SIEMENS

Navigator *syngo* Operator Manual

SOMATOM® Emotion Duo

Version A40A

Siemens Medical Solutions, Computed Tomography
Siemensstr. 1, D-91301 Forchheim, Germany

Headquarters: Berlin and Munich
Siemens AG, Wittelsbacher Platz 2, D-80333 Munich, Germany

Print No. C2-019-4.620.04.02.02 (Navigator *syngo* Operator Manual – Part 1)
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Printed in the Federal Republic of Germany
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CE 0123

CE
0123

Manufacturer’s note:

This product bears a CE marking in accordance with the provisions of the Council Directive 93/42/EEC of June 14th, 1993 concerning medical devices.

The CE marking applies only to medico-technical products/ medical products introduced in connection with the above-mentioned comprehensive EC directives.

The original language of this document is english.

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SOMATOM® Esprit+

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K *Pulmo (Option)*

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M *Calcium Scoring (Option)*

N *DynEva CT (Option)*

O *Volume (Option)*

Introduction to the Operator Manuals

Welcome to the Navigator - the main console of your SOMATOM scanner.

The Navigator is equipped with the pioneering multi modality software: *syngo*.

To make it easier for you to work with the system, the following documentation is included in the scope of supply.

SOMATOM Operator Manual

In this manual, you will find a description of the hardware components of the system and their operation.

Here you will find:

- Information about **safety measures** you must heed when handling the CT scanner
- An **overview** of all **components of the system** and the **accessories**
- Instructions on **system operation**
- Instructions on **quality assurance**

Online Help

The Online Help explains operation of the system’s software.

It includes:

- Detailed instructions on **patient administration**
- A detailed description of **examination procedures**
- Instructions on **image reconstruction** and **image manipulation**

Quick Guide Operator Manuals (optional)

The optional Quick Guide and the Quick Guide Options operator manuals are designed to be a short reference for basic operating steps and the most important functions of your computer tomograph during examinations.

These guides serve as a guideline to help you with your examination routine. The Quick Guide operator manuals are only valid in connection with the Online Help and the SOMATOM Operator Manual and the safety instructions contained therein.

System Owner Manual

In this manual, you will find the details and preconditions for operation of this CT-scanner:

- Information on **correspondence** with the authorities, on **regulations** and **test protocols**.
- Dosimetry and Image Performance Report.
- A listing of **labels** and **technical data**.
- Information on **operation**, **maintenance** and **disposal**.

Navigator *syngo* Operator Manual (option)

This operator manual is not included in the scope of supply. You can order it separately from your Siemens representative.

The Navigator *syngo* Operator Manual contains detailed step-by-step instructions for operation of the system software. It also contains an **introductory part** for users without computer experience or knowledge of the system.

This operator manual is only valid in connection with the SOMATOM Operator Manual and the safety instructions contained therein.

Safekeeping of manuals

Always store manuals in an easily accessible location in the vicinity of the system.

Validity of the operator manual

This operator manual is only valid for the stated software version and in conjunction with the latest release note.

The release note can extend the validity of the operator manual to following versions.

Purpose of the equipment

These manuals describe the application and operation of the SOMATOM.

Device type	SOMATOM is a computed tomography system.
Type of application	SOMATOM is suitable for the generation and processing of tomographic images of patients for diagnostic purposes.
Site of application	SOMATOM can be operated in the X-ray department of a hospital or doctor's practice.
Authorized users	SOMATOM must only be used by persons with the necessary specialist knowledge, e.g. doctors or trained radiologists.

Structure of the manuals and text layout

The two manuals are subdivided into individual parts (Part **A**, Part **B** etc.).

At the beginning of each part you will find a detailed table of contents. The overview and introduction chapter which follows outlines the topic dealt with in this part.

In the chapters, a number of text sections are highlighted by symbols.

Operating step

Individual steps of an instruction are indicated by a lozenge.

✧ Perform these operating steps.

Background information

Tips and additional information about a topic are marked with an arrow.

➪ In these kind of paragraphs you will find interesting additional information about the topic being described.

Lists

Items in a list are marked by squares.

❑ This character preceeds each item in a list.

Cross-references

A topic is often closely related to another topic or is described in detail at another location in the manual. In order to keep the manuals down to a manageable size and to show you how topics are interrelated, cross-references are used.

Cross-references are marked with thin arrows and are highlighted in italics:
→ Navigator Operator Manual, chapter A.1, *Basics for Beginners*

Names and designations used

All names and data of patients and institutions that are used in this operator manual are entirely fictional.

Any resemblance to names of existing people or organizations past or present is entirely coincidental.

Configuration-dependent designations, such as names of drives, network nodes, and databases, that are used in this operator manual are usually not the same as the designations to be found on a particular installation of the system in a particular hospital.

Your opinion

Nobody and nothing is perfect. No doubt, it would be possible to improve these manuals, too.

Please give us your opinion and your suggestions for improvement. To make this easier for you we have attached a form in → System Owner Manual

Copy this form (2 pages) and mail or fax your answer to the address provided. We will take account of your suggestions in the next edition. Thank you for your trouble.

PART A

Basics

A.1 *Basics for Beginners*

A.2 *Configuring the User Interface*

A.3 *Service Functions*

A.4 *First Steps*

CHAPTER

A.1 Basics for Beginners

This chapter is addressed to beginners with little experience using computers and Windows NT®.

It is intended to enable you to use the applications and enter data.

You are first given a short overview of the user interface of the program. After that, an explanation is given of how to operate the computer using the mouse and keyboard.

This chapter also explains the command and input elements on the program's user interface.

Operating system

The program *syngo*® uses the operating system Windows NT®.

➩ *syngo*® is a registered trademark of Siemens AG.

Logon and program start

After you have switched on the system you are automatically logged on as *syngo* user.

The applications start automatically.

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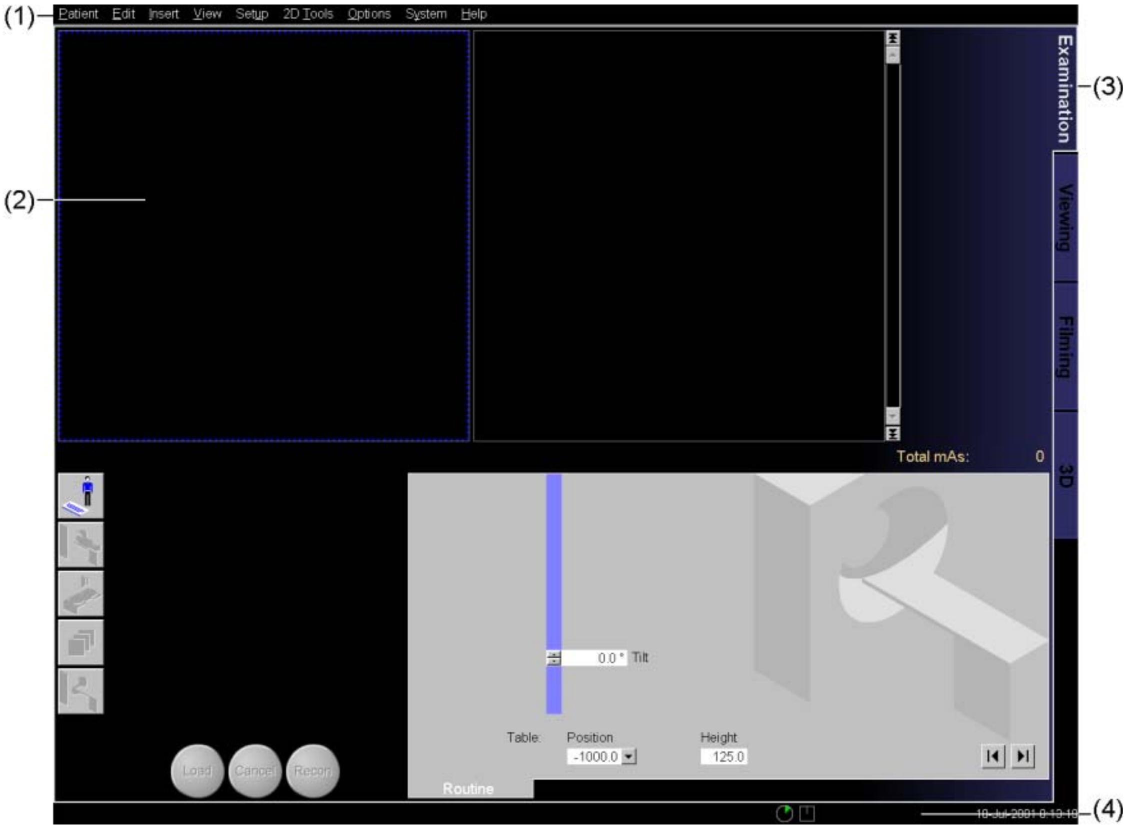
Configuration-dependent designations, such as names of drives, network nodes, and databases, that are used in this operator manual are usually not the same as the designations to be found on a particular installation of the system in a particular hospital.

The application program

After start up the user interface of the program appears on your screen.
It is subdivided into the following areas:



Total mAs: 0

0.0 ° Tilt

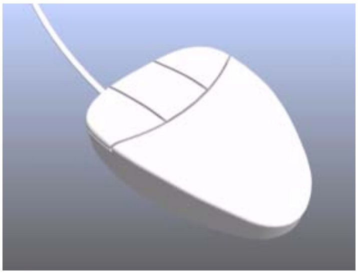
Table: Position -1000.0 Height 125.0

(1) Menu bar
(2) Image and workspace of the task cards
(3) Tabs of the task cards
(4) Status bar

Mouse and keyboard

In order to execute commands on the computer or to input data you can use the mouse and/or the keyboard.

The mouse



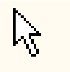
Your mouse has three buttons.

You can start actions of the program with the mouse buttons.
With the left button you select objects and start applications and actions.
With the right button you open popup menus.
With the center buttons you change the window values of images.

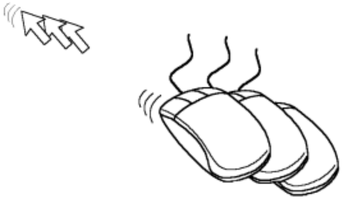
With the mouse you can:

❑ Move the mouse pointer
❑ Select and mark objects
❑ Copy and move objects
❑ Start applications and actions
❑ Edit images
❑ Call up menus

The mouse pointer



The mouse pointer follows every movement of the mouse on the screen.



➪ If you have lost sight of the mouse pointer, simply move the mouse.

Depending on the application which is currently active and the action you want to perform, the appearance of the mouse pointer can change.

Cursor

✧ Position the mouse pointer in a field in which you want to enter text.

The mouse pointer changes its shape and becomes a vertical line. It is now a text cursor indicating where characters typed in will appear.

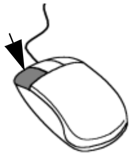
Using the mouse

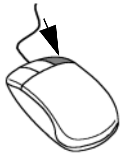
First place the mouse pointer on an object, for example an image. You can then perform the following actions:

Single click

Press a mouse button briefly and release it again. Do not move the mouse while doing this.

You select an object with the left mouse button,
with the right mouse button you call up popup menus.

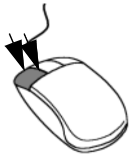




Double click

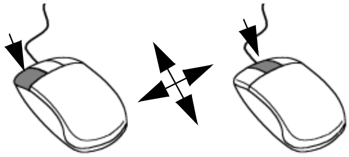
Double-clicking means pressing the mouse button twice in quick succession and then releasing the button again.

Double-clicking is used to start programs, for example.



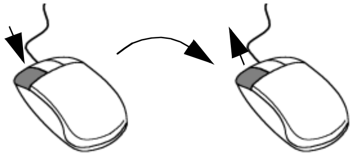
Dragging

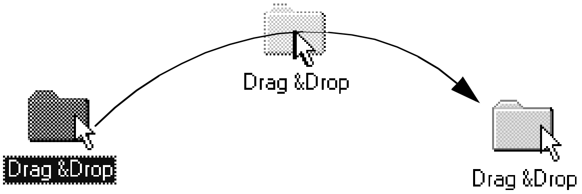
Press the mouse button and move the mouse while holding the button down. With this action you can draw graphics, for example (left mouse button), or set window levels (center mouse button).



Drag & drop

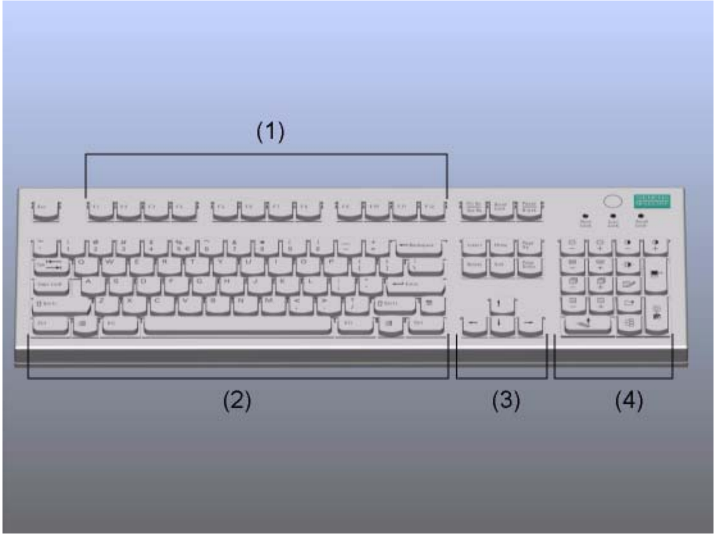
Click an object with the left mouse button, move it while holding the mouse button down and release the mouse button again.





The keyboard

You use the keyboard to enter text and numbers. You can also call up certain functions and start programs using key combinations and the keys of the numeric keypad.



(1) Function keys
(2) Typewriter keyboard
(3) Cursor keypad
(4) Symbol keypad

Using the keyboard

You can execute almost all commands both with the mouse and with the keyboard.

Entering text and numbers

You normally use the keys on the typewriter keyboard to enter text and numbers or commands.

Deleting characters

With the **Backspace** key you can delete the character in front of the text cursor and with **Del** the character following the text cursor. If a text is marked you can use either of these keys to delete it.

Moving the cursor

With the cursor keys ←↓↑ →you can move the text cursor within a text entry field. With the keys **Home** and **End** you move the cursor to the first and last position within the text.

Calling up help

An on-line help is supplied with the program. To call up the context-sensitive help, click on the **Help** button of dialogs (if available), or simply click the cursor at the dialog, screen area (e.g. chronicle), or subtask card and press **F1**.

Calling up the popup menu

With a single click of the right mouse key you can call up a pop menu for the selected object or active area of the screen (except **Viewing**).
→ Page A.1–5, *Using the mouse*

Calling up task cards

With the function keys **F5 to F8**, you call up the individual task cards.
→ Page A.1–31, *Task cards*

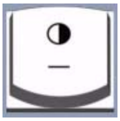
Starting applications and functions

The “symbol keypad” of your system looks different from the numeric keypad of a standard PC keyboard. In your system functions have been assigned to these keys, which you can easily identify by the images on these keys.

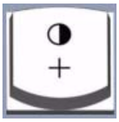
➪ If your system is **not** equipped with the original Siemens keyboard, you can call up these functions and programs with the corresponding keys of your standard numeric keypad.

Window Center - (Num **Num**)
(Brightness -)

Window Center + (Num **/**)
(Brightness +)



Window Width - (Num *****)
(Contrast -)



Window Width + (Num **-**)
(Contrast +)

Not used for CT.

Scroll study back (Num **7**)

Scroll study forward (Num **8**)

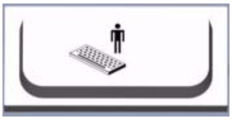
Scroll series back (Num **4**)

Scroll series forward (Num **5**)

Scroll image back (Num **1**)

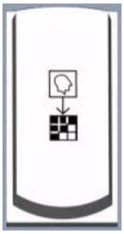
Scroll image forward (Num **2**)

Correct image text (Num **6**)
(not supported in this software version)

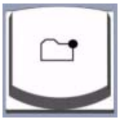


Call up **Patient Registration** (Num **0**)

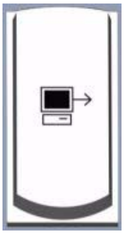
Call up **Patient Browser** (Num **.**)



Copy to **Film Sheet** (Num **Enter**)



Mark (Num **3**)



Send To Node 1 (Num **+**)

Using shortcuts

With the key combinations **Ctrl** plus another key or **Alt** plus another key, you can give commands to your computer very quickly.

➩ You can execute all functions by pressing the **Alt** key together with the key of the letter underlined in the menu item or on the button. In this way, you can operate the program without using the mouse.

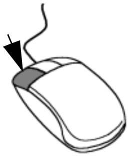
Here is a table of the most important key combinations:

Alt + **F4**	Close **Patient Browser**
Ctrl + **Tab**	Switch active task card / page through stack of cards
Ctrl+**Shift** + **Tab**	Switch active task card backwards / page through stack of cards backwards
Ctrl + **C**	Copy
Ctrl + **I**	Import data
Ctrl + **P**	Expose film job
Ctrl + **S**	Save (only **3D** task card)
Ctrl + **X**	Cut (only **Filming** task card)
Ctrl + **V**	Paste
Ctrl + **W**	Save window values

Entering commands and data

You always have several options for entering commands or data on the computer. You can use the mouse and/or the keyboard.

Selecting objects



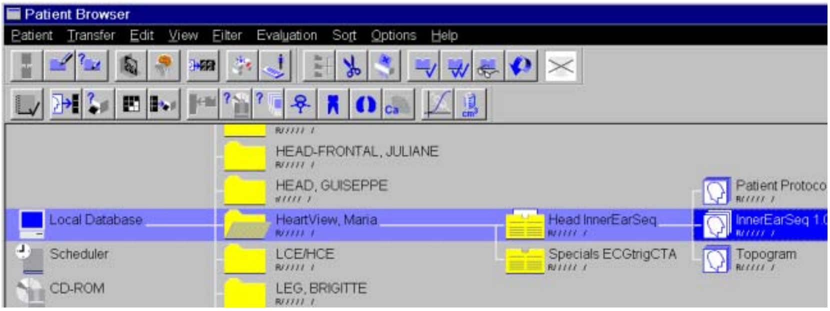
You can select an object (e.g. an image or a patient) by clicking it with the left mouse button.

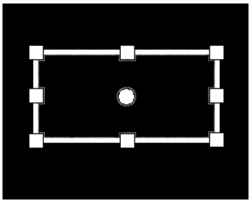
➪ Selected objects are marked. Images are given a border, graphic objects such as ROIs (region of interest) are displayed with grab handles, icons and text (e.g. in list entries) are shown highlighted (e.g. white on black).

Examples:

❑ The selected patient entry in the window of the **Patient Browser** is displayed highlighted (left).

❑ Resizing handles (small squares) are visible on the selected border (right).





Selecting several objects

You select an object with the mouse and then press the **Ctrl** or the **Shift** key.

With the **Ctrl** key you can select other **individual** objects**.**

✧ Press the **Ctrl** key and keep it pressed.

✧ Click all the objects that you want to select.

✧ Click a selected object a second time to deselect it again.

With the **Shift** key you can select **entire blocks** of objects.

✧ Select the first object.

✧ Press the **Shift** key and hold it pressed.

✧ Click another object.
All the objects in between are selected as well.

Deselecting objects

You can deselect selected objects by selecting another object or by clicking the background with the mouse.

Moving or copying objects

You can move or copy objects (e.g. images) from one location to another location on the screen.

Drag & drop

This means picking up an object, dragging it and dropping it again.

✧ Click an object with the left mouse button, e.g. a series, and hold the mouse button down.

✧ Press the **Ctrl** key if you want to copy the object.

✧ Drag the object to another location with the mouse (into another task card or window).

✧ Release the mouse button and the object will be moved or copied to the new location.

→ Page A.1–5, *Using the mouse*

Cut/copy & paste

Another way of moving objects is via the **cut & paste** or **copy & paste** functions.

✧ Select the object you want to move or copy.

✧ Call up **Edit > Cut** or use the shortcut **Ctrl + X** if you want to move the object.

Or

✧ Call up **Edit > Copy** or use the shortcut **Ctrl + C** if you want to copy the object.

The object is moved or copied to the Windows clipboard. It remains there until you cut or copy another object that will then replace the previous one.

✧ Click the new location.

✧ Call up **Edit > Paste** or use the shortcut **Ctrl + V** to move or copy the object to this new location.

→ Page A.1–11, *Using shortcuts*
→ Page A.1–33, *Using menus*

Double-clicking

If you double-click on an object with the left mouse key, the standard function of the associated function menu, which also depends on the object type, is executed. You can transfer a selected object to another application with a double click.

Menus

You can also use the entries of the dropdown menus to pass objects from one application to another.

✧ Select the object(s) you want to pass onto another task card.

✧ Call up the relevant menu item.
→ Page A.1–33, *Using menus*

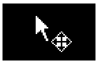
Changing the image display

You can change the display of an image with the mouse:

- Setting window levels (windowing)
- Changing the image size (zooming)
- Moving the image (panning)

For windowing you use the center mouse button. For zooming and panning you first switch the mouse to zoom/pan mode and then use the left mouse button to change the image display.
→ Page E.4–16, *Zooming and panning images*

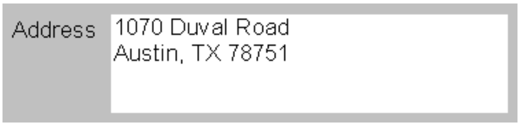
✧ Move the mouse pointer onto the image, press the center or left mouse button and hold it pressed. If you now move the mouse you change the way the image is displayed.



For zooming (left cursor) and panning (right cursor) the mouse cursor changes shape.

Entering text

If you click a text entry field with the mouse, the mouse pointer becomes a text cursor (vertical bar).



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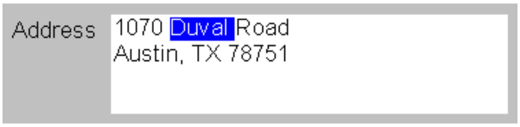
✧ Enter the text via the keyboard.

➪ You can also enter text into a combo box.
→ Page A.1–27, *Combo box*

Marking text

You can mark text by moving the cursor across the text while holding the left mouse button down. The text is displayed highlighted.



Address
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Austin, TX 78751

Marking words

✧ Double-click with the left mouse button while the cursor is inside a word. The word is marked.

Deleting text

✧ Mark the text with the mouse. Press the **Del** or the **Backspace** key. The text is deleted.

Windows

In the Windows® operating system programs are displayed in windows. When you start an application it is called up in a window.

Layout of windows

You will find the following graphic elements in a window:

(1) Title bar
The title bar displays the name of the program you are currently working in.

(2) Title bar icon
Icon for opening a menu for window commands

(3) Menu bar
This contains the functions of the program in dropdown menus.

(4) Tool bar
This contains the icons for starting functions and programs.

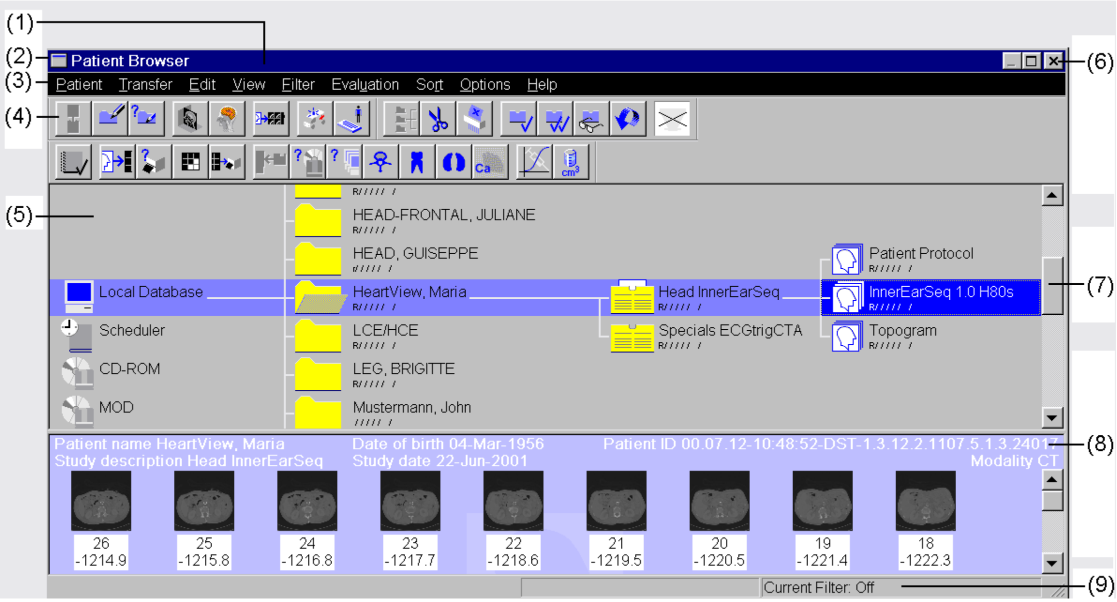
(5) Workspace
Here you can execute the functions of the program.

(6) Window buttons
Buttons for controlling the window display
Here you minimize, maximize or close the window.

(7) Scroll bar
If the content of the window is too large to be displayed, scroll bars are displayed on the right and lower edge of the window.

(8) Border
Place the mouse on the border to resize the window.

(9) Status bar
This displays the instructions and feedback from the program.



Patient name HeartView, Maria
Study description Head InnerEarSeq
Date of birth 04-Mar-1956
Study date 22-Jun-2001
Patient ID 00.07.12-10:48:52-DST-1.3.12.2.1107.5.1.3.24017
Modality CT

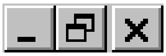
Current Filter: Off

Resizing and moving a window

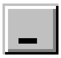
You can change the window display (window, full screen or icon), the size of the window and the position of the window.

Changing the type of window

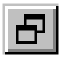
In the top right-hand corner of the title bar you will find three buttons with which you can change the size and position of windows.



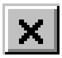
With these buttons you can change the active window as follows:



✧ Click on the left-hand button with the left mouse button and the window is minimized.



✧ Click the center button to toggle between full screen size and window size. If you click the button again you switch back to the previous size.



✧ Click on the right button to close the window and therefore the application as well.

Or

✧ Click on the Windows title button and select the corresponding entry in the menu.

⇨ Not all of these functions are available in all windows.

Resizing the window

Move the mouse pointer onto the border of the window and its appearance changes. Depending on where you place the mouse pointer it can take on one of the following shapes:

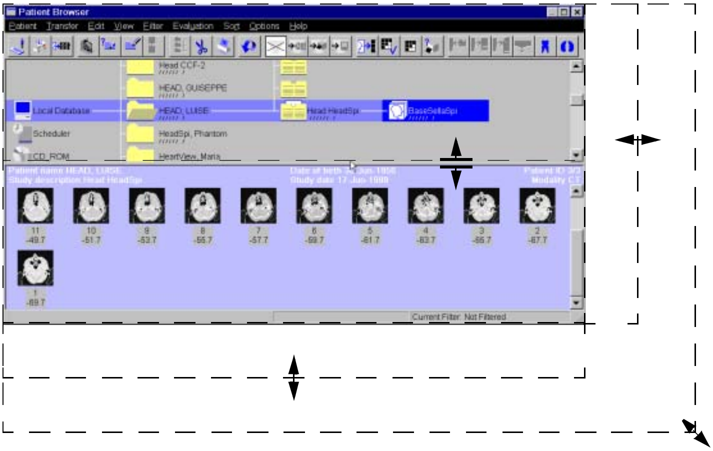
↕ ❑ On the lower or upper edge it becomes a vertical double arrow.
Now you can change the **height of the window**.

↔ ❑ On the left or right edges it changes to a horizontal double arrow.
Now you can change the **width of the window**.

⤡ ❑ On a corner of the border it becomes a diagonal double arrow.
Now you can change the **height and width of the window**.

⇳ ❑ On the interior border line it becomes a broken double arrow (if the window is subdivided).
You can change the **height of the window sections**.

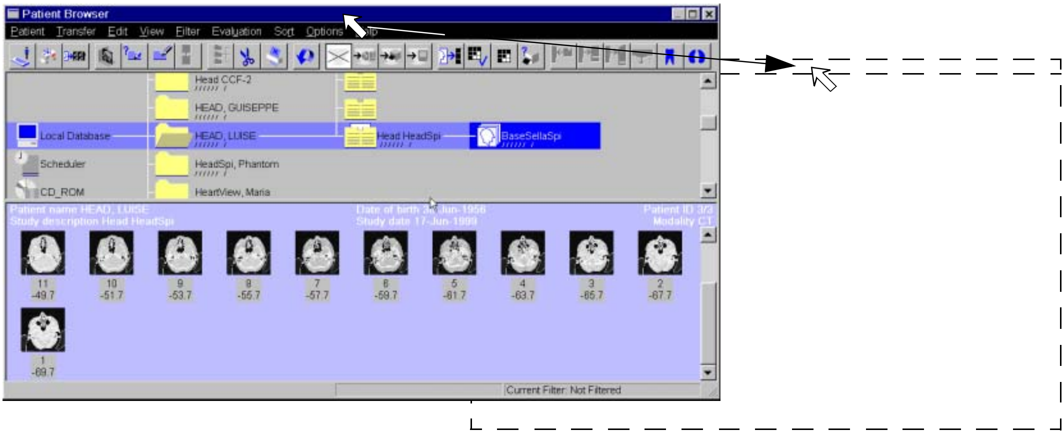
✧ Press the left mouse button and drag the border to the new position while holding the mouse button down.



Changing the position of the window

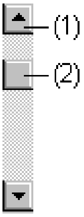
You can move the window to any position on the screen as long as it is not maximized or minimized.

✧ Click the title bar and drag the window to the new position holding the mouse button down.



Moving the content of the window

On the scroll bars you will find the arrow buttons and a scroll box with which you can move the content of the window. Depending on whether the window is too short or too narrow to display its content the scroll bar will appear on the right or below the window.



✧ Click an arrow button (1) with the left mouse button. The screen content is shifted a small distance in the direction of the arrow.

✧ Click the scroll box (2) and drag it with the mouse. The screen content is moved continuously in the corresponding direction.

✧ Click any point on the scroll bar with the mouse. The screen content is moved toward this point by a distance which is proportional to the distance of this point from the scroll box.

Switching between windows

Very often several windows or tab cards are open at the same time, for example, if you are looking for a patient using the **Patient Browser** before you start an examination.

Active window

The active window is in the foreground.
The title bar of the active window has a different color from that of the inactive window.

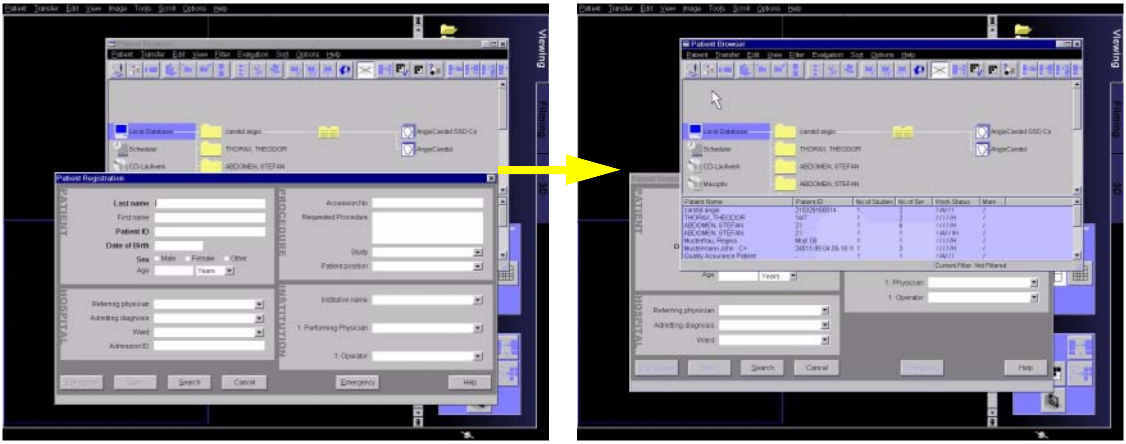
➩ You can move objects (e.g. images) from an active window to a window in the background (**drag & drop**) as long as both windows are visible.

Switching windows

If you want to switch from one window to another visible window click on the corresponding window.

It moves to the foreground, and the color of the title bar changes. It is now the active window in which you can work.

Example: **Patient Browser** and **Patient Registration**.

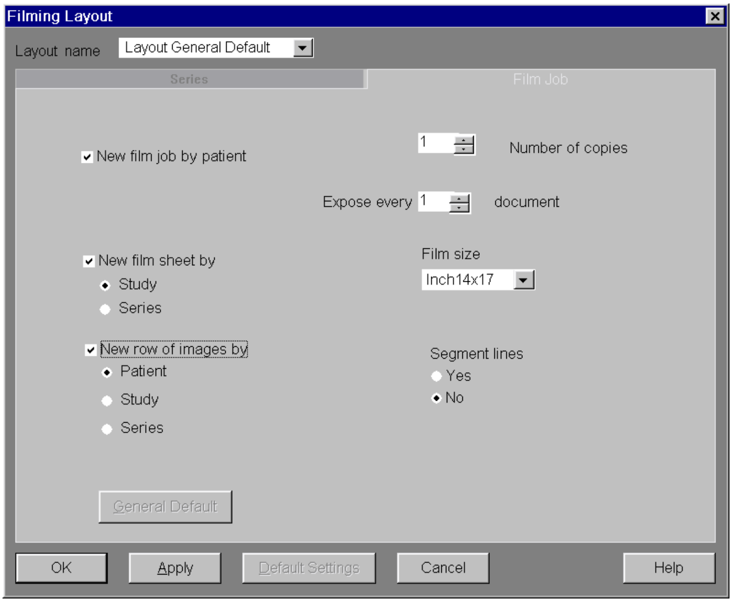


Dialog boxes

Dialog boxes are used to enter data or to select or confirm settings.

They are usually displayed after you have called up a function.

Example:



Filming Layout

Layout name: Layout General Default

☑ New film job by patient

1 Number of copies

Expose every 1 document

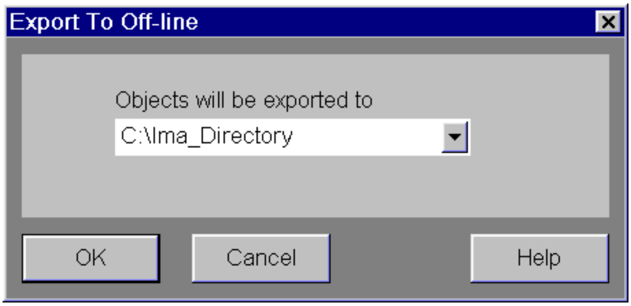
☑ New film sheet by
- ● Study
- ○ Series

Film size: Inch14x17

☑ New row of images by
- ● Patient
- ○ Study
- ○ Series

Segment lines
- ○ Yes
- ● No

Example:
You want to export data to your hard disk and therefore call up **Transfer > Export To Off-line**.
The **Export To Off-line** dialog box will be displayed.



Export To Off-line

Objects will be exported to

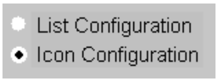
C:\Ima_Directory

In a dialog box you will find entry fields, selection lists, radio buttons or checkboxes to select options and buttons with which you can accept or reject inputs.

Operating elements in boxes and on tab cards

In dialog boxes and on tab cards you will find various operating elements that you can use to enter data or make selections.

Radio buttons



You can select options by clicking them with the left mouse button. You can only select one option at a time.

Check box

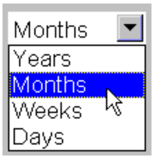
✧ Click the rectangle with the left mouse button.

A cross or checkmark appears. The option is then selected.

✧ Click the rectangle again to deselect the option.

More than one option can be selected this way.

Selection list



✧ Click the arrow to the right of the selection list with the left mouse button to open the selection menu.

✧ Move the mouse pointer down the list and the entries are highlighted one after the other.

✧ Click on the entry you want to select.

Entry field

Date of Birth 16.10.1923

Here you can enter text or numbers.

✧ Click into the entry field with the mouse pointer. Then enter the text at the text cursor.

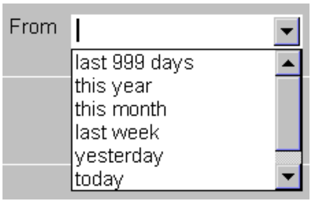
Spin box

1 Copies

In a spin box you can select values.

✧ Click one of the arrows with the left mouse button to increase the set value (up) or decrease it (down), or enter a value in the entry field.

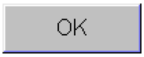
Combo box



This field is a combination of an entry field and a selection list. You can either select entries from the list or type them in on the keyboard.

Buttons for executing commands

By clicking on a button you start an action. A dialog box contains several buttons, for instance:



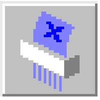
- All the settings in the window become valid and the window is closed. In some dialog boxes **OK** triggers an action, for example, filming.

- Same as **OK**, except that the window is not closed.

- The dialog box is exited without making any changes.

- A help text about the dialog box is displayed.

Buttons for calling up functions

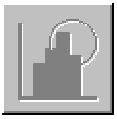


You can start many functions in the program both via the menus or via the icon buttons.

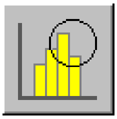
You find icon buttons on the tool bars, on the subtask cards, or in the control area of the task cards. They allow fast and intuitive execution of functions simply by clicking on the buttons.

Dimmed fields and buttons

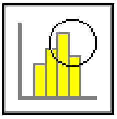
There are a number of functions which you can only execute if you have selected an image, for example, or loaded data into the task card. Buttons and input fields are dimmed (shown gray or shaded) if you cannot execute the function assigned to them.



Dimmed button, the function cannot be started.

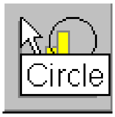


The button is no longer dimmed, you can start the function.



The icon is active, for example, you can now draw a ROI on an image.

Tool tips



If you place the mouse cursor over an icon, a short text about this function is displayed. The tool tip disappears again after a few seconds.

Using tab cards

Tab cards are arranged in stacks so that you can place them in the foreground easily by clicking on a tab. When you activate a tab card it is placed in the foreground. You can only start a function from an **active tab card**.

Activating a tab card

✧ Click a tab to activate a card.

The active tab card has a different background color than the inactive tab cards.

The settings and data that you have entered on the tab card which was previously active are not changed when it moves back into the background. When you call up this tab card again you will find all the data and settings unchanged.

There are two types of tab cards:

❑ Task cards
❑ Subtask cards

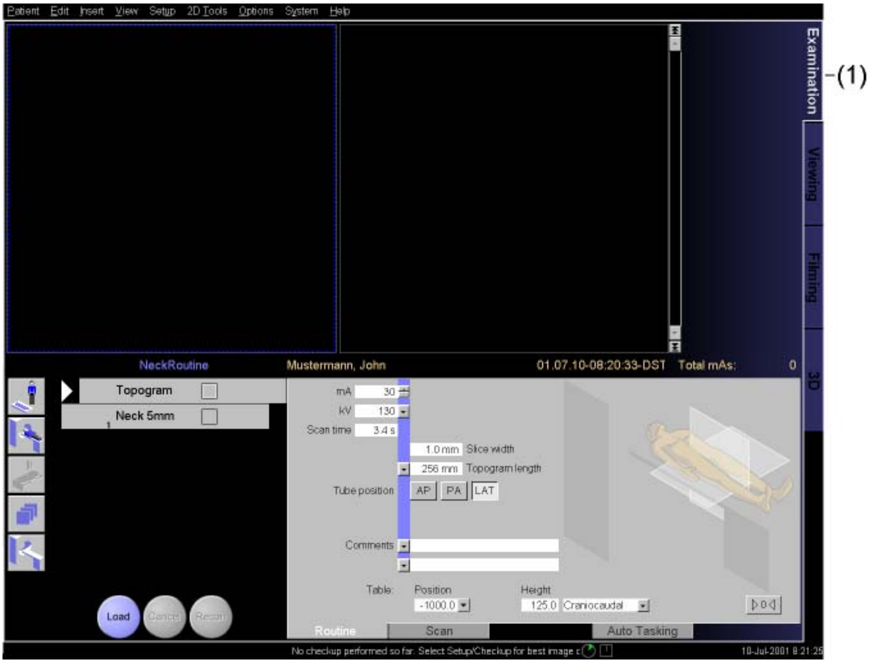
Task cards

The arrangement of the task cards reflects routine operation in the hospital or practice and their layout supports the examination procedure, for example:

- You can perform an examination in the **Examination** task card.
- You can view the results and process them in the **Viewing** task card.
- You edit your film sheet in **Filming**
- You postprocess images 3-dimensionally in **3D**.

Calling up using the tabs

✧ Click the tab (1) on the right-hand side of the screen to activate a task card.



Mustermann, John 01.07.10-08:20:33-DST Total mAs: 0

mA 30
kV 130
Scan time 3.4 s
1.0 mm Slice width
256 mm Topogram length
Tube position LAT
Comments
Table: Position -1000.0 Height 125.0 Craniocaudal

No checkup performed so far. Select Setup/Checkup for best image c

10-Jul-2001 8:21:25

Calling up using the function keys

You can also switch to each task card using the function keys.

✧ Press the **F5** key to switch to the **Examination** task card.

✧ Press the **F6** key to switch to the **Viewing** task card.

✧ Press the **F7** key to switch to the **Filming** task card.

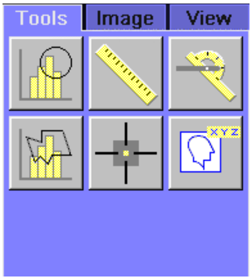
✧ Press the **F8** key to switch to the **3D** task card.

Subtask cards

On task cards you will find smaller cards, called subtask cards.

They are used for the following purposes:

❏ Tool boxes, e.g. for graphic evaluation
❏ Setting parameters
❏ Calling up functions and programs



Using menus

In order to keep the screen clearer, actions are grouped together in dropdown menus.

Application-specific menus

The menu bar changes with the task card that is currently active or the window that is currently open. This way only the functions are accessible which are relevant for the respective application.

Patient Browser menu bar

The menu bar of the **Patient Browser** window contains the following entries:

Viewing menu bar

The menu bar of the **Viewing** task card contains the following entries:

Filming menu bar

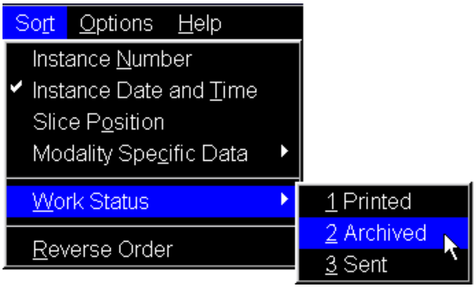
The menu bar of the **Filming** task card contains the following entries:

3D menu bar

The menu bar of the **3D** task card contains the following entries:

Dropdown menus of the menu bar

The menu bar consists of a row of dropdown menus. Via these menus a series of functions and settings is accessible.



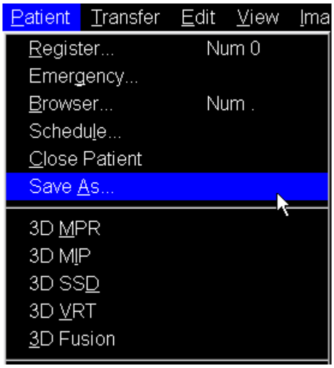
Selecting a menu

- ✧ Click a menu item in the menu bar with the left mouse button.
  The dropdown menu is opened.
  The menu item is highlighted.
- ✧ Move the mouse pointer down the menu bar and each drop-down menu opens and closes in turn.
  Only the dropdown menu on which the mouse pointer is placed remains open.

Closing the menu

- ✧ If you do not want to select a function click the menu title again or click on the background outside the dropdown menu.

Selecting an action

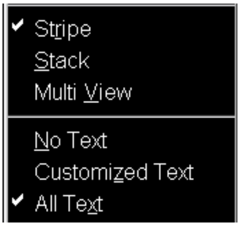


✧ Move the mouse pointer down a dropdown menu. The entries are highlighted one after the other.

✧ Stop at the action you want to execute.
Click on it with the left mouse button.
The action is started and the menu closed.

➩ Menu entries followed by an ellipses open dialog boxes (e.g. **Browser...**).
Menu entries without an ellipses call up an action directly (e.g. **Expose Film Task**).

Options

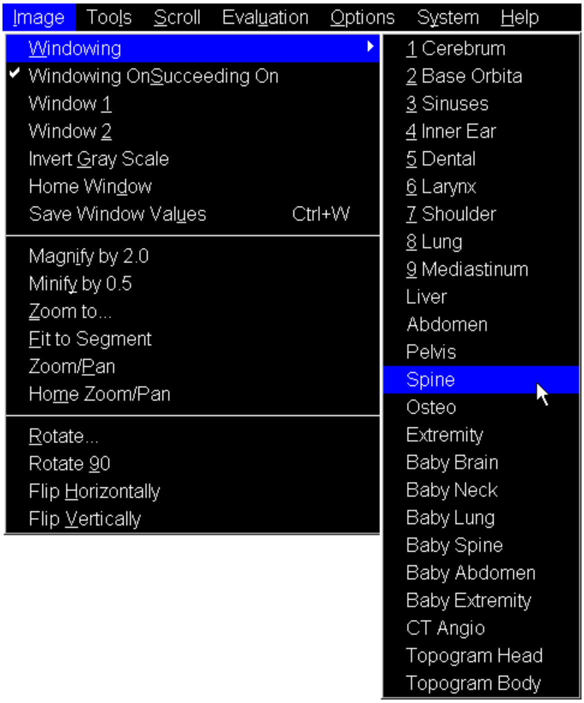


Some menu items when clicked do not seem to perform any action. However, if you look at the dropdown menu again you will see that the menu item has a checkmark next to it. The associated option is now active.

✧ Click the menu entry again to deactivate the option.

Submenu

Some lines in the dropdown menu have a small arrow on the right-hand side. If you move down to one of these arrows with the mouse pointer a submenu is displayed.



Popup menus

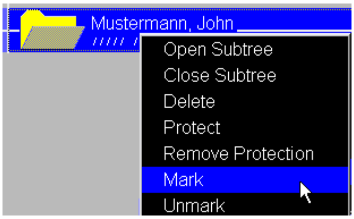
Popup menus contain context-specific information. That means a different popup menu will appear depending on the type of object you have selected. This menu offers you actions that can be performed on this object.

Calling up popup menus

✧ First select an object with the left mouse button.

✧ Call up the popup menu by pressing the right mouse button.
The menu belonging to the current object type is displayed.

Selecting an action



✧ Move the mouse pointer over the menu.
The entry on which the mouse pointer is placed will be highlighted. With a single click (right or left mouse button) you can start the function.

➩ If you have not selected an object and click on the right mouse button a context menu is also opened. This menu now provides you with actions that are meaningful in the currently active task card or window as long as nothing is selected.

Status bar

The status bar at the bottom edge of the window shows you messages and instructions.

It is subdivided into three columns:

- In the first column examination-specific information is displayed.
- In the second column you will see warnings and messages.
- If functions are being executed in the background you will see the application as an icon in the third column.

Action history

The actions executed by the program are automatically logged together with information about whether each step was successfully terminated or whether an error occurred. You can query a list of the last entries in the history at any time.

✧ Click on the task bar with the left mouse key to list the last commands and program actions.

➪ You can determine the number of entries in the log in the **History Size** dialog box that you call up by clicking the status bar with the right mouse key.

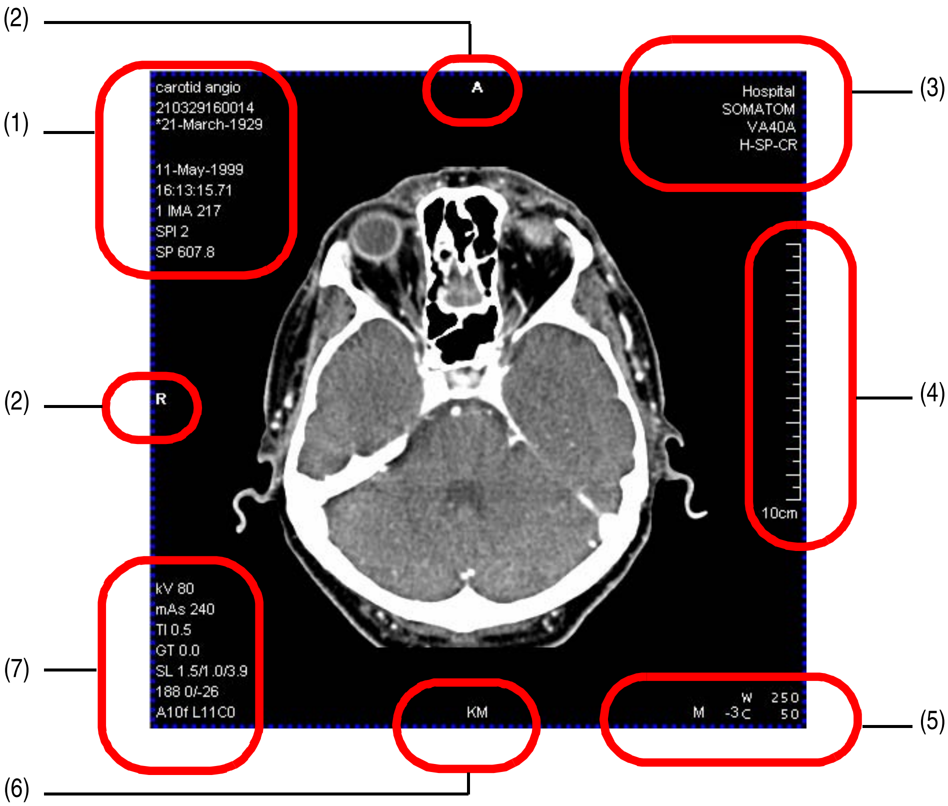
Text information in medical images

In images various information is displayed as image text. This text information identifies the patient and documents examination and image parameters.

Image texts are grouped by content and displayed in the four corners and along the bottom and right-hand edges of each image.

Depending on the configuration of your system as well as on the modality with which an image was acquired, individual items of information are displayed in an image.

⇨ With the **Image Text Editor** you can define which text elements are to be displayed in the images.
→ Page A.2–8, *Configuring image text*



(1) Patient and examination data
(2) Orientation labels
(3) System-specific information and patient position
(4) Scale bar
(5) Window and pixel values
(6) Image comment
(7) Scan and reconstruction parameters

Contents of the image text components

The following tables list the information contained in the image text components.

Patient and examination data

In the upper left corner of an image, patient and examination data are displayed.

Image text	**Abbreviation**	**Example**
Patient name	-	carotid angio
Patient ID	-	210329160014
Date of birth	-	*21-March-29
Acquisition date	-	11-May-99
Acquisition time	-	16:13:15.71
Series and image number	-	1 IMA 217
Scan type or image type and scan number	TOP (topogram) SEQ (sequence) SPI (spiral, last image) ROT (rotation mode) RTD (real time display) MON (monitoring) MUL (multiscan) STA (static) ICD (interventional cine display)	TOP 1 SEQ 135 SPI 2 ROT 23 RTD 123 MON 34 MUL 2 STA 3 ICD 23
Slice position	SP	SP 607.8

Scan and reconstruction parameters

In the lower left corner you see the parameters with which the image was acquired.

Image text	Abbreviation	Example
Contrast/bolus agent	+C	+C
Voltage	kV	kV 80
mAs (exposure)	mAs	mAs 240
Scan time	TI	TI 0.5
Gantry tilt	GT	GT 0.0
Slice width or slice width / collimation or slice width / feed per rotation or slice width / collimation / feed per rotation	SL	SL 1.0 or SL 5.0 / 2.5 SL 5.0 / 4.1 SL 3.0 / 1.0 / 4.1
Size and center (x/y) of Field of View	FoV	188 0/-26
Convolution kernel (kernel) and reconstruction parameters	-	A10f L11CD

System-specific information and patient position

In the upper right corner the name of your institution, the system name and software version as well as the patient position and the view position are displayed.

Image text	Abbreviation	Example
Institution	-	Hospital
Manufacturer's model name	-	SOMATOM
Software version	-	VA40A
Patient position (direction and position) and view position	H (head first) F (feet first) LL (left lateral) RL (right lateral) SP (supine) PR (prone) CR (cranial) CA (caudal)	H-SP-CR or H-SP (topogram mode)

Window and pixel values

In the lower right corner the current window values and the pixel value at the cursor position in the image (mini mean) are shown.

Image text	Abbreviation	Example
Window width (contrast)	W	W 250
Window center (brightness)	C	C 50
Mini mean	M	M -3

Exiting the program

The system shuts down in two stages

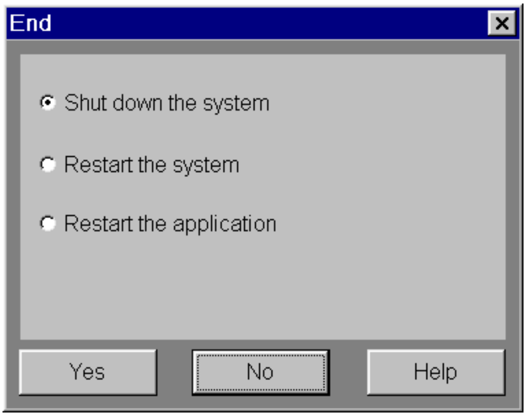
❏ Termination of the application program

❏ Shutdown of the operating system

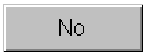
Before you can shut down the system, you must exit all applications.

✧ In the main menu, call up **System > End**.

The **End** dialog box is displayed.



● Shut down the system
○ Restart the system
○ Restart the application

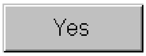


➩ If you do not want to exit, click on **No**. You return to the user interface.

Shutting down the operating system

With the **End** dialog box, you shut down the system to switch it off.

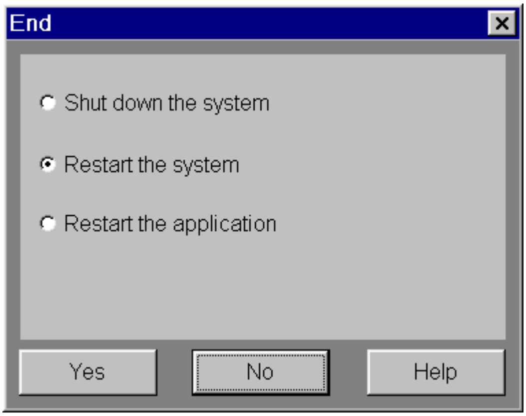
✧ Select the “Shut down the system” option.



✧ Confirm with **Yes**.
The system is shut down.

Restarting the system

If you want to restart the system, select the second option in the **End** dialog box.



End

○ Shut down the system

● Restart the system

○ Restart the application

✧ Click on **Yes**.

The system is restarted.

Restarting syngo

✧ Click the third option in the **End** dialog box to restart only the *syngo* application program.

CHAPTER
A.2

Configuring the User Interface

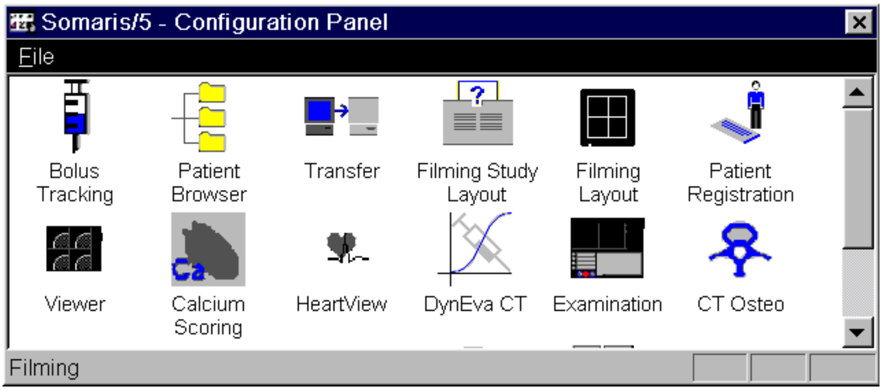
You can configure task cards, windows, and individual functions of the program, i.e. adapt them to your requirements.

To configure windows and task cards you first call up the **Configuration Panel** where you will find icons representing various applications. You then double-click on an icon to open the corresponding configuration window.

For example, you can define which buttons the tool bar of the **Patient Browser** window contains.

Calling up the Configuration Panel

✧ Call up **Options > Configuration...** to open the **Configuration Panel**.



Calling up configuration windows

Configured program parts are represented by icons in the **Configuration Panel**.

Patient Browser

✧ Double-click on the icon to display the configuration window for the **Patient Browser**.
→ Chapter D.7, *Configuring the Patient Browser*

Transfer

✧ Double-click on the icon to display the configuration window for the archiving and network functions.
→ Chapter F.6, *Configuring data transmission*

Filming Study Layout

✧ Double-click on the icon to display the configuration window for assignment of study-specific film layouts.
→ Chapter G.7, *Configuring Filming Layout*

Filming Layout

✧ Double-click on the icon to configure film layouts or create new film layouts.
→ Chapter G.7, *Configuring Filming Layout*

Patient Registration

✧ Double-click on the icon to configure the patient registration.
→ Chapter B.5, *Configuring Patient Registration*

Viewer

✧ Double-click on the icon to configure the **Viewing** task card.
→ Chapter E.8, *Configuring the Viewing Task Card*

✧ Call up **Options > Configure 3D** in the main menu of the **3D** task card to configure the **3D** application.
→ Chapter H.13, *3D Configuration*

➪ You can call up the **3D** configuration only when a patient is loaded in the **3D** task card.

Bolus Tracking

✧ Double-click on the icon to change individual settings for an examination with CARE Bolus.
→ Page C.8–28, *Configuring the CARE Bolus*

HeartView

✧ Double-click on the icon to select the mean value to be used for calculation in HeartView examinations.
→ Page C.7–12, *Configuration*

CT Osteo

✧ Double-click on the icon to adapt the evaluation functions of the **Osteo** task card to your requirements.
→ Page J.4–1, *Configuring Osteo Evaluation*

CT Pulmo

✧ Double-click on the **CT Pulmo** icon in the **Configuration Panel** dialog box to call up the configuration window for this task card.
→ Page K.4–1, *Extended functions in Pulmo*

DynEva CT

✧ Double-click on the icon to adapt the evaluation functions of the **DynEva** task card to your requirements.
→ Page N.5–1, *Configuring DynEva*

CT Volume

✧ Double-click on the icon to adapt the evaluation functions of the **Volume** task card to your requirements.
→ Page O.4–1, *Configuring Volume Evaluation*

Calcium Scoring

✧ Double-click on the icon to adapt the evaluation functions of the **CalciumScoring** task card to your requirements.
→ Page M.5–1, *Configuring CaScoring*

Examination

✧ Double-click on the icon to adapt the evaluation functions of the **Examination** task card to your requirements.
→ Page C.13–1, *Configuring Examinations*

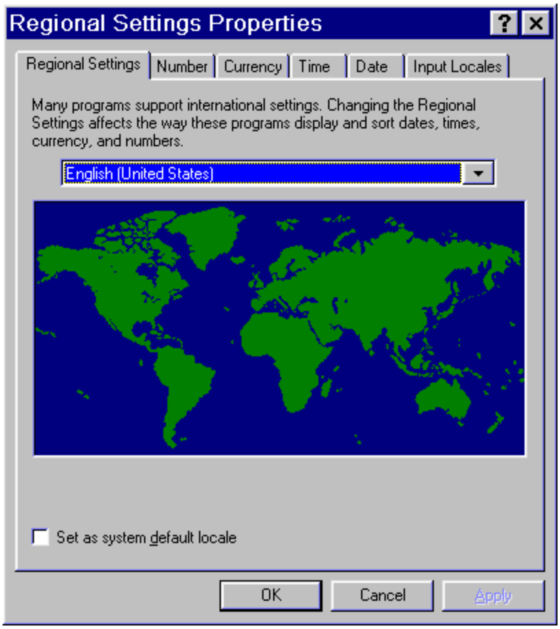
Defining the regional settings

Under **Regional Settings**, you can define the language of the user interface and other settings, such as the date format.

✧ Double-click on this icon.

Regional Settings

The configuration for regional settings appears.



Regional Settings Properties

Many programs support international settings. Changing the Regional Settings affects the way these programs display and sort dates, times, currency, and numbers.

English (United States)

☐ Set as system default locale

➩ The user interface for the regional settings is always in English whatever language is set.

Setting the language

✧ Select the language you require on the **Regional Settings** subtask card and confirm with **OK**.

The application is restarted with the new language.

NOTE

A restart of the system is necessary to apply the change of the language.

Other regional settings

You can make further settings on the other subtask cards.

✧ In particular, define the format for the **Date** and **Time**.

➪ We recommend to select the short date style.

Configuring image text

With the **Image Text Editor** you can define which text elements will be displayed in the images.

ImageText
Editor

✧ Double-click on this icon of the *syngo* **Configuration Panel**.

The configuration editor **Image Text Configuration** is displayed.

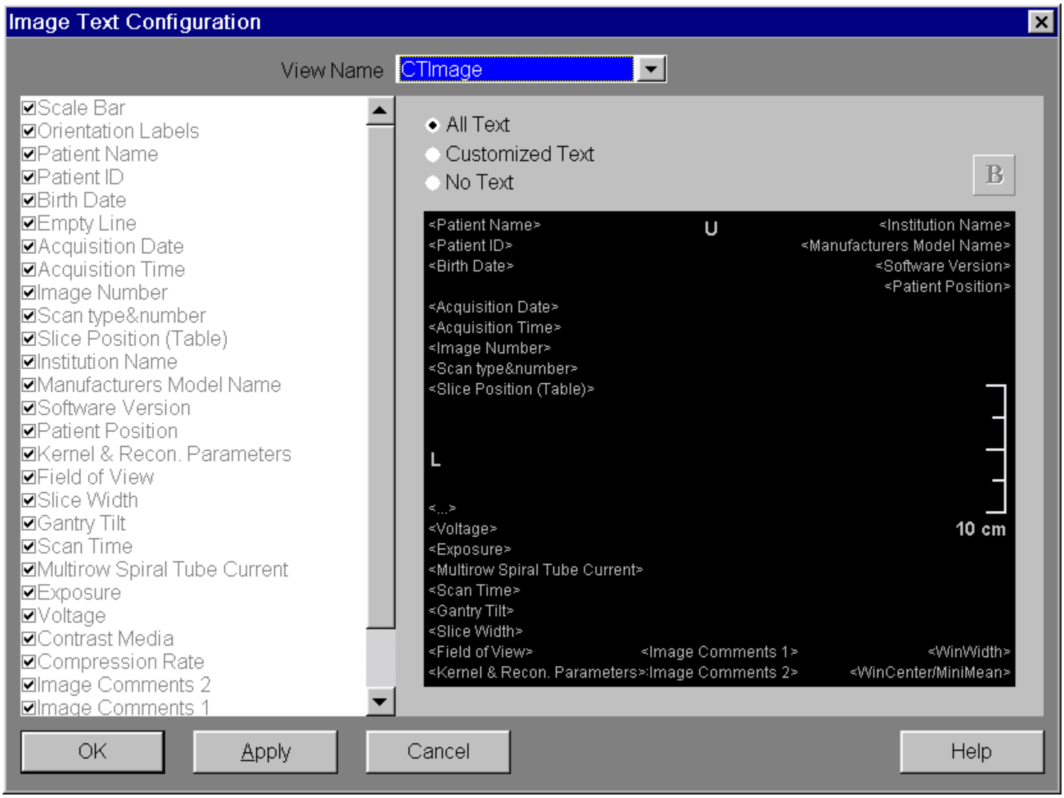


Image Text Configuration

View Name: CTImage

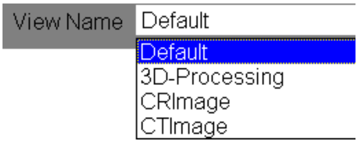
☑ Scale Bar
☑ Orientation Labels
☑ Patient Name
☑ Patient ID
☑ Birth Date
☑ Empty Line
☑ Acquisition Date
☑ Acquisition Time
☑ Image Number
☑ Scan type&number
☑ Slice Position (Table)
☑ Institution Name
☑ Manufacturers Model Name
☑ Software Version
☑ Patient Position
☑ Kernel & Recon. Parameters
☑ Field of View
☑ Slice Width
☑ Gantry Tilt
☑ Scan Time
☑ Multirow Spiral Tube Current
☑ Exposure
☑ Voltage
☑ Contrast Media
☑ Compression Rate
☑ Image Comments 2
☑ Image Comments 1

● All Text
○ Customized Text
○ No Text

Image type

You can define individual settings for each modality.

➩ The default setting is used if no other setting is specified for the displayed image.

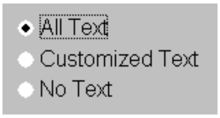


View Name Default

✧ Select the type of image you require from the selection list **View Name**.

The setting for this text selection is displayed.

Number of texts



● All Text
○ Customized Text
○ No Text

You can change the default text mode.

✧ Click on the required option button.

❑ **All Text**
All available text information is displayed in the images.

❑ **Customized Text**
You can make a selection from the available texts.

❑ **No Text**
No texts will be displayed in the images.

NOTE

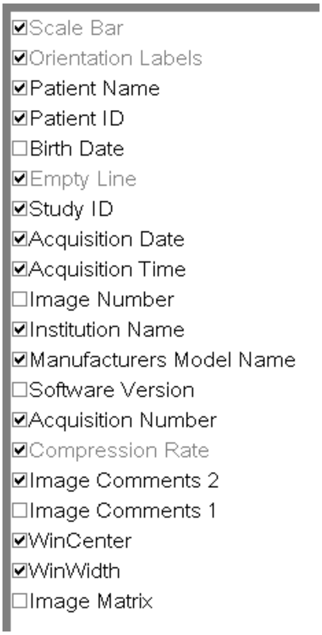
If you select the setting **No Text**,
no orientation marks or scale will be displayed either!

Text selection

If you have selected the **Customized Text** option, you can put together any text selection.

✧ Activate or deactivate the required checkboxes.

The text selection is displayed.



- ☑ Scale Bar
- ☑ Orientation Labels
- ☑ Patient Name
- ☑ Patient ID
- ☐ Birth Date
- ☑ Empty Line
- ☑ Study ID
- ☑ Acquisition Date
- ☑ Acquisition Time
- ☐ Image Number
- ☑ Institution Name
- ☑ Manufacturers Model Name
- ☐ Software Version
- ☑ Acquisition Number
- ☑ Compression Rate
- ☑ Image Comments 2
- ☐ Image Comments 1
- ☑ WinCenter
- ☑ WinWidth
- ☐ Image Matrix

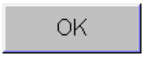
➩ Depending on the configuration of your system it might not be possible to display some texts.

NOTE

Patient Name cannot be displayed without orientation labels.

Exiting a configuration window

As soon as you have changed settings in a configuration window, you can exit the configuration window with or without saving your changes.



✧ Click on the **OK** button to save all your settings and exit the configuration window.

✧ Click on the **Apply** button to save your settings but leave the window open.

✧ Click on **Vendor Default** to restore the original settings.

✧ Click on **Cancel** to cancel configuration, reject all settings and close the window.

CHAPTER

A.3 Service Functions

The system provides a range of service functions for maintenance, checking, and configuring the system for authorized users, i.e. system administrators.

➪ For service-technical reasons, the user interface of the service functions is always in english independent of the national language selected.

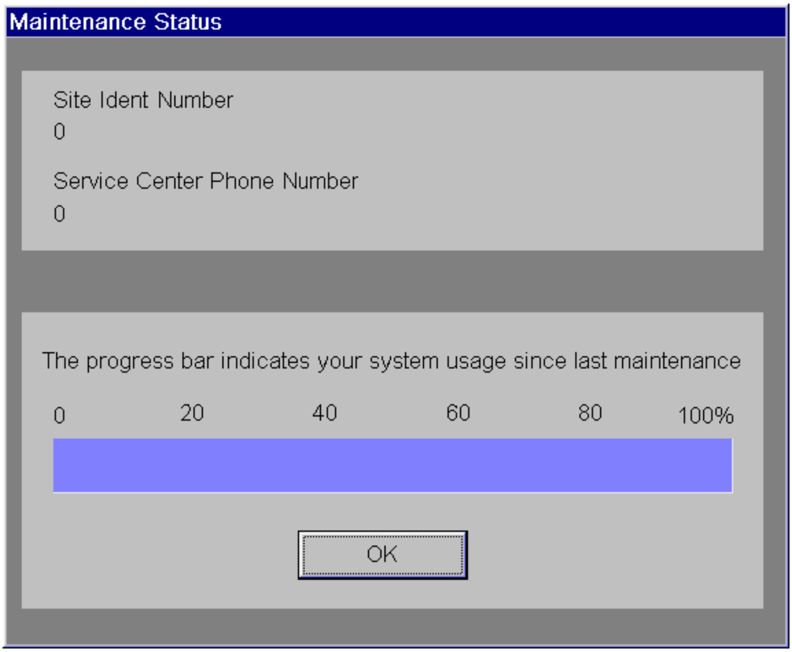
Displaying the maintenance status

To ensure smooth operation, your system must be maintained at certain intervals.

The system contains a dialog box which shows you when your system must be inspected again.

✧ Call up **Options > Maintenance...**.

The **Maintenance Status** dialog box is displayed.



Site Ident Number
0

Service Center Phone Number
0

The progress bar indicates your system usage since last maintenance

➪ On monochrome monitors, it might be difficult to see the progress bar.

The progress bar shows you when the next maintenance of your system is due by means of a colored display.

As long as the display is in the green range, you can close the window again with **OK**. If the bar moves into the red range, you can only close this window again after maintenance has been performed.

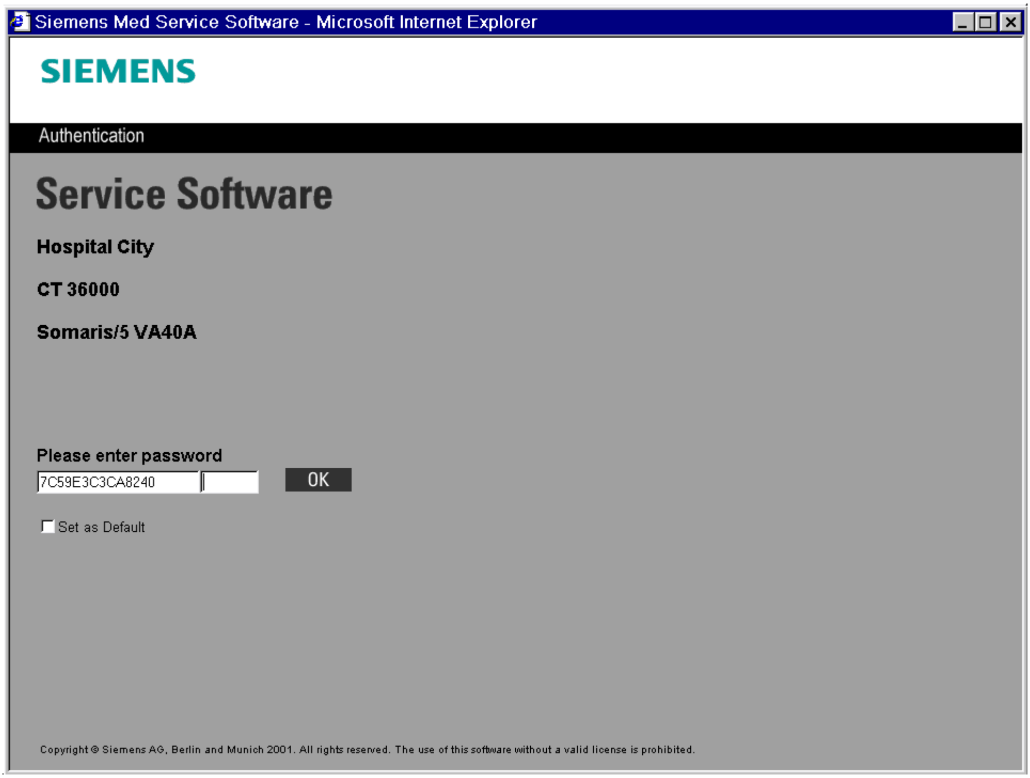
➩ In that case, move the window to one side, finish off the examination, and contact Siemens Service.

➩ For further information, please contact your Siemens Service or your system administrator.

Local Service

In addition to the user-specific configuration, there is a configuration level for authorized users.

✧ Select **Options > Local Service...** to call up the **Authentication** window.



Service Software

Hospital City

CT 36000

Somaris/5 VA40A

Please enter password
7C59E3C3CA8240

Depending on the configuration access rights in your system, several service levels are available.

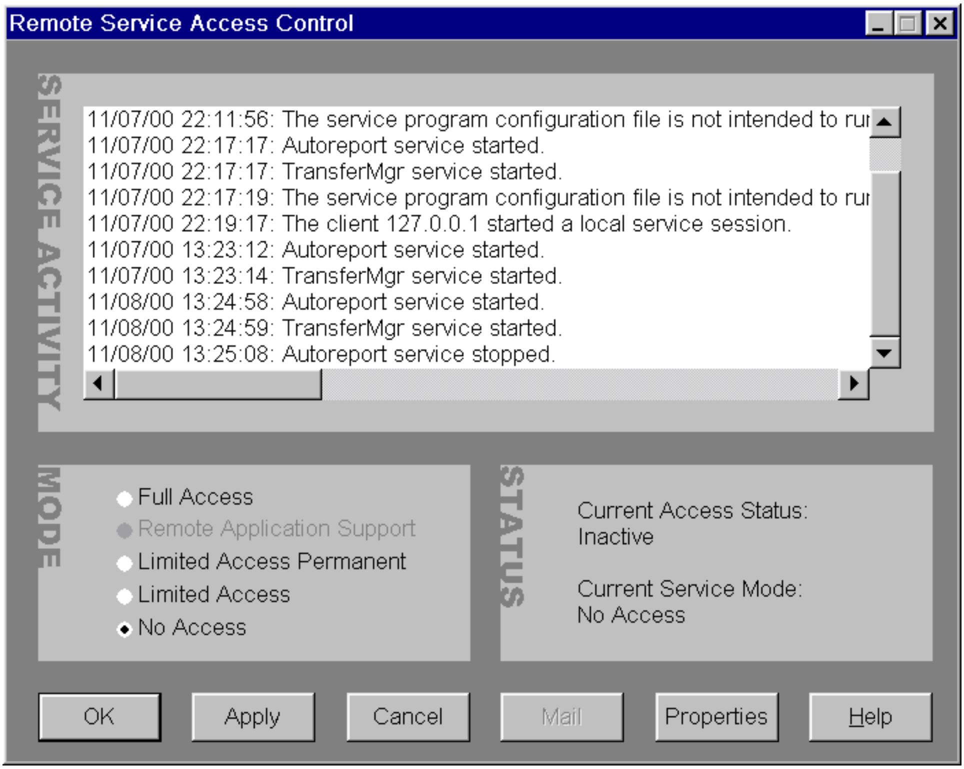
➪ For further information, please contact your Siemens Service or your system administrator.

Remote Service Access

Your system can also be serviced by Siemens Service via modem.

In the **Remote Service Access Control** window, you can grant access rights to service so that service personnel can perform maintenance.

✧ Call up **Options > Remote Service...** to display the **Remote Service Access Control** dialog box.



```
11/07/00 22:11:56: The service program configuration file is not intended to rur
11/07/00 22:17:17: Autoreport service started.
11/07/00 22:17:17: TransferMgr service started.
11/07/00 22:17:19: The service program configuration file is not intended to rur
11/07/00 22:19:17: The client 127.0.0.1 started a local service session.
11/07/00 13:23:12: Autoreport service started.
11/07/00 13:23:14: TransferMgr service started.
11/08/00 13:24:58: Autoreport service started.
11/08/00 13:24:59: TransferMgr service started.
11/08/00 13:25:08: Autoreport service stopped.
```

○ Full Access
○ Remote Application Support
○ Limited Access Permanent
○ Limited Access
● No Access

Current Access Status:
Inactive

Current Service Mode:
No Access

NOTE

As long as you have assigned full access rights to service, i.e. maintenance is in progress, you cannot continue working with your system.

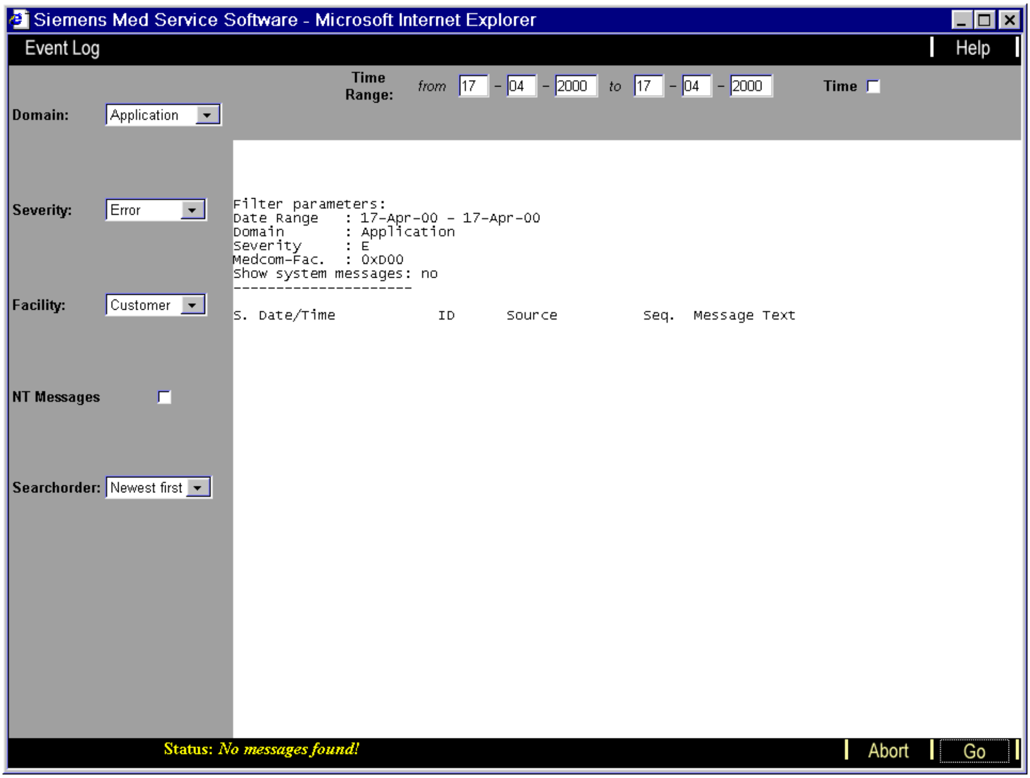
✧ Select **Limited Access** or **No Access** and click **OK** or **Apply** to continue.

➩ For further information, please contact your Siemens Service or your system administrator.

Logbook

Your system has a logbook that records all system and application-relevant events, for example error messages.

✧ Call up **Options > Event Log...** to display the **Event Log** dialog box.



Time Range: *from* 17 – 04 – 2000 *to* 17 – 04 – 2000 **Time** ☐

Domain: Application

Severity: Error

Facility: Customer

NT Messages ☐

Searchorder: Newest first

```
Filter parameters:
Date Range   : 17-Apr-00 - 17-Apr-00
Domain       : Application
Severity     : E
Medcom-Fac.  : 0xD00
Show system messages: no
---------------------

S. Date/Time            ID      Source          Seq.  Message Text
```

Status: *No messages found!*

You can select the type and date of the messages that you want to display.

➩ For further information, please contact your Siemens Service or your system administrator.

CHAPTER
A.4 First Steps

The following pages provide you with a short introduction to working with your computer tomograph.

Here you can familiarize yourself with the typical procedure for a routine examination with all its individual steps using the example of a cranial phantom or any other phantom you might have:

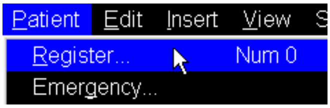
- ❏ After the phantom has been positioned you enter the data required for examination with the patient registration.
- ❏ Then scan a topogram and perform two spiral scans.
- ❏ With the examination data, you can calculate the slice images and perform initial image evaluation.
- ❏ For detailed postprocessing, load the images onto the **Viewing** card with the **Patient Browser** and evaluate them there in detail.
- ❏ On the **Filming** card, you can collect the images for documentation on film sheet and send them via network for further postprocessing.

NOTE

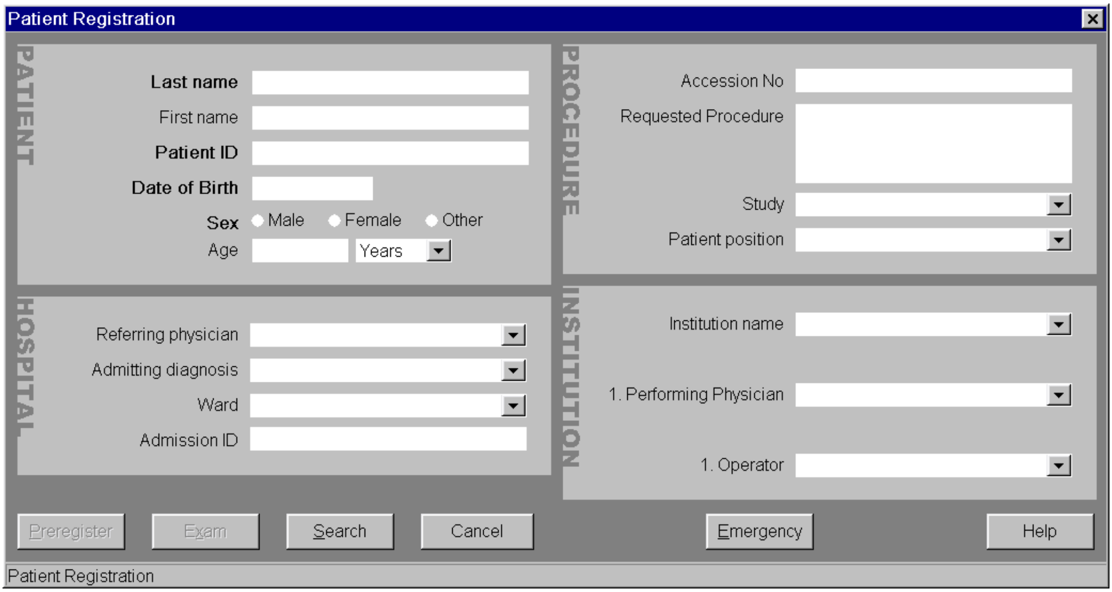
Do **not** perform these first steps on a patient. Use one of the phantoms supplied or your own cranial phantom for the examination described.

Registering a patient

Before you can examine a patient, you must register the patient.



✧ Call up **Patient > Register** in the main menu.



Entering the necessary data

The fields that you must always fill in for an examination are shown in **bold** type.

✧ Enter a patient name (**Last name**).

✧ Enter a **Patient ID**.

✧ Enter the **Date of birth**.

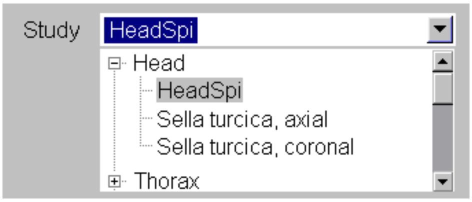
✧ Click on the **Sex**.

➪ This data is necessary to meet the DICOM requirements.

Patient position: Head First - Supine

✧ Click on the arrow next to the **Patient position** field and select a patient position.

Selecting an examination

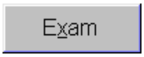


Study: HeadSpi

- Head
  - HeadSpi
  - Sella turcica, axial
  - Sella turcica, coronal
- Thorax

✧ Click on the arrow next to the **Study** field.

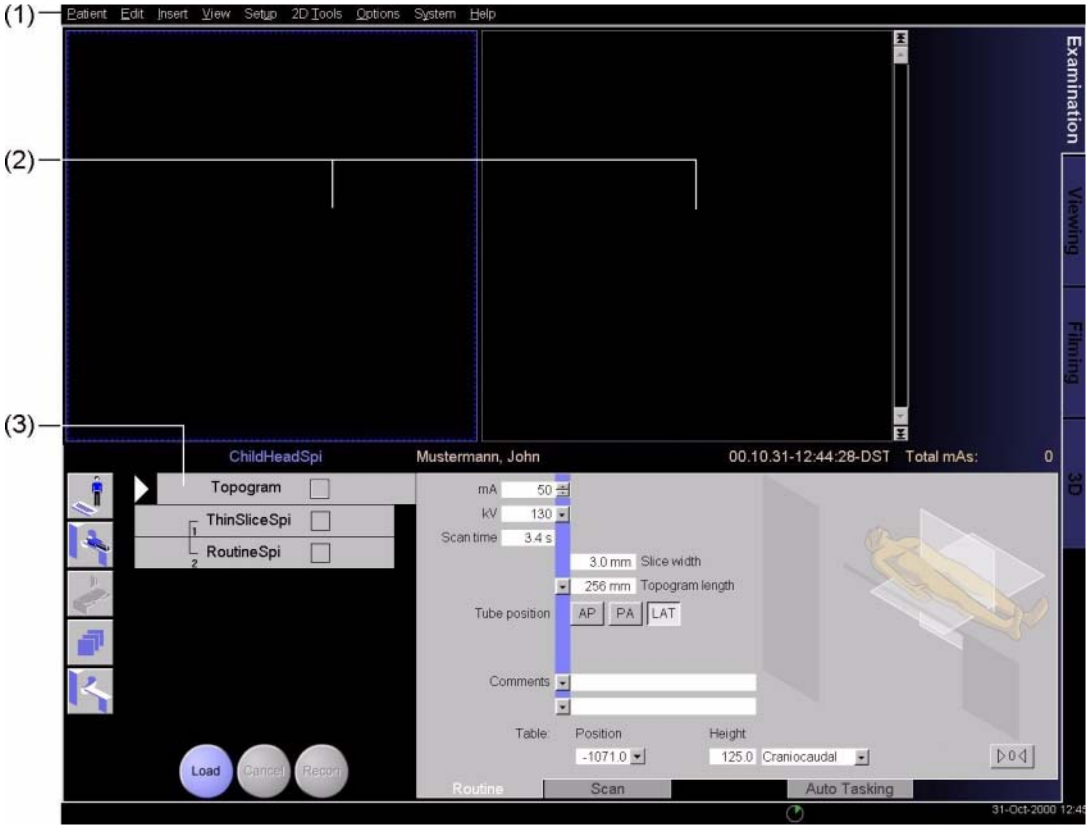
✧ Click on the **+** sign in the list which is opened out in front of **Head**. Select **HeadSpi** after that.



✧ Close the patient registration with the **Exam** button.

Examining a patient

You now see the examination card.



ChildHeadSpi Mustermann, John 00.10.31-12:44:28-DST Total mAs: 0

mA 50
kV 130
Scan time 3.4 s
3.0 mm Slice width
256 mm Topogram length
Tube position AP PA LAT
Comments
Table: Position -1071.0 Height 125.0 Craniocaudal

(1) Main menu
(2) Topo segment (left) and tomo segment (right)
(3) Chronicle

Scanning a topogram

The first examination step, the topogram, is already selected in the chronicle.

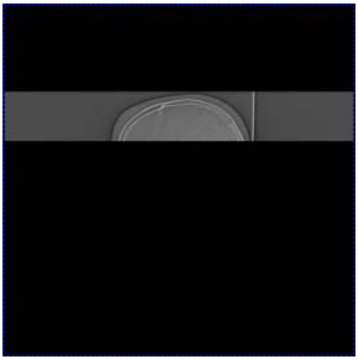
✧ Click on **Load**.

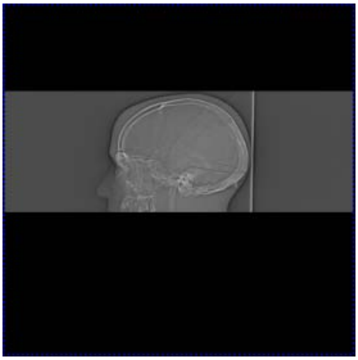
✧ Press the **Start** button on the control box.

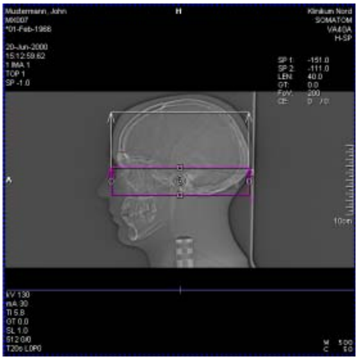
> **CAUTION**
>
> **Source of danger**: Radiation in the scanning room after the **Start** button has been pressed
>
> **Consequence**: Radiation damage possible
>
> **Remedy**: Leave the scanning room before initiating scanning. Or wear protective clothing.

➪ Depending on the actual table position you are prompted to press MOVE before the scan trigger is released.

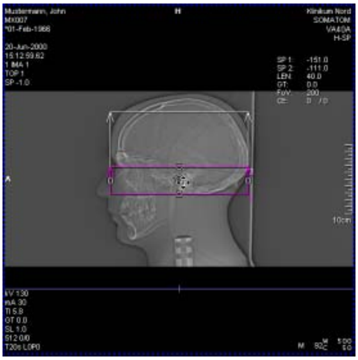
The topogram is scrolled down in the topo segment while it is being scanned.







Adapting ranges

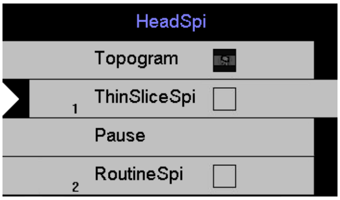


The examination ranges of the following scans are displayed in the topogram according to the scan protocol selected.

✧ Select the ranges by clicking on the corresponding entry in the chronicle.

✧ Click on a handle on the horizontal border lines. Hold the mouse button down and enlarge or reduce the range concerned.

First spiral scan



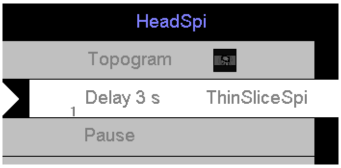
✧ Click on the first spiral scan in the chronicle.

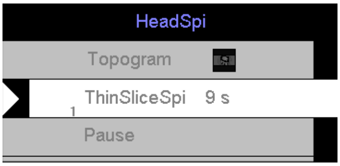
✧ Click on the **Load** button.

✧ Press the **Move** button on the control box.

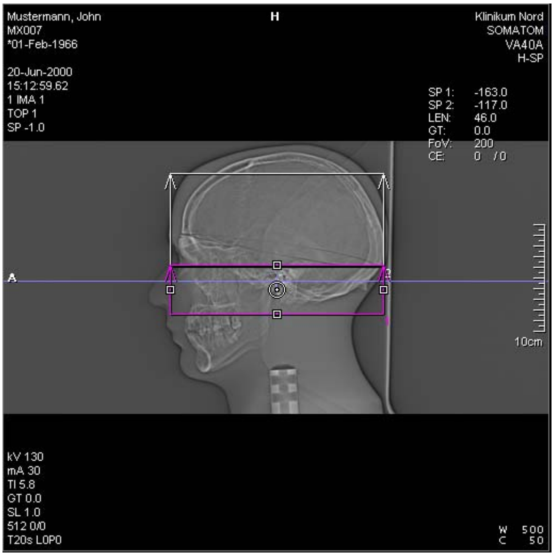
✧ Then press the **Start** key.

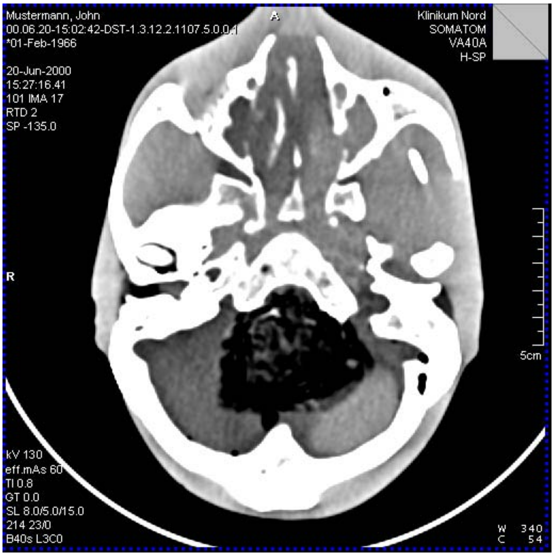
After a delay has elapsed, scanning begins. The remaining scan time is displayed.





You can see the progress of scanning in the topo segment. The slice images are displayed continuously with reduced image quality in the tomo segment.





Next spiral scan

After the first spiral scan is completed, the system pauses.

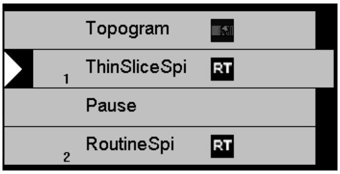
✧ Press the **Move** button on the control box until the starting position for the next scan is reached.

✧ Press the **Start** button on the control box.

The next scan is automatically started after the delay has elapsed. The system pauses after the range has been scanned completely.

Reconstructing images with full matrix

You now reconstruct slice images from the scan data and have different image fields of view displayed. First, calculate an overview image for setting the fields of view.



Topogram
1 ThinSliceSpi RT
Pause
2 RoutineSpi RT

✧ Click on the first spiral scan in the chronicle.

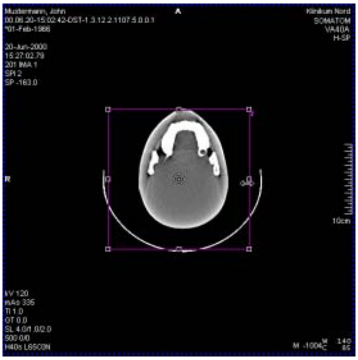
Recon job ● 1 ○ 2 ○ 3

✧ Select the **Recon** subtask card and select a new recon job.

✧ Click on the **Overview** button to display an overview image of the entire scan field.

⇨ Displaying the overview image can take some time.

In the tomo segment, the first reconstruction target (numbered with “1”) for this spiral scan is displayed.



✧ Click on one of the handles displayed.

✧ Hold the mouse button down and reduce or enlarge the field of view.

Recon job ○ 1 ○ 2 ● 3

✧ Select the third recon job on the **Recon** subtask card and set the field of view in the same way.

✧ Then start reconstruction of the first spiral scan with the **Recon** button.

✧ Then repeat these steps for the second spiral scan.

Evaluating images

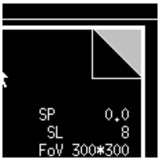
✧ Call up **2D Tools > Graphics** and **2D Tools > Image Manipulation**.

HeadSpi Mustermann, John 008 Total mAs: 9065

Recon job ● 1 ○ 2 ○ 3

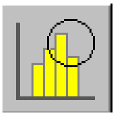
Slice width 3.0 mm
Kernel H30s medium smooth
Window Base Orbita
FoV 200 mm
Center X 0 mm
Center Y 0 mm
Mirroring None
Extended CT scale ☐

Begin -1201.0 mm
Recon begin -1201.0 mm
Image Order Caudocranial
Recon increment 3.0 mm
No. of images 14
Recon end -1161.0 mm
End -1161.0 mm



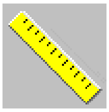
SP 0.0
SL 8
FoV 300*300

✧ Scroll through the tomo segment to the image that you want to evaluate using the dog-ears.

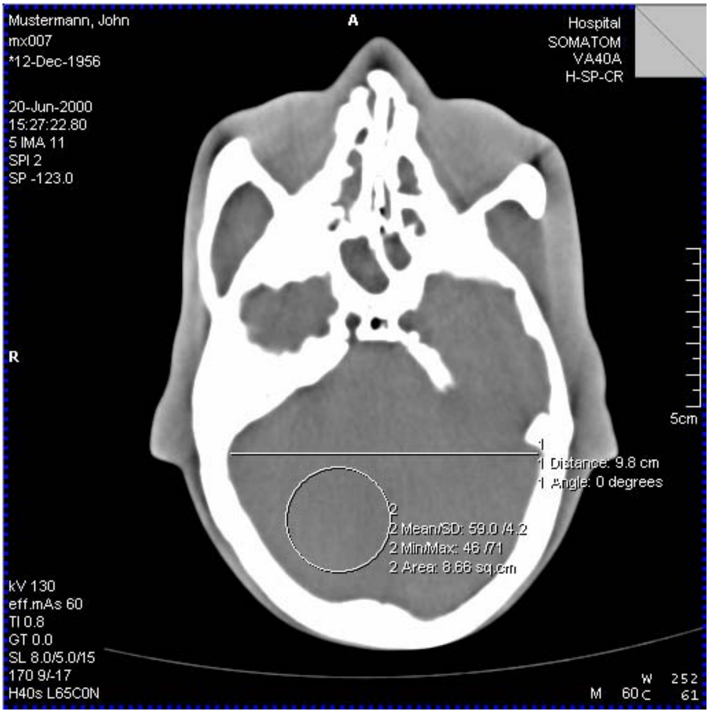


✧ Click on the **Circle** button to draw in and evaluate a region of interest (ROI).

✧ Drag open a circle holding the left mouse button down and release the mouse button again. The smallest, largest, mean density value and the size of the area are displayed.



✧ Click on the **Distance** button and drag a line between the required start and end point holding the left mouse button down to measure the distance.



Ending an examination

✧ Click on **End Exam** on the **Examination** card.

✧ Click on **Yes** in the dialog box displayed to delete the raw data of the examination of the phantom.

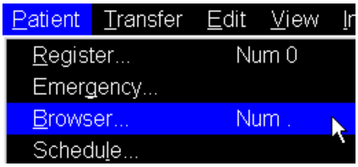
➪ So a later reconstruction will not be possible any more.

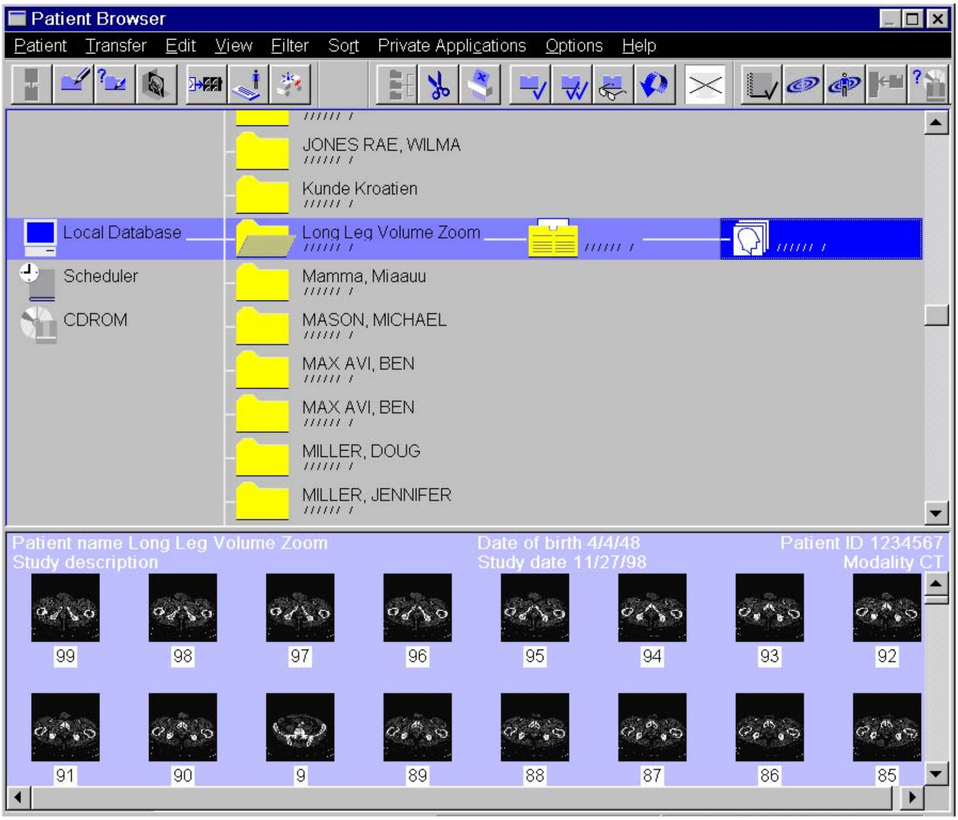
The images of your examination have already been saved. The examination card is empty again.

Retrieving and postprocessing images

With the **Patient Browser**, you can search for images of the examination in your database and then transfer them to the **Viewing** task card for evaluation.

✧ First click on the **Viewing** card and then call up **Patient > Browser** in the main menu.



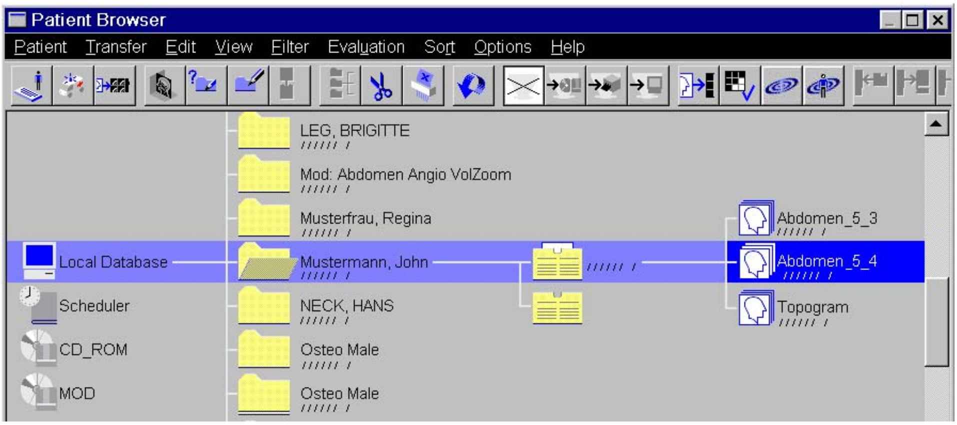


JONES RAE, WILMA
Kunde Kroatien
Long Leg Volume Zoom
Mamma, Miaauu
MASON, MICHAEL
MAX AVI, BEN
MAX AVI, BEN
MILLER, DOUG
MILLER, JENNIFER

Patient name Long Leg Volume Zoom Date of birth 4/4/48 Patient ID 1234567
Study description Study date 11/27/98 Modality CT

Searching for patient data and loading for evaluation

✧ Scroll through the list of patients in your local database with the scroll bar.



As soon as you have found the patient you are looking for:

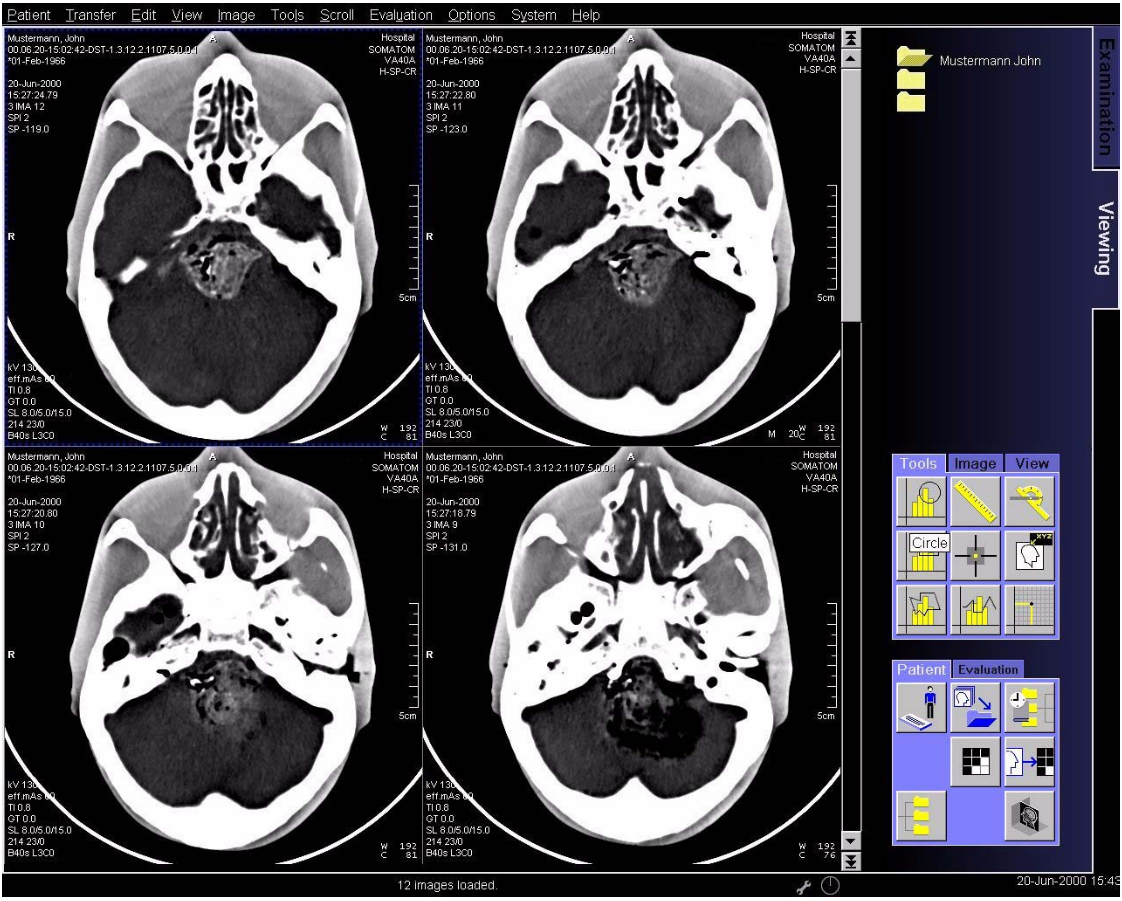
✧ Click on the patient entry.
All the studies of the patient are displayed.

✧ Then click on the entry of the study you require.

✧ Finally double-click on the entry of the scan series that you want to evaluate.

The **Patient Browser** window is closed.

You can see the images of the loaded scan series on the **Viewing** task card. The associated patient folder is displayed in the top right-hand corner of the card.



12 images loaded.

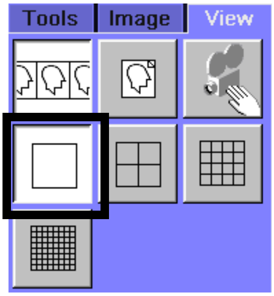
Scrolling through the series

✧ Use **Image+** and **Image-** on the symbol keypad of your keyboard to scroll through the scan series.

✧ Click on the image that you want to evaluate.

The image is now selected and has a blue dotted border.

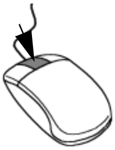
Selecting a large-format layout



✧ Click the **View** card in the subtask card stack into the foreground.

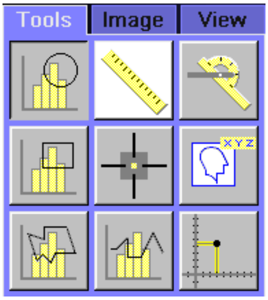
✧ Select layout 1:1.

Windowing an image



✧ Move the mouse in the image holding the center mouse button down:
up/down (changing the window center)
right/left (changing the window width)

Measuring a distance

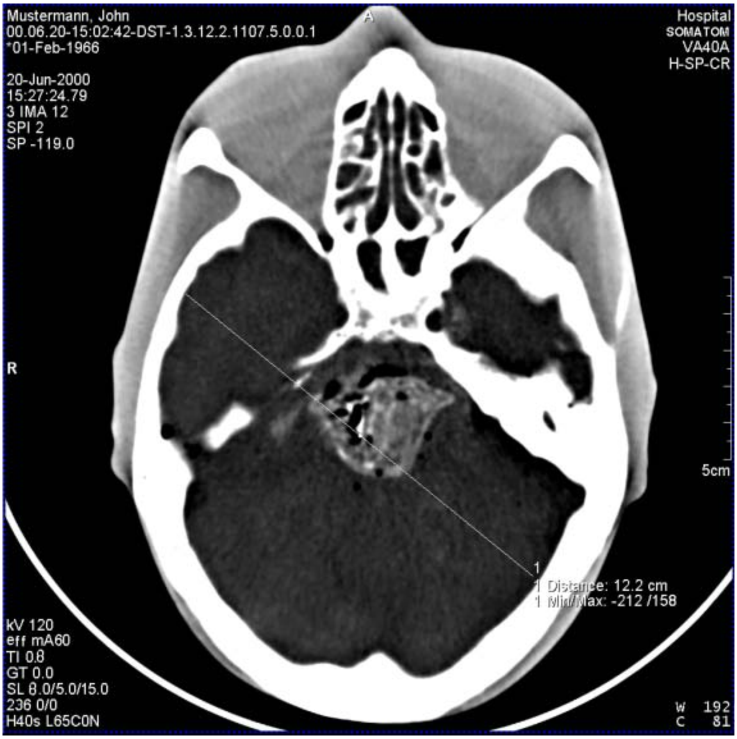


✧ Click the **Tools** card in the card stack into the foreground.

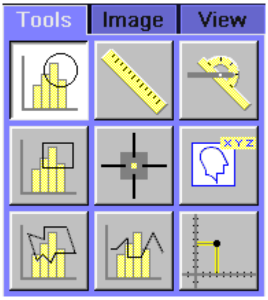
✧ Click on the **Distance** button to measure the distance between two points in the image.

✧ Place the mouse cursor on a starting point of the distance line, hold the left mouse button down and drag the line to the end point.

As soon as you release the mouse button, the distance is displayed in the image in centimeters.



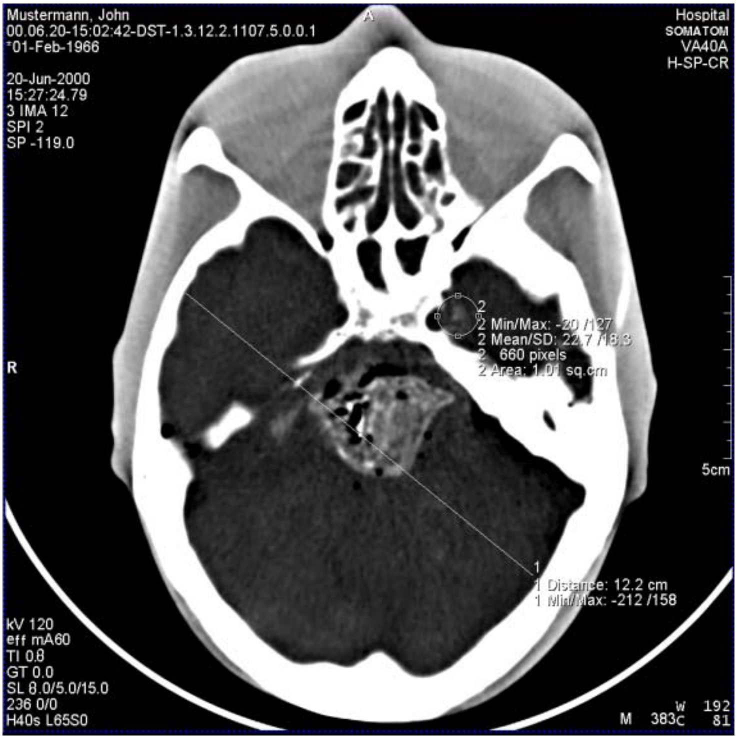
Evaluating an area



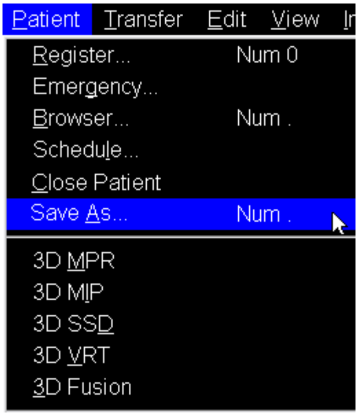
✧ Click on the **Circle** button on the **Tools** card to draw and evaluate a circular region of interest (ROI) in your image.

✧ Draw a circle in the image holding the left mouse button down.

As soon as you release the mouse button, the evaluation results of the ROI are displayed in the image.



Saving an image



✧ Call up **Patient** > **Save As**.

⊙ Save images in new series: TestImage

✧ Enter a designation in the dialog box displayed next to **Save images in new series** and click on **OK**.

Sending an image through the network

✧ Select an image in the image area.

✧ Call up **Transfer > Send To Node 1** to send the image to this preconfigured address in the network.

➪ For sending images, your system has to be connected to a network.

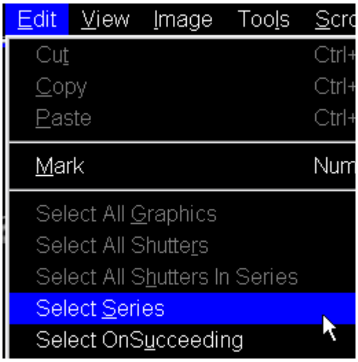
Filming images

After postprocessing and evaluation you can expose the examination results on film for reporting.

✧ Select the images in the **Patient Browser** and transfer them to the **Viewing** task card.
→ Page A.4–14, *Retrieving and postprocessing images*

➪ If necessary you can refresh the **Patient Browser** display with **View** > **Refresh**.

✧ Click on an image in the image area of the **Viewing** card holding the **Ctrl** key down.



✧ Call up **Edit > Select Series** from the main menu.

The complete series is now selected.

Transferring images for filming

✧ Click on the **Copy to Film Sheet** button on the **Patient** subtask card.

All the selected images are transferred to the **Filming** task card.

Calling up Filming

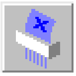
✧ Click on the **Filming** tab on the right-hand edge of the screen.

✧ If more than one film sheet is displayed, page through the film sheets of your selected series using the dog-ears (top right corner of the image area).

Deleting an image

✧ With the left mouse button, click on an image that you do not want to film.

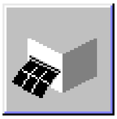
The image now has a blue dotted border.



✧ Click on the **Delete** button.

The image is deleted from the film sheet.

Exposing images on film



✧ Click on the **Expose Film Task** button to document the images on film.

PART
B

Patient Registration

B.1 Introduction

B.2 Registering an Emergency Patient

B.3 Registering a New Patient

B.4 Registering a Known Patient

B.5 *Configuring Patient Registration*

CHAPTER
B.1 Introduction

Before you can examine a patient with your system, you must register him or her. Registration means that you give your system all the information about a patient that it requires for an examination.

Depending on how registrations are organized in your hospital and how much time you have for registration, you can choose between different patient registration procedures.

Emergency registration

If a patient is admitted who is in an extremely critical condition and must therefore be examined and treated immediately, call up emergency registration. This reduces the time before you can begin the examination to a minimum.

Registration

However, if you want to register a patient for an examination, then you first enter his or her patient data or call it up from the database and then examine the patient.

Preregistration

If you want to prepare the system to examine a patient at a later point in time, then you can preregister the patient.
For example, you can enter the data in the morning for all the patients to be examined during the day. When you want to begin an examination, simply call up this data and edit it, if necessary. This saves time during the examinations.

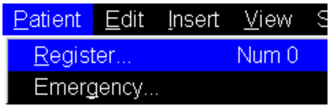
HIS/RIS query

If your system is linked to, and licensed and registered for an HIS/RIS system (hospital and radiology information system), you can call up data for the patient to be examined.

Calling up patient registration

You can call up patient registration both in the **Patient** menu and by using icon buttons on various task cards and from the **Patient Browser**. You can choose between emergency registration and normal registration.

Patient menu

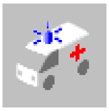


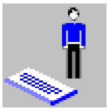
✧ Call up **Patient > Emergency** or **Patient > Register...**.

The **Emergency Registration** or the **Patient Registration** window is then displayed.

Or

Buttons

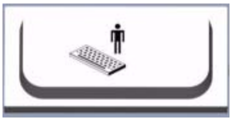




✧ Click on the icon button on the task cards or on the tool bar of the **Patient Browser**.

Or

Symbol keypad

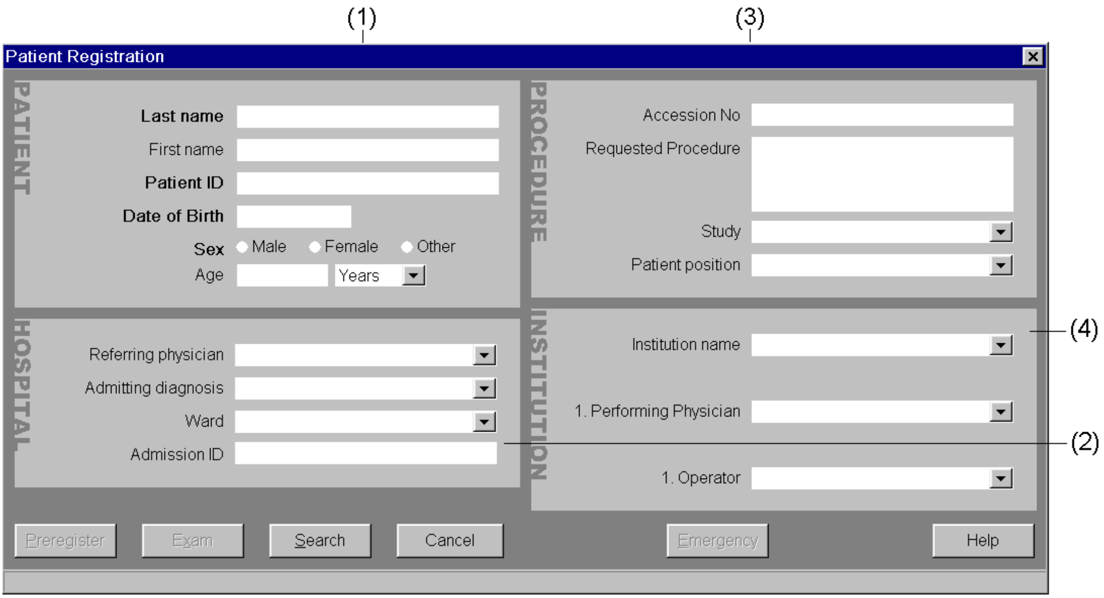


✧ Press the **Patient Register** key on the symbol keypad.

The Patient Registration window

The **Patient Registration** window is subdivided into four areas into which you can enter the following data:

(1) Personal data of the patient (PATIENT)
(2) Referral data (HOSPITAL)
(3) Study-specific data (PROCEDURE)
(4) Institution data (INSTITUTION)



Personal data of the patient

In the **PATIENT** area, you can enter all the personal details and any additional information about the patient.

NOTE

Patient name, patient ID, date of birth and sex
are used for unique identification of a patient in the
databases or on archive media.

Referral data

In the **HOSPITAL** area, you can enter the referring physician, the preliminary diagnosis, preliminary admission ID, and the hospital ward in which the patient is located.

Study-specific data

In the **PROCEDURE** area, you can enter information about the planned examination, e.g. the patient position and the examination to be conducted.

Institution data

In the input fields of the **INSTITUTION** area, you can register the name of your hospital or practice and the names of your examinations personnel.

CHAPTER
B.2

Registering an Emergency Patient

If an emergency patient is admitted to your institution, it is essential to be able to examine and treat the patient immediately without wasting time entering the patient's data.

In such cases call up emergency registration and switch to the **Examination** task card immediately.

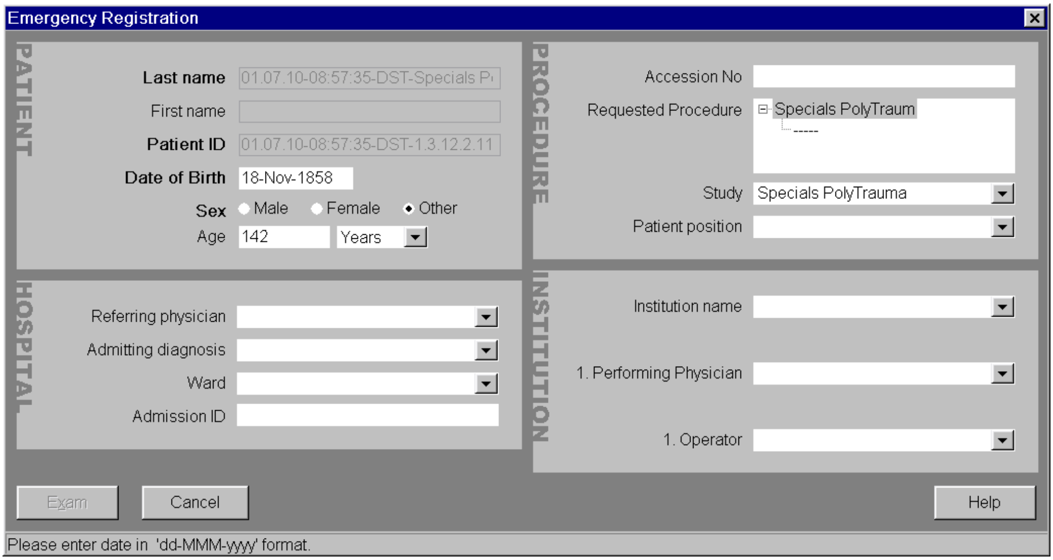
Or you conduct an emergency registration from the **Patient Registration** window if this is already open.
→ Page B.3–3, *Emergency registration in the Patient Registration window*

In this way, you can reduce the time between admission of the emergency patient and the beginning of the examination to a minimum.

You can complete the data about this patient in the **Patient Browser** later on.
→ Page D.4–2, *Correcting patient or examination data*

Patient emergency window

After you have called **Patient > Emergency...** in the main menu or in the **Patient Browser** menu, the **Emergency Registration** window is displayed.



Emergency Registration

Last name 01.07.10-08:57:35-DST-Specials P
First name
Patient ID 01.07.10-08:57:35-DST-1.3.12.2.11
Date of Birth 18-Nov-1858
Sex ○ Male ○ Female ● Other
Age 142 Years

Referring physician
Admitting diagnosis
Ward
Admission ID

Accession No
Requested Procedure ⊟ Specials PolyTraum

Study Specials PolyTrauma
Patient position

Institution name
1. Performing Physician
1. Operator

Please enter date in 'dd-MMM-yyyy' format.

Performing an emergency registration

The system has already entered unique codes for the patient name and the patient ID, in case, for example, it is not possible to communicate with the patient. You only have to add a few items of data before you can start examining the patient.

Codes for patient name and ID

The code for **Last name** comprises the date, time, and an abbreviation for daylight-saving time (DST) or standard time (STD) and (depending on configuration) the preset study description, for example: “99.12.31-23:59:00-STD-Thorax-Trauma”.

In the field for **Patient ID**, there is a combination of the date, time, abbreviation for daylight-saving or standard time, and the identification number of your system (unique worldwide).

⇨ The ID entered automatically is only valid locally, that is, it is not transmitted to the RIS system.

Adding necessary data

Date of Birth 16.10.1923

Date of Birth 18.11.1858

The cursor is in the input field for the date of birth.

✧ Enter the date of birth of the patient.

Or

✧ Skip the date of birth by pressing the tab key, e.g. if you do not know it.
Your system then uses the provisional date of birth (18.11.1858).

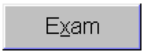
Sex ○ Male ○ Female ● Other

✧ Enter the sex of the patient.

Or

✧ Skip this data by pressing the tab key.
Your system then enters “**Other**” for the sex.

Registration



✧ Click on the **Exam** button to register the emergency patient.

The **Examination** task card is opened and you can begin with the examination immediately.

> **NOTE**
>
> Depending on the configuration it might be necessary to enter, for instance, the planned examination and the patient position in the **Emergency Registration** window before you can register the emergency patient.

As soon as you have more time after the examination you can complete the patient and examination data of your emergency patient using the **Patient Browser**. You then also replace the codes and provisional data by the correct data (e.g. the complete patient name).
→ Page D.4–2, *Correcting patient or examination data*

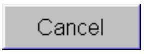
NOTE

You cannot perform emergency registration during a running examination.

✧ First finish off or interrupt the current examination and then register your emergency patient.

Canceling emergency registration

You can cancel emergency registration at any time, e.g. if you have accidentally called up the **Emergency Registration** window instead of the **Patient Registration** window.



✧ Click on **Cancel** to stop emergency registration. You return to the application from which you called up the emergency registration.

CHAPTER
B.3

Registering a New Patient

No data are yet stored on your system about a patient who has not yet been examined in your hospital or practice.
Before an examination you must therefore enter all the data about this patient.

Registration

If you enter the patient's data and want to examine the patient immediately then you must fill in at least those input fields whose names are displayed **bold**.

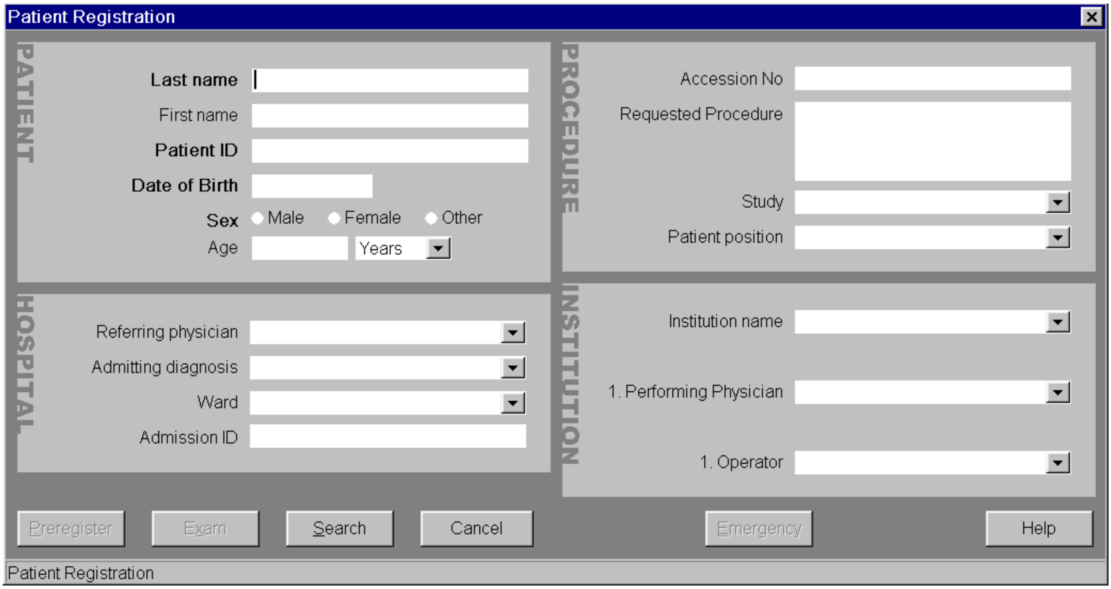
Preregistration

If you only want to preregister the patient for later examination, his or her sex, name, patient ID, and date of birth is sufficient.

You will enter the data of a new patient in the empty **Patient Registration** window.

✧ Call up the **Patient Registration** window.
→ Page B.1–3, *Calling up patient registration*

➪ If you call up patient registration from the **Patient Browser** make sure that you have not selected a patient or study there.



Emergency registration in the Patient Registration window

You can conduct an emergency registration from the **Patient Registration** window at any time.

✧ Click on the **Emergency** button to activate the **Examination** task card and to begin with the examination.

Provisional patient code and patient number

If you have already entered a patient name, your system places the term “EMERGENCY” in front of the last name of the emergency patient to be identified. If a study description is also specified, it is appended to the end of the patient ID.

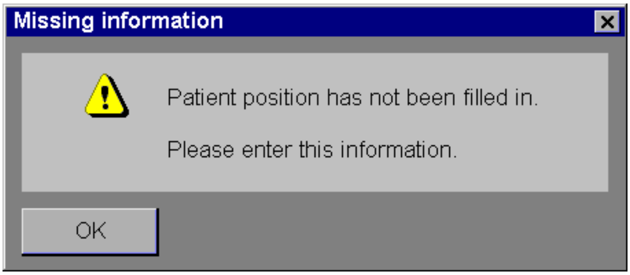
Example: If the last name is “Miller” and the study description “Thorax Trauma”, your system uses the ID “EMERGENCY-Miller-Thorax-Trauma” as the patient name.

➪ If you have not entered a name, the system forms the code in the same way as for registration in the **Emergency Registration** window.
→ Page B.2–3, *Codes for patient name and ID*

Entries in the **Patient ID** field are overwritten by the automatic identification made up of the date, time, abbreviation for daylight-saving or standard time, and the identification number of your system (unique worldwide).
→ Page B.2–3, *Codes for patient name and ID*

Patient and examination data entered

All the other patient and examination data that you have already entered in the **Patient Registration** window, are taken over unchanged. Your system displays a message box if information which is mandatory for the examination of the emergency patient is missing (e.g. patient position).



Patient position has not been filled in.

Please enter this information.

OK

✧ Close the message window with **OK**.

Emergency

✧ Add missing data in the **Patient Registration** window before you click on **Emergency** again.

➪ Depending on the configuration, your system automatically enters “**Other**” as the sex and “11/18/1858” as the date of birth, if you do not enter these data. If you enter the age instead of the date of birth, the system calculates the date of birth from the current date.

After the examination or later on you can complete or correct the data about the emergency patient using the **Patient Browser**.
→ Page D.4–2, *Correcting patient or examination data*

Entries in the PATIENT area

After you have called up patient registration, the cursor is in the input field for patient name in the **PATIENT** area.

The **Exam** and **Preregister** buttons remain deactivated until you have entered all the information required to register or preregister a patient.

Personal patient data include name, patient number, age, and sex. This data uniquely identifies the patient in your databases.

✧ Enter the last name and the first name for your patient.

Patient ID RJ-1923-10051997

✧ Enter a patient number.

If you do not enter a patient number, your system automatically generates an identification code from the date, time, abbreviation for daylight-saving or standard time, and the identification number of your system (unique worldwide).
→ Page B.2–3, *Codes for patient name and ID*

Date of Birth 16.10.1923

✧ Enter the date of birth of the patient.

➪ The input format for the date of birth depends on the regional settings of your operating system. The valid input format is displayed in the status line.

➪ You may separate day, month, year with '-', '.' or '/' or a blank. You can enter the month numerically or as a three-letter abbreviation.
You can enter the year with four or two digits.
Examples: Mar/21/55 or 3-21-1955 or 21 03 55.

➪ Enter the year of birth with four digits for patients over 100 years old. Only dates of birth after 18.11.1858 are processed correctly.

Sex ○ Male ○ Female ● Other

✧ Enter the sex of the patient.

Your system has already calculated the age of the patient from the date of birth you entered above.

✧ Check the age shown. If it is incorrect you must correct the date of birth.

➪ If you do not know the date of birth you can enter the estimated age here. The system then calculates a date of birth from the current date. In the selection field next to it you can enter whether the age is in years, months or days (for example for infants).

NOTE

Check once more that the patient name, patient number, date of birth, and sex are correct to avoid confusion with other patients.

Entering admission data

In the **HOSPITAL** area you can enter information about admission of the patient to your practice.

Referring physician: Dr. Winter

✧ Enter the name of the physician (e.g. family doctor) who referred the patient or select one from the selection list.

Admitting diagnosis: Meniscus Trauma

✧ Enter the admitting diagnosis or select it from the selection list.

Ward Surgery A

✧ Enter the ward where the patient is staying or select it from the selection list.

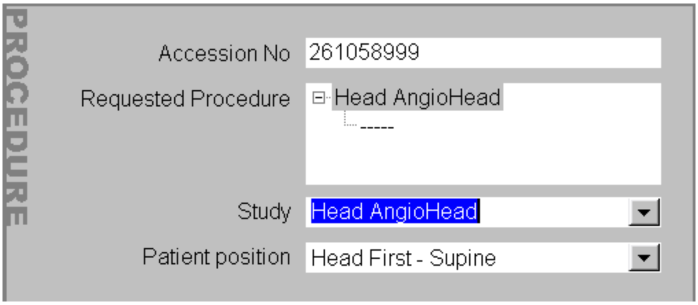
Admission ID

✧ Enter a preliminary patient number.

➩ In **Registration Configuration** you can define the entries in these selection lists.
→ Page B.5–2, *Defining entries in the selection list*

Entering examination data

In the **PROCEDURE** area you can enter information about the examination to be conducted.



Accession No 261058999

Requested Procedure Head AngioHead

Study Head AngioHead

Patient position Head First - Supine

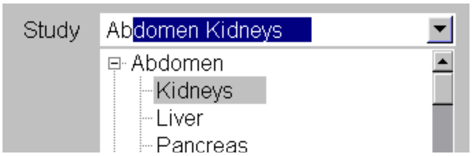
Entering one study

If only one study is possible during a session you can define it in the **Study** input field.

Study Ab

✧ Enter the first few letters of the required study.

The study list opens up and the first study which matches your entry is highlighted and placed in the input field.



Study Abdomen Kidneys

✧ If you click on a study in this list it is placed in the input field immediately.

It then also appears in the field **Requested Procedure** immediately.

Requested Procedure Head Routine
Head Cerebrellum

Or

✧ Scroll through the study list with the scroll bar until you find the required region of the body.

✧ Click on the ⊞ symbol in front of this entry to display all the studies grouped together for this region.
The ⊞ symbol becomes a ⊟ symbol.

✧ Click on the ⊟ symbol to hide the studies again.

✧ Click on the study you require in the selection list.

It then appears in the **Study** input field.

Entering the patient position

For the examination and the ensuing evaluation it is essential that the patient position is entered correctly.

➪ During the registration for the examination and on the **Examination** task card, you can change the patient position entered again.

After you have entered the requested examination, you enter the position that the patient is to adopt during the examination.

➪ In the **Examination** task card you can change the patient position again.

Patient position: Head First - Left Lateral

✧ Select the patient position for the (first) study in the selection list. The patient position is defined as direction - position.

Direction:

❑ **Head First**
The patient is lying with his or her head toward the examination unit.

❑ **Feet First**
The patient is lying with his or her feet toward the examination unit.

Position:

❑ **Left Lateral**
The patient is lying on the left-hand side.

❑ **Right Lateral**
The patient is lying on the right-hand side.

❑ **Supine**
The patient is supine.

❑ **Prone**
The patient is prone.

Administration number

The administration numbers are intended for internal management numbers of the external examinations.

If you have compiled a study list the following data refer to all studies in the list.

Accession No 35GHUPT89

Configuration-dependent input and output field for the access number of the study assigned by the RIS (radiological information system).

Entering institution data

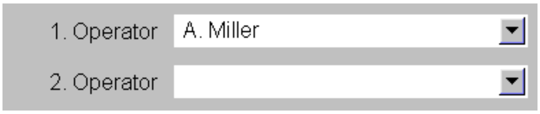
In the **INSTITUTION** area, you enter the information about the examining institution and the examination personnel. This information can be helpful if the examination results are passed on to a different organization for reporting.


Institution name: UCLA

✧ Enter the name of the hospital or practice or select it from the selection list.


1. Performing Physician:
2. Performing Physician:

✧ Enter the name of the examining physician or physicians or select them from the selection list.


1. Operator: A. Miller
2. Operator:

✧ Enter the name of the operator or operators or select them from the selection list.

➪ In **Registration Configuration** you can define the entries in these selection lists.
→ Page B.5–2, *Defining entries in the selection list*

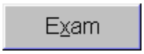
Completing data entry

After you have entered all the necessary patient data in the **Patient Registration** window, you can register the patient for the ensuing examination or preregister him or her for examination later on.

Registering a patient for the examination

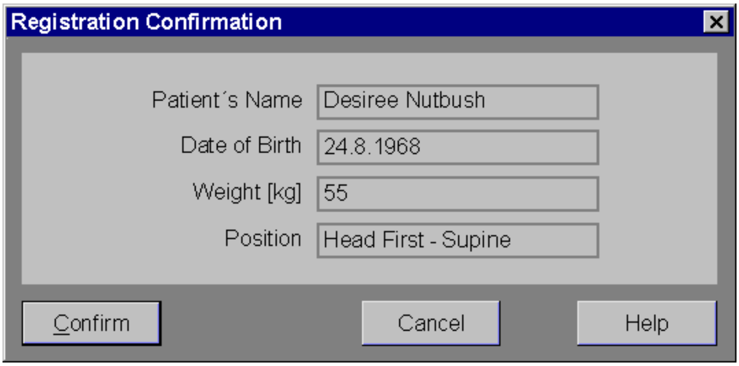
If you want to examine the patient directly afterwards, register the patient now. The ensuing examination is conducted with the data that you have entered.

Registration



✧ Click on the **Exam** button.

Depending on the configuration of your system, a dialog box appears in which you must confirm the patient position, weight, and, if necessary, the date of birth of the patient.



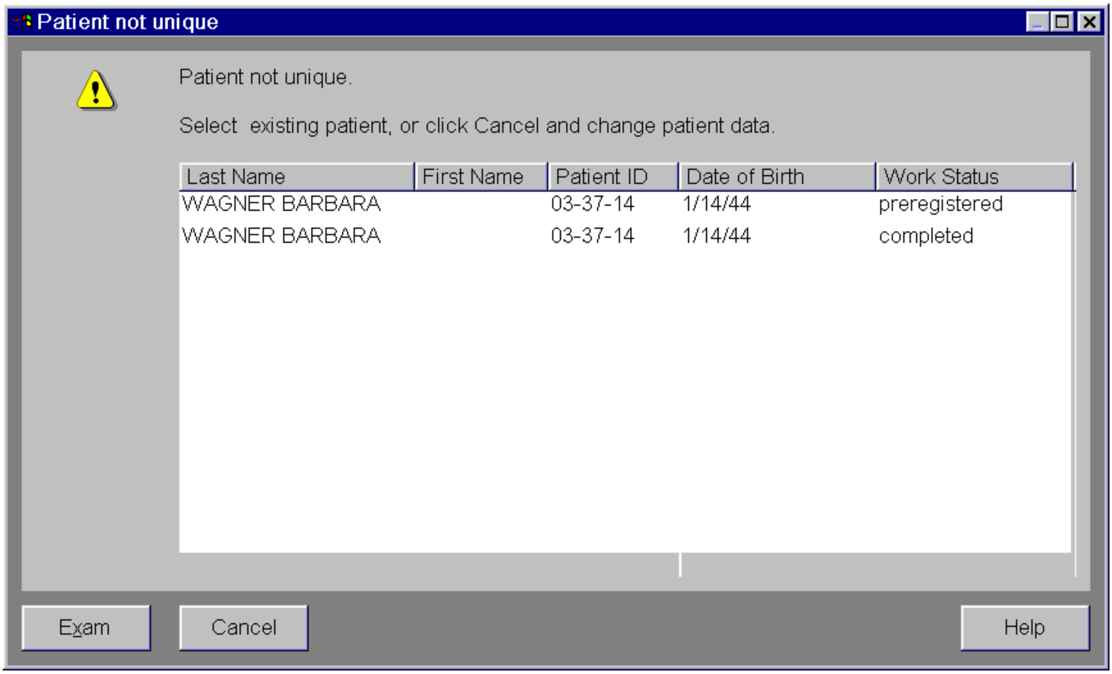
Patient´s Name: Desiree Nutbush
Date of Birth: 24.8.1968
Weight [kg]: 55
Position: Head First - Supine

✧ Confirm the information with **Confirm**.

➩ Click on **Cancel**, if this data is not correct. You will return to the **Patient Registration** window.

Patient already known to the system

When you have confirmed the patient data the system checks whether a patient with this personal data has already been pre-registered or is stored in the local database. If so, the **Patient not unique** dialog box is displayed.



Patient not unique.

Select existing patient, or click Cancel and change patient data.

Last Name	First Name	Patient ID	Date of Birth	Work Status
WAGNER BARBARA		03-37-14	1/14/44	preregistered
WAGNER BARBARA		03-37-14	1/14/44	completed

Exam

✧ Mark the patient entry and confirm by clicking the **Exam** button.

Or

Cancel

✧ Click on **Cancel** to cancel registration in order to change the patient data.

Depending on your configuration the system checks during registration whether the relation between the age and the weight is plausible. If the system finds a mismatch, registration is canceled. You then return to the **Patient Registration** window and you can correct your entries.

After successful completion of all checks, the following message appears in the footer of the **Patient Registration** window: “Transferring patient to examination...”.

The patient is now registered for the examination.

The **Patient Registration** window is closed and you return to the **Examination** task card.

Preregistering a patient

You can preregister the patient with the data entered if you want to conduct the examination later on. You can call up the patient when you start the examination and therefore save time during routine examinations.
→ Page B.4–1, *Registering a Known Patient*

Preregistration

✧ Click on the **Preregister** button.

The system checks whether the patient has already been preregistered or is already stored in the database and displays the dialog box **Patient not unique** if necessary.
→ Page B.3–19, *Patient already known to the system*

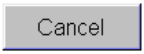
After that the following message appears in the footer of the **Patient Registration** window:
“Preregistering patient...”.

The patient is put in the schedule. All the input fields of the **Patient Registration** window are now empty again. You can enter the data of the next patient.

➪ The data of a patient may appear twice in the scheduler if the patient has been preregistered at two consoles, simultaneously. In that case, delete one of the entries.
→ Page D.5–16, *Deleting data*

Canceling patient registration

You can cancel entering patient data any time. All data that are entered in the **Patient Registration** window are lost.



✧ Click on the **Cancel** button.

The **Patient Registration** window is closed and you return to the application from which you called up patient registration.

CHAPTER

B.4

Registering a Known Patient

A patient who is preregistered or has already been examined in your hospital or practice is known to your system.

If you want to register a known patient for an examination you do not need to enter the patient's data again. You can search for the patient in the databases and place the information stored in the **Patient Registration** window, which saves time during registration.

HIS/RIS-query	If the data of the patient has already been entered via an HIS/RIS system, you can call up that data from the hospital network and place it in the scheduler. The patient is then preregistered.
Preregistered patient	If the patient is preregistered you call up the data entered previously and add to it, if necessary. After that you register the patient for examination.
Patient already examined	You can use the personal data of a patient who has already been examined from the database. Check the data, correct it, if necessary, and enter the new examination data. After that, register the patient for the ensuing examination or preregister the patient if you do not want to examine him or her until later on.

Performing an HIS/RIS query

With an HIS/RIS query, the patient data entered in the hospital network is updated at specific intervals.

Automatic query

Depending on the configuration, your system either queries data intended for your workstation, or data from the HIS/RIS system intended for other workstations with the same modality.
→ Page B.5–11, *Selecting a worklist*

This process is triggered automatically at specific intervals if you activate it in the configuration window of **Patient Registration.**
→ Page D.2–4, *Updating the scheduler*
→ Page B.5–10, *HIS/RIS query*

Manual query

You can also query the HIS/RIS system manually at any time.

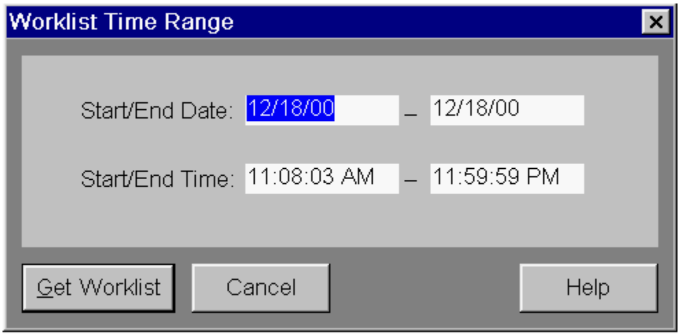
✧ Call up **View > Update Worklist** in the **Patient Browser** or double-click on the **Scheduler** symbol.
→ Page D.2–4, *Updating the scheduler*

➪ Before you start looking through the patient data in the databases, make sure that the scheduler contains all the patient data required for the examination.

Defining the worklist time range

If configured, the window **Worklist Time Range** appears when you make a manual HIS/RIS query. In it you can define the start and end time of the patient data entered in the HIS/RIS system for your query.
→ Page B.5–11, *Defining the scope of the worklist*

You can delimit the worklist range to a period of interest to you, for example, to all the patient data entered that day.



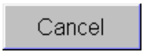
Start/End Date: 12/18/00 – 12/18/00

Start/End Time: 11:08:03 AM – 11:59:59 PM

✧ Enter the start and end point (date and time) of your worklist query.

✧ Click on **Get Worklist** to call up the updated worklist for the defined period.
→ Page B.4–7, *Search list*

Or



✧ Click on **Cancel** to close the **Worklist Time Range** window without updating the worklist.

Searching in the Patient Registration window

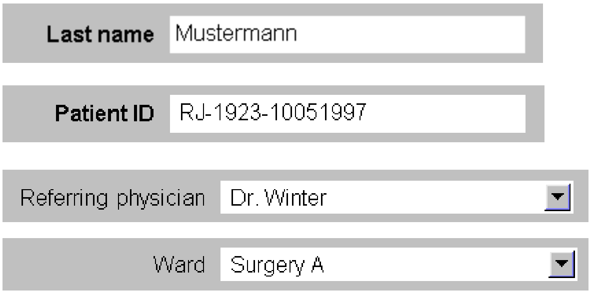
You can search for patient data in the databases from the **Patient Registration** window and then use the data for registration.

Entering search information

✧ Call up the **Patient Registration** window.

➪ If you call up registration from the **Patient Browser**, make sure that no patient or study is currently selected there to ensure that the registration dialog opens empty.

✧ Enter the data known to you in the fields Last name, Patient ID, Referring physician and Ward.
→ Page B.3–5, *Entries in the PATIENT area*



Last name Mustermann

Patient ID RJ-1923-10051997

Referring physician Dr. Winter

Ward Surgery A

➪ It does not matter whether your entries contain upper or lower case letters.

Wildcards for patient name, ID, physician and ward

If you know only part of the name or part of the ID of the referring physician, or the ward of the patient you are looking for, you can use an asterisk "*" as a wildcard.

A wildcard stands for any number of characters (letters and/or numbers).

⇨ You can use up to two asterisks "*" as wildcards in the input field, before and/or after the known part of the name or ID.

⇨ If you leave one or more fields empty, the search is performed as if you had entered an "*".

⇨ If you enter first and last names of a patient for the search, you must separate them by a "*".

Example of a patient name

If you enter “Mill*”, the names “**Mill**er” and “**Mill**”, but not “Ha**mil**ton” will be found.

Example of a patient ID

If you enter “*sy*”, the patient IDs “GO18EN**SY**39987” and “**SY**HODSON40425” will be found.

Starting a search

As soon as you have entered the data known to you, you can start the search.

✧ Click on **Search**.

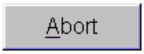
The **Search** button turns into the **Abort** button.

The databases of your system are now searched for the patient with the data entered.

➩ In **Registration Configuration** you can define which databases (e.g. local database, database in network, archive) are to be searched.
→ Page B.5–5, *Configuring the patient search*

Canceling a search

You can cancel a search at any time, for example, if you have made a mistake entering the name.

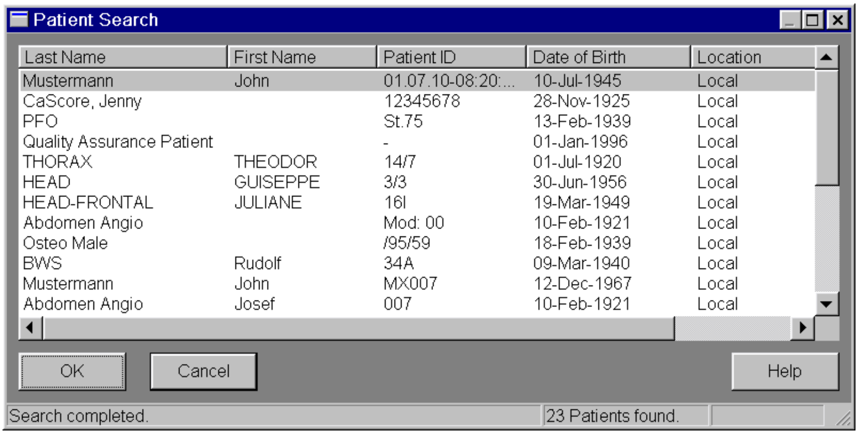


✧ Click on **Abort**.

The search is canceled and you return to the **Patient Registration** window. No data is transferred. The **Abort** button turns back into the **Search** button.

Search list

In the **Patient Search** window, the patients found in the databases are listed. The hit list is displayed as soon as more than one patient is found.



Last Name	First Name	Patient ID	Date of Birth	Location
Mustermann	John	01.07.10-08:20:...	10-Jul-1945	Local
CaScore, Jenny		12345678	28-Nov-1925	Local
PFO		St.75	13-Feb-1939	Local
Quality Assurance Patient		-	01-Jan-1996	Local
THORAX	THEODOR	14/7	01-Jul-1920	Local
HEAD	GUISEPPE	3/3	30-Jun-1956	Local
HEAD-FRONTAL	JULIANE	16l	19-Mar-1949	Local
Abdomen Angio		Mod: 00	10-Feb-1921	Local
Osteo Male		/95/59	18-Feb-1939	Local
BWS	Rudolf	34A	09-Mar-1940	Local
Mustermann	John	MX007	12-Dec-1967	Local
Abdomen Angio	Josef	007	10-Feb-1921	Local

Search completed. 23 Patients found.

➩ In **Registration Configuration** you can set which patient data are to be displayed in the **Patient Search** window.
→ Page B.5–5, *Configuring the patient search*

Status bar

The status bar shows the progression of the search in the **Patient Search** window. Here you can see:

- ❑ which database is being searched,
- ❑ to what extent this database has already been searched (in %),
- ❑ how many patients have already been found.

Accepting patient data

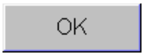
Even after the first patient has been found, the search for further patients in the databases is continued. As soon as a second patient has been found, your system displays the **Patient Search** window with the hit list.

One patient found

If only one patient has been found at the end of the search, his or her personal data are automatically placed in the **Patient Registration** window.

For a preregistered patient, all data previously entered are transferred to the **Patient Registration** window.

More than one patient found



If more than one patient is found, select the patient you require from the search list and transfer that patient's data.

✧ Select the patient in the search list and click on **OK**.

Or

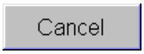
✧ Double-click on the required patient.

The personal data of the selected patient, for preregistered patients all data entered previously, are placed in the **Patient Registration** window.

The **Patient Search** window is closed.

Patient not found

If the hit list does not contain the required patient or if no patient has been found, you might not have entered the name or patient number correctly, or the data of the patient are stored in a database that you have not searched.



✧ Click on **Cancel** if a hit list was displayed without the patient you require.

The **Patient Search** window is closed and you are in the **Patient Registration** window again.

✧ Repeat your search with changed entries and/or extend the search to further databases.

⇨ In **Registration Configuration** you can define which databases to include in the search.
→ Page B.5–5, *Configuring the patient search*

Searching in the Patient Browser

You can also use the **Patient Browser** to search for a patient in the scheduler and local database and in the archive. You can then transfer the data to the **Patient Registration** window. You can simplify your search by filtering and sorting the patient data.
→ Page D.2–6, *Scrolling through and selecting patient data*
→ Page D.2–38, *Calling up additional information about a patient*

✧ First select the database from which you want to transfer the patient data.

✧ Search and select the required patient in the navigation area or in the content area of the **Patient Browser**.

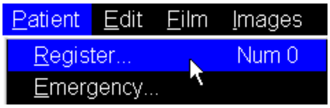
Or

✧ Select the study or studies of the patient that you want to perform or repeat.

Or

✧ Select the series of the patient that you want to perform or repeat.

Transferring data to registration



✧ Call up the **Patient Registration** window with **Patient > Register....**

Or

✧ Click on the icon button on the toolbar.

Or

✧ Drag the selected data into the **Patient Registration** window (**drag & drop**).

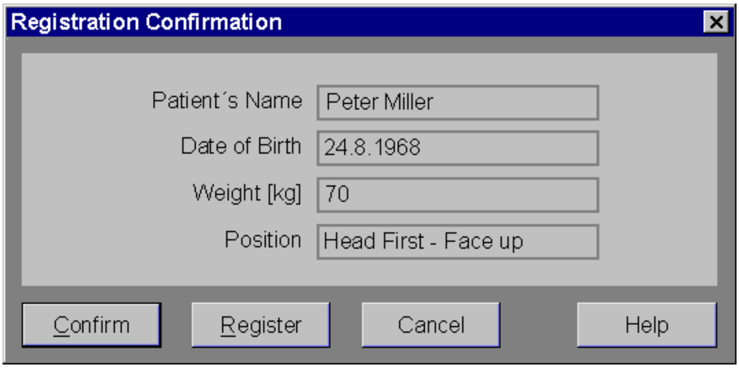
Registering a patient directly

You can also register a preregistered patient for the examination directly if all the data required for the examination have been entered.

✧ To do that, double-click on the procedure or the procedure step in the scheduler.

The data are directly transferred to the examination card.

Once all the data required for registration have been entered, and depending on the configuration, the window **Registration Confirmation** appears in which you must confirm entries such as patient name or date of birth, etc.



Patient´s Name: Peter Miller
Date of Birth: 24.8.1968
Weight [kg]: 70
Position: Head First - Face up

Confirm

✧ Click on **Confirm** if all entries are correct.

The window **Patient Registration** closes and the examination card is displayed.

Or

Register

✧ Click on **Register** if you want to change the patient data.

The **Patient Registration** window appears in which you can make any necessary changes.
→ Page B.4–13, *Completing your entries*

➪ If not all of the fields required for registration are completed, the window **Patient Registration** is called up automatically.

✧ Click on **Cancel** to close the window **Registration Confirmation** automatically without registering the patient.

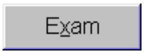
Completing your entries

After you have transferred the patient data you searched for into the **Patient Registration** window, check that it is correct and if necessary add the missing data before registering the patient.

→ Page B.3–9, *Entering admission data*
→ Page B.3–11, *Entering examination data*
→ Page B.3–16, *Entering institution data*

➪ Depending on the configuration of your system, it may only be possible to correct HIS/RIS data partially.

Registering



✧ Click on **Exam** if you want to examine the next patient.

The patient is registered for examination.

The examination data will be transferred to the **Examination** task card and you can begin with the examination.

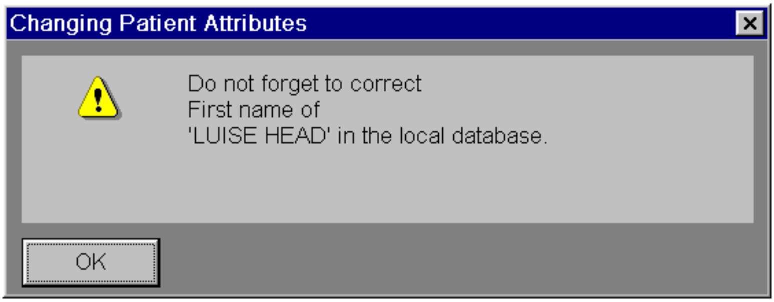
Or

Preregister

✧ Click on **Preregister** to preregister the patient.

Corrected patient data

If you have transferred the patient from the local database and made corrections to that patient’s personal data in the **Patient Registration** window, this message box appears.


Changing Patient Attributes

Do not forget to correct
First name of
'LUISE HEAD' in the local database.

➪ Do not forget to correct the patient data in the original record later on.
→ Page D.4–2, *Correcting patient or examination data*

Searching and registering in the HIS/RIS system

If you cannot find a particular patient in the databases although he or she has been entered in the HIS/RIS system, you can search through the entire HIS/RIS system with a worklist query.

If configured, you can also use this method to access patient data intended for other workstations and modalities.

Calling up a patient worklist query

✧ Enter the patient data that you know in the **Patient Registration** window.

➪ As empty fields are treated like "wildcards", you should complete at least one of the fields so that the search result is better manageable.
You will find information about "wildcards" for a patient search on
→ Page B.4–5, *Wildcards for patient name, ID, physician and ward*.

➪ You cannot use a patient ID entered automatically as a search term.

Starting a search

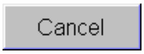
✧ Click on **Get worklist**.

The **Get worklist** button turns into the **Abort** button.

➪ The HIS/RIS system is now searched for patients with the entered data.

Canceling a search

You can cancel a search at any time, e.g. if you have made a mistake entering the name.

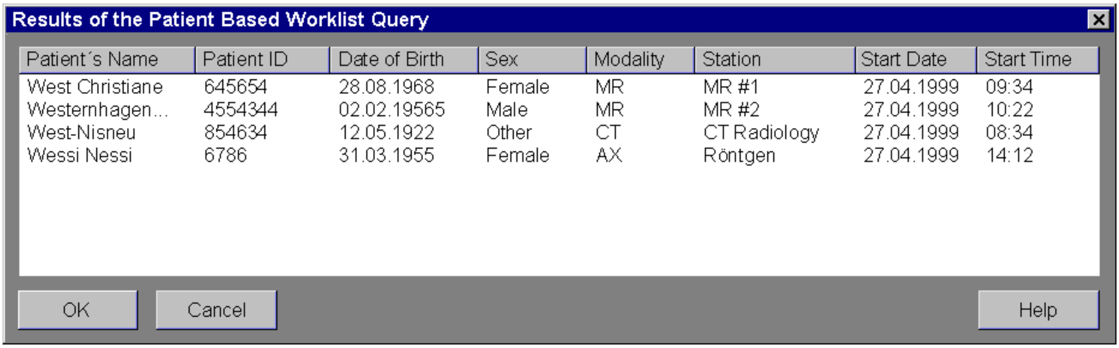


✧ In that case, click on **Cancel**.

The search is canceled without any data being transferred.

Search list of the worklist query

The patient data found in the HIS/RIS system are listed in the window **Results of the Patient Based Worklist Query**. The search list is also displayed if only one patient has been found.

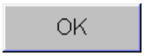


Patient´s Name	Patient ID	Date of Birth	Sex	Modality	Station	Start Date	Start Time
West Christiane	645654	28.08.1968	Female	MR	MR #1	27.04.1999	09:34
Westernhagen...	4554344	02.02.19565	Male	MR	MR #2	27.04.1999	10:22
West-Nisneu	854634	12.05.1922	Other	CT	CT Radiology	27.04.1999	08:34
Wessi Nessi	6786	31.03.1955	Female	AX	Röntgen	27.04.1999	14:12

➪ All the data found for a particular patient is automatically pre-registered in the **Scheduler** for the intended modality.

Accepting patient data

✧ Select a patient from the search list.



✧ Click on **OK**.

Or

✧ Double-click on a patient entry.

➪ You can close the **Results of Patient Based Worklist Query** window with **Cancel**.

The data of the selected patient is transferred to the **Patient Registration** window.

➪ If the fields in the **Patient Registration** window contain the data of another patient, they are overwritten by the data of the new patient.

Patient not found

If you have not found the patient you are looking for, correct your entries, if necessary, and start the search again.

CHAPTER
B.5

Configuring Patient Registration

You can adapt patient registration flexibly to the individual requirements of your examination practice.

You can change the following default settings:

❏ The entries in the selection lists of the **Patient Registration** window.

❏ Selection of the databases that you want to be searched when using the search function and the search procedure and display of the search results.

❏ Worklist settings, if a HIS/RIS system is connected.

✧ Call up the **Configuration Panel** (**Options > Configuration...** in the main menu).

✧ Call up the configuration window for patient registration.

Patient
Registration

➩ In the **Basics** part of this manual you can read how to call up and exit configuration windows, save changes, or reset settings back to the as-delivered state.
→ Chapter A.2, *Configuring the User Interface*

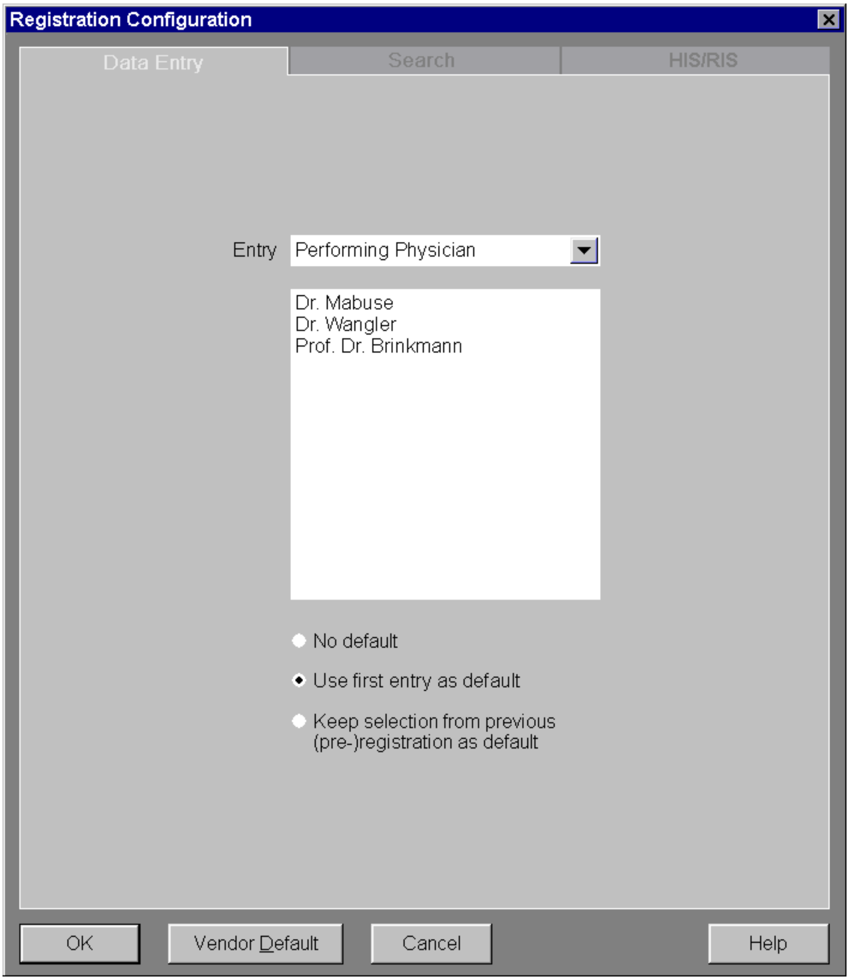
The **Registration Configuration** window is displayed with the cards **Data Entry, Search**, and **HIS/RIS**.

➩ The card **HIS/RIS** is only displayed if your system is connected to the HIS/RIS system and configured and licensed accordingly.

Defining entries in the selection list

You create selection lists in the **Data Entry** tab card. During patient registration, you can then make use of these entries. In this way, you save time during data entry and avoid typing errors.

✧ Click **Data Entry** tab card into the foreground.



Entry: Performing Physician

Dr. Mabuse
Dr. Wangler
Prof. Dr. Brinkmann

○ No default
● Use first entry as default
○ Keep selection from previous (pre-)registration as default

Possible selection lists

You can change and add to the selection lists for the following input fields if these fields are shown on the **Patient Registration** window:

☐ Referring physician
☐ Admitting diagnosis
☐ Ward
☐ Name of the institution
☐ Name of the performing physician
☐ Name of the operator

Creating entries

Each selection list can contain up to 50 entries.


Entry Referring Physician

✧ Select under **Entry** which selection list you want to edit.

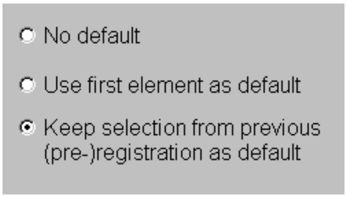

Dr. King

✧ Enter new entries in the text input field and correct or delete the existing entries.

➪ Make sure that the entries which are required most often are as near to the top of the dropdown list as possible.

Default entries

For each selection list you can define whether and which entries are preselected in an input field when you call up patient registration.



○ No default

○ Use first element as default

● Keep selection from previous (pre-)registration as default

✧ Choose one of these three options:

❏ **No default**
When you call up the patient registration the input field is empty.

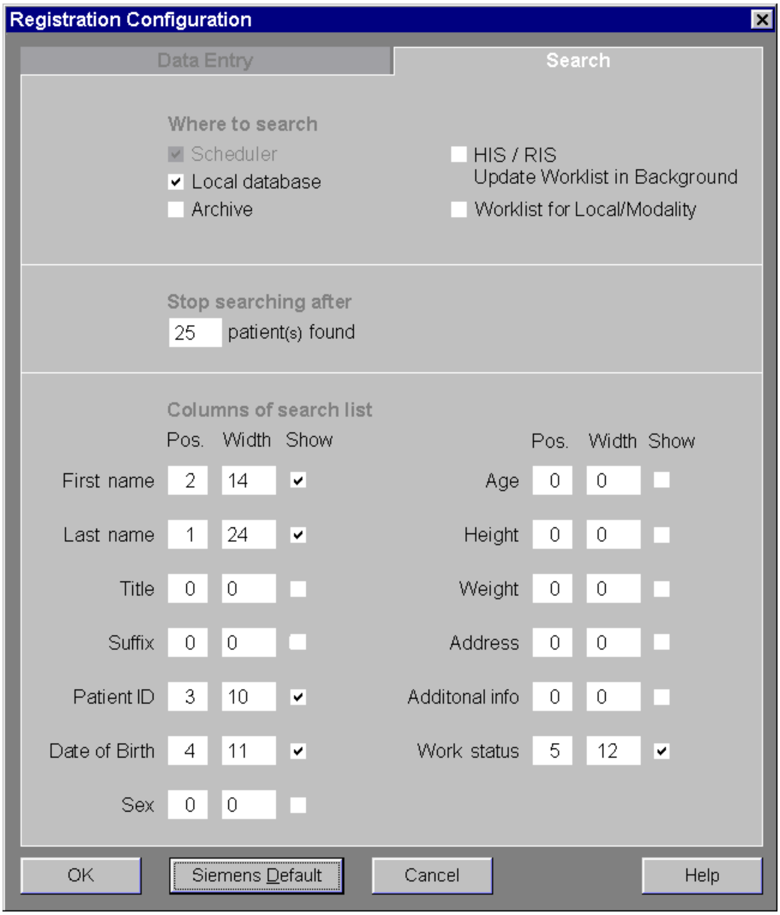
❏ **Use first element as default**
When you call up the patient registration the first entry from the selection list is already in the input field.

❏ **Keep selection from previous (pre-)registration as default**
When you call up the patient registration the entry you selected for the last patient you (pre-)registered is already in the input field.

Configuring the patient search

In the **Search** tab card you can define which databases are to be searched during a patient search, after how many hits the search is terminated, and what information the search list is to contain.

✧ Click the **Search** tab card into the foreground.



Registration Configuration

Where to search

☑ Scheduler
☑ Local database
☐ Archive
☐ HIS / RIS
Update Worklist in Background
☐ Worklist for Local/Modality

Stop searching after

25 patient(s) found

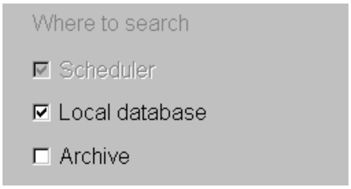
Columns of search list

	Pos.	Width	Show
First name	2	14	☑
Last name	1	24	☑
Title	0	0	☐
Suffix	0	0	☐
Patient ID	3	10	☑
Date of Birth	4	11	☑
Sex	0	0	☐
Age	0	0	☐
Height	0	0	☐
Weight	0	0	☐
Address	0	0	☐
Additonal info	0	0	☐
Work status	5	12	☑

Databases

During a patient search the following databases can be searched:

- ❑ Scheduler
  (contains all preregistered patients)
- ❑ Local database
  (contains all patients who have been examined in the past and whose data have not yet been archived)
- ❑ Local archive
  (contains all patients that are stored on the data media currently inserted)



Where to search

☑ Scheduler

☑ Local database

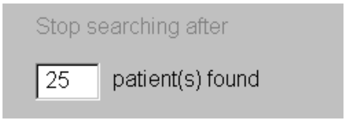
☐ Archive

✧ Select the databases that you want to search during the patient search.

⇨ It is not possible to exclude the scheduler from the search.

Limiting the number of patients found

You can have the search stopped once a certain number of patients have been found.



Stop searching after

25 patient(s) found

✧ Enter after how many hits you want the patient search to be abandoned.

Display of the search list

Here you can select which data items of the patients found will be listed in the **Patient Search** window and how the display is to appear.
You can have the following information displayed:

- Personal data
  You can have some or all of the information that you have entered in the **PATIENT** area displayed in the search list.
- Admission data
  Information about the referring physician and ward from area **HOSPITAL**.
- Information about hospital/practice
  The name of the hospital/practice that you have entered in area **INSTITUTION**.
- Location
  The network node where the data of the patient displayed in the search list are stored.


Pos.
2

✧ Enter the column of the search list in which the information is to be entered.


Width
14

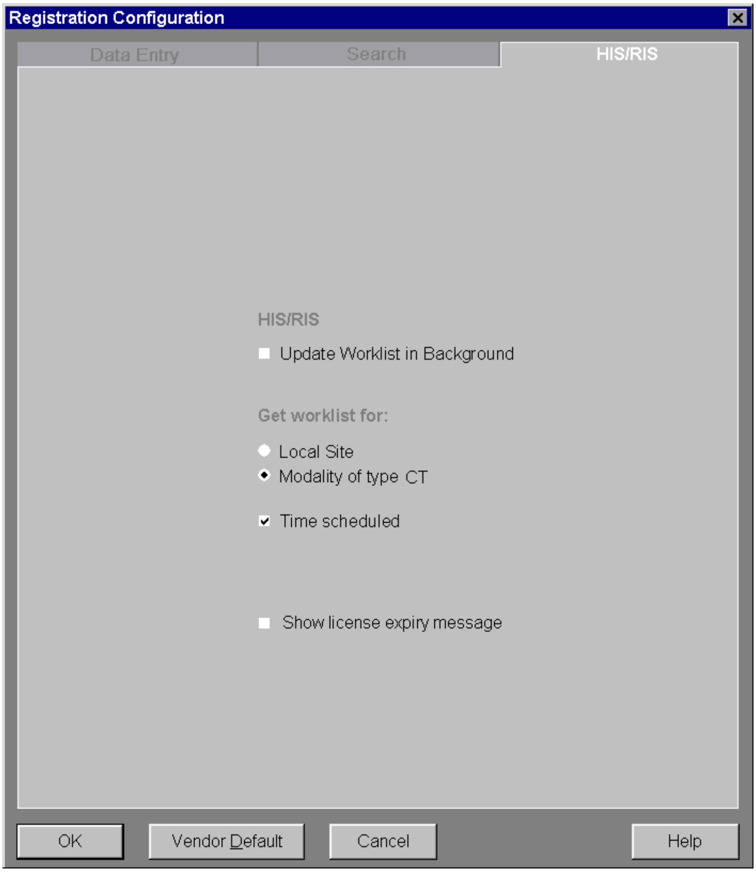
✧ Enter the column width (number of characters).


Show
☑

✧ Click the information that you want to display.

Configuring the HIS/RIS system

If your system is connected to an HIS/RIS system (hospital or radiology information system), you can also select the HIS/RIS card.



HIS/RIS

☐ Update Worklist in Background

Get worklist for:

○ Local Site
● Modality of type CT

☑ Time scheduled

☐ Show license expiry message

HIS/RIS query

With the HIS/RIS system, you can regularly update the scheduler with new patient data from registration. This process is triggered automatically at regular intervals if you activate it.

☑ HIS / RIS
Update Worklist in Background

✧ Click on the check box to have your system initiate a HIS/RIS query at regular intervals.
→ Page B.1–2, *HIS/RIS query*
→ Page D.2–4, *Updating the scheduler*

⇨ If your system is equipped with a main and a satellite console you should start the HIS/RIS query from only *one* console. This console must then be connected directly to the hospital network.

Selecting a worklist

Generally, your system only queries the patient data intended for your workstation. However, you can also call up data that are intended for other workstations of the same modality in the HIS/RIS system.

☑ Worklist for Local/Modality

✧ Click on the option field **Local Site** to query all the data intended for your workstation.

Or

✧ Click on the option field **Modality of type...** (in this case **CT**), if configured.

The system queries all the patient data of your institute intended for all the workstations of the modality in question.

Defining the scope of the worklist

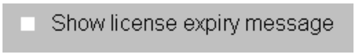
You can limit the extent of the worklist to a defined time range.

✧ Click on the control box to narrow down the worklist, for example, to the patient entries for the current day only.
→ Page B.4–3, *Defining the worklist time range*

➪ You can only define the scope of the worklist in the manual HIS/RIS query.

Display expiry date of license

The use of the worklist for the management of your patients is subject to a restricted license which you must renew in good time before the expiry date.



☐ Show license expiry message

✧ Click on the control box if you want a message to appear as of 30 days before expiry of the license for the use of the worklist.

License expired

The license for worklist expires in 8 days.

☐ Don't show this message again.

PART

C Examination

C.1 Introduction

C.2 Preparing for an Examination

C.3 *Topogram / Planning Ranges*

C.4 *Control Scan*

C.5 *Spiral*

C.6 *Sequence*

C.7 *HeartView CT (Option)*

C.8 *CARE Bolus (Option)*

C.9 *CARE Vision CT (Option)*

C.10 *Reconstruction*

C.11 *Image Processing and Evaluation*

C.12 *Scan Management*

C.13 *Configuring Examinations*

CHAPTER
C.1 Introduction

After you have registered a patient for examination, position him or her in the planned position on the examination table, if necessary, using the appropriate positioning aids.
’ SOMATOM Operator Manual, chapter C.3, *Positioning the Patient*

After that, perform the examination from the console in the control room. While doing this, you are working on the **Examination** task card with which you can control and monitor all examination operations.

During the examination, you observe the patient through the observation window in the control room. Using the intercom system that you operate via the control box, you can hear the patient at all times and give him or her instructions.

On the following pages, you will find a short overview of the **Examination** task card and its operating elements. The chapters after that then guide you step by step through an examination from the examination preparations to configuration of your system.

Examination procedure

Your SOMATOM is a system which is optimized for clinical operation. Routine examinations are largely automated:

Preparing for an examination

Before scanning, check whether the data about the planned examination has been entered correctly and correct this, if necessary. At this time, you also define the procedure of individual examination steps.

Obtaining a topogram

The first scan that you perform will generally be a topogram. You define the examination range in the topogram.

Performing a control scan

You use a control scan to check whether the examination range is correct. You can also define the field of view again in such a way that the subsequent tomograms “fit”.

Spiral scan or sequence scan

As part of the actual examination, you will perform one or more measurements over the set range. Depending on the diagnostic problem and the examination region, you will use either spiral technique or sequence technique.

Reconstruction and image evaluation

Tomograms are calculated (reconstructed) from the collected raw data and stored. You can already postprocess and evaluate this image material during the examination.

Ending the examination

If you have obtained all the images required for the diagnostic problem, end the examination and release the patient. You can then register the next patient for examination or use other applications to evaluate the examination results.

Examination task card

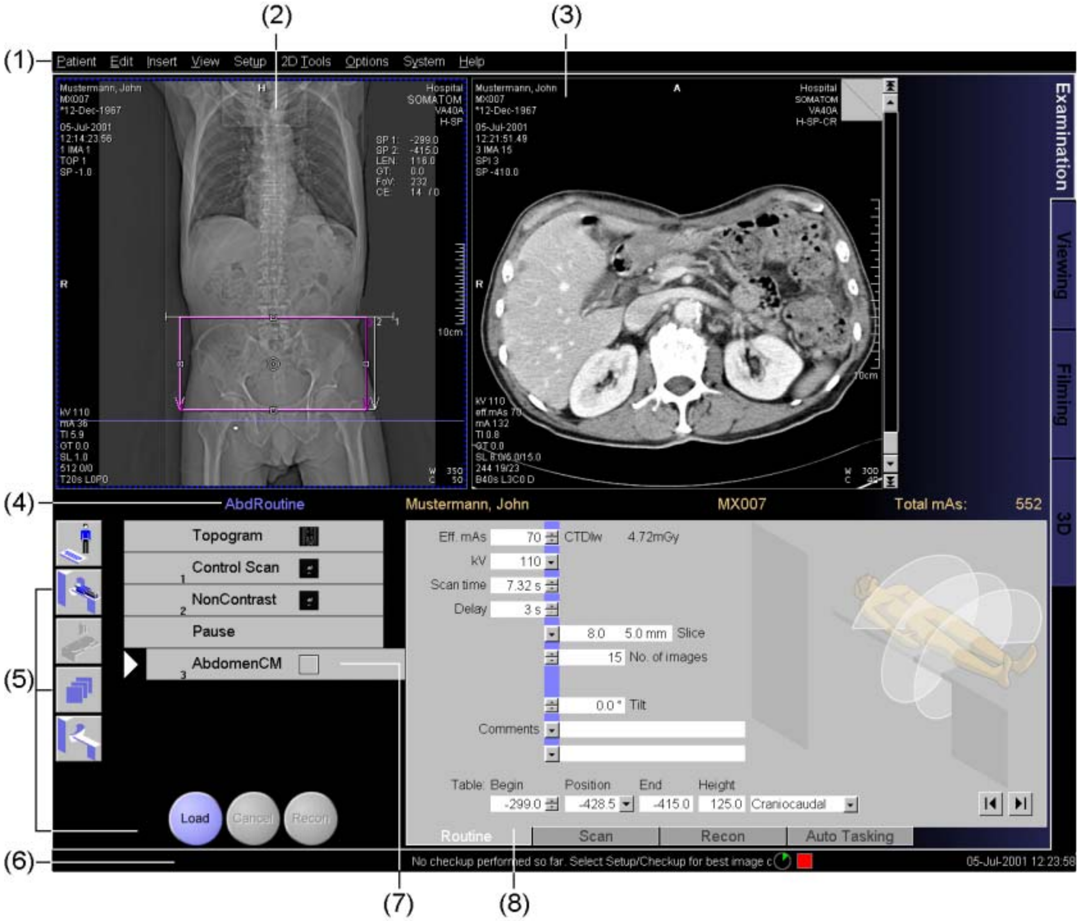
As soon as you have registered a patient for examination, the **Examination** task card moves into the foreground. This is the card on which you perform examinations.

If you have switched to the **Viewing** card in the meantime, you can return to the **Examination** card by clicking on its tab and continue your work there.

✧ Click on the tab to call up the **Examination** task card.

On the **Examination** card, you will see the following elements and areas:

(1) Main menu bar
(2) Topo segment
(3) Tomo segment
(4) Title bar
(5) Buttons for controlling the examination
(6) Status bar
(7) Chronicle
(8) Subtask cards



Mustermann, John MX007 Total mAs: 552

Eff. mAs 70 CTDIw 4.72mGy

kV 110

Scan time 7.32 s

Delay 3 s

8.0 5.0 mm Slice

15 No. of images

0.0 ° Tilt

Comments

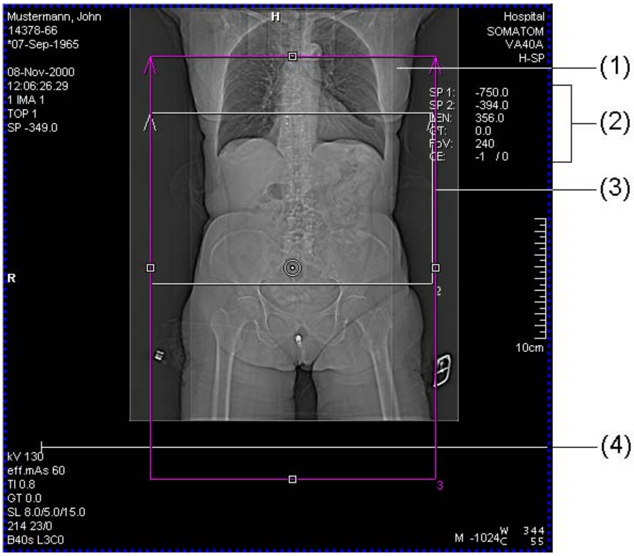
Table: Begin -299.0 Position -428.5 End -415.0 Height 125.0 Craniocaudal

No checkup performed so far. Select Setup/Checkup for best image c

05-Jul-2001 12:23:58

The topo segment

You usually begin your examination with a topogram scan. The topogram is always displayed in the top left quadrant of the **Examination** task card, the topo segment. This is where you define the ranges for your scans graphically.



Mustermann, John
14378-66
*07-Sep-1965

08-Nov-2000
12:06:26.29
1 IMA 1
TOP 1
SP -349.0

Hospital
SOMATOM
VA40A
H-SP

SP 1: -750.0
SP 2: -394.0
LEN: 356.0
CT: 0.0
FoV: 240
CE: -1 / 0

kV 130
eff.mAs 60
TI 0.8
GT 0.0
SL 8.0/5.0/15.0
214 23/0
B40s L3C0

M -1024 W 344 C 55

(1) Topogram
(2) Data about the range
(3) Range
(4) Current table position

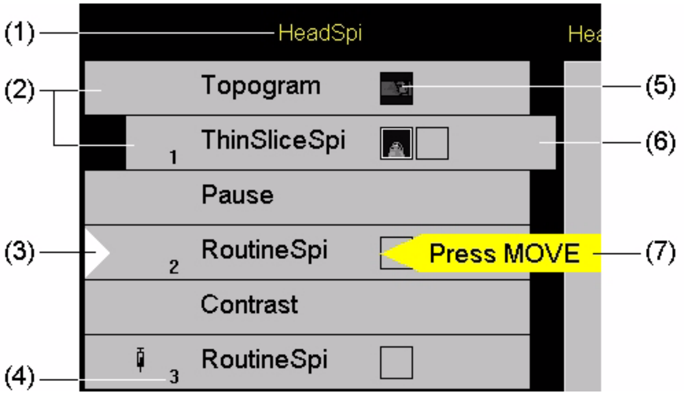
The tomo segment

The tomographic images are displayed in the tomo segment (top right quadrant) of the **Examination** card. Here, you can scroll through your scans, plan the reconstruction of new images, and use graphic tools for a first evaluation of the examination results.

(1) Dog ears for scrolling
(2) Scroll bar
(3) Image text information
(4) Reconstruction target

The chronicle

During patient registration, you decide which examination to perform. You will then find the individual examination steps of the selected scan protocol listed in the chronicle one after the other.



(1) Designation of the examination (scan protocol name)
(2) Examination steps of the scan protocol
(3) Next examination step (marked by a triangle)
(4) Number of a scan range
(5) Recon icon
(6) Selected examination step (corresponds to the subtask cards)
(7) Prompt to take action

Scan series

Your system processes the data of a scan to form a set of tomographic images (tomograms). You can obtain further sets of tomographic images with every new image reconstruction. In the chronicle, an icon is displayed with a miniature tomogram (thumbnail image) to the right of the name of the examination step.
→ Page C.1–10, *Status of the examination*

Each set of tomograms is stored and managed in the database as a (scan) **series** under the name listed in the chronicle.

➪ A series can also consist of an individual scan only, e.g. a topogram, control scan or raw data.

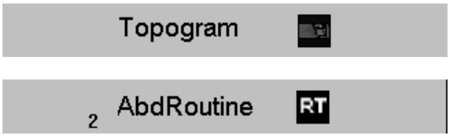
Selected series

You can see that an examination step is selected in the chronicle by the fact that the entry is shifted to the right. All information and settings of the subtask cards always refer to this selected examination step.

To select an examination step in the chronicle just click on the entry.

Status of the examination

The scan protocol is listed in the chronicle in chronological order and executed from top to bottom during the examination. By the entries, you can immediately see which scans have already been performed and which are pending:



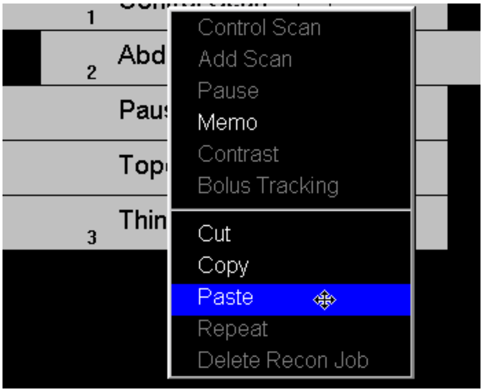
- A scan that contains at least one recon icon with a thumbnail image has already been performed.

- The next series to be scanned is marked by a triangle on the left-hand border of the chronicle.

- All other planned scans have only **empty** recon icons just like the next series to be scanned.

Popup menu

In the chronicle, you can change the procedure of an examination. You use the entries of the main menu or call up a popup menu with the right mouse key to modify examination steps or insert new steps.

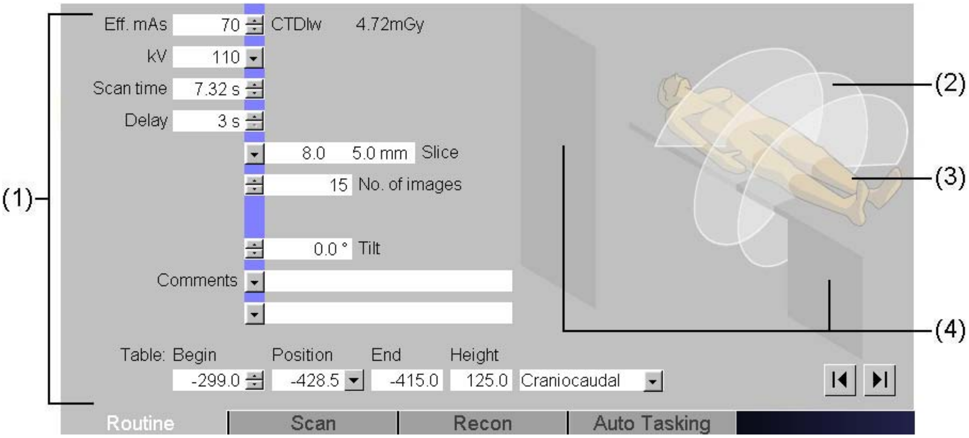


The subtask cards

Your system performs the scans with certain settings that you can view and change on the subtask cards. When you select a scan series in the chronicle, the associated parameter settings are displayed on the subtask cards.

Routine subtask card

For many examinations, it is enough to work with the **Routine** subtask card, because it contains all the important scan settings. A diagram (graphic patient model) is displayed for each examination step by which you can see the patient position and scanning mode set.



Eff. mAs 70
CTDIw 4.72mGy
kV 110
Scan time 7.32 s
Delay 3 s
8.0 5.0 mm Slice
15 No. of images
0.0 ° Tilt
Comments
Table: Begin -299.0 Position -428.5 End -415.0 Height 125.0 Craniocaudal

(1) Settings for scanning
(2) Scanning mode (here: spiral)
(3) Patient position (here: head first, supine)
(4) Model of the gantry and table top

If you want to change settings that are not listed on the **Routine** card, use the other subtask cards to adapt the examination specially to your requirements:

Scan subtask card

All parameters that your system will use for scanning are listed on the **Scan** subtask card.

Recon subtask card

The images are calculated from the raw data using the reconstruction parameters that are set on the **Recon** subtask card.

Auto Tasking subtask card

Use the subtask card **Auto Tasking** to film automatically images or transfer them to other applications (e.g. for further processing) and for billing purposes (MPPS).

Routine subtask card

A contrast agent pause is included in the chronicle for examinations with contrast agent. The **Routine** subtask card is displayed with additional information for contrast agent administration for this entry.

Trigger subtask card

The conditions for automatic start of spiral or sequence acquisition are defined on the **Trigger** subtask card for the optional examinations **CARE Bolus** and **HeartView CT**.

Graphic selection and editing

During your examination, you will often have to edit graphics: to delimit the region that you want to examine in the topogram and to draw fields of view in the tomograms for image reconstruction. To do this you will work with the mouse in the topo or tomo segment. On the following pages, you will find a brief explanation of the basic steps involved in graphic editing.

Graphic objects

On the **Examination** task card, you will work with cutlines and ranges in the topo segments and with fields of view in the tomo segment. These are drawn as a line or box, which are both graphic objects.

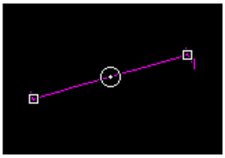
Center point

You can recognize a graphic object by the fact that a center point is shown in its center when it is selected.

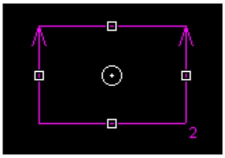
Grab handles

To edit a graphic object, you can also use the grab handles at the end of a line or on the sides of a box.

(1)



(2)



(1) Line with center point and grab handles
(2) Box with center point and grab handles

Editing graphic objects

You can enlarge, reduce, tilt (only in topograms), and move the graphic objects drawn in the topo or tomo segment in order to edit the corresponding range or field of view.

Selecting a graphic object

You must first select the graphic object that you want to edit in the topo or tomo segment.

✧ Click on the graphic object with the mouse.

The grab handles of the object are displayed.

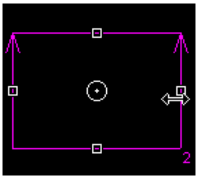
✧ Click on another graphic object.
The grab handles of the graphic object previously selected are shown again.

Resizing

↕ ↔

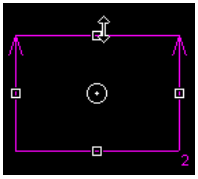
✧ Move the mouse cursor onto a grab handle to change the size of a graphic object.

The mouse cursor changes shape.



✧ Drag the handle inward (toward the center point) holding the left mouse key down to reduce the graphic object.

Or

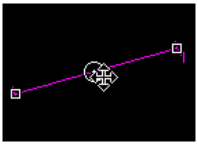


✧ Drag the handle outward (away from the center point) holding the left mouse key down to enlarge the graphic object.

Repositioning

✧ Move the mouse cursor onto the center point of a graphic object to move it.

The mouse cursor changes shape.

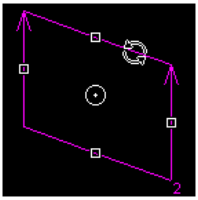


✧ Drag the graphic object to the required new position holding the left mouse key down.

Inclining (tilting)

✧ Move the mouse cursor onto one of the horizontal border lines of the graphic object to tilt it.

The mouse cursor changes shape.



✧ Drag the line up (or down) holding the left mouse key down to tilt the graphic object.

➩ It is only possible to tilt graphic objects in **lateral topograms**.

Using the intercom system

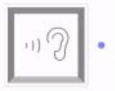
You use the intercom system to communicate with the patient in the examination room. You operate the intercom system on the control box.

Talking to the patient

✧ Press the **Call Patient** key on the control box and hold it pressed while talking to the patient.

➪ While you are holding the **Call Patient** key pressed, the loudspeaker in the control room is muted. You cannot hear the patient.

Listening to the patient



✧ Press the **Hear Patient** key to listen to what the patient is saying.

The loudspeaker in the control room is now permanently activated and reproduces all sounds entering the microphones in the examination room. This function is indicated by a green LED.

✧ Click on the **Hear Patient** key again if you want to mute the loudspeaker again.

Setting the intercom system

You usually only adapt the volume and noise suppression of your intercom system to the local conditions once in the **API / Comment Setup** dialog box.
→ Page C.13–8, *Setting the intercom system*

CHAPTER
C.2

Preparing for an Examination

Before you start an examination, you must make several preparations on the console in the control room.

For routine examinations, these preparations are usually limited to checking and possibly adding to the data which you have already entered during patient registration.

For examinations that differ from normal routine, you can adapt the examination procedure defined in a routine scan protocol to your individual requirements.

Selecting an examination

Usually, you will tell the system what examination you want to perform during patient registration by selecting a routine scan protocol.

A scan protocol is used to plan an examination. All the individual steps of the examination and the sequence in which they are performed are defined in it.

A variety of routine protocols for standard examinations are stored on your system and you can access them. That saves time and the suggestions of these scan protocols are suitable for most routine examinations.

If the data about the pending examination was only entered incompletely or incorrectly during registration, you can add to this or correct this now.

NOTE

Special scan protocols with a lower radiation dose and other settings for image calculation have been created for examinations of children.

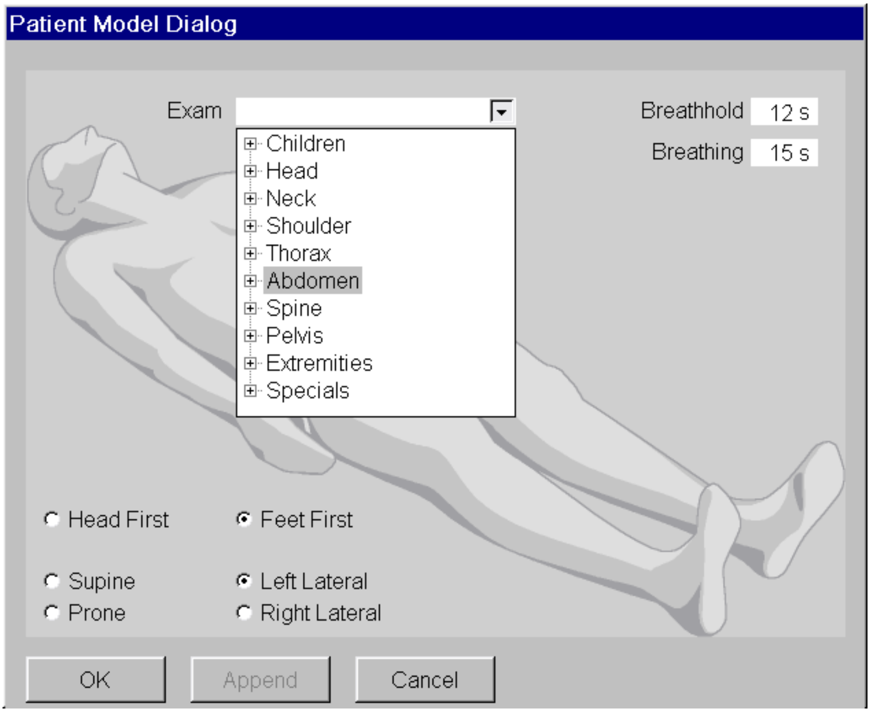
Make sure that you have selected one of these scan protocols and not a protocol for adults if you are examining a child. (e. g. *ChildHead* instead of *HeadSpi*)

➪ You can change the procedure for routine scan protocols individually for the ensuing examination. However, these changes **only** apply to the current examination.
→ Page C.2–23, *Adapting routine scan protocols*

Selecting a scan protocol

If you have not selected an examination region, a patient position and method for the examination during patient registration, the **Patient Model Dialog** dialog box is opened automatically.

Patient Model Dialog



Patient Model Dialog

Exam

- ⊞ Children
- ⊞ Head
- ⊞ Neck
- ⊞ Shoulder
- ⊞ Thorax
- ⊞ Abdomen
- ⊞ Spine
- ⊞ Pelvis
- ⊞ Extremities
- ⊞ Specials

Breathhold 12 s

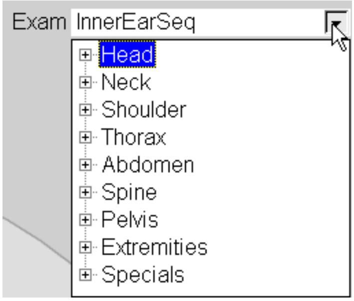
Breathing 15 s

○ Head First ● Feet First

○ Supine ● Left Lateral

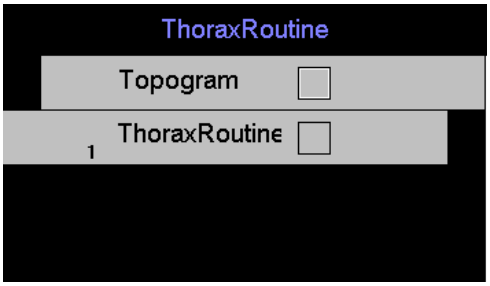
○ Prone ○ Right Lateral

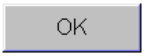
Selecting an examination



- Click on the arrow next to the **Exam** text field in the **Patient Model Dialog** dialog box.
  A list of the examination regions is opened up.
- Click on the ⊞ symbol in front of the entry to display all routine scan protocols for this examination region.
  (Click on the ⊟ symbol to hide this list again.)
- Click on the scan protocol you require.

As soon as you have selected a scan protocol, the corresponding examination is displayed in the chronicle with its individual steps.



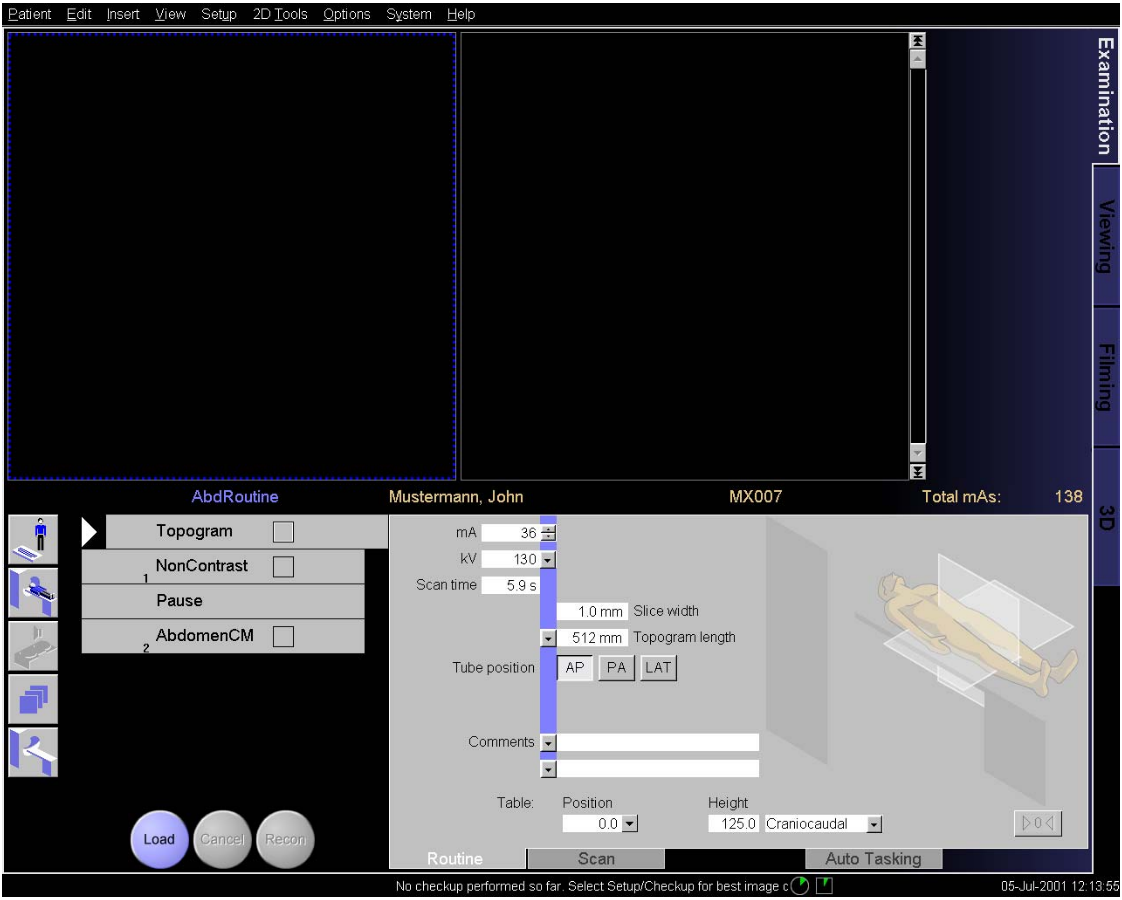


- Click on **OK** to confirm your choice and close the **Patient Model Dialog** dialog box.

Selecting a different scan protocol

If you have already entered an examination when you called up the **Examination** card, the **Patient Model Dialog** dialog box is not displayed.

Instead you can see the individual steps of the scan protocol which you decided on during registration in the chronicle. You can begin with this examination immediately.



AbdRoutine Mustermann, John MX007 Total mAs: 138

mA 36
kV 130
Scan time 5.9 s
1.0 mm Slice width
512 mm Topogram length
Tube position AP PA LAT
Comments
Table: Position 0.0 Height 125.0 Craniocaudal

No checkup performed so far. Select Setup/Checkup for best image c

05-Jul-2001 12:13:55

If the examination region and method were not selected correctly during registration, you can subsequently change this.

✧ Click on the **Exam** button to open the **Patient Model Dialog** dialog box.

Changing the examination region and method

✧ Select a new routine scan protocol from the selection list.
→ Page C.2–4, *Selecting a scan protocol*

OK

✧ Click on **OK** to confirm the changes to the scan protocol.

The new scan protocol is now shown in the chronicle instead of the protocol selected during registration.

Appending a scan protocol

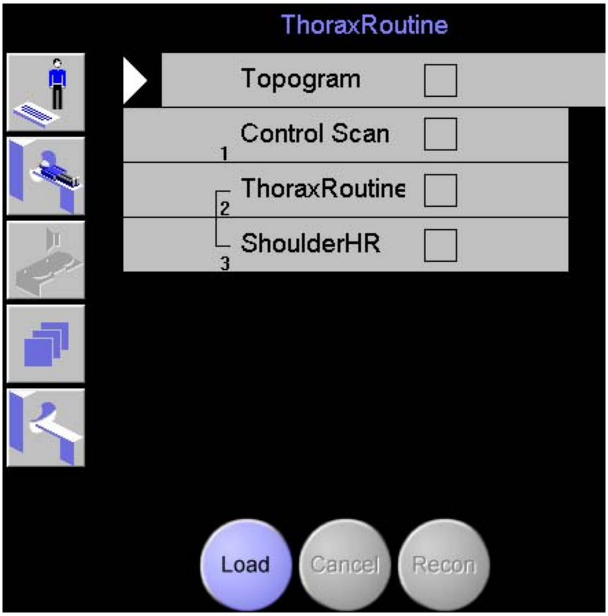
Sometimes, you will have to perform a series of more than one examination on a patient during one session.

✧ Click on the **Exam** button to open the **Patient Model Dialog** dialog box.
→ Page C.2–4, *Patient Model Dialog*

Append

✧ Select a scan protocol and click on the **Append** button.

All the steps of the second examination are now appended to the first scan protocol in the chronicle.



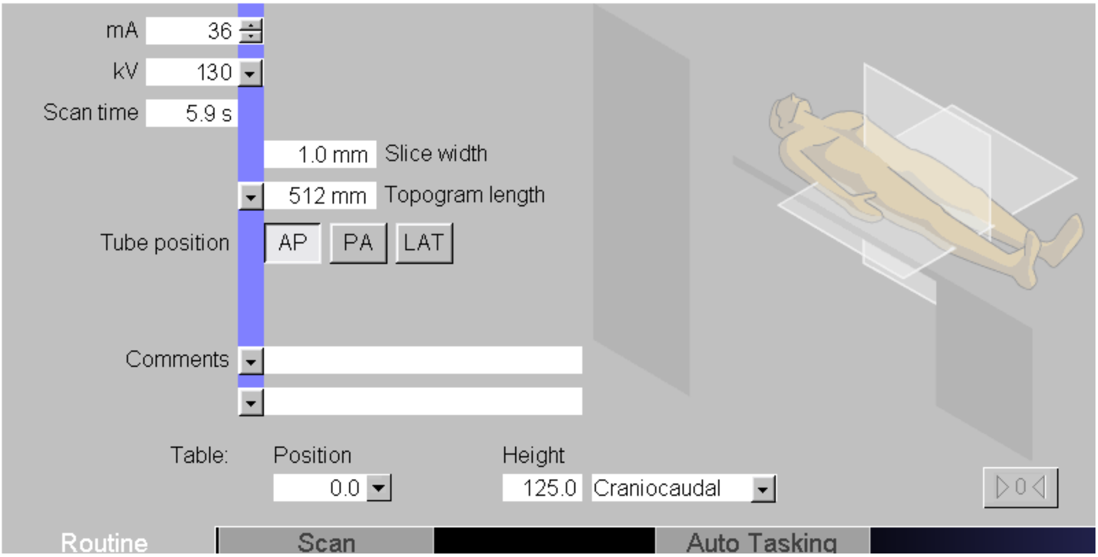
The **Patient Model Dialog** dialog box is closed.

✧ Open the **Patient Model Dialog** again if necessary to append further scan protocols to your examination list.

➩ If you do not want to perform all the individual steps of this chain of routine scan protocols, you can remove individual scans from the chronicle.
→ Page C.2–23, *Adapting routine scan protocols*

Changing the patient position

After you have called up **Examination** you can see a diagram of the patient on the **Routine** card shown in the position that you stated during registration (e. g. *head first*, *supine*).



mA 36

kV 130

Scan time 5.9 s

1.0 mm Slice width

512 mm Topogram length

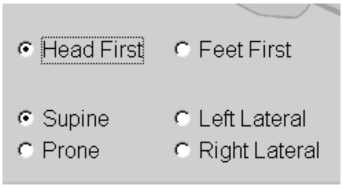
Tube position AP PA LAT

Comments

Table: Position 0.0 Height 125.0 Craniocaudal

If you entered the patient position incorrectly during registration or have had to reposition the patient before beginning the examination, you can now change the patient position.

✧ Click on the **Exam** button to open the **Patient Model Dialog** dialog box.
→ Page C.2–4, *Patient Model Dialog*



● Head First ○ Feet First

● Supine ○ Left Lateral
○ Prone ○ Right Lateral

✧ Select the correct patient position using the radio buttons and confirm with **OK**.

➩ If you have already started the first scan of the examination (e.g. the topogram scan) and want to reposition the patient, end the current examination and register the patient again.

Automatic functions

Your system provides several automatic functions to ensure that scanning is performed quickly and comfortably:

- Automatic processing of consecutive spiral and sequence acquisitions (**Auto Range**).
  → Page C.2–28, *Processing auto range*
- Full reconstruction of the images in parallel with the examination (spiral: Metro Recon).
- Real time reconstruction of the images with reduced image quality, simultaneous with scanning (**RTD**). This automatic function is activated for spiral scans (alternative for Metro Recon).
- Full quality reconstruction of an overview image at the end of the spiral range after scanning (**Last Image Display**).
- Automatic patient instruction system (**API**)
- Automatic loading of all images into the **Viewing** task card.
- Automatic forwarding of images to the **Filming** task card parallel with reconstruction (**Auto filming**).
  → Page C.2–19, *Automatic Filming*
- Automatic archiving and sending of all images after the examination has been finished.
  This function can be activated in the **Transfer Configuration** window and on the **Auto Tasking** subtask card.

Reconstruction parallel with examination

Spiral scans can be reconstructed both parallel with scanning with full image quality (Metro Recon) or at the end of the examination range of the spiral (replay of last image). As an option, RTD provides real-time displays with almost complete image quality.

Metro Recon is set as default reconstruction mode. You can change this setting by switching the **Metro Recon** button.

✧ Leave **Metro Recon** deactivated to reconstruct your spiral scan with full image quality but delayed to scanning.

Or

✧ Click on the **Metro Recon** button to activate Last Image Display (only if RTD is not available).

➪ A tomogram with full image quality is reconstructed and displayed at the end of the examination range of the spiral.

Or

✧ Click on the **Metro Recon** button to activate RTD and reconstruct images synchronously with scanning (RTD available).

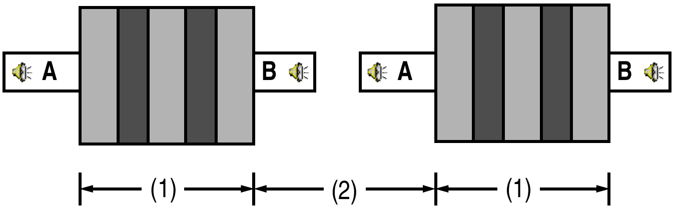
Automatic patient instruction

In many examinations, it is important to give the patient instructions on breathing during the scan. The automatic patient instruction system (**API**) synchronizes these instructions with the scanning procedure.

Each instruction consists of two texts:

❑ Text A is played back before a scan
(e.g. “Breathe in - Hold your breath”)

❑ Text B is played back after a scan
(e.g. “Breathe normally again”)

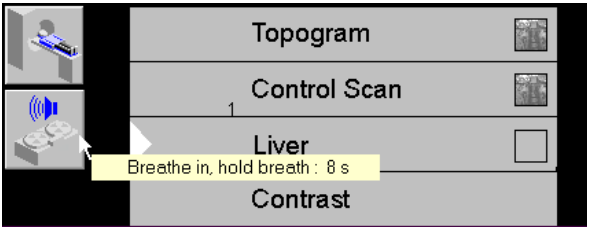


(1) During the scan, the patient holds his or her breath (**Breathhold time**)

(2) During the scan interruption, the patient continues to breathe (**Breathing time**)

Checking a preset API

It is useful to use the automatic patient instruction system (**API**) for a whole range of routine scan protocols. A pair of announcement texts is preselected for each of these scan protocols.



Breathe in, hold breath : 8 s

✧ Move the mouse cursor onto the **API** button to check which pair of announcement texts is preselected. A short designation of the API currently set is displayed.

➪ On the **Scan** subtask card, you can select from among different pairs of announcement texts.
→ Page C.5–57, *Selecting an API text*

Activating API

The automatic patient instruction is active if an announcement text is selected and the **API** button is pressed.

✧ Click on the **API** button.
The button is then shown white.

The patient will now hear text A before the scan. After the scan has been completed or has been interrupted, the patient will hear text B.

➪ If you do not want to use the **API** for all measurements, you can deactivate it and reactivate it again later during the examination. You cannot activate the **API** during scans that have already begun.

Deactivating API

✧ Click on the **API** button again to deactivate the automatic patient instruction.
The button then appears gray.

Entering a breathholding time

Your system takes the breathholding time as a basis for examinations with an automatic breathholding command, e.g. for planning spiral lengths and sequence scan clusters.

When examining a patient who is short of breath, reduce the breathholding time in the **Patient Model Dialog** dialog box.

✧ Click on the **Exam** button to open the **Patient Model Dialog** dialog box.
→ Page C.2–4, *Patient Model Dialog*

Breathhold 12 s

✧ Enter a shorter breathholding time (in seconds).

⇨ The **Breathhold** input field is only evaluated if you have applied the automatic patient instruction system (**API**) for the current examination.
→ Page C.2–12, *Automatic functions*

⇨ If you want to perform a sequence examination with an automatic breathholding command, during which only **one** scan is performed per breathholding phase, enter **1 second** for the breathholding time.

Entering a breathing time

Breathing 15 s

The breathing time is the duration time the patient can use to breath out and in again during the examination.

✧ Enter a longer breathing time (in seconds) if necessary.

➩ The **Breathing** input field is only evaluated if you have applied the automatic patient instruction system (**API**) for the current examination.

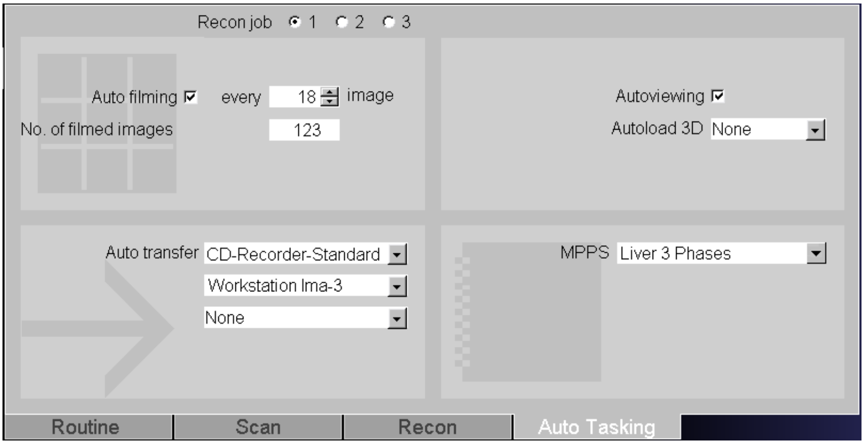
Automatic image transfer

On the **Auto Tasking** subtask card you can define which images and data are automatically transferred to other applications.

In the Chronicle you can select the examination steps for automatic image transfer one after the other. On the Auto Tasking card you can determine which actions are to be started automatically for each Recon job.

✧ Click on the examination step in the Chronicle for which you want to set automatic image transfer.

✧ Click the **Auto Tasking** card into the foreground.



Recon job ● 1 ○ 2 ○ 3

Auto filming ☑ every 18 image

No. of filmed images 123

Autoviewing ☑

Autoload 3D None

Auto transfer CD-Recorder-Standard

Workstation Ima-3

None

MPPS Liver 3 Phases

Recon job

Recon job ● 1 ○ 2 ○ 3

✧ Click on the radio button for the reconstruction job for which you want to define automatic functions.

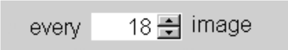
Automatic Filming

Depending on your examination plan it could be useful to provide image material on film or paper for reporting as quickly as possible. With Automatic Filming, the reconstructed images are automatically transferred to the virtual film sheet.

Auto filming ☑

✧ Click on the **Auto filming** checkbox to activate automatic filming.

➪ If **Automatic exposure** is activated on the **Filming** task card, the images are automatically exposed after transfer to film.



every 18 image

✧ In the spinbox you can define whether every nth image or all images (n = 1) of the examination are to be transferred to the Filming task card.

The number of images to be filmed is output.

No. of filmed images 123

➪ If you want to deactivate **Automatic filming**, click on the **Auto filming** checkbox again.

Automatic loading into Viewing

With **Autoviewing** you can transfer the images of the selected reconstruction job to the **Viewing** task card (exception: in biopsy mode and in CAREVision mode, the images are always transferred). You can then switch directly to the **Viewing** task card and perform a detailed 2D evaluation with the images of the current examination.
→ Part E, *Viewer*

➪ Tomograms calculated with reduced image quality (RT images for spiral) are not transferred.

✧ To activate automatic loading into the **Viewing** task card, click into the **Autoviewing** checkbox.

The function is marked with a checkmark.

➪ If you want to deactivate automatic loading into the **Viewing** task card, click on the **Autoviewing** checkbox again.

Automatic loading in 3D

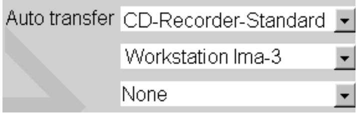
With **Autoload 3D** you can transfer the images of the reconstruction job to the **3D** task card automatically.

✧ Select the required display mode for **3D** from the list.

The images are transferred to the 3D subtask card in the selected output type.

➪ If you want to deactivate automatic loading into 3D, select "None" from the selection list.

Auto transfer



With the selection lists of **Auto transfer** you define to which databases or data media images of a recon job are to be sent automatically.

✧ Select the addresses required for data transfer from the selection lists.

The image data are automatically stored on the selected data media or sent to the network node after reconstruction.

➪ To deactivate one or all functions of Auto transfer, select "None" in the relevant list.

MPPS

On patient registration your system creates a performance report in which the steps performed during the examination (Modality Performed Procedure Step = MPPS) are entered
→ Chapter D.5, *Maintaining your Data*

Each series (that is, recon job performed) is assigned an MPPS description that matches the name of the scan protocol used. If you have changed the scan protocol selected during registration for the examination, you can adapt the MPPS description for each recon job accordingly.

MPPS Liver 3 Phases

✧ Select the required MPPS description.

Or

MPPS New entry

✧ Select *"New entry"* and enter an appropriate MPPS description.

Or

MPPS None

✧ Enter "*None*" if you do not want to place the recon job in question in the performance report.

➩ If the MPPS list has been expanded for a recon job and the change has been accepted by the system, the new entry becomes available for all recon jobs.

NOTE

If a reconstruction has been completed, you cannot assign any other MPPS description to this recon job.

Adapting routine scan protocols

If the suggestions of the routine scan protocols are not adequate for the planned examination, select a scan protocol that meets your requirements as nearly as possible. Then modify the examination in this protocol in the Chronicle on the **Examination** task card.

If you also want to make scan protocols you have changed available for subsequent examinations, store them.
→ Chapter C.13, *Configuring Examinations*

Adding examinations steps

You can expand the routine scan protocols by additional examinations steps:

❑ Control scans, pauses, contrast agent pauses, and comments you can insert using the pop-up menu (right mouse key) of the Chronicle. Or you can use **Edit** and **Paste** in the main menu of the **Examination** task card.

❑ You can insert additional examinations by concatenating several routine protocols. After that you can move the examination steps and delete steps that you do not require.

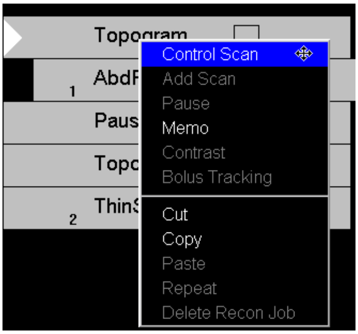
❑ You can insert an additional scan after the last scanned range using **Add Scan** from the menu. An additional scan can be inserted after a sequence range with table feed or alter a spiral scan.
→ Page C.6–40, *Performing additional scans*

❑ Use **Copy** and **Paste** or **Repeat** to repeat examination steps of a scan protocol.
→ Page C.2–30, *Moving, copying, deleting, renaming examination steps*

➪ You cannot insert another examination step in front of an examination step that has already been completed.

Inserting a control scan

Before you begin scanning a spiral or sequence, it is useful to check the position of the scan range and the field of view by means of a single scan.



✧ Place the mouse cursor at the step of your routine scan protocol **before** which you want to insert a control scan.

✧ Call up the popup menu of the chronicle (right mouse key), and click on **Control Scan** with the left mouse key.

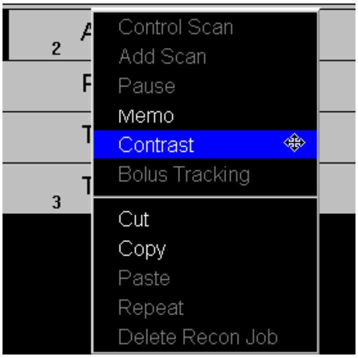
Or

✧ Select the entry in the chronicle and call up **Insert > Control Scan** in the main menu.

Now a control scan is included in the chronicle.

Inserting a contrast-medium pause

A contrast-medium pause allows you to inject contrast medium before scanning a spiral or sequence.



- Place the mouse cursor at the first range from which you want to scan with contrast medium.
- Call up the popup menu of the chronicle and click on **Contrast**.

Or

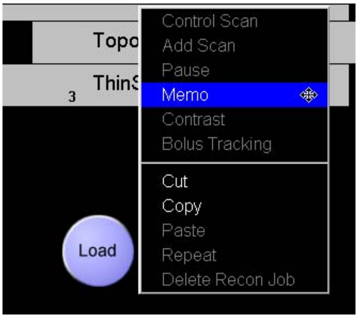
- Select the entry in the chronicle and call up **Insert > Contrast** in the main menu.

A contrast-medium pause is included in the examination.

The following examination steps are marked with the contrast-medium symbol and the contrast-medium label (+C) appears on the images.

Inserting a comment

You can explain the examination procedure with short memo or instruction texts.



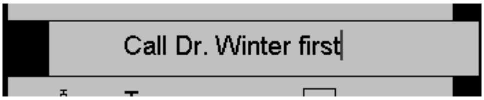
✧ Place the mouse cursor at the section of the examination **before** which you want to insert a comment.

✧ Call up the popup menu (right mouse key) of the chronicle, and insert a **Memo**.

Or

✧ Select the entry in the chronicle and call up **Insert > Memo** in the main menu.

A memo line is inserted in the chronicle.



Call Dr. Winter first

✧ Click on the "Memo" entry in the chronicle and enter your comment text (up to 18 characters).

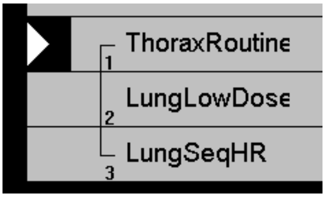
✧ Click into the image area of the **Examination** card to terminate text input mode.

➪ If you have made a typing error you can cancel your change with the **ESC** key.

➪ If you delete the text and then press the **Return** key, the memo entry is removed again.

Processing auto range

Auto ranges are examination step sequences that are performed by the system one by one without the user intervening, i.e. when one examination area has been scanned, scanning of the next is automatically started (exception: increase of gantry tilt).



Auto ranges are usually included in contrast agent administration when precise to-the-second timing of the scans is decisive to the examination result. Auto ranges are indicated in the chronicle by bracketing off the relevant examination steps.

Forming an auto range

To form an auto range you have to delete the pauses between the examination steps that you want to combine.

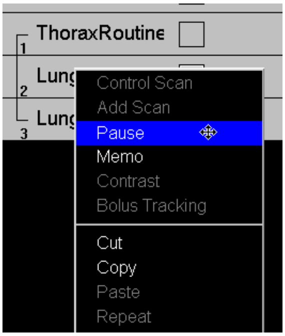
✧ Delete the pause or control scan between two sequences or spirals.
→ Page C.2–32, *Deleting an examination step*

NOTE

You can also combine one spiral and one sequence to form an auto range. For technical reasons, the spiral must be acquired before the sequence.

Canceling an auto range

You can cancel an auto range by inserting a pause. You must then trigger the individual examination steps manually.



✧ Place the mouse cursor on the second or next examination step in the auto range.

✧ Select **Pause** in the popup menu of the chronicle.

Or

✧ Select the entry in the chronicle and call up **Insert > Pause** in the main menu.

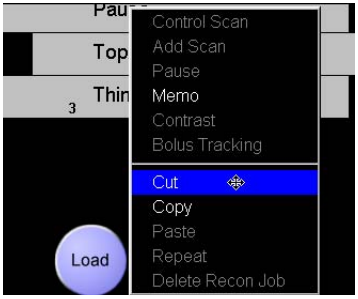
A pause is inserted in the chronicle. The examination steps before and after the pause are no longer combined to form an auto range.

➩ An auto range can also be interrupted by inserting a contrast agent pause or a control scan. However, the control scan is then linked to the previous scan to form an auto range.

Moving, copying, deleting, renaming examination steps

In routine examinations, it is sometimes useful not to perform all the steps suggested in the scan protocol in order to save time. In some cases, you might want to repeat steps or change the sequence of examination steps.

Moving an examination step

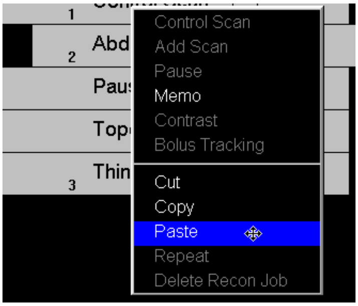


- Place the mouse cursor at the step that you want to move.
- Call up the popup menu (right mouse key) of the chronicle and select **Cut**.

Or

- Select the step in the chronicle and call up **Edit > Cut** in the main menu.

- Now select the examination step **before** which you want to place the step you have just cut.

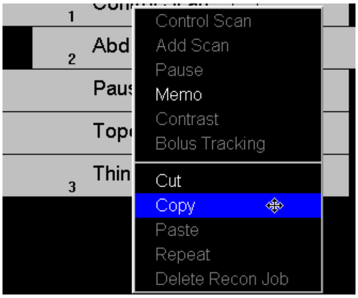


- Call up the popup menu of the chronicle and select **Paste**.

Or

- Call up **Edit > Paste** in the main menu.

Copying the examination step



✧ Place the mouse cursor at the step that you want to copy.

✧ Call up the popup menu of the chronicle and select **Copy**.

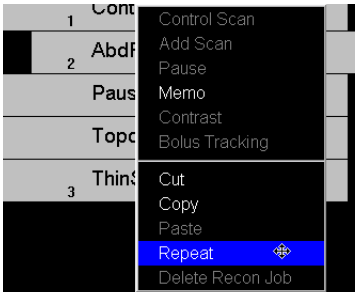
Or

✧ Select the step in the chronicle and call up **Edit > Copy** in the main menu.

✧ Click on the examination step **before** which you want to insert the step you have copied.

✧ Insert the examination step with **Paste** (popup menu) or with **Edit > Paste** (main menu).

Repeating an examination step



✧ Place the mouse cursor at the step that you want to repeat.

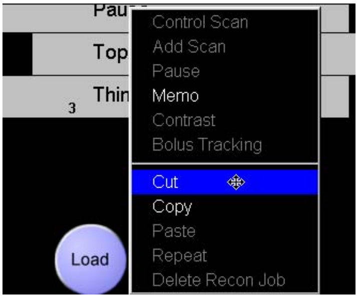
✧ Call up the popup menu (right mouse key) of the chronicle and select **Repeat**.

Or

✧ Select the step in the chronicle and call up **Edit > Repeat** in the main menu.

Deleting an examination step

✧ Mark the step that you want to delete in the chronicle.



✧ Call up **Cut** in the popup menu of the chronicle or **Edit > Cut** in the main menu.

➪ If you have accidentally deleted a topogram or another acquisition series, use **Paste** straight afterwards to undo deletion. You can also call up the **Patient Model Dialog** dialog box and insert the same scan protocol again with **Append**. Then delete the unwanted examination steps.
→ Page C.2–8, *Appending a scan protocol*

Renaming an examination step

✧ Click into the name of the examination step that you want to rename, and extend the selection.

✧ Enter the new name and then click into the image area on the **Examination** card to terminate text input mode.

➪ If you have made a typing error you can cancel your change with the **ESC** key.

➪ It is not possible to rename contrast-medium pauses.

Routine subtask card in contrast agent examination

There are several examinations which are always performed with contrast-medium injection. In such cases, you insert a contrast medium pause in the chronicle in front of the contrast agent scans.
→ Page C.2–26, *Inserting a contrast-medium pause*

Record the details of contrast agent administration on the **Routine** subtask card that is displayed for the contrast agent pause. In that way you ensure that your examination can be reproduced later on.

➩ Always document the details of your contrast-medium injection. This information might be significant for the interpretation of examination results.

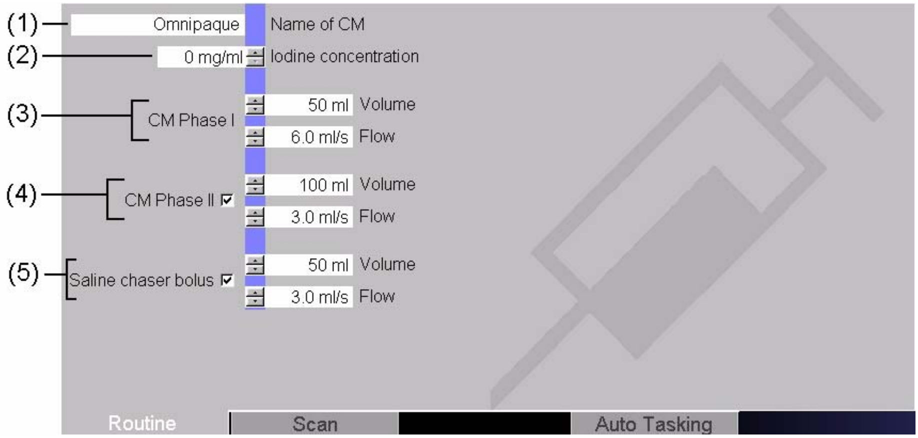
NOTE

It is the individual responsibility of the physician to define the settings for contrast agent administration for the specific patient.

Displaying the Routine subtask card

✧ Click on a contrast-medium pause in the chronicle.

➪ Default values are initially displayed in the input fields of the **Routine** card for contrast agent administration.



Omnipaque Name of CM
0 mg/ml Iodine concentration
CM Phase I 50 ml Volume
6.0 ml/s Flow
CM Phase II ☑ 100 ml Volume
3.0 ml/s Flow
Saline chaser bolus ☑ 50 ml Volume
3.0 ml/s Flow

(1) Name of the contrast medium
(2) Iodine concentration
(3) Volume and flowrate of first contrast agent phase
(4) Volume and flowrate of second contrast agent phase
(5) Volume and flowrate of saline solution administered as a chaser

Name of the contrast medium

Omnipaque Name of CM

✧ Enter the name of the contrast medium.

Concentration

0 mg/ml Iodine concentration

✧ Enter the iodine concentration. You can obtain this information from the manufacturer’s data.

Quantity of contrast medium

50 ml Volume

✧ Enter the quantity of contrast medium to be injected, or set the value using the spin box.

Flow rate

6.0 ml/s Flow

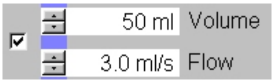
✧ Enter the flow rate.

Second contrast agent phase

If you have planned a second phase for contrast agent administration, you can enter the relevant information under **CM Phase II**.

CM Phase II ☑ II

✧ Check the **CM Phase II** checkbox so that you can enter the data of the second contrast agent phase.



☑ 50 ml Volume

3.0 ml/s Flow

✧ Enter the contrast agent volume and flowrate.

Chaser phase

If you want to administer a saline solution chaser, enter it in the lower input fields.

Saline chaser bolus ☑ 50 ml Volume

3.0 ml/s Flow

✧ Check the checkbox **Saline chaser bolus** and enter the volume and flowrate of the chaser solution.

CHAPTER
C.3

Topogram / Planning Ranges

During patient registration or preparation for an examination, you have selected a routine scan protocol for the planned examination.

The first examination step in your scan protocol is the acquisition of a topogram. Topograms are overview images in which you define the anatomical regions to be examined.

Topograms are acquired with a constant tube position, constant table feed and without gantry tilt.

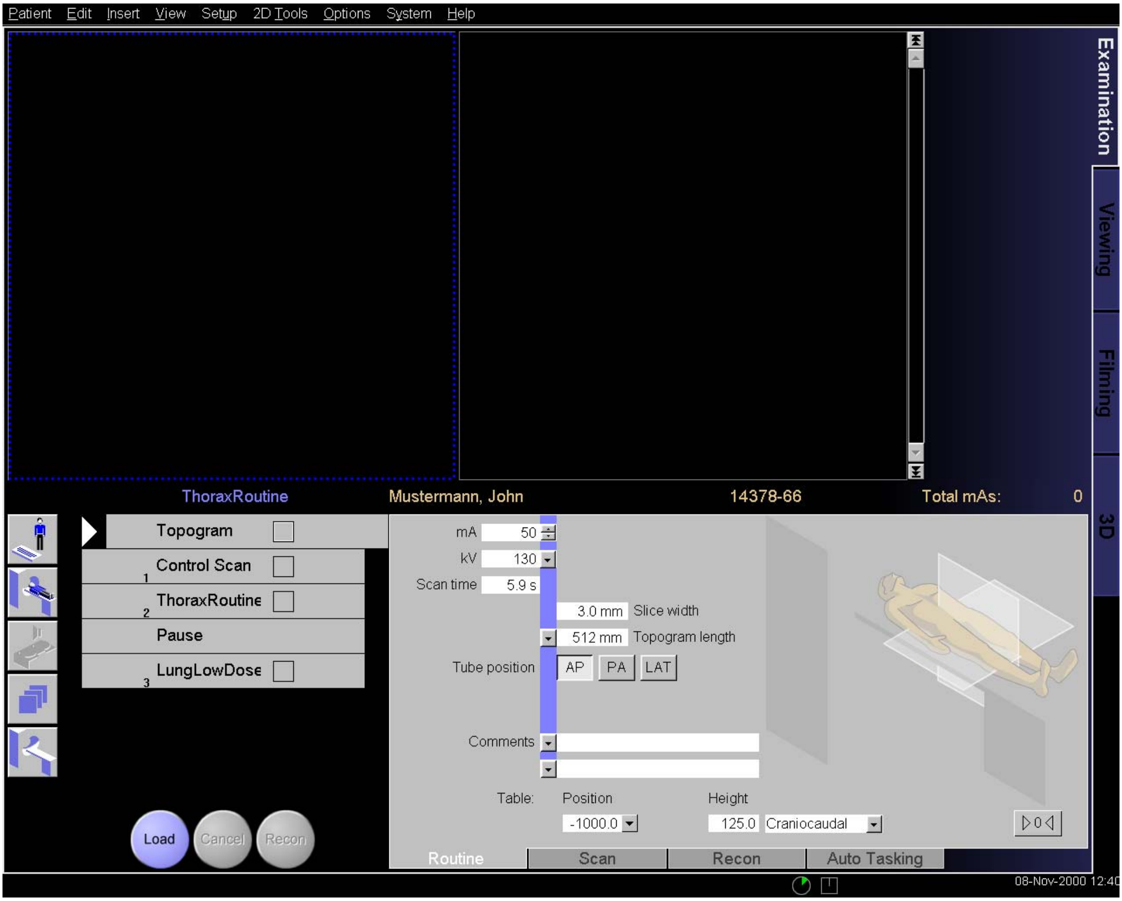
Your system suggests routine topograms for standard examinations and draws standard ranges into the topogram acquired. You will always have to adapt the size of the ranges slightly so that they match the individual anatomy of the patient.

In this chapter, you will read how to prepare a topogram and how to acquire a routine topogram. You will learn how to modify the ranges and adapt topogram parameters.

➪ If you do not want to perform a topogram scan, delete this examination step from the chronicle.
→ Page C.2–23, *Adapting routine scan protocols*
In that case, continue reading on
→ Page C.3–31, *Planning ranges without a topogram*

Preparing a topogram

If you have already entered an examination during patient registration and call up **Examination**, you can see the individual steps of this examination listed in the chronicle. The first scan, the topogram, is selected.



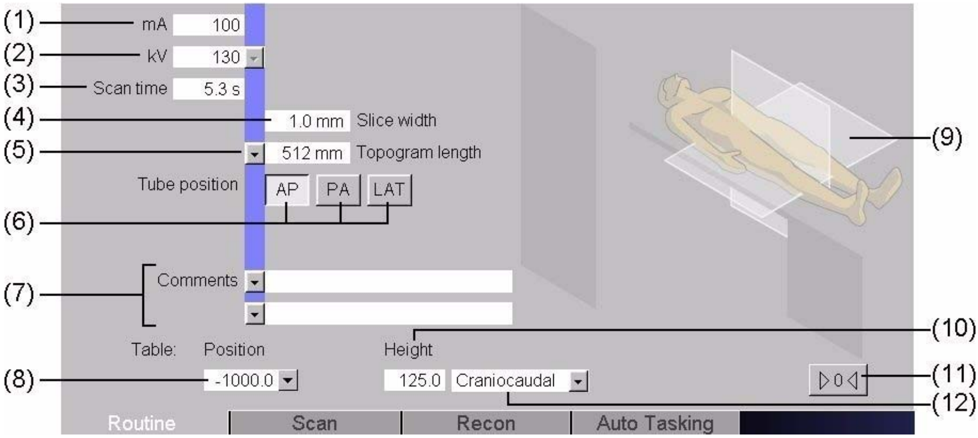
ThoraxRoutine
Mustermann, John
14378-66
Total mAs: 0

Topogram ☐
1 Control Scan ☐
2 ThoraxRoutine ☐
Pause
3 LungLowDose ☐

mA 50
kV 130
Scan time 5.9 s
3.0 mm Slice width
512 mm Topogram length
Tube position AP PA LAT
Comments
Table: Position -1000.0 Height 125.0 Craniocaudal

08-Nov-2000 12:40

On the **Routine** subtask card, you can see all the settings required for your routine topogram.


mA 100
kV 130
Scan time 5.3 s
1.0 mm Slice width
512 mm Topogram length
Table: Position -1000.0
Height 125.0
Craniocaudal

(1) Tube current
(2) Tube voltage
(3) Scan time (duration of radiation exposure)
(4) Slice thickness
(5) Topogram length in mm
(6) Tube position
(7) Comment lines
(8) Horizontal table position
(9) Patient model
(10) Table height
(11) Zeroing button
(12) Scan direction

Using the input fields and buttons, you can change the settings before a topogram is acquired.

The values displayed in the input fields are predefined by the selection of the routine scan protocol. You can adapt these presettings as required.
→ Page C.3–29, *Scan subtask card for topograms*

⇨ For Osteo examinations, you should only change the horizontal table position and gantry tilt. All other scan parameters are predefined and should not be modified.

On the patient model in the right-hand half of the **Routine** subtask card, you can see which patient position was entered during registration or examination preparation.

NOTE

Make sure that this patient position is correct and change it if necessary before you start scanning.

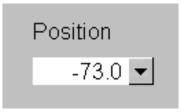
→ Page C.2–10, *Changing the patient position*

Moving the patient in the initial position

Before scanning, you move the patient into the starting position of the topogram. Take the scan direction for topogram acquisition into account.

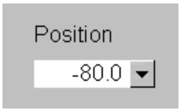
You can always set the initial position of the topogram using the operating elements in the examination room, because only here can you see the light marker and estimate the path through the gantry. Should it be necessary to correct the table position from the console, you can control the table with the following functions:

Horizontal table position


Position
-73.0

The **Position** field always shows you the horizontal table position **relative** to a selectable reference point.

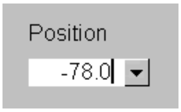
➪ Initially, the reference point of the previous examination is valid. Later on, you can define the starting position of the topogram as the reference point for the ensuing examination.
→ Page C.3–7, *Setting the table position to zero*


Position
-80.0

✧ Enter a smaller value (in mm) to extend the table further into the gantry and confirm with the **Return** key.

➪ You must always enter the target position, not the distance, by which you want to move the table.

✧ Press the **Move** key on the control box to trigger table movement.


Position
-78.0

✧ Enter a larger value, confirm with the **Return** key, and press **Move** to retract the table out of the gantry by a small distance again.

Or

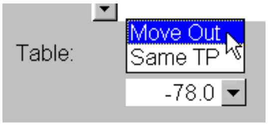


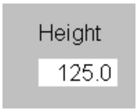
Table: -78.0

✧ Click on the arrow ▾ next to the display for the table position.

✧ Select **Move Out** and then press the **Move** key to move the patient table and support out of the gantry completely. The table top moves completely out immediately.

> **NOTE**
>
> With **Move Out**, you can move the patient out of the gantry very fast in the event of an emergency.

Table height



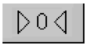
Height 125.0

On the **Routine** subtask card, you can see the current height of the patient table (in mm). The numeric values are absolute and always state the distance of the table top from the center of rotation of the tube detector system.

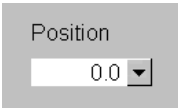
➪ You can only change the table height using the gantry operator fields in the examination room.
→ SOMATOM Operator Manual, chapter B.2, *The Scan Unit (Gantry)*

Setting the table position to zero

You can define the initial position for the topogram as the reference point for all the following scans.



✧ Click on the **Zero** button to set the current table position to zero.



During the scans, the **relative displacement** of the table top with respect to the initial position of the topogram is now always displayed.

➩ You can correct the table position again and press the **Zero** button again as long as you have not started to scan the topogram.

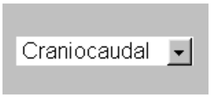
NOTE

If you do **not** set the table position to zero,
all table position values of your measurements refer to the last set zero position.

✧ Take this into account when evaluating your results!

Selecting the scan direction

After you have moved the patient table into the initial position, select the scan direction for the topogram.



✧ Select **Craniocaudal** in the selection list to set the scan direction from *head to feet*.

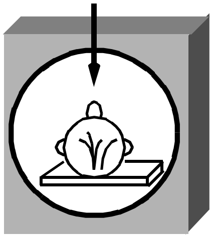
Or

✧ Select **Caudocranial** in the selection list to set the scan direction from *feet to head*.

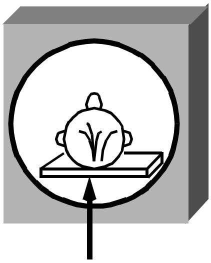
The data you enter about the patient position and selected scan direction determine whether the table top must move into the gantry while the topogram is being acquired or out of the gantry.

Defining the tube position

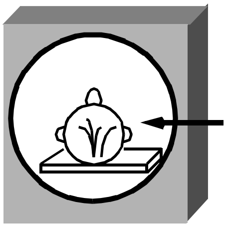
Topograms are acquired with a constant tube position.



AP



PA



Lateral
(Feet first)

For your topogram, you can select one of the following tube positions:

AP

❑ **AP** (from above)
The angle is 270°.

PA

❑ **PA** (from below)
The angle is 90°.

LAT

❑ **Lateral** (from the side)
The angle is 0° (default setting) for radiation from the right. The radiation comes from the right-hand side of the patient if the patient position is “Feet first”.

➪ On request, Siemens Service can also set **Lateral** to 180°, i.e. radiation from the left to avoid exposure directed to the operators console.

✧ Click on one of the buttons to define the tube position.

Checking and adapting scan parameters

Routine topograms suggest scan parameter settings to you. These default settings are shown on the **Routine** subtask card. In most cases, these parameters are suitable.

Tube voltage


kV 80

You can improve the contrast in the display of soft tissue by increasing the tube voltage.

✧ Select a value from the selection list.

Setting topogram length

With the topogram length, you can define the length of the region to be scanned (in mm) for the topogram. In the routine scan protocols, a topogram length appropriate for the region to be examined has already been defined.


512 mm Topogram length

✧ Select another topogram length from the selection list, if the suggested value is not suitable.

Depending on the topogram length selected, the system determines:

❑ the necessary scan time

❑ the magnification factor for displaying the topogram

❑ the optimum Field of View (topogram width)

Display depending on the topogram length:

Topogram length	Magnify factor (max.)	Topogram width (FoV)
128	1.0	512
256	1.0	512
512	1.0	512
768	0.5	1024
1024	0.5	1024

➩ The magnification of the topogram can be changed after scanning.
→ Page C.3–23, *Changing the topogram display*

Shortened topogram

Depending on the initial position of the patient table, the table top can reach its final position during scanning before the entire topogram length has been scanned.

In that case, a message is displayed in the status bar,
e.g.: “Topogram length reduced to 716 mm”.

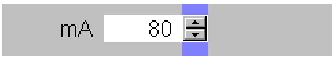
✧ Select a shorter topogram length.

Or

✧ Leave the setting for the topogram length unchanged. You then automatically obtain a shortened topogram.

➩ Shortened topograms are displayed with the zoom factor that was set for the topogram originally selected.

Tube current



mA 80

The tube current corresponds to the intensity of the radiation. A value should be selected that provides satisfactory image quality with a minimum radiation dose for the patient. The build of the patient and the diagnostic problem of the examination should be taken into account here.

✧ Set the tube current via the spin box.

Scan time

Scan time 5.3 s

The scan time indicates how long acquisition of the topogram will take. This is the length of time that the patient must hold his or her breath in response to a breathholding instruction during a topogram.

➪ The radiation dose can be calculated from the radiation intensity (dose rate) and the scanning time. You can only change it by changing the topogram length.

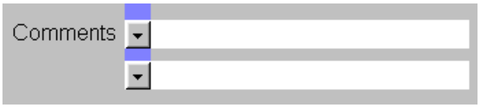
Slice width

1.0 mm Slice width

The slice width is constant for topograms. It cannot be changed.

Selecting comments

You can display up to two comment lines in the topogram.



✧ Select one or two comment lines from the selection lists.

➪ You can create and edit standard comments in the setup.
→ Page C.13–3, *Creating standard comment texts*

Or

✧ Enter free comment texts in one or in both of the two input fields.

Performing a topogram scan

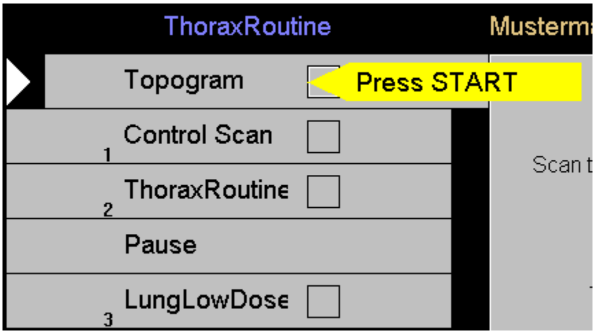
After you have made all preparations for your topogram, you can start scanning.

Confirming parameters

First load the settings into the scan system.

✧ Click on the **Load** button (below the chronicle).

The scan parameters are loaded, the prompt **Press START** appears in the chronicle.



The system is ready for scanning. You can trigger acquisition of the topogram with the **Start** key on the control box.

Or

✧ Click on **Cancel** to cancel readiness for scanning again.

NOTE

For acquisition of a topogram, the gantry **must** be vertical. If the gantry is tilted (more than 5°), **Press MOVE to tilt** is displayed in the chronicle after the topogram parameters have been loaded.

✧ Press the **Move** key on the control box to put the gantry into the vertical position.
Only then does **Press START** appear in the chronicle and you can begin scanning.

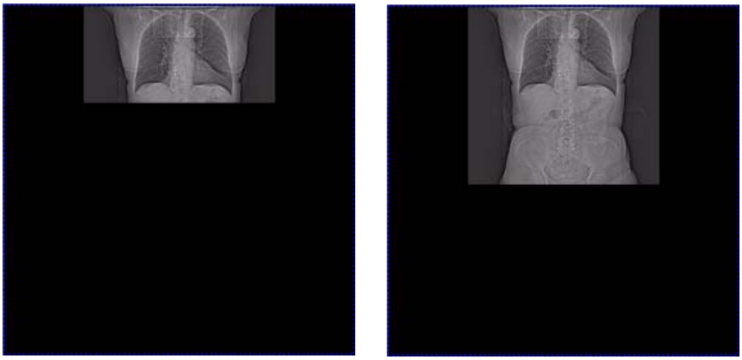
Scanning

You always trigger topogram acquisition from the console. You cannot use the optional footswitch for topograms.

✧ Press the **Start** key on the control box to start scanning.

After the delay time has elapsed, scanning begins. The image is build up in the topo segment as scanning progresses.

➪ If you scan with automatic patient instruction, the announcement is made during the delay time.

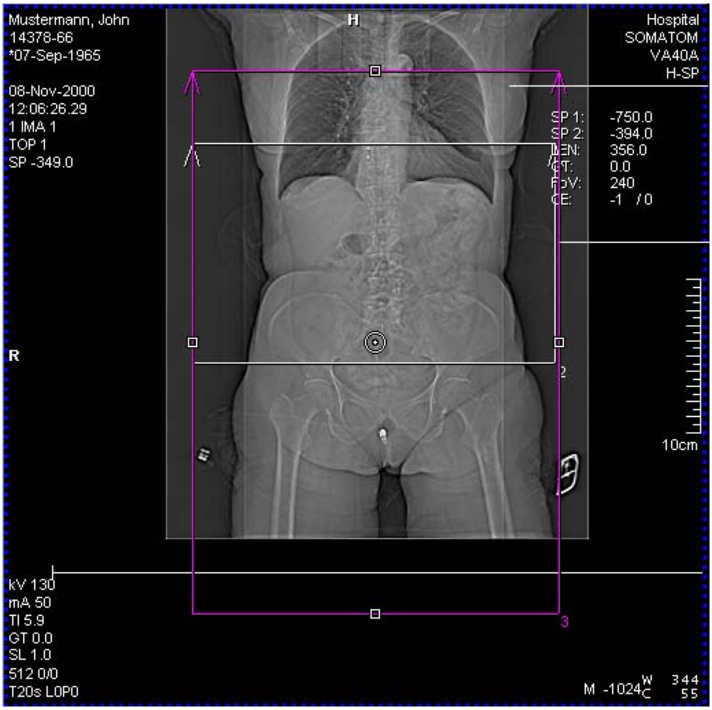


You can see the current scanning position by the separator line of the topogram. It moves from the lower to the upper or the upper to the lower edge of the image during scanning depending on the scan direction you have set.

End of scanning

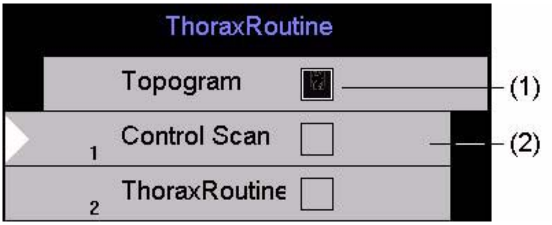
As soon as the set topogram length has been scanned, the system automatically terminates scanning.

The examination regions suggested in the routine scan protocol are now displayed in the topogram.



Display in the chronicle

The topogram is labeled as **scanned** in the chronicle, i.e. a thumbnail topogram appears in the recon icon. At the same time, the next examination step is selected.

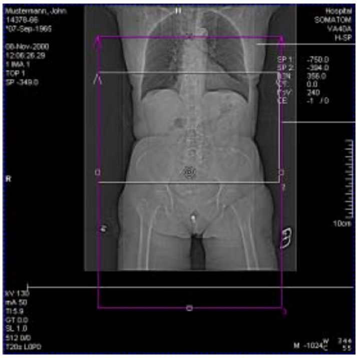


(1) Recon icon with thumbnail topogram
(2) Next examination step

Display in the topo segment

Topograms are always displayed in the same way in the topo segment:

- The head of the patient is at the top, whatever the patient's real position.
- The topogram is always a front view, regardless of whether the patient is lying supine or prone.
- For all lateral tube positions, the patient is always facing the left in the topogram (patient table always on the right).



Suspending scanning

You can follow the progress of topogram acquisition on the screen.

As soon as all the areas of interest for your examination have been acquired, you can suspend acquisition before the entire topogram length has been scanned. In this way, you can prevent the patient from being exposed to radiation for longer than absolutely necessary.

✧ Press the **Suspend** key on the control box.

Acquisition of the topogram is terminated prematurely.

Or

✧ Click on the **Suspend** button.

You obtain a **shortened topogram** and can continue to work with it.
→ Page C.3–21, *Adapting ranges*

➩ Shortened topograms are displayed with the magnification factor that was set for the topogram length originally selected.
→ Page C.3–10, *Setting topogram length*

Stopping scanning

In an emergency, you can stop scanning a topogram just as you can stop acquiring any other type of scan.

✧ In an emergency, press the **Stop** key on the control box.

Radiation is stopped immediately and the system is blocked. You can continue the examination after you have pressed **Continue**.
→ Page C.12–23, *Restoring system readiness*

Adapting ranges

After you have finished the scan, you can see one or more examination ranges marked in the topogram. The current position of the scanning plane (tube detector system) with respect to the patient is indicated by a thin horizontal line across the entire topogram segment.
→ Page C.3–17, *End of scanning*

You must usually adapt the ranges suggested by the routine scan protocol to the anatomy of the patient in question. For this purpose, you can move, lengthen/shorten, and for lateral topograms also tilt ranges or modify the Field of View.

CAUTION

Source of danger: Scan lines at wrong position for OSTEO examination

Consequence: Wrong diagnosis

Remedy: Check position of scan lines in the mid of the vertebrae

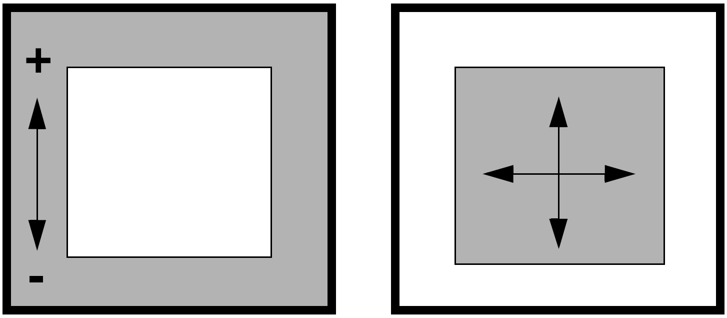
Depending on the selected scan protocol, the following can be marked on the topogram:

- A single range
- Several ranges on top of each other (e.g. for examinations with contrast medium in which the same region is to be acquired in different contrast medium phases).
- Several contiguous ranges
  (regions with the same Field of View that touch or are very close, such as for head examinations).
- One or more cutlines in addition to the range(s) to mark planned single scans.

Changing the topogram display

When planning areas of examination, it is helpful, especially on shortened topograms, to adapt the size and position of the topogram in the topo segment to your needs (**zoom/pan**).

Depending on where you place the mouse cursor in the topo segment, you can enlarge or reduce the topogram or pan it in the segment.



Zooming **Panning**

✧ Select **2D Tools > Zoom & Pan On** in the main menu to activate the mouse function for zooming and panning.

✧ Place the mouse cursor close to the edge of the segment.

✧ Drag the mouse cursor up or down holding the left mouse key pressed to enlarge or reduce the topogram.

Or

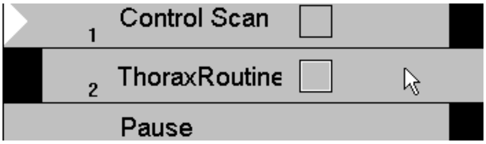
✧ Place the mouse cursor in the center of the topogram.

✧ Drag the mouse cursor in the direction in which you want to pan the topogram holding the left mouse key pressed.

Selecting ranges

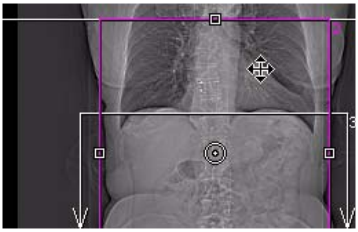
If more than one range or cutline is shown in your topogram, the range of the next examination step is initially selected in your chronicle. If you want to edit another range or another cutline, you must first select it.

Selecting a range or cutline



✧ Click on the entry of the corresponding scan in the chronicle.

Or



✧ Click on the range in the topogram.

Additional text information

In the top right-hand corner of the topo segment, you can see several items of data about the size and position of the selected range or cutline.

```
Klinikum Nord
SOMATOM
VA40A
H-SP
SP 1:   -1050.0
SP 2:   -1264.0
LEN:    214.0
GT:     0.0
FoV:    238
CE:     -1   / 0
```

❏ **SP 1:** Scan position for the first image

❏ **SP 2:** Scan position for the last image
(not for cutlines)

❏ **LEN:** Length of the range
(not for cutlines)

❏ **GT:** Gantry tilt

❏ **FoV:** Field of View

❏ **CE:** Center (x/y coordinates) of the Field of View

Modifying the ranges and cutlines

You can alter a selected range quickly and simply by changing its graphic display in the topo segment.

To do this, use the graphic processing techniques already described.
→ Page C.1–14, *Graphic selection and editing*

Moving a range or cutline

✧ Place the mouse cursor on the center of the selected range or cutline.

The cursor changes shape.

✧ Drag the range or cutline to the required position holding the left mouse key down.

Snapping mechanism

If you move a range or cutline in the vicinity of another range, the two ranges are joined together by a mechanism. The Field of View and the gantry tilt must be the same for both ranges or cutlines.

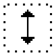
➪ You can change the capture range in the **Examination Configuration**.
→ Page C.13–22, *Snap distance*

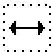
Changing range length; Changing the Field of View

✧ Place the mouse cursor on the handle on the upper or lower boundary to change the length of the range.

Or

✧ Place the mouse cursor on the handle on the right or left boundary to change the Field of View of the range.



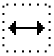


The cursor changes shape.

✧ Drag the cursor in the required direction holding the left mouse key down.

Changing the Field of View of a cutline

✧ Place the mouse cursor on the right or left end handle of the cutline to change the Field of View.



The cursor changes shape.

✧ Drag the mouse cursor towards the outside of the cutline to enlarge the FoV on one side.

Likewise, to reduce the FoV drag the mouse cursor toward the center.

➩ The FoV of a control scan must always be a little larger than the FoV of the following scans so that their Fields of View can be displayed in the control scan and adapted.

Tilting a range or cutline

In topograms that have been acquired with a lateral tube position, you can tilt the range or cutline. The tilt corresponds to the gantry tilt during the scan.

✧ Place the mouse cursor on the upper or lower boundary of the range, but not on one of the grab handles.

Or

✧ Place the mouse cursor on any position between the center and the ends of the cutline.

The cursor changes shape.

✧ Drag the cursor up or down holding the left mouse key down.

➩ The gantry tilt can also be set numerically on the **Routine** subtask card.

Change the ranges until they cover the anatomical regions that you want to examine in an optimum way.

Then begin acquiring a control scan.
→ Chapter C.4, *Control Scan*

Multiselection of ranges

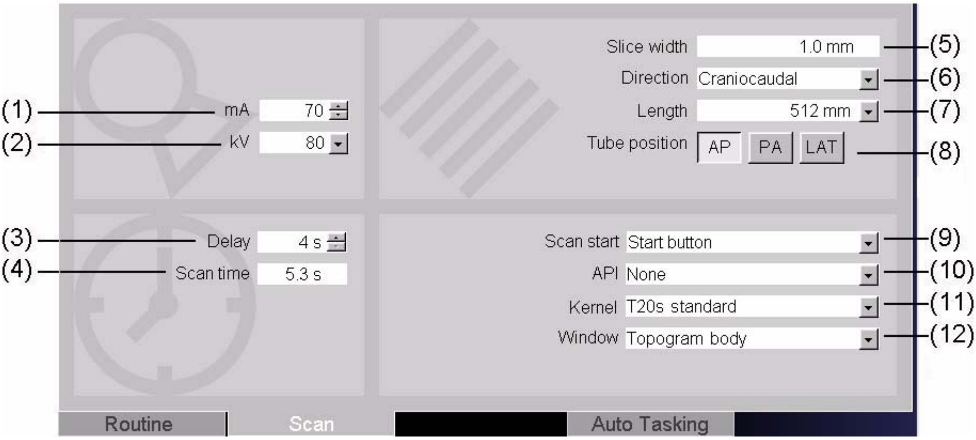
You can use the group selection to apply your modifications of one range to all following ranges of the scan protocol.

➩ The Field of View and the gantry tilt must be the same for all ranges concerned.

✧ Press the **Shift** key after modification of one range *before* you release the left mouse key.

Scan subtask card for topograms

The Scan subtask card contains the scanning and reconstruction parameters of topogram acquisitions. You can define the scan parameters of the Routine card here in the same way. For scans with API, also select the breath holding command. All other parameters are predefined in the scan protocol and cannot be changed.



mA 70
kV 80
Delay 4 s
Scan time 5.3 s
Slice width 1.0 mm
Direction Craniocaudal
Length 512 mm
Scan start Start button
API None
Kernel T20s standard
Window Topogram body

(1) Tube current (radiation intensity)
(2) Tube voltage
(3) Delay time
(4) Scan time (duration of radiation exposure)
(5) Slice width
(6) Scan direction
(7) Topogram length
(8) Direction of radiation / tube position
(9) Scan start
(10) Automatic patient instruction system
(11) Kernel
(12) Window

Selecting an instruction text

You can only activate automatic patient instruction for an examination step if an instruction text is selected.

API breathing

✧ Select the breathing instruction you want to acquire the topogram with (e.g. **Expiration**).

Or

✧ Select **None** if you want to deactivate automatic patient instruction for your topogram.

➪ In the **API / Comment Setup** dialog box, you can edit announcement texts for automatic patient instruction, delete announcements or add new announcements.
→ Page C.13–2, *API and comment texts*

Planning ranges without a topogram

Only in rare cases (e.g. for babies) should you omit scanning a topogram and start with the spiral or sequence scans immediately in order to keep the total radiation exposure of the patient as low as possible.

Setting the table position

✧ Move the patient table into the starting position of the first range using the gantry operator panels in the examination room.
→ SOMATOM Operator Manual, page C.3–5, *Positioning patients*

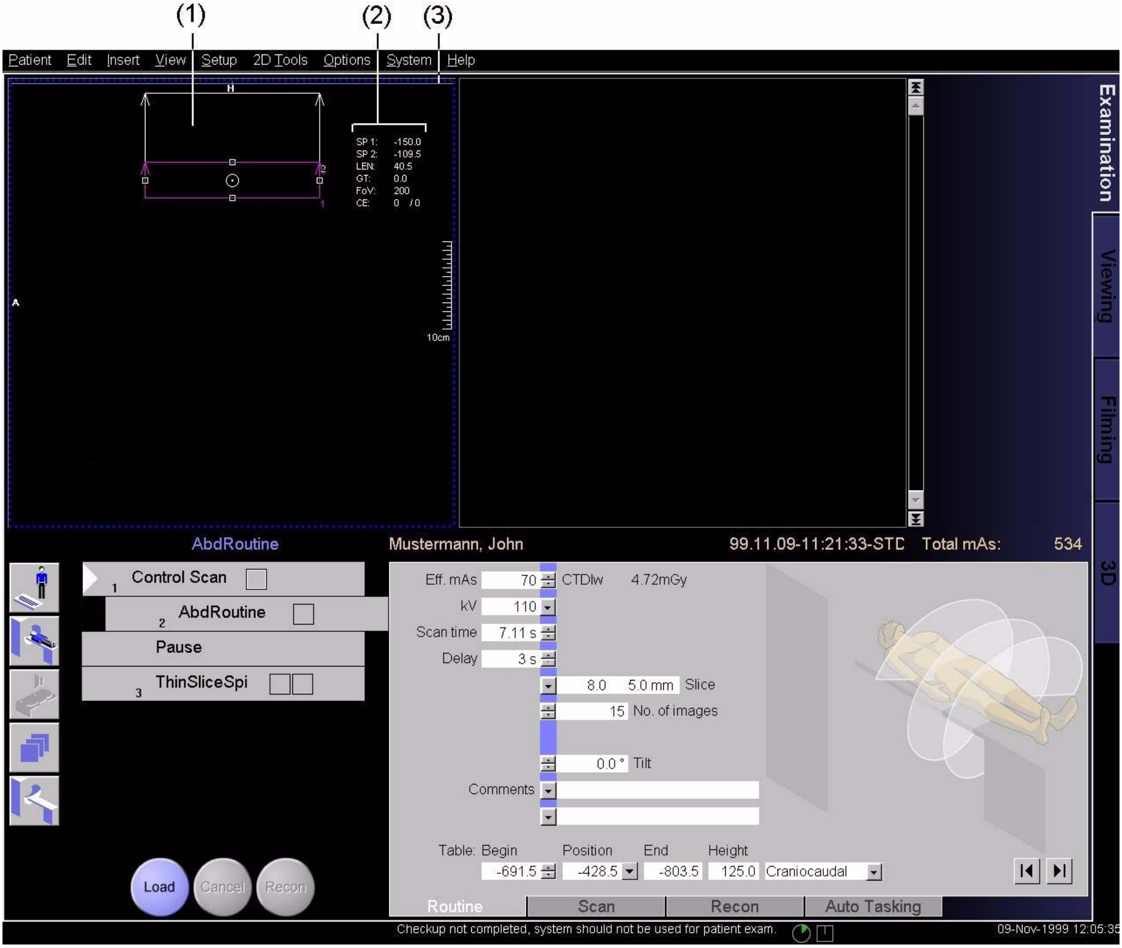
✧ Place the table position on the gantry to zero.

➯ If you do not define a new reference point, all table position values refer to the last set zero position.

Ranges without topogram

✧ Delete the topogram from the chronicle if you want to begin the examination without acquiring a topogram first.
→ Page C.2–23, *Adapting routine scan protocols*

The next examination step is now selected. The examination ranges suggested in the routine scan protocol are displayed in the otherwise empty topo segment.



SP 1: -150.0
SP 2: -109.5
LEN: 40.5
GT: 0.0
FoV: 200
CE: 0 / 0

Mustermann, John 99.11.09-11:21:33-STD Total mAs: 534

1 Control Scan ☐
2 AbdRoutine ☐
Pause
3 ThinSliceSpi ☐☐

Eff. mAs 70 CTDIw 4.72mGy
kV 110
Scan time 7.11 s
Delay 3 s
8.0 5.0 mm Slice
15 No. of images
0.0 ° Tilt
Comments

Table: Begin	Position	End	Height	
-691.5	-428.5	-803.5	125.0	Craniocaudal

Checkup not completed, system should not be used for patient exam.
09-Nov-1999 12:05:35

(1) Ranges or cutlines of the following scans
(2) Data about the selected range
(3) Current table position (at top of the segment)

The topo segment shown represents the entire length of 512 mm. After you have zeroed the table position, the current table position is shown at the top edge of the image.

✧ Set the size and position of the ranges marked in the same way as in a scanned topogram.
→ Page C.3–21, *Adapting ranges*

➪ You can use the numeric data about the range selected shown in the top right-hand corner of the topo segment as an aid.
→ Page C.3–25, *Additional text information*

CHAPTER C.4 Control Scan

In the previous sections, you learned how to prepare an examination. You selected a routine scan protocol and defined the ranges using a topogram.

If you have entered a control scan as the next examination step in the chronicle, it will now be selected. With the control scan, you can check the following settings for the ensuing scan series:

☐ Start line for the first range

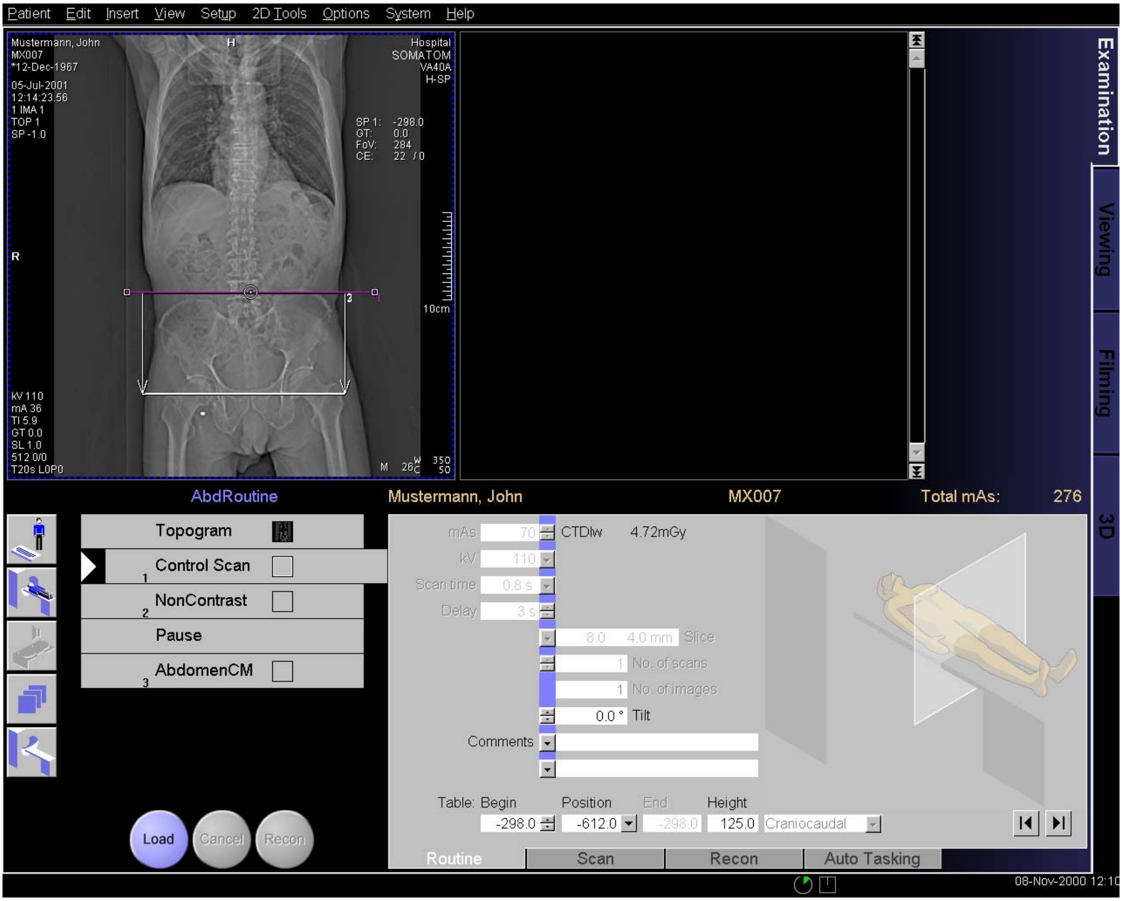
☐ Position of the patient

☐ Size (Field of View) and position of the planned reconstruction target

➩ If you do not want to check these settings and accept the parameter suggestions from the routine scan protocol, you do not need to perform a control scan.
→ Page C.2–32, *Deleting an examination step*
In that case, start the spiral scan or sequence scan.
→ Chapter C.5, *Spiral*, → Chapter C.6, *Sequence*

Performing a control scan

You perform the control scan with the scan parameters that are set in the routine scan protocol for the following sequence or spiral. These parameters are already entered on the **Routine** subtask card of the control scan and are displayed dimmed there.



Mustermann, John
MX007
*12-Dec-1967
05-Jul-2001
12:14:23.56
1 IMA 1
TOP 1
SP -1.0

Hospital
SOMATOM
VA40A
H-SP

SP 1: -298.0
GT: 0.0
FoV: 284
CE: 22 / 0

kV 110
mA 36
TI 5.9
GT 0.0
SL 1.0
512 0/0
T20s L0P0

M 26 C W 350 50

AbdRoutine · Mustermann, John · MX007 · Total mAs: 276

Topogram
1 Control Scan ☐
2 NonContrast ☐
Pause
3 AbdomenCM ☐

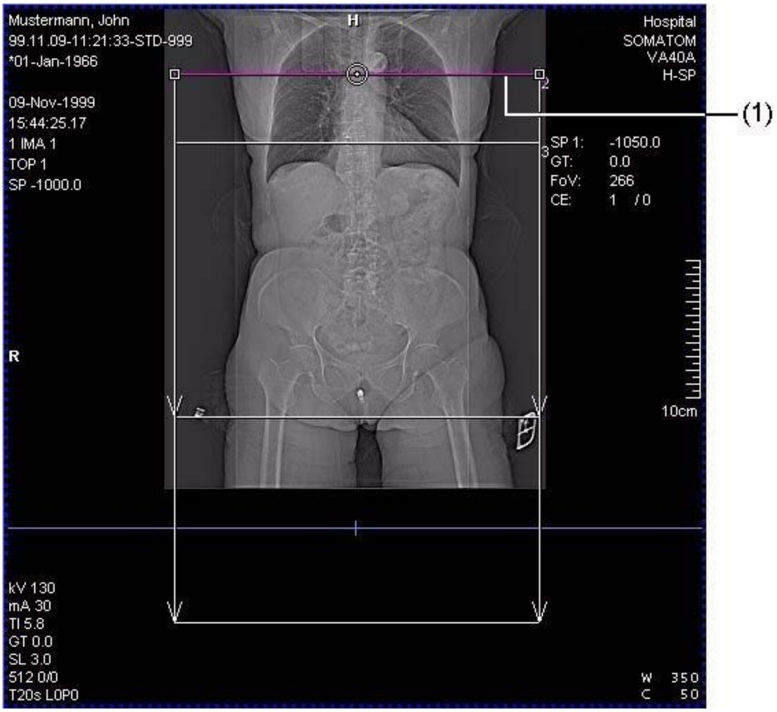
mAs 70 · CTDIw 4.72mGy
kV 110
Scan time 0.8 s
Delay 3 s
Slice 8.0 4.0 mm
No. of scans 1
No. of images 1
Tilt 0.0 °
Comments

Table: Begin -298.0 · Position -612.0 · End -298.0 · Height 125.0 · Craniocaudal

08-Nov-2000 12:1

Positioning the control scan

By default, the control scan is planned at the beginning of the following range. You can see this position by the cutline drawn in the topo segment.



Mustermann, John
99.11.09-11:21:33-STD-999
*01-Jan-1966

09-Nov-1999
15:44:25.17
1 IMA 1
TOP 1
SP -1000.0

Hospital
SOMATOM
VA40A
H-SP

SP 1: -1050.0
GT: 0.0
FoV: 266
CE: 1 / 0

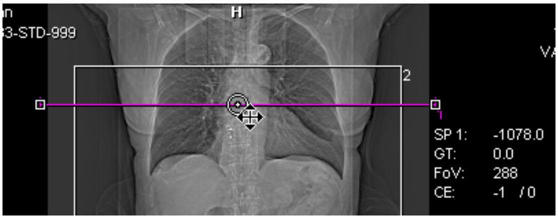
kV 130
mA 30
TI 5.8
GT 0.0
SL 3.0
512 0/0
T20s L0P0

W 350
C 50

(1) Cutline of control scan

Perhaps, you would like to check the image quality and reconstruction parameters at another position. In that case, you can reposition the cutline both graphically and numerically.

Graphic setting



SP 1: -1078.0
GT: 0.0
FoV: 288
CE: -1 / 0

✧ Move the cutline of the control scan to the required position in the topogram using the mouse.
→ Page C.3–26, *Moving a range or cutline*

Or

Numeric setting

Table: Begin
-142.0

✧ Enter the required horizontal table position on the **Routine** subtask card.

Performing the scan

The cutline for the control scan is now positioned, all further scan settings have already been defined on the **Routine** card. You now confirm the scan parameters, move the patient table to the starting position (if necessary), and start the scan.

Confirming the scan parameters

✧ Click on the **Load** button beneath the chronicle.

The preset scan parameters are loaded, and the system is ready to scan.

Moving the patient table into the starting position

If the patient table is not yet at the correct position, the **Press MOVE** prompt appears in the chronicle.

✧ Press the **Move** key on the control box until the starting position is reached and table movement stops.

Or

✧ Click on the **Cancel Move** button if you want to perform the control scan at the current table position.

The **Press START** prompt is displayed in the chronicle.

Starting the control scan

✧ Press the **Start** key on the control box.

Or

✧ Start scanning with the footswitch.

The system starts the control scan. When it has finished, the control scan is marked as scanned in the chronicle by a miniature image on the recon icon. The next examination step has now been selected.

Interrupting the control scan

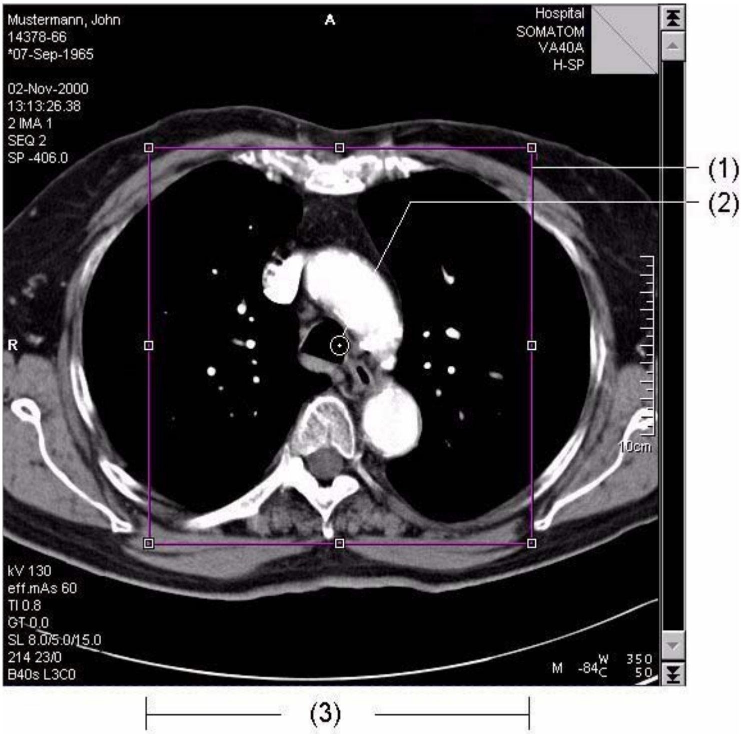
In an emergency, you can interrupt the control scan at any time.

✧ Press the **Stop** key on the control box.

Radiation is interrupted immediately and the system is blocked. You can resume the examination after you have pressed **Continue**.
→ Page C.12–23, *Restoring system readiness*

Checking the reconstruction settings and scan parameters

As soon as you have completed the control scan, it is displayed in the tomo segment and the reconstruction targets (we usually call it the field of view or FoV) of the following scan series are also displayed.



(1) Number of the FoV (reconstruction task number)
(2) Center of the FoV
(3) Size of the FoV

Checking the range

Using the control scan, you can make sure that you have really positioned the range at the beginning of the region which is to be examined.

✧ Check whether the control scan results in the expected image.

✧ Change the size and position of the range in the topo segment, if necessary.
→ Page C.3–21, *Adapting ranges*

Checking the position of the patient

The control scan can also be used to make sure that the patient is positioned symmetrically (e.g. for examinations of the inner ear) if precise comparison of the two sides is of clinical importance.

✧ Check whether the control scan results in the expected image.

✧ If necessary, adjust the position of the patient.

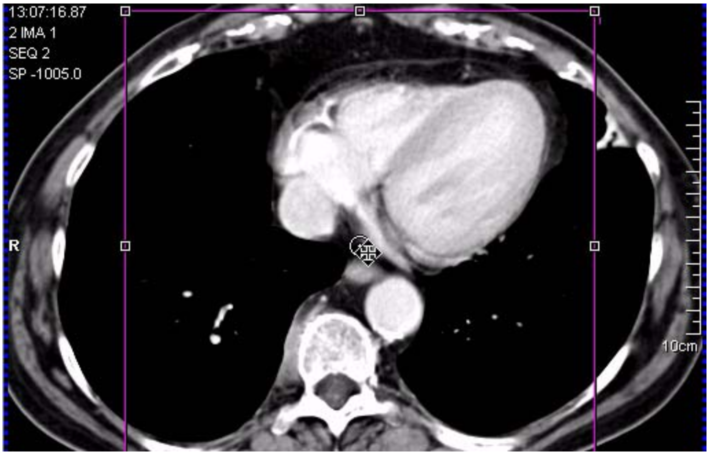
➩ Because only small changes to the position are usually required, it is not necessary to repeat the topogram in such cases.

Adjusting the fields of view

With the graphic positioning of the fields of view (FoV), you can define what square areas of the slices are to be the visible images. This adaptation in the control scan is useful to reconstruct the following scan series with the optimum FoV.

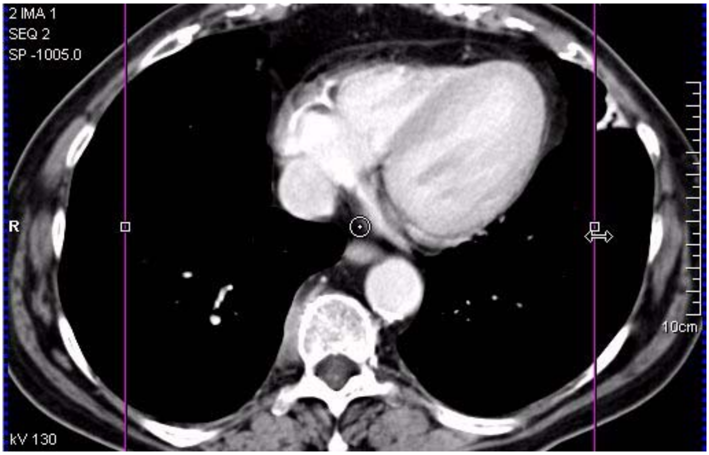
In the tomo segment, the FoV for the next scan has already been selected. The FoVs of the following scans are selected initially if they match the FoV and the gantry tilt of the next range in the scan protocol. Then they can be adapted to the region of interest in a single action.

Moving the FoV



✧ Check the position of the first (selected) FoV. Move the center, if necessary.
→ Page C.3–26, *Moving a range or cutline*

Changing the size of the FoV



✧ Check the size of the FoV and change it, if necessary.
→ Page C.3–27, *Changing range length; Changing the Field of View*

➩ If reconstructions are planned with a different FoV, select the individual fields of view by their recon icon in the chronicle or by their numbers on the **Recon** card. On the **Recon** card, you can also change the envisaged reconstruction settings.
→ Page C.10–20, *Changing reconstruction parameters*

➩ For parallel calculation of the tomograms during scanning, only the first field of view of a measurement is relevant.

Creating an overview image

A control scan is reconstructed with the field of view that was set for it in the topogram during planning of the examination. The field of view is always somewhat larger than the preset FoV of the following scans (otherwise, it would not be possible to display the field of view of the ranges in the control scan).
→ Page C.3–27, *Changing range length; Changing the Field of View*

If the FoV of the control scan is too small to display the region of interest, you can calculate the entire scanned tomographic image without releasing radiation again.

✧ In this case, select the **Recon** card and select a new recon job.

✧ Click on the **Overview** button to display the entire scan field.
→ Page C.10–6, *Creating the overview image*

✧ Enlarge the field of view and click on the **Recon** button to reconstruct the control scan again.

Checking image quality

Check whether you are happy with the image quality of the control scan. If small changes to the scan parameters are necessary, it is enough to make these changes for the following scans and then resume the examination. In rare cases, it might be necessary to repeat the control scan with changed parameters.

Repeating the control scan

If the control scan does not show the required image or the required image quality, change the settings of the following scan series accordingly. If necessary, you can repeat the control scan to check the new parameters.

✧ Define the new scan settings for the following spiral scan or sequence.
  → Page C.5–3, *Preparing for a spiral*
  → Page C.6–4, *Preparing for a sequence*

✧ Insert a further control scan **in front of** the next scan series in the chronicle to check the changed scan parameters.
  → Page C.2–25, *Inserting a control scan*

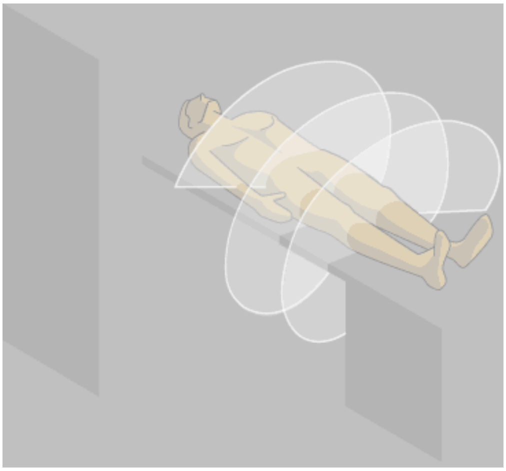
✧ Repeat the control scan.

CHAPTER
C.5 Spiral

Two alternative scanning methods are used for acquiring slice images on the CT scanner: spiral scans and sequence examinations.

With your CT scanner, you will mostly perform examinations using the spiral technique; for the sequence technique, see:
→ Chapter C.6, *Sequence*

A so-called spiral scan is a continuous data scan of a volume of the body with continuous table feed during the scan.



Spiral scans provide gapless volume data of a region of the body from which almost any number of images can be reconstructed afterwards.

With continuous table feed and permanent rotation of the X-ray tube, spiral scanning is a very fast method. It is therefore possible to scan relatively long ranges within one breathhold time using the spiral technique.

It is also possible to increase the speed of examination by increasing the table feed during each rotation of the X-ray tube. This allows you to scan even longer ranges without any significant loss in image quality and to keep the radiation exposure of the patient as low as possible.

Because of the facilities for reducing the exposure of the patient while obtaining complete and largely artifact-free volume data that permit great variability in reconstruction, the spiral CT is now the recommended method in most routine scan protocols.

Preparing for a spiral

Once you have scanned the topogram and made a control scan, if necessary, the system selects the first examination step of the following scan series in the chronicle.

You can see which scanning method is selected by the patient model on the **Routine** subtask card.
→ Page C.1–12, *The subtask cards*

The scan parameters suggested by the routine scan protocol are entered in the input and selection fields of the card. In most cases, this data is suitable for your examination. The size and positioning of the range in the topogram depend on the patient and must therefore be adapted for each new patient.
→ Page C.3–21, *Adapting ranges*

Before you continue with the examination, check the scan parameters on the **Routine** subtask card as described below.

⇨ If you want to use automatic functions, such as automatic patient instruction, you must activate them before you start scanning.
→ Page C.2–12, *Automatic functions*

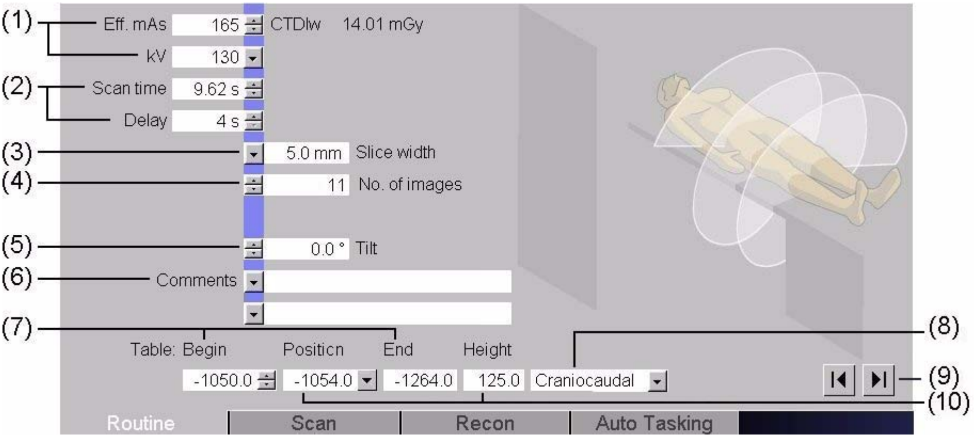
NOTE

If more than one scan series, i.e. more than one range, is planned for the spiral examination, you must check the scan parameters of these ranges individually. Initially, the first scan series is selected.

✧ Select the next or a following scan series in the topo segment or the chronicle to display its scan parameters on the **Routine** card.

✧ Make the changes in all series for which the new settings are to apply. Select the first range again before you start scanning.

Routine subtask card



Eff. mAs 165 CTDIw 14.01 mGy
kV 130
Scan time 9.62 s
Delay 4 s
5.0 mm Slice width
11 No. of images
0.0 ° Tilt
Comments

Table: Begin	Position	End	Height	
-1050.0	-1054.0	-1264.0	125.0	Craniocaudal

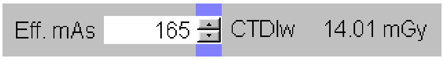
(1) Radiation parameters
(2) Time settings
(3) Slice width
(4) Number of images
(5) Gantry tilt
(6) Comment lines
(7) Range
(8) Scan direction
(9) Buttons for step-by-step table movement into/out of the gantry
(10) Current table position

Checking the radiation parameters and slice width

The radiation parameters and slice width determine the image quality and the radiation exposure of the patient.

If you are not yet familiar with scanning operation on your computer tomograph, you should stick to our suggestions for parameter selection. Of course, you can also make changes to the parameters, for example, to optimize the image quality when examining especially slender or corpulent patients.

Eff. mAs per image



Eff. mAs 165 CTDIw 14.01 mGy

✧ Define the Eff. mAs and confirm with the **Return** key.
The larger the value the sharper the image and the less noise is in it. But the radiation dose for the patient is also increased.

Based on the current scan parameter settings the CT dose index **CTDIw** (in mGy) is calculated and displayed next to the **Eff. mAs** input field.

➪ The display of the CTDI value can be configured in the **Local Service** dialog box**.**

Tube voltage

kV 80

✧ Select the tube voltage.
You can improve the contrast of the soft tissue displayed by selecting higher values.

Slice width

The slice width must be adapted to the size of the objects that you want to display with the examination. This is already taken into account in the routine scan protocols for individual examinations.

If you want to chose another setting anyway, you should bear in mind that the scan time is increased with a smaller slice and that this also increases the radiation exposure of the patient.

5.0 2.5 mm Slice width

✧ Chose a slice width in the selection list if you want to change the set value.

➩ The possible slice widths that are provided for selection in the list depend on the set slice width mode.
→ Page C.5–55, *Slice-width mode*

Changing the time settings

The time settings are very important for spiral scans. The scan time must not be longer than the time the patient can hold his or her breath and must also be matched to the contrast medium kinetics. Shortening the scan time places a load on the X-ray tube and can cause a conflict with the X-ray tube monitoring. The delay time must be adapted to the filling and dispersal time of the contrast medium.

Scan time

The system calculates the scan time of a spiral scan from the rotation time of the X-ray tube (equivalent to the “scan time” of a control scan), the length of the range, and the table feed per rotation suggested in the routine scan protocol.
→ Page C.5–48, *Special scan settings*


Scan time 9.62 s

✧ Set the time for the spiral scan using the spin buttons.
The shorter the scan time the higher the table feed per rotation of the tube-detector system.

➪ Where parameter conflicts arise you can easily adapt the scan time to the Eff. mAs and delay time with the scan assistant.
→ Page C.12–5, *Adapting scan parameters with the scan assistant*

Setting the delay time

The routine protocol suggests a delay time suitable for the region to be examined. The delay time is the time from pressing the **Start** key to when the scan begins. Note that it is not possible to set a delay smaller than a certain minimum delay time, because the scanning system requires a short preparation period.

For acquisition with contrast medium, select the flooding time of the contrast medium used as the delay.

Delay 3 s

✧ Change the delay time using the spin buttons, if necessary.

➪ Activating the API announcement text increases the minimum delay time, which might cause the delay you set to be increased automatically. If this happens, a message is displayed on the status bar. Remember that this value will automatically be changed back if you deactivate the API.

NOTE

With the delay time you define the length of the interruption between two consecutive scans in an auto range.

Changing the range and scan direction

You can plan the size and position of the scanning ranges graphically in the topo segment. On the **Routine** subtask card you will find the exact start and end position of the spiral.

Spiral length

Table: Begin -85.5

End -355.5

In the fields **Table: Begin** and **End**, you can enter the positions at which you want to take the first and last image. If you change **Begin**, the position of the range is changed accordingly. If you enter a new value for **End**, the length of the range is adapted.

➪ The range actually scanned is always longer than the spiral length you have entered, because the system requires starting and concluding rotations. Spiral acquisitions of a few millimeters only are therefore not advisable. This applies especially to small slice thicknesses.

✧ Set the spiral length using the entry fields and confirm your settings with the **Return** key.
The changes are displayed immediately in the topo segment.

Or

✧ Move the boundary lines of the examination range in the topo segment.
The changes are displayed immediately on the **Routine** subtask card.

Gantry tilt

As for the beginning and end of ranges, you can plan the gantry tilt for tomographs with lateral patient position graphically in the topo segment.
→ Page C.3–28, *Tilting a range or cutline*

➩ The tilt of the range in the topogram is displayed as gantry tilt in the topo segment.

0.0 ° Tilt

The current gantry tilt is always displayed on the **Routine** card. Before you start scanning, you can tilt the gantry to another angle.

➩ The range must be selected then.

✧ Select the required gantry tilt using the spin buttons or change it numerically.

✧ Press the **Move** key on the control box until the new gantry tilt has been reached.

NOTE

If an increase in the gantry tilt has been planned for an examination step in an auto range, you must confirm it manually with **Move**. A message appears in the chronicle prompting you to tilt the gantry.

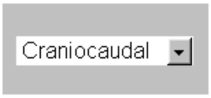
Scan direction

In the routine scan protocol, the caudiocranial scan direction is preset for examinations of the skull and the craniocaudal scan direction for examinations of the body. If more than one range is planned for an examination, the same scan direction is usually set for all of them in the routine scan protocol.

In contrast-medium series in which the same examination range is scanned several times, the patient table moves back to the starting position between two scans.

You can change the scan direction, for example to shorten the time for table movement between scanning two identical ranges. If you are examining the same region first in the craniocaudal and then (with contrast medium) in the caudiocranial direction, you save the time for repositioning the table.

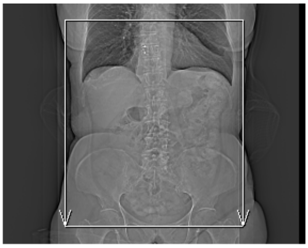
✧ Select the range for which you want to change the scan direction in the chronicle or in the topo segment.



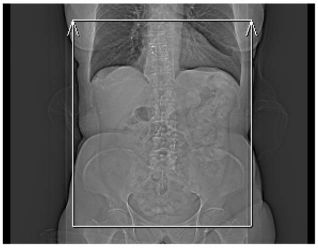
✧ Select the new scan direction on the **Routine** subtask card.

For example, you can plan the following procedure to minimize the distances the patient table has to travel for an examination in three phases:

(1)



(2)



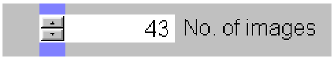
(3)

(1) Craniocaudal
(2) Caudocranial
(3) Craniocaudal

Number of images

Because the scanning procedure is extremely fast, one image per second is calculated with a reduced image quality simultaneously with the spiral scan (only RTD). At a rotation time of, for example, 1 second, you therefore obtain exactly one image per rotation of the scanning system. If MetroRecon or Last Image Display is activated, the scans are reconstructed with full image quality parallel with scanning.
→ Page C.5–41, *Starting reconstructions*

The number of images provides a measure of the size of the steps with which the range will be constructed with a full matrix. If you want to know the increment, i.e. the reconstruction step width, then look on the **Recon** subtask card.
→ Page C.10–29, *Increment for a spiral*

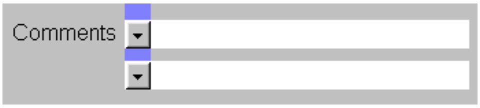


✧ Set how many images you want to create with a full matrix within the first reconstruction using the spin buttons.

➪ The increment is adapted upon changing the number of images.
→ Page C.10–29, *Increment for a spiral*

Entering comments

Comment texts are displayed on the reconstructed images and filmed together with the images.



✧ Select one or two comment lines from the selection lists.

➪ You can create and edit standard comments in the **API / Comment Setup** dialog box.
→ Page C.13–3, *Creating standard comment texts*

Or

✧ Enter free comment texts in one or two input fields.

➪ Comment texts are inherited to the following ranges up to the range of which the comment text has already been modified.

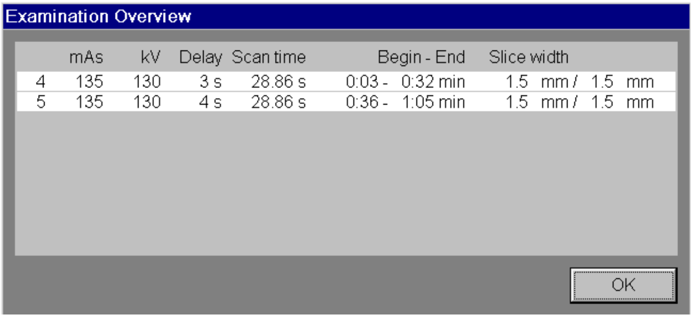
Displaying the parameter overview

The scan parameters for the spiral acquisition selected in the chronicle are displayed on the **Routine** subtask card.

You can view the most important scan settings for the examination steps of an auto range in an overview.

✧ In the chronicle, select an entry in the auto range.

✧ Call up **View > Examination Overview** in the main menu to display a parameter overview of the auto range.



Examination Overview

	mAs	kV	Delay	Scan time	Begin - End	Slice width
4	135	130	3 s	28.86 s	0:03 - 0:32 min	1.5 mm / 1.5 mm
5	135	130	4 s	28.86 s	0:36 - 1:05 min	1.5 mm / 1.5 mm

Multiscan (spiral without table feed)

One variation of a spiral examination is scanning without table feed. You can use this type of scan to determine changes in the density over a defined period (usually after contrast agent administration).

Calling up Multiscan

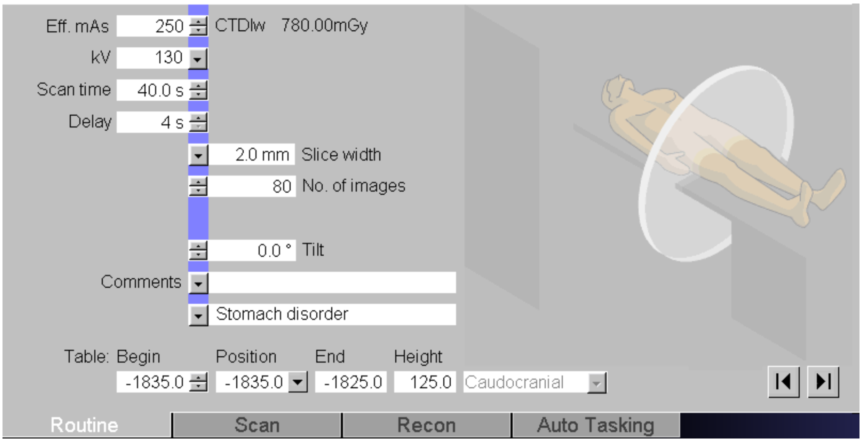
To acquire multiscans you require special scan protocols. Select these during registration or in the patient examination window under "*Specials*".
→ Page C.2–2, *Selecting an examination*

Setting scan and recon parameters

After you have selected the Multiscan examination, you will set the necessary parameters on the Routine, Scan, and Recon subtask cards. With Multiscan most of the parameters have already been defined. During scanning, the raw data are always reconstructed with full image quality (Metro Recon).

➪ The reconstruction range of a spiral without table feed is time-dependent. It requires individual settings of the reconstruction parameters.
→ Page C.6–20, *Serio scans (sequence without table feed)*

Routine card



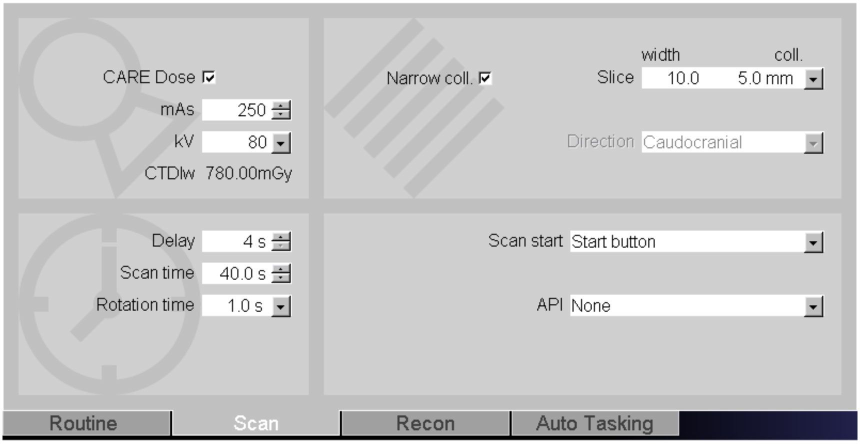
Eff. mAs 250 CTDIw 780.00mGy
kV 130
Scan time 40.0 s
Delay 4 s
2.0 mm Slice width
80 No. of images
0.0 ° Tilt
Comments
Stomach disorder
Table: Begin -1835.0 Position -1835.0 End -1825.0 Height 125.0 Caudocranial

Scan time 40.0 s

✧ Enter the duration of the multiscan in the **Scan time** spinbox

Scan card

In addition to the usual scan parameters, you can decide whether you want to set continuous radiation or radiation with dose modulation (CARE Dose). If the **CARE Dose** function is active, the radiation doses vary throughout a scan depending on the tissue. If there is a high proportion of soft tissue the dose is lower than if there is a high proportion of bone. The image quality is not affected.



CARE Dose ☑
mAs 250
kV 80
CTDIw 780.00mGy
Narrow coll. ☑
Slice width 10.0 coll. 5.0 mm
Direction Caudocranial
Delay 4 s
Scan time 40.0 s
Rotation time 1.0 s
Scan start Start button
API None

CARE Dose ☑

✧ Select **CARE Dose** to set scanning with modulated radiation.

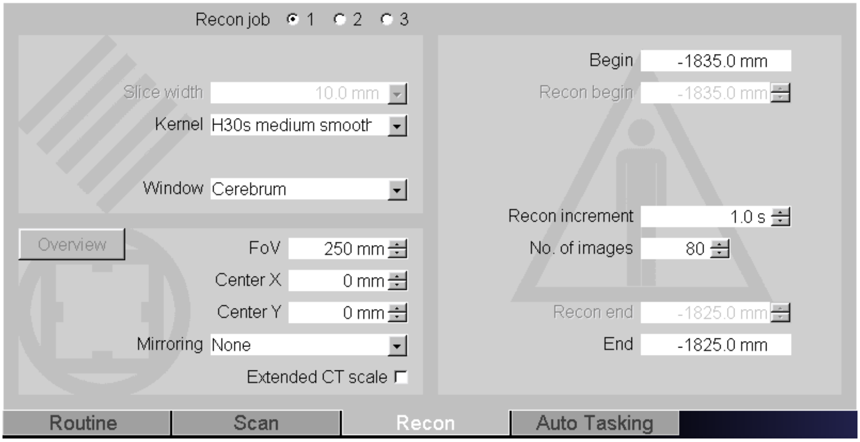
Or

CARE Dose ☐

✧ Deselect **CARE Dose** to scan with continuous radiation.

Recon card

On the Recon subtask card you can check the window and image settings and define the time difference between two consecutive images.



Recon job ● 1 ○ 2 ○ 3

Slice width 10.0 mm

Kernel H30s medium smooth

Window Cerebrum

FoV 250 mm

Center X 0 mm

Center Y 0 mm

Mirroring None

Extended CT scale ☐

Begin -1835.0 mm

Recon begin -1835.0 mm

Recon increment 1.0 s

No. of images 80

Recon end -1825.0 mm

End -1825.0 mm

Because scanning is performed at the same table position, the reconstruction range is a time window. The time difference between two consecutive images is determined by the **Recon increment**.

Recon increment 1.1 s

✧ If necessary, change the **Recon increment**.

⇨ The default value for the **Recon increment** is equivalent to the rotation time, the minimum value is 0.1 s. If the rotation time changes, the **Recon increment** is adapted automatically.

No. of images 18

The number of images is automatically adapted to the **Recon increment** set.

Scanning a spiral

After you have checked the scan parameters for your spiral examination and changed them, if necessary, you can begin scanning the first range.

Automatic check of scan settings

When you change or confirm scan settings, the system checks whether the selected settings cause conflicts with the tube monitoring. If necessary, the system will adjust the scan settings within the preset organ-specific limits.

If you are required to intervene, the system displays a conflict message (certain items on the **Routine** subtask card are displayed in yellow) and helps you find the scan settings suitable for your purposes.
→ Chapter C.12, *Scan Management*

➩ If an API text is selected for the spiral (**Scan** subtask card) and the scan time exceeds the set breath holding time, a message to that effect appears in the status bar.
→ Page C.12–9, *Breathholding time too short*

Performing a scan

If you have made a control scan and then did not have to change any scan settings for the spiral, the system is still ready for scanning. You can start scanning your spiral by moving the system into the starting position.

Directly after scanning a topogram or after changing the parameter settings on all subtask cards, you must first confirm the scan parameters at the first Recon job before continuing.

Confirming the parameters

✧ Click on the **Load** button to confirm the scan parameters for the spiral scan.

The **Press MOVE** prompt is displayed in the chronicle, if the patient table is not yet in the starting position.

Moving to the starting position

✧ Press the **Move** key on the control box until the patient table is in the starting position for the spiral.

Or

✧ Click on the **Cancel Move** button if you want to begin the spiral at the current table position.

➪ **Cancel Move** is not possible if the current table position is close to or behind the end of the range.

The patient table then moves back until the first image can be reconstructed at this table position.

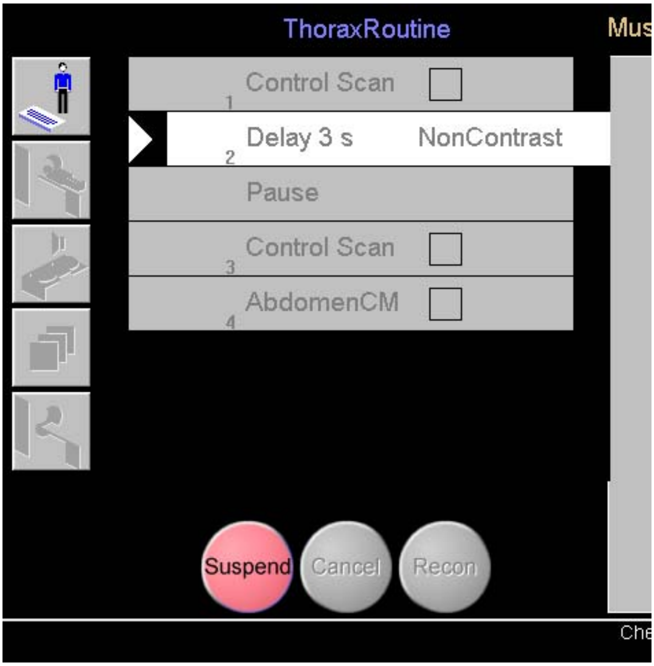
The **Press START** prompt is displayed in the chronicle.

Starting the spiral

✧ Press the **Start** key on the control box (or press the foot-switch) to start the spiral scan.

The delay time elapsing until radiation is released is displayed in the chronicle.

➪ If you are scanning with automatic patient instruction, the announcement is made during the delay time.



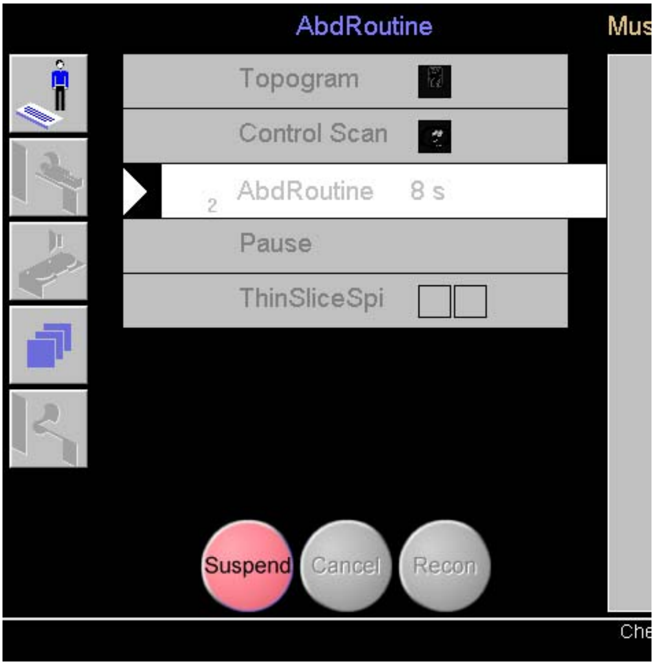
After the countdown has elapsed, the system starts scanning.

Tracing the scanning procedure

You can observe the progress of your scan on the screen so that you can intervene immediately if problems arise.

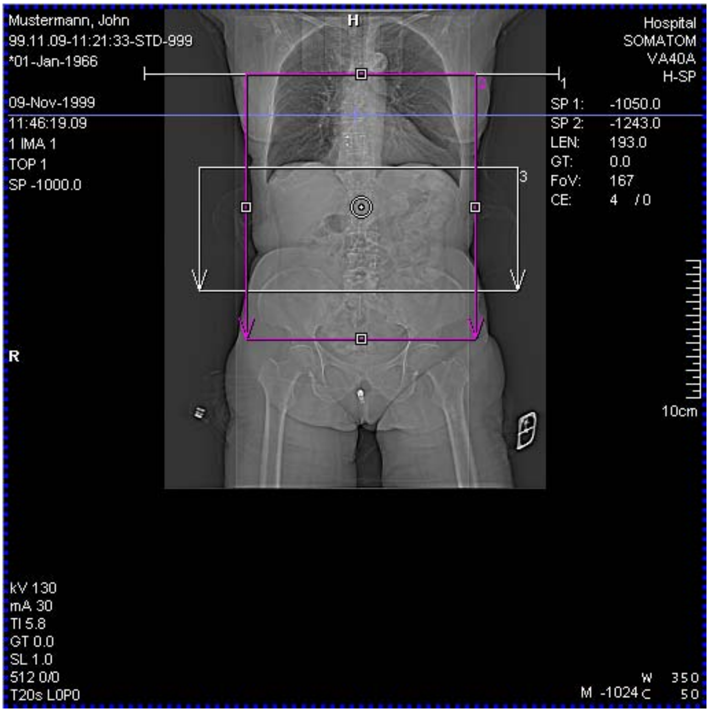
Time display in the chronicle

In the chronicle, you can see the scan time still to go.



Display in the topo segment

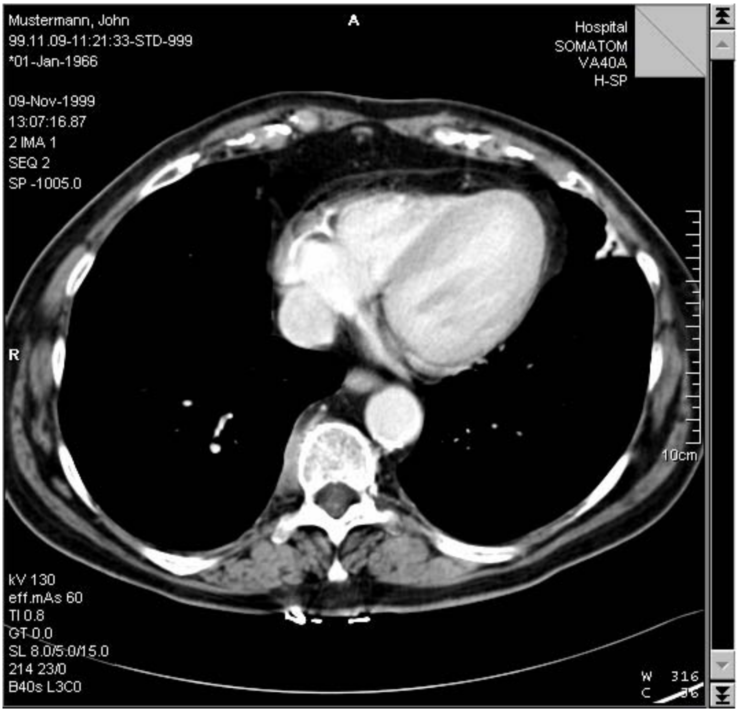
A line over the entire width of the topo segment indicates the position at which scanning is currently being conducted. This line moves from the starting position to the end of the range as scanning progresses.



Display in the tomo segment

During the spiral scan, one tomogram is calculated each second with a reduced image quality (**RTD** images) and displayed in the tomo segment for you to check the examination.

➪ You can reconstruct the raw data with a full matrix after the spiral scan.
→ Page C.5–41, *Starting reconstructions*



Suspending a scan

You can suspend a spiral scan at any time. If you suspend the spiral before sufficient data for full-quality reconstruction of an image have been collected, you can restart scanning of the same range.

At all subsequent positions in the scan, you can suspend the spiral to continue with the next range or to terminate the examination.

Suspend buttons

✧ Press the **Suspend** key on the control box.

Or

✧ Click on the **Suspend** button to suspend scanning.

Scanning is terminated.

The system is still ready for scanning.

Restarting the scan

If you have terminated the spiral scan shortly after starting scanning, the suspended scan series remains loaded in the chronicle. You can restart scanning of the same range.

➯ If necessary, change the scanning parameters on the **Routine** card. After this, you must confirm the new parameters with **Load** before restarting the scan.

✧ Press the **Start** key on the control box (or press the footswitch) to start the scan of this spiral series.

Suspension in an extreme emergency

✧ In an emergency, press the **Stop** key on the control box.

Radiation is stopped immediately and the entire system is blocked. You can resume the examination after you have pressed **Continue** in the dialog window displayed.
→ Page C.12–23, *Restoring system readiness*

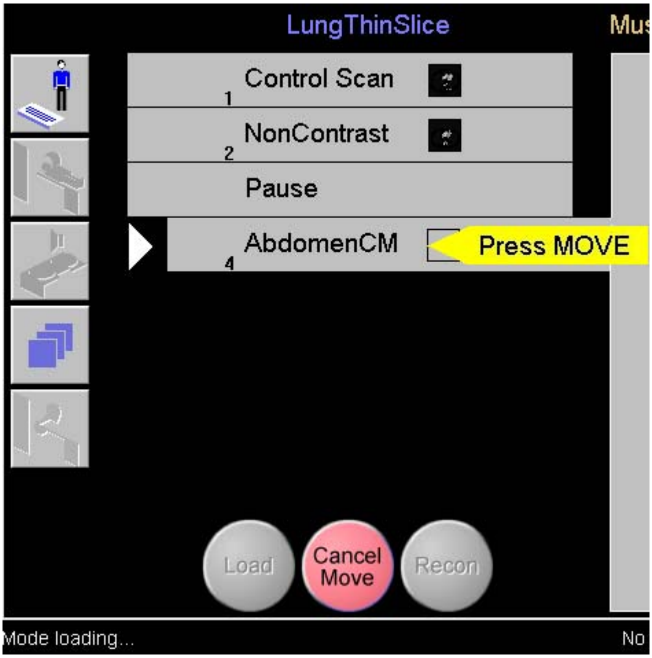
Continuing examination after suspension

If you have suspended the scan because you have already obtained all the images that you want from a range, then continue with the next examination step.

➪ If you accidentally interrupt spiral scanning before the end of the examination range or if the scan was aborted, copy the examination step (**Repeat** in the chronicle), adapt the scan range, and then scan the remaining range.
→ Page C.2–31, *Repeating an examination step*

The previous scan series is finished and marked as scanned by a stamp image in the recon icon in the chronicle. The system calculates the radiation dose of the patient accumulated so far.
→ Page C.5–31, *Total radiation dose*

The next scan is selected in the chronicle. You are prompted to **Press MOVE**.



Moving to the next range

✧ Press the **Move** key on the control box until the patient table is in the starting position for the next range.

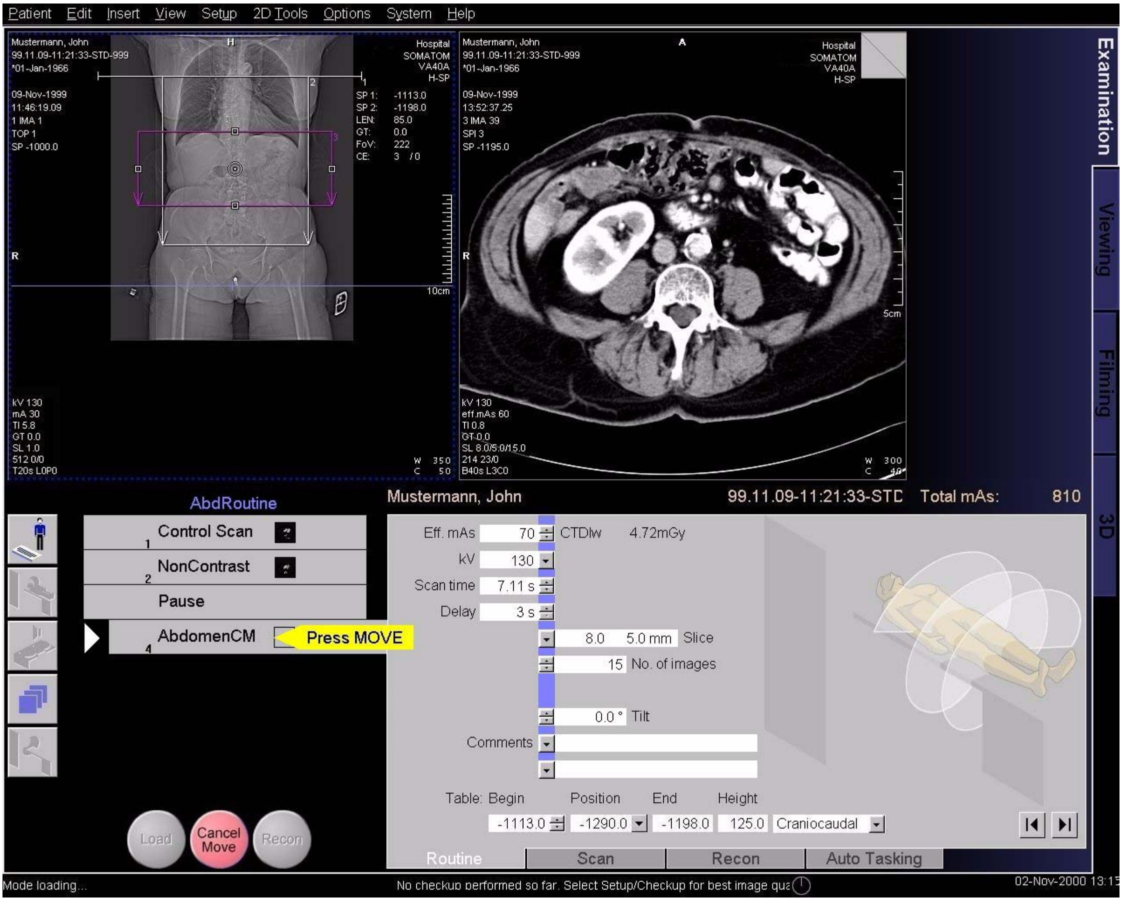
Or

✧ Click on **Cancel Move** if you want to start the next range at the current table position.
→ Page C.5–22, *Moving to the starting position*

Now continue your examination with the next series.
→ Page C.5–33, *Starting the next scan manually*

End of the range reached

After you have completed the scan of the first range, the image last reconstructed is displayed in the tomo segment.



Mustermann, John 99.11.09-11:21:33-STD Total mAs: 810

Eff. mAs 70 CTDIw 4.72mGy

kV 130

Scan time 7.11 s

Delay 3 s

8.0 5.0 mm Slice

15 No. of images

0.0 ° Tilt

Comments

Table: Begin -1113.0 Position -1290.0 End -1198.0 Height 125.0 Craniocaudal

Mode loading...

No checkup performed so far. Select Setup/Checkup for best image qua

02-Nov-2000 13:15

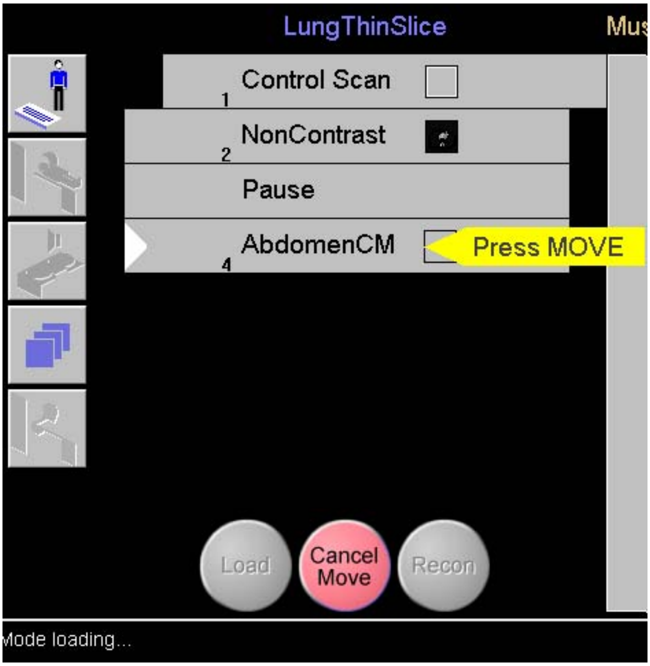
Total radiation dose

The radiation dose accumulated so far is displayed in the title bar above the subtask cards behind the patient name. It is updated after every interruption in scanning and at the end of a scanning step.


Mustermann, John 14378-66 Total mAs: 810

Display in the chronicle

The spiral is marked as scanned in the recon icon in the chronicle. The next examination step is selected.



Next scan in an auto range

The second and subsequent acquisition series of an auto range are started automatically by your system unless the gantry tilt has to be increased. In that case, the prompt Press Move is displayed in the chronicle.

✧ Hold the **Move** key on the control box down until the new gantry tilt is set.

The next scan starts automatically after the delay time has elapsed.

Or

✧ Click on the Cancel Move button if you want to keep the current gantry tilt.

✧ Then click on the Start button on the control box (or press the footswitch) to continue the scan.

Starting the next scan manually

If the next examination step is not part of an auto range, the system stops and remains ready for scanning. You then start acquisition of the next examination range manually.

Approaching the starting position

If the patient is not yet in the starting position for the next examination range, the prompt **Press MOVE** is displayed in the chronicle.

✧ Keep the button **Move** on the control box pressed until the patient table stops at the starting position for the next acquisition series.

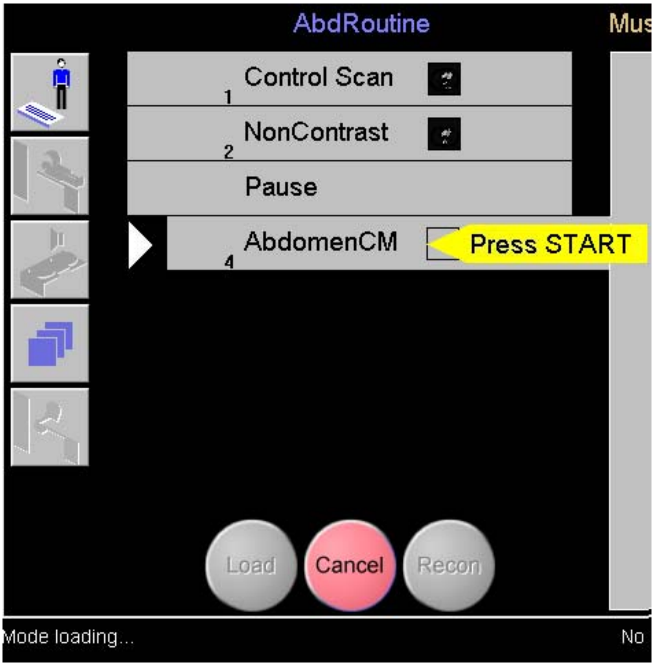
Or

✧ Click on **Cancel Move** if you want to start the next examination range at the current table position.

The patient table then moves back slightly so that the first image can be acquired at this table position.

Starting the next scan series

The next scan series is selected in the chronicle and the prompt **Press START** is displayed.



Possible actions

❏ Continue scanning immediately
→ Page C.5–23, *Starting the spiral*

❏ Inject contrast medium and then continue scanning

❏ Change the measurement settings for the next scan series
→ Page C.5–3, *Preparing for a spiral*

❏ Reconstruct the old scan series with a full matrix
→ Page C.5–41, *Starting reconstructions*

➪ Whenever you change settings on the **Routine** subtask card, the system is not immediately ready for scanning. If there is no **Start** request after changes, you must first click on the **Load** button.
→ Page C.5–22, *Performing a scan*

Completing an examination

You have executed the last examination step in the chronicle.

Depending on the configuration reconstruction of all open recon jobs is automatically initiated.

Before you let the patient leave the examination room, make sure that your scans are complete by using Topo Graphics.

It also makes sense to conduct the reconstruction with a full matrix to check the quality of the data while you can still repeat individual scans.

If you cannot conduct reconstructions that you might still need at the moment, because you have to start the next examination, make sure that the raw data are saved for later reconstruction runs.

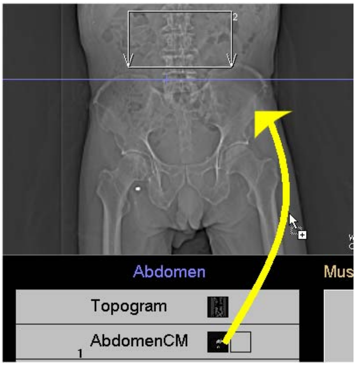
Only then terminate the examination to start the next examination or to work on another data set.

Displaying cutlines in the topogram

Documenting the scans as ranges and cutlines in the topogram is part of completing an examination.

Starting Topo Graphics via drag&drop

You can use the drag&drop function of the chronicle to have images of an individual series displayed as cutlines in the topogram.

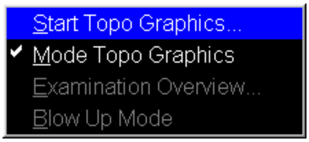


✧ Select a topogram in the chronicle.

✧ Select the recon icon of a reconstructed series in the chronicle.

✧ Drag the recon icon to the topo segment and drop it onto the topogram.

Starting Topo Graphics via menu



✧ Select a topogram in the chronicle and call up **View > Start Topo Graphics** in the main menu.

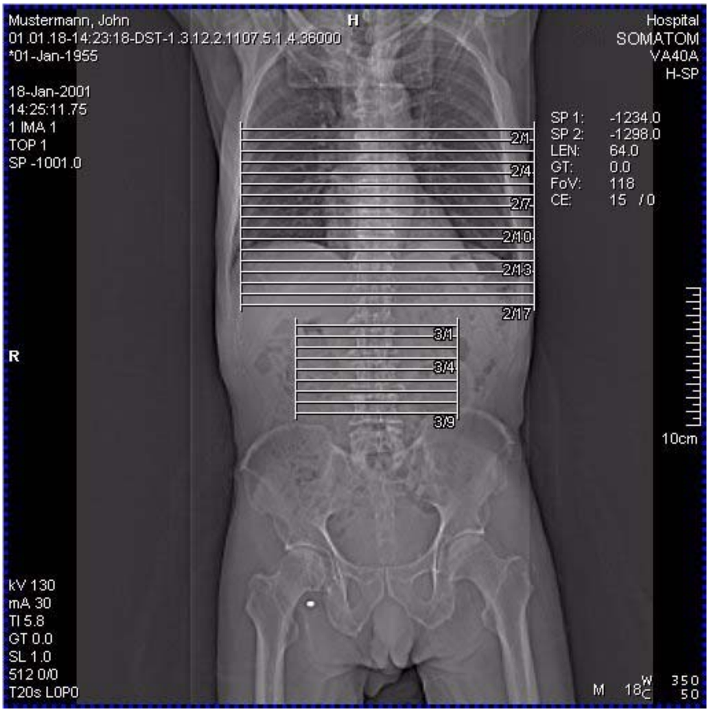
The **Patient Browser** window is opened. The current examination is already selected.

✧ Select the images or series for the examination that you wish to have drawn in the topogram as cutlines or ranges.
→ Page D.2–6, *Scrolling through and selecting patient data*

➩ If you do not change the preselection, all the images of the examination reconstructed with full matrix are used for the display in Topo Graphics.

✧ Call up **Patient > Update Topo Graphics** in the **Patient Browser**.

In the topogram, the reconstruction targets of all ranges and cutlines are marked. On the right-hand edge, you can see the number of the scan series and the image number.



⇨ You can zoom and pan the topogram display, if necessary.
→ Page C.3–23, *Changing the topogram display*

Changing the topogram

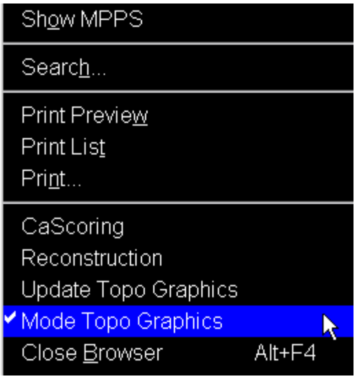
If you have acquired several topograms in the course of the examination (e.g. several perspectives), you can display the selected images as cutlines.

✧ Select the topogram in the chronicle.

✧ Call up **Patient > Update Topo Graphics** in the Patient Browser to display the cutlines in the topogram.

Saving Topo Graphics

If you want to document the topogram with the displayed cutlines onto film or save it for subsequent applications, **Topo Graphics** mode must be switched on when you terminate the examination.



✧ Check that **Mode Topo Graphics** is activated in the menu **Patient** of the **Patient Browser** or in the **View** menu of the **Examination** task card.
Activate the mode if necessary.

The examination regions and cutlines are stored together with the topogram as soon as you terminate the examination with **Patient > End**.

Switching off Topo Graphics

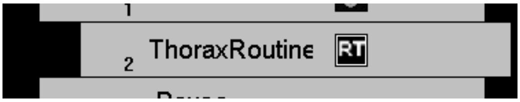
✧ Deselect **Mode Topo Graphics** in the menu **Patient** of the **Patient Browser** again.

In the topo segment, the ranges and cutlines are again displayed normally.

The topogram is stored **without** cutlines when the examination is terminated.

Starting reconstructions

The scan protocol of the current examination is still loaded in the chronicle and the system is still ready to scan if **Auto Recon** is not activated. You can now reconstruct the series just scanned with the full image quality. Or you can define new recon jobs with different settings to obtain sufficient diagnostic material with different fields of view.



✧ Select the scan series in the chronicle that you want to reconstruct.

✧ Create new recon jobs, if necessary.
→ Page C.10–14, *Appending new jobs*

✧ Change the preset image parameters on the **Recon** subtask card, if necessary.
→ Page C.10–20, *Changing reconstruction parameters*

➩ Remember that the parameters set on the **Auto Tasking** subtask card are considered for new recon jobs as well.

✧ Click on the **Recon** button underneath the chronicle to start reconstruction.

➩ You can read details about image reconstruction and planning of new reconstruction fields of view in
→ Chapter C.10, *Reconstruction*

Saving raw data for postprocessing

You can calculate the additional images with different reconstruction parameters at a later time. To do that, make sure that the raw data are delete protected before starting the next examination.

Automatic saving of the raw data

Your system stores the reconstructed scans in your local database. If not all planned reconstructions have been performed for a scan series, the raw data belonging to that study are protected from deletion.

The empty recon icons in the chronicle indicate for which scan series reconstructions still have to be performed, i.e. for which there are open reconstruction jobs. These also include the reconstruction jobs that have so far only been performed in **Guide View** quality (**RTD** images) with reduced image quality.

- Series **with open** recon jobs

- Series **without open** recon task

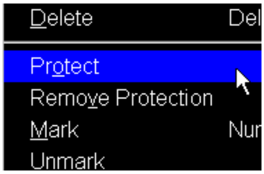
✧ Define one open reconstruction job for all scan series that you want to reconstruct later.
→ Page C.10–14, *Appending new jobs*

Saving raw data in the Patient Browser

As an alternative to creating open reconstruction tasks, you can also protect raw data of a scan or examination from deletion in the **Patient Browser**.

✧ Call up **Patient > Browser** in the main menu.

✧ Select the raw data concerned in the navigation or content area.
→ Page D.2–10, *Selecting raw data*



✧ Call up **Edit > Protect** in the main menu of the **Patient Browser** or **Protect** in the popup menu (right mouse key). The raw data are now protected from deletion.

NOTE

Catch up on outstanding reconstructions of your scans quickly. If you have protected raw data from deletion, remember to remove it again in the **Patient Browser** after you have processed the data.
→ Page D.5–20, *Protecting data from deletion*

In this way, you make sure that future examinations are not delayed, because old raw data are occupying necessary storage space.

Ending an examination

Make sure that all the necessary tomographic images required for the diagnosis have been reconstructed with the required quality or that the raw data have been protected from deletion.

You can now end the examination in order to start with the next one.

End Exam

✧ Click on the **End Exam** button.

Or

✧ Call up **Patient > End Exam** in the main menu to end the current examination.

Or

✧ Register a new patient and confirm with **Yes.**

The scan protocol of the patient, all reconstructed images, and the raw data of the scan series with open reconstruction tasks are stored.

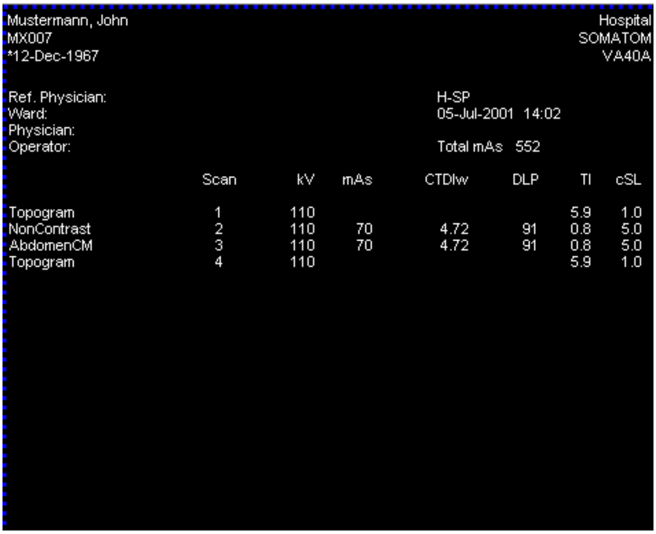
The gantry moves back to the scanning position for AP topograms.

⇨ If all planned reconstructions have been performed for each scan series of the examination the **Recon Controller** dialog box for easy deletion of the raw data is displayed.
→ Page C.10–34, *Deletion of raw data*

Patient protocol

As soon as you conclude the examination with **End Exam**, your system creates a patient protocol if this option is selected in the **Examination Configuration**.
→ Page C.13–17, *Patient-related default settings*

In the patient protocol you will see an overview of the examinations you have performed together with the examination steps and the most important scan parameters.



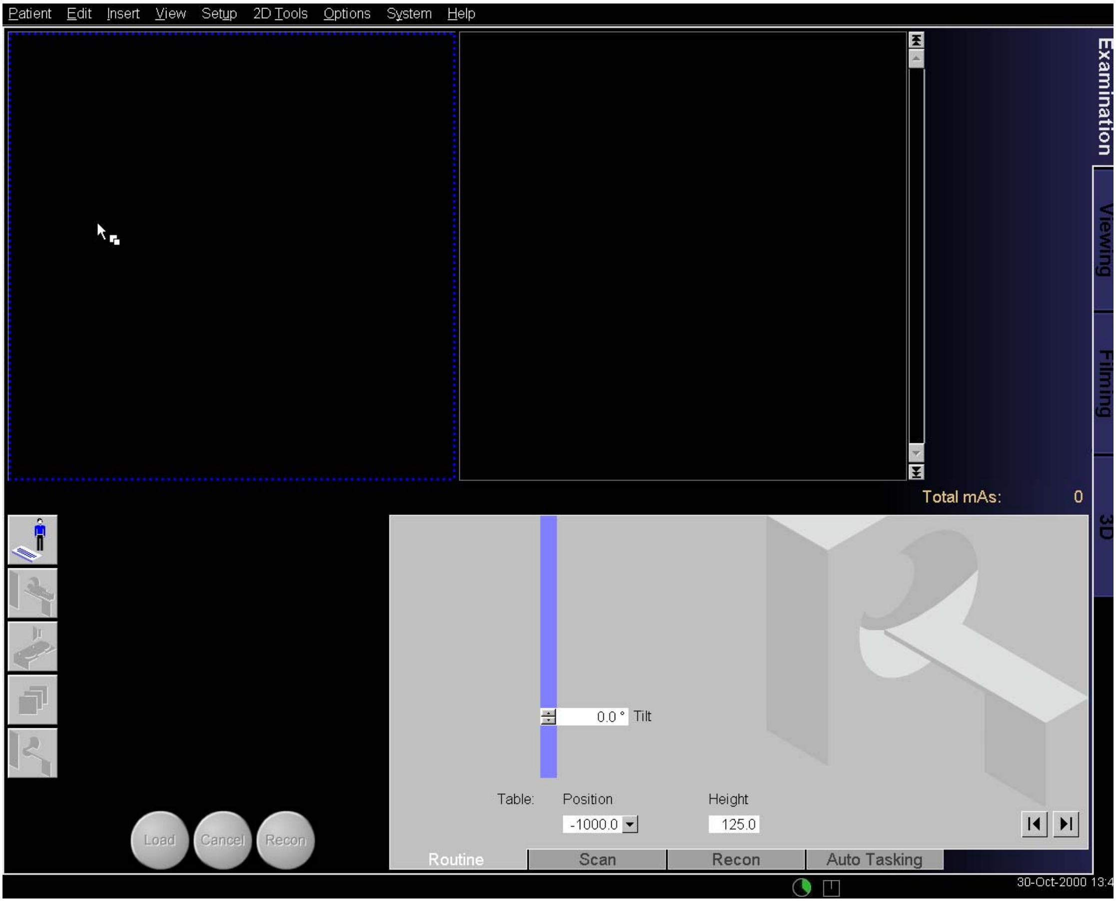
```
Mustermann, John                                                   Hospital
MX007                                                              SOMATOM
*12-Dec-1967                                                         VA40A

Ref. Physician:                                    H-SP
Ward:                                              05-Jul-2001  14:02
Physician:
Operator:                                          Total mAs   552

                        Scan      kV     mAs     CTDIw     DLP     TI    cSL

Topogram                 1       110                                5.9   1.0
NonContrast              2       110      70      4.72      91     0.8   5.0
AbdomenCM                3       110      70      4.72      91     0.8   5.0
Topogram                 4       110                                5.9   1.0
```

➪ In the patient protocol, the **mAs** and **CTDI** value is taken over from the **Routine** card. For scans with the CARE function activated, these values are above the values really used.

The patient protocol is stored as an additional series of the study in the local database and is indicated by a special icon in the **Patient Browser**.

Examination task card

The **Examination** task card is now empty.



You can register the next patient or select a new examination for the same patient via the patient registration window.

NOTE

End Exam resets the accumulated radiation dose count. The counting starts again for the next examination.

This is also the case if you perform an examination on the same patient.

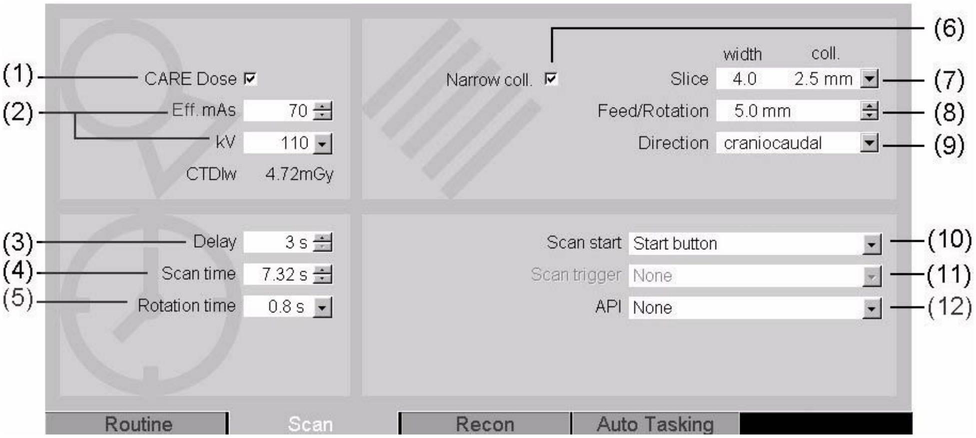
Special scan settings

When you select a routine scan protocol, all the main scan parameters for the examination of a region of the body in spiral mode are already set.

In the section *Preparing for a spiral*, you have learned how to adapt scan parameters which experience has shown always need to be adapted, how to check them before you begin scanning, and how change them, if necessary.
→ Page C.5–3, *Preparing for a spiral*

On the following pages, you will read how to find and change parameters of a spiral examination which have to be changed less frequently.

✧ Click the **Scan** subtask card into the foreground.



CARE Dose ☑
Eff. mAs 70
kV 110
CTDIw 4.72mGy

Delay 3 s
Scan time 7.32 s
Rotation time 0.8 s

Narrow coll. ☑
Slice width 4.0 coll. 2.5 mm
Feed/Rotation 5.0 mm
Direction craniocaudal

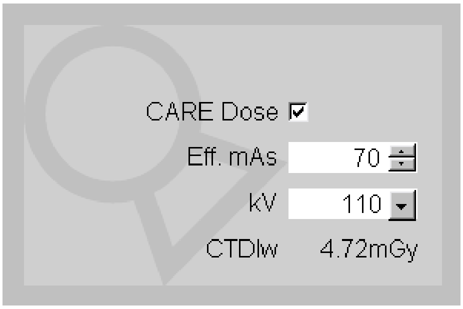
Scan start Start button
Scan trigger None
API None

(1) Dose modulation
(2) Radiation parameters
(3) Delay time
(4) Scan time
(5) Rotation time
(6) Slice width mode
(7) Effective and collimated slice width
(8) Table feed per rotation
(9) Scan direction
(10) Scan start
(11) Scan trigger (defined in scan protocol, grayed out)
(12) API text pair

Radiation parameters

You have already checked and adapted, if necessary, the mAs and the tube voltage on the **Routine** subtask card.

You can also view and modify these settings on the **Scan** card, if necessary, in order to improve the image quality or to minimize the radiation exposure of the patient. The CT dose index **CTDIw** displayed (in mGy) is calculated based on the scan parameters currently set.
→ Page C.5–6, *Checking the radiation parameters and slice width*



CARE Dose ☑

Eff. mAs 70

kV 110

CTDIw 4.72mGy

CARE Dose

In addition to the usual radiation parameters, you can decide whether you want to set continuous radiation or radiation with dose modulation (CARE Dose). If the **CARE Dose** function is active, the radiation doses vary throughout a scan depending on the tissue.

CARE Dose ☑

✧ Select **CARE Dose** to set scanning with modulated radiation.

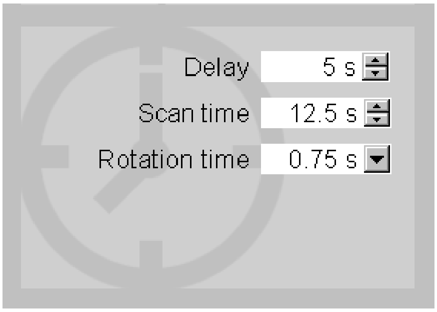
Or

CARE Dose ☐

✧ Deselect **CARE Dose** to scan with continuous radiation.

Time settings

In this part of the **Scan** card, you can modify the time settings for your scan.



Delay 5 s

Scan time 12.5 s

Rotation time 0.75 s

Delay time

Delay 4 s

✧ Set the time delay between the scan trigger and the onset of radiation using the spin buttons.
→ Page C.5–9, *Setting the delay time*

Rotation time

The rotation time is the time that the X-ray tube requires for one rotation.

The shorter the rotation time the longer the ranges that can be scanned between two respiration phases.

Longer rotation times are recommended if high resolutions are required for very small structures.

You have already checked with the control scan whether the image quality with the default rotation time is sufficient for your requirements. The "scan time" of the control scan corresponds to the rotation time of the following spiral.

If the control scan does not give an adequate image, you must change the rotation time for the spiral.

Rotation time 0.75 s

✧ Select a rotation time from the selection list.
The options provided are organ-specific.

➪ We recommend checking the rotation time again with a second control scan.

If you change the rotation time, the system adapts the scan time of the selected examination range. If necessary, the system will automatically set a kernel which is adapted to the new rotation time.

Scan time

The scan time is the period that the system requires to scan a range. It results from the rotation time, the length of the range, and the table feed per rotation.

Before the system begins scanning, it checks whether the set breathholding time of the patient is exceeded by the current scan time (only if an API text is defined). The tube monitoring checks the scan time for the load on the X-ray tube. If it is not possible to scan within the set scan time, your system displays a conflict message.
→ Page C.12–2, *Spiral too long*

Scan time 40.0 s

✧ Change the scan time using the spin buttons, if necessary.

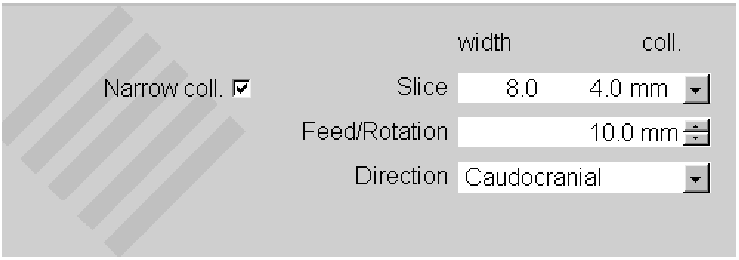
If you set a new scan time, your system automatically adapts the table feed per rotation. In the slice setting area of the **Scan** card, you can see the current table feed.

Feed/Rotation 10.0 mm

Slice settings

In the preparations for your spiral scan, you have checked the slice width and the scan direction and changed them on the **Routine** subtask card, if necessary.
→ Page C.5–3, *Preparing for a spiral*

You can view and modify these settings at any time on the **Scan** subtask card.



Narrow coll. ☑

	width	coll.
Slice	8.0	4.0 mm
Feed/Rotation		10.0 mm
Direction	Caudocranial	

Changing the table feed

You can also alter the table feed per rotation on the **Scan** subtask card. If you increase the table feed per rotation, the scan time is shortened. Your system lengthens the scan time if you set a smaller value.

Feed/Rotation 10.0 mm

✧ Increase the table feed using the spin buttons in order to scan the range faster.
→ Page C.5–53, *Scan time*

Slice-width mode

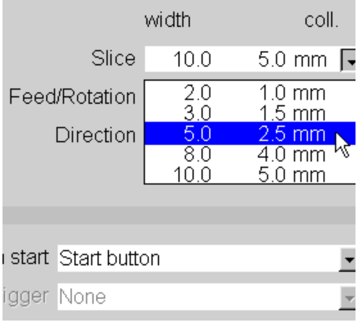
Your computer tomograph is equipped with a multi-row detector. Per rotation of the tube-detector system, several slices are scanned simultaneously. If you use the **Narrow Collimation** technique, the scan data of multiple detector rows are used to calculate one (fused) slice.

Narrow coll. ☑

✧ Click on the check box to activate the **Narrow coll.** slice width mode.
This reduces the partial volume artifacts and image noise.

Or

✧ Deactivate **Narrow coll.**.
The scan time for the range is shorter than with **Narrow coll.** for the same slice width.

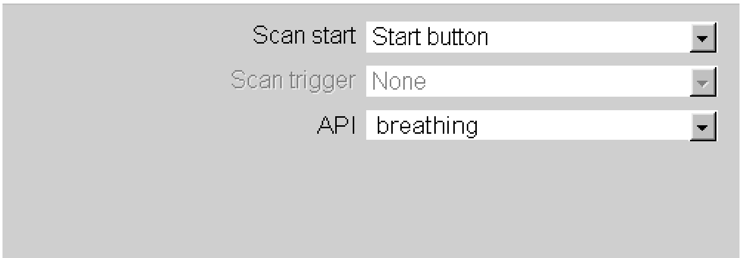


✧ After that, select the required slice width in the selection list.

When selecting the slice width, it is the first value (**Slice width**) which is relevant to you, because it is a measure of the slice width represented in one image. The **collimated slice width** is used for additional information. All slice widths that belong to the same collimation can be reconstructed afterwards.

Performing a scan

In this part of the **Scan** subtask card you select the scan starter and the text of the API announcement.



Scan start: Start button

Scan trigger: None

API: breathing

Defining the Scan start

You will usually control your scans from the console. As an alternative, you can start the scans from the examination room using the footswitch.

Scan start: Start button

✧ Select the **Start** key (on the control box) or the footswitch (in the examination room) as the scan trigger.

➪ Scan triggering by footswitch is set if the scan has to be triggered in the examination room for interventional examinations.

Selecting an API text

For examinations with automatic patient instruction, you have to select a pair of announcement texts.

A suitable pair of announcement texts is usually preset in the routine scan protocol.

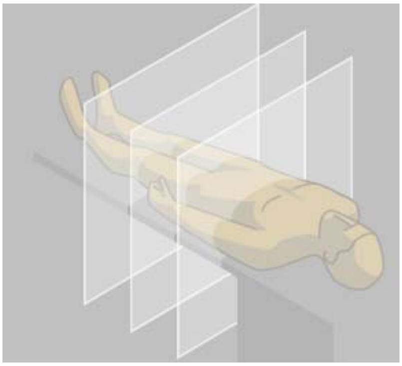
API breathing

✧ Check the selection and select a new pair of texts from the list, if necessary.

➪ You can read how to create new announcement texts and place them in the selection list on
→ Page C.13–5, *Recording and processing API texts*

CHAPTER C.6 Sequence

Sequence examinations provide a series of individual slice scans over a defined range with a constant slice width and increment.



Use of the sequence method

Although you can perform most of your examinations in spiral mode, sequence examinations are useful, for example, for very small ranges, because the tube-detector system needs no starting and concluding rotations.

To scan the lung with high resolution, we recommend the sequence mode. With it, you can scan a very thin slice (typically 1 or 2 mm) every 1 or 2 cm, i.e. you can scan with gaps.

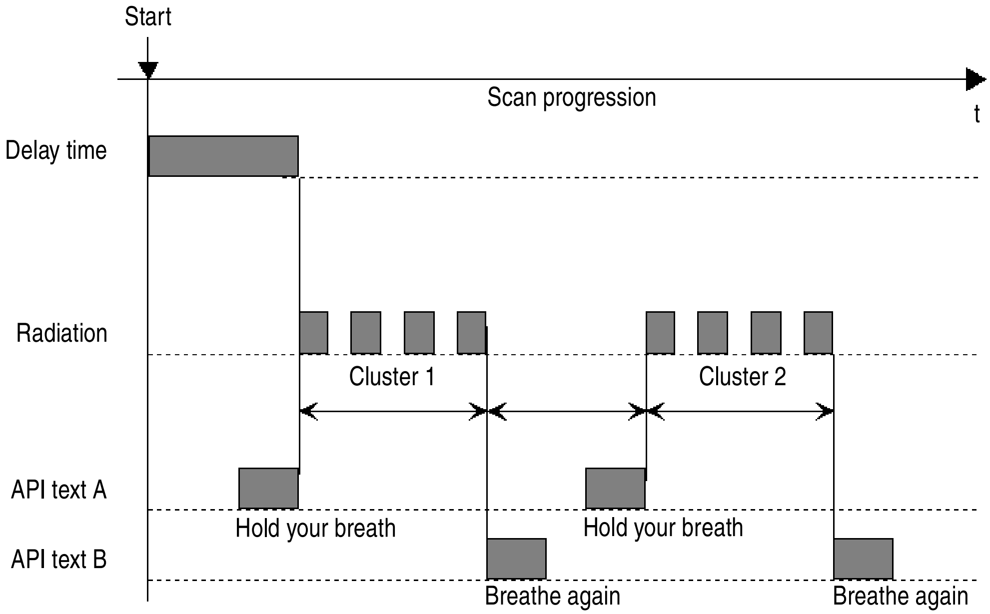
Long ranges can be scanned without interruption with sequence examinations, just as for spiral examinations.

Automatic clustering

For long sequence examinations with breathing instructions, the system groups the scans that are possible within one respiration phase automatically to form so-called clusters. Before and after every cluster, your system plays back the breathing command and in the pauses between the clusters, the patient can breathe again.

The length of a cluster and therefore also the number of scans per cluster depends on the breathholding time set, generally 18 seconds.
→ Page C.2–16, *Entering a breathholding time*

⇨ You can shorten the duration of a cluster at any time by pressing the **Suspend** and **Start** buttons.
→ Page C.6–32, *Suspending a scan*

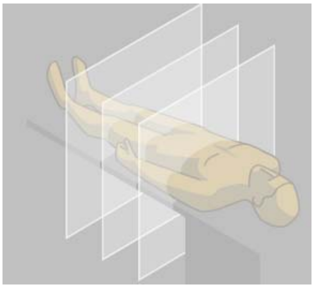


NOTE

For scans with API, you should set a short cycle time to be able to scan as many slices per cluster as possible.
→ Page C.6–61, *Cycle time*

Preparing for a sequence

After you have scanned the topogram, the system has selected the first examination step of the following scan series in the chronicle.



You can see which scan mode is selected by the patient model on the **Routine** subtask card.
→ Page C.1–12, *The subtask cards*

The scan parameters suggested by the routine scan protocol are entered in the input and selection fields. In most cases, these data are suitable for your examination. The size and positioning of the range in the topogram depend on the individual patient and therefore have to be adapted for each new patient.
→ Page C.3–21, *Adapting ranges*

Before you continue with the examination, check the scan parameters on the **Routine** subtask card.

- ➪ If you want to use automatic functions, such as automatic patient instruction system, you must activate them before you start scanning.
  → Page C.2–12, *Automatic functions*
- ➪ On Osteo scan protocols, all scan and reconstruction parameters are default settings and should not be altered. You should only change the horizontal table position and the gantry tilt in the subtask card.

NOTE

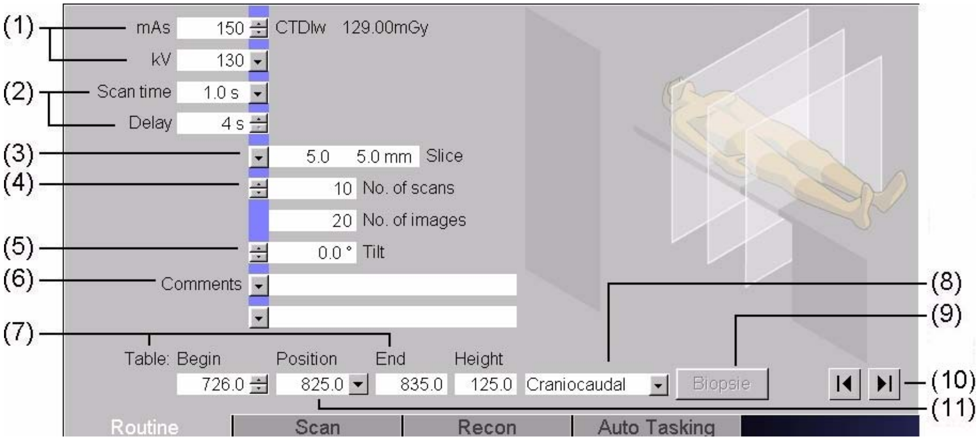
If more than one scan series, i.e. more than one range, is planned for the sequence examination, you must check the scan parameters of these ranges individually. Initially, the first scan series is selected.

✧ Select the next or a following scan series in the topo segment or in the chronicle to have the scan parameters displayed on the **Routine** card.

✧ Make the changes in all series to which the new settings apply.

✧ Before you start scanning, select the first range again.

Routine subtask card



mAs 150 CTDIw 129.00mGy

kV 130

Scan time 1.0 s

Delay 4 s

5.0 5.0 mm Slice

10 No. of scans

20 No. of images

0.0 ° Tilt

Comments

Table: Begin 726.0 Position 825.0 End 835.0 Height 125.0

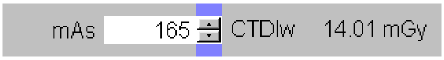
Craniocaudal

(1) Radiation parameters
(2) Time settings
(3) Slice width
(4) Number of images
(5) Gantry tilt
(6) Comment lines
(7) Range
(8) Scan direction
(9) Biopsy button
(10) Buttons for step-by-step table movement into/out of the gantry
(11) Current table position

Checking the radiation parameters, scan time, and slice width

The routine scan protocol suggests radiation parameters that in most cases ensure excellent image quality with low radiation exposure of the patient. In individual cases (e.g. for corpulent patients), it might be necessary to change the default settings slightly.

mAs per image



mAs 165 CTDIw 14.01 mGy

✧ Enter the mAs per image and confirm with the **Return** key. The larger the value the sharper the image and the less noise is in it. But the radiation dose for the patient is also increased.

Based on the current scan parameter settings the CT dose index **CTDIw** (in mGy) is calculated and displayed next to the **mAs** input field.

Tube voltage

kV 80

✧ Select the tube voltage. Higher values improve the contrast in the display of soft tissue.

Scan time

Scan time 1.5 s

✧ Select the scanning time per scan.
The local resolution is better the longer the rotation time is. But with long rotation times, the probability of motion artifacts also increases.

Slice width

The slice width must be adapted to the size of the objects that you want to display during the scan. This is already taken into account in the routine scan protocols for individual examinations.

If you want to chose another setting anyway, make sure that the scan time is increased with a smaller slice width which increases the radiation exposure of the patient.

5.0 5.0 mm Slice width

✧ Choose a slice width in the selection list if you want to change the set value.

⇨ The possible slice widths are provided for selection in the list depending on the set slice-width mode.
→ Page C.6–63, *Slice-width mode*

Setting the delay time

The **Routine** protocol suggests a delay time suitable for the region to be examined. This is the time from pressing the **Start** key to when the scan begins. Note that it is not possible to set a delay smaller than a certain minimum delay time, because the scanning system requires a short preparation time.


Delay 3 s

✧ Change the delay time using the spin buttons, if necessary.

➩ Activating the API announcement text increases the minimum delay time, which might cause the delay you set to be increased automatically. If this happens, a message is displayed on the status bar. Remember that this value will automatically be changed back if you deactivate the API.

NOTE

With the delay time you define the length of the interruption between two consecutive scans in an auto range.

Changing the range and scan direction

You can plan the size and positioning of the ranges graphically in the topo segment. Before scanning the sequence, you can see the start and end position of the first range and the current table position on the **Routine** card.

Length of the range

Before you start scanning, you can change the settings of the ranges again.

✧ Adapt the starting and end positions of a range and confirm your settings with the **Enter** key.
The changes are displayed immediately in the topo segment.

Or

✧ Move the boundary lines of the examination range in the topo segment.
The changes are immediately applied on the **Routine** subtask card.

Number of scans

The system calculates the number of scans from the length of a range and the selected slice width taking the set table feed into account, which is usually the same as the slice width.

On the **Routine** subtask card, the number of scans calculated is displayed. If you change this value, you can lengthen or shorten the range by individual scans.


55 No. of scans

✧ Set a larger (or smaller) number of scans using the spin buttons if you want to lengthen (or shorten) the range accordingly.

The new end position of the scan series is displayed in the topo segment and in the **Table: ... End** field of the **Routine** subtask card.

Gantry tilt

Like for the beginning and end of ranges, you can plan graphically in the topo segment for tomograms with a lateral patient position that are scanned with a tilted gantry.
→ Page C.3–28, *Tilting a range or cutline*

0.0 ° Tilt

The current gantry tilt is always displayed on the **Routine** card. Before you start scanning, you can tilt the gantry to another angle.

✧ Select the required gantry tilt using the spin buttons.

Or

✧ Change the tilt numerically for each range.

Press the **Move** key on the control box until the new gantry tilt has been reached.

> **NOTE**
>
> If an increase in the gantry tilt has been planned for an examination step in an auto range, you must confirm it manually with Move. A message appears in the chronicle prompting you to tilt the gantry.

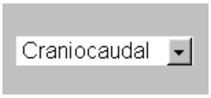
Scan direction

In the routine scan protocol, the caudiocranial scan direction is preset for examinations of the skull and the craniocaudal scan direction for examinations of the body. If more than one range is planned for an examination, the same scan direction is usually set for all of them in the routine scan protocol.

In contrast-medium series in which the same examination range is scanned several times, the patient table moves back to the starting position between two scans.

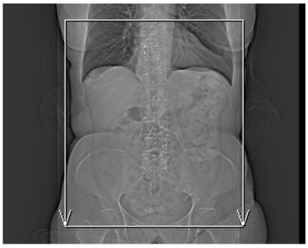
You can change the scan direction, for example to shorten the time for table movement between scanning two identical ranges. If you are examining the same region first in the craniocaudal and then (with contrast medium) in the caudiocranial direction, you save the time for repositioning the table.

✧ Select the range for which you want to change the scan direction, in the chronicle or in the topo segment.

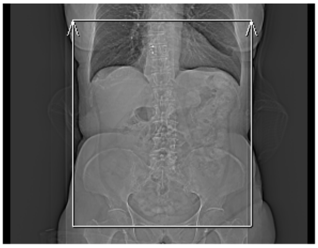


✧ Select the new scan direction on the **Routine** subtask card.

(1)



(2)



(3)

(1) Craniocaudal
(2) Caudocranial
(3) Craniocaudal

Number of images

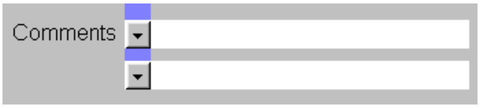
On systems with a multi-row detector, the number of images states how many single images you can obtain from the total measured data of the scan series.
(Number of scans x number of images per scan).

20 No. of images

The number of images displayed depends on the range length and on the slice settings which can be modified on the **Scan** subtask card.
→ Page C.6–62, *Slice settings*

Entering comments

Comment texts are displayed on the reconstructed images and filmed or printed together with the images.



✧ Select one or two comment lines from the selection lists.

➪ You can create and edit standard comments in the **API / Comment Setup** dialog box.
→ Page C.13–3, *Creating standard comment texts*

Or

✧ Enter free comment texts in one or two input fields.

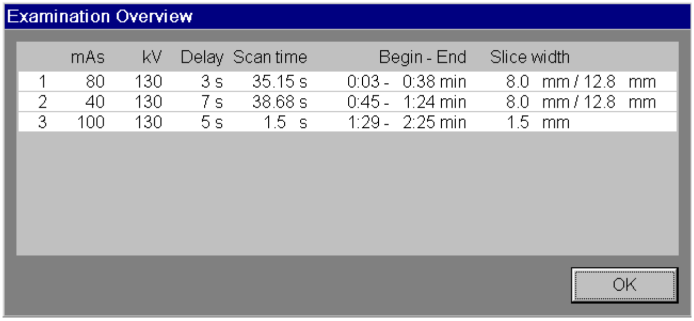
Displaying the parameter overview

The scan parameters for the sequence acquisition selected in the chronicle are displayed on the **Routine** subtask card.

You can view the most important scan settings for the examination steps of an auto range in an overview.

✧ In the chronicle, select an entry in the auto range.

✧ Call up **View > Examination Overview** in the main menu to display a parameter overview of the auto range.



	mAs	kV	Delay	Scan time	Begin - End	Slice width
1	80	130	3 s	35.15 s	0:03 - 0:38 min	8.0 mm / 12.8 mm
2	40	130	7 s	38.68 s	0:45 - 1:24 min	8.0 mm / 12.8 mm
3	100	130	5 s	1.5 s	1:29 - 2:25 min	1.5 mm

➪ If you are not planning any special sequence scans such as **Biopsy** or **Serio**, continue on
→ Page C.6–26, *Scanning a sequence*

Preparing special sequence scans

Special scanning procedures such as serio scans, which are also executed in a sequence, are very easy to set in the **Routine** and **Scan** subtask cards.

In the following, you will find a description of the scanning procedures listed:

❏ Sequence with gaps

❏ Dynamic scan series (serio)

❏ Biopsy

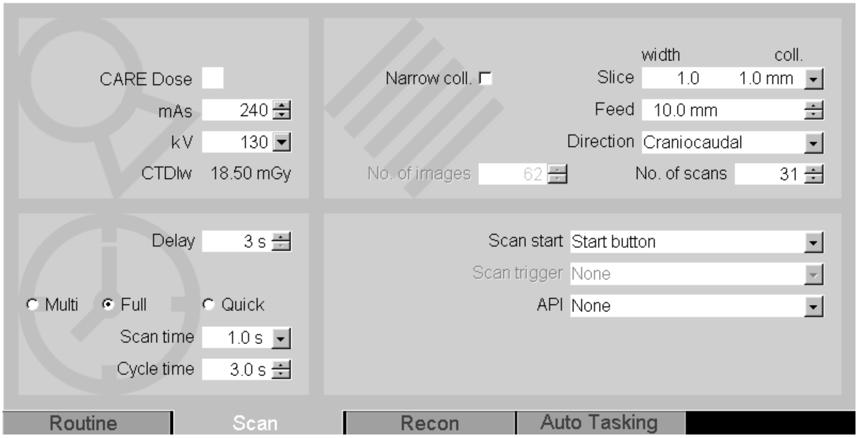
➪ You will find more information about HeartView CT examinations and CARE Bolus examinations in
→ Chapter C.7, *HeartView CT (Option)*
→ Chapter C.8, *CARE Bolus (Option)*

Sequence with gaps

Apart from high resolution examinations of the lung, gapless scanning sequences are the rule for all examinations. The single scans are contiguous without gaps or overlap, and the patient table is moved by the distance of one slice width between scans. If the slice width is changed, the table feed is therefore automatically adapted to the new slice width.

In some examinations, it can be useful to increase the distance between slices, i.e. to scan with gaps. In high resolution pulmonary examinations, you might want to adapt the distance between scans to the diagnostic problem.

✧ Switch to the **Scan** subtask card to change the table feed.



CARE Dose ☐
mAs 240
kV 130
CTDIw 18.50 mGy

Narrow coll. ☐

	width	coll.
Slice	1.0	1.0 mm

Feed 10.0 mm
Direction Craniocaudal
No. of images 62
No. of scans 31

Delay 3 s
○ Multi ● Full ○ Quick
Scan time 1.0 s
Cycle time 3.0 s

Scan start Start button
Scan trigger None
API None

Feed 4.0 mm

✧ Increase the table feed (per scan).

The table feed is the distance between two scans (i.e. the gap). As soon as you increase the table feed, the system automatically reduces the number of scans; the range is not altered.

The message “Table feed is not equal to slice thickness” is displayed in the status bar.

NOTE

Whenever you change the slice width, the system sets the table feed to achieve scanning without gaps or overlap. You therefore always have to set the increased table feed **after** setting the slice width.

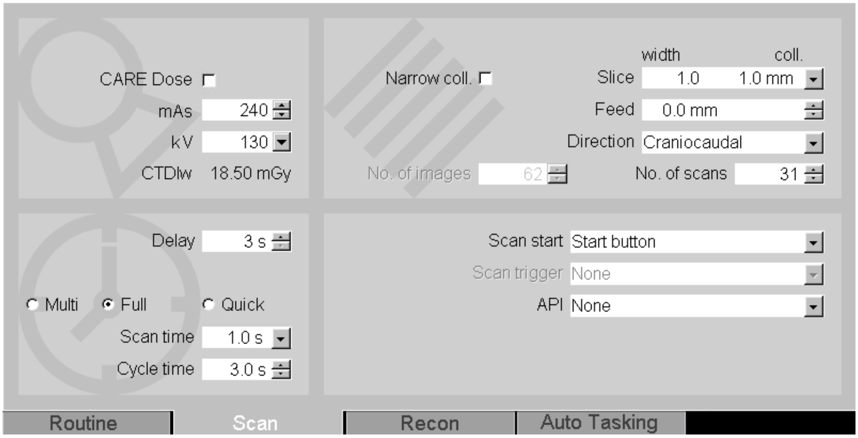
Serio scans (sequence without table feed)

One variation of the sequence examination is acquiring a scan series without table feed. You can use this to determine changes in density over a defined period (usually after contrast-medium injection).

➩ No automatic clustering is performed for these scans, even if the scan time exceeds the set breath holding time.

✧ Determine the position of a slice which is representative of the organ using the topogram and, if necessary, control scans.
→ Chapter C.4, *Control Scan*

✧ Switch to the **Scan** subtask card to set up the sequence scans without the table feed.



CARE Dose ☐
mAs 240
kV 130
CTDIw 18.50 mGy

Narrow coll. ☐
width coll.
Slice 1.0 1.0 mm
Feed 0.0 mm
Direction Craniocaudal
No. of images 62
No. of scans 31

Delay 3 s
○ Multi ● Full ○ Quick
Scan time 1.0 s
Cycle time 3.0 s

Scan start Start button
Scan trigger None
API None

Converting a range to a cutline

Feed 0.0 mm

Plan the examination area for the Serio scan series as a cutline.

✧ Set the table feed to “0” on the **Scan** card.
The range becomes a cutline.

✧ Move the cutline in the topogram to the required scanning position.

Defining the number of scans

No. of scans 20

✧ Define the number of scans to be taken.

➪ You should set a slice width with **one** image per scan (i.e. the number of scans and slices are equal). Otherwise, you will obtain a range with more than one image at different table positions at one scanning time.
→ Page C.6–62, *Slice settings*

Setting the cycle time

The system now plans the stated number of scans without the patient table being moved between the scans. The scans are taken at defined time intervals.

You must set the time intervals between scans, the cycle time, to the expected change in density, i.e. the contrast-medium kinetics.

✧ Increase the cycle time to lengthen the pauses between scans.

Biopsy mode

In biopsy mode, the examining physician can trigger individual scans in the examination room at freely selected table positions. The individual tomogram scans are observed on a second monitor located in the examination room.

A detailed representation of the organ structures in the tomographic image allows precise localization of the lesion and the surrounding region. The physician can therefore plan the path of the puncture in the transversal cut precisely, avoiding critical structures such as vessels, nerves, or the intestine.

Preparation

Usually, you locate the structure to be punctured with a spiral scan.
→ Chapter C.5, *Spiral*

The path of access and the point of insertion are then marked on the skin surface. This is also the scan position for the scan sequence in biopsy mode.

Activating biopsy mode

✧ Click on the Biopsy button in the **Routine** card to activate biopsy mode for the sequence.

➪ Biopsy mode cannot be performed for scans in an auto range, or **HeartView CT** and **CARE Bolus** examinations.

Special aspects of biopsy mode

The following aspects of examinations in biopsy mode must be taken into account:

❏ Individual scans are always acquired at the current table position with minimum start delay.

❏ Any horizontal and vertical table position within the collision limit can be selected.

❏ You must always trigger the individual scans via the start button or footswitch. Automatic table feed is not performed after the scan.

❏ If you set a low table height for the scan, the patient is located outside the scan center. Reduced image quality results.

❏ If **Autoload Viewer** is activated, every image is immediately transferred to the **Viewing** card and can be displayed in full screen display.

❏ Hand Care is activated for Quick Scan to reduce exposure of the physican’s hands.

NOTE

If the patient is incorrectly positioned in the scan field, the images may be useless. This results in an unnecessary radiation exposure of the patient.

Please make sure that you set the horizontal and vertical table position correctly before scanning.

Activating biopsy mode

Biopsy

✧ Click on the **Biopsy** button on the **Routine** card to activate biopsy mode for the sequence.

The following examination steps are marked with the biopsy icon.

➪ Biopsy mode cannot be used for scans in an Auto Range and for HeartView CT and CARE bolus examinations.

Deactivating biopsy mode

Biopsy

✧ Click on the **Biopsy** button again to deactivate biopsy mode for the sequence.

Scanning a sequence

After you have checked the scan parameters for your sequence examination and changed them, if necessary, you can begin scanning the first range.

Automatic check of scan settings

When you change or confirm scan settings, the system checks whether the selected settings cause conflicts with the tube monitoring. If necessary, the system will adjust the scan settings within the preset organ-specific limits.

If you are required to intervene, the system displays a conflict message and helps you find the scan settings suitable for your purposes.
→ Chapter C.12, *Scan Management*

Starting scanning

After you have checked the scan parameters for your sequence scans, start the first scan. The system then scans slice by slice. The table is moved automatically between scans.

Confirming the parameters

✧ Click on the **Load** button to confirm the set scan parameters.

The **Press MOVE** prompt is displayed in the chronicle, if the patient table is not yet in the starting position.

Moving to the starting position

✧ Press the **Move** key on the control box until the patient table is in the starting position for the sequence.

Or

✧ Click on the **Cancel Move** button if you want to begin the sequence at the current table position.

➪ **Cancel Move** is not possible if the current table position is close to or behind the end of the range.

The **Press START** prompt is displayed in the chronicle.

Starting the sequence

✧ Press the **Start** key on the control box (or press the foot-switch) to start the sequence scan.

The delay time elapsing until radiation is released is displayed in the chronicle.

➪ If you are scanning with automatic patient instruction system, the announcement is made during the delay time.

After the countdown has elapsed, the system starts scanning the first slice.

Tracing the scanning procedure

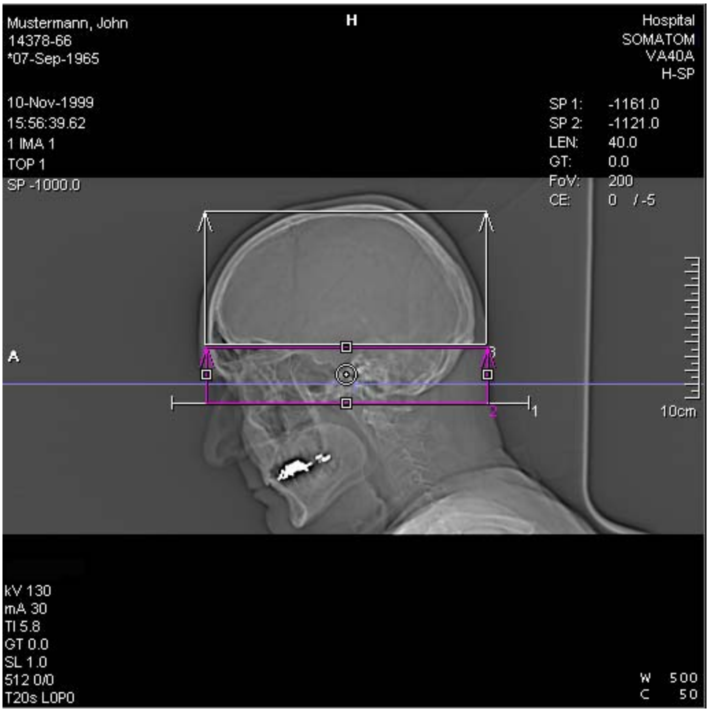
You can observe the progress of your scan on the screen so that you can intervene immediately if problems arise.

Display in the chronicle

In the chronicle, you can see how many scans have been completed already and how many are planned in total.

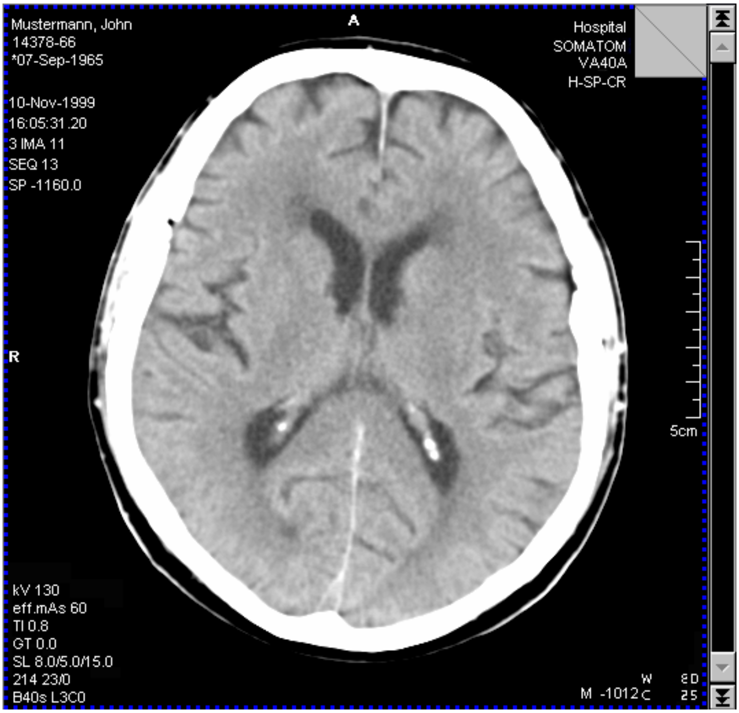
Display in the topo segment

A line over the entire width of the topo segment marks the position at which a slice is being scanned. This line moves from the starting position to the end of the range as scanning progresses.



Display of the slice scans

After each scan, a tomogram is calculated of the set field of view. You can see the image with the number and associated text in the tomo segment after a short delay.



✧ Check the images displayed during the scan.

If the patient is uncooperative or you are worried that the examination might fail for other reasons, stop scanning and repeat the unclear images.

Suspending a scan

At all positions in the scan, you can suspend the sequence to continue with the next range or to terminate the examination.

➩ If suspending the sequence is not required, continue on
→ Page C.6–37, *End of the range reached*

Suspend buttons

✧ Click on the **Suspend** button to suspend scanning.

Or

✧ Press the **Suspend** key on the control box.

Scanning is terminated.

The system is still ready for scanning.

Restarting the scan

If you have terminated the sequence shortly after starting scanning, the suspended scan series remains loaded in the chronicle. You can restart scanning of the same range.

➪ If necessary, change the scanning parameters on the **Routine** card. After this, you must confirm the new parameters with **Load** before restarting the scan.

✧ Press the **Start** key on the control box (or press the footswitch) to start the scan of this sequence series.

Suspension in an extreme emergency

✧ In an emergency, press the **Stop** key on the control box.

Radiation is stopped immediately and the entire system is blocked. You can resume the examination after you have pressed **Continue** in the dialog window displayed.
→ Page C.12–23, *Restoring system readiness*

Continuing examination after suspension

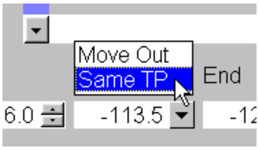
The previous scan series is finished and marked as scanned by a miniature tomogram in the recon icon in the chronicle. The system calculates the radiation dose of the patient accumulated so far.
→ Page C.6–38, *Total radiation dose*

➩ If you accidentally interrupt sequence scanning before the end of the examination range or if the scan was aborted, copy the examination step (**Repeat** in the chronicle), adapt the scan range, and then scan the remaining range.
→ Page C.2–31, *Repeating an examination step*

Repeating part of a range

If you have suspended scanning because the patient moved and a number of scans are therefore unusable, you can now repeat these scans. First move the patient table back to the position of the first unsuccessful image.

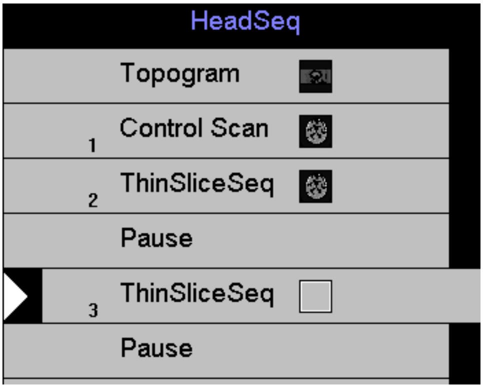
✧ Page to the first unsuccessful image in the tomo segment by repeatedly clicking on the inner dog ear in the top right-hand corner with the mouse.
→ Page C.10–9, *Scrolling in the tomo segment*



✧ Click on **Same TP** in the selection list of the table position.

- Press the **Move** key on the control box until the patient table stops.
- In the chronicle, copy the examination step with **Repeat** and adapt the start and the end of the scan range, if necessary.
  → Page C.2–31, *Repeating an examination step*

A new examination step is inserted in the scan protocol with which you can scan the missing scans up to the end of the range.



HeadSeq
Topogram
1 Control Scan
2 ThinSliceSeq
Pause
3 ThinSliceSeq ☐
Pause

- Click on the **Load** button to confirm the set scan parameters.

The **Press MOVE** prompt is displayed in the chronicle.

- Click on **Cancel Move** to start the range at the current table position.
- Press the **Start** key on the control box (or press the foot-switch) to continue to scan the range.

Moving to the next range

If you have suspended the scan because you have already obtained all the images required for the diagnosis, then continue with the next examination step.

The next scan is selected in the chronicle. You are prompted to **Press MOVE**.

✧ Press the **Move** key on the control box until the patient table is in the starting position for the next range.

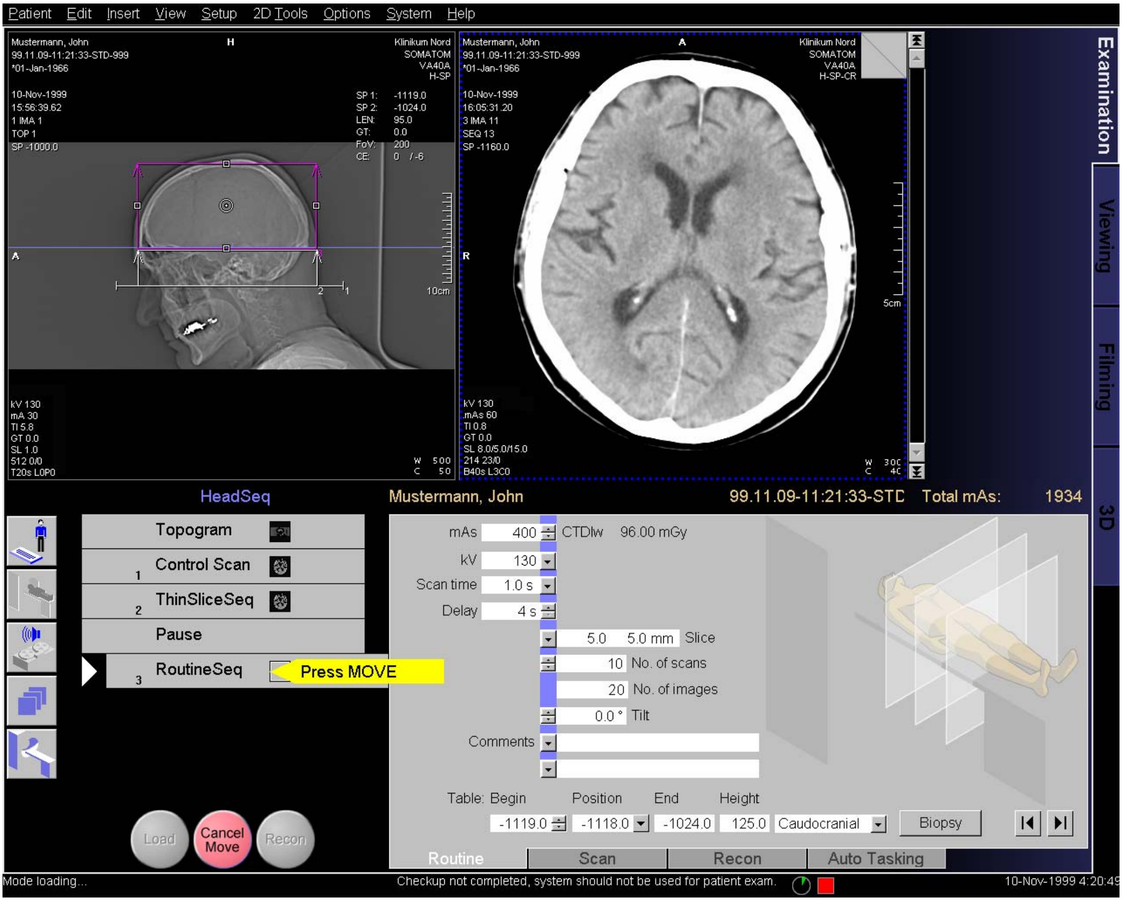
Or

✧ Click on **Cancel Move** if you want to start the next range at the current table position.

Now start the next scan series.
→ Page C.6–40, *Adding scans*

End of the range reached

After scanning of the first range has been completed, the last slice scan is reconstructed and displayed in the tomo segment. The patient table stops at the set end position.



Mustermann, John 99.11.09-11:21:33-STD Total mAs: 1934

mAs 400 CTDIw 96.00 mGy
kV 130
Scan time 1.0 s
Delay 4 s
5.0 5.0 mm Slice
10 No. of scans
20 No. of images
0.0 ° Tilt
Comments

Table: Begin -1119.0 Position -1118.0 End -1024.0 Height 125.0 Caudocranial

Mode loading...

Checkup not completed, system should not be used for patient exam.

10-Nov-1999 4:20:49

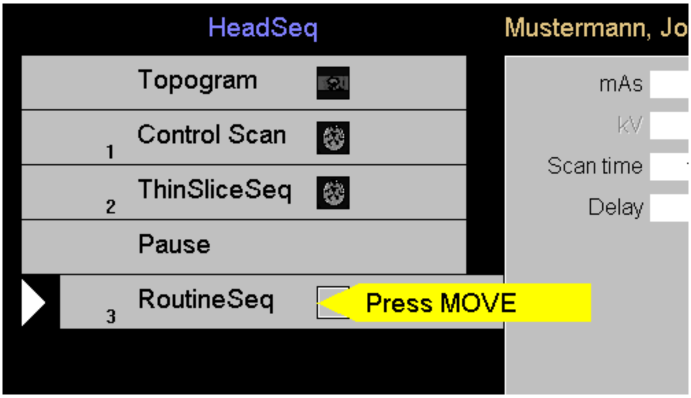
Total radiation dose

The radiation dose accumulated so far is displayed in the title bar above the subtask cards behind the patient name. It is updated after every interruption in scanning and at the end of a scanning step.

Mustermann, John 14378-66 Total mAs: 810

Display in the chronicle

The sequence is marked as scanned in the recon icon in the chronicle. The next examination step is selected.



Next scan in auto range

The second and following scan series of an auto range are started automatically by your system unless the gantry inclination has to be increased. In that case, the prompt **Press Move** appears in the chronicle.

- Hold the **Move** key on the control box down until the Gantry tilt is set.

Or

Cancel Move

- Click on **the button Cancel Move** if you want to retain the current gantry tilt.

- Then press the Start key on the control box (or press the footswitch) to continue the scan.

Performing additional scans

If individual images of your scan are unusable because of motion artifacts, or you want to perform late scans at individual table positions, make additional scans. The additional tomographic images are stored in a series together with the previous images of the range.

Adding scans

When appending additional scans to the end of a range, the system always scans with the same table feed and the same slice width (e.g. distance between the scans: with or without gaps) set for this range.

✧ Choose **Add scan** from the menu to get the entry in the scan protocol.

✧ Press the **Start** key on the control box (or footswitch) to make a further scan.

A **Pause** entry is automatically inserted between the selected range and the added scan.

Additional scans are always individual scans, i.e. if you require several additional scans, you must press the **Start** key for each one. The table is moved automatically by the system.

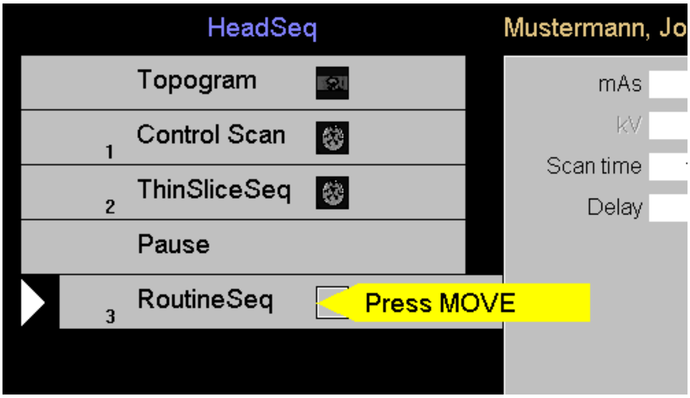
✧ If you do not require any more additional scans, press the **Move** key and continue your examination with the next scan.
→ Page C.6–41, *Starting the next scan manually*

Starting the next scan manually

If the next examination step is not part of an auto range, the system stops and remains ready to scan. You then start the scan of the next examination area manually.

Moving to the starting position

If the patient table is not in the starting position for the next examination range, the message **Press MOVE** is displayed in the chronicle.

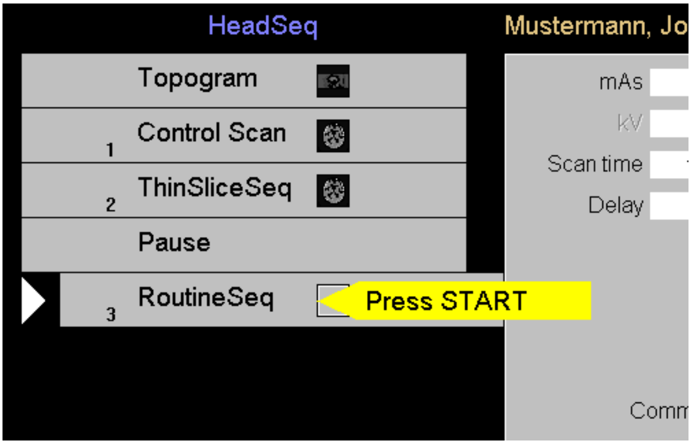


✧ Hold the **Move** key on the control box down until the patient table stops at the starting position for the next scan series.

Or

✧ Click on **Cancel Move** below the chronicle if you want to start the next range at the current table position.

In the chronicle, the next step is now selected and the **Press START** prompt displayed.



Possible actions

- ❏ Continue scanning immediately
  → Page C.6–28, *Starting the sequence*
- ❏ Inject contrast medium and then continue scanning
- ❏ Change the measurement settings for the next scan series
  → Page C.6–4, *Preparing for a sequence*

➪ Whenever you change settings on all subtask card, the system is not immediately ready for scanning. If there is no **Start** request after changes, you must first click on the **Load** button.
→ Page C.6–27, *Starting scanning*

Completing an examination

You have executed the last examination step in the chronicle.

Before you let the patient leave the examination room, make sure that your scans are complete by using the examination overview (topographics).

If you cannot conduct reconstructions that you might still need at the moment, because you have to start the next examination, make sure that the raw data are saved for later reconstruction runs.

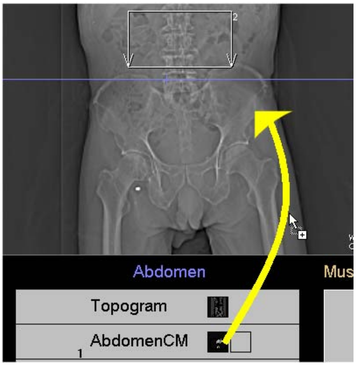
Only then terminate the examination to start the next examination or to work on another data set.

Displaying cutlines in the topogram

Documenting the scans as ranges and cutlines in the topogram is part of completing an examination.

Starting Topo Graphics via drag&drop

You can use the drag&drop function of the chronicle to have images of an individual series displayed as cutlines in the topogram.



✧ Select a topogram in the chronicle.

✧ Select the recon icon of a reconstructed series in the chronicle.

✧ Drag the recon icon to the topo segment and drop it onto the topogram.

Starting Topo Graphics via menu

✧ Select a topogram in the chronicle and call up **View > Start Topo Graphics** in the main menu.

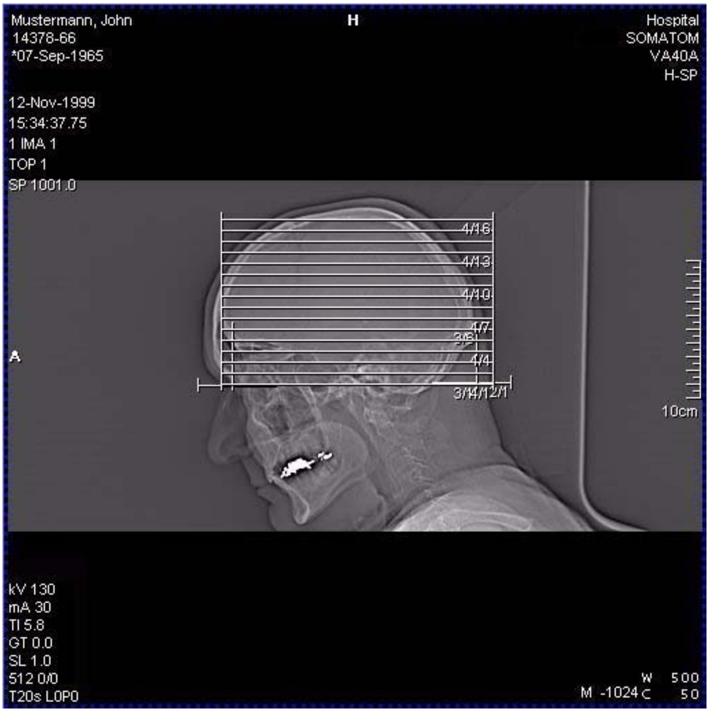
The **Patient Browser** window is opened. The current examination is already selected.

✧ Select the images or series for the examination that you wish to have drawn in the topogram as cutlines or ranges.
→ Page D.2–6, *Scrolling through and selecting patient data*

➪ If you do not change the preselection all the images of the examination reconstructed with full matrix are used for the display in Topo Graphics.

✧ Call up **Patient > Update Topo Graphics** in the **Patient Browser**.

In the topogram, the reconstruction targets of all ranges and cutlines are marked. On the right-hand edge, you can see the number of the scan series and the image number.



➩ You can zoom and pan the topogram display, if necessary.
→ Page C.3–23, *Changing the topogram display*

Changing the topogram

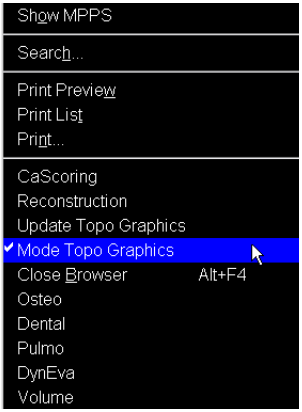
If you have acquired several topograms in the course of the examination (e.g. several perspectives), you can display the selected images as cutlines.

✧ Select the topogram in the chronicle.

✧ Call up **View > Start Topo Graphics** in the Patient Browser to display the cutlines in the topogram.

Saving Topo Graphics

If you want to document the topogram with the displayed cutlines onto film or save it for subsequent applications, **Topo Graphics** mode must be switched on when you terminate the examination.



✧ Check that **Mode Topo Graphics** is activated in the menu **Patient** of the **Patient Browser** or in the **View** menu of the **Examination** task card.
Activate the mode if necessary.

The examination regions and cutlines are stored together with the topogram as soon as you terminate the examination with **Patient > End Exam**.

Switching off Topo Graphics

✧ Deselect **Mode Topo Graphics** in the menu **Patient** of the **Patient Browser** again.

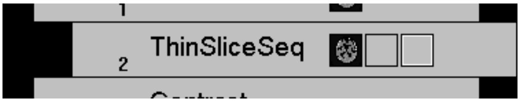
In the topo segment, the ranges and cutlines are again displayed normally.

The topogram is stored **without** cutlines when the examination is terminated.

Repeating reconstructions

The scan protocol of the current examination is still loaded in the chronicle and the system is still ready to scan. You can reconstruct the series you have just scanned as often as required and with different parameters to create different fields of view or to calculate separate images for bone and soft tissue, for example.

✧ Select the scan series in the chronicle that you want to reconstruct again.



✧ Set the required image parameters on the **Recon** subtask card.
→ Page C.10–20, *Changing reconstruction parameters*

✧ Click on the **Recon** button underneath the chronicle to start reconstruction.

⇨ You can read details about image reconstruction and planning of new reconstruction fields of view in
→ Chapter C.10, *Reconstruction*

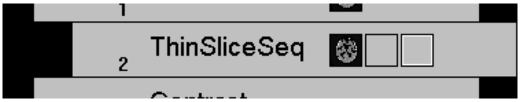
Saving raw data for postprocessing

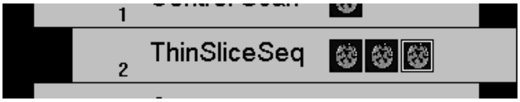
You can calculate the additional images with different reconstruction parameters at a later time. Make sure that the raw data of your sequence are saved before you continue with the next examination.

Automatic saving of the raw data

Your system always stores reconstructed tomograms in your local database automatically. As long as not all planned reconstructions have been performed for a scan series, the raw data belonging to that series are protected from deletion.

The empty recon icons in the chronicle indicate for which scan series reconstructions still have to be performed, i.e. for which there are open reconstruction jobs.





✧ Define one open reconstruction task for all scan series that you want to reconstruct later.
→ Page C.10–14, *Appending new jobs*

Saving raw data in the Patient Browser

As an alternative to creating open reconstruction tasks, you can also provide raw data of a scan or examination with delete protection in the **Patient Browser**.

✧ Call up **Patient > Browser** in the main menu.

✧ Select the raw data concerned in the navigation or content area.
→ Page D.2–10, *Selecting raw data*

✧ Call up **Edit > Protect** in the main menu of the **Patient Browser** or **Protect** in the popup menu (right mouse key). The raw data are now protected from deletion.

> **NOTE**
>
> Catch up on outstanding reconstructions of your scans quickly. If you have protected raw data from deletion, remember to remove it again in the **Patient Browser**.
> → Page D.5–20, *Protecting data from deletion*
>
> In this way, you make sure that future examinations are not delayed, because old raw data are occupying necessary storage space.

Ending an examination

Make sure that all the necessary tomographic images required for the diagnosis have been reconstructed with the required quality or that the raw data has been saved.

You can now end the examination in order to start with the next one.

End Exam

✧ Click on the **End Exam** button.

Or

✧ Call up **Patient > End Exam** in the main menu to end the current examination.

The scan protocol of the patient, all reconstructed images, and the raw data of the scan series with open reconstruction tasks are stored.

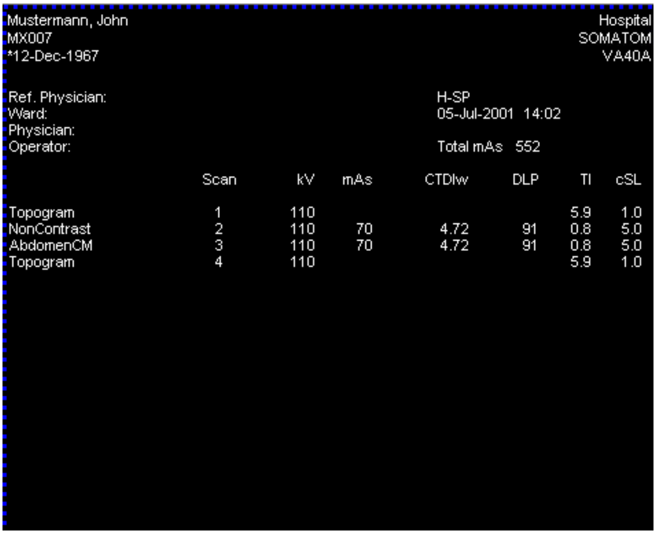
The gantry moves back to the scanning position for AP topograms.

➪ If all planned reconstructions have been performed for each scan series of the examination the **Recon Controller** dialog box for easy deletion of the raw data is displayed.
→ Page C.10–34, *Deletion of raw data*

Patient protocol

As soon as you conclude the examination with **End Exam**, your system creates a patient protocol if this option is selected in the **Examination Configuration**.
→ Page C.13–17, *Patient-related default settings*

In the patient protocol you will see an overview of the examinations you have performed together with the examination steps and the most important scan parameters.



Mustermann, John
MX007
*12-Dec-1967

Hospital
SOMATOM
VA40A

Ref. Physician:
Ward:
Physician:
Operator:

H-SP
05-Jul-2001 14:02

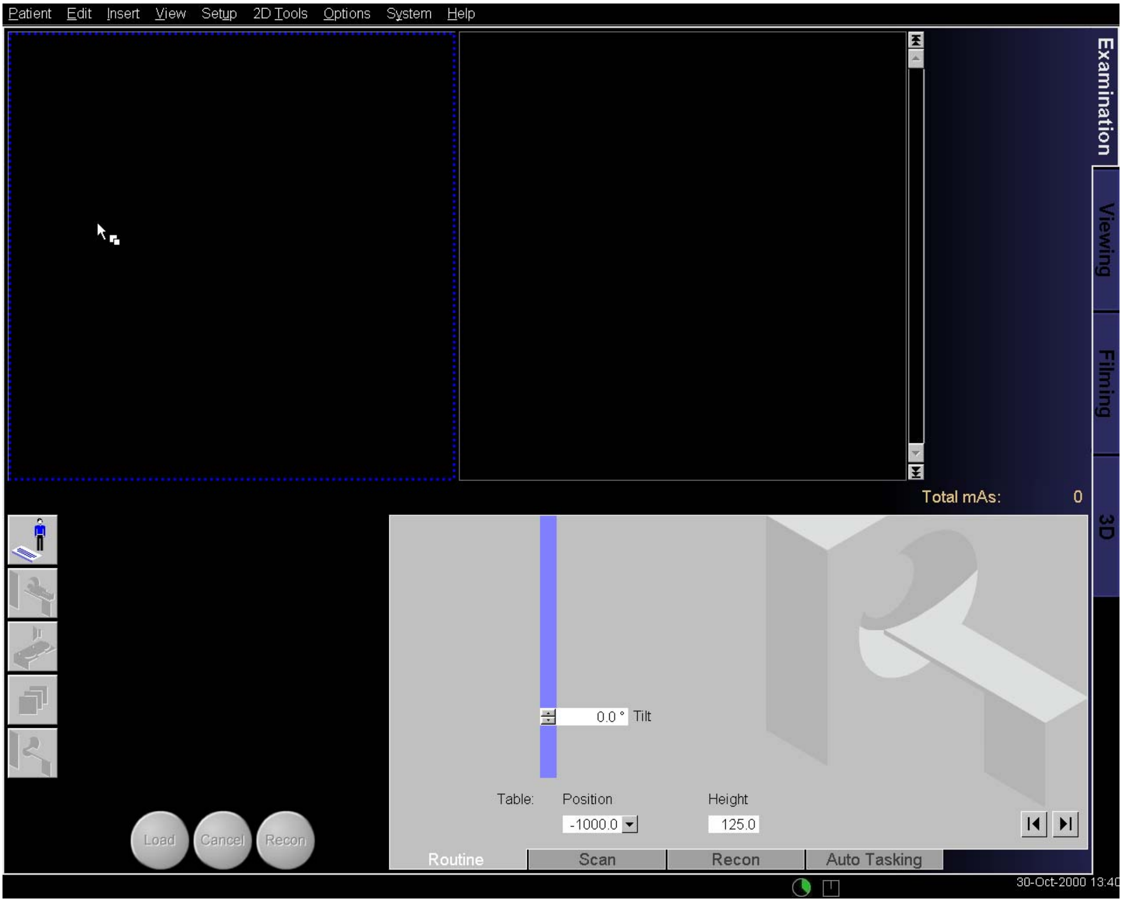
Total mAs 552

	Scan	kV	mAs	CTDIw	DLP	TI	cSL
Topogram	1	110				5.9	1.0
NonContrast	2	110	70	4.72	91	0.8	5.0
AbdomenCM	3	110	70	4.72	91	0.8	5.0
Topogram	4	110				5.9	1.0

➪ In the patient protocol, the **mAs** and **CTDI** value is taken over from the **Routine** card. For scans with the CARE function activated, these values are above the values really used.

The patient protocol is stored as an additional series of the study in the local database and is indicated by a special icon in the **Patient Browser**.

Examination task card The **Examination** task card is now empty.



You can register the next patient or select a new examination for the same patient via the patient registration window.

NOTE

End Exam resets the accumulated radiation dose count. The counting starts again for the next examination.

This is also the case if you perform an examination on the same patient.

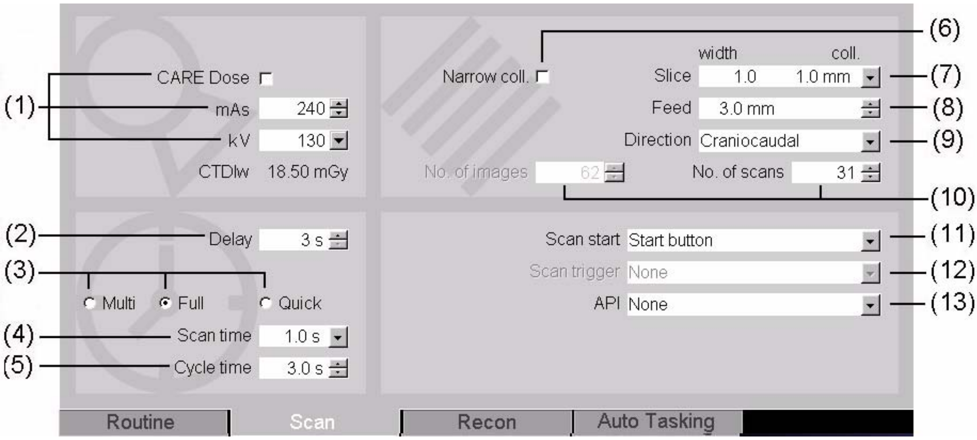
Special scan settings

When you select a routine scan protocol, all the main scan parameters for the examination of a region of the body in sequence mode are already set.

In the section *Preparing for a sequence*, you have learned how to adapt scan parameters which experience has shown need to be adapted to the individual situation frequently, how to check them before beginning scanning, and how to change them, if necessary.
→ Page C.6–4, *Preparing for a sequence*

On the following pages, you will read how to find and change parameters of a sequence examination which have to be changed less frequently.

✧ Click the **Scan** subtask card into the foreground.



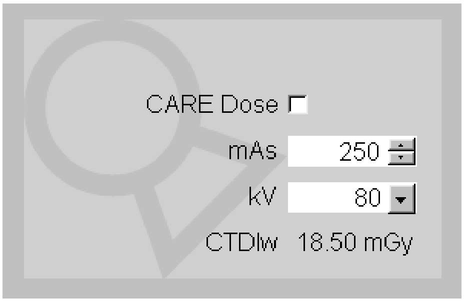
CARE Dose ☐
mAs 240
kV 130
CTDIw 18.50 mGy
Delay 3 s
○ Multi ● Full ○ Quick
Scan time 1.0 s
Cycle time 3.0 s
Narrow coll. ☐
Slice width 1.0 coll. 1.0 mm
Feed 3.0 mm
Direction Craniocaudal
No. of images 62
No. of scans 31
Scan start Start button
Scan trigger None
API None

(1) Dose modulation and radiation parameters
(2) Delay time
(3) Scan time mode
(4) Scan time
(5) Cycle time
(6) Slice-width mode
(7) Slice width and collimated slice width
(8) Feed
(9) Scan direction
(10) Number of images and number of scans
(11) Scan-Start
(12) Scan trigger
(13) API text pair

Radiation parameters

You have already checked and adapted, if necessary, the mAs and the tube voltage on the **Routine** subtask card.

You can also view and modify these settings on the **Scan** card, if necessary, in order to improve the image quality or to minimize the radiation exposure of the patient. The CT dose index **CTDIw** displayed (in mGy) is calculated based on the scan parameters currently set.
→ Page C.6–7, *Checking the radiation parameters, scan time, and slice width*



CARE Dose ☐
mAs 250
kV 80
CTDIw 18.50 mGy

CARE Dose

In addition to the usual radiation parameters, you can decide whether you want to set continuous radiation or radiation with dose modulation (CARE Dose). If the **CARE Dose** function is active, the radiation doses vary throughout a scan depending on the tissue.

CARE Dose ☑

✧ Select **CARE Dose** to set scanning with modulated radiation.

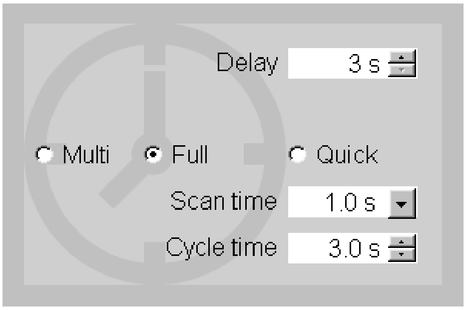
Or

CARE Dose ☐

✧ Deselect **CARE Dose** to scan with continuous radiation.

Time settings

In this part of the **Scan** card, you can modify the time settings for your scan.



Delay 3 s

○ Multi ● Full ○ Quick

Scan time 1.0 s

Cycle time 3.0 s

Delay time

Delay 4 s

✧ Set the time delay between starting the scan trigger and the onset of radiation using the spin buttons.
→ Page C.6–9, *Setting the delay time*

Scan-time mode

The scan-time mode defines to what extent and how often the tube-detector system rotates during a scan.

The larger the angle of rotation, the higher the reconstructible image quality, but the time required for one scan and the patient dose also increase.

✧ Select a scan time mode using the radio buttons.

- **Multi** (multiple rotation)
  Multi implements a 720° rotation per scan. **Multi** is used to minimize artifacts due to peristaltics and image noise. Improvement of image quality is usually greater than just by increasing the radiation dose.
- **Quick**(part rotation)
  Quick implements a 270° rotation per scan. **Quick** is used, for instance, in **HeartView CT** examinations.
- **Full** (full rotation)
  The default **Full** implements one full rotation per scan (360°).

Scan time


Scan time 1.5 s

Depending on the set scan-time mode, the system provides different scan times for your scan.

✧ Select a scan time in the selection list to define the time per scan.

Cycle time


Cycle time 3.0 s

The cycle time consists of the scan time and a pause. The time the system plans for the pauses is the time it requires to become ready for the next scan.

✧ Increase the cycle time using the spin buttons to plan longer pauses between scans.

The following scenarios will help you set the cycle time:

❑ You are conducting an examination with API. In order to be able to perform as many scans as possible during one breathholding time, select a short cycle time.

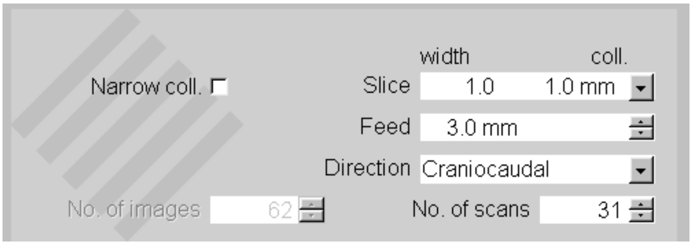
❑ You want to make sure that image reconstruction can keep up with the scan. Select a longer cycle time so that your system has enough time between two scans to reconstruct the last scan.

❑ You are conducting a dynamic CT series without table feed. With the cycle time, you can define the time intervals between the slice scans.

Slice settings

In the preparations for your sequence scan, you have checked the slice settings and the scan direction and changed them on the **Routine** subtask card, if necessary.
→ Page C.6–4, *Preparing for a sequence*

You can view and modify these settings at any time on the **Scan** subtask card.



Narrow coll. ☐

Slice width 1.0, coll. 1.0 mm

Feed 3.0 mm

Direction Craniocaudal

No. of images 62

No. of scans 31

You can also decide whether you want gapless data acquisition or scanning with gaps during preparation for an examination and set the table feed accordingly.
→ Page C.6–18, *Sequence with gaps*

Slice-width mode

Your computer tomograph is equipped with a multi-row detector. Per scan, i.e. per rotation of the tube-detector system, not one but multiple slices are scanned simultaneously. If you use the **Narrow Collimation** technique, the raw data of multiple detector rows are used to calculate one (fused) slice.

✧ Click on the check box to activate the **Narrow coll.** slice-width mode.
This reduces the partial volume artifacts and image noise.

Or

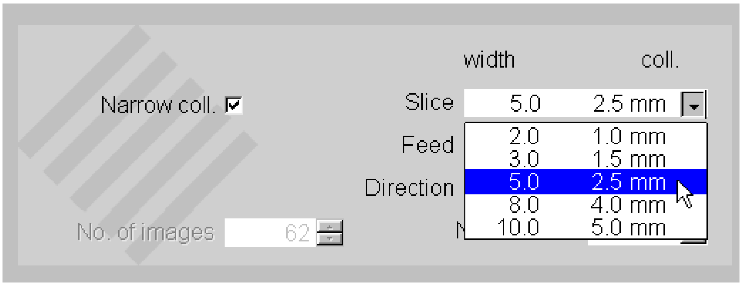
✧ Deactivate **Narrow coll.**.
The scan time for the range is shorter than with **Narrow coll.** for the same slice width.

NOTE

When you activate or deactivate **Narrow coll.**, your system automatically sets a **new collimated slice width**. This collimated slice width is selected in such a way that the images can be created with the slice width and slice-width mode originally selected.

Slice width and collimated slice width

In the **Slice** selection list, each slice width is shown with its corresponding collimated slice width. After scanning, all slice widths of the same collimation can be reconstructed from the raw data.



Narrow coll. ☑

	width	coll.
Slice	5.0	2.5 mm
	2.0	1.0 mm
	3.0	1.5 mm
	5.0	2.5 mm
	8.0	4.0 mm
	10.0	5.0 mm

No. of images 62

Number of images

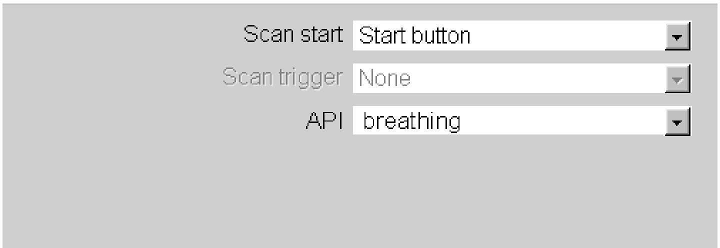
No. of images 10

The number of images indicates how many images will be reconstructed **in total** for the current slice setting in the selected series (number of scans x images per scan).

➪ If you change the number of scans, the number of images is changed accordingly.

Starting scanning

In this area of the **Scan** card, you can select the scan trigger and the text of the API announcement.



Scan start Start button

Scan trigger None

API breathing

Defining the Scan start

You will usually control your scans from the console.
As an alternative, you can start the scans from the examination room using the footswitch.

Scan start Start button

✧ Select the **Start** key (on the control box) or the footswitch (in the examination room) as the scan start.

➩ Scan triggering by footswitch is set if the scan has to be triggered in the examination room for interventional examinations.

Selecting an API text

For examinations with automatic patient instruction system, you have to select a pair of announcement texts.

A suitable pair of announcement texts is usually preset in the routine scan protocol.

API breathing

✧ Check the selection and select a new pair of texts from the list, if necessary.

➩ You can read how to create new announcement texts and place them in the selection list on
→ Page C.13–5, *Recording and processing API texts*

CHAPTER
C.7 HeartView CT (Option)

Physiological movements of organs cause artifacts and make unambiguous image interpretation more difficult if not impossible.

The HeartView CT option provides a way of suppressing motion artifacts caused by heart beating. This is done by synchronizing the data acquisition with the physiological movement of the heart. For that purpose, the heart rate is traced with an ECG unit and evaluated for the scan resolution or data reconstruction.

Prospective sequence

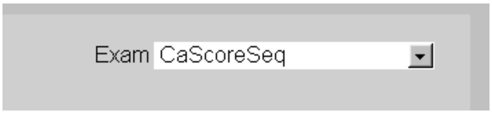
With this method, the individual scans of a sequence measurement are performed with ECG triggering. The scan trigger is a physiological signal (the R wave). After reconstruction of the raw data, you obtain tomographic images of a certain phase of the heart beat.

Preparing for the examination

In addition to the usual preparations in the examination room and on the console, some actions specific to HeartView CT are required.

Registering the patient

✧ Call up patient registration and complete the patient and examination data.
→ Part B, *Patient Registration*



Exam CaScoreSeq

✧ Select the required HeartView CT scan protocol and register the patient for examination.

⇨ The selection list receives protocols for sequence measurement with ECG triggering.

Positioning the patient

✧ Position the patient on the patient table and immobilize him or her using the positioning accessories, if necessary.
→ SOMATOM Operator Manual, chapter C.3, *Positioning the Patient*

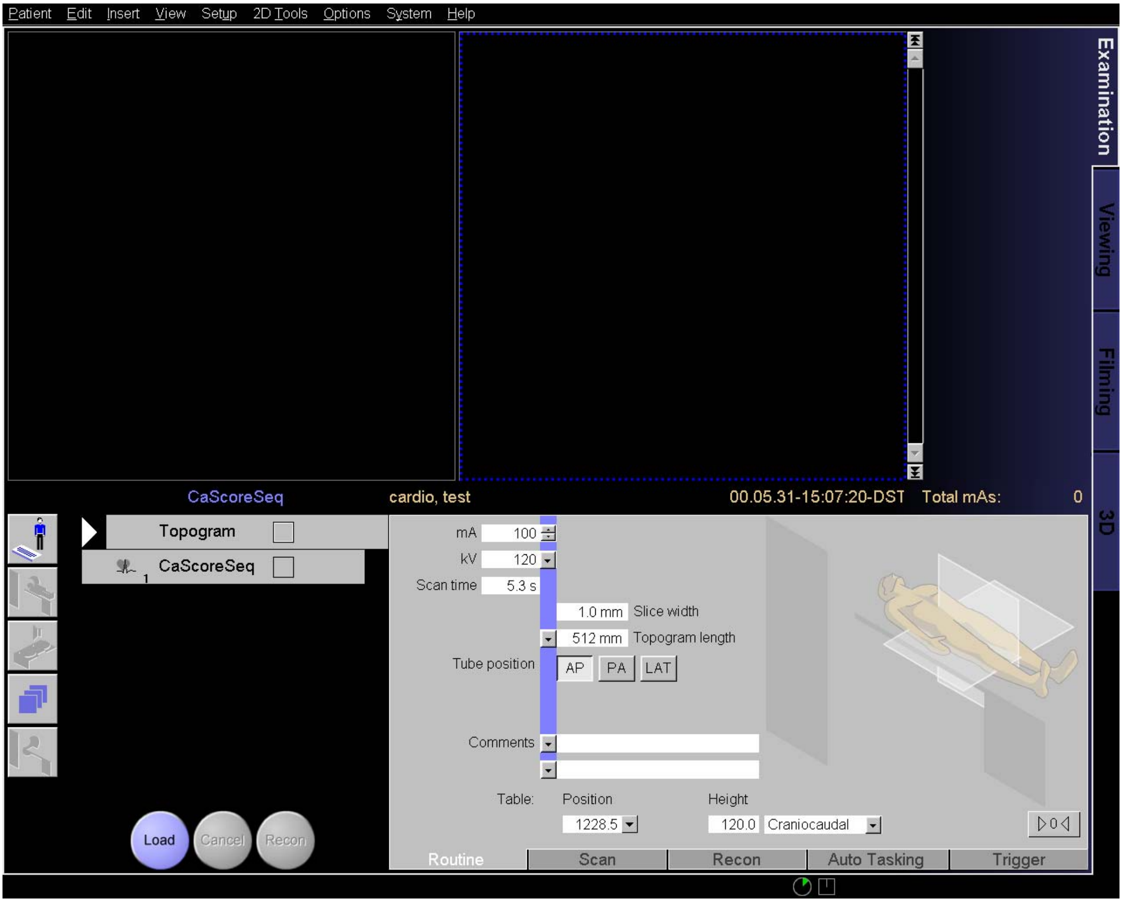
Applying ECG electrodes

✧ Apply the ECG electrodes. Please observe the instructions of the manufacturer.

✧ Connect the ECG unit.

The Examination card for HeartView CT

After registration, the **Examination** task card is displayed. A **Trigger** card is also included in the **HeartView CT** platform.

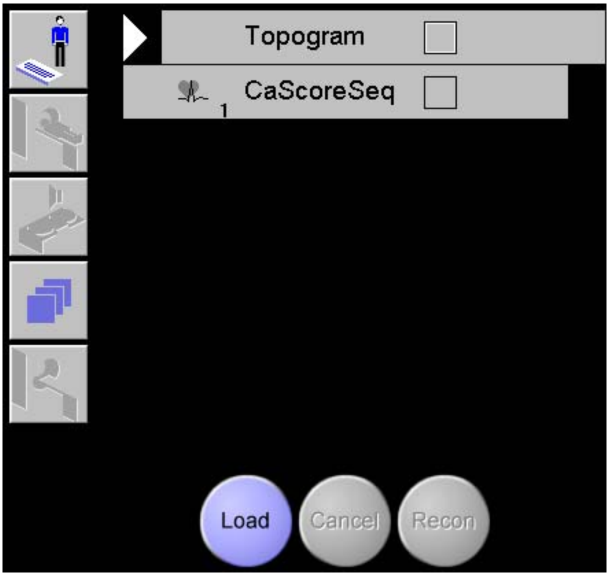


CaScoreSeq cardio, test 00.05.31-15:07:20-DST Total mAs: 0

mA 100
kV 120
Scan time 5.3 s
1.0 mm Slice width
512 mm Topogram length
Tube position
Comments
Table: Position 1228.5 Height 120.0 Craniocaudal

HeartView CT scan protocol in the chronicle

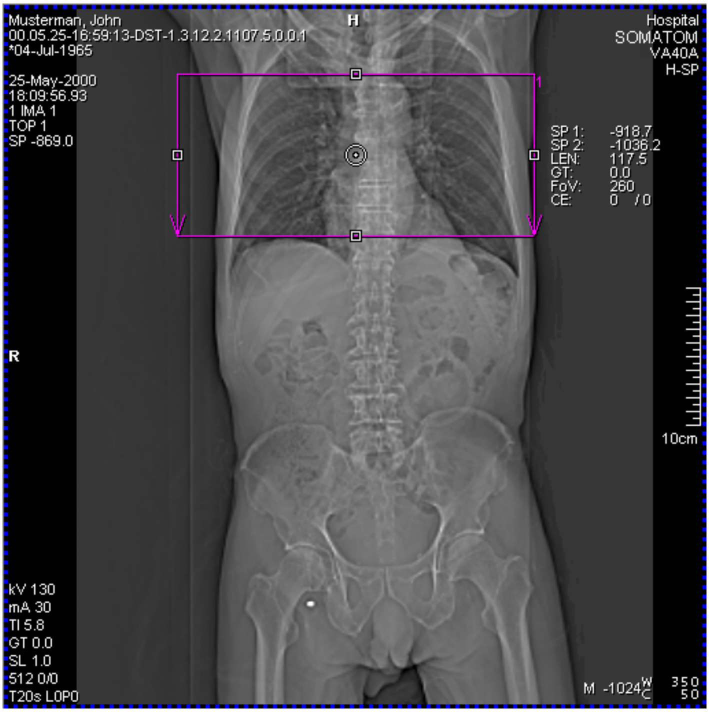
If you select a **HeartView CT** mode during patient registration, you can see the individual steps in the Chronicle. The ECG-triggered steps are marked with a heart icon.



➩ If you have not yet selected a scan protocol during patient registration or you want to switch protocols, select the required examination in the **Patient examination** window.
→ Page C.2–4, *Selecting a scan protocol*
→ Page C.2–6, *Selecting a different scan protocol*

Acquiring a topogram

Topogram acquisition and definition of the examination ranges for examinations with HeartView CT are performed in the same way as for standard examinations.
→ Chapter C.3, *Topogram / Planning Ranges*



Preparing for scanning with contrast agent

You perform a HeartView CT examination with administration of contrast agent just like a “normal” contrast agent examination. Administering contrast agent improves delimitation of certain structures, such as the heart walls, lumina etc.
→ Page C.2–26, *Inserting a contrast-medium pause*
→ Page C.2–33, *Routine subtask card in contrast agent examination*

NOTE

For scans with contrast agent you should always activate the synthetic trigger so that a scan does not have to be stopped if problems arise with the ECG signal.
→ Page C.7–10, *Synthetic trigger*

ECG-triggered sequence

During sequence measurement with ECG triggering, the system calculates the duration of a cardiac phase (R-R interval) in advance (prospectively). The individual scans are then triggered on every recorded R wave after the delay time you selected.

Setting scan parameters

On the **Routine** and **Scan** cards you can check the scan parameters preset in the scan protocol and change them if necessary.
→ Page C.6–4, *Preparing for a sequence*

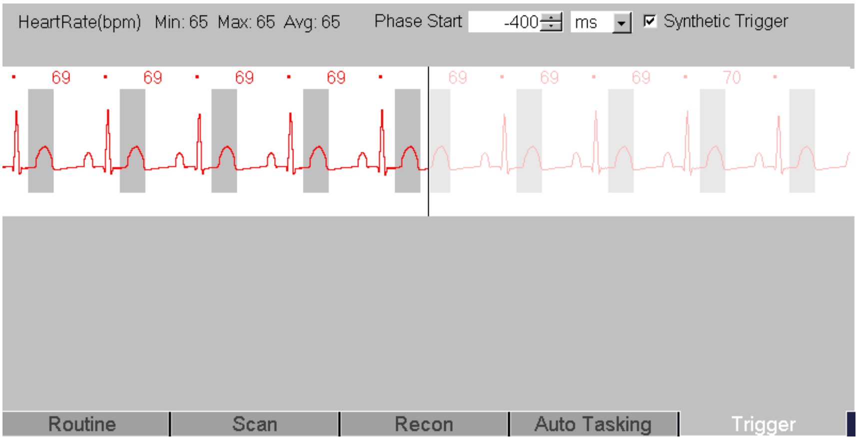
➪ The cycle time is set to the minimum value (e.g. 1.3s) and cannot be altered.

Setting trigger parameters

On the **Trigger** subtask card you can define in which cardiac phase the scans are to be performed.

Trigger subtask card

On the **Trigger** card, the ECG signal of the patient is displayed online. In the upper right-hand area, you will find the input fields for the trigger parameters.

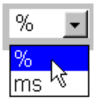


In the ECG, the current heart rate is displayed for each heart beat, and the minimum, maximum, and average heart rates of the last 30 s are displayed (all in beats per minute).

The R waves are marked by a blue dot.

Trigger delay for sequence

With the trigger delay you define how long after or before occurrence of an R wave the scan is to be started.



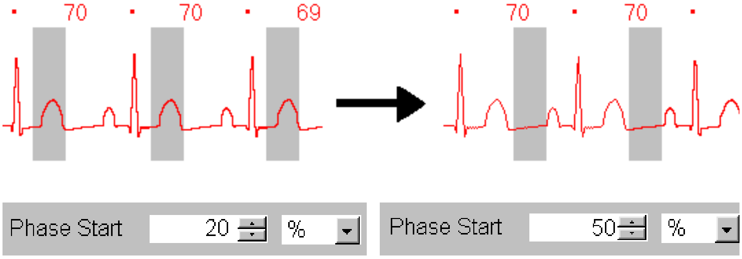
✧ Select **ms** (absolute delay) or **%** (relative delay) as the trigger unit in the selection box.


Phase Start 20 %

✧ Set the trigger delay in the spin box in the **Phase Start** field.

A positive value means a delay after the R wave. A negative value means that the starting point of the scan window is before next estimated R wave.

On every change in the trigger delay, the position of the scan window in the ECG is adjusted accordingly. In this way you can check when you have reached the correct value.



Phase Start 20 %

Phase Start 50 %

Synthetic trigger

The synthetic ECG trigger is an aid for when the ECG unit no longer provides acceptable R-wave pulses during scanning. It is especially useful for examinations with contrast agent if it is absolutely necessary to continue scanning. The R-wave signals are then generated by the system using the synthetic trigger.

➪ If the R-wave signals are lost before the spirals are started, readiness to scan is canceled by the system.

☑ Synthetic Trigger

✧ Click on this checkbox to allow activation of the synthetic trigger during the spiral.

Acquiring a control scan

You can no longer change the trigger settings for reconstruction after acquiring the sequence. You should therefore use the control scan to check the scan parameters and especially the trigger parameters.

➪ For the control scan, the scan and trigger parameters of the following sequence scan are acquired.

✧ Insert a control scan in front of the sequence.
→ Page C.2–25, *Inserting a control scan*

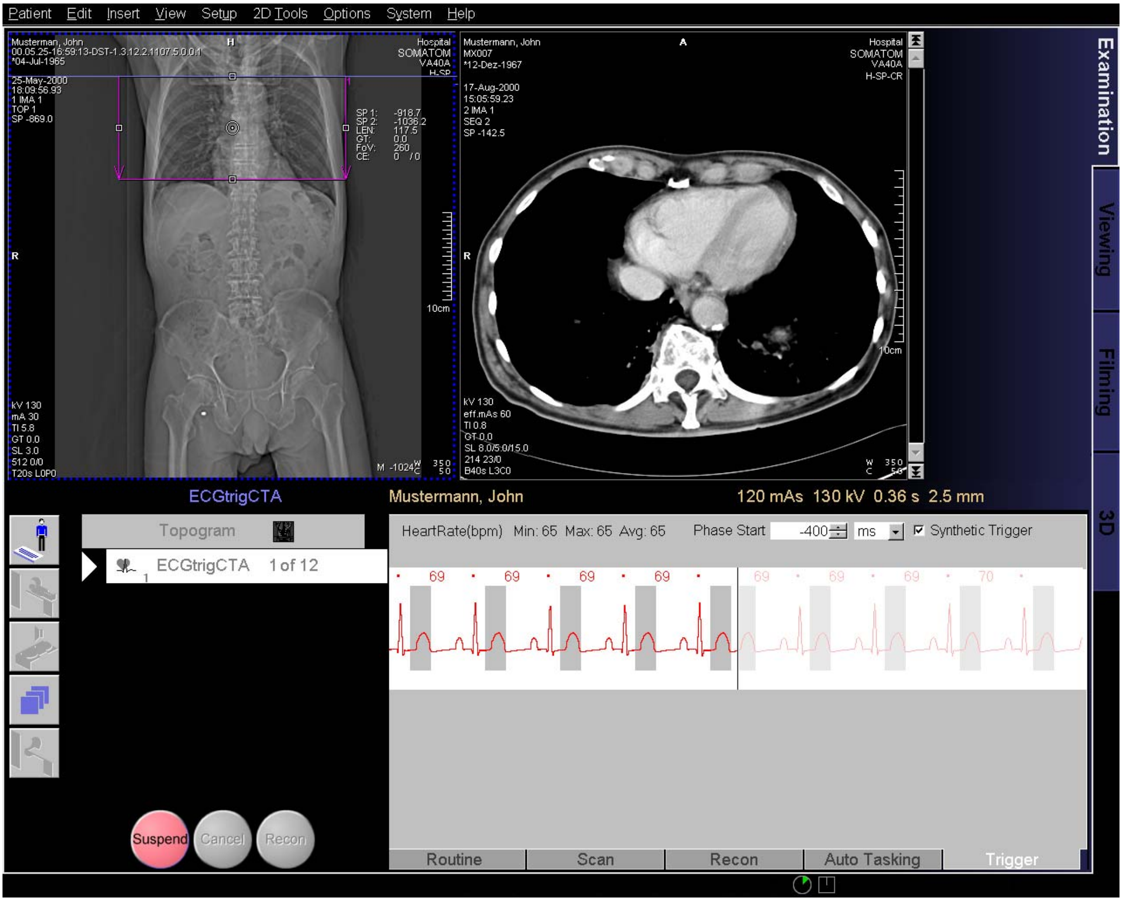
✧ Acquire the control scan and check the set scan and trigger parameters.
→ Chapter C.4, *Control Scan*

If any changes to the scan parameters or trigger settings are necessary, you can modify the parameters of the sequence accordingly and check them with a second control scan.

Acquiring a sequence

You perform sequence measurement and subsequent reconstruction in the usual way.
→ Page C.6–26, *Scanning a sequence*
→ Page C.10–3, *Reconstructing the scan series*

➩ After you have started the scan, the scanned scan windows are marked with pink lines. It is then no longer possible to change the trigger delay time.



Mustermann, John 120 mAs 130 kV 0.36 s 2.5 mm

HeartRate(bpm) Min: 65 Max: 65 Avg: 65 Phase Start -400 ms ☑ Synthetic Trigger

Configuration

In the **HeartView Configuration**, you can make the following settings:

❑ Mean value calculation of R-R intervals for sequence triggering

✧ Call up **Options > Configuration** in the main menu.

✧ Double click on the configuration symbol in the configuration panel.

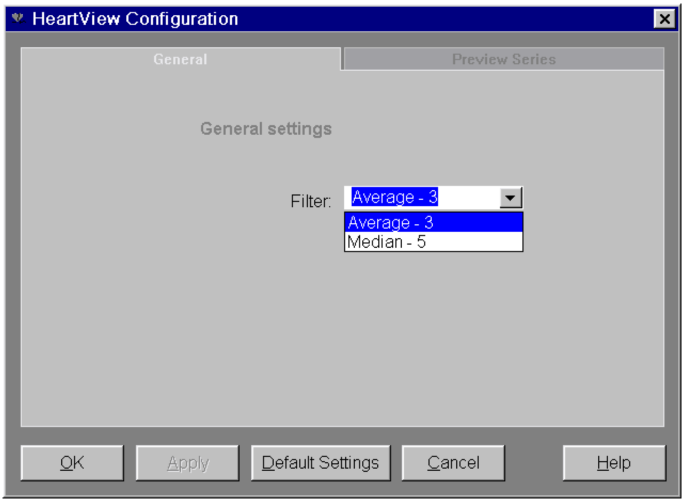
HeartView

Setting the mean value

For the prospectively triggered sequence, the mean value of the preceding R-R intervals is used to calculate the expected R peaks.

In the **General** subtask card you can set which of the preceding R-R intervals will be used to calculate the average R-R interval.

✧ Click the **General** subtask card into the foreground.



General settings

Filter: Average - 3

✧ Select **Average - 3** to have the mean value calculated from the last 3 preceding R-R intervals.

Or

✧ Select **Median - 5** to have the mean value set to the third-largest value of the last five R-R intervals.

CHAPTER
C.8

CARE Bolus (Option)

Many CT examinations are scanned with intravenously administered contrast medium (e.g. examinations for diagnosing tumors or CT angiography examinations).

Contrast media are used to increase the image contrast in the relevant regions and make the chronology of certain processes clearer.

CARE Bolus is a supplementary option for SOMATOM which allows optimum synchronization of the contrast medium bolus with the spiral scan.

Course of examination

CARE Bolus is integrated in the course of examination of the SOMATOM. As soon as you activate CARE Bolus, all the displays for contrast medium flow-in and parameter input appear on the task card.

❑ **Calling up an examination with spiral**
You register the patient with a spiral scan protocol.

❑ **Measuring a topogram**
The same as for normal CT examinations.

❑ **Planning examination ranges**
Once you have scanned the topogram you plan the examination range of the spiral graphically.

❑ **Activating CARE Bolus**
Insert CARE Bolus before spiral acquisition.

❑ **Planning and executing the pre-monitoring scan**
The pre-monitoring scan is used to identify a suitable slice for the monitoring scan.

- ❑ **Preparing the monitoring scan**
  Draw a trigger ROI into the tomogram of a pre-monitoring scan to monitor contrast medium flow-in and define the contrast medium threshold which must be reached before the imaging spiral can start.

- ❑ **Contrast medium administration, starting the monitoring scan**
  Once the contrast medium has been administered, the system waits for the specified delay time and then starts the monitoring scan (typically with lower dose).

- ❑ **Tracking contrast medium flow-in**
  Contrast medium flow-in in the trigger ROI is calculated during the scan and then displayed as a curve in the Trigger subtask card.

- ❑ **Automatic spiral start**
  As soon as the threshold value entered for contrast medium flow-in in the trigger ROI is reached, the imaging spiral starts automatically.

NOTE

You can start the spiral manually at any time if you think that a movement of the patient has displaced the trigger ROI or if the trigger threshold is too high.
→ Page C.8–37, *Enable/Disable START key*

Planning examination ranges

In order to plan the examination ranges of pre-monitoring, monitoring, and spiral scans, you must first perform an overview scan (topogram).

Scanning a topogram

A topogram is measured with CARE Bolus in the same way as other CT examinations.
→ Page C.3–2, *Preparing a topogram*
→ Page C.3–14, *Performing a topogram scan*

Setting the scan parameters for the spiral

Before you insert additional examinations steps for CARE Bolus, define the scan parameters for the spiral, as these parameters are used for the pre-monitoring and monitoring scan.

Planning the examination range of the spiral

First define the examination range for spiral acquisition based on the topogram.

✧ Select the spiral in the chronicle.

✧ Move the examination area graphically in the tomogram or define it numerically on the **Routine** subtask card.

Checking and modifying scan parameters

You can modify scan parameters in the usual way on the Routine or Scan cards.

Check the default scan parameters and, if necessary, adapt them to the requirements of the examination.
→ Page C.5–3, *Preparing for a spiral*

Activating CARE Bolus

Once you have defined all the scan parameters for spiral acquisition you can activate CARE Bolus.

Activating CARE Bolus for the next spiral

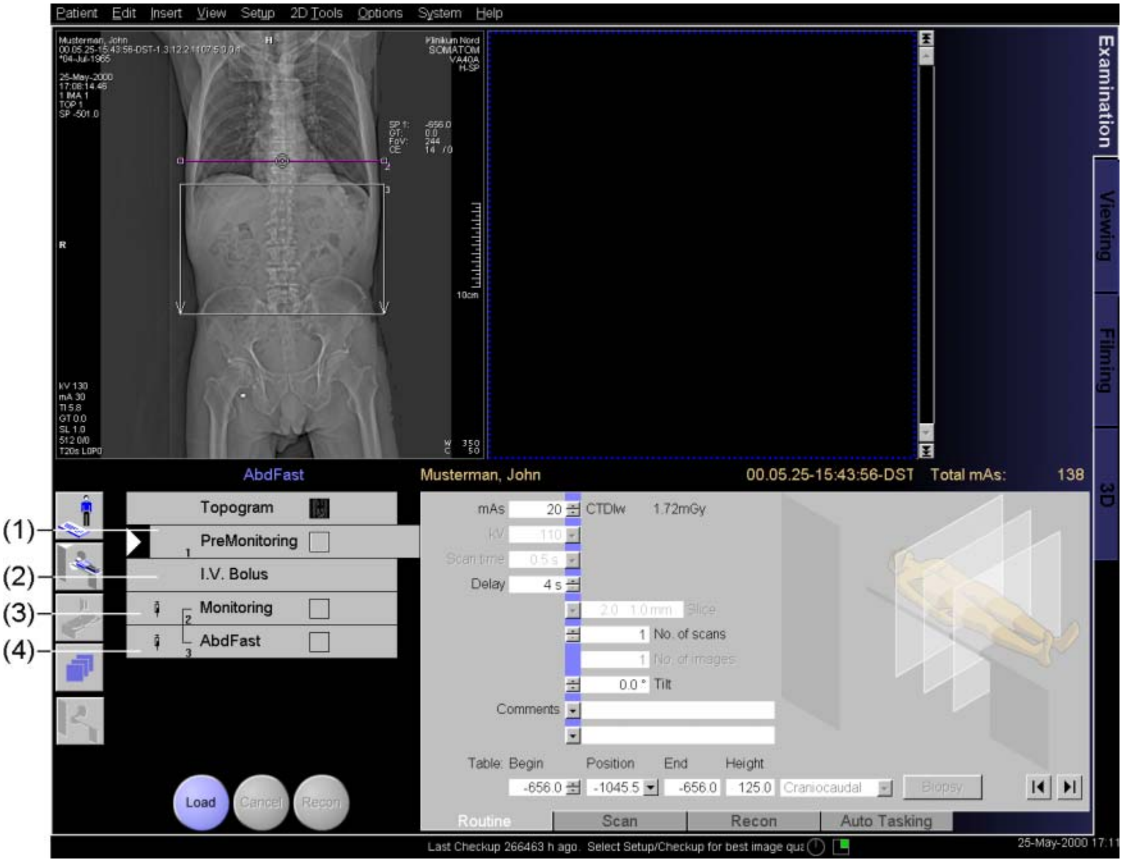
In one step, you now insert a pre-monitoring scan, a contrast medium pause (I.V. Bolus), and a monitoring scan in front of the spiral. You can insert CARE Bolus only once in a scan protocol.

> **NOTE**
>
> You can only activate CARE Bolus if the scan that you have selected is to be acquired with spiral technology and has not yet been measured.
>
> Otherwise, the menu items in the main menu and popup menu are grayed out.

✧ In the chronicle, click on a spiral scan that has not yet been measured to select it.

✧ Call up **Insert > Bolus Tracking** in the main menu or **Bolus Tracking** in the popup menu (right mouse click) of the chronicle.

All the examination steps required for CARE Bolus are displayed in the chronicle



Musterman, John 00.05.25-15:43:56-DST Total mAs: 138

mAs 20 CTDIw 1.72mGy
kV 110
Scan time 0.5 s
Delay 4 s
2.0 1.0 mm Slice
1 No. of scans
1 No. of images
0.0 ° Tilt
Comments
Table: Begin -656.0 Position -1045.5 End -656.0 Height 125.0 Craniocaudal

Last Checkup 266463 h ago. Select Setup/Checkup for best image qua

25-May-2000 17:11

(1) Pre-monitoring scan
(2) Contrast medium pause (I.V. Bolus)
(3) Monitoring scan
(4) Spiral for imaging

Deactivating CARE Bolus

If CARE Bolus is specified in the chronicle but you do not want to use it for the current diagnostic problem, delete the pre-monitoring scans, the monitoring scan, or I.V. Bolus.

✧ Select one of the CARE Bolus entries in the chronicle.

✧ Call up **Edit > Cut** in the main menu or **Cut** in the popup menu.

⇨ Removing one step in the examination deletes the entire CARE Bolus scan protocol.

Planning and executing a pre-monitoring scan

When you have completed acquisition of the topogram and planned the examination range for the spiral, the pre-monitoring scan is displayed in the chronicle as the next step in the examination.

Defining the number of pre-monitoring scans

On the **Routine** subtask card, you can see all the scan parameters for the pre-monitoring scan(s).

NOTE

A pre-monitoring scan is always acquired using sequence technique and without contrast medium.


3 No. of scans

✧ First specify how many scans you want to perform in the pre-monitoring scan (max. 10 scans possible without conflict warning).

➪ Select several pre-monitoring scans if you are not sure which slice is most suitable for monitoring contrast medium flow-in.

In the topogram you now see an examination range instead of a cut line for the pre-monitoring scan.

Moving pre-monitoring scans

You can define the starting position of the pre-monitoring scan in the same way as the starting position of the spiral.

✧ Click on the entry **PreMonitoring** in the chronicle.

✧ Move the cut line or the examination range of the pre-monitoring scan to the required position.
→ Page C.3–21, *Adapting ranges*

➪ If you move the position of the pre-monitoring scan toward spiral start, the cut line/range of the pre-monitoring scan automatically jumps to the starting point of the spiral. You can define the capture range in the window **Bolus Tracking Configuration** individually.
→ Page C.8–28, *Configuring the CARE Bolus*

Adapting the field of view (FoV)

You can use the pre-monitoring scans not only to identify the slice for the monitoring scan but also to check the field of view of subsequent scans.

✧ Set the FoV on the **Recon** subtask card, the setting is used for the following scans.

Or

✧ Adapt the FoV for the pre-monitoring scan and subsequent scans graphically in the topogram.

Adapting the mAs value

You can perform the pre-monitoring scan, monitoring scan, and imaging scan with different mAs values. Whereas you will need an mAs value for the spiral that will ensure diagnostic image quality, much lower mAs values are sufficient for the monitoring/ pre-monitoring scan.

The scan protocol initially suggests the same mAs value for the pre-monitoring scan as for the monitoring scan

You can increase this value. This will give the pre-monitoring scans a better image quality which can be useful for positioning the trigger ROI.

✧ Set the mAs value for the pre-monitoring scans on the **Routine** subtask card.

Initiating scanning

✧ After you have checked all the scan parameters, click on the button **Load** to transfer the parameters of the pre-monitoring scan to the scan system.

✧ Then press the **Start** key on the control box to start the pre-monitoring scan.

Or

✧ Start the pre-monitoring scan with the footswitch

The pre-monitoring scans are displayed in the tomo segment.

Preparing the monitoring scan

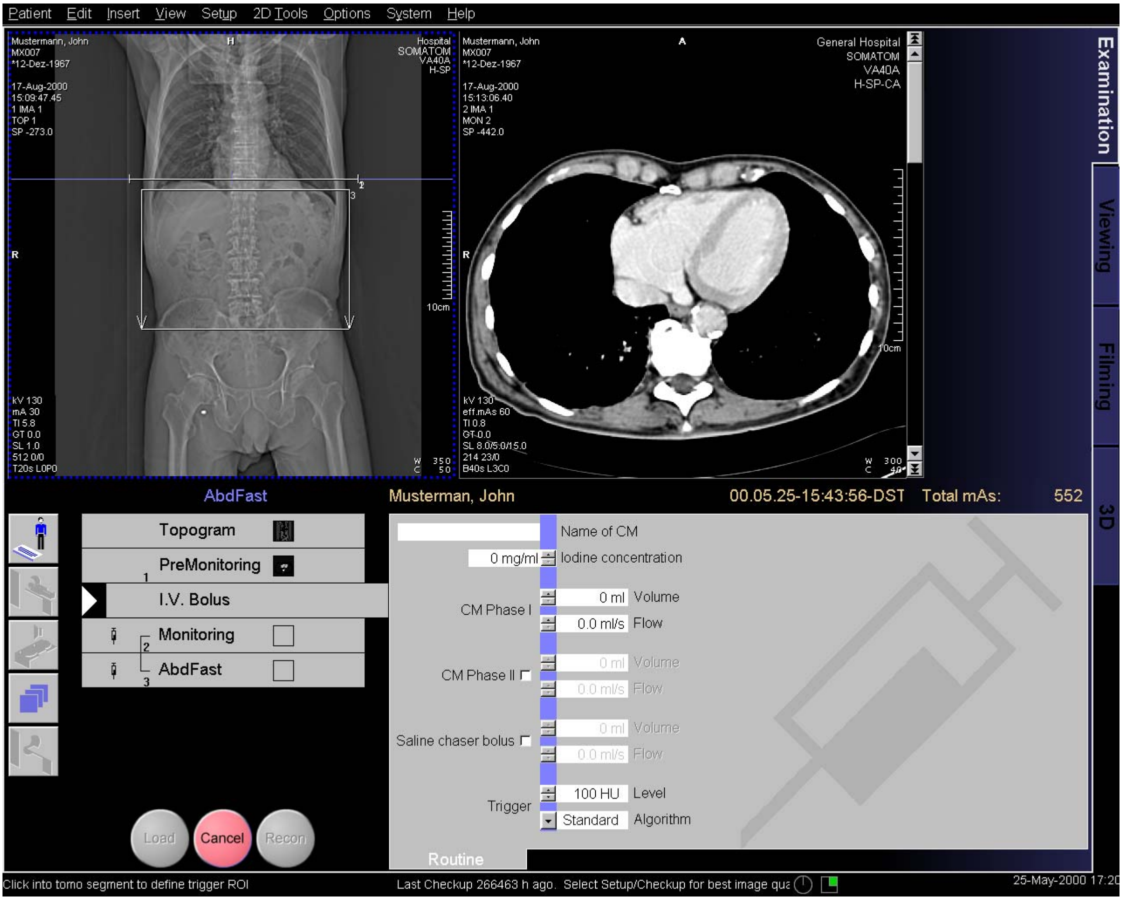
When you have completed the pre-monitoring scan, scroll through the tomograms to localize the slice that is most suitable for monitoring contrast medium flow-in. In that tomogram define an area (trigger ROI) in which the system is to measure flow-in of the contrast medium regularly.

Then check and modify the parameters of the current contrast medium protocol, as well as the scan parameters of the monitoring scan and the subsequent spiral scan.

Defining a Trigger ROI

The contrast medium pause **I.V. Bolus** is now selected in the chronicle. In the subtask card stack, you can see the **Routine** card for entering contrast medium data and defining the trigger threshold value.

➪ This information is stored with the scan protocol at the end of the examination.



AbdFast Musterman, John 00.05.25-15:43:56-DST Total mAs: 552

1 Topogram
PreMonitoring
I.V. Bolus
2 Monitoring ☐
3 AbdFast ☐

		Name of CM
	0 mg/ml	Iodine concentration
CM Phase I	0 ml	Volume
	0.0 ml/s	Flow
CM Phase II ☐	0 ml	Volume
	0.0 ml/s	Flow
Saline chaser bolus ☐	0 ml	Volume
	0.0 ml/s	Flow
Trigger	100 HU	Level
	Standard	Algorithm

Click into tomo segment to define trigger ROI

Last Checkup 266463 h ago. Select Setup/Checkup for best image qua

25-May-2000 17:20

Selecting pre-monitoring scans

✧ With the dog-ears click through the image stack in the tomo segment to select an image in which the relevant trigger area is clearest.

Or

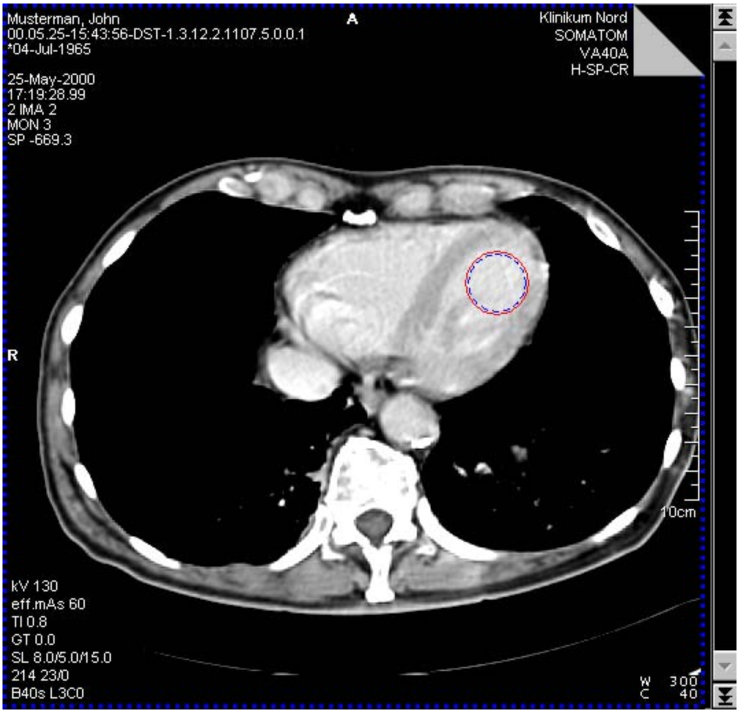
✧ Scroll using the scroll bar

Defining the ROI

✧ Position the cursor into the center of the trigger area and then press the left mouse button.

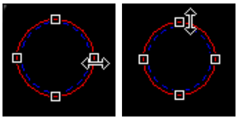
You can now see a trigger ROI of a predefined size positioned around that center.

➩ The predefined size of the trigger ROI depends on the configuration.
→ Page C.8–33, *Size of the trigger ROI*



You can now correct the position and size of the ROI.

✧ Click into the ROI keeping the left mouse key pressed and move the ROI to the required position.



✧ Click on the outline of the ROI and, keeping the left mouse key pressed, move it out (larger) or in (smaller).

NOTE

On very small structures you can zoom the pre-monitoring scan to make it easier to draw in the ROI.
→ Page E.4–16, *Zooming and panning images*

Heavily zoomed images can be fuzzy. In that case, create another reconstruction job with a smaller field of view. Reconstruct the pre-monitoring scan for trigger ROI definition again with an optimum field of view.
→ Page C.10–10, *Reconstruction progress*

In the default setting, the ROI is divided into a visible area (solid line border) and an active area (dotted line border). The visible area should be used for positioning the trigger ROI, the system evaluates the area inside the active ROI.

➪ In the **Bolus Tracking Configuration**, you can hide the active area individually.
→ Page C.8–28, *Configuring the CARE Bolus*

Defining contrast medium parameters

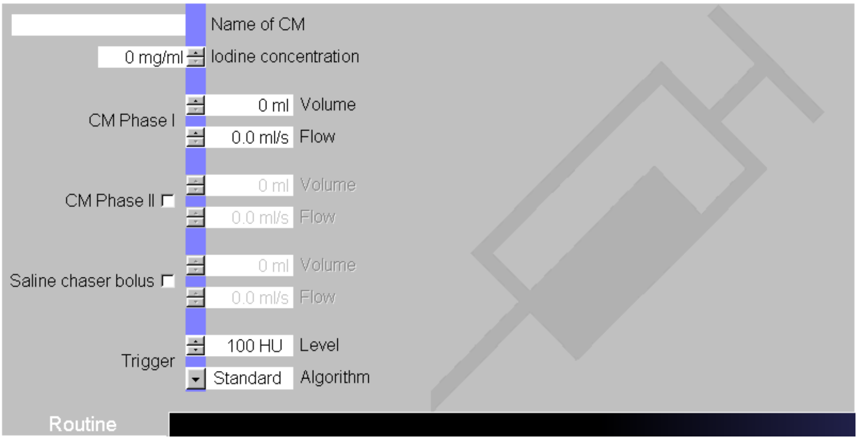
When you have completed ROI definition, check the contrast medium data of the scan protocol. Then define the trigger threshold value at which the imaging spiral is to be triggered.

Checking the contrast medium data

On the **Routine** task card you can see all the suggestions made by the scan protocol for contrast medium administration.
→ Page C.2–33, *Routine subtask card in contrast agent examination*

You can accept these suggestions and set the injector accordingly. If you want to use other contrast medium values, define them after you have programmed the injector in the **Routine** subtask card.

➩ The information entered is stored with the scan protocol at the end of the examination.



Name of CM
0 mg/ml Iodine concentration
CM Phase I
0 ml Volume
0.0 ml/s Flow
CM Phase II ☐
0 ml Volume
0.0 ml/s Flow
Saline chaser bolus ☐
0 ml Volume
0.0 ml/s Flow
Trigger
100 HU Level
Standard Algorithm

➪ If you insert CARE Bolus into a scan protocol subsequently, all contrast medium values are reset to 0.

NOTE

It is the responsibility of the physician concerned to define the settings for contrast medium administration patient specifically.

Setting the trigger threshold value

In spiral scans with CARE Bolus, initialization of scanning with the spiral is coordinated with the contrast medium bolus, i.e., scanning should start as soon as a specific contrast medium concentration (contrast medium density value) is reached in the trigger ROI. This density threshold value has already been entered for your examination via the selected scan protocol.

Trigger 100 HU Level

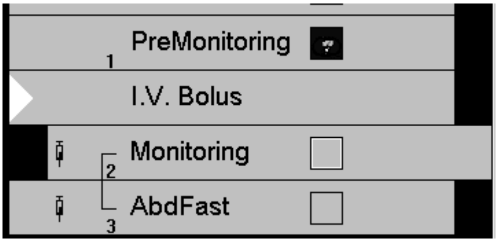
✧ Check the trigger threshold value on the **Routine** subtask card and change it, if necessary.

➪ You can also correct the trigger threshold value on the **Trigger** subtask card graphically.
→ Page C.8–18, *Checking the threshold value*

Setting scan parameters for the monitoring scans

Once you have made all the settings for the trigger threshold value, select the monitoring scan in the chronicle and check and correct the scan parameters, if necessary.

✧ Click on the entry **Monitoring** in the chronicle to select that examination step.



The most important parameters of this scan are displayed on the **Routine** card. The subtask card stack now also has another tab (**Trigger**).

Adapting the mAs value

A relatively low mAs dose (20 mAs) is preset for monitoring scans, as this type of scan is only used to check contrast medium flow-in. A lower image quality is sufficient for this step.


mAs 20 CTDIw

You can increase the mAs value, but this also increases the patient's exposure to radiation.
→ Page C.5–6, *Eff. mAs per image*

Changing the scan time

✧ If necessary, you can alter the default acquisition time for each image to improve the local resolution.
→ Page C.5–53, *Scan time*

➩ You can also set **Quick** rotation instead of **Full** rotation to reduce the scan time.
→ Page C.6–60, *Scan-time mode*

Setting the start delay

The time delay between pressing the **Start** button and triggering the first monitoring scan must be coordinated with contrast medium flow-in. The value you set depends on the physical condition of the patient concerned. For extremely corpulent patients, for example, you should set a longer time delay.


Delay 12 s

✧ Change the start delay via the spin box.

Number of scans

You can specify the maximum number of monitoring scans to be performed via **No. of scans**. Currently, the maximum number of scans is 50 (without conflict warning).


30 No. of scans

✧ Change the number of monitoring scans via the spin box.

Setting the cycle time

Via the cycle time you can specify at which frequency monitoring scans are to be performed and contrast medium flow-in is checked in the area of the trigger ROI.

The shorter the interval between scans, the more precisely arrival at the trigger threshold value can be defined. However, in that case correspondingly more monitoring scans are acquired.

✧ To set the cycle time click the **Scan** subtask card into the foreground.

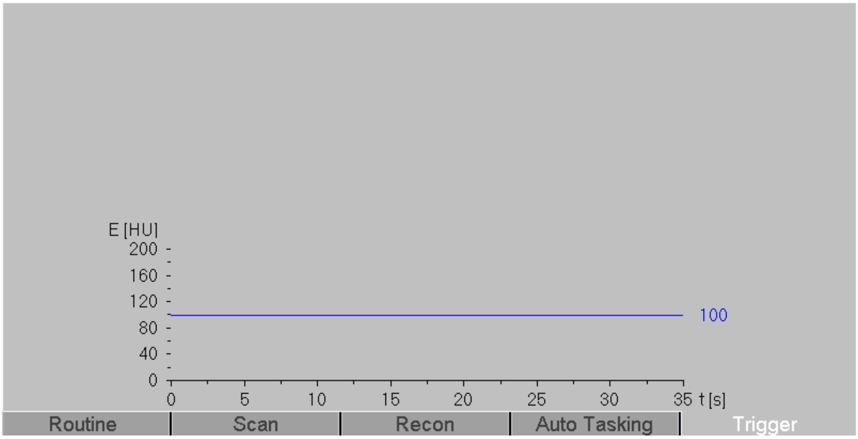

Cycle time 1.0 s

✧ Change the cycle time if you want to increase or decrease the intervals between individual scans.

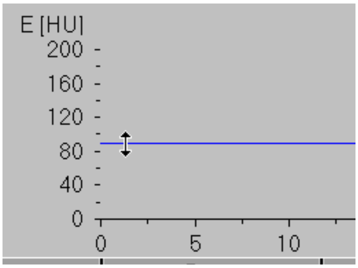
Checking the threshold value

Before you start checking the scan parameters for the spiral scan, you can once more check the trigger threshold value graphically.

✧ Click the **Trigger** subtask card into the foreground.



Here you can graphically change the trigger threshold value one more time.



✧ With the left mouse key, click on the threshold value line in the diagram.

✧ Keep the mouse key pressed and pull the line up or down to increase or reduce the trigger threshold value.

➪ You can extend the y-axis by dragging the trigger line towards a higher value. In that case, do not forget to redefine the trigger threshold value to be used.

Checking the FoV for the spiral

The field of view initially has the same settings as the FoV of the previous monitoring scan.

✧ If you have reduced the size of the FoV for the monitoring scan, you can now increase it again for the spiral scan or create an overview image and adapt the FoV in it.
→ Page C.10–5, *Adapting a reconstruction target*
→ Page C.10–14, *Repeating reconstruction*

Contrast medium administration, monitoring scan, spiral

Once you have made all the scan parameter settings for the monitoring scans and completed the imaging spiral, you can start scanning.

> **NOTE**
>
> If an error occurs during monitoring scanning or subsequent spiral scanning, you must stop the injector and the CT scanner manually. If necessary, you can repeat the monitoring or premonitoring scan.
> → Page C.2–31, *Repeating an examination step*

Loading scan parameters

First select the monitoring scan and then the spirals in the chronicle.

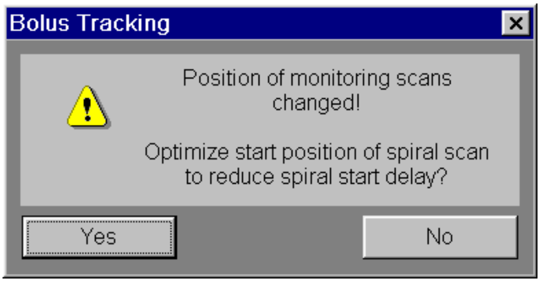
Accept

✧ Click on the button **Accept** to confirm the parameters of these examination steps.

> **NOTE**
>
> With **Accept** you confirm the selected pre-monitoring scan for the next monitoring scan, and the size and position of the trigger ROI.
>
> You cannot select another pre-monitoring scan without repeating the pre-monitoring measurements.

Optimizing the spiral starting position

If you have placed the monitoring scans at a different table position to the planned start of the spiral scan, a prompt is displayed as soon as you click on **Accept**, asking you to optimize the starting position of the spiral.



Bolus Tracking

Position of monitoring scans changed!

Optimize start position of spiral scan to reduce spiral start delay?

The system optimizes the start position by automatically moving the start of the spiral to the position of the monitoring scan (a minimum delay of 2 seconds is set).

➩ The snap distance can be configured or deactivated in the **Bolus Tracking Configuration**.
→ Page C.8–36, *Range for snap distance*

As a result, the patient table does not first have to be returned to the start position of the spiral when the contrast medium threshold is reached and the monitoring scan is complete.

Yes

✧ Click on **Yes** to accept the start position of the monitoring scan for spiral monitoring

Or

No

✧ Click on **No** if a start delay is acceptable to you.

➪ Differing monitoring scan and imaging spiral start positions might be necessary if the ideal slice for monitoring contrast medium flow-in is located in the center of the examination range of the spiral, e.g. for structures in which the vessels through which the contrast medium flows are not graphically "at the top" or "at the bottom"

Contrast medium administration and scan start

✧ Now start contrast medium administration via the injector.

✧ At the same time start the monitoring scan with the foot pedal.

Or

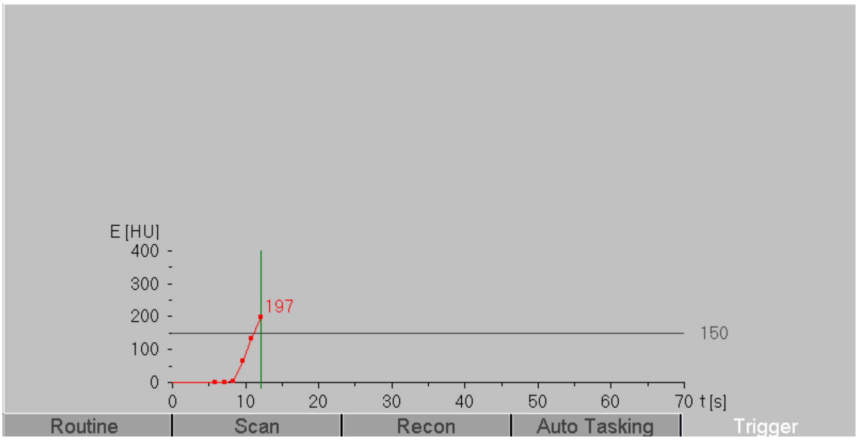
☢

✧ Start the monitoring scan via the **Start** button on the control box.

Monitoring scan sequence

After the specified delay time, the system starts the monitoring scan.

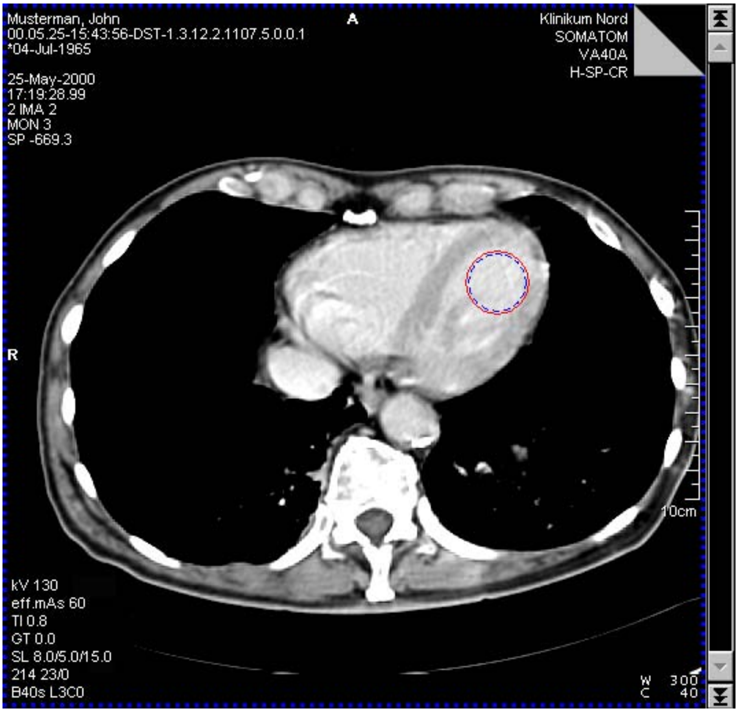
In the subtask card stack, the **Trigger** card is placed in the foreground.



In the card **Trigger**, flow-in of the contrast medium is expressed as a curve. The contrast medium density value actually reached is displayed next to the curve.

When the examination is complete, the contrast medium curve is stored in the database as an image together with the examination results.

In the tomo segment the reconstructed images of the monitoring scan are displayed parallel to the scan.



NOTE

For optimum system performance, you should not work in any other task card while the monitoring scan is being performed.

Starting the spiral automatically

As soon as the set threshold value within the ROI is reached, the spiral scan is automatically triggered.

Starting the spiral manually

If the development of the contrast medium curve on the **Trigger** card shows you that the trigger threshold value will be reached at a very late stage or not at all, you can also start the spiral manually.

☢

✧ Press the **Start** button on the control box while the monitoring scan is still running.

Or

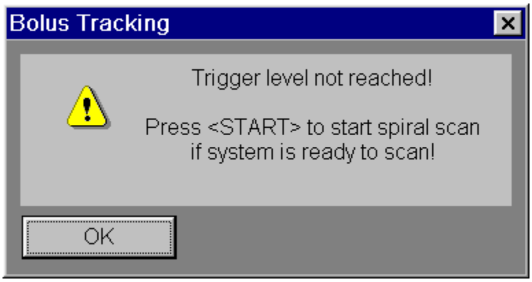
Start Spiral

✧ Click on the **Start spiral** button in the chronicle.

The monitoring scan is canceled and the imaging spiral starts immediately.

Trigger threshold value not reached

If the trigger threshold is not reached even after the number set for the monitoring scan, the following message appears.



Trigger level not reached!

Press <START> to start spiral scan if system is ready to scan!

Here again, you can start the spiral manually.

Spiral scan

The imaging spiral runs like any other spiral scan, whether it is started automatically or manually.
→ Page C.5–22, *Performing a scan*

Reconstruction and documentation of images

When the spiral is complete, you can reconstruct the images of the examination from the raw data of the spiral.
→ Page C.10–1, *Reconstruction*

➪ The system does not store any raw data for the monitoring scan, so you cannot reconstruct any images from this scan.

You can now view, evaluate, and document the reconstructed images in the normal way.
→ Page C.11–1, *Image Processing and Evaluation*

Configuring the CARE Bolus

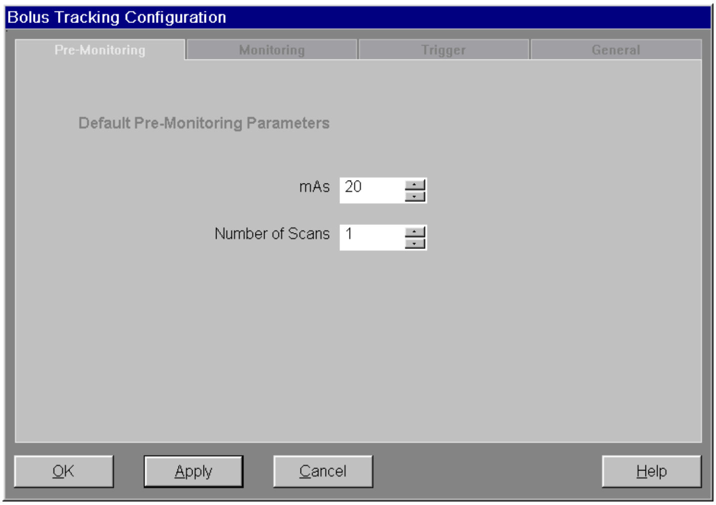
Your system provides some default settings for an examination with CARE Bolus. You can change them individually in the window **Bolus Tracking Configuration**.

✧ Call up **Options > Configuration** in the main menu.

Bolus Tracking

✧ Double click on the configuration symbol in the configuration panel.

The window **Bolus Tracking Configuration** with the **Pre-Monitoring**, **Monitoring**, **Trigger**, and **General** subtask cards is displayed:



Bolus Tracking Configuration

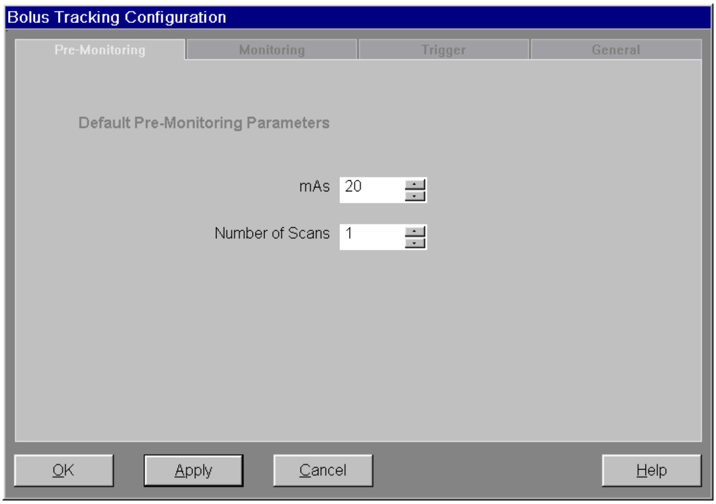
Default Pre-Monitoring Parameters

mAs 20

Number of Scans 1

Changing Pre-Monitoring parameters

On the **Pre-Monitoring** subtask card you can change the default settings of the pre-monitoring scans.



Default Pre-Monitoring Parameters

mAs 20

Number of Scans 1

mAs

The mAs default setting for the pre-monitoring scan(s) should be set to a value that produces the best possible image quality at the lowest possible radiation exposure.

mAs 20

✧ Increase or decrease the **mAs** value via the spin box.

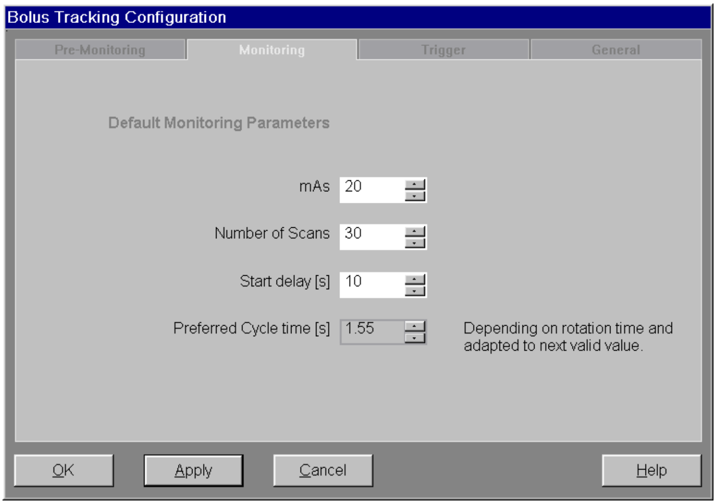
Number of pre-monitoring scans

Number of Scans 1

✧ Specify how many pre-monitoring scans you usually intend to perform (max. 10 scans possible without conflict warning).

Changing Monitoring parameters

On the **Monitoring** subtask card you can change the default settings of the monitoring scans.



Bolus Tracking Configuration

Default Monitoring Parameters

mAs 20

Number of Scans 30

Start delay [s] 10

Preferred Cycle time [s] 1.55

Depending on rotation time and adapted to next valid value.

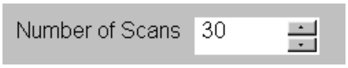
mAs

The mAs value for pre-monitoring scans should be preset to a default value because this image material is not required for diagnostic purposes.

mAs 20

✧ Increase or decrease the **mAs** value via the spin box.

Number of monitoring scans

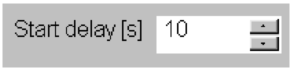


Number of Scans 30

✧ Specify how many monitoring scans you usually intend to perform (max. 50 scans possible without conflict warning).

Start delay

The start delay depends on the physical condition of the examined patient. The default setting should be adapted to the physical condition of an “average patient”.



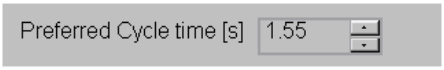
Start delay [s] 10

✧ Set the default start delay via the spin box.

Preferred cycle time

Via the cycle time you can specify at which frequency monitoring scans are to be performed and contrast medium flow-in is checked in the area of the trigger ROI.

➩ The values for the preferred cycle time depend on the rotation time. If necessary, the system adapts the value entered to the next valid value.

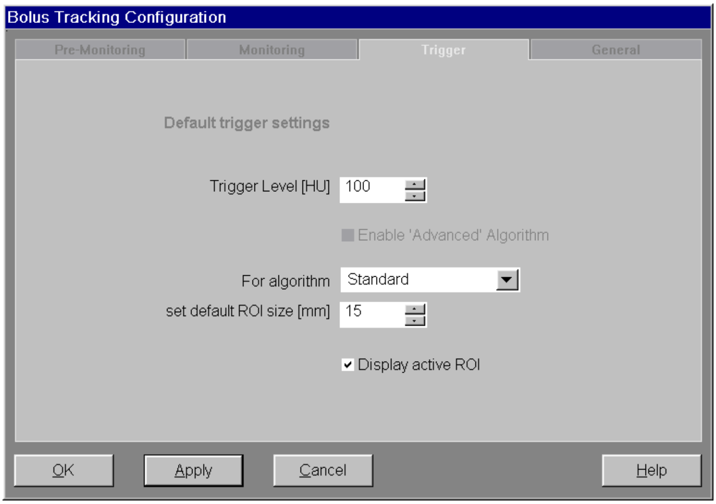


Preferred Cycle time [s] 1.55

✧ Change the default cycle time via the spin box, if necessary.

Changing Trigger parameters

On the **Trigger** subtask card you can change the default settings for the triggering parameters.



Default trigger settings

Trigger Level [HU] 100

☐ Enable 'Advanced' Algorithm

For algorithm Standard

set default ROI size [mm] 15

☑ Display active ROI

Trigger threshold value

Trigger Level [HU] 100

The trigger threshold value for triggering the spiral scan is preset for examinations with CARE Bolus. You can change this default setting for future CARE Bolus examinations.

✧ Enter your own default setting in the input field **Trigger Level [HU]**.

Algorithm

In a later program version you can select different algorithms for evaluating the active trigger ROI.

For algorithm Standard

For the default standard algorithm, an increase in the contrast medium flow-in must occur in all pixels of the ROI. By dividing the trigger ROI into two areas it is ensured that the active ROI covers the scan range when the visible ROI is positioned more precisely.

Size of the trigger ROI

The default ROI consists of a visible and an active ROI. Contrast medium flow-in is monitored in the active ROI.

You can increase or reduce the standard size of the trigger ROI. The sizes of both ROIs change proportionally.

set default ROI size [mm] 15

✧ Enter the value for the required ROI via the spin box.

Displaying the active trigger ROI

Both areas of the ROI are displayed to make it easier for you to position the trigger ROI as precisely as possible. However, you can also hide the active ROI if you want to.

☑ Display active ROI

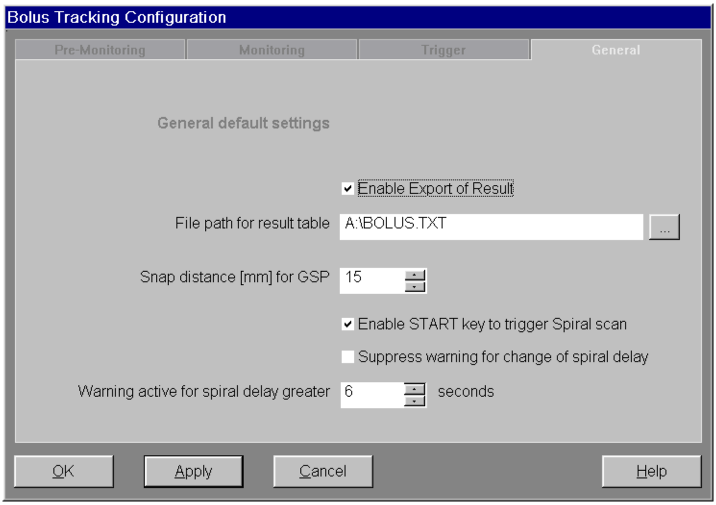
✧ To do that, click on the checkmark in the **Display active ROI** check box.

The checkmark disappears. As a default setting the active ROI is no longer displayed.

➪ The visible area is for positioning the trigger ROI. The system evaluates the area inside the active ROI.

Changing General parameters

On the **General** subtask card you can configure the export of results and general settings of the Bolus Tracking examination.



General default settings

☑ Enable Export of Result

File path for result table: A:\BOLUS.TXT

Snap distance [mm] for GSP: 15

☑ Enable START key to trigger Spiral scan

☐ Suppress warning for change of spiral delay

Warning active for spiral delay greater: 6 seconds

Export of results

If you intend to save the results of your Bolus evaluation to diskette you have to activate the **Enable Export of Results** check box.

☐ Enable Export of Result

✧ Click on the **Enable Export of Results** check box to activate this function.

File path for result table

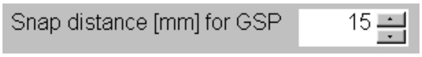
✧ Enter the path and file name you want to save your results with.

Range for snap distance

A capture range mechanism supports you with the graphic positioning of examination ranges and cut lines in the topogram.

Whenever you move a line or a range into the vicinity of another, the start line that you have moved jumps to the start of the adjacent arrange. As a result, a minimum start delay of 2 seconds is achieved.

You can configure the capture range to make it easier to plan the optimum starting position.



Snap distance [mm] for GSP 15

✧ You can increase or decrease the capture range in the input field **Snap Distance [mm] for GSP**.

➪ To switch off the snapping mechanism just enter zero as snap distance.

CAUTION

Source of danger: The snap distance is set to an unusually high value (e.g. 300 mm).

Consequence: The spiral range snaps to the starting position of the pre-monitoring and monitoring scan. The end of the range is moved by the same distance such that part of the examination region may be outside the range.

Remedy: Check the position of the range in the topogram after snapping. Only set moderate snap distances.

Enable/Disable START key

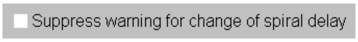
Normally the spiral scan is started automatically as soon as the preset threshold value has been reached. Yet, you have the option of triggering the spiral scan manually with the START key on the control box.

☑ Enable START key to trigger Spiral scan

✧ Activate and deactivate the START key via the check box.

Spiral delay

You can have a warning displayed if the delay of the spiral start is increased above a certain value (e.g. if you move the spiral start away from the start position of the monitoring scans a warning will be displayed per default).



☐ Suppress warning for change of spiral delay

✧ Deselect the **Suppress warning for change of spiral delay** check box to activate the warning function.

Warning active for spiral delay greater 6 seconds

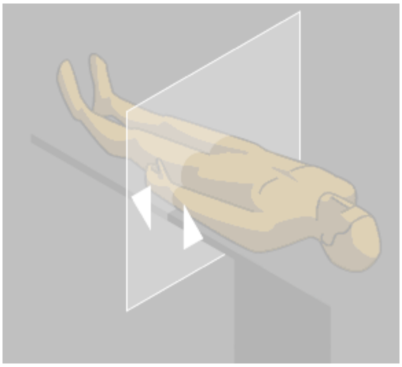
✧ Set the default spiral delay which is to be considered for the display of a warning.

➩ A warning is displayed whenever the delay for the start of the spiral exceeds this value.

CHAPTER
C.9 CARE Vision CT (Option)

The option **CARE Vision CT** is a special examination mode for such interventions as biopsies, drainages, and analgesic therapy performed in the examination room itself.

With **CARE Vision CT** the examining physician can trigger scans in the examination room at freely selected table positions.



Tomographic acquisitions are monitored on a second monitor installed directly in the examination room. The detailed representation of organ structures in the tomographic image permits precise control of the operation so that critical structures such as blood vessels, nerves, or intestines are not harmed.

Special aspects

The following aspects of **CARE Vision CT** examinations must be taken into account:

- The scan is always acquired at the current table position with minimum start delay.
- The horizontal and vertical table position can be freely selected within the collision limits.
- You must always control the scan with the foot switch. A scan in **CARE Vision CT** is started by pressing the foot pedal and finished by releasing it. Once the scan has started, no automatic table feed occurs.
- If you have set a low table height for the scan, the patient will be located outside the scan center. This results in reduced image quality.
- The rotation time (lowest value), slice thickness mode (narrow collimation), and table feed per scan (0) are preset and cannot be changed.
- The raw data of the **CARE Vision CT** scans is not stored. Subsequent reconstructions are therefore not possible.

CARE Vision CT accessories

Use the following accessories for **CARE Vision CT** examinations:

❏ Foot switch for triggering scans
The scan is triggered as soon as you press the foot switch and keep it pressed.
→ SOMATOM Operator Manual, page B.2–14, *Scanning footswitch (optional)*

❏ Monitor
You can monitor surgical intervention during the scan at the monitor in the examination room.
→ SOMATOM Operator Manual, page B.4–10, *Monitor(s)*

Preparing CARE Vision CT

For your examinations with **CARE Vision CT** you will load special scan protocols that are stored in your system. You will then execute a topogram and localize the position for the surgical intervention, usually with a spiral acquisition. You will then define the scan and reconstruction parameters for the **CARE Vision CT** acquisitions and start scanning.

Calling up CARE Vision CT

You can activate **CARE Vision CT** by selecting a particular scan protocol during patient registration or in the window **Patient Model Dialog** on the **Examination** card.
→ Page B.3–11, *Entering examination data*
→ Page C.2–4, *Selecting a scan protocol*

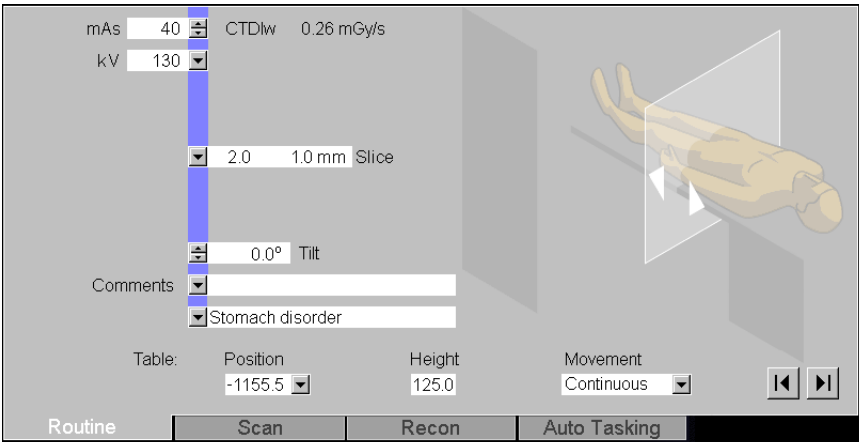
You can append additional examination steps using the control of the chronicle and so easily extend your **CARE Vision CT** examination.
→ Page C.2–23, *Adapting routine scan protocols*

Defining parameters

Once you have executed the topogram acquisition and adapted the examination area, set the scan parameters for your **CARE Vision CT** examination in the usual way on the **Routine** and **Scan** subtask cards. Unlike a sequence or spiral examination, here the majority of the parameters are preset and cannot be altered.

Subtask card Routine

The selection list **Movement** is displayed instead of the selection list for scan direction. Here you specify the step length that the table must travel when you jog it by tapping the symbol keys on the gantry operating console.



mAs 40

kV 130

CTDIw 0.26 mGy/s

2.0 1.0 mm Slice

0.0° Tilt

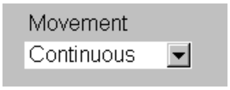
Comments

Stomach disorder

Table: Position -1155.5

Height 125.0

Movement Continuous



Movement: Continuous

✧ Select **Continuous** if the table is to move by 0.5 mm on every "tap".

Or

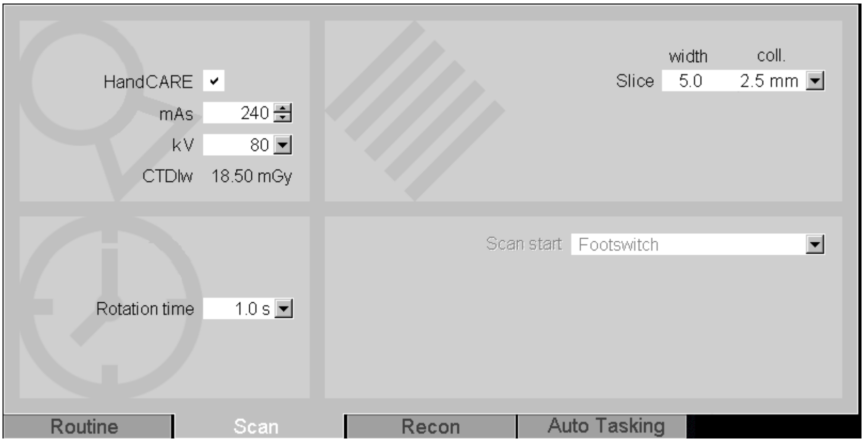
✧ Select **Incremental** and enter your own step length in the input field.

➩ A short "tap" moves the table by 0.5 mm (**Continuous**) or by the set step length (**Incremental**). Pressing and keeping pressed moves the table continuously (speed accelerates after two seconds)

✧ Set the tube voltage, the mAs value and the slice thickness for your **CARE Vision CT** scans.

Subtask card Scan

In addition to the scan parameters on the **Routine** subtask card you can also choose between continuous radiation and radiation with pauses (**Hand CARE**) on the **Scan** subtask card. If the **Hand CARE** function is activated, radiation is interrupted during a scan phase if the rotating X-ray tube is located in the upper part of the gantry. This reduces radiation exposure for patient and physician standing next to the scanner.



HandCARE ☑

mAs 240

kV 80

CTDIw 18.50 mGy

Slice width 5.0, coll. 2.5 mm

Scan start Footswitch

Rotation time 1.0 s

HandCARE ☑

✧ Select **HandCARE** to set scanning with reduced radiation (one image will be reconstructed on each rotation of the tube/detector system).

Or

HandCARE ☐

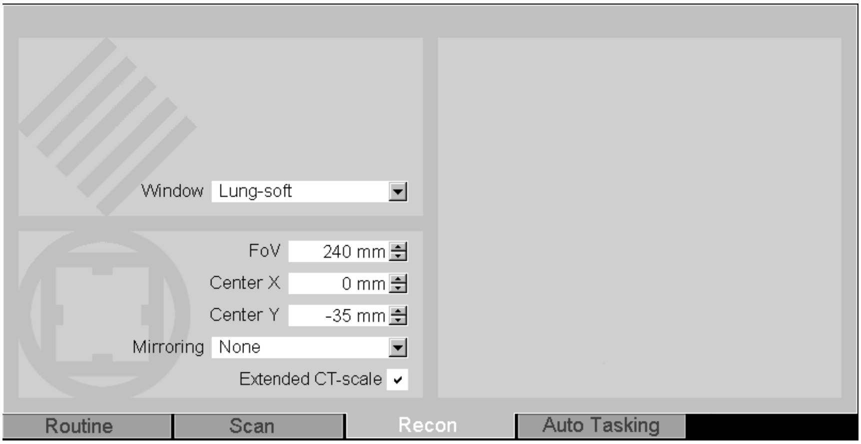
✧ Deselect **HandCARE** to scan with continuous radiation (the maximum possible number of images are reconstructed).

Scan start Footswitch

You always control the scan with the foot switch.

Subtask card Recon

All you now have to do is check and, if necessary, correct the window settings and parameters for the image settings in the **Recon** task card. These settings are applied to the tomogram display during the examination.



Window Lung-soft

FoV 240 mm

Center X 0 mm

Center Y -35 mm

Mirroring None

Extended CT-scale ☑

Window Abdomen

✧ Select a window that is suitable for the type of tissue to be reconstructed.

✧ Change the image settings, if necessary.
→ Page C.10–25, *Image settings*

Performing CARE Vision CT

Once you have defined the scan and reconstruction parameters, switch the scanner ready to scan.

Load

✧ Confirm the scan protocol with **Load**.

➪ When you have loaded the scan protocol and before all further scans, the start prompt is displayed.

Controlling the scanner

The physician specifies the duration of radiation with the foot switch and the horizontal table movement using the symbol keys on the gantry operating console. Surgical intervention is monitored on the tomograms at the monitor of the Navigator and in the examination room.

➪ Ensure that the field of view is set correctly.

Scanning

The scan is performed for as long as the foot switch for triggering the scan remains pressed.

When you release the foot switch scanning is terminated and the system is again ready to scan.

➪ After start of the first scan the gantry tilt can not be altered.

Moving the table

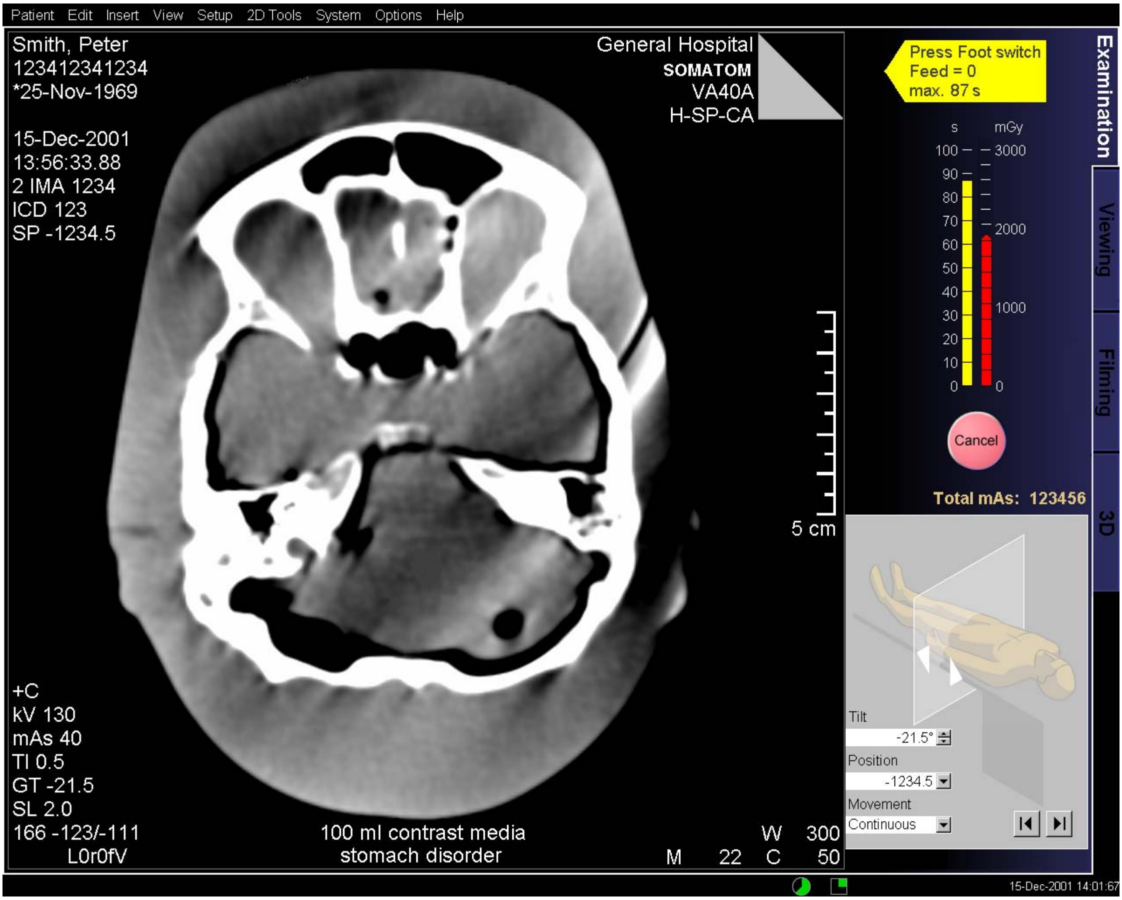
The patient table can be moved during scan pauses using the gantry field.

☐ A short "tap" moves the table by 0.5 mm or by the set step length
→ Page C.9–5, *Subtask card Routine*

☐ Press and keep pressed - continuous table movement (speed accelerates after two seconds)

Tomogram display

The acquired tomograms are displayed in large format on the screens in the control room and in the examination room. If the **HandCARE** function is activated, all tomograms are stored in the local database. If **HandCARE** is not used, the tomograms acquired over the last three seconds are stored in each scan pause.



Press Foot switch
Feed = 0
max. 87 s

Total mAs: 123456

Tilt: -21.5°

Position: -1234.5

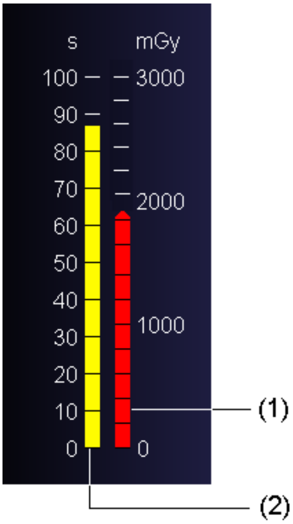
Movement: Continuous

Radiation dose and scan time

Information about the radiation dose and scan time is given in the top right-hand area of the **Exam** card.

Applied dose and remaining scan time

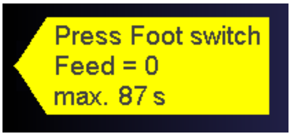
The radiation dose so far applied and the remaining scan time is displayed continuously by a progress indicator. The increase of the radiation dose is indicated by a change of color of the progress indicator and by a warning triangle (maximum dose).



(1) Radiation dose in milliGrays

(2) Scan time in seconds

Maximum scan time



Press Foot switch
Feed = 0
max. 87 s

During scan pauses the maximum possible scan time is displayed by the start prompt and the progress indicator. It decreases as the tube load increases and increases in the scan pauses.

Closing CARE Vision CT

Once you have completed the last scan required for the intervention you can close **CARE Vision CT** mode.

✧ Click on **Cancel** on the right-hand side of the **Exam** card to deactivate the system’s readiness to scan.

✧ Continue with the next scan listed in the chronicle or close the examination with **End Exam**.

NOTE

With **End Exam** the display for the entire radiation dose is reset; it starts from the beginning again on the next examination.

This also applies if you perform a subsequent examination on the same patient.

CHAPTER
C.10 Reconstruction

In a sequential or spiral scan, the first step is always the acquisition of raw data. You can largely influence the quality of these raw data via the scan parameters.
→ Page C.5–3, *Preparing for a spiral*
→ Page C.6–4, *Preparing for a sequence*

In a next step, tomographic images are calculated from the raw data according to the reconstruction parameters. The scan parameters and reconstruction parameters together determine the quality of the CT images.

After scanning, you can no longer change the scan parameters, but you can have different images calculated from the raw data by applying different reconstruction parameters to the same set of data.

This is useful if you want to optimize the image display after a scan. And there are examinations which always involve two or more image displays, such as soft tissue and pulmonary images in the thorax or the separate display of the right and left hip in addition to overview images of the pelvis.

Reconstruction during scanning

An initial set of tomographic images is already reconstructed in parallel with each scan. During sequence scans, there is a small time delay before reconstruction with full image quality (**Metro Recon**). A spiral scan can either be reconstructed in **Metro Recon** mode or as last image at the end of the spiral scan (**Last Image Display**). As an option, RTD offers real time imaging with nearly full image quality.

Reconstruction after scanning

You will usualy reconstruct full quality images parallel with scanning in **Metro Recon** mode. If multiple reconstructions are useful, you decide whether to perform these reconstructions immediately after scanning or later on. If **RTD** or **Last Image Display** was used during spiral scanning full reconstruction of the raw data must be performed after scanning, as well.

Reconstruction at a later time

As long as there are still raw data of an examination in the system, you can calculate further images with altered reconstruction parameters as often as you require. Search for the required patient in the **Patient Browser** and then transfer the raw data for reconstruction to the **Examination** card.
→ Page D.3–9, *Reconstructing images*

Reconstructing the scan series

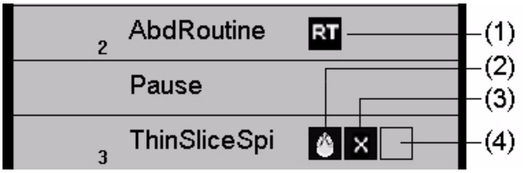
Regardless of whether you want to reconstruct the examination data straight after scanning or not until a later time, a reconstruction job must have been created. It contains all the parameters and settings with which you want your system to calculate the images.

The scan protocol which is based on the current examination data already contains one or more reconstruction jobs for each scan series.

On the **Recon** subtask card, you can change the reconstruction parameters, e.g. if you want to repeat a reconstruction with new settings. Here you can also define the number of reconstruction jobs.

Reconstruction jobs

Reconstruction jobs appear as boxes (recon icons) next to the entry for the scan series in the chronicle. You can see the processing state that the reconstruction job is in by the way the box is displayed.



(1) RT reconstruction job
(2) Completed reconstruction job
(3) Interrupted reconstruction job
(4) Open reconstruction job

If all the planned reconstruction jobs for a series have been completed, then you must create new jobs for further reconstructions.
→ Page C.10–14, *Repeating reconstruction*

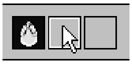
The RT reconstruction jobs designate scan series that were only reconstructed during scanning with reduced image quality in **Guide View**. These jobs are treated as open, because you will usually have the associated scans calculated again with full image quality.

Adapting a reconstruction target

With the field of view (FoV), you define the square area of an image that you want reconstructed and that should fill the segment when the resulting image is displayed.

With the FoV, you also define the magnification factor, i.e. you determine the visibility of details.

You have already limited the required FoV in the topogram and perhaps also optimized it using the control scan. After you have calculated the first scans of a series, you can define the FoV again to make it fit the region of interest as precisely as possible.



✧ Click on the recon icon of the job in the chronicle whose field of view you want to edit.

➩ If you click on a completed reconstruction job (recon icon with a miniature tomogram), the images already reconstructed are displayed. In this case you can of course no longer change the FoV.

Creating the overview image

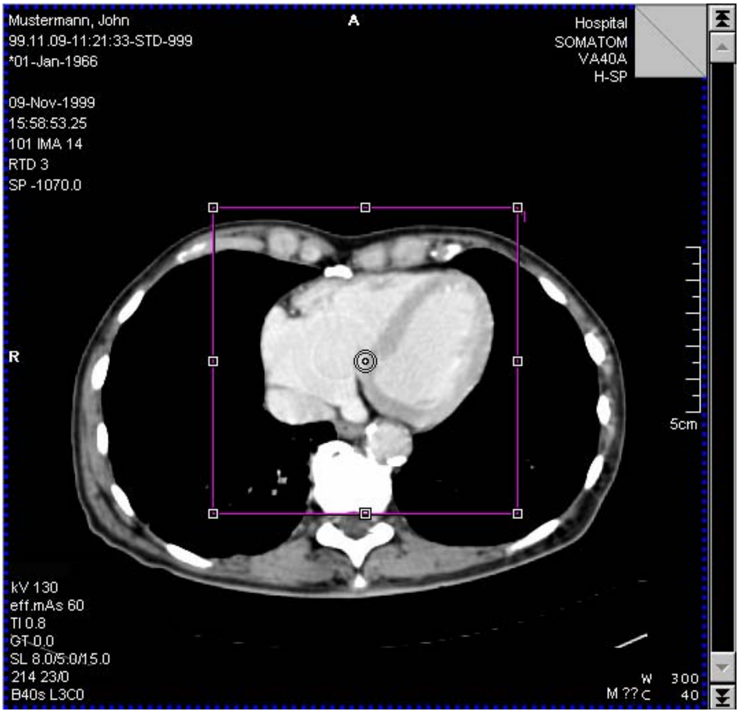
Overview

If you want to enlarge or pan the field of view beyond the edge of the image, have an overview image displayed with maximum FoV.

✧ Click the **Recon** subtask card into the foreground and select the **Overview** button on it.

The overview image is displayed in the tomo segment. The field of view previously set is displayed, and you can pan it and enlarge it.

➪ You can plan all FoVs of this range in the overview image.



➪ On the **Recon** card, you can define at what table position the overview image is reconstructed.
→ Page C.10–28, *Start of reconstruction range*

Panning the FoV

✧ Move the mouse onto the displayed center of the field of view.

The mouse cursor changes shape.

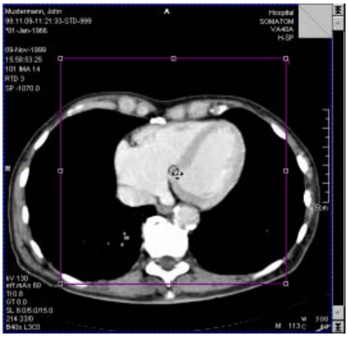
✧ Move the center holding the left mouse key down to change the position of the FoV.

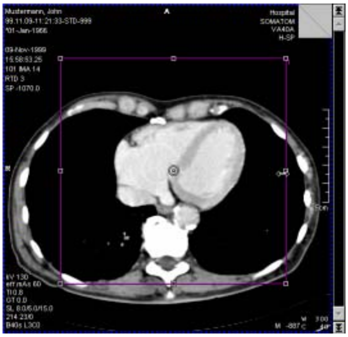
Enlarging or reducing the FoV

✧ Move the mouse onto one of the handles.

The mouse cursor changes shape.

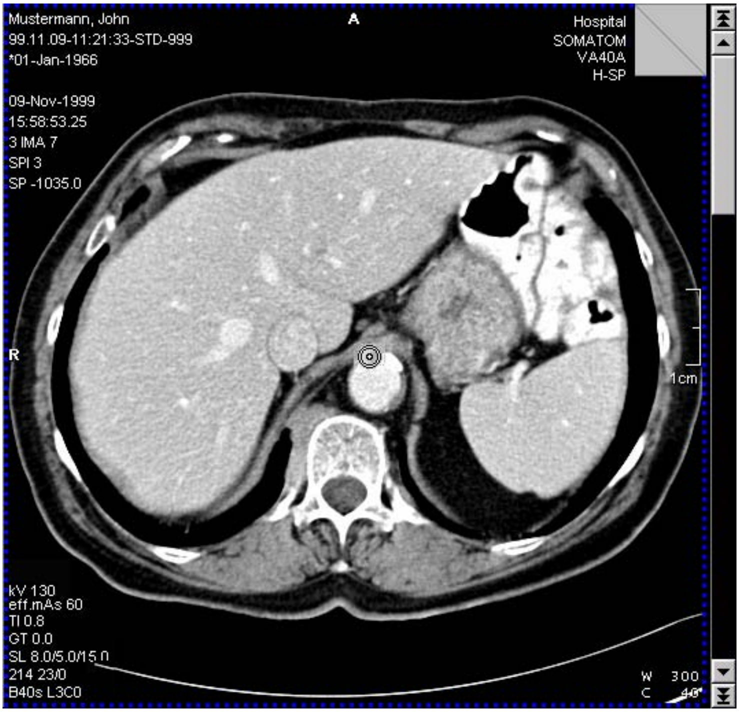
✧ Drag the handle inward while holding the left mouse key down to reduce the FoV, or outward to enlarge the FoV.



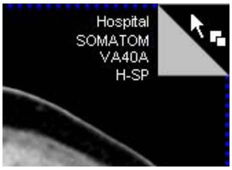


Reconstruction without an overview image

You do not require the overview image, if you want to enlarge details from the image displayed. Use the image displayed in the tomo segment. After you have clicked the corresponding recon icon, the FoV is displayed and is already selected.



Scrolling in the tomo segment



If you want to change the field of view in another tomographic image, scroll through the image stack using the dog ear in the top right-hand corner.

✧ Click on the inner triangle with the mouse to scroll back by one image.

✧ Click on the outer triangle to scroll forward by one image.

Or

✧ Use the scroll bar.

➪ If the region of interest is not completely visible on the images, first create an overview image and adapt the FoV there.
→ Page C.10–6, *Creating the overview image*

➪ It is also possible to set the size and position of the FoV numerically.
→ Page C.10–25, *Setting the FoV numerically*

Starting reconstruction

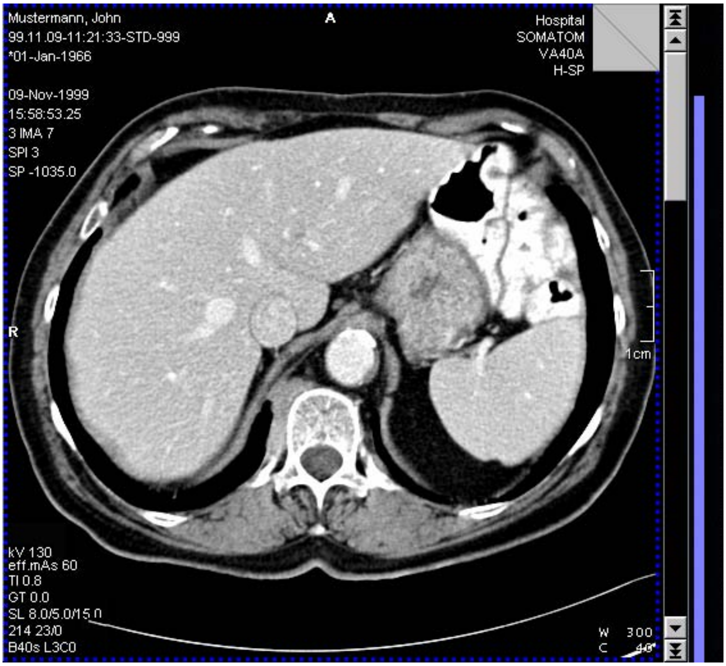
✧ Click on **Recon** to start reconstruction of the scan series currently selected.
The **Recon** button turns into the **Hold Recon** button.

Tomographic images are calculated from the raw data of the series in question for the set field of view and are displayed in the tomo segment.

If more than one open reconstruction job has been defined for the selected series, then the other jobs are executed as well.
→ Page C.10–16, *Executing open reconstruction jobs*

Reconstruction progress

You can see the calculated images displayed one after the other in the tomo segment. You can follow the reconstruction progress by the bar display on the right-hand border.



After the reconstruction jobs have been executed, the last reconstructed scan is displayed in the tomo segment.

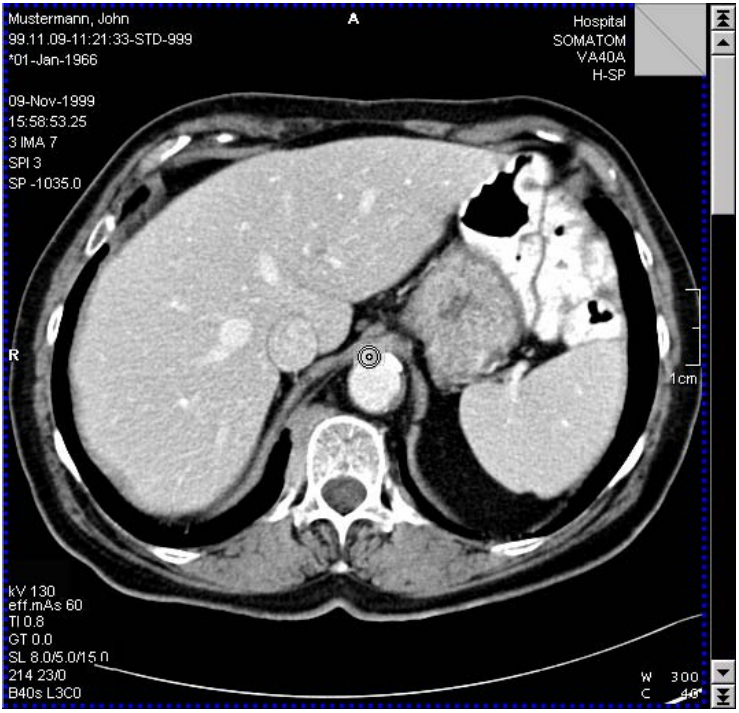
Holding reconstruction

You can suspend reconstruction at any time. For example, if you see that the region of interest is moving out of the image or if you want to perform graphic evaluation of an image. You can also stop reconstruction altogether, if you have to examine an emergency patient.

Hold Recon

✧ Click on **Hold Recon** to suspend reconstruction.

The **Hold Recon** button turns into the **Recon** button. In the tomo segment, you can see the image last reconstructed with the center of the Field of View displayed.



Mustermann, John
99.11.09-11:21:33-STD-999
*01-Jan-1966

09-Nov-1999
15:58:53.25
3 IMA 7
SPI 3
SP -1035.0

Hospital
SOMATOM
VA40A
H-SP

kV 130
eff.mAs 60
TI 0.8
GT 0.0
SL 8.0/5.0/15.0
214 23/0
B40s L3C0

W 300
C 40

For example, you can now update the FoV in the tomo segment and then resume reconstruction.
→ Page C.10–5, *Adapting a reconstruction target*

➪ You can only change the windowing values and the image settings on the **Recon** subtask card. All other parameters are dimmed.

Preliminary graphic evaluation

Using the graphic tools on the **Examination** card, it is possible to perform graphic evaluations in the tomograms displayed. You can evaluate areas in a ROI and distances, lengths, and angles.
→ Page C.11–12, *Evaluating images*

The graphic elements drawn in (e.g. a ROI) can then be automatically copied to the following reconstructed tomograms.

✧ Call up **2D Tools > Hold Graphics On** in the main menu.

If you continue reconstruction, the graphic elements drawn in are transferred to each new tomogram of the series.

Resuming reconstruction

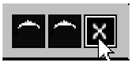
✧ Click on the **Recon** button to resume reconstruction without a gap.

➪ If you have interrupted reconstruction because of an emergency patient, you must load the examination data with the **Patient Browser** again first.
→ Page D.3–9, *Reconstructing images*

Stopping reconstruction

If you want to stop reconstruction altogether, i.e. not resume it again later, you must delete the reconstruction job.

✧ Click on **Hold Recon** to stop the current reconstruction.



✧ Select the reconstruction job in the chronicle with the appropriate recon icon.

✧ Call up **Edit > Delete Recon Job** in the main menu to delete this reconstruction job.

Or

✧ Select **Delete Recon Job** in the popup menu of the chronicle.

➪ If you do not delete the job, it is still considered open and will be continued during the next reconstruction.

Repeating reconstruction

While the raw data of a scan is accessible, you can start additional reconstruction jobs as often as required to create further optimized images. However, you must first create new jobs when all the reconstruction jobs previously planned have been executed.

Appending new jobs

For each additional reconstruction of a scan series, you require a new reconstruction job.

✧ Select the scan series that you want to reconstruct again in the chronicle.

✧ Click the **Recon** card into the foreground.

Recon job ● 1 ○ 2 ○ 3

✧ Click the second radio button to plan a second reconstruction job.

➪ If two reconstruction jobs already exist, click on the third radio button to create a third job.

Deleting recon jobs

Three reconstruction jobs for each scan series can be managed in the chronicle. If a scan series already has three completed reconstruction jobs, you must first delete one or two of these old jobs before you can create new jobs.

➪ By deleting a completely or partially executed reconstruction job, you do **not** delete the images created with it. You cannot delete images by deleting recon icons.

✧ Select one of the completed reconstruction jobs in the chronicle.

✧ Call up **Edit > Delete Recon Job** in the main menu or **Delete Recon Job** in the popup menu of the chronicle to delete the reconstruction job.

✧ Repeat these two steps if you want to delete a further reconstruction job.

➪ The last remaining reconstruction job cannot be deleted.

Executing open reconstruction jobs

On the previous pages, we have shown you how to select and process reconstruction jobs in the chronicle and how to perform a reconstruction.

If you have not reconstructed all scans at the end of an examination, some reconstruction jobs will still be open. Here, we describe how you can execute open reconstruction jobs of an individual scan or all open reconstruction jobs of an examination.

Reconstructing an individual scan

✧ Select the scan series that you want to reconstruct in the chronicle.

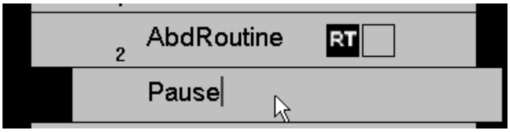
✧ Click on **Recon** to start reconstruction.
The **Recon** button turns into the **Hold Recon** button.

All open reconstruction jobs of the selected scan are executed one after the other.

➩ If the scan has not been completed, your system is still ready to scan and the **Recon** button is dimmed. The **Recon** button is also not active if no more reconstruction jobs are open.

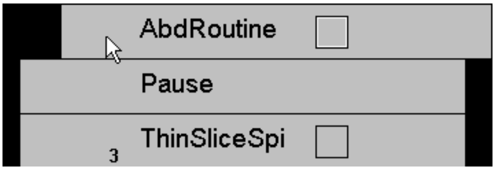
Reconstructing all scans

If you want to execute all open reconstructions in one go, you only have to make sure that none of the scans performed so far is selected. The scan protocol of the current examination is still loaded in the chronicle and the system is ready to scan if **Auto Recon** is not activated.
→ Page C.13–14, *Automatic functions*



✧ Select a pause, contrast, or comment entry in the chronicle if you want to execute all open reconstruction jobs.

Or



✧ Instead, select a scan that you have not yet started.

➪ If no entry is selected in the chronicle, all open reconstruction jobs are taken into account.

✧ Click on **Recon** to start reconstruction.
The **Recon** button turns into the **Hold Recon** button.

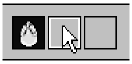
All open reconstruction jobs are executed in the sequence in which they appear in the chronicle.

Completing reconstruction

All raw data of the scan series containing reconstruction jobs which are still open, are protected from deletion. Raw data that is no longer required, because all the necessary images have been calculated, are no longer delete protected when the examination is completed. They will be overwritten with the raw data of the next or following examinations

Saving raw data

You might want to keep the raw data even though the reconstruction jobs have been executed. To protect these data from overwriting, simply create a new reconstruction job.



✧ Check whether at least one open reconstruction job exists for a scan series whose raw data you want to retain.

✧ Create a new recon job, if that is not the case. The raw data are now write-protected.
→ Page C.10–14, *Appending new jobs*

➩ If you want to reconstruct the raw data later, search for the scan series in the **Patient Browser** and then load it onto the **Examination** card.
→ Page C.10–17, *Reconstructing all scans*

Allowing raw data to be deleted

If you are sure that you no longer want to reconstruct the examination data currently loaded, you can allow these raw data to be deleted.

In this way, you can make space in the raw data memory of your system for data of new examinations.

✧ Make sure that no open recon jobs exist for the scan series of the examination.
Delete all open recon jobs from the chronicle.
→ Page C.10–15, *Deleting recon jobs*

➩ When you finish the examination (**End Exam**) the **Recon Controller** dialog box for easy deletion of the raw data is displayed.
→ Page C.10–33, *Ending reconstruction*

NOTE

Always catch up on missing reconstruction runs of your scans as quickly as possible. In that way, you can make sure that future examinations are not delayed because old raw data is taking up memory space.

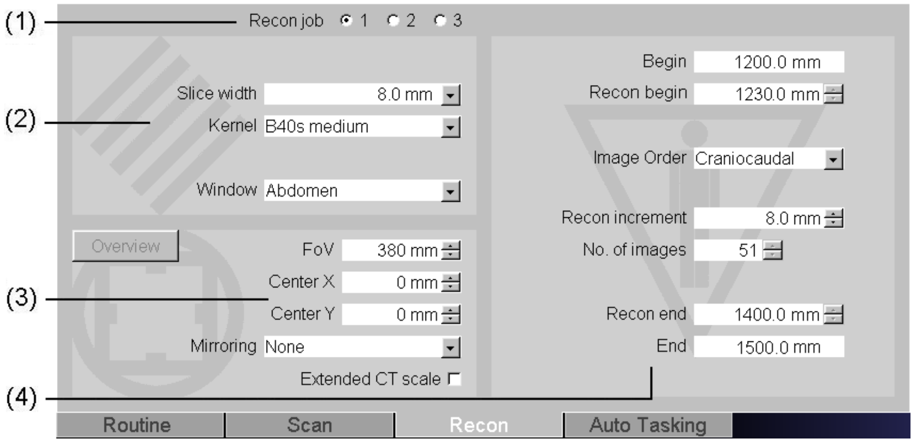
You should archive and then delete from the local database raw data that you do not require in the near future, but still want to save.
→ Page D.6–2, *Archiving data*

Changing reconstruction parameters

When you change the reconstruction parameters, you influence the size of the field of view, the image display, and the degree of overlap between the calculated images of a series.

Calling up the Recon subtask card

✧ Click the **Recon** subtask card into the foreground, if you want to check and change the reconstruction parameters.



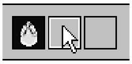
Recon job ● 1 ○ 2 ○ 3

Slice width 8.0 mm
Kernel B40s medium
Window Abdomen
FoV 380 mm
Center X 0 mm
Center Y 0 mm
Mirroring None
Extended CT scale ☐

Begin 1200.0 mm
Recon begin 1230.0 mm
Image Order Craniocaudal
Recon increment 8.0 mm
No. of images 51
Recon end 1400.0 mm
End 1500.0 mm

(1) Number of the reconstruction job
(2) Reconstruction algorithm
(3) Image settings
(4) Reconstruction range

Selecting a reconstruction job



✧ Click on the recon icon of the job whose reconstruction settings you want to view or process in the chronicle.

Or

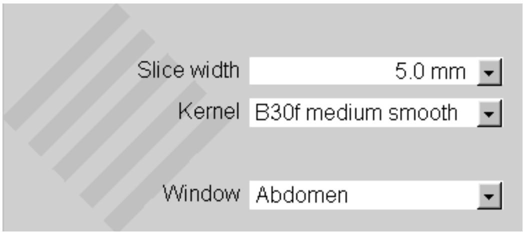
✧ Select a scan series in the chronicle.

Recon job ● 1 ○ 2 ○ 3

✧ Select the radio button of the reconstruction job that you want to edit on the **Recon** subtask card.

Reconstruction algorithm

In this part of the card, you define how the images are to appear. Via the selection of a kernel you set whether you want the images to be smooth or with greater detail resolution and what slice width the images are to have.



Slice width 5.0 mm
Kernel B30f medium smooth
Window Abdomen

Slice width

For reconstruction after a spiral scan, you can also set a slice width which is greater than the collimated slice width during the scan. The selection of slice widths which you can choose depends on the slice width mode.

Slice width 5.0 mm

✧ Select a slice width from the selection list.

Kernel

Via the kernel, you can regulate the image sharpness and resolution. The different kernel categories refer to the region of the body, the type of tissue, and whether the patient is a child. Make sure that you select the correct kernel for your examination.

The following table is for illustration purposes only and may vary with software version:

Region	Kernel	description
Body	B10 B20 B30 B40 B50 B60 B70	very smooth smooth medium smooth medium moderate sharp medium sharp sharp
Head	H10s H20s H30s H40s H50s H60s H70s	very smooth smooth medium smooth medium moderate sharp medium sharp sharp
Child head	C20s C30s C60s	smooth medium smooth medium sharp
UHR	U90s	ultra sharp

The second part of the kernel designation, the index number with the preceding abbreviation for the kernel category, is a measure of the resolution.

The higher the index number of a kernel, the more pronounced the contrast differences will be, and the higher the resolution will be, i.e. for bone and lung images. With a low index number, the images appear smoother. These kernels are suitable for soft tissue images in order to demarcate wide area tissue structures better.


Kernel B30f medium smooth

✧ Select a suitable kernel from the selection list.

➪ The selection list only contains the kernels that are permissible for the region of the body selected in the routine scan protocol.

Window

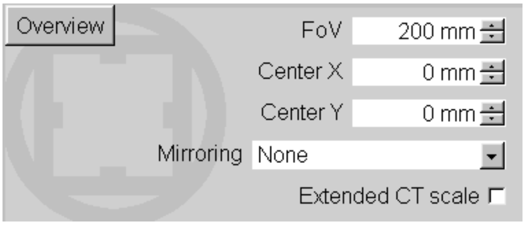

Window Abdomen

✧ Select a window which is suitable for the type of tissue that you want to reconstruct.

➪ For fine adjustment during or after reconstruction, you can use the tuning knobs on the control box, for example.

Image settings

The image settings include the field of view, the type of image mirroring, and the CT scale.



FoV 200 mm

Center X 0 mm

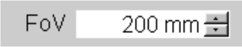
Center Y 0 mm

Mirroring None

Extended CT scale ☐

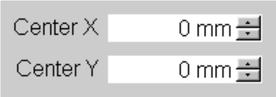
Setting the FoV numerically

You will generally define the FoV graphically in the topogram or in a tomographic image. If you have a lot of experience or want to reproduce the precise value of a reference image, you can enter the size and position of the FoV numerically. Every change to the FoV is displayed graphically in the topo and in the tomo segment.



FoV 200 mm

✧ Enlarge or reduce the FoV numerically by selecting the required size using the spin buttons (increment 1 mm).



Center X 0 mm

Center Y 0 mm

✧ Position the FoV numerically by setting the coordinates X and Y for the center via the spin buttons (increment 1 mm).

➪ With the **Overview** button, you can reconstruct an overview image.
→ Page C.10–6, *Creating the overview image*

Mirroring

The position of the patient during the examination determines whether and in what direction the scans are automatically mirrored in order to obtain a standard view of the images. The following mirroring modes for a reconstruction are possible:

- Up-down (vertical mirroring)
- Left-right (horizontal mirroring)
- Both (vertical and horizontal mirroring)
- None

Mirroring None

✧ Select the required mirroring in the selection list if you want to reconstruct images in a view other than the standard view.

Extended CT-scale

Foreign bodies of strongly absorbent material (e.g. implantations or endoprotheses made of iron or titanium) appear white on the images, if their density values are above the CT-scale typical for tissues. Extending the CT-scale enables you to see the density differences at the edges of these objects and to display them in gray-scale values with a suitable window setting.

Extended CT scale ☐

✧ Click the **Extended CT-scale** check box to reconstruct over the maximum density value range.

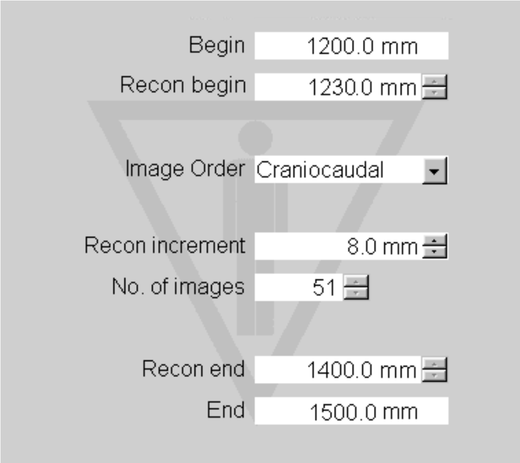
Instead of from -1024 HU to +3071 HU, the CT-scale now covers the range from -10240 HU to +30710 HU.

➪ The density values of deletion artifacts occurring inside strongly absorbent foreign bodies cannot be displayed by extending the CT-scale for physical reasons.

Reconstruction range

You will usually reconstruct all the scans of a range, i.e. calculate tomographic images over the entire scanned length.

On the **Recon** subtask card, you can, however, restrict the reconstruction range. This is useful if you know from the image reconstruction that was carried out in parallel with the scanning that the first or last images of the range are not relevant for your diagnostic problem.



Begin 1200.0 mm

Recon begin 1230.0 mm

Image Order Craniocaudal

Recon increment 8.0 mm

No. of images 51

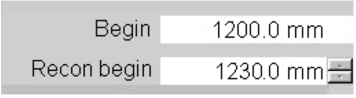
Recon end 1400.0 mm

End 1500.0 mm

➩ The **Recon increment** is only displayed for spiral scans.

Start of reconstruction range

For the start of the reconstruction range, enter the table position at which you want the first image to be reconstructed. If you create an overview image, it is also calculated at the **Recon begin** table position.



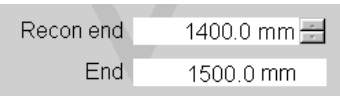
Begin 1200.0 mm

Recon begin 1230.0 mm

✧ Set the start of the reconstruction range using the spin buttons.

End of reconstruction range

The end of reconstruction range is the table position at which the last image is going to be reconstructed.



Recon end 1400.0 mm

End 1500.0 mm

✧ Set the end of reconstruction using the spin buttons.

➪ The beginning and end of the reconstruction range must be within the scanned range (between **Begin** and **End**).

➪ If you only want to calculate one image, select the same position for the end of the reconstruction range as for the start of the reconstruction range.

Image Order

In a recon job you define the direction in which the reconstructed images are sorted by their image number.

Image Order Craniocaudal

✧ Select *craniocaudal* or *caudocranial*.

➪ In the **Patient Browser** you can sort an image series in reverse order if necessary.

Number of images

No. of images 51

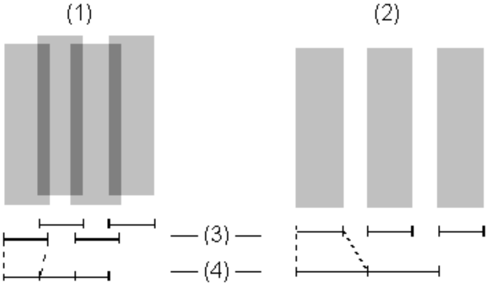
Here, the total number of images is displayed that you will obtain from a reconstruction run. It depends on the length of the range set, the slice width, and for spirals also on the increment (increment during reconstruction).

Increment for a spiral

Recon increment 8.0 mm

You have acquired a body volume without gaps with a spiral and can now calculate tomographic images at any position contiguously, overlapping, or with gaps.

Depending on what reconstruction increment you have selected compared with the slice width set, the images will be contiguous (default setting), they will overlap (image distance < slice width), or gaps will arise between the images (image distance > slice width).



(1) Overlapping images
(2) Images with gaps
(3) Slice width
(4) Image distance

Overlapping images

Slices reconstructed to overlap have the advantage that partial volume effects are reduced and the image transitions are smoothed during postprocessing.

Recon increment 8.0 mm

✧ Set the increment to be smaller than the slice thickness to obtain overlapping images.

No. of images 51

The number of images is increased accordingly.

Images with gaps

You can use reconstruction with gaps, for example, to obtain an overview of the scanned range with fewer images.

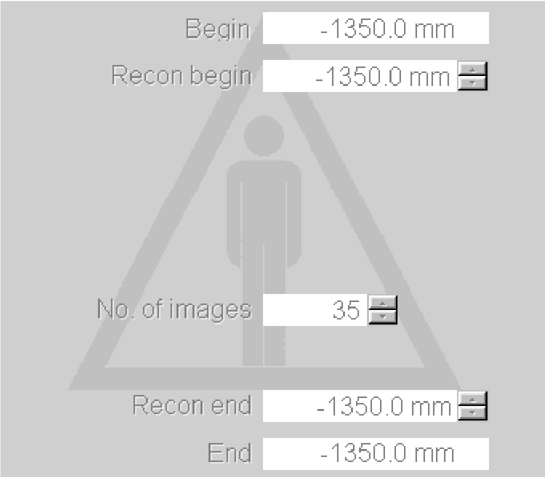
Recon increment 8.0 mm

No. of images 51

✧ Increase the increment if you want to calculate the images with gaps.

Sequence without table feed

Dynamic scan series acquired with the sequence technique consist of slice scans taken at time intervals at the same table position. The value for the beginning (**Begin**) and the end of scanning (**End**) is thus identical.



Begin -1350.0 mm

Recon begin -1350.0 mm

No. of images 35

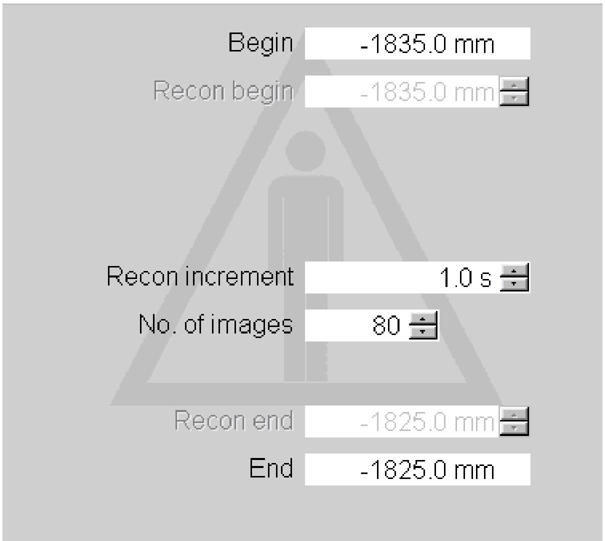
Recon end -1350.0 mm

End -1350.0 mm

The entries for the reconstruction range are dimmed in this case. All the scanned slices are therefore always reconstructed.

Multiscan

Because scanning is performed at the same table position, the reconstruction range is a time window. The time difference between two consecutive images is determined by the **Recon increment**.



Begin -1835.0 mm
Recon begin -1835.0 mm
Recon increment 1.0 s
No. of images 80
Recon end -1825.0 mm
End -1825.0 mm

Recon increment 1.1 s

✧ If necessary, change the **Recon increment**.

➪ The default value for the **Recon increment** is equivalent to the rotation time, the minimum value is 0.1 s. If the rotation time changes, the **Recon increment** is adapted automatically.

No. of images 18

The number of images is automatically adapted to the **Recon increment** set.

Ending reconstruction

You can complete the examination after you have performed all the required reconstructions and, if necessary, have performed an initial image processing and evaluation.
→ Chapter C.11, *Image Processing and Evaluation*

✧ Click on the **End Exam** button to end processing the examination data.

Or

✧ Call up **Patient > End Exam** in the main menu.

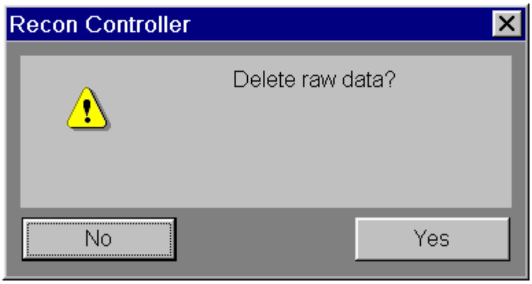
Or

✧ Register the next patient and confirm with **Yes**.

All the reconstructed images are saved as well as the raw data of the scan series with open reconstruction jobs.

Deletion of raw data

If all planned reconstructions have been performed for each scan series of the examination (no open recon jobs) the **Recon Controller** dialog box is displayed.



Delete raw data?

Yes

✧ Click on **Yes** to delete all raw data of the examination.

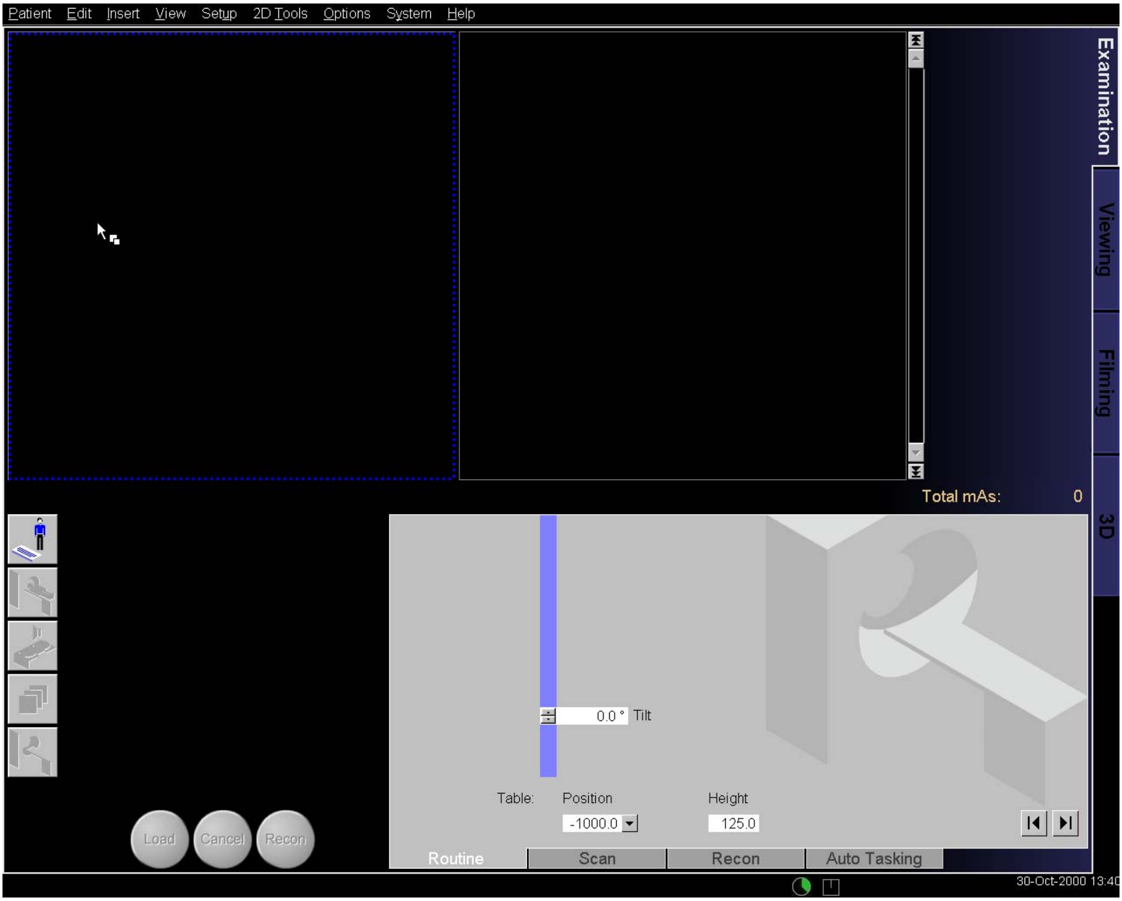
Or

No

✧ Click on **No** if you want to reconstruct raw data of the examination again, later.

The **Examination** task card is now empty.

You can now examine another patient or load the data from another examination from the **Patient Browser** and reconstruct the scans in it.



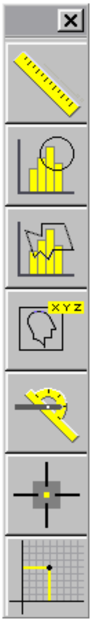
CHAPTER C.11 Image Processing and Evaluation

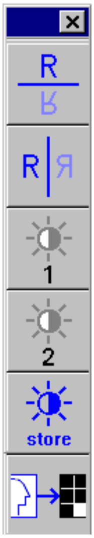
Already during the examination, you have the opportunity to evaluate the examination results simultaneously with or after reconstruction of the scans.

On the **Examination** task card, a number of graphic tools are available to you. You can use them to process and statistically evaluate both the topogram and any image selected in the tomo segment.

For detailed postprocessing of the examination results after you have completed the examination, you can use the **Viewing** task card.
→ Page E.1–2, *Calling up the Viewing task card*

Displaying the graphic tools





The graphic tools of the **Examination** task card are accessible via two tool bars. Display them, if necessary.

✧ Call up **2D Tools > Graphics** in the main menu to display the tools for graphic evaluation.

✧ Call up **2D Tools > Image Manipulation** in the main menu to display the tools for image processing.

The tool bars appear to the right of the tomo segment, but can be moved to any other position.

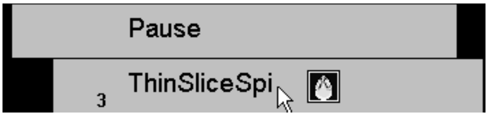
✧ Click into the title bar with the mouse and move the tool bar to the required position holding the left mouse key down.

To hide the tool bar, click on the small button with the cross.

Selecting a topogram and images

You can postprocess and evaluate both a topogram and the images in the tomo segment of the **Examination** task card.

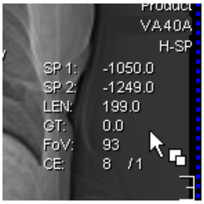
Selecting a scan



✧ Click on an entry in the chronicle to select a scan series for processing.

Selecting the topogram

In the topo segment, the topogram of this series is displayed and selected for evaluation. Of course, you can switch to the tomo segment at any time and resume your work in the topo segment later on.



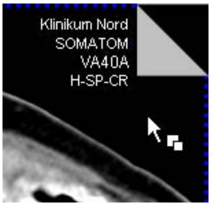
SP 1: -1050.0
SP 2: -1249.0
LEN: 199.0
GT: 0.0
FoV: 93
CE: 8 /1

✧ Click into the topo segment with the mouse to select the topogram for evaluation again.

➩ The segment selected has a blue dotted border.

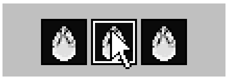
Single image

In the tomo segment, you first see the last image of the first reconstruction task when you select a series in the chronicle.



✧ Click into the tomo segment with the mouse to process and/or evaluate images there.
The tomo segment has a blue dotted border.

✧ Scroll to the first image in the stack that you want to process using the dog ears.
→ Page C.10–9, *Scrolling in the tomo segment*



✧ If you want to display the images of another reconstruction task in the tomo segment, click on the corresponding recon icon in the chronicle.

Images up to the end of series

If you want your processing steps to apply to all the following images of a series, set the image selection to "up to end of series".

✧ Call up **2D Tools > Select on Succeeding**.

Or

✧ Select **2D Tools** in the popup menu.

All images are selected from the displayed image up to the end of the stack.

Complete series

To process all tomograms in the image stack at once, select the complete series.

✧ Call up **2D Tools > Select Series** to select all images of the series.

Editing image display

Before you evaluate the examination images, we recommend optimizing the display parameters in order to provide the best display of the regions relevant in this examination.

You can adapt the window values, enlarge the field of view, and pan the region of interest into the center of the image in the tomo or topo segment.

Setting the window values

By optimizing the window settings, you can ensure that the diagnostically relevant areas are easily visible on the images or in the topogram.

Scope for windowing

On the **Examination** task card, you can chose between two scopes of action for changing the window settings just like on the **Viewing** task card.
→ Page E.4–4, *Setting the scope*

❏ Windowing on succeeding

✧ Select **2D Tools > Windowing On Succeeding** in the main menu if you want to window all the images up to the end of the series from the image displayed onward.

➩ If you want to window the entire stack of images (i.e. the entire series) scroll to the first image of the stack.

❏ Windowing on selection

✧ Deselect **2D Tools > Windowing On Succeeding** in the main menu to window individual images.

➩ With the **Ctrl** key, you can select several images for processing at the same time.
→ Page E.3–36, *Selecting images explicitly*

During reconstruction, **Windowing On Succeeding** is activated and the tomo segment is selected. You only need to select a suitable window setting once, and this is then also applied to the images calculated afterwards.

Windowing with the mouse

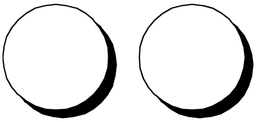
- ✧ Define the scope for windowing.
- ✧ Click on the image or the first image that you want to window, or select the topogram.
- ✧ Move the mouse left/right while holding the center mouse key down to change the contrast (window width).

Or

- ✧ Move the mouse up/down while holding the center mouse key down to change the brightness range (window position).

Windowing with the control box

Instead of the mouse, you can also use the two tuning knobs on the control box to set the window values in the topogram or for very fine adjustment in the reconstructed scans.
→ SOMATOM Operator Manual, page B.4–8, *The control box*



- ✧ Define the scope for windowing.
- ✧ Click on the image or the first image that you want to window, or click into the topo segment.
- ✧ Set the required window values with the tuning knobs.

Fixed window values

Depending on the region of the body or organ examined, your system suggests two sets of window values. You can call these values up, readjust them, and save them with the corrected values for future work.

➪ You can define the default values for the fixed window values organ-specifically in the **Viewing Configuration**.
→ Page E.8–8, *Organ-specific and user-specific window values*

✧ Select the image or images or the topogram to which you want to assign the predefined window values.

➪ Fixed window values are assigned only to individually selected images.

Window1/Window2

✧ Click on the **Window1** or **Window2** button to assign the corresponding window values.

After you have optimized the window settings using the mouse or the tuning knobs on the control box, you can save the new window values with the selected CT images. These images are then always displayed with these window values when retrieved from the memory.

Store Window

✧ Click on this button to store the changed window settings for **Window1** and **Window2**.

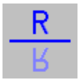
Changing the view of the image

In the tomo segment, you can mirror, enlarge/reduce, or move the images.

Flipping images

✧ Click on the image in the tomo segment that you want to flip.

✧ Click on the **Flip Vertically** button to flip the image from left to right.



✧ Click on the **Flip Horizontally** button to flip the image from top to bottom.

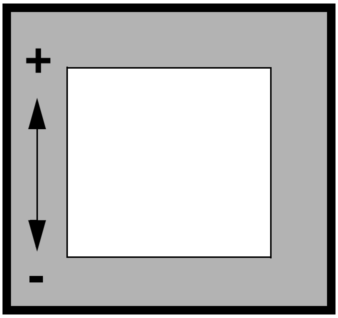
➪ It is not possible to flip topograms.

Enlarging/reducing and panning

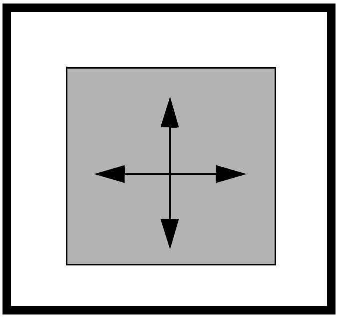
✧ Select **2D Tools > Zoom & Pan On** in the main menu to activate the mouse function for zooming and panning.

In this way, you switch the function of the left mouse key from “Select images/graphic objects” to “Zoom/pan”.

Depending on whether you place the mouse cursor in the center of your image or near the edge, you can enlarge/reduce the image or pan the field of view.



Zooming



Panning

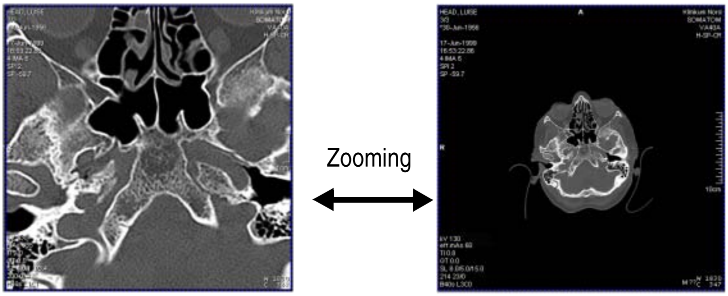
✧ Click near the edges of the image that you want to zoom or click on the edge of the tomo segment.

The mouse cursor changes shape.

✧ Drag the mouse cursor up while holding the left mouse key down to enlarge the selected images.

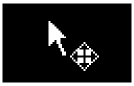
Or

✧ Drag the mouse cursor down while holding the left mouse key down to reduce the selected images.



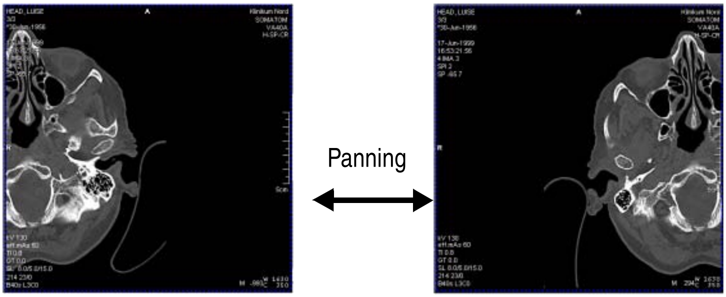
Or

✧ Click into the center of the tomo segment to pan the field of view.



The mouse cursor changes shape.

✧ Drag the mouse cursor in the direction in which you want to pan the selected images while holding the left mouse key down.



Evaluating images

With the graphic tools on the **Examination** card, you can evaluate areas, measure distances, lengths and angles and evaluate pixels. To do that, draw graphic elements on the examination images that you want your system to evaluate statistically.

➩ Graphic and text elements are only stored in an image when you process the last series to have been reconstructed.

➩ You can create and save images with the corresponding text and graphic annotations on the **Viewing** task card.
→ Chapter E.7, *Saving and Documenting Images*

CAUTION

Source of danger: Distance measurements in the topogram

Consequence: Incorrect measurement values due to the projection technique used

Remedy: Only perform distance measurements in the topogram in the longitudinal direction (head-foot direction)

Evaluating areas

You can mark areas of interest in the images with so-called ROIs (**R**egions **O**f **I**nterest) and have them evaluated statistically. You can draw ROIs either as circles or freehand.

✧ Select the image that you want to evaluate.

Circular ROI

✧ Click on the **Circle** button to draw in a circular ROI.

✧ Drag open a circle holding the left mouse key down and then release the mouse key again.

Freehand ROI

✧ Click on the **Irregular ROI** button if you want to draw a non-circular ROI.

✧ Drag the mouse around the relevant region of the image while holding the left mouse key down.

Or

✧ Draw the ROI as a polygon by defining its vertices with a mouse click (left mouse key).

Or

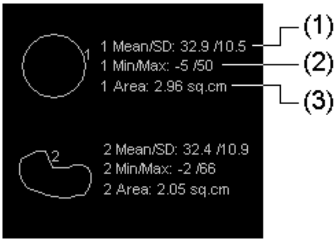
✧ Combine the two steps by holding the left mouse key down for free drawing and appending straight lines with mouse clicks.

✧ When you have finished your ROI, close it with a double-click.

The system connects the start and end points to form an enclosed region.

Evaluating the ROI

As soon as you have drawn your ROI, it is evaluated statistically and the results are displayed in the tomo segment. The ROIs and the associated statistical data are numbered.



1 Mean/SD: 32.9 /10.5
1 Min/Max: -5 /50
1 Area: 2.96 sq.cm

2 Mean/SD: 32.4 /10.9
2 Min/Max: -2 /66
2 Area: 2.05 sq.cm

(1) Mean/SD
Mean value and standard deviation
(2) Min/Max
Highest and lowest density value
(3) Area
Area of the ROI in cm^2

Deactivating ROI mode

While the **Circle** or **Irregular ROI** button is active, you can draw in further ROIs.

✧ To deactivate the ROI drawing mode again, click on the **Circle** or **Irregular ROI** button again.

⇨ If you select another evaluation or image processing function, ROI drawing mode is also deactivated.

Measuring distances

You can use the graphic tools of the **Examination** task card to draw lines in the tomographic images and measure distances with them.

Drawing a distance line

- Click on the **Distance** button to activate distance measurement.
- Drag out a line between two points in the image while holding the left mouse key down to measure the distance.
- Repeat this step if you want to measure further distances.

The length and the angle with the horizontal line is displayed for each line.

Deactivating distance measurement

- Click on the **Distance** button again if you want to deactivate distance measurement again.

➩ If you select another evaluation or image processing function, the distance measurement is also deactivated.

Measuring an angle

To measure an angle, draw in two lines of any length to create the legs of the angle you want your system to measure. The two lines do not need to intersect within the image. The system calculates a virtual point of intersection (not visible to you) and calculates the angle between the two (extended) lines.

Defining the angle

✧ Click on the **Angle** button to activate angle measurement.

✧ First drag out one line while holding the left mouse key down. This represents the first leg of the angle.

✧ Draw another line for the second leg. This can be in any position in the image.

➩ Pull each line toward the origin of the angle or away from the origin of the angle otherwise the complementary angle with respect to 180° will be calculated.
→ Page E.5–27, *Measuring an angle*

Deactivating angle measurement

✧ Click on the **Angle** button again if you want to deactivate angle measurement again.

➩ If you select another evaluation or image processing function, angle measurement is also deactivated.

Measuring pixels with the crosshair

Using the crosshair you can determine the position of pixels and angles with reference to a starting point and two axes at right angles to each other in several images at the same time.

Displaying the crosshair

✧ Select the image or images in which you want to display the crosshair.

✧ Call up **Tools > Crosshair** or click on the **Crosshair** icon button.

The crosshair is displayed in the selected images.

Measuring with the crosshair

✧ Click on the points in the image whose position you want to determine.

The crosshair and the measuring points are stored with the image and can be filmed and/or printed with it.

➪ You can also change the measuring method by switching between **Polar** and **Carthesian** measurement.

Hiding the cross-hair

✧ Click again on the **Cross-hair** button if you want to deactivate angle measurement again.

➪ If you select another evaluation or image processing function, angle measurement is also deactivated.

Displaying Hounsfield values with the pixel lense

If you move the mouse cursor over the image in the tomo segment, the mean Hounsfield value of a 5x5 pixel area is calculated at the current cursor position and output in the bottom right-hand corner of the segment (e.g. “M 44”).

With the pixel lense, you can place these averaged Hounsfield values next to the point of measurement in the image.

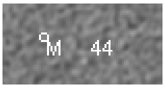
✧ First select the image in the tomo segment for your evaluation.

Activating the pixel lense

✧ Click on the **Pixel Lense** button to activate the pixel lense.

✧ Move the mouse cursor to the current position in the image. You can see the mean pixel value (in HU) in the bottom right-hand corner of the segment.

Entering pixel values



You can label any number of positions in the image and have the associated pixel values displayed.

✧ Click on the required position in the image with the left mouse key while the pixel lense is active.

The position is marked with a small circle and the mean pixel value is displayed to the right of it.

✧ Repeat this step if you want to calculate further positions and display the pixel value in the image.

Deactivating the Pixel Lense

✧ Click on the **Pixel Lense** button again if you want to deactivate the pixel lense.

➩ If you select another evaluation or image processing function, the Pixel Lense is also deactivated.

Annotating images

You can annotate interesting or abnormal regions in the images with text.

Entering text

Annotate

✧ Click on the **Annotate** button to switch to text input mode.

✧ Click to the point in the image at which you want to insert text with the left mouse key.

✧ Enter the required text in the text field displayed and press the **Return** key on the keyboard.

✧ Repeat the two steps if you want to enter further comment texts.

Exiting text input mode

✧ Click on the **Annotate** button again if you want to exit text input mode again.

➩ If you select another evaluation or image processing function, the text input mode is also deactivated.

Moving text

✧ Click on the text with the left mouse key, but not on the grab handles.

✧ Drag the text to the new position.

Changing text

✧ Double-click on the text with the left mouse key to change it. The mouse cursor changes into a text cursor (rectangle) and is located on the first position of the text.

Deleting graphic elements and text

You can delete graphic elements and annotations that you have inserted in the tomo segment at any time.

Deleting graphic elements and text individually

✧ Click on the graphic or text that you want to delete with the left mouse key. The evaluation tools must be active at the time.

✧ Call up **2D Tools > Delete Graphics** in the main menu or press the **Del** key on the keyboard to delete the selected text/graphic element.

➪ If you want to delete more than one graphic element in the displayed image, hold the **Ctrl** key down while clicking on the required graphic objects one after the other with the mouse.

Removing all graphic elements and texts

✧ Select the image or the images to remove the graphic elements and text annotations.
→ Page C.11–3, *Selecting a topogram and images*

✧ Call up **2D Tools > Select All Graphics** in the main menu. In the selected images, all text and graphic elements have now been selected.

✧ Call up **2D Tools > Delete Graphics** in the main menu or press the **Del** key on the keyboard to delete all the selected texts and graphics.

Storing images with graphics

You will usually perform only a preliminary evaluation with the tools of the Examination card. The Viewer task card is intended for detailed evaluation of the examination results. However, if you want to continue to use individual images processed in advance, you can store them from the Examination card.

➪ The tomograms from each reconstruction are already automatically stored in the local database. Only when you want to store the images with graphic evaluation (e.g. ROIs), you have to do that manually.

Storing images

✧ Select the image that you want to store.

✧ Call up **2D Tools > Save Image**.

A copy of the original image is created and stored together with the graphic objects and evaluations.

Filming images

✧ Select the images that you want to film or print.

✧ Click on the **Copy to filmsheet** button

All selected objects are transferred to the **Film** task card.

CHAPTER C.12 Scan Management

For your examinations, you will use the routine scan protocols suggested by your system in most cases. These have been designed in such a way that you can perform scan series quickly and smoothly.

But even if you change the scan parameters and adapt a scan protocol to your special requirements, your system ensures a problem-free examination.

To achieve this, your system checks the following points at the beginning of each scan:

- ❑ Is the planned length of the spiral or sequence possible with the scan parameters set?
- ❑ Can the spiral be scanned during a breathhold?
- ❑ Can the X-ray tube cool off sufficiently in the scan pauses?
- ❑ Is there enough memory for the data of the following scan?

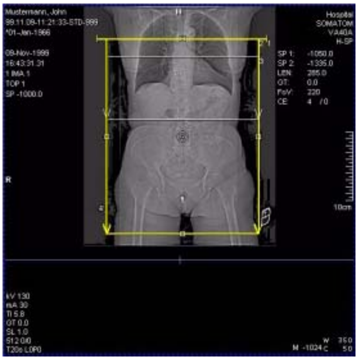
If a scan is not possible with the current settings, this is displayed immediately in the chronicle, on the subtask cards, and in the topo segment. Your system helps you find suitable scan settings and take the necessary measures to be able to continue the examination with the next scan.

Spiral too long

During preparation of the spiral examination, the X-ray tube monitor checks the expected temperature increase of the X-ray tube. If the spiral is too long for the effective mAs set, the system blocks loading of the scan parameters.

During scans with **API**, your system also checks whether the calculated scan time exceeds the set breathhold time of the patient. In this case, you must shorten the scan time or, if possible, increase the breathhold time.

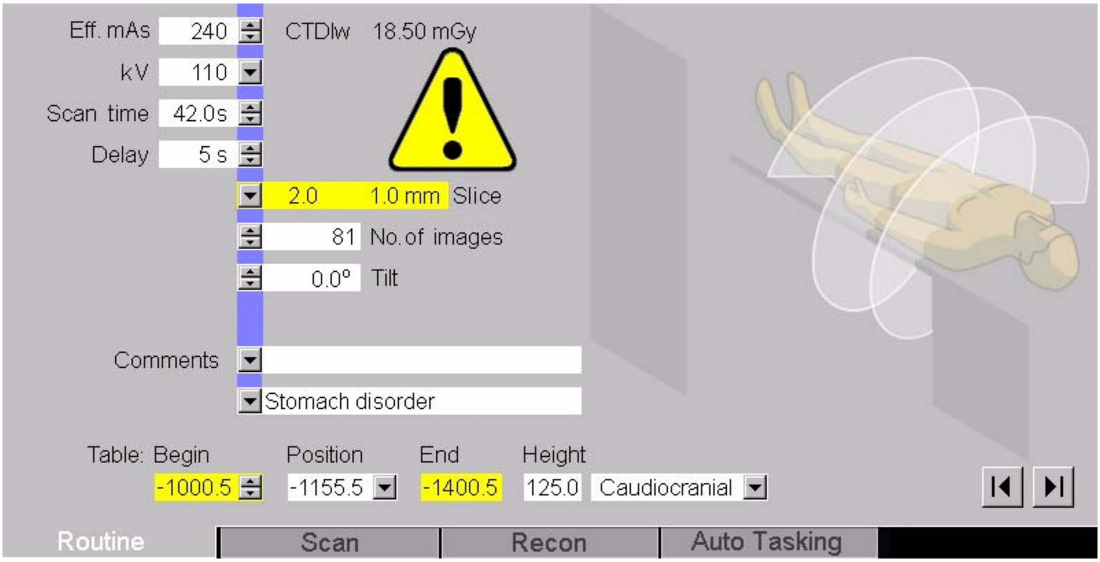
Display in the topo segment



In the topogram, you can see the range which is not possible with the current scan settings with a yellow border. The other, unblocked ranges and cutlines of your examination are still shown white.

Display on the subtask cards

On the **Routine** and **Scan** subtask cards, the input fields with impermissible parameter values have a yellow background and a warning triangle is displayed on the **Routine** card.



Eff. mAs 240

kV 110

Scan time 42.0s

Delay 5 s

CTDIw 18.50 mGy

2.0 1.0 mm Slice

81 No. of images

0.0° Tilt

Comments

Stomach disorder

Table: Begin -1000.5

Position -1155.5

End -1400.5

Height 125.0

Caudiocranial

Restoring readiness for scanning

You can restore readiness for scanning and start the spiral scan in one of the following ways:

- Call up the **Scan Assistant** dialog box. In it, you can make the most important parameter changes simply and quickly.
- You can change the scan settings on the **Routine** or **Scan** subtask card. To achieve that, have your system make suitable suggestions.
- Reduce the length of the range or split the range.

You can continue with your examination as soon as the warning triangle has disappeared from the **Routine** card.

The range in the topo segment and the input fields on the **Routine** and **Scan** cards are then displayed in the usual way.

Adapting scan parameters with the scan assistant

Some of the scan parameters of a spiral scan influence each other. If you change one parameter, this often has an effect on the permissible value range of other parameters.

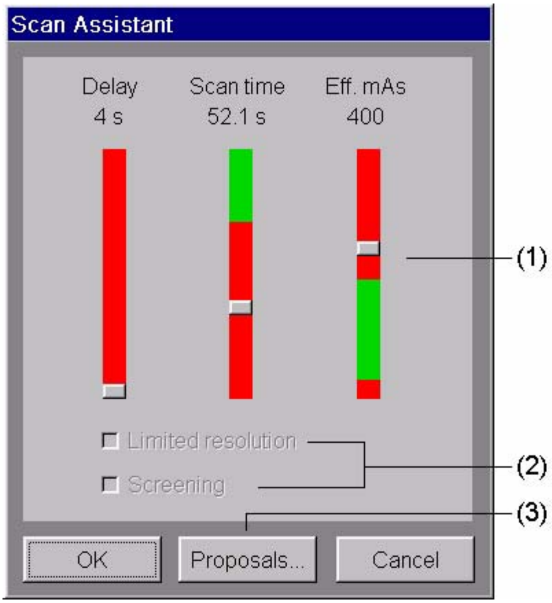
Your system takes these relations into account and provides the scan assistant to help you find a parameter combination suitable for your purposes in a simple way so that you can continue with your examination quickly.

Calling up the scan assistant

✧ Click on the warning triangle on the **Routine** subtask card to call up the scan assistant.

The **Scan Assistant** dialog box is displayed.

Scan Assistant dialog box



(1) Sliders for adapting the most important scan parameters

(2) **Limited resolution** and **Screening** check boxes
These options are set by your system (in preparation).

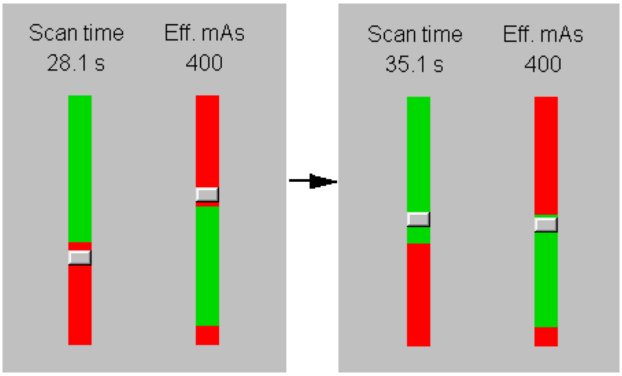
(3) **Proposals** button to display suggestions about setting parameters

Sliders in the Scan Assistant window

Using the sliders, you can set the delay, the scan time, and the effective mAs. By the position of the slider, you can see whether one or more parameter values are permissible (green range) or not permissible (red range).

As soon as you move a slider, the value ranges of the other parameters are updated.

If the effective mAs and scan time are in the red range, for example, it is enough to move the slider for the scan time into the green range. The slider for the effective mAs is then also in the green range.



Scan time 28.1 s
Eff. mAs 400

Scan time 35.1 s
Eff. mAs 400

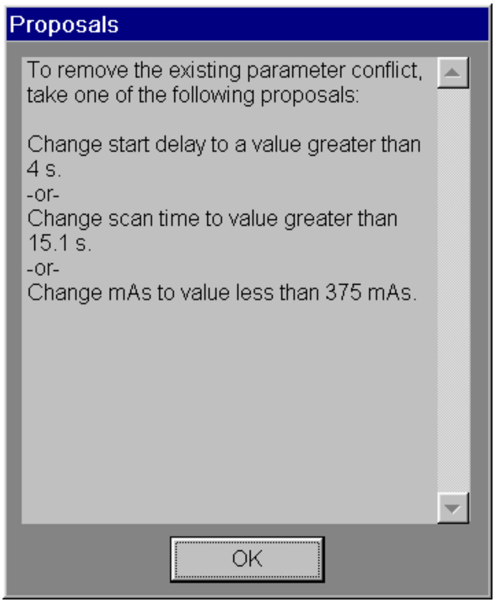
Displaying change suggestions

Proposals...

If you want to set parameters numerically, first have your system suggest suitable measures.

✧ Click on **Proposals** in the **Scan Assistant** dialog box to display the **Proposals** window.

➪ If you click on **OK** in the **Scan Assistant** window while a slider is still in the red range, the **Proposals** window is displayed automatically.



Proposals

To remove the existing parameter conflict, take one of the following proposals:

Change start delay to a value greater than 4 s.
-or-
Change scan time to value greater than 15.1 s.
-or-
Change mAs to value less than 375 mAs.

After closing the scan assistant, you can make the suggested parameter changes on the **Routine** or **Scan** card.

✧ Click on **OK**.
You return to the **Scan Assistant** window.

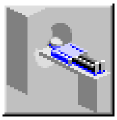
Cancel

✧ Click on **Cancel** to close the scan assistant without changing the scan settings.

Breathholding time too short

For long spiral scans with automatic patient instruction (**API**), the planned scan time can exceed the set breathholding time. A corresponding message is then output in the status bar.

However, very often, patients can hold their breath for a considerably longer time than that set. Given sufficient cooperation from the patient, you should therefore increase the breathholding time before changing other scan parameters.



✧ Click on **Exam** to display the **Patient Model Dialog** dialog box.
→ Page C.2–4, *Patient Model Dialog*

Breathhold 20 s

✧ Enter a longer breathholding time.

If the new breathholding time is also too short to scan the spiral, you must shorten the scan time, e.g. by splitting the range.
→ Page C.12–10, *Splitting the examination range*

Modifying the examination range

If you do not want to change the scan parameter settings you should shorten or split the range.

Reducing the length of the range


Table: Begin -85.5 End -355.5

✧ Set a smaller range by entering a new start and/or end position.

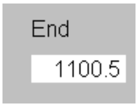
Or

✧ Shorten the range graphically in the topo segment.
→ Page C.3–26, *Modifying the ranges and cutlines*

Splitting the examination range

If you are not performing a contrast-medium examination, you can usually split long examination ranges without any problem. The X-ray tube can cool down sufficiently in the pauses between two sections.

✧ Copy the scan series concerned in succession in the chronicle.
→ Page C.2–31, *Repeating an examination step*


End 1100.5

✧ Shorten the range for the first of the two scan series.
The new end position is displayed on the **Routine** card.


Table: Begin -142.0

✧ Set the start position of the second scan series to the end position of the first scan.

Your system inserts a pause between the two examination steps in the chronicle in which the X-ray tube can cool down.

Sequence too long

Scanning a very long range with a high mAs setting causes a greater load on the X-ray tube. If the scan is not possible for that reason, the X-ray tube monitor blocks readiness for scanning. The message “Cooling impossible” is displayed in the chronicle.

Display in the topo segment and on the subtask cards

In the topogram, the range concerned is displayed yellow.
→ Page C.12–2, *Display in the topo segment*

On the **Routine** and **Scan** subtask cards, input fields with impermissible parameter values are displayed with a yellow background.

Delay 4 s

Parameter value permissible

mAs 240

Parameter value impermissible

Restoring readiness for scanning

On the **Routine** or **Scan** subtask cards or in the topogram, you must adapt the scan settings to restore readiness for scanning and to be able to start the sequence scan.
You have the following options:

❑ Reducing the mAs

❑ Selecting a larger slice width

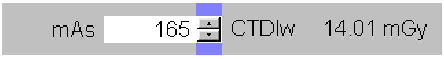
❑ Reducing or splitting the range

❑ Increasing the scan time for the range

As soon as the range in the topo segment and the input fields on the **Routine** and **Scan** cards are displayed with the normal white background again, you can begin with the examination.

Reducing the setting for mAs

You will usually reduce the mAs, because this has a great effect on the load on the X-ray tube. It is often enough to make small changes that scarcely impair the image quality. Reducing the mAs also reduces the patient dose.



mAs 165 CTDIw 14.01 mGy

✧ Set a smaller mAs value per image to reduce the load on the X-ray tube.

Increasing slice thickness

Depending on the region of the body and organ you are examining, you have a certain degree of freedom in selecting the slice width.

5.0 2.5 mm Slice width

✧ Select a larger slice width to cover the range with fewer scans.
This reduces the load on the X-ray tube, but also reduces the resolution along the longitudinal axis of the body.

Modifying the range

If you do not want to change the scan parameter settings you should shorten or split the range.

Reducing the number of scans

55 No. of scans

✧ Reduce the number of scans to shorten the range.

Or

Reducing the length of the range

Table: Begin -85.5 End -355.5

✧ Set a smaller range by entering a new start and/or end position.

Or

✧ Shorten the range graphically in the topo segment.
→ Page C.3–26, *Modifying the ranges and cutlines*

Splitting the range

If you are not performing a contrast-medium examination, you can usually split long examination ranges without any problem. The X-ray tube can cool down sufficiently in the pauses between two sections.
→ Page C.12–10, *Splitting the examination range*

Modifying time settings

Another way of reducing the load on the X-ray tube is to increase the scan time for the set examination range.

Increasing the scan time

Scan time 1.5 s

✧ Select a longer scan time per image. In this way, you can achieve the required mAs with a reduced X-ray tube power. However, the total scan time does increase.

Increasing the scan pauses

In the pauses between scans, the X-ray tube cools down. You can increase the scan pauses.

Cycle time 3.0 s

✧ Increase the cycle time on the **Scan** card, which also increases the scan pauses.

➩ If you are scanning with **API**, remember that if you increase the cycle time, fewer scans are performed per cluster.
→ Page C.6–2, *Automatic clustering*

X-ray tube cooling delays required

If you plan to perform many scans at short intervals, X-ray tube cooling delays might be necessary although the scan parameters of each individual scan series do not exceed the limit values.

Display in the topo segment and on the subtask cards

The ranges concerned are drawn yellow in the topo segment. Some scan parameters have a yellow background on the **Routine** and **Scan** cards.
→ Page C.12–2, *Display in the topo segment*
→ Page C.12–3, *Display on the subtask cards*

Scan Controller dialog box

When you load the scan parameters into the measuring system, the **Scan Controller** dialog box is displayed.

✧ Click on **Load** if you want to start the first measurements with the current settings.

Or

✧ Click on **Cancel** to change the measurement settings.

Restoring readiness for scanning

You can continue your examination in one of the following ways:

- ❏ Start scanning the first range(s). Then wait until the X-ray tube has cooled down sufficiently and continue scanning of the following ranges as planned.
- ❏ Increase the delay times for the planned scan series and then start the examination.
- ❏ Change the scan parameters to reduce the load on the X-ray tube in order to be able to begin the scan series without additional delay times.
  → Page C.12–2, *Spiral too long*
  → Page C.12–11, *Sequence too long*

Waiting for a cooling delay to elapse

You will usually allow a cooling delay to elapse before continuing with your examination rather than change scan parameters. This also reduces the additional delays of the following scans and minimizes the deviations from the planned examination schedule.

Your system continuously checks the current temperature of the X-ray tube, calculates the required delay for the ensuing scan series, and updates the display in the topo segment and on the subtask cards.

✧ Click on the **Load** button to confirm the set scan parameters.

✧ Press **Start** on the control box to start scanning of the first range.

✧ After scanning of the first range has been completed, wait until the cooling delay has elapsed, if necessary.

✧ Click on the **Load** button to confirm the scan parameters for the next range and start scanning again.

Accepting longer delay times

If the examination is not bound to a fixed schedule, you can set longer delays for the current and following scan series. Further scans are then possible without new cooling delays.

✧ Set longer delay times for the following scans on the **Routine** or **Scan** card or in the scan assistant.
→ Page C.12–5, *Adapting scan parameters with the scan assistant*

Load

✧ Confirm the new delay times with **Load**.

The system is now ready for scanning and the **Press START** prompt is displayed in the chronicle.

☢

✧ Press **Start** on the control box to start the following scan.

Memory insufficient

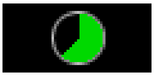
During the course of an examination, large quantities of data are collected and stored in the raw data memory. Images are reconstructed from the raw data that are stored in the local database.

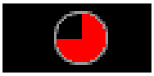
Your system monitors the memory capacity of the local database and the raw data memory. Your system informs you before a scan if you have to make space.

Storage of image data not possible

By the storage symbol on the status bar, you can see how much space has already been taken up in the local database. If the filled capacity rises above 75%, the icon changes color from green to red.

Storage capacity





✧ Archive the patient and examination data in time and delete them in the **Patient Browser** to ensure that sufficient capacity is always available.
→ Page D.6–2, *Archiving data*

Image data memory full

If the available space in the local database is no longer sufficient to store all the images of the following scan, the start trigger is blocked.

A popup window with the message
“Disk capacity exceeded. Images must be deleted” is displayed.

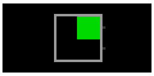
✧ Delete patient and examination data that you no longer require or that has been archived in the **Patient Browser** to make space.
→ Page D.5–16, *Deleting data*

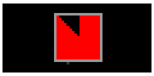
➭ If enough space is available for the following scan series but not for the entire examination, you are informed about this on the status bar. The start trigger is released in this case.

Storage of raw data not possible

You can see by the storing icon (square) on the status bar how much space has already been taken up in the raw data memory. If the load of the raw data memory rises above 75%, the color of the icon changes form green to red.

Memory allocation raw data





Raw data memory full

If too little raw data memory is available for the following scan, the start trigger is blocked.

A popup window with the message
“Disk capacity exceeded. Raw data must be reconstructed” is displayed.

✧ Delete raw data that is no longer required in the **Patient Browser** to make space.
→ Page D.5–16, *Deleting data*

➪ If there is enough memory for the following scan but not for the entire examination, you are informed about that on the status bar. The start trigger is not blocked.

NOTE

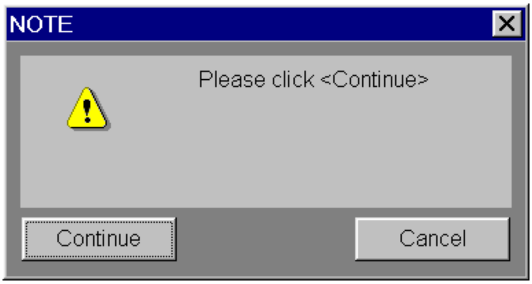
Always perform missing reconstructions quickly to avoid old raw data taking up memory capacity unnecessarily.

Restoring system readiness

It is necessary to restore system readiness if a scan was interrupted by a fault that cannot be automatically remedied by your system or because you pressed the **STOP** key.

Restoring system readiness after a prompt

The **NOTE** dialog box is always displayed if you have interrupted the scan with the **STOP** key or if the automatic attempt to restore the system to readiness for operation after a fault has failed three times.



Please click <Continue>

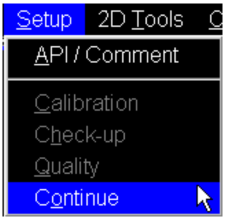
✧ Click on **Continue** to restore the readiness of your scan system.

Or

✧ Click on **Cancel** to interrupt the process.
The **NOTE** dialog box is displayed again as soon as you attempt to load scan parameters into your scan system.

Restoring system readiness manually

If you find a fault but your system does not display the **NOTE** dialog box, you can restore system readiness through the main menu, too.



✧ Call up **Setup > Continue** in the main menu to make your system ready for operation again.

If this does not remedy the fault:

✧ Switch your system off and on again or contact Siemens Service.

CHAPTER
C.13

Configuring Examinations

During installation of your CT scanner, Siemens Service has already set up the system so that you can start examinations immediately.

In the **Examination** task card, you can change or add to the preconfigured settings in order to adapt your system to your method of working or requirements.

You can make the following configuration settings:

☐ Set up API and comment texts and the intercom system

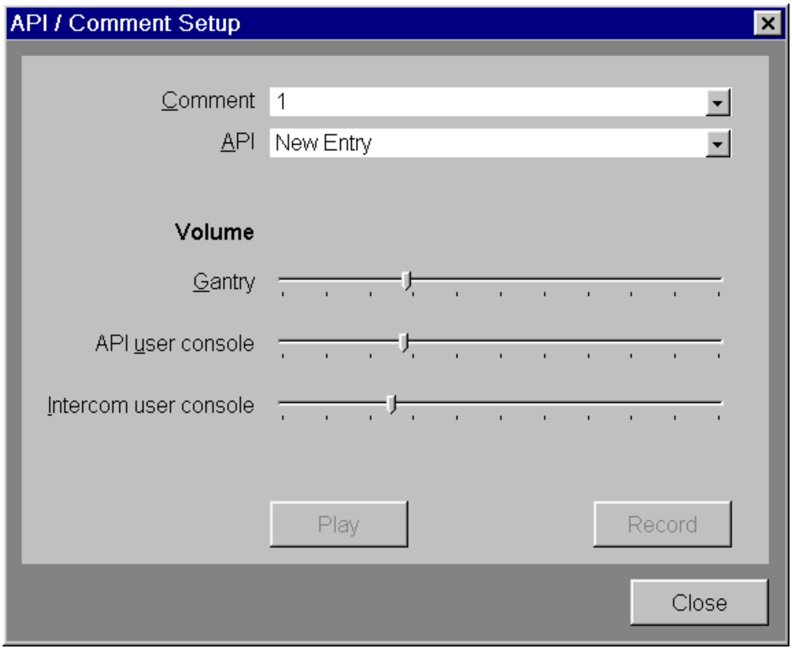
☐ Create and store individual scan protocols

☐ Design a general working procedure for your examination

API and comment texts

With the **API / Comment Setup** dialog box, you can manage the standard comment texts, record announcement texts for the automatic patient instruction function (in preparation) and set up your intercom system.

✧ Call up **Setup > API/Comment** to open the **API / Comment Setup** dialog box.



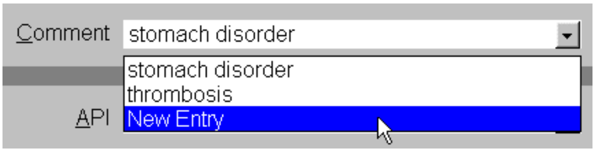
Comment 1

API New Entry

Creating standard comment texts

The images of a CT examination can contain up to two comment lines. Before a scan, define which texts you want to display. You can fill in these comment lines on the **Routine** or **Contrast** subtask cards, or simply select a suitable comment from the list. Here you will learn how to create or change the list of most frequently needed comment entries.

Creating a comment text

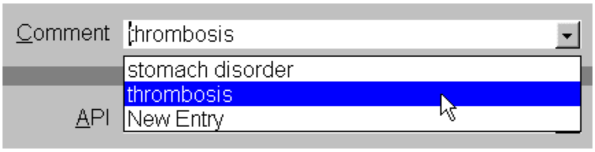


- ✧ Select either an old entry to overwrite from the **Comment** selection list or select **New Entry** to add a new standard comment text.
- ✧ Enter the new comment text.
- ✧ Press the **Return** key of your keyboard.

The standard comment is placed in the **Comment** selection list of the **Routine** and **Contrast** subtask cards.

Deleting a comment text

The **Comment** selection list can contain up to 24 standard comment texts. You should delete entries that you no longer require to keep the comment selection lists on the **Routine** and **Contrast** subtask cards clear.



✧ Select the standard comment text that you want to delete from the selection lists.

✧ Delete the entry in the **Comment** entry field using the **Del** key on your keyboard.

✧ Press the **Return** key to confirm deletion.

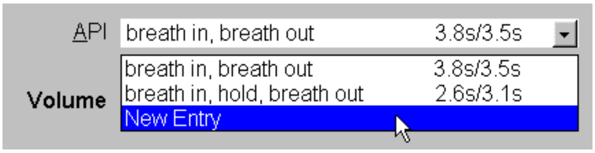
The comment now no longer appears in the **Comment** selection lists on the **Routine** or **Contrast** subtask cards.

Recording and processing API texts

For many scans, breathing commands are required. Have the instructions played back in a coordinated manner during the examination using the automatic patient instruction system (**API**).
→ Page C.2–14, *Automatic patient instruction*

To do that, record the required **API** texts once, which you can then use any number of times for your examinations.

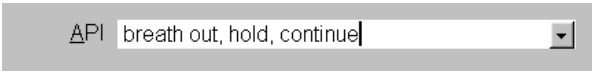
Recording API


API breath in, breath out 3.8s/3.5s

✧ Select the entry “New Entry” at the end of the **API** selection list, if you want to record a new instruction.

Or

✧ Select an instruction from the **API** selection list that you want to record over.


API breath out, hold, continue

✧ Overwrite the previous entry (or **New Entry**) with an unambiguous short designation and confirm with the **Return** key.

The **API** will from now on be managed and can be called up under the name you entered.

➪ If you only want to rerecord an instruction, leave the name unchanged. Press the **Return** key immediately.

✧ Click on the **Record** button to have the system ready for recording.

✧ Press the **Call Patient** key on the control box and hold the key pressed while you speak **Text A** into the integrated microphone.
→ SOMATOM Operator Manual, page B.4–8, *The control box*

✧ Press **Call Patient** a second time and speak **Text B** into the microphone.

➪ If you want to add pauses, then hold the **Call Patient** key pressed down for a little while after the announcement. In this way, you can give the patient more time to follow instruction A before scanning begins. Your recording (texts A + B) cannot be longer than 25 seconds.

Playing back an API

After recording, you should play the announcements back once to check that they are understandable.

✧ Select the patient instruction that you want to listen to from the **API** selection list.

✧ Click on the **Play** button to play back the announcements.

Like during an examination, the announcements are played back both on the loudspeaker on the console and on the loudspeaker on the gantry.

✧ Press the **Hear Patient** key on the control box to hear how the announcements can be understood via the loudspeakers on the gantry.

Deleting the API

Your system manages up to 50 different pairs of **API** texts. To keep the **API** list clear, you should delete old announcements that you no longer require.

✧ Select the instruction that you want to delete from the **API** selection list.

✧ Delete the entry in the API entry field (**Del** key) and press the **Return** key of your keyboard to delete the instruction from the API list.

➪ If you have accidentally deleted the entry, press the **Esc** key instead of the **Return** key. The old instruction is then retained.

Setting the intercom system

Your intercom system works with constant loudspeaker settings that you usually have to adapt to the local conditions only once. You can readjust these settings at any time as long as no scan is in progress.

Changing the volume

✧ Move the **Gantry** slider to the right to increase the volume of your announcements in the examination room, or to the left to reduce the volume.

✧ Move the **API user console** slider to the right to increase the volume of the **API** announcements on the console or to the left to make them quieter.

➪ You cannot set the volume on the console to be greater than on the gantry in the examination room.

✧ Move the **Intercom user console** slider to the right to increase the volume for the patient when **Hear Pat** is switched on.
By sliding the slider to the left, you can reduce the volume.

Closing API / Comment Setup

As soon as you have created an **API** announcement or a comment text, they are stored immediately. However, the settings for the intercom system with the slide switches are initially only temporary.

If you exit the **API / Comment Setup** dialog box, you can accept the changed volume and noise suppression of your intercom system or reset the settings to the original status.

Close

✧ Click on the **Close** button if you want to close the **API / Comment Setup** dialog box with the current slider positions for the intercom system.

Or

☒

✧ Close the window with the close-window button (top right on the title bar of the window) if you want to reset the changed volume and noise suppression.

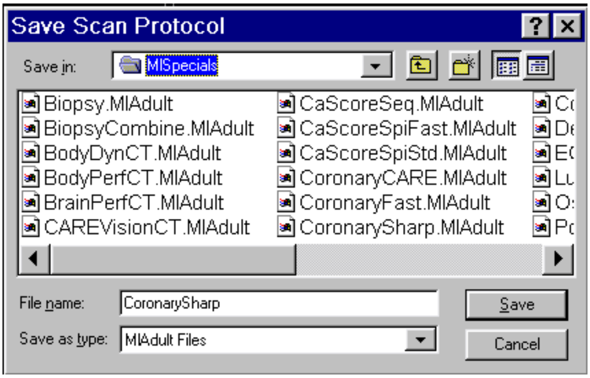
Individual scan protocols

Your system contains a series of routine scan protocols that prescribe individual examination steps and the sequence in which they are performed. You can, however, adapt the scan procedure to your own requirements.

Store the scan protocols you have modified so that you can use them again in future examinations.

✧ Change an existing scan protocol to suit your requirements.
→ Page C.2–23, *Adapting routine scan protocols*

✧ Select **Edit > Save Scan Protocol** in the main menu to call up the dialog box **Save Scan Protocol**.



Save in: MISpecials

File name: CoronarySharp

Save as type: MIAdult Files

- In the selection list **Save as type**, select the directory for the region in question.
- Enter a name for the scan protocol under **File name** or select an existing scan protocol which you can overwrite.

- Then click on **OK**.

The modified scan protocol is then stored in the **Exam** selection list of the **Patient Model Dialog** and the **Patient Registration** window.

> **NOTE**
>
> When storing altered protocols, do not mix head and body scan protocols. For example, do not store a head mode in MIAbdomen.

Procedure for examinations

You can adapt and expand preconfigured settings to adapt the examination procedure to your working methods.

You can make the following configurations:

❑ Activate/deactivate automatic functions during examination

❑ Patient-related default settings

❑ Settings for the topo segment

✧ Call up the **Configuration Panel**
(**Options > Configuration** in the main menu).

Examination

✧ Select the configuration window of the **Examination** task card.

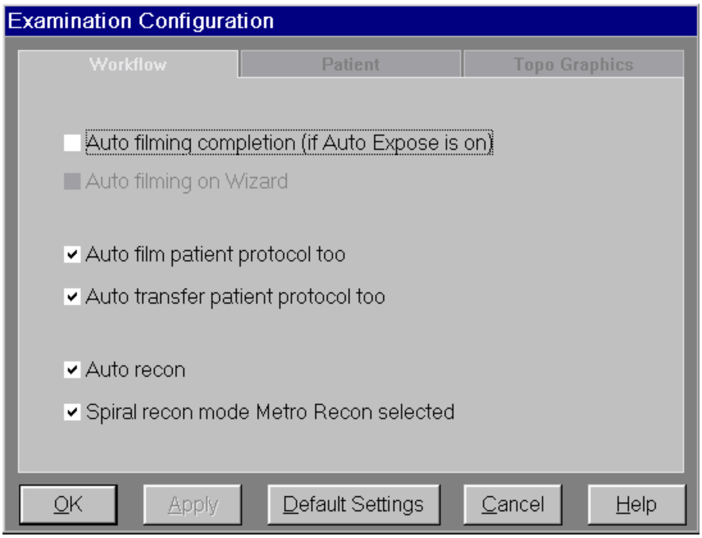
The window **Examination Configuration** with the subtask cards **Workflow**, **Patient**, and **Topo Graphics** is displayed.

In the Basics part of this manual you can read how to call up and exit configuration windows, save changes, or reset settings back to the as-delivered state.
→ Chapter A.2, *Configuring the User Interface*

Automatic functions

On the **Workflow** subtask card you will make the settings for automatic filming and reconstruction and for automatic data transfer.

✧ Click the **Workflow** subtask card into the foreground.



☐ Auto filming completion (if Auto Expose is on)

☐ Auto filming on Wizard

☑ Auto film patient protocol too

☑ Auto transfer patient protocol too

☑ Auto recon

☑ Spiral recon mode Metro Recon selected

Closing a film task

☑ Auto filming completion (if Auto Expose is on)

✧ Check the **Auto filming completion** checkbox if you want to close the film jobs once you have transferred them to the **Filming** task card.

➪ With End Exam the last filmsheet is printed automatically, even if it is not filled completely.

Auto filming on Wizard

With **Auto filming on Wizard** you transfer the images to be filmed automatically to the Wizard.

☑ Auto filming on Wizard

✧ To do that, check the checkbox **Auto filming on Wizard**.

➪ This field is dimmed on devices with only one console.

Filming the patient protocol

You can automatically film the patient protocol together with the examination images.

☑ Auto film patient protocol too

✧ To do that, check the checkbox **Auto film protocol too**.

As soon as you have activated **Auto filming** for at least one Recon task, the patient protocol is also filmed.

Transferring the patient protocol

To transfer the patient protocol to other output media, activate **Auto transfer patient protocol too**.

☑ Auto transfer patient protocol too

✧ To do that, check this checkbox.

The patient protocol is transferred for automatic data transfer together with the examination images to the addresses that you have selected on the **Recon** subtask card.

Reconstruction

If all Recon tasks are to be executed straight after spiral and sequence acquisition, use **Auto recon**.

☑ Auto recon

✧ To do that, check this checkbox.

The raw data are automatically reconstructed according to the parameters defined in the Recon tasks as soon as scanning is complete.

Metro Recon

You can reconstruct spiral acquisitions in parallel with the examination either in real-time (RTD) / Last Image Display or with a delay with full image quality (Metro Recon).

☑ Spiral recon mode Metro Recon selected

✧ Check the checkbox **Spiral recon mode Metro Recon selected** to set Metro Recon as the default reconstruction mode.

Or

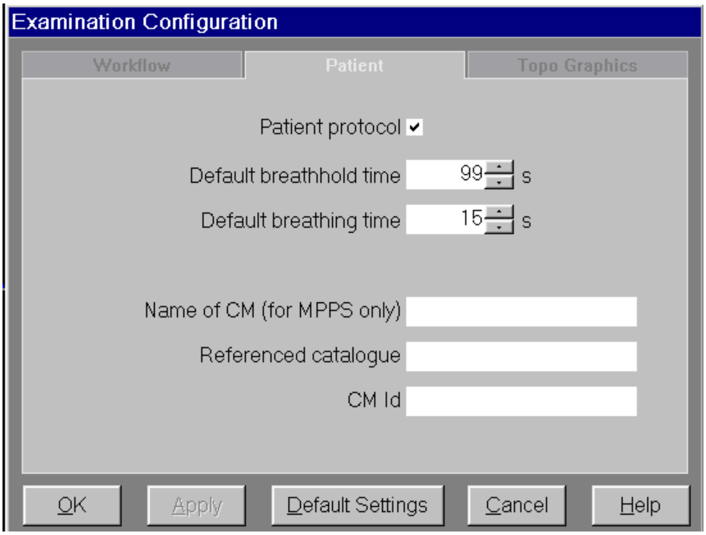
✧ Uncheck the checkbox.
Last Image Display or RTD mode is set as default during the spiral scan.

Patient-related default settings

On the **Patient** subtask card you activate the creation of the patient protocol and define the default settings for breathing time and contrast medium administration.

✧ Click the **Patient** subtask card into the foreground.

.



Patient protocol ☑

Default breathhold time 99 s

Default breathing time 15 s

Name of CM (for MPPS only)

Referenced catalogue

CM Id

Patient protocol

Patient protocol ☑

✧ Check the checkbox **Patient protocol** if you want a patient protocol to be created for your examinations.

Breathing time and breathhold time

When you call up the **Patient Model Dialog** window it already contains default values for the breathhold and breathing time. You can change these default settings.

Default breathhold time 99 s

✧ Enter your own default setting for the breathhold time.

Default breathing time 15 s

✧ Enter you own default setting for the breathing time.

➪ For sequence acquisitions with **API**, the breathhold time and breathing time is taken into account for the compilation of scan clusters and calculation of scan pauses.

Contrast medium specifications

If you always use the same contrast medium, enter details of it in the lower area of the **Patient** card. These data are used for the performance documentation (MPPS).
→ Page D.5–8, *Performance documentation*

✧ Enter the name of the contrast medium in input field **Name of CM**.

Catalog name

✧ Enter the catalog name of the contrast medium in input field **Referenced catalogue**.

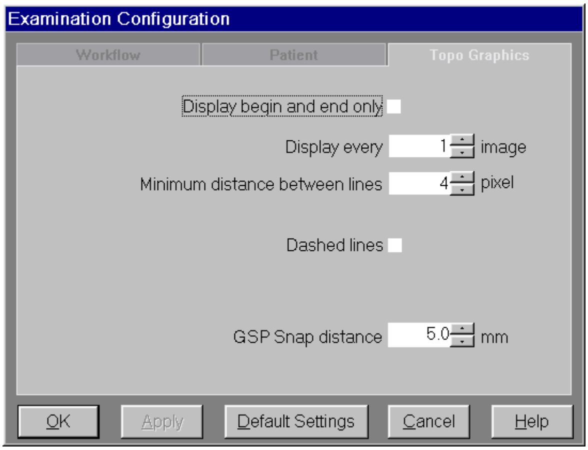
Identification

✧ Enter the ID of the contrast medium in input field **CM Id**.

Topo segment

On the **Topo Graphics** subtask card, you define the snap distance for the graphic slice positioning and the cut line and range display (Topo Graphics) in the topogram.

✧ Click the subtask card **Topo Graphics** into the foreground.



Display begin and end only ☐

Display every 1 image

Minimum distance between lines 4 pixel

Dashed lines ☐

GSP Snap distance 5.0 mm

Topo Graphics display


Display begin and end only ☑

✧ Check the checkbox **Display begin and end only** if only the beginning and the end of an examination range is to be displayed.

Or


Display every 1 image

✧ Specify whether every (display every 1 image) or every n-th image is to be displayed as a cut line.


Minimum distance between lines 4 pixel

✧ Also enter the minimum distance between two cut lines to be displayed in Topo Graphics.


Dashed lines ☑

✧ Check the checkbox **Dashed lines** to display the cutlines in the topogram as dashed lines.

Snap distance

A capture range mechanism supports you with the graphic positioning of examination ranges and cut lines in the topogram.

Whenever you move a line or a range into the vicinity of another, the start line that you have moved jumps to the start or end of the adjacent range.

You can configure the capture range to make it easier to plan the optimum starting position.

GSP Snap distance 5.0 mm

✧ Increase of decrease the snap distance in input field **GSP Snap distance**.

PART
D

Patient Browser

D.1 Introduction

D.2 Searching for and Displaying Patient Data

D.3 Transferring Data to other Applications

D.4 *Correcting Data*

D.5 *Maintaining your Data*

D.6 *Archiving, passing on, or filming data*

D.7 *Configuring the Patient Browser*

CHAPTER

D.1 Introduction

The **Patient Browser** supports you with administration of the patient and examination data that are stored in the databases of your system.

With the **Patient Browser** you can search for data in a fast and uncomplicated way and then process that data in the browser or in the task cards.

When to use the Patient Browser

- ❏ To examine a patient that has already been examined once before with your system
- ❏ To view the images of a patient from earlier examinations in order to compare them with current results
- ❏ To comment or postprocess images after an examination
- ❏ To correct incorrect information for a patient stored in your system
- ❏ To archive patient and examination data or to send them to another location in your hospital via the network
- ❏ To expose images of a patient onto film for reporting or documentation purposes

Databases and drives

In the **Patient Browser** you access patient and examination data that is stored in the various databases of your systemor on external data media such as CDs or MODs.

Scheduler

The scheduler contains the data of all preregistered patients. This database gives you an overview of all patients who have been preregistered for examination. Here you can search for a patient to register him or her for an examination.

The scheduler can be updated with data from an HIS/RIS system either automatically or manually if the system is connected to one

Local database

The local database is the area of your system in which the patient data and results of current examinations are stored.

➪ If the data volume in the local database increases, the access times become longer and examinations are slowed down. Therefore you should regularly move data from your local database to archive media.

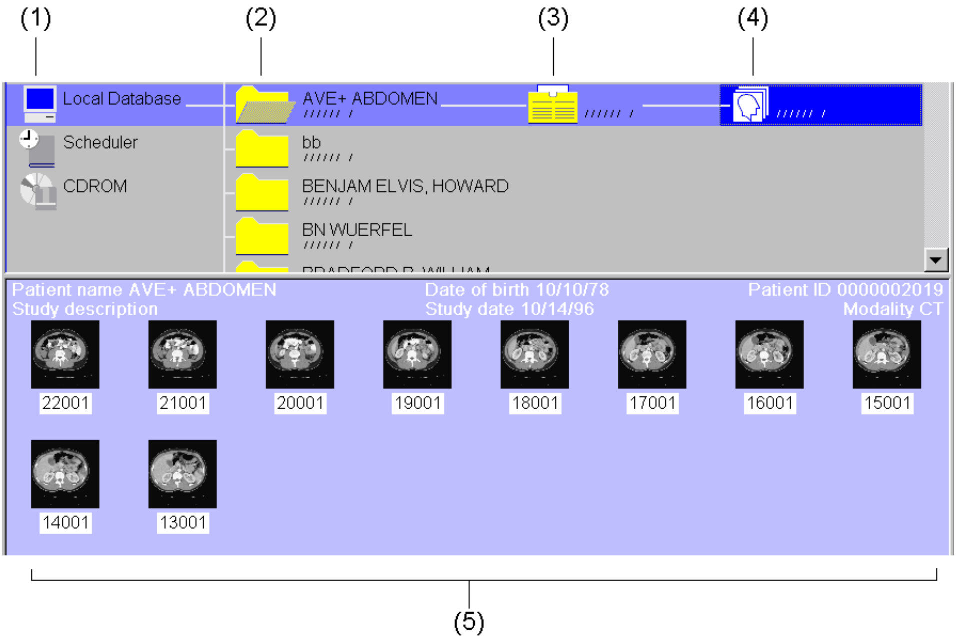
Connected drives

One or more MOD drives and, possibly, CD drives are connected to your system. The icons with the drive names provide a quick way of accessing these archiving media. As soon as an examination has been completed and evaluated you should archive the examination data and then delete it from the local database.

Data levels

In the databases and on the external data media, the patient and examination data are structured hierarchically. This structure helps you find examination results quickly.

➪ The display of the data levels depends on the configuration.



Patient name AVE+ ABDOMEN
Date of birth 10/10/78
Patient ID 0000002019
Study description
Study date 10/14/96
Modality CT

(1) Database
(2) Patient
(3) Study
(4) Series
(5) Instances

➪ Depending on the database, the work status of each database entry is displayed as an abbreviation. You will find information about the processing status on
→ Page D.5–2, *Defining the work status*

Patient

The examination data of different patients are stored by the names of the patients in your database.

Study / Procedure

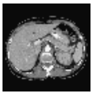
A study is an examination which is conducted to find answers to a particular question, usually as a result of a referral. A study consists of one or more series. In the **Scheduler**, the planned **Procedure** is stored at this level.

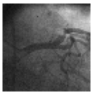
Series / Procedure Step

All the images of a measurement or of an image-processing operation are designated to a series. In the **Scheduler**, the **Procedure Steps** for the examination are listed at this level.

➩ **Procedure Steps** are not displayed for patients preregistered locally (i.e. at this workstation).

Instances / Action Item





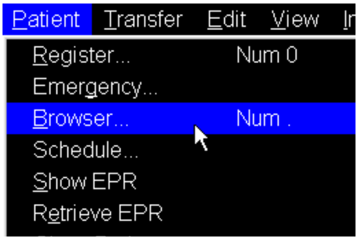
On the lowest data level, the **Instance Level**, the individual images (left hand fig.) are stored and, depending on the modality, the data sets from which images can be generated (e.g. raw data, center fig.) and waveforms, 3D objects and multiframe images (right hand fig.), too. All entries on the **Instance Level** are generally referred to as images.
In the **Scheduler**, you will find the individual **Action Items** for the **Procedure Step** in question at this point.

➩ **Action Items** are not displayed for patients preregistered locally (i.e. at this workstation).

Calling up the Patient Browser

You can call up the **Patient Browser** window either from the main menu or by using the symbol keypad.

Main menu



✧ Call up the **Patient Browser** in the main menu by selecting the entry **Patient > Browser....**

Or

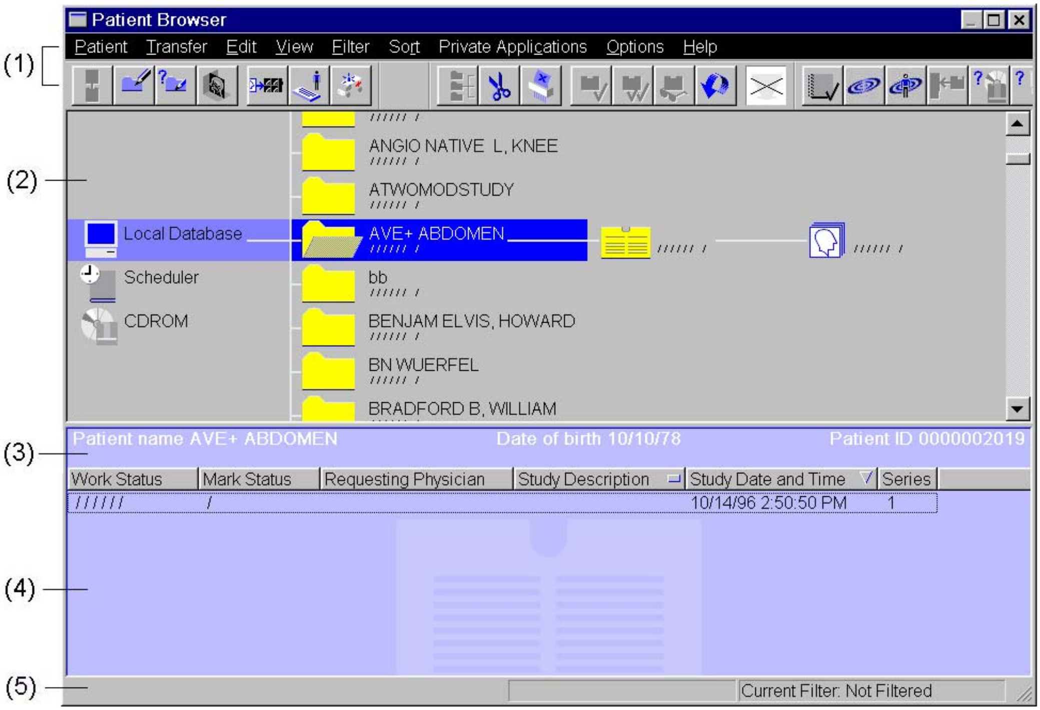
Symbol keypad

✧ Press the **Browser** key on the symbol keypad (Num **.**).

The Patient Browser window

When you call up the **Patient Browser**, the **Patient Browser** window is displayed and placed in the foreground.

The window is subdivided into various processing areas and therefore provides you with access to your data in a clearly laid out manner.



Patient name AVE+ ABDOMEN Date of birth 10/10/78 Patient ID 0000002019

Work Status	Mark Status	Requesting Physician	Study Description	Study Date and Time	Series
//////	/			10/14/96 2:50:50 PM	1

Current Filter: Not Filtered

(1) Menu and tool bar
(2) Navigation area
(3) Information area
(4) Content area
(5) Status bar

Tool bar

You can work on the data you have selected using the menus or the icon buttons on the tool bar.

➩ In **Browser Configuration** you can define which buttons the tool bar contains.
→ Page D.7–2, *General settings*

➩ You can hide the toolbar by deselecting **View > Toolbar**.

Navigation area

The lower data levels for the selected databases, patients, examinations, and series are displayed graphically in the navigation area.

Using the mouse you can select patient, study, series or image data in order to edit it or to transfer it to other applications. Every selection you make in the navigation area is automatically shown in the content area.

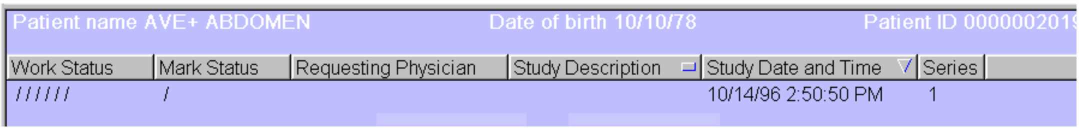
Information area

In the information area you can see brief information about the patient and study selected. When the navigation area is hidden, you can also see which database is open and which data level is displayed.
→ Page D.1–13, *Showing and hiding window sections*

Content area

In the content area you will see a list of the studies or procedures for the patient selected in the navigation area. If you select the lower data levels, you can see which series or procedure steps are stored for a study and which images or action items are stored for a series or procedure step.

⇨ In **Browser Configuration** you can define which information is to be displayed for each entry.
→ Page D.7–2, *General settings*



Patient name AVE+ ABDOMEN Date of birth 10/10/78 Patient ID 000000201

Work Status	Mark Status	Requesting Physician	Study Description	Study Date and Time	Series
//////	/			10/14/96 2:50:50 PM	1

In the content area you can also select patient and examination data for further processing.

⇨ You can toggle between a list display or image stamp display.
→ Page D.1–14, *Display of lists and image stamps in the content area*

Customizing the Patient Browser window

You can alter the display of the **Patient Browser** window and in this way optimize it for your way of working. For example, you can have a certain area enlarged in order to view as much data as possible at one time.

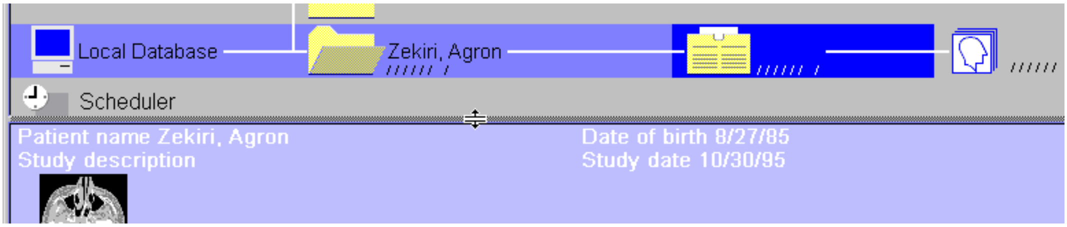
Changing the window size

You can enlarge, reduce, and pan the **Patient Browser** window on your screen as you require.
→ Page A.1–20, *Resizing and moving a window*

Enlarging and reducing the navigation and content areas

You can change the height of the navigation and content areas with respect to one another using the mouse. The larger you make the navigation area the smaller the content area will become and vice versa.

- Move the mouse cursor to the border of the navigation area. The cursor changes shape to a small vertical double arrow.



Patient name Zekiri, Agron
Study description
Date of birth 8/27/85
Study date 10/30/95

- Drag the line down to enlarge the navigation area and reduce the content area.

Or

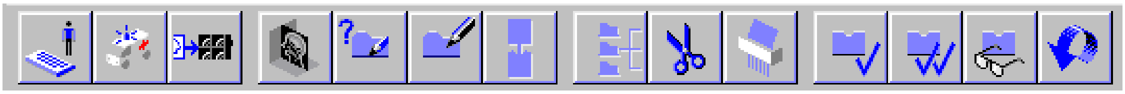
- Drag the line up to reduce the navigation area and enlarge the content area.

➩ In the image stamp display, the content area can only be enlarged or reduced in steps so that image stamps are not cut off.
→ Page D.1–14, *Display of lists and image stamps in the content area*

Moving the tool bar

If you have the tool bar displayed, it usually appears directly below the menu bar of the **Patient Browser**.

You can also place the tool bar on the lower border or at the side of the **Patient Browser** window.

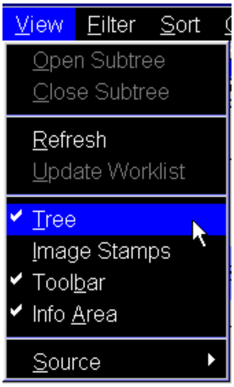


✧ Click on the tool bar but not on any of the buttons with the mouse.

✧ Drag the tool bar to the border of the window where you want to place it and release the mouse key.

➪ Experience has shown that directly below the menu bar is the best position. It is easily accessed and is not in the way of any processing activities.

Showing and hiding window sections



You can have the tool bar, navigation area, and information area either displayed or not, in order to create more room in the **Patient Browser** window.

✧ Click on **View > Toolbar** to hide or show the tool bar.

✧ Click on **View > Info Area** to hide or show the information area.

✧ Click on **View > Tree** to hide or show the data structure in the navigation area.

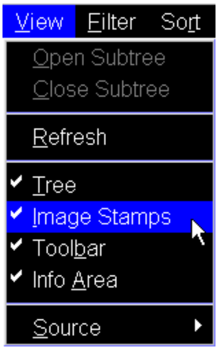
If the data structure is not displayed, the data level set in the configuration is displayed in the content area. In the navigation area, you can see which database these entries belong to.
→ Page D.7–15, *Single view of the content area*

➩ When switching to tree/single view, the previous selection will not be retained.

➩ In order to switch between the databases in the navigation area you must first display the tree structure.

Display of lists and image stamps in the content area

If you have selected a study or series in the navigation area, all the associated series and images are displayed in the content area. With the **View** menu you can toggle between a list or image stamp display.



✧ Click on **View > Image Stamps** to have series and images displayed as image stamps (menu entry has a checkmark) or as a list in the content area (no checkmark next to menu entry).

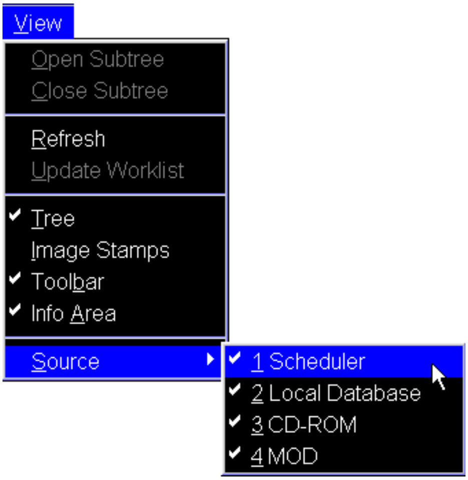
➩ In **Browser Configuration** you can define what information the list entries and the image stamps contain.
→ Page D.7–6, *Hierarchical view in the navigation and content area*

Showing and hiding databases and drives

You can have individual databases and drives either displayed or not in the navigation area depending on whether you need them for your work.

✧ Call up **View > Source** to open a submenu.

✧ Select the databases and drives that you want to have displayed as an icon in the navigation area.



⇨ The names of the submenu entries depend on the service configuration of your system.

Customizing the table in the content area

The list display of patient and examination data in the content area consists of a table. You can alter the preset column widths for each column.

✧ Click on the header of the table in the content area with the mouse cursor.

✧ Drag the right column boundary to the right to enlarge the column.

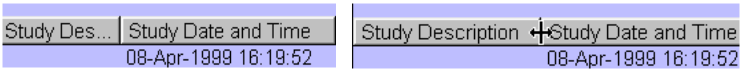


Image stamps

Series, or images of a patient are represented in the **Patient Browser** by a small image referred to as an image stamp.

If you click on an image stamp with the mouse the object will be selected.

Double-click or **drag & drop** loads the data into the task card that is at the top of the stack of cards, e.g. the **Viewing** card.

CHAPTER
D.2

Searching for and Displaying Patient Data

In the **Patient Browser** window you can view all the patient and examination data stored in the databases of your system and on external archiving media.

You can search for patient data to examine a patient again or to review, film, or archive his or her images.

You can search for patient data in the **Patient Browser** by navigating through the data levels of the window by mouse click or using the keyboard.

You can speed up your search by sorting the data displayed, e.g. alphabetically by the last name of the patient, or by filtering the data displayed and only viewing a certain subset.

Displaying information levels

When searching for patient and examination data you move through the navigation area with the mouse or you select **Open Subtree** in the **View** menu to open lower data levels.

Displaying a data tree

✧ Click on the icon of a patient entry in the navigation area of the **Patient Browser** window to view that patient's data levels.

Only the first subobject is displayed down to its lowest level.

In the content area you can see a list of all studies that are available for that patient.

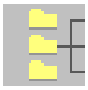
✧ Click on another patient to hide the first patient's data tree and view the information levels of the other patient instead.

Opening a data tree

✧ Select an entry in the navigation area.

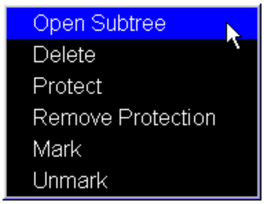
✧ Select the menu entry **View > Open Subtree** to view all the entries of lower data levels (open up the data tree completely).

Or



✧ Click on this button on the tool bar.

Or



✧ Call up the popup menu with the right mouse key and click on **Open Subtree**.

➪ The function **Open Subtree** is especially useful if you have selected several patients simultaneously.

➪ If you select the icon for a database or drive the **Open Subtree** menu item and the button remain dimmed. At this level you cannot open the data tree.

Closing a subtree

✧ Call up **View > Close Subtree** in the main menu or **Close Subtree** in the popup menu to close the lower information levels again.

Updating the scheduler

If your system is connected to an HIS/RIS system, the scheduler is automatically updated at regular intervals with information from the registration depending on the service configuration. You can also start this updating operation manually. In this way you can ensure that you are always working with the latest data.

✧ Select **View > Update Worklist** to update the scheduler.

Or

✧ Double-click on the icon for the scheduler to update it and then open it.

➪ Depending on the configuration, the **Worklist Time Range** window is displayed in which you can limit the time frame for your query.
→ Page B.4–3, *Defining the worklist time range*

In the **Patient Browser**, all patients who are preregistered for examination on your system are now displayed.

Updating the display of the databases

Changes and additions to database entries that you make on your workstation or are made via the network are automatically displayed in the **Patient Browser** window. You can initiate this updating manually, too, if the automatic process is delayed.

✧ Call up **View > Refresh** to update the display of the navigation and content areas.

Or

✧ Click on this button.

NOTE

If you are working on a satellite console, you must update the database with the **Refresh** key.

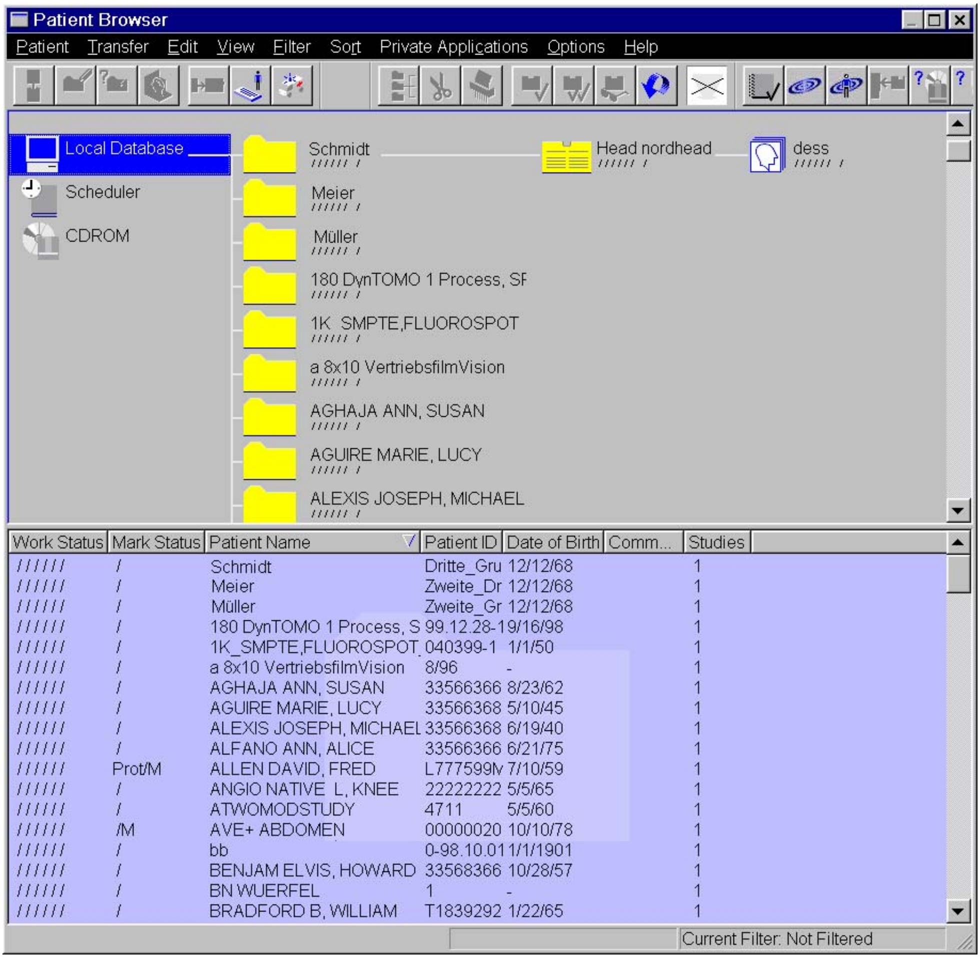
Scrolling through and selecting patient data

You can search for a patient’s examination data in the databases in order to process it further.

After you have called up the **Patient Browser** window for the first time the local database will open. All the patients stored in it are listed in the navigation and content area.

The data levels of the first patient are displayed in the navigation area.

➪ If you call up the **Patient Browser** again later, it appears in the display last set.



Work Status	Mark Status	Patient Name	Patient ID	Date of Birth	Comm...	Studies
//////	/	Schmidt	Dritte_Gru	12/12/68		1
//////	/	Meier	Zweite_Dr	12/12/68		1
//////	/	Müller	Zweite_Gr	12/12/68		1
//////	/	180 DynTOMO 1 Process, S	99.12.28-1	9/16/98		1
//////	/	1K_SMPTE,FLUOROSPOT	040399-1	1/1/50		1
//////	/	a 8x10 VertriebsfilmVision	8/96	-		1
//////	/	AGHAJA ANN, SUSAN	33566366	8/23/62		1
//////	/	AGUIRE MARIE, LUCY	33566368	5/10/45		1
//////	/	ALEXIS JOSEPH, MICHAEL	33566368	6/19/40		1
//////	/	ALFANO ANN, ALICE	33566366	6/21/75		1
//////	Prot/M	ALLEN DAVID, FRED	L777599N	7/10/59		1
//////	/	ANGIO NATIVE L, KNEE	22222222	5/5/65		1
//////	/	ATWOMODSTUDY	4711	5/5/60		1
//////	/M	AVE+ ABDOMEN	00000020	10/10/78		1
//////	/	bb	0-98.10.01	1/1/1901		1
//////	/	BENJAM ELVIS, HOWARD	33568366	10/28/57		1
//////	/	BN WUERFEL	1	-		1
//////	/	BRADFORD B, WILLIAM	T1839292	1/22/65		1

Current Filter: Not Filtered

Now select a database in the navigation area and search for the patient you require. You then open the lower levels of information until you have found the data you are looking for of the patient concerned.

Example

For example, to select certain images of a patient for processing you can open the information levels patient, study, and series one after the other until the images you require are listed or displayed (as image stamps) in the content area.

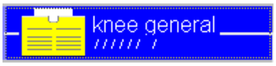
✧ Click on the icon for the database in which the patient is stored in the navigation area.

✧ If necessary, scroll through the list of patients using the scroll bar until you have found the patient you require.

➪ You will find the patient you are looking for even faster if you press the key for the first letter of the patient's name on the keyboard. The selection then jumps to the first patient entry with this initial letter.

ALLEN DAVID, FRED
////// Prot/M

✧ Click on the patient you are looking for in the navigation area to view the information levels stored for this patient as icons. All the studies of this patient are displayed in the content area.



knee general
////// /

✧ Click on a study in the navigation area to select it and to view all the associated series.

t2 me2d sag
////// /

✧ Click on a series in the navigation area to select it and to obtain an overview of all the images contained in it in the content area.

✧ Click on an image in the content area to select it.

➩ Depending on whether you have clicked on **View > Image Stamps** or not, the series and images are displayed as image stamps or listed in the content area.
→ Page D.1–10, *Customizing the Patient Browser window*

Data selection with the keyboard

Using the keyboard you can reach various data entries in the **Patient Browser** very quickly. The key assignment for the selection options in the active area (navigation or content area) is summarized in the following table.

Key	Selection	Key	Selection
Home	First entry	**End**	Last entry
Page up	First visible entry	**Page down**	Last visible entry
↑	Entry one line up (same level)	↓	Entry one line down (same level)
←	Entry left (level up in navigation area)	→	Entry right (level down in navigation area)
Tab or **Shift** + **Tab**	Toggle between the navigation and content area	Letter	1st entry with the appropriate starting letter

➩ If you press the **Ctrl** key at the same time, the entry is not selected. To select it press the space bar afterwards.

Selecting raw data

The raw data of a scan series are stored in the same data level as the images and can be selected in the same way in the content area.

The image number, date and time, slice width, slice position, and annotation text are not defined in a raw data set. For that reason, the corresponding fields remain blank in the list and image stamp display, unlike for images.

Multiple selection

You can also select several patients at once, for example, to archive their data, or you can select several images of one patient in order to review them.

✧ Mark the patient entries or examination data you require in the navigation or content area with the mouse keeping the **Ctrl** key pressed.
→ Page A.1–13, *Selecting several objects*

Or

✧ Select the first entry you require in the navigation or content area. Hold the **Shift** key pressed and extend your selection using the keyboard.
→ Page D.2–9, *Data selection with the keyboard*

➩ Multi-select is only possible on one data level in the tree display. Data selected must belong to the same entry at the next highest data level (e.g. several series of one study but not several series of different studies).

Filtering data

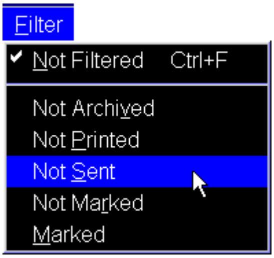
If the volume of data in the navigation and content areas is very large, you can simplify the search for patient data by filtering the data. You then only view a certain selection of patients, studies, series, and images.

Using standard filters

When filtering your data you can use filter criteria that are offered by default by your system. These are available to you on the menu bar or with the buttons on the tool bar.

➪ In **Browser Configuration**, you can add standard filters to or remove them from the menu bar or toolbar.
→ Page D.1–8, *Tool bar*

Filter menu

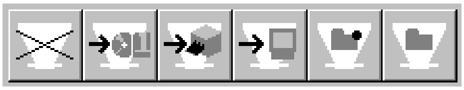


✧ Select one of the filtering criteria in the **Filter** menu of the **Patient Browser.**

These default filters evaluate the status or marking of data on all data levels.
→ Page D.5–2, *Defining the work status*
→ Page D.5–6, *Marking examination data*

Or

Filters on the tool bar



✧ Call up a standard filter using the tool bar.

➪ In **Browser Configuration** (**Options > Configure Browser...**) you can configure the contents of the tool bar.
→ Page D.7–3, *Tool bar*

Depending on the filtering criterion selected these data are now displayed:

Not Archived
Only the data which have not been archived are displayed.

Not Printed
Only the data which have not yet been printed are displayed.

Not Sent
Only the data which have not yet been sent in the network are displayed.

Not Marked
Only the data which are not marked are displayed.

Marked
Only marked data are displayed.

Deactivating the filter


Current Filter: Marked

A filter remains active until you replace it by another filter.

The status bar shows you which filter is currently being applied.

➪ If you exit the **Patient Browser** and call it up again later on, the last filter that has been selected is still active.

✧ Call up **Filter > Not Filtered** or click on the icon button to have all the data displayed again (unfiltered).

Creating a user-defined filter

Using the **Patient Browser** you can also create your own filter criteria in order to filter the database according to a combination of conditions.

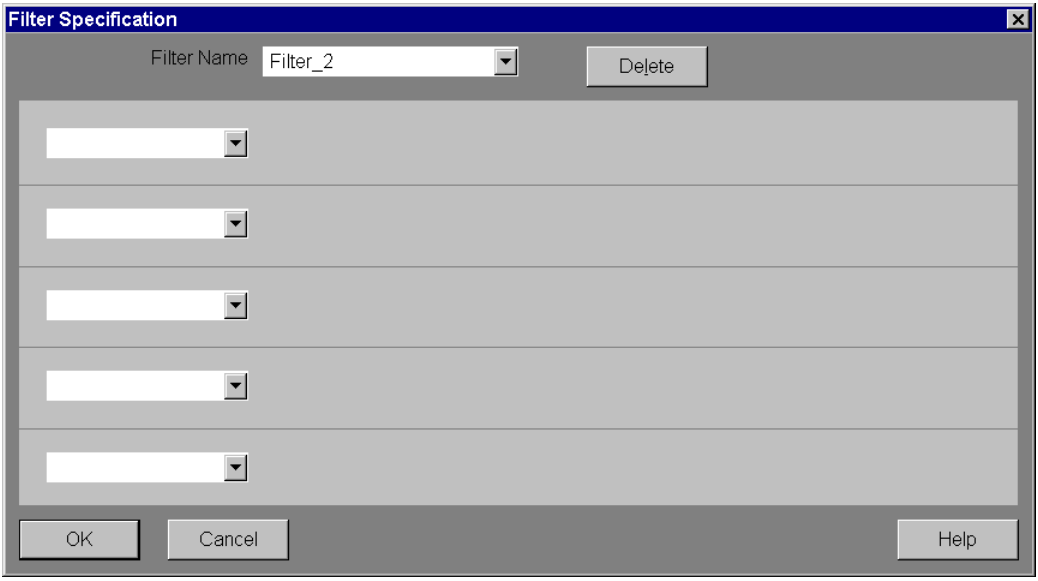
If you keep self-defined filters general, you can use them frequently to have a certain subset of the data displayed in a quick and uncomplicated manner.

If you define very specific filters, you can search for patient and examination data in a direct and time-saving way.

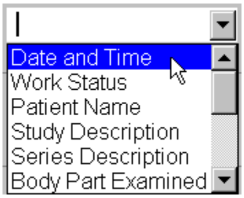
Creating a filter

✧ Call up **Options > Filter Settings....**

The **Filter Specification** dialog box is displayed with input fields for the filter name and five filtering criteria.

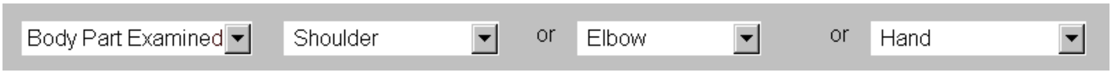


✧ Enter a suitable name in the **Filter Name** field by which your filter is to be known.



✧ Select one of the filtering criteria offered in the selection list.

Depending on which criterion you select, input fields combined with **and, or** or **From ... to** appear or the criterion has *no* additional input field.



Body Part Examined Shoulder or Elbow or Hand

✧ Enter conditions in the input field combined with ’**or**’ of which at least one must be fulfilled.

Work Status Completed and Read and Approved

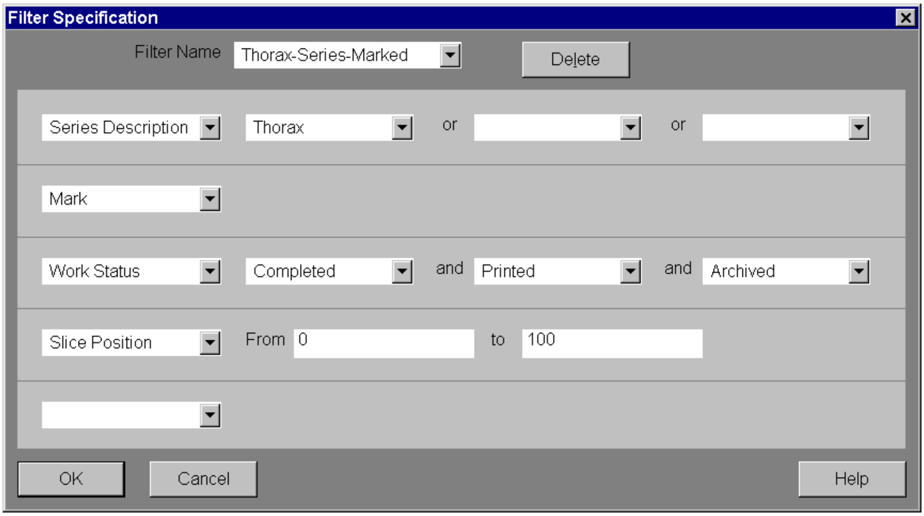
✧ Enter conditions in the input fields combined with ’**and**’ that must all be fulfilled.

Patient Name From A to F

✧ In the input fields combined with ’**From - to**’ enter the range in which the data you are searching for must be contained.

Example of a user-defined filter

The following user-defined filter was created to find a particular series of a thorax examination in a database.



Filter Name: Thorax-Series-Marked

Series Description: Thorax

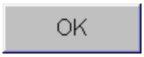
Mark

Work Status: Completed and Printed and Archived

Slice Position From 0 to 100

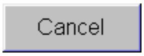
This filter only selects marked series that have already been completed, filmed, and archived and that were acquired with a slice position between 0 and 100.

Saving a filter



✧ Click on **OK** to save the filter. You will return to the **Patient Browser** window.

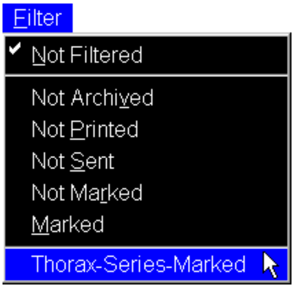
Or



✧ Click on **Cancel** to return to the **Patient Browser** window without saving the new filter.

Using user-defined filters

User-defined filters are placed in the **Filter** menu as additional menu entries.



✧ Call up, for example, **Filter > Thorax-Series-Marked**, to filter all data to your criteria.

Removing user-defined filters

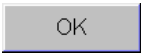
When you no longer require a user-defined filter, you can remove it from the **Filter** menu again to keep the menu clear.

✧ Call up the **Filter** dialog box and select the filter you want to delete in the selection list next to **Filter Name**.

Filter Name Thorax-Series-Marked

✧ Click on **Delete** to remove the filter from the list.

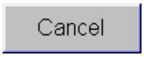
✧ If necessary, select further filters from the selection list and remove them in the same way.



✧ Then click on **OK** to confirm deletion of the filter.

You return to the **Patient Browser** window.

Or



✧ Click on **Cancel** to keep all filters as they were.

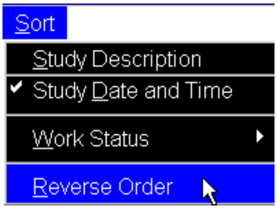
Sorting data

You can sort the data displayed in the **Patient Browser** by various criteria. This enables you to output the data in a certain sequence and makes it easier to find certain patient and examination data.

✧ Select a data level in the navigation area in order to view the patients, studies, series, or images you want to sort in the content area.

➪ In the **Scheduler**, you can only sort by patient name (also in reverse order).

Sort menu



✧ Open the **Sort** menu.

Depending on the data level displayed in the content area different sorting criteria will be provided.

✧ Click on one of the sorting criteria stated.

Depending on the criterion selected, the data in the content area are sorted alphanumerically or chronologically, or by whether the sorting criterion has been fulfilled completely, partially or not at all.

✧ Call up **Sort > Reverse Order** to reverse the sequence.

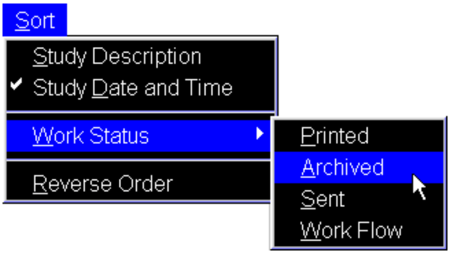
➪ In the navigation area, too, the data are resorted by the same criteria as in the content area.

Example of sorting data

Suppose you want to finish archiving the examination data of a patient. To facilitate this task you want to have the studies of the patient listed in the order unarchived, partially archived, archived in the content area.

✧ Select the patient in the navigation area.

✧ Call up **Sort > Work Status > Archived**.



✧ Call up **Sort > Reverse Order**.

In the content area the studies are displayed in the order unarchived, partially archived, completely archived.

Printing out a data list

If your system is connected to a printer, you can print out examination data in the form of a list. On printing out, the information displayed in the content area is displayed.

✧ Display the required patient and examination data in the content area.
→ Page D.2–6, *Scrolling through and selecting patient data*

⇨ To print out the content area, you can work both in the tree display and in the single display.
→ Page D.1–13, *Showing and hiding window sections*

Displaying the print preview

✧ Call up **Patient > Print Preview...** to have the printout displayed in a preview.

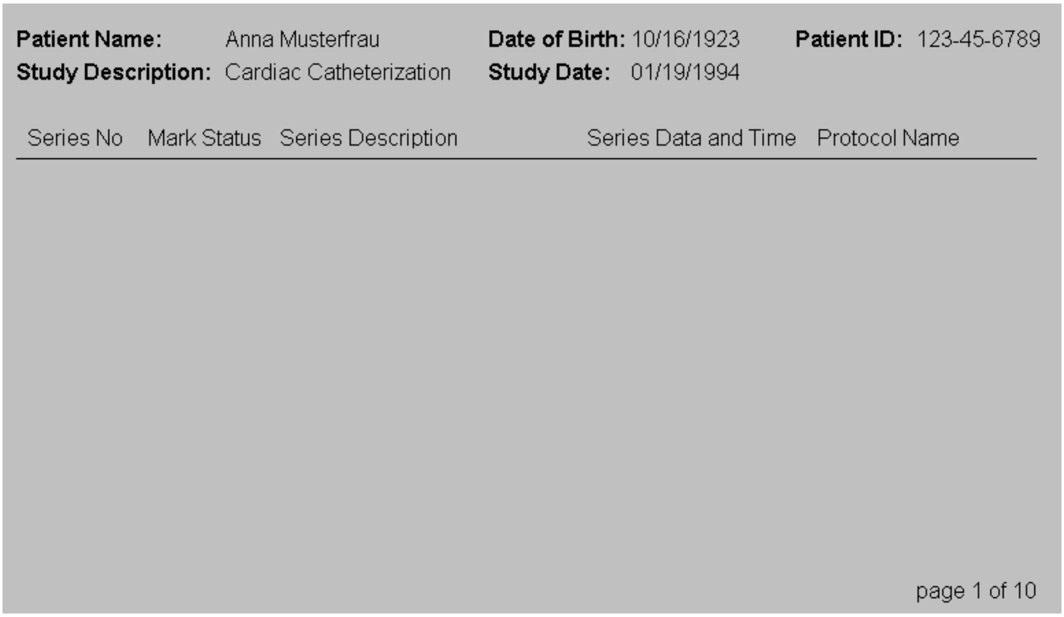
☒

✧ Click on **Close window** to close the print preview again.

Printing out a list

✧ Call up **Patient > Print List** to print out the data listed in the content area.

In a list of patients, the content and date of creation of the list is stated in the header of the printout. For all other data levels, the content of the information area is also printed.



Patient Name: Anna Musterfrau **Date of Birth:** 10/16/1923 **Patient ID:** 123-45-6789
Study Description: Cardiac Catheterization **Study Date:** 01/19/1994

Series No	Mark Status	Series Description	Series Data and Time	Protocol Name

page 1 of 10

➪ This list is always printed out in English.

Changing printer settings

You can change the printer settings (e.g. page margins) in the Windows NT print dialog.

✧ Call up **Patient > Print...** and make the required settings in the dialog box shown.

OK

✧ Click on **OK** to apply the new settings.

Reading data from archive media

You can import patient and examination data archived or exported onto a data medium in DICOM format into your system (into the local database) if a drive has been installed and configured appropriately.

➪ With the current program version, you can only import DICOM data.

➪ Single images in DICOM or bitmap format can also be imported by the file system.
→ Chapter F.4, *Exporting and importing images*

✧ Click on the icon of a data medium in the navigation area to display all the patient data stored there.

Data media

Depending on the drive setting of your system, you can read data from the following media:

❑ MOD (magneto optical disk) 5.25"

❑ CD or CD-R

❑ 3.5" diskettes

→ Page F.2–2, *Backup on local data media*

Changing data media

✧ Call up **Transfer > Eject from...** and select the appropriate drive from the list which is then displayed.

✧ Remove the data medium from the drive and insert the new medium into the corresponding drive.

Or

✧ Call up **Transfer > Eject From <drive name>**, or press the eject button on the CD drive and change the medium.
→ Page F.2–3, *Inserting and ejecting media*

➪ MODs that are written by other systems should only be inserted with write-protection.

Showing/hiding data sources

With **View** > **Source**, you can hide or display archiving media individually in the navigation area.
→ Page D.1–15, *Showing and hiding databases and drives*

Selecting data

You search and select patient and examination data from archive media by clicking through the data levels in the navigation area.

➪ You can speed up your search by filtering and/or sorting the data.
→ Page D.2–12, *Filtering data*
→ Page D.2–20, *Sorting data*

Importing data

You can import the patient and examination data selected in the archive medium into the local database, e.g. to evaluate it, to send it through the network, or to store it on another data medium.

✧ Call up **Transfer > Import** to import the selected data from the data medium or network node into your local database.

Or

✧ Click on the icon button on the tool bar.

Searching for and importing data in the network

With **Patient Search**, you can retrieve patient and examination data from workstations that are working with other DICOM program systems or older SOMATOM program versions and are therefore not displayed in the navigation area.

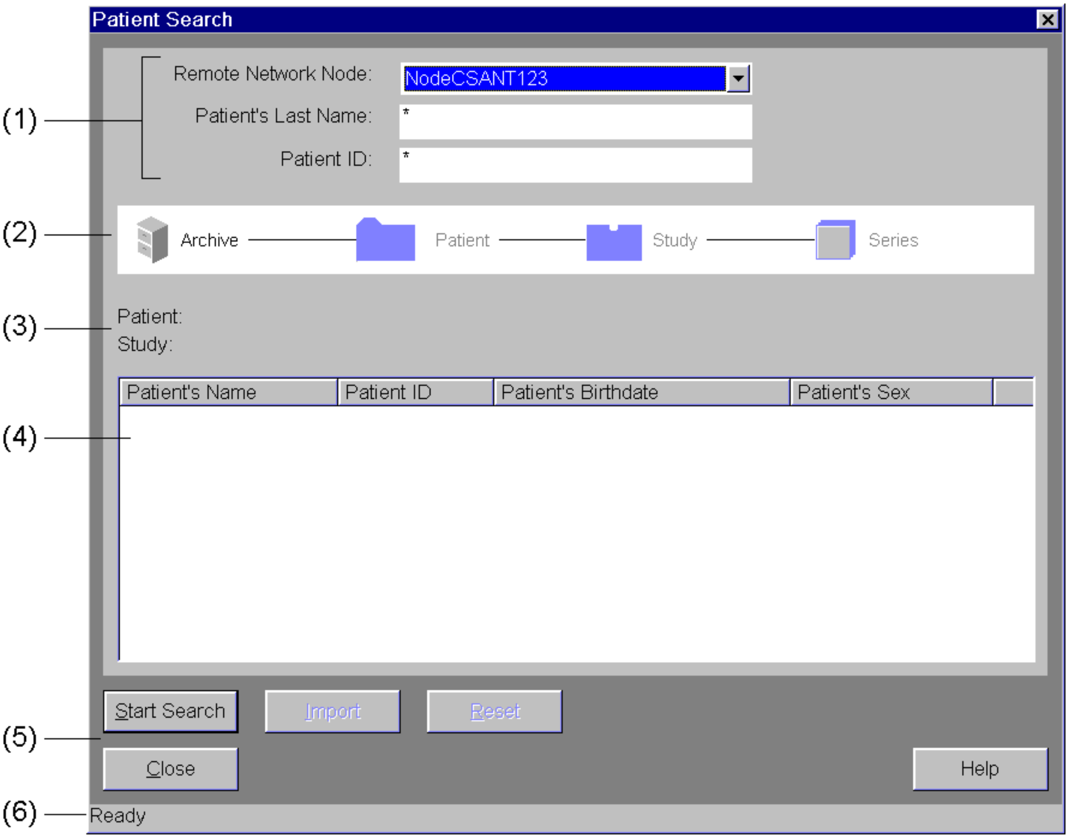
You can import the required data into your local database via the network and work on your workstation in the usual way, e.g. loading the data into the **Viewing** task card for evaluation.

➩ You can retrieve patient and examination data only from workstations that are set up as a network node and support **Patient Search**.

Calling up Patient Search

You can perform your data search in the **Patient Search** window. There you enter the search criteria, start the search, and select the data to import.

✧ Call up **Patient > Search...** in the main menu to display the **Patient Search** window.



Remote Network Node: NodeCSANT123

Patient's Last Name: *

Patient ID: *

Patient:

Study:

Ready

(1) Input fields for search criteria
(2) Navigation bar
(3) Information area
(4) Search output list
(5) Buttons
(6) Status bar

Searching for data

Just like in the navigation area of the **Patient Browser**, with **Patient Search** you first search for the patient you require. After that, you open the lower data levels until you have found the studies, series, or images concerned.

Starting a search for a patient

Remote Network Node MagicViewRoundTheCorner

✧ Select the network node on which the data searched for are located.

Patient's Last Name: M*

Patient ID: *

✧ Enter the last name and ID of the patient searched for.

➪ The following characters are not permitted: ^ = \

➪ The search distinguishes between upper and lower case! Enter the characters correctly.

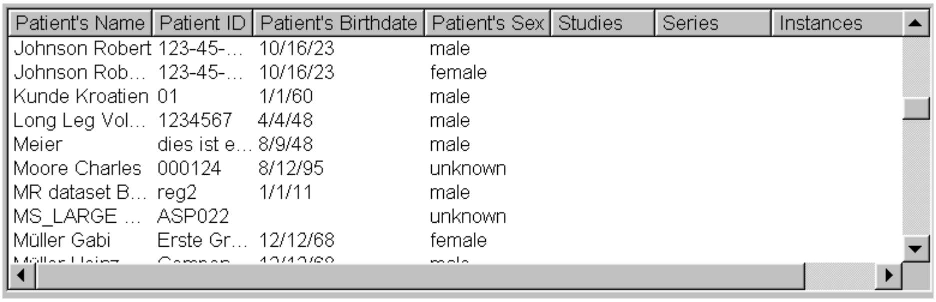
➪ If you only know part of the name or the patient ID, you can also use the character * as wildcard.
→ Page B.4–5, *Wildcards for patient name, ID, physician and ward*

✧ Click on the **Start Search** button to start with the search.

➪ The **Start Search** button changes to **Stop Search** which you can use for aborting the query at any time (e.g. when the required data has been found already). You can also cancel the search with the **Esc** key on the keyboard.

Search result

All the patients found during the search are displayed with their attributes in the search list.



Patient's Name	Patient ID	Patient's Birthdate	Patient's Sex	Studies	Series	Instances
Johnson Robert	123-45-...	10/16/23	male			
Johnson Rob...	123-45-...	10/16/23	female			
Kunde Kroatien	01	1/1/60	male			
Long Leg Vol...	1234567	4/4/48	male			
Meier	dies ist e...	8/9/48	male			
Moore Charles	000124	8/12/95	unknown			
MR dataset B...	reg2	1/1/11	male			
MS_LARGE ...	ASP022		unknown			
Müller Gabi	Erste Gr...	12/12/68	female			

The archive icon is marked on the navigation bar. This tells you that the database level is open and its content is being displayed in the search list (as in the content area of the **Patient Browser**).

➪ The archive symbol can stand, for example, for the local database of the network node.

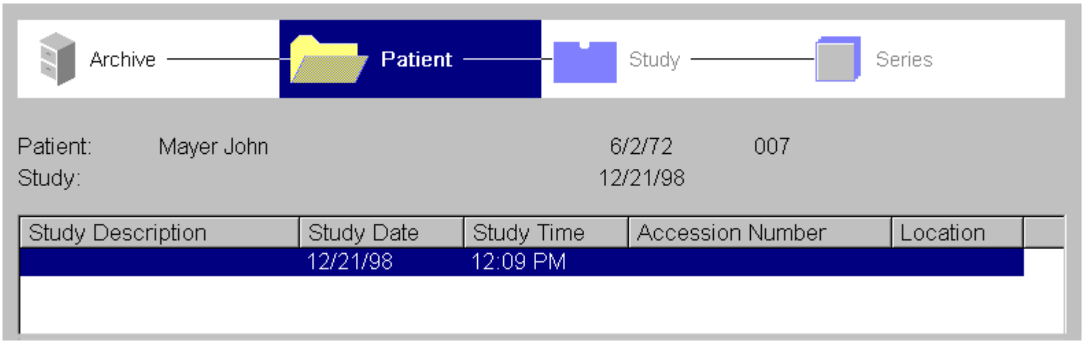
Listing studies

Mayer John

✧ Select *one* patient from the search list with the mouse.

✧ Click on **Start Search** to open the “**Patient**” data level and to have all the studies of this patient displayed in the search list.

Using the personal data displayed in the information area (name, ID, and date of birth), you can see to which patient the studies listed belong.



Patient: Mayer John 6/2/72 007
Study: 12/21/98

Study Description	Study Date	Study Time	Accession Number	Location
	12/21/98	12:09 PM		

NOTE

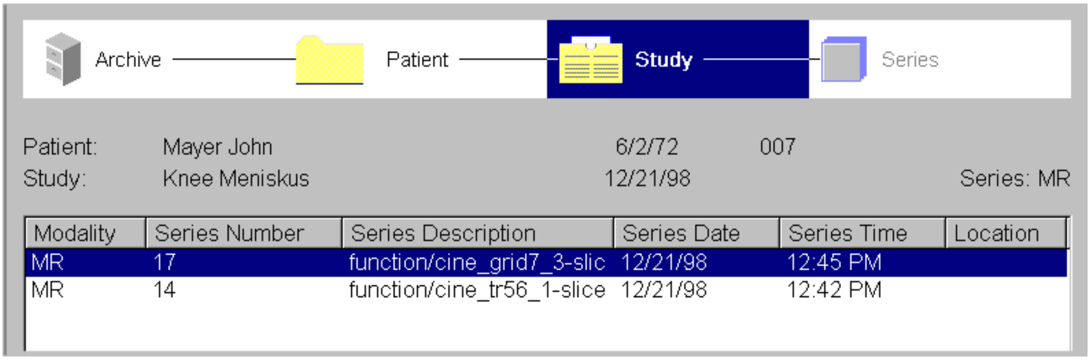
If the ID of the patient is not unique, studies may be listed which do not belong to the patient selected and displayed in the information area.

Listing series

✧ Select a study in the search list with the mouse.

✧ Click on **Start Search** to open the “**Study**” level and list all series of this study.

In the information area, you can see the selected study and the study date below the patient data.



Patient: Mayer John 6/2/72 007
Study: Knee Meniskus 12/21/98 Series: MR

Modality	Series Number	Series Description	Series Date	Series Time	Location
MR	17	function/cine_grid7_3-slic	12/21/98	12:45 PM	
MR	14	function/cine_tr56_1-slice	12/21/98	12:42 PM	

Listing images

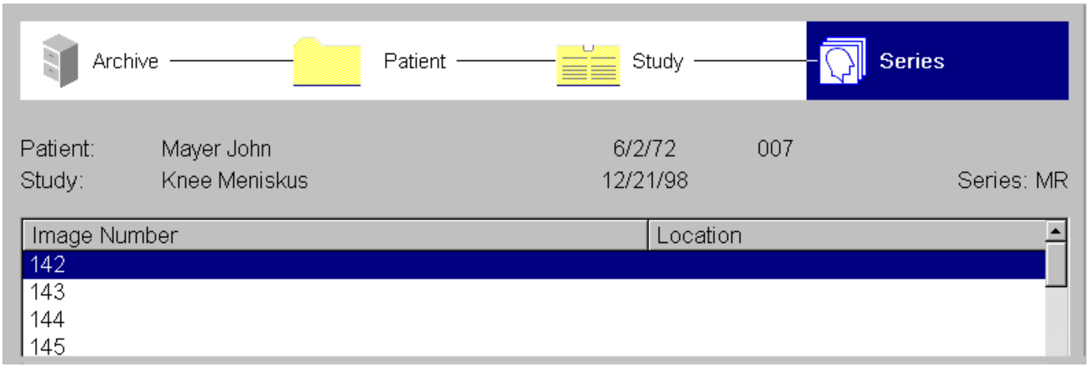
MR

✧ Select a series from the search list.

Start Search

✧ Click on **Start Search** to open the “**Series**” data level.

In the search list, you can see the numbers of all images that belong to the series concerned. The designation of the series is displayed in the information area.



Patient: Mayer John 6/2/72 007
Study: Knee Meniskus 12/21/98 Series: MR

Image Number	Location
142	
143	
144	
145	

Another series, study, or other patient

If you are searching for the images of another series or study or for another patient, then first switch to the appropriate data tree and open the lower data levels again.

➩ Please note: As soon as you select another entry on a data level, the result lists on the lower data levels are deleted.

✧ Click on the “**Study**” icon on the navigation bar if you are searching for another series.
All series of the selected study are listed.

Or

✧ Go back to selection of another study on the “**Patient**” data level by clicking on the icon.
All studies of the patient are listed.

Or

✧ Click on the “**Archive**” data level if you require the data of another patient.

➩ Depending on the system setting, this data level might be dimmed. You will then already find the patients with their studies in the search list on the “**Patient**” data level.

✧ Select the required entry from the search list and have the associated data displayed on the next lowest data level with **Start Search**.

Selecting another network node

If the required data are not at the address stated, switch to another network node and continue your search there.

✧ Click on **Reset** to terminate the data search on the previous network node.

✧ Select another network node and start your data search there.
→ Page D.2–29, *Starting a search for a patient*

Importing data

After you have found the required study, series, or images, transfer them to your workstation for further processing.

Availability of images

You can only import data from selected network nodes to your system if those data have been “released” for that purpose. This is indicated in the search list by an attribute in the column **Location**.

➩ Whether and how the attribute is set in the column **Location** depends on which type of network node you have selected. Please ask your system manager for further details.

For example, some network nodes enter the following information in the column **Location**:

- **Online**
  Studies, series, or images can be imported.
- **Nearline**
  The data objects are available inside a "jukebox". No operator is required to insert the storage medium in.
- **Offline**
  Studies, series, or images cannot be imported.
  The personnel at the network node must first be informed that the data in question must be put online.

Starting importing data

✧ Select the study or one or more series or image(s) that you want to import into your database from the search list.

✧ Click on the **Import** button.

The selected data are copied from the network node to your workstation and displayed in the navigation and content area.

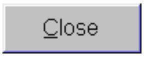
✧ Click on the **Import Stop** key if you want to cancel reading in prematurely.

Checking data transmission

Just as for archiving or exporting you can view and process import processes.

✧ Call up **Transfer > Local Job Status** or **Transfer > Network Job Status**.
→ Chapter F.5, *Checking data transfer*

Ending Patient Search



✧ Click on the **Close** button to close the **Patient Search** window.

➪ If you have triggered a patient search it is now canceled. However, if you are in the process of importing data, importing continues in the background.

Calling up additional information about a patient

If your hospital has an intranet, you can call up information about a patient from other departments in your hospital using a Web browser with which *syngo* provides an interface. This applies to data that has been entered in an HIS or similar information system.

The additional information about the patient (e.g. concerning allergies, implants, preliminary examinations) might bear relevance to the pending examination or evaluation of more recent examination results.

Use the EPR Web browser (EPR = Electronic Patient Record) to call up the data.

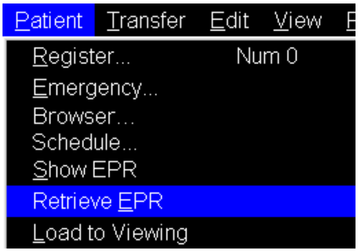
➪ At any one time the Web browser only displays the EPR for *one* patient. You can view but not import the data of the patient with the EPR Web browser.

➪ The first time you launch the Web browser you must log on (see the operating instructions of your Web browser).

➪ The *syngo* interface must be individually adapted to the EPR Web browser by your system administrator.

Calling up the EPR Web browser

To display the electronic report for a particular patient, select a patient (or a study, series, instances) from the **Patient Browser** or in another task card.



✧ Call up **Patient > Retrieve EPR** in the main menu to display the EPR Web browser.

Or

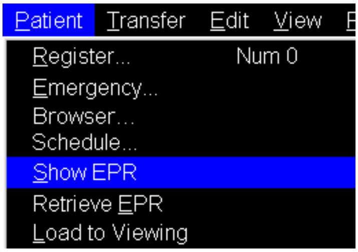
✧ Click on **Retrieve EPR** in the tool bar.

The EPR Web browser starts up and the information available for the selected patient is displayed.

➩ If you click with the mouse outside the EPR Web browser, the window is placed in the background.

Placing the EPR Web browser in the foreground

You can call up the Web browser with the same patient data again.



✧ To do that, call up **Patient > Show EPR** in the main menu.

Or

✧ Click on **Show EPR** in the tool bar.

The EPR Web browser is again displayed with the same contents.

Closing the EPR Web browser

✧ Call up **File > Close** to close the EPR Web browser.

The EPR Web browser is closed.

CHAPTER
D.3

Transferring Data to other Applications

You have found the patient and examination data you require in the **Patient Browser** window and would now like to make use of this data in another application.

❑ You would like to examine the patient again.

❑ You would like to view and possibly review the patient's stored images.

❑ You would like to process and evaluate images three-dimensionally for special diagnostic problems.

❑ You want to reconstruct images, e.g., because a complete reconstruction of all images had not been possible immediately after the examination, because of a lack of time.

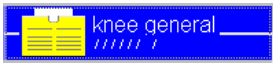
Registering the patient again

Before you can examine a patient stored in the local database or in one of the archive media again, you must register this patient for a new examination. You can also call up and preregister the patient on the **Wizard** and register for examination on the Navigator later.

ALLEN DAVID, FRED
////// Prot/M

✧ Click on the required patient entry in the navigation or content area of the **Patient Browser**.

Or



knee general
////// /

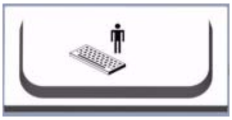
✧ Select the study or studie(s) of the patient that you want to perform or repeat.

✧ Call up the patient registration with **Patient > Register...**.

Or

✧ Click on the icon button on the tool bar.

Or



✧ Press the **Patient Register** key on the symbol keypad (Num **0**).

Or

✧ Drag the selected data into the open **Patient Registration window** (**drag & drop**).

In the **Patient Registration** window you can check the patient data and correct it if necessary. You can add to the examination data and register the patient whom you can then examine right away.
→ Chapter B.4, *Registering a Known Patient*

Viewing and processing images

With the **Patient Browser** you can transfer the images of one or more patients from the local database to the **Viewing** task card for viewing and editing.

Depending on which data level you are in, you can transfer the following image material to the **Viewing** card:

❏ All images of one or more patients

❏ All images of one or more studies

❏ All images of one or more series

❏ One image or more than one image

For transferring images to the **Viewing** task card you can either use the menu bar or the tool bar or you simply double-click the images or **drag & drop** them onto the **Viewing** task card with the mouse.

All images of a patient, a study or series

✧ Select the patient, study, or series in the navigation or content area of the **Patient Browser**.

✧ Call up **Patient > Load to Viewing** or click on the button on the tool bar to transfer the associated images to the **Viewing** task card.

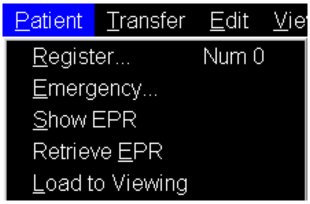
Or

✧ Click the **Viewing** card to the top of the stack.

✧ Then double-click on the required data object. Or select the data using the keyboard and press the **Return** key.

➪ Using multiple selection in the navigation or content area you transfer the images of *more than one* patient, study, or series to the **Viewing** task card.
→ Page D.2–11, *Multiple selection*

One or more than one image of a patient



✧ Click the **Viewing** card to the top of the stack.

Or

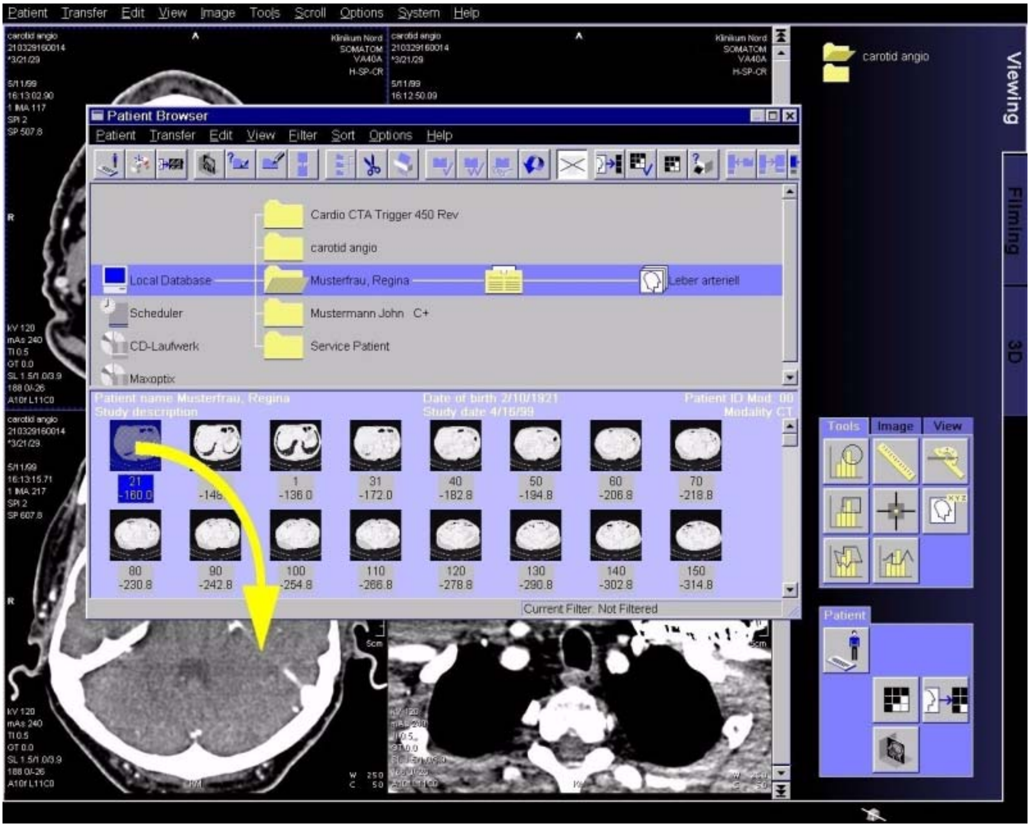
✧ Select more than one image in the content area and transfer it to the **Viewing** card with **Patient > Load to Viewing** or the **Load to Viewing** button on the tool bar.
→ Page D.2–11, *Multiple selection*

Drag & drop

In addition to the methods described above you can also transfer images to the **Viewing** task card by **drag & drop**. In this way you can determine in which segment the first of your selected images is to be displayed.

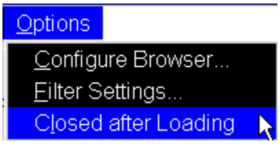
✧ Reduce and/or move the **Patient Browser** window so that you can see the image area of the **Viewing** task card.

✧ Drag the selected images to the desired segment on the **Viewing** task card.



➪ If the task card is not in the foreground you can also drag the images from the **Browser** onto the corresponding tab. The task card moves into the foreground and the images are loaded into the image area.

Closed after Loading



If you have selected the **Closed after Loading** setting in the **Options** menu, the **Patient Browser** window is closed after transfer of the images.

✧ Call up **Options > Closed after Loading** to activate this function.

If the option is not checked, the **Patient Browser** remains open in the foreground even after you have loaded images into the **Viewing** card. To process images you can always switch manually to the **Viewing** task card.

✧ To do that, click on the **Close** button in the top right corner of the **Patient Browser**.

In the **Viewing** task card you can view and edit the transferred images.
→ Part E

Processing images in 3D

As the result of an examination you obtain images of a certain volume which are stored in your local database. You can combine the two-dimensional slices of a suitable series to form a three-dimensional representation of the region of interest and you can process and evaluate it in the **3D** task card.

✧ Select a patient or one or more of his or her studies, series or images (at least 4) in the navigation or content area of the **Patient Browser**.

✧ Call up **Patient > MPR** or click on the icon button to start image processing as multiplanar reconstruction (MPR).

Or

✧ Call up **Patient > MIP** or click on the icon button to start maximum intensity projection (MIP).

Or

✧ Call up **Patient > SSD** or click on the icon button to start surface shaded display (SSD).

Or

✧ Call up **Patient > VRT** to start the volume rendering technique as the image processing.

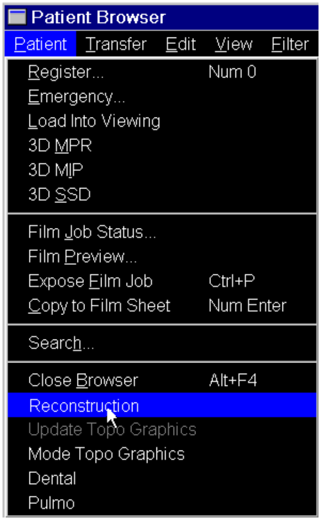
If you have selected more than one suitable series or an especially large series, the **Series List** dialog box is displayed. As soon as you have decided on a series there, you can perform three-dimensional image processing on the **3D** task card.
→ Chapter H.2, *Transferring Images to 3D*

Reconstructing images

Depending on how much time you have between examinations, you can reconstruct the images of an examination immediately after scanning or at a later point in time.

✧ Select the required study or series of the patient for image reconstruction in the local database or archive.

➩ You can only reconstruct studies or series if they contain unprocessed reconstruction jobs. The raw data were then saved after the examination.



✧ Call up **Patient > Reconstruction** to pass the selected data to the **Examination** task card.

In the **Examination** task card you can now start the unprocessed reconstruction jobs or define new ones.

➩ By activating **Patient > Mode Topo Graphics** you can have the scans documented as ranges and cutlines in the topogram even after completing an examination
→ Page C.5–36, *Displaying cutlines in the topogram*

Private applications

Via the main menu **Private Applications** of the **Patient Browser** you have the opportunity to use the functions or other application programs of your *syngo* system, too.

In the **Patient Browser** you can select patient and examination data and pass it on to programs you intend to use for further processing.

➩ In the **Browser Configuration** you can define with which application programs you want to work in your *syngo* system.

Passing on data to another application

✧ Select the data that you want to process in the navigation or content area of the **Patient Browser**.

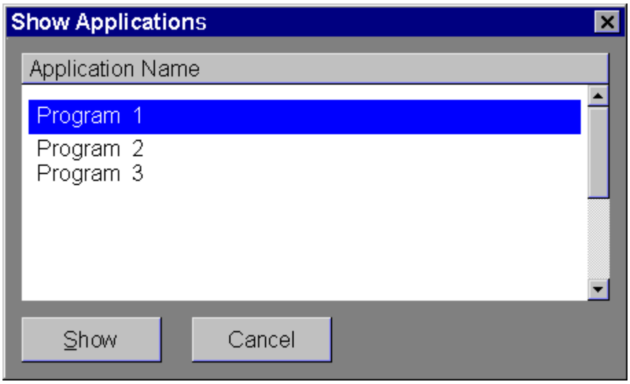
✧ Call up the menu **Private Applications** and click on the required program entry.

The data selected in the **Patient Browser** are loaded into the application program.

Showing an application program

✧ Call up **Private Applications > Switch to....**

The dialog box **Show Applications** appears with a list of all configured application programs.



✧ Select the program from the list to which you have passed the patient and examination data.

Show

✧ Click on **Show** to switch to the application program.

The program user interface moves into the foreground. You can process the loaded patient and examination data with the functions provided there.

CHAPTER
D.4 Correcting Data

Every now and then it is necessary to correct patient data or to add information about the study data, series and instances of a patient.

For example, if you have examined an emergency patient, that patient is first stored by a provisional identification. Later on you can add the patient's full name, correct patient ID and all the other personal information and information about the examination conducted.

You can use the **Patient Browser** to search for this patient in the database and then call up a dialog box in which you can process the data.

➪ The data of the Service Patient cannot be altered. The same applies to data that have been imported via an HIS / RIS system or which are linked with such a system.

➪ Whether and what changes can be made to data linked with **MPPS** depends on the working status.
→ Page D.5–8, *Performance documentation*

History of changes

Every time you change the data of a patient or examination, this is recorded in a history of changes on your system. The correction list is maintained for each object level. You can view the history of changes for an entry in the **local database** at any time in order to see what changes have been made to it.

Correcting patient or examination data

You can correct or add to the personal data of a patient or information about that patient’s studies in the local database.

If you want to change archived data or data from another workstation, you must first import it into the local database. However, the original data remain unchanged.
→ Page D.2–24, *Reading data from archive media*

✧ Select the patient, study, series or images that you want to correct in the navigation or content area of the **Patient Browser**.

✧ Call up **Edit > Correct**.

Or

✧ Click on the icon button on the tool bar to open the **Correct** dialog box.

➪ You cannot correct data that was delete-protected with **Edit > Protect**. You must first remove the delete protection with **Edit > Remove Protection**.

➪ Data that are used by other applications cannot be corrected, either. The corresponding entries in the **Correct** dialog box are then dimmed.

Selected patient

On the title bar of the **Correct** window, you can see which patient and data you have selected.

Correct

"ROBERTS MELISSA SUE" on "Local"

1 Patient selected

Content display

In the first line of the window of the header line, the number of studies, series, and images which are selected for correction is displayed.

Entering data

In the input and selection fields of the **Correct** window you can see the information that has been stored for the selected patient or selected study or series so far.

✧ Correct or add to the selected data.

➪ Depending on the data level in which you want to correct data, some fields of the dialog box might be dimmed.

➪ When you enter very long comments in the **Comment** input field only the first part of the text is displayed in the **Viewing** task depending on the selected layout. A third or fourth comment line is not displayed, either.

➪ Multiple values are represented by an asterisk and cannot be changed (except instance level).

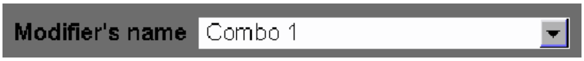
Updating a current examination


☑ Update data acquisition

If you have called up the **Correct** window from the examination card, you can incorporate the changes in the current examination.

✧ Select the checkbox **Update data acquisition**.

Signing for changes


Modifier's name Combo 1

✧ Enter your name under **Modifier's name** or select your name from the selection list.

This will indicate who made the changes to the patient and examination data for further reference. If your name is not yet in the selection list, it will now be placed in the list automatically.

➪ If you do not specify a name, the name with which you logged onto the system is taken as the modifier.

Saving changes

OK

✧ Click on **OK** to save the new data and place the changes in the history of changes.

The system first checks whether the predefined data are correct and the date of birth entered is consistent with the specified age. After that, the changed data are accepted into the system.

Or

Cancel

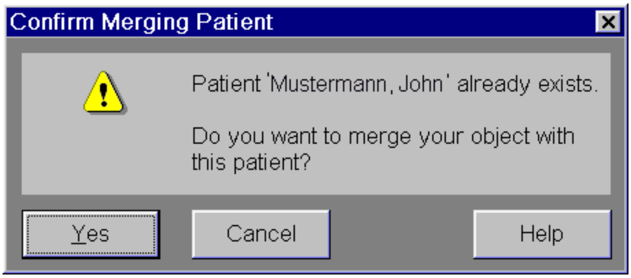
✧ Click on **Cancel** to reject the corrections. The data remain unchanged and no entry is placed in the history of changes.

➩ As soon as you start data correction with **OK**, a dialog window is displayed with the **Cancel** button. With this key you can still cancel your changes as long as the save operation has not been completed.

One patient stored in the database twice

A patient whose name was spelled incorrectly during an examination or who was once registered as an emergency patient is stored in the database twice.

As soon as you save the corrected patient name, the dialog box asks you whether you want to merge the examination data of the two patient entries or not.



Patient 'Mustermann, John' already exists.

Do you want to merge your object with this patient?

OK

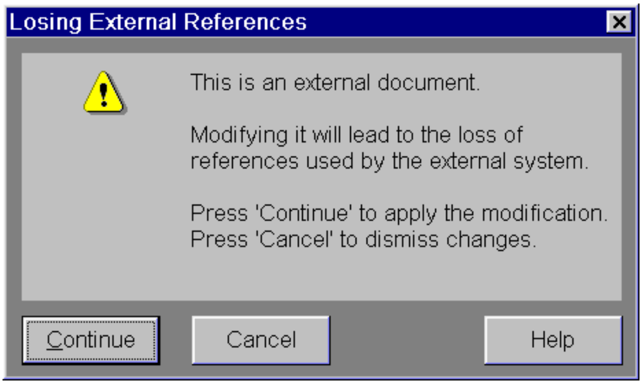
✧ Click on **OK** to store all the selected data under the corrected patient name.

Cancel

✧ Click on **Cancel** to cancel correction of the data.
No changes will be made.

Changing external data

If you change patient and examination data that you have previously imported into your local database (e.g. from another archiving medium) or that was imported into your system (e.g. via HIS/RIS), the **Losing External References** message box is displayed.



This is an external document.

Modifying it will lead to the loss of references used by the external system.

Press 'Continue' to apply the modification.
Press 'Cancel' to dismiss changes.

Continue

✧ Click on **Continue** to save the changed data in your local database.

If you then transfer the corrected data back to its original location, it is stored in addition to the original data.

Or

Cancel

✧ Click on **Cancel** to cancel the process.

Moving data

The images of a patient are grouped together by examination and series into hierarchical groups. If find that the structure is not correct, you can regroup the examinations and series by moving them.

➯ If you move external data imported into your local database and then transfer them back to their original location in a different combination, they will be stored in addition to the original data.
→ Page D.4–7, *Changing external data*

Restrictions

The data of the Test Patient cannot be moved. The same applies to data imported via an HIS/RIS system or linked with such a system.

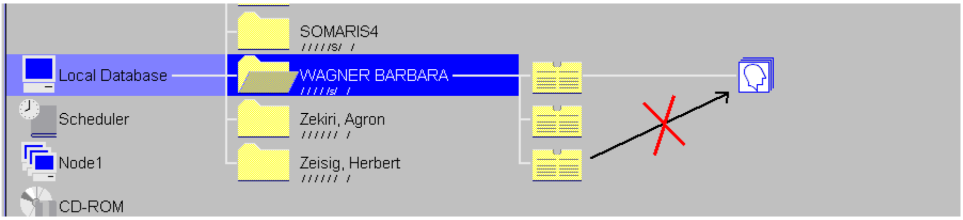
You can only group together examination data that were acquired by the same examination method with the same patient position.

You cannot move data that are already opened in another application (e.g. the **Viewing** card) or are delete-protected with **Edit > Protect**.

You can only move studies into other studies or patient entries, series into other series or studies, images into other series.

❑ For example, you can move images from one series into another series or all images of one series into another study.

❑ For example, you cannot move the images of a study into an individual series of another study.



➪ If you want to move linked external objects, select this function with multiple selection because otherwise the reference to the unselected objects will be lost.

Drag & drop or cut & paste

You can move data either with the mouse (**drag & drop**) or using the **Edit** menu (**cut & paste**).

➩ If you accidentally cut and move data by **drag & drop**, you can cancel the operation at any time with the **Esc** key.

✧ Select the study or studies, series, images, or the one image that you want to move.

✧ Drag the selected data to the target position and release the mouse key.

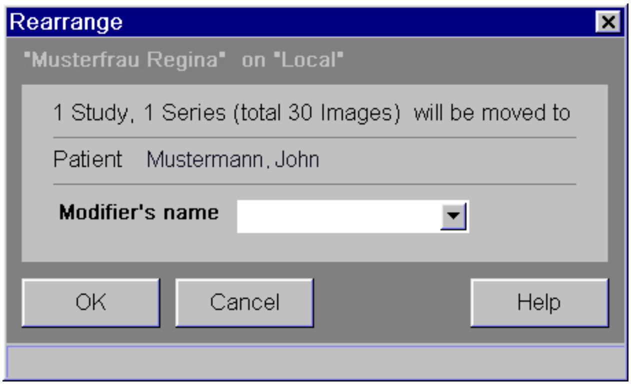
Or

✧ Call up **Edit > Cut** or click the icon button on the tool bar.

✧ Click on the target position.

✧ Call up **Edit > Paste** or click on the icon button on the tool bar.

The **Rearrange** dialog box will be displayed.



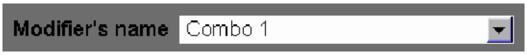
"Musterfrau Regina" on "Local"

1 Study, 1 Series (total 30 Images) will be moved to

Patient Mustermann, John

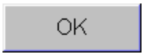
Modifier's name

Just like when correcting patient and examination data, moving data is also recorded in the history of changes.
→ Page D.4–12, *Displaying a history of changes*


Modifier's name Combo 1

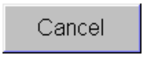
✧ Enter your name in the **Rearrange** dialog box or select it from the selection list.

➪ If you do not specify a name, the name with which you logged onto the system is taken as the modifier.



✧ Click on **OK** to confirm your entry. The data are moved and the changes are recorded in the history of changes together with your name.

Or



✧ Click on **Cancel** to cancel the move.

Displaying a history of changes

The correction list is a sort of log of your local database that is created separately for each data level. Here you can always see what changes and additions have been made to the data of patient and to the information about the patient's examinations.

✧ Select the patient, study, series or image stored in the local database whose history of changes you want to view.

✧ Call up **Edit > History** to display the **Correct & Rearrange History** window with a chronological list of changes.

Or

✧ Click on the icon button on the tool bar.

➪ In the **Correct & Rearrange History** window you cannot make changes yourself. All entries are made by your system.

Series ' ', Study ' TEETH2 ' of patient ' SMITH KATHY ' on ' Local '

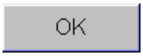
Attribute	Original Setting	Corrected Setting	Date & Time	Modifier's Name
> Patient name	SMITH LOUIE P..	SMITH KATHY	12/19/00 2..	meduser
> Study Description	TOOTH	TEETH	12/19/00 2..	meduser

Depending on the data level of the selected data different information is listed in the **Correct & Rearrange History** window:

- ❑ **Title**
  Here you can see the data record to which the logged changes belong.
- ❑ **Attribute**
  This column lists the corrected entries.
- ❑ **Original Setting** and **Corrected Setting**
  These two columns show you the corrected entry before and after the change.
- ❑ **Date & Time**
  This column of the table shows you the date and time of the change.
- ❑ **Modifier’s name**
  In the last column in the table you can see who has made the corrections.

➪ If an object has been moved, the entry is marked ">" under **Attribute** in window **Correct & Rearrange History**.

➪ Depending on how many levels have changed when you change an object, up to four lines of texts can be inserted into the table.



✧ Click on **OK** to close the history display again.

CHAPTER D.5 Maintaining your Data

If you maintain your data collection regularly you can keep your data management clear and access times to the databases short. This is an important contribution to the efficiency of daily examinations.

❏ You can obtain information about the work status of patient and examination data and can edit it. In this way you can record the processing stage that a patient's images are at.

❏ You can mark important examination data so that you will find it more easily later on.

❏ You can delete patient or examination data that has already been archived from the local database.

Defining the work status

The work status indicates the processing stage of patient and examination data. This status is indicated as an abbreviation in every list entry in the content area. Except “read” and “verified” all work states will be set by the system.

➪ Via the work status, you can define, for example, preconditions for archiving and sending data.
→ Chapter F.6, *Configuring data transmission*

Abbreviations com/p/a/s/e/r/h

The abbreviation consists of seven parts:

- **com**/p/a/s/e/r/H - the first part provides information about the progress of the study and whether the results have been checked by the physician:
  The study has been **com**pleted (**com**/...)
  The images have already been **rea**d (**rea**/...)
  The images and examination data have already been **ver**ified (**ver**/...).
- com/**p**/a/s/e/r/H - the second part states whether
  all (.../**P**/...),
  a part of (.../**p**/...), or
  no (.../ /...)
  images of this patient, study, or series have been **p**rinted or exposed on film.

- com/p/**a**/s/e/r/H - the third component shows the following status:
  (.../**A**/...) Data have been **a**rchived completely
  (.../**AC**/...) Data have been archived and committed
  (.../**AV**/...) Data have been archived and checked
  (.../**A?**/...) Archiving and checking data is pending
  (.../**Af**/...) Archiving and checking data has failed
  (.../**a**/...) Part of the data has been archived
  (.../ /...) No data have been archived
- com/p/a/**s**/e/r/H - by the fourth component you can see with which scope and status the images of the patient, examination, or series have been sent via the network:
  (.../**S**/...) Data have been **s**ent completely
  (.../**SC**/...) Data have been sent and committed
  (.../**SV**/...) Data have been sent and checked
  (.../**S?**/...) Sending and checking data is pending
  (.../**Sf**/...) Sending and checking data has failed
  (.../**s**/...) Part of the data has been sent
  (.../ /...) No data have been sent.
- com/p/a/s/**e**/r/H - the fifth component states whether
  all (**E**/...),
  part (**e**/...) or
  none (/...)
  of the images of this patient, examination, or series have been **e**xported to data medium.

- com/p/a/s/e/**r**/H - the sixth part indicates whether
  all (**R**/...),
  a part of (**r**/...) or
  no (/...)
  images of this patient, study, or series have been imported into your local database via the network (**r**eceived).
- com/p/a/s/e/r/**H** - the seventh part indicates whether changes have been made to this record, i.e. whether a **h**istory of changes has been created (.../**H**)
  or not (.../).

➩ Note that capital or lower case letters indicate that *all* (capital letter) or some (lower case letter) of the data have been processed.

Entering the work status

Most of the entries in the work status abbreviation are made automatically as soon as a data record has been processed (e.g. an image has been exposed on film).

As a user, you can enter the following work statuses for studies and series in your local database:

❑ **com**/... (completed) - study has been completed
❑ **rea**/... (read) - the images have been reviewed by the physician
❑ **ver**/... (verified) - the images have been approved.

➪ The “completed” flag is set automatically.

✧ Call up **Edit > Set State** and select the work status that you want to assign.

Or

com rea ver

✧ Click on the relevant icon button on the tool bar.

➪ Please note that automatic data transfer might be triggered by assigning the “completed” status. If automatic data transfer has been defined at image level, you must trigger data transfer manually.
→ Page F.6–2, *Automatic data transfer*

➪ Assignment of a work status is not possible in the **Scheduler**.

Marking examination data

With the **Patient Browser** you can mark individual items of patient or examination data in order to find them and process them more quickly later on.

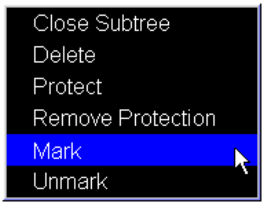
➩ With the **Filter** menu you can search for marked data specifically.
→ Page D.2–12, *Filtering data*

Marking items

✧ Select one or more patients, studies, series, or images in the navigation area or content area.

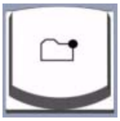
✧ Call up **Edit > Mark** in the main menu of the **Patient Browser** to mark the selected patient and examination data.

Or



✧ Open a popup menu in the navigation or content area with the right mouse key (or **Shift** + **F10**) and select **Mark**.

Or



✧ Press the **Mark** key on the symbol keypad (Num **3**).

Display of marked data

Mark Status
Prot/M

You can recognize marked patient and examination data in the content area by the list entry ’M’ in the **Mark Status** column.

Unmarking items

- Select the data which you want to unmark in the navigation or content area.
- Call up **Edit > Unmark**.

Or

- Remove the mark with **Unmark** in the popup menu (right mouse key or **Shift** + **F10**).

Performance documentation

After completion of an examination and all associated evaluations, you can document the work you have done in a performance report. This report can then be used, for example, for invoicing the costs.

Your system creates the performance report during patient registration. During examination and postprocessing of the examination results, the report is updated.

Editing the performance documentation

Before you conclude your work on the examination by archiving, check and add missing entries to the performance report.

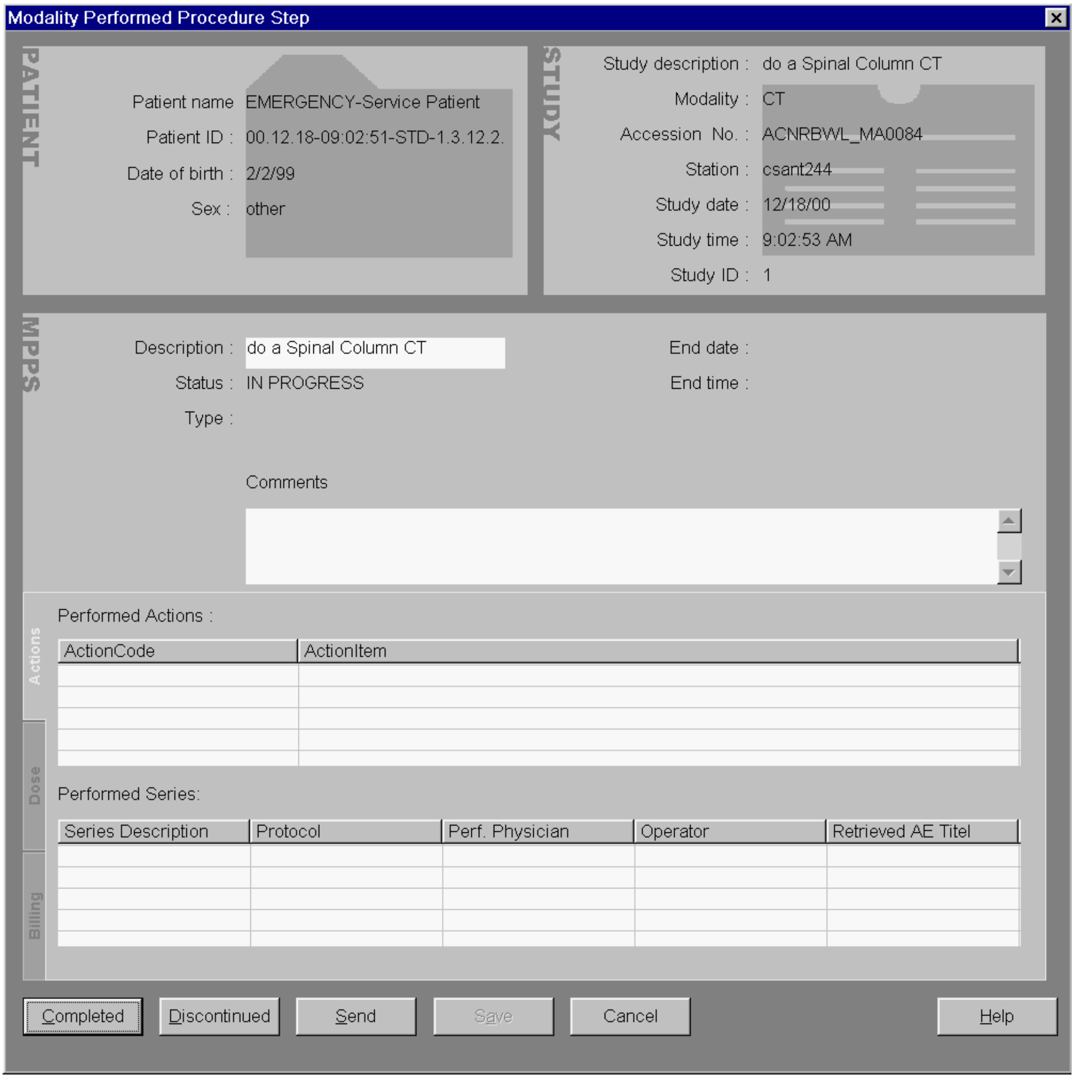
✧ Select the patient, the examination, or one of the associated series or images from the **Patient Browser**.

✧ Call up **Patient > Show MPPS**.

Or

✧ Click on the button on the toolbar.

The window **Modality Performed Procedure Step** is displayed.



Patient name EMERGENCY-Service Patient
Patient ID : 00.12.18-09:02:51-STD-1.3.12.2.
Date of birth : 2/2/99
Sex : other

Study description : do a Spinal Column CT
Modality : CT
Accession No. : ACNRBWL_MA0084
Station : csant244
Study date : 12/18/00
Study time : 9:02:53 AM
Study ID : 1

Description : do a Spinal Column CT
Status : IN PROGRESS
Type :
End date :
End time :

Comments

Performed Actions :

ActionCode	ActionItem

Performed Series:

Series Description	Protocol	Perf. Physician	Operator	Retrieved AE Titel

MPPS status

As soon as you select a series the **MPPS** status in the field **Status** is displayed. It consists of three parts (e.g. "COMPLETED"/"HIS"/"S"):

The first part provides information about the processing status:

- "IN PROGRESS" if **MPPS** is currently being processed,
- "COMPLETED" if **MPPS** is complete,
- "DISCONTINUED" if **MPPS** has been canceled,
- "OPEN" (at the **Patient/Study** level) if at least one **MPPS** has the status IN PROGRESS,
- "DONE" (at the **Patient/Study** level) if no **MPPS** has the status IN PROGRESS,
- " ", if no **MPPS** exists.

The second part describes the location at which the working step has been planned:

- "HIS", if the planned working step has been assigned via the HIS/RIS system,
- "LOC" if the working step has been planned locally,
- " ", if you are on the **Patient/Study** level.

The third part provides information about the work status in a message to the HIS/RIS-System:

- "s", if creation of the performance report has been successfully sent to the HIS/RIS system,
- "S" if COMPLETED/DISCONTINUED has been successfully sent to the HIS/RIS system,
- " " if you are on the **Patient/Study** level.

Checking data

✧ Check the entries for the patient and examination in the areas **PATIENT**, **STUDY**, and **MPPS**.

✧ Correct the data and enter a comment, if necessary.

➩ You cannot make entries in all fields.

Displaying Actions, Dose, Billing

In the lower part of the window **Modality Performed Procedure Step**, the examination data are listed on three subtask cards ordered by different aspects. You can select them by clicking on their tab.

Examination steps

✧ Click the **Actions** card into the foreground to display a list of the examination steps performed.

Dose information

✧ Click on the **Dose** card to display a list of the data in connection with the radiation exposure (e.g. applied dose).

Cost information

✧ Click on the **Billing** card for a cost-related statement of the services rendered and the materials consumed (film sheets).

Printing, sending, concluding a report

If all data in the performance report are entered correctly, you can close the report and therefore also the examination. If further working steps are planned, you can save the report temporarily and conclude it later.

Depending on operational requirements, you can print out the report or pass it on to the HIS/RIS system.

Saving

✧ Click on the **Save** button to save your changes to the report.

The examination has not yet been concluded.

Or

Concluding

✧ Click on the **Completed** button to conclude the report and the examination.

A message indicating this is sent to the HIS/RIS system, if connected.

➩ You cannot make any further changes to the performance report.

Or

Exiting as discontinued

✧ Click on the **Discontinued** button if you do not want to continue examination.

The report is also concluded and a message indicating that is sent to the HIS/RIS system, if connected.

➩ You cannot make any further changes to the performance report.

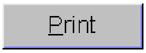
Or

Sending to the HIS/RIS

✧ Click on the **Send** button to mark the report as "in progress" and pass it on the HIS/RIS system.

Or

Printing out



✧ Click on the **Print** button to print out the performance report on a connected printer.

Closing the performance report without saving

The **Modality Performed Procedure Step** window is automatically closed if you conclude, save, or send a report. If you have only opened the report to print it out or view it, close it without changes.

☒

✧ Click on **Close window** to exit the dialog box.

Deleting data

If an examination has been completed and all the examination results and images have been reviewed and commented, you can archive the data and then delete it from the database.

> **NOTE**
>
> When you have archived data on MOD you should remove the MOD from the drive first, before you start deleting this data from the local database.

✧ Select the data that you want to delete in the navigation area or content area.

➪ You can also select raw data for deletion explicitely, e.g. if recon tasks have been planned for a series which you do not need to reconstruct again.
→ Page D.2–10, *Selecting raw data*

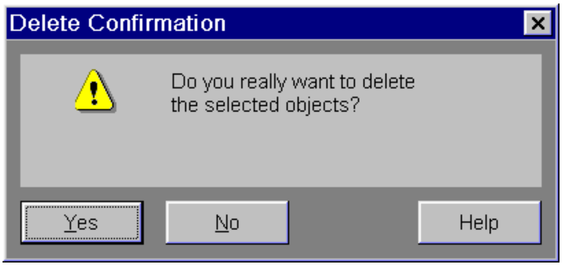
✧ Call up **Edit > Delete** in the main menu of the **Patient Browser** or open a popup menu and select **Delete** there.

Or

✧ Click on the button on the tool bar.

➪ Please note that you cannot delete data objects stored on MOD with the menu **Edit > Delete**. It is only possible to delete the entire page of a MOD by formatting.

A dialog box appears in which you can again confirm that you really want to delete the data you have selected.



Do you really want to delete the selected objects?

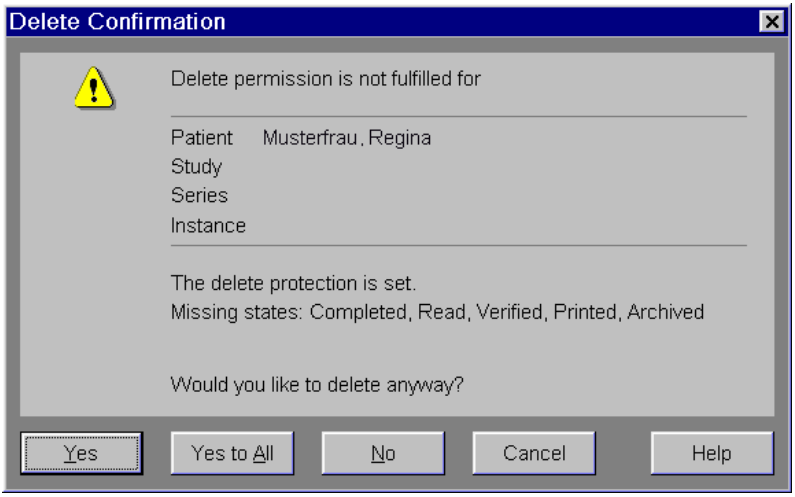
✧ Confirm the question with **Yes** to delete the selected patient and examination data.

➪ You can turn this confirmation dialog box off in **Browser Configuration**. After that, unprotected data will always be deleted immediately without confirmation.
→ Page D.7–2, *General settings*

➪ If the data have been delete-protected expressly or because of their work status, a dialog box to that effect appears.
→ Page D.5–18, *Deleting data with missing work status*

Deleting data with missing work status

If you attempt to delete data for which the work status does not allow deletion, a message box is displayed.



Delete permission is not fulfilled for

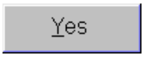
Patient Musterfrau, Regina
Study
Series
Instance

The delete protection is set.
Missing states: Completed, Read, Verified, Printed, Archived

Would you like to delete anyway?

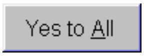
In this message box you can see why you cannot delete the selected data. For example, because it is first necessary to perform a number of processing steps before it can be deleted.

➪ In the **Browser Configuration** you can define in which work status you are allowed to delete data.
→ Page D.7–2, *General settings*



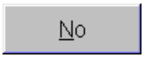
✧ Click on **Yes** to delete the data record stated in the message box despite the missing states.

Or



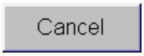
✧ Click on **Yes to All** if you have selected more than one data record for deletion and you want to delete all the records regardless of their work status.

Or



✧ Click on **No** in order not to delete the data record stated in the message box.

Or



✧ Click on **Cancel** to cancel deletion.

Protecting data from deletion

You can protect patient and examination data from accidental deletion.

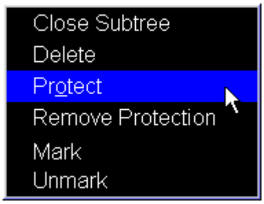
✧ Select the data that you want to protect against deletion in the navigation or content area.

✧ Call up **Edit > Protect** in the main menu of the **Patient Browser**.

Or

✧ Click on the icon button on the tool bar.

Or



✧ Select **Protect** in the popup menu (right mouse key or **Shift** + **F10**).

You can now no longer simply delete the selected data. Delete protection always includes all lower data levels and the related entries of the higher data levels. For example, if you protect a study entry you can no longer delete the individual images of that study nor the patient entry.

⇨ Data that you have assigned delete protection to, are protected from both moving and correction.
→ Page D.4–8, *Moving data*
→ Page D.4–2, *Correcting patient or examination data*

Display of delete-protected data

Mark Status

Prot/M

Patient and examination data that are assigned delete protection can be identified by the list entry ’prot’ in the **Mark Status** column in the content area.

Removing delete protection

If you want to correct, move, or delete data without a message box being displayed, you must remove the delete protection again.

✧ Call up **Edit > Remove Protection** in the main menu or **Remove Protection** in the popup menu to remove the delete protection.

Or

✧ Click on the icon button in the tool bar.

CHAPTER
D.6

Archiving, passing on, or filming data

To backup data and to reduce the amount of data stored in the local database you should archive patient and examination data at regular intervals. For archiving you can equip your system with a MOD drive or a CD burner, or connect the system to a central archive via the network.

If your system is connected to a network, you can transfer examination data to other workstations. If your system is equipped with the appropriate drive, you can also export data to data media in order to pass them on.

To process or otherwise use images with other applications, you export them into the file system.

Finally you can use the **Patient Browser** to film images for documentation or reporting.

Select the required patient and examination data in the navigation area or content area of the **Patient Browser** window. After that start archiving, sending, or filming with the appropriate menu item or by using the tool bar.

Archiving data

With the function **Archive To...** you can save patient and examination data to local exchangeable data media (to MOD = magneto optical disk or CD-R = CD recordable) or to an archive via the network.
→ Chapter F.2, *Archiving data*

Inserting an MOD or CD-R

✧ Insert the required medium into the drive.

✧ If necessary, format and rename a new MOD in the dialog automatically displayed.
→ Page F.2–8, *Labeling an MOD*

✧ Select the data that you want to archive in the navigation or content area of the **Patient Browser**.

Standard MOD

✧ Call up **Transfer > Archive To MOD**.

Or

✧ Click on the icon button.

The data are archived on the default MOD drive.

✧ After archiving, click on the drive icon concerned in the navigation area to ensure that all data were copied to the MOD.

Standard CD-R

✧ Call up **Transfer > Archive To CD-R**.

Or

✧ Click on the icon button.

The data are selected for archiving on CD-R.
Depending on the configuration of your system, archiving is performed in single-session mode or in multi-session mode.
→ Page F.2–15, *Archiving to a single session CD-R*
→ Page F.2–22, *Archiving to multi session CD-R*

Selecting a destination (MOD, CD-R, or archive)

✧ Call up **Transfer > Archive To...**.

Or

✧ Click on the icon button.

✧ Select the archiving destination you require in the **Archive To** dialog box.

Archive

✧ Click on **Archive** to archive the data on the selected destination.

Burning a CD-R

The actual procedure for storage to CD-R, recording a CD-R, starts automatically or can be triggered manually.
→ Page F.2–18, *Starting the write operation automatically*
→ Page F.2–19, *Starting the write operation manually*

Passing on data

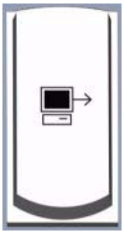
Transfer of examination data (e.g. to other workstations for evaluation) is possible both via the hospital's network and by data medium.

Sending via the network

If your system is connected to a network, you can send patient and examination data to other workstations via the network with the **Send To...** function.
→ Page F.3–2, *Sending in the network*

✧ Select the patient, study, series or the images in the navigation area or content area.

Standard address

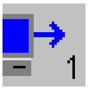


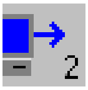
✧ Press the **Send To Node 1** key on the symbol keypad.

Or

✧ Call up **Transfer > Send To Node 1** or **Transfer > Send To Node 2** to send the data to one of the preconfigured addresses in the network.

Or





✧ Click on one of the two icon buttons on the tool bar.

The data are sent to the selected address.

Selecting a destination

✧ Call up **Transfer > Send To....**

Or

✧ Click on the appropriate button on the toolbar instead.

✧ Select the network address(es) you require in the **Send To** dialog box.

Send

✧ Click on **Send** to send the selected data to the required address(es).

Exporting to data medium

If there is no network connection, you can write the data to a data medium (MOD or CD-R) with the function **Export To...** in order to pass them on.
→ Page F.3–5, *Exporting to data medium*

✧ Select the required data in the navigation or content area.

✧ Call up **Transfer > Export To...**

✧ Select the data medium you require in the **Export To** dialog box.

Export

✧ Click on **Export** to save the data on the selected data medium.

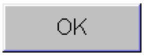
Exporting images to the file system

If you want to process images with other programs, you can export them to a defined directory on your system hard disk in certain image formats (**Export To Off-line**).
→ Page F.4–2, *Exporting images to the file system*

✧ Select the images for export and call up **Transfer > Export to Off-line**.

✧ Select the required directory in the **Export to Off-line** dialog box.

✧ Select the required image format (DICOM, TIFF, bitmap, or JPEG).



✧ Click on **OK** to save the selected images as individual files.

Filming

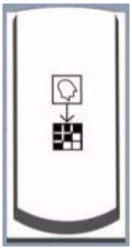
You can use the **Patient Browser** to send single images or all images of one or more patients, studies or series to the **Filming** task card.

Transferring images to Filming

✧ Select the data in the navigation or content area.

✧ Call up **Patient > Copy to Film Sheet** or click on the icon button.

Or



✧ Press the **Copy to Film Sheet** key on the symbol keypad.

Or

✧ Click the **Filming** card to the top of the stack and double-click on the entries that you want to film in the **Patient Browser**.

Or

✧ Drag the selection to the **Filming** task card with the mouse (**drag & drop**).
Just like loading the images into the **Viewing** task card you can determine in which segment of the film sheet the images are to appear.
→ Page D.3–5, *Drag & drop*

With one of the above commands, all the selected images are transferred to the **Filming** task card. Depending on whether **Auto Expose** has been activated there, the images are exposed on film immediately, as soon as a film sheet is full, or they are first collected in a film job.
→ Chapter G.2, *Automatic/Manual Filming*

Film preview

✧ Call up **Patient > Film Preview** to view a preview showing how the images will be filmed or printed.

Or

✧ Click on the **Film Preview** icon button on the tool bar.

Exposing images on film

You can expose or print a patient's images that you have collected in a film job from the **Patient Browser**. To do that you do not have to switch to the **Filming** task card first.

✧ Call up **Patient > Expose Film Task** to transfer all images in the film job to the camera or printer.

Or

✧ Click on the icon button on the tool bar.

➩ If you have transferred more than one patient's images to the **Filming** task card so that more than one film job exists, a dialog box is displayed. In this dialog box you can select the film job you wish to expose on film or print on paper.
→ Page G.2–9, *Exposing a film job*

➩ You cannot expose "multiframe images" directly from the **Patient Browser**. You must first load them into the **Viewing** task card.
→ Page E.7–12, *Filming/printing images*

Film Task Status

You can obtain an overview of all film jobs that have already been sent to a camera or printer and, for example, change the sequence in which they are to be processed.
→ Page G.5–3, *Viewing and manipulating film jobs*

✧ Call up **Patient > Film Task Status** to display the **Film Job Status** dialog box with a list of all pending film jobs.

Or

✧ Click on the icon button on the tool bar.

CAUTION

When a MOD is formatted all the data stored on it is lost irretrievably!

CHAPTER
D.7

Configuring the Patient Browser

With the **Browser Configuration** dialog box you can adapt the **Patient Browser** to your method of working.

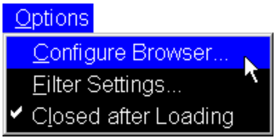
You can change the following settings:

❏ General settings such as the layout of the tool bar and the display of the work status.

❏ The hierarchical view of the information levels (patient, study, series, image) in the navigation and content area.

❏ The display of the individual information levels (study, series, image) in the content area.

❏ Selection of user-defined applications in the **Private Applications** menu (you can call up the corresponding configuration window directly in the **Private Applications** menu).



✧ Call up **Options > Configure Browser...** in the menu bar of the **Patient Browser**.

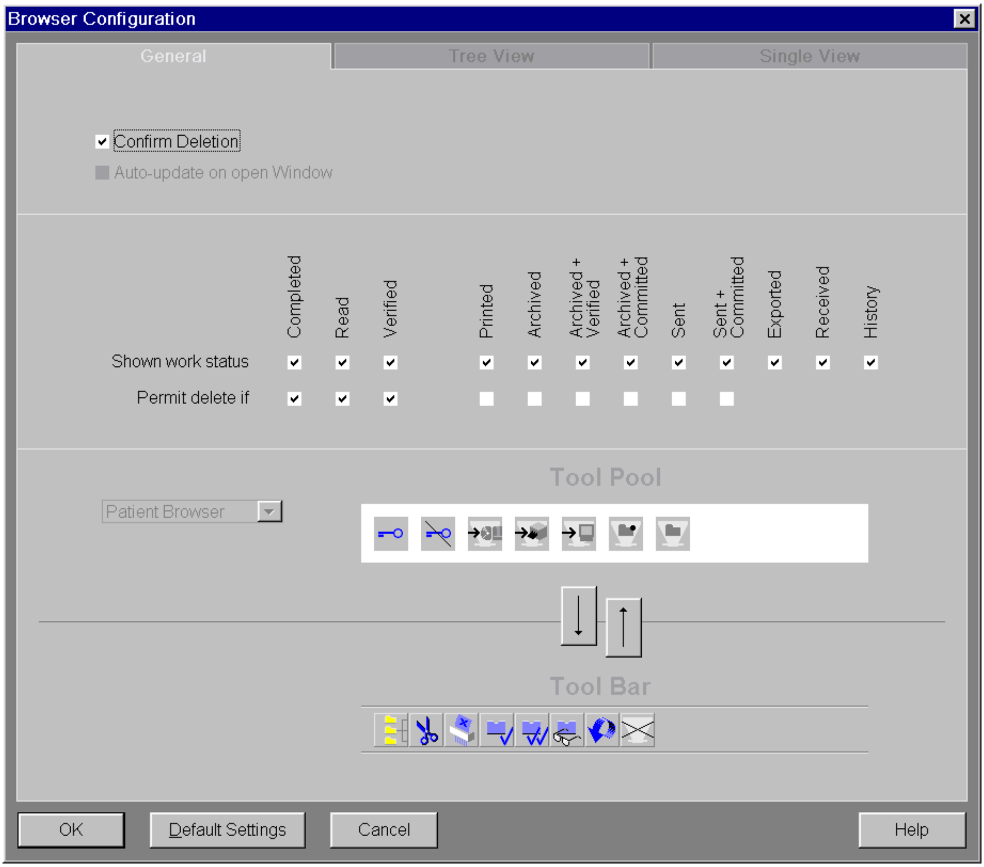
The **Browser Configuration** window with the three tab cards **General**, **Tree View** and **Single View** is displayed.

➪ In the **Basics** part of this manual you can read how to call up and exit configuration windows, save changes, or reset settings back to the as-delivered state.
→ Chapter A.2, *Configuring the User Interface*

General settings

On the **General** tab card you can configure the tool bar of the **Patient Browser**, define which work status is displayed for the examination data, and set the influence of the work status on delete permission.

✧ Click the **General** tab card into the foreground to activate this card.



☑ Confirm Deletion
☐ Auto-update on open Window

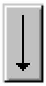
	Completed	Read	Verified	Printed	Archived	Archived + Verified	Archived + Committed	Sent	Sent + Committed	Exported	Received	History
Shown work status	☑	☑	☑	☑	☑	☑	☑	☑	☑	☑	☑	☑
Permit delete if	☑	☑	☑	☐	☐	☐	☐	☐	☐			

Tool bar

You can place buttons for the functions of the **Patient Browser** that you require frequently on the tool bar and remove rarely-used functions.

➪ In a later software version you can also configure functions of other applications in the **Patient Browser** tool bar by using the application selection list (dimmed in this version).

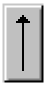
✧ Select an action that you want to place as an icon button on the tool bar from the **Tool Pool**.



✧ Click on the down arrow to place the button on the **Tool Bar**.

✧ Repeat this step until the **Tool Bar** contains all the buttons you require.

✧ If you want to remove an icon button from the tool bar, select the corresponding action on the **Tool Bar**.



✧ Click on the up arrow to remove the button from the **Tool Bar**.

Work status

In the middle part of the **General** tab card you can define which work status is displayed in the content area for the examination data and in which processing state data is released for deletion.

Display of work status

	Completed	Read	Verified	Printed	Archived	Archived + Verified	Archived + Committed	Sent	Sent + Committed	Exported	Received	History
Shown work status	☑	☑	☑	☑	☑	☑	☑	☑	☑	☑	☑	☑
Permit delete if	☑	☑	☑	☐	☐	☐	☐	☐	☐			

✧ Select the check box for a work status if you want this work status to be displayed in the content area of the **Patient Browser**.

➪ You will find information about the work status on
→ Page D.5–2, *Defining the work status*

Delete authorization

Permit delete if	☑	☑	☑	☐	☐	☐	☐	☐	☐

✧ Select the check box of a work status. Data without this status cannot be deleted without explicit confirmation in a message box.

Delete confirmation

The default setting is to have your system display a confirmation window before each deletion even if the data concerned have already reached the work status required for deletion. This further reduces the risk of data being deleted accidentally. You can activate and deactivate this confirmation in the configuration.


☑ Confirm Deletion

✧ Click on the **Confirm Deletion** check box to have a confirmation box displayed every time before data is deleted.

A check mark in the check box shows that deletion confirmation is activated.

Or

✧ Deselect the check box to suppress the confirmation for deletion.

CAUTION

Source of danger: Deletion confirmation activated

Consequence: Loss of data possible

Measure: Do not deactivate deletion confirmation

Hierarchical view in the navigation and content area

On the **Tree View** tab card you can define what information is listed in the content area of the **Patient Browser** in the hierarchy levels (e.g. patient). You can also hide hierarchy levels in the navigation and content areas. You can also configure the icon display of series and images.

✧ Click the **Tree View** tab card into the foreground.

Selecting a database

✧ Select **Scheduler** to define the display of preregistered patient data in the **Patient Browser**.

Or

✧ Pick **Database** from the selection list of databases to configure the local database view.

➪ The names and information that appear on the card **Tree View** for the different data levels differ depending on the database that you have called up (e.g. **Study** in the local database corresponds to **Procedure** in the scheduler).

Selecting a data level

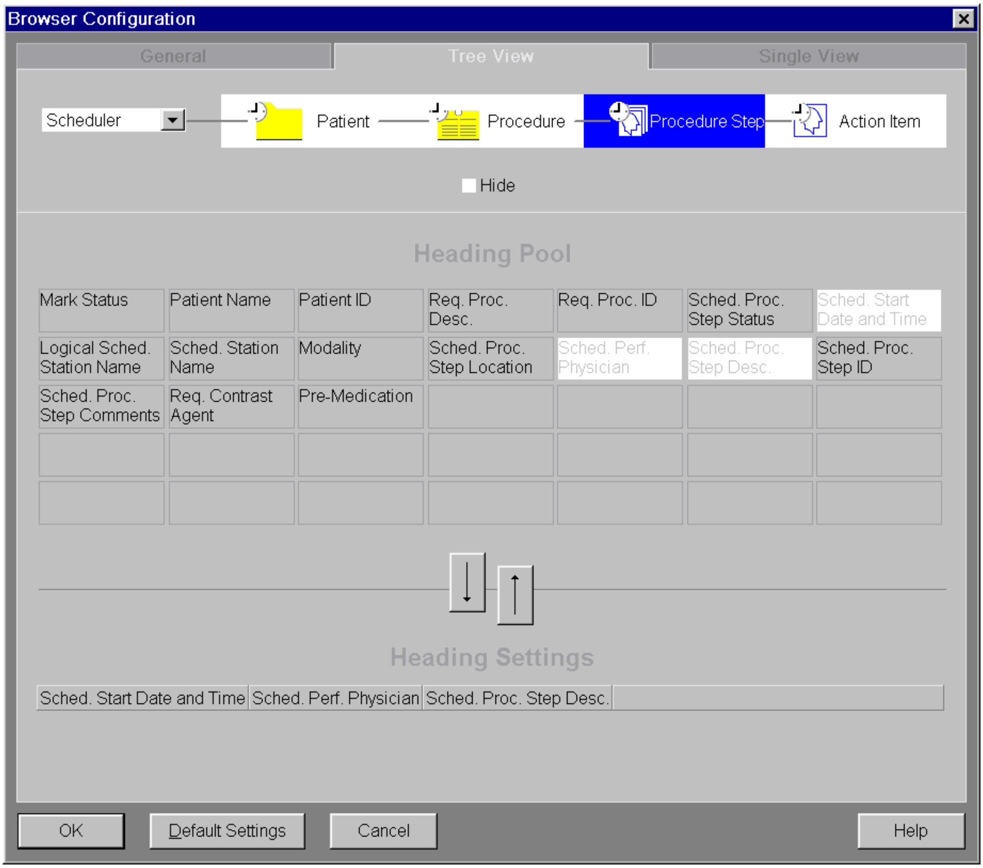
✧ Select the hierarchy level **Patient**, **Procedure**, **Procedure Step** or **Action Item** in the scheduler.

Or

✧ Select the hierarchy level **Patient**, **Study**, **Series** or **Instance** in the local database

➪ The **Tree View** tab card differs slightly depending on the hierarchy level selected. On the **Series** level the **Modality** selection list is also displayed. On the **Instance** level the selection list **Data Type** appears instead.

Example: Data level Procedure Step/Scheduler



Scheduler

☐ Hide

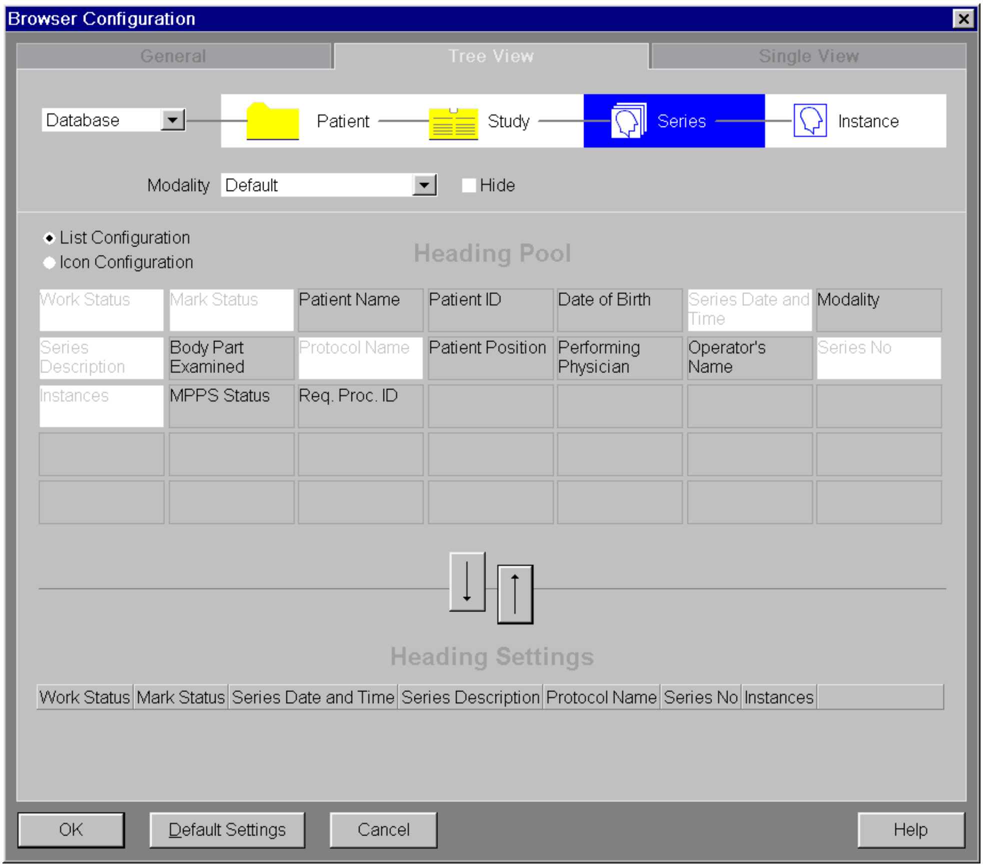
Heading Pool

Mark Status	Patient Name	Patient ID	Req. Proc. Desc.	Req. Proc. ID	Sched. Proc. Step Status	Sched. Start Date and Time
Logical Sched. Station Name	Sched. Station Name	Modality	Sched. Proc. Step Location	Sched. Perf. Physician	Sched. Proc. Step Desc.	Sched. Proc. Step ID
Sched. Proc. Step Comments	Req. Contrast Agent	Pre-Medication				

Heading Settings

Sched. Start Date and Time	Sched. Perf. Physician	Sched. Proc. Step Desc.

Example: Data level Series / Local database



Database

Modality Default ☐ Hide

● List Configuration

○ Icon Configuration

Heading Pool

Work Status	Mark Status	Patient Name	Patient ID	Date of Birth	Series Date and Time	Modality
Series Description	Body Part Examined	Protocol Name	Patient Position	Performing Physician	Operator's Name	Series No
Instances	MPPS Status	Req. Proc. ID				

Heading Settings

Work Status	Mark Status	Series Date and Time	Series Description	Protocol Name	Series No	Instances	

List entries

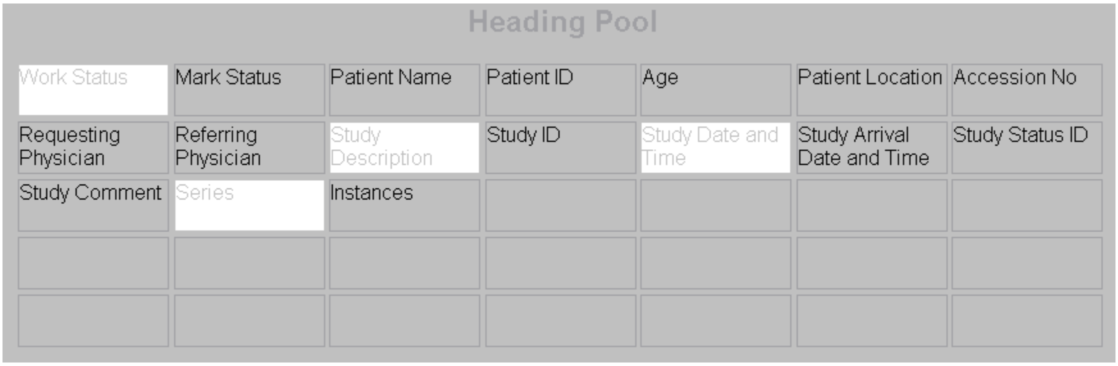
You can make the content area of the **Patient Browser** clearer by having your own selection of information listed.

Adding list entries

✧ In the **Heading Pool** select which entries you want to have displayed in the content area.

➪ Select the entries in the sequence in which you want to have them displayed.

➪ For detailed description of the **Heading Pool** entries please refer to
→ Chapter P.2, *Parameter Glossary*.



Heading Pool

Work Status	Mark Status	Patient Name	Patient ID	Age	Patient Location	Accession No
Requesting Physician	Referring Physician	Study Description	Study ID	Study Date and Time	Study Arrival Date and Time	Study Status ID
Study Comment	Series	Instances				

↓

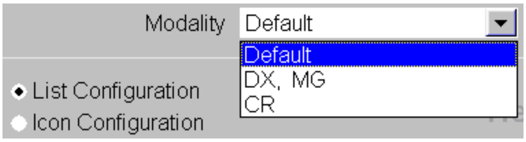
✧ Click on the down arrow to place the entry in the **Heading Settings** for the table in the content area.

✧ Repeat this step until the table contains all the required entries in the content area.

➪ If an entry is dimmed in the **Heading Pool** it is already contained in the **Heading Settings** and vice versa.

Modality-specific entries

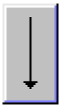
In series (local database), the information displayed in the content area is modality dependent. Depending on the modality you can also define specific entries in the content area.



✧ Select a modality on the data level **Series** if you want to create list entries in the content area.

Or

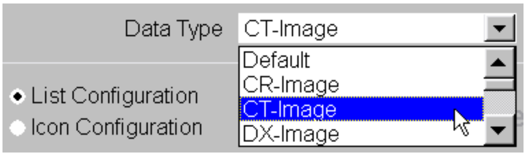
✧ Select **Default** to define the information to be displayed with series of different modalities, or for which no modal-specific settings can be made.



✧ Transfer the required list entries from the **Heading Pool** to the **Heading Settings**.

Data type specific entries

The list display of images in the content area depends on the data type. You can select the list entries specifically for each data type from the relevant **Heading Pool**.



Data Type: CT-Image

● List Configuration

○ Icon Configuration

✧ Select a data type on the **Instance** data level if you want to create list entries in the content area specifically for the images of that data type.

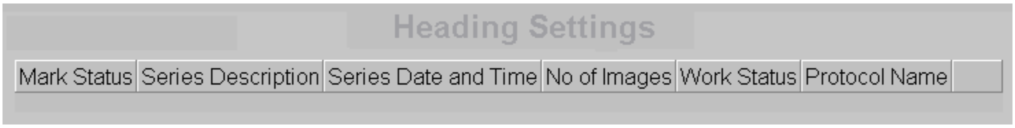
Or

✧ Select **Default** to define which information is to be displayed in the content area for images of different data types, or for which no data type specific settings can be made.

↓

✧ Transfer the required list entries from the **Heading Pool** to the **Heading Settings**.

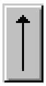
Removing list entries



Heading Settings

Mark Status	Series Description	Series Date and Time	No of Images	Work Status	Protocol Name

✧ Select an entry in the **Heading Settings** if you want to remove it from the table.



✧ Click on the up arrow to remove the entry from the table in the content area.

Hiding data levels

You can define which of the hierarchy levels, study, series, or instance you want displayed in the navigation and content area.

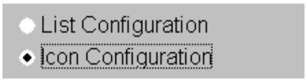
☑ Hide

✧ Click on the **Hide** check box to hide this data level.

List display / image stamp display

For display of series and images in the content area you can choose between display as a list and display as image stamps (icons). You can label the image stamps with up to two entries. To assign these entries proceed exactly as for definition of the list entries in the content area.

→ Page D.7–10, *List entries*

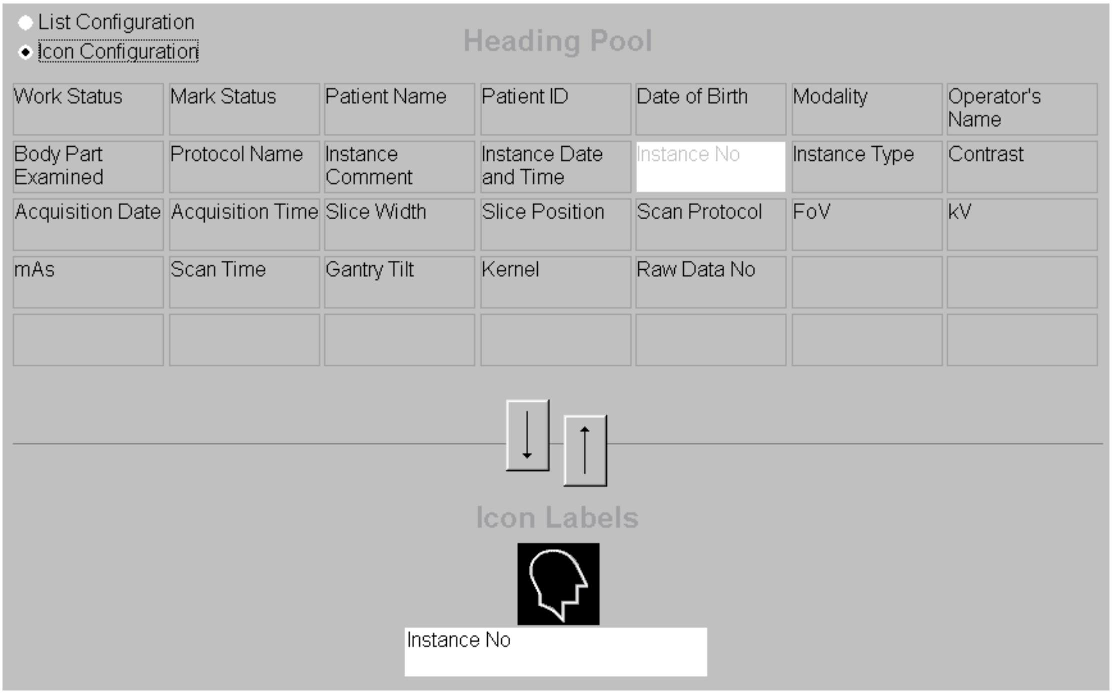


○ List Configuration

● Icon Configuration

✧ Click on the **Icon Configuration** option button.

✧ Select the entries in the **Heading Pool** with which you want to label the entries for series and images and click on the down arrow. The entries now appear in the **Icon Labels** box.



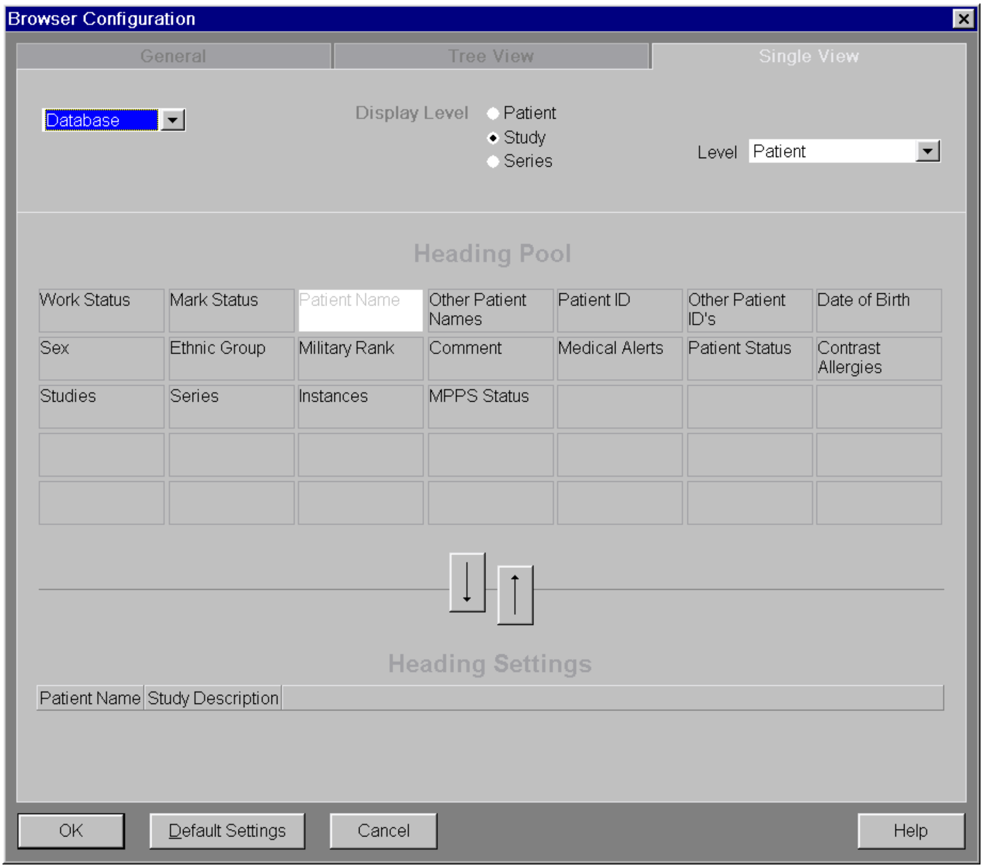
○ List Configuration

● Icon Configuration

Single view of the content area

In the card **Single View**, define to which hierarchy level data are to be displayed if the navigation area is hidden. Each data entry is displayed in exactly one line.

✧ Click the **Single View** tab card into the foreground and select the database you want to configure.
→ Page D.7–6, *Selecting a database*



Database

Display Level ○ Patient ● Study ○ Series

Level Patient

Work Status	Mark Status	Patient Name	Other Patient Names	Patient ID	Other Patient ID's	Date of Birth
Sex	Ethnic Group	Military Rank	Comment	Medical Alerts	Patient Status	Contrast Allergies
Studies	Series	Instances	MPPS Status			

Patient Name | Study Description

Setting the data level

In the single view, the content area always shows the same data level.

✧ Select the data level that you want to have displayed when switching from the **Tree View** to the **Single View** in the content area.

It depends on the data level that you have set for the single view of the content area what information can be displayed about the list entries. For example, if you have set the **Series** level to be displayed, you can have information from the levels patient, study, and series displayed in the list of series.

Combining list entries

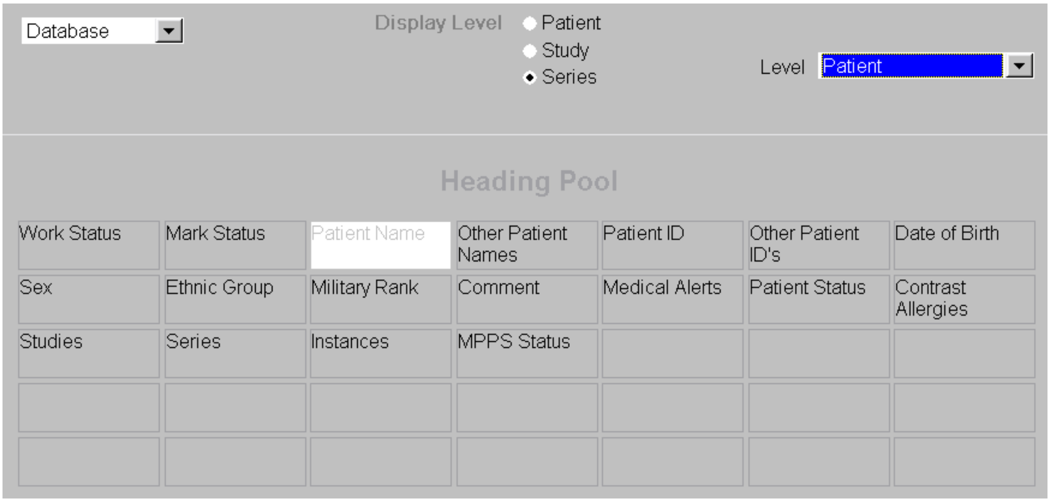
You can configure the single view of the content area in a similar way as the hierarchical view of the navigation and content area.
→ Page D.7–6, *Hierarchical view in the navigation and content area*

You can combine list entries of different information levels by varying the data level for the pool in the **Heading Pool** from which you then select the required entries.

✧ Define the data level in the selection list from which you want to take list entries for the content area in the **Heading Pool**.

The **Heading Pool** now contains all the possible list entries from the selected information level.

➪ For detailed description of the **Heading Pool** entries please refer to
→ Chapter P.2, *Parameter Glossary*.



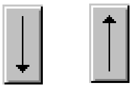
Database

Display Level ○ Patient ○ Study ● Series

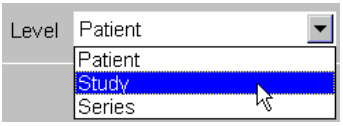
Level Patient

Heading Pool

Work Status	Mark Status	Patient Name	Other Patient Names	Patient ID	Other Patient ID's	Date of Birth
Sex	Ethnic Group	Military Rank	Comment	Medical Alerts	Patient Status	Contrast Allergies
Studies	Series	Instances	MPPS Status			



✧ Click on a list entry in the **Heading Pool** and move it into the **Heading Settings** with the arrow down key or remove a list entry from the **Heading Settings** with the arrow up key.



Level Patient

Patient
Study
Series

✧ Now select another **Level**, if necessary, to place list entries of another data level from the **Heading Pool** into the **Heading Settings**.

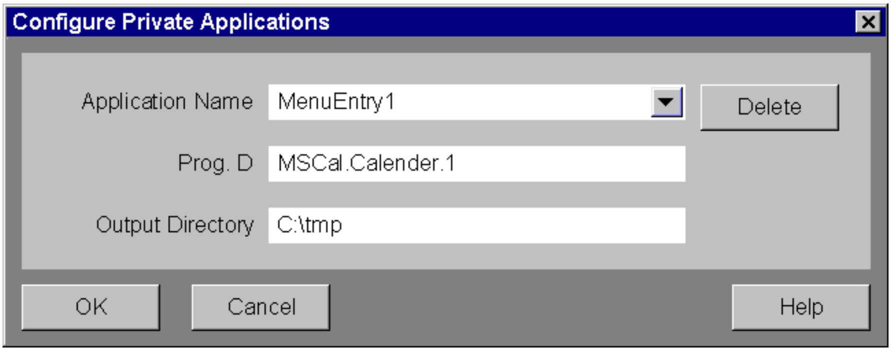
➪ For the **Series** data level, you can set up modality- or data type-specific list entries for the content area.
→ Page D.7–11, *Modality-specific entries*
→ Page D.7–12, *Data type specific entries*

Configuring user-defined applications

Via the menu **Private Applications** in the **Patient Browser** you can use other application programs for processing patient and examination data in your *syngo* system. You can set up these programs in the window **Configure Private Applications** for use in the *syngo* system.

✧ Call up **Private Applications > Configure...** in the main menu of the **Patient Browser**.

The dialog box **Configure Private Applications** is displayed.



Application Name: MenuEntry1

Prog. D: MSCal.Calender.1

Output Directory: C:\tmp

Adding a program

Application Name MenuEntry1

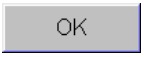
✧ Enter a program name by which you want to call the application in the *syngo* system in the future.

Prog.ID MSCal.Calender.1

✧ Enter the program ID under which the application program is registered on your computer.

Output Directory C:\tmp

✧ Enter the directory on your system hard disk to which the data are to be sent from the **Patient Browser**.



✧ Click on **OK** to add the application program to the menu **Private Applications**.

Removing a program

You can remove any programs from the menu **Private Applications** that you no longer want to call up from the *syngo* system.

✧ Call up **Private Applications > Configure...**.

✧ In the dialog box **Configure Private Applications**, select the application program in question from the **Application Name** selection list.

✧ Click on **Delete** and confirm with **OK** to remove the entry from the **Private Applications** menu.

PART
E

Viewing

E.1 *Introduction*

E.2 *Loading and Displaying Images*

E.3 *Scrolling and Selecting Images*

E.4 *Processing Images*

E.5 *2D Evaluation*

E.6 *Dynamic Image Postprocessing*

E.7 *Saving and Documenting Images*

E.8 *Configuring the Viewing Task Card*

CHAPTER

E.1 Introduction

On the **Viewing** task card, you can view the results of an examination and evaluate it or prepare it for diagnostics.

You can also use the **Viewing** task card to compare image material of different examinations and, depending of configuration, of different patients.

Loading and displaying images

You can first load the images using the **Patient Browser** or from the **3D** task cardinto the **Viewing** task card. Here you can select one of various ways of arranging the image material and displaying it in the clearest way for your diagnostic problem.

Processing and evaluating images

On the **Viewing** task card, you can then process and evaluate the images:

❏ You can change window values, enlarge, pan, rotate, and flip images.

❏ You can highlight regions of interest (ROIs) using drawing tools (circles, rectangles, lines), provide them with comment texts, and evaluate them statistically.

❏ You can display measured values for pixel points or ranges and measure distances and angles on the images.

Storing, filming and transferring images

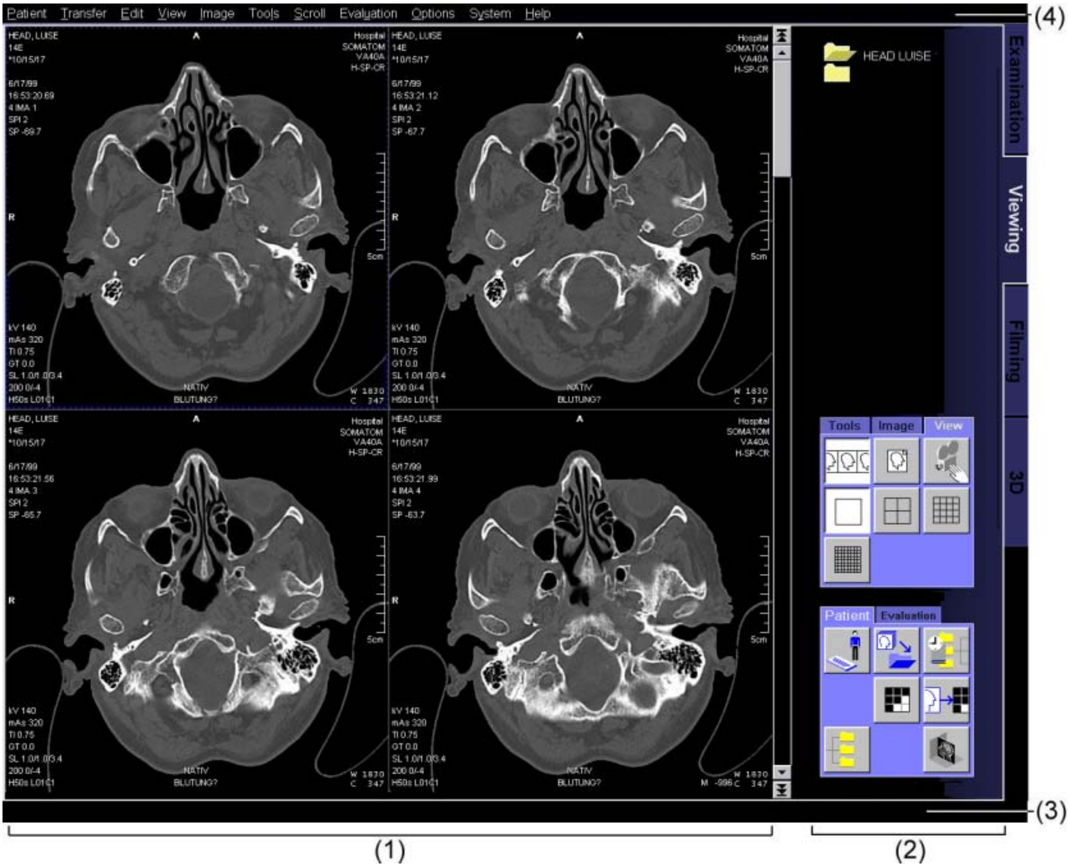
You can then save the images you have processed and evaluated, you can print them or expose them on film or send them to other locations in your hospital.

Calling up the Viewing task card

As soon as you have loaded images into the **Viewing** task card, the task card moves into the foreground. But you can also switch to other applications at any time and resume image processing on the **Viewing** task card later.

✧ If the **Viewing** task card is currently not in the foreground, click on the tab on the right-hand edge of the screen to activate the card.

The **Viewing** task card is divided into four main areas:



(1) Image area
(2) Control area
(3) Status bar for system messages
(4) Menu bar with specific entries for viewing and processing images

The image area

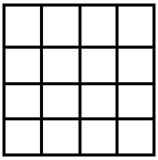
In the image area, the images that you have loaded into the **Viewing** task card are displayed. Depending on the division of the screen and the number of images loaded, you can only see some of the images. The remaining images are in the background.

Layout of the image area

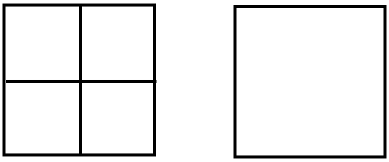
The image area is subdivided into segments. One image is displayed in each segment.

Depending on whether you want to see an overview of the loaded images, or whether you require a display which is suitable for reporting, you can choose between different layouts:

- In a small format layout, several images are displayed at once.
- In a large format layout, you can only see a few images on the screen, but these images are displayed large enough for you to see details.



Small format layout

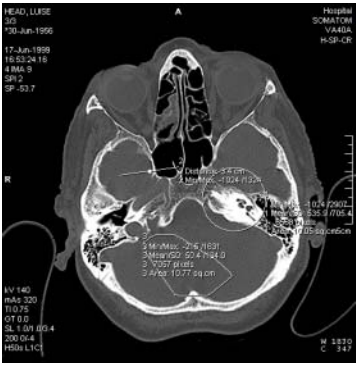


Large format layouts

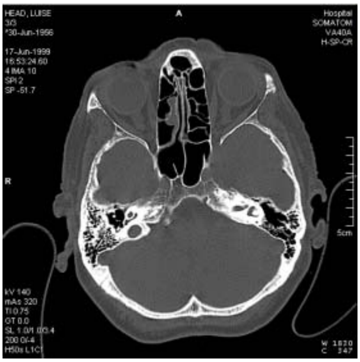
Image, text and graphic objects

In the image area, medical images are displayed. These may also contain text information that is stored in the system about the patient and the study.

The images can also be provided with graphics (ROIs, measurements etc.) and text comments as part of processing in the **Viewing** task card.



Medical image with text and graphic elements

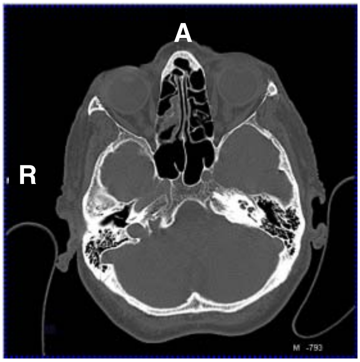


Medical image with study data displayed

Medical image without text and graphic elements

Image orientation

On each image, you can see orientation labels displayed at the edge of the image. They always show you the current image orientation, i.e. after rotation or mirroring, you can see immediately which side of the patient corresponds to which side of the image.



The letters have the following meanings:

- ❏ L stands for left
- ❏ R stands for right
- ❏ A stands for anterior
- ❏ P stands for posterior
- ❏ H stands for head
- ❏ F stands for feet

➪ For images that are not displayed in an anatomical standard view (e.g. oblique cuts), the orientation labels consist of two or three letters.
→ Page H.3–2, *The patient coordinate system*

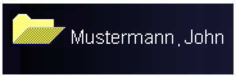
The control area

In the control area, you will find all the tools you need to select image material, arrange the screen display and process images.

Here you can also control data exchange with other parts of the program and call up other applications.

You can call up these functions easily using buttons and work much faster than via the menu bar.

Patient information



Mustermann, John

In the upper part of the control area, you can see the names of the patients whose images are currently loaded in the **Viewing** task card. Up to three patients (depending on the system configuration) can be loaded into the **Viewing** task card at one time.

Here you can select the image data of a patient you want to process next.

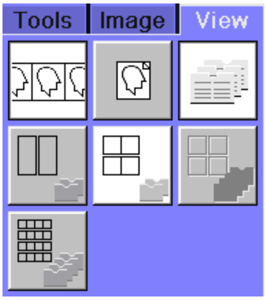
The open patient folder shows you whose images are currently visible in the image area.

➩ If you use the option for comparing examination data of different patients, this group folder is labeled with the names of the loaded patients (e.g. "Brown, Smith" if the group folder contains the data of two patients, or "Brown, Smith..." if it contains the data of three or more patients).

➩ For longer names only the first part is displayed.

Subtask cards

On the subtask cards, you can see the buttons which you use to call up the processing tools, define display modes, transfer image data and switch to other applications.

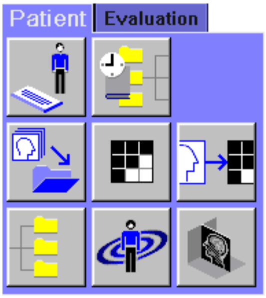


The stack of cards in the center of the control area contains the **Tools**, **Image** and **View** subtask cards.

❑ The left-hand card of the stack is called **Tools** and contains buttons for image evaluation and commenting.

❑ On the center card, **Image**, you will find buttons for image processing.

❑ The right-hand card, **View,** contains buttons for setting the layout.



On the **Patient** subtask card in the lower part of the control area, you will find buttons with which you can film/print images, for example after processing, or send images to other work stations for reporting. Here you can also call up **Patient Registration** or the **Patient Browser** directly.

CHAPTER
E.2

Loading and Displaying Images

In the **Viewing** task card, you can view and process examination images that are stored in the local database of your system, an archive medium or a network node.

In the **Patient Browser** window, you have access to this data. You can search for patients, studies, series or individual images and load them onto the **Viewing** task card.

You can also transfer series from the **Examination** task card to the **Viewing** task card immediately after an examination, automatically.
→ Page C.2–20, *Automatic loading into Viewing*

Moreover, you can view and process the images that you have generated in the **3D** task card and transferred to the **Viewing** task card.
→ Page H.12–3, *Transferring images to the Viewing task card*

Transferring images with the Patient Browser

You can search for image data that you have stored in the local database or in the archive using the **Patient Browser** and then load it onto the **Viewing** task card.

As soon as you load image material you decide whether you want to view or evaluate the images or series of one patient, or whether you want to compare the image material of different patients. You transfer a patient to a patient folder. If you want to compare the examination results of different patients you create a group folder.

⇨ You cannot load raw data, patients with unreconstructed raw data and reports into the **Viewing** task card.

Creating a patient folder

If you want to view and evaluate the images of a patient, transfer them to the patient folder on the **Viewing** task card.

✧ Place the **Viewing** task card into the foreground by clicking on the tab.

The task card is still empty at this point.

✧ Call up the **Patient Browser** (**Patient > Browser...**).

✧ Search for the required patient(s), study(s), series or one or more images in the navigation or content area.

✧ Double-click on the entry or entries that you were looking for and they will be loaded into the **Viewing** task card.

Or

✧ Select the entries and call up **Patient > Load to Viewing**, or click on the **Load to Viewing** button on the tool bar.

Or

✧ Drag your selection onto the **Viewing** task card with the mouse (drag & drop).

➪ Before you load the image data of a patient with **drag & drop**, you must first open a new (empty) patient folder. The images of any patient folder already open are otherwise removed from the **Viewing** card if this folder is not in Multi View Mode. If you **drag & drop** images into a folder (Multi View Mode) they are added to the existing ones.
→ Page E.2–9, *Load the folder*

➪ If the task card is not in the foreground you can also drag the images from the **Browser** onto the corresponding tab. The task card moves into the foreground and the images are loaded into the image area.

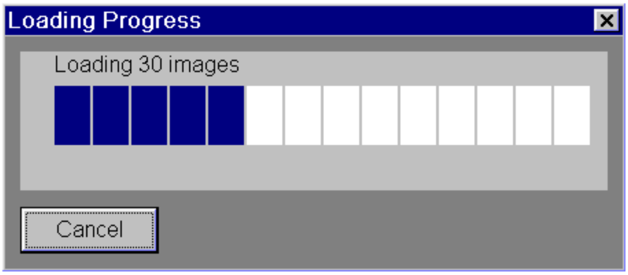
Close after loading

The **Patient Browser** will be closed if the **Closed after Loading** option has been selected.
→ Page D.3–7, *Closed after Loading*

➪ The **Browser** remains open when you load images by **drag & drop**.

Stopping loading

Loading a large series with very many images can take a long time. You can then see a progress indicator showing you how far the loading progress has progressed.



Loading 30 images

You can stop loading.

Cancel

✧ Click on the **Cancel** button.

The images of the new patient are now displayed in the **Viewing** task card grouped by series.

Loading color images

You can also load color images into the **Viewing** task card (True Color and Pseudo True Color). If the images cannot be displayed, you obtain an error message.

✧ Please contact your system administrator.

Loading images of another patient (configuration dependent)

Before you start evaluating the first loaded images, you can first transfer all the examinations and patients that you want to view and edit in a single session into the **Viewing** task card.

✧ Click on a closed patient folder in the upper control area of the **Viewing** task card to open it.

✧ Select the images of another patient from the **Patient Browser** and pull them onto the **Viewing** task card (**drag & drop**).

The new images are transferred to the opened folder. The patient name appears next to the open folder.

In the **Viewing** task card, you can manage up to two patients (configurable). If you load a third patient, the folder of the patient you opened first will be closed again. If you want to process the images of this patient again, you need to reload the images.

Loading additional images/ series

You can add more images, series, and examinations of the same patient to a patient folder at any time.

✧ In the **Viewing** task card, open the patient folder in which you want to load additional image material.

✧ Open the **Patient Browser** and select additional image material of the patient already loaded.

✧ Transfer those images with a double-click or with **Patient > Load to Viewing**, or click on the **Load to Viewing** button in the toolbar or load them by **drag & drop**.

The images are distributed to the patient folders in question by the program and appended to the image material contained in them (studies to studies, series to series and images to images).

➪ Images of series or studies that are already in the **Viewing** card are not loaded a second time. Instead, you receive the message: “Already loaded images skipped”.

Creating a group folder

If you want to compare the results of different patients in the **Viewing** task card, first create a group folder.

The name of this group folder consists of the name of the patient contained in it (Brown, Smith, ...).

Load the folder

✧ Open the **Patient Browser**.

✧ There, select all the patients, examinations, and series that you want to compare in the **Viewing** task card.

✧ Transfer that data by **drag & drop** to the **Viewing** card.

Or

✧ Transfer those images by double-click, or with **Patient > Load to Viewing**, or click on the **Load to Viewing** button in the toolbar.

The program automatically creates a group folder and switches to study comparison mode.

You can also load several patient data into an existing patient folder.

✧ Switch the folder to multi view mode.

✧ Load additional patient data by **drag & drop**.

These patient data are added to the existing data and the existing folder now turns into a group folder.

Displaying images and series

After you have loaded images into the **Viewing** task card, you can choose between different views.

In this way, you can arrange the display of the image material in the way which is most helpful for your diagnostic problem.

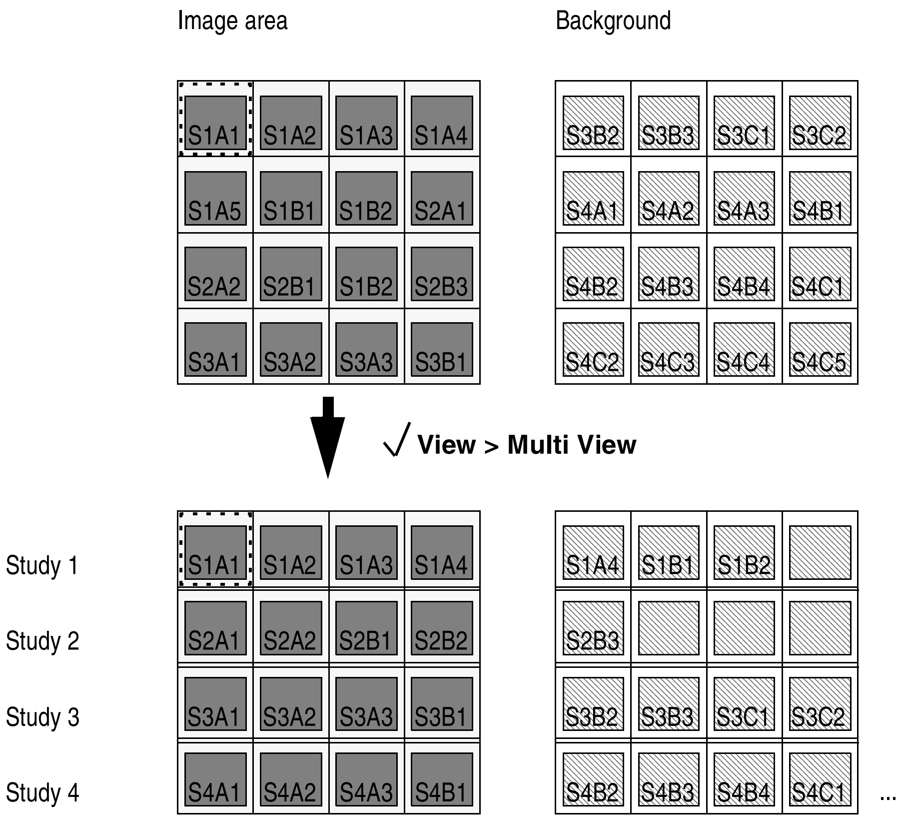
Normal mode or study comparison mode

If you have loaded several examinations of a patient in the **Viewing** task card, the images of those studies and series are first displayed one after the other, starting with the images of the first loaded study. If you want to view the images of further examinations, you must page to them.
→ Page E.3–2, *Scrolling*

If you want to compare the results of the various examinations you have loaded directly, you can switch from normal view mode to study comparison mode.

✧ Call up **View > Multi View** to activate study comparison mode.

In this view, the screen is subdivided into areas in which the results of different examinations are displayed one below the other.



✧ Deselect the option **View > Multi View**, or click on the button again to return to normal mode.

➩ If you created a group folder when you loaded your images, i.e. loaded the examinations of several patients in a folder, study comparison mode is already activated. In that case, you cannot switch to normal mode.

Image-stripe display or stack display

Medical images are always displayed in the image area of the **Viewing** task card grouped by studies or series.

Depending on whether you want to view or evaluate individual images of a series or whether you want to compare series with each other, you can select either image-stripe display or stack display.

You can switch from one view to another.

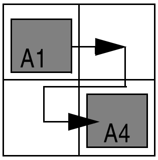
Image-stripe display

Select image-stripe display to view the loaded series of a study one after the other image by image.

✧ Call up **View > Stripe** to activate this display mode.

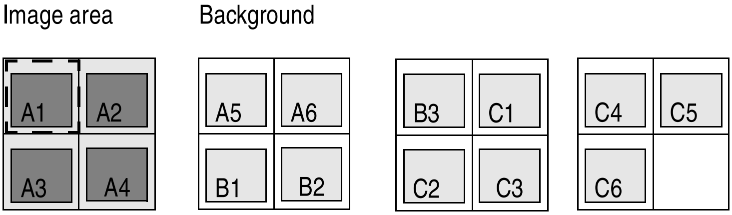
Or

✧ Click on the **Stripe** button on the **View** subtask card.



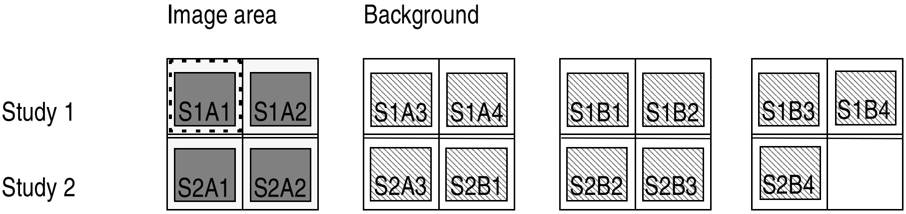
In **normal mode** you can now see the images of the first loaded series displayed in the image area from top left to bottom right.

If more than one series of a patient is loaded, you can see the first images of series A. To view the images of the other series, you must first scroll to them.



In **study comparison mode** you see the images of the examination first loaded in the first row, starting with the first image of the first series. In the second row, you see the images of the second examination etc.

All the images and series of an examination that can no longer be displayed from left to right in the image area, are placed in the background. To display those images, you must page to them.



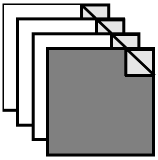
Stack display

If you want to **compare** the images of **various series** of one study, you best select stack display.

✧ Call up **View > Stack** to activate this display mode.

Or

✧ Click on the **Stack** button on the **View** subtask card.



All images of a series are now stored in a stack one on top of the other. You can see the first image of each series.

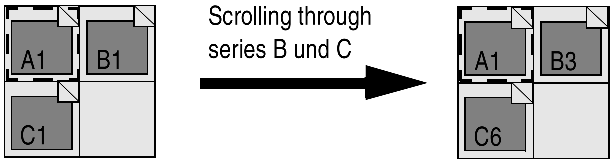
If more than one series of a patient is loaded in **normal mode**, the images of these series are arranged in stacks from top left to bottom right. Each stack has dog ears for scrolling.

✧ Click on the top or bottom (inner or outer triangle) of a dog ear to display the previous or next image of the stack.

This way you can compare any image of one series with any image of another loaded series.

Image area

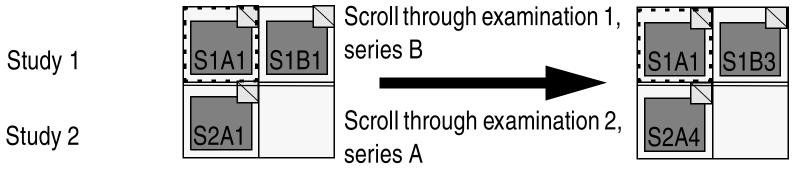
Image area



View when first called up

Possible display for comparison purposes

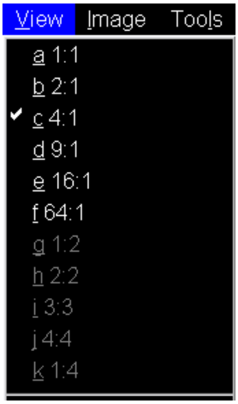
In **study comparison mode**, the loaded series of the various examinations are also stored in stacks. Here again, you can scroll through the series with the dog ears and compare different images with each other.



Division of the image area

With the division of the image area, you define the number and size of the segments in the image area.

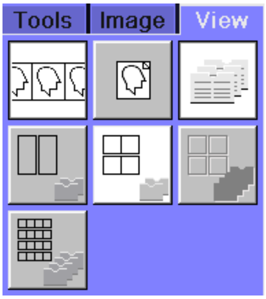
Switch to a large format display with just a few images on the screen if you want to see diagnostic details. Select a small format display to obtain an overview.



✧ Select a layout in the **View** menu.
The current layout is now marked with a checkmark.

Or

✧ Select a layout with the buttons on the **View** subtask card.

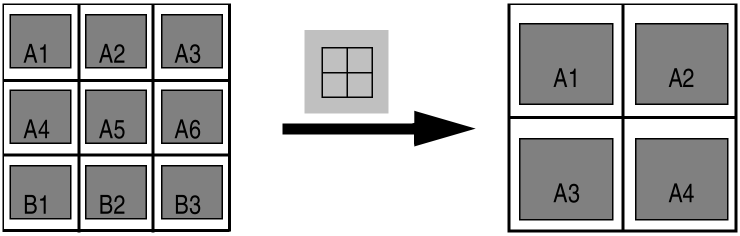


When you select a new layout, the division of the image area is changed, but the sequence of the images displayed remains the same.

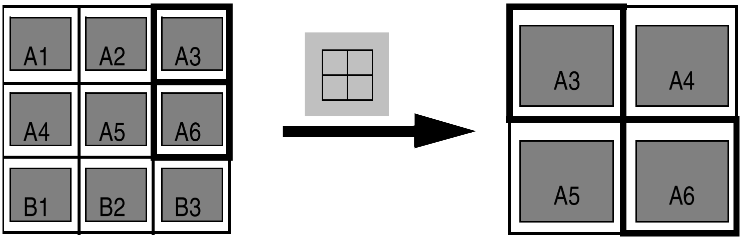
If you selected images before you selected a new layout, you will see the loaded images in the new view starting with the first selected image.
→ Page E.3–31, *Selecting images*

➪ In study comparison mode different layouts are used. The non-comparison layouts are dimmed.

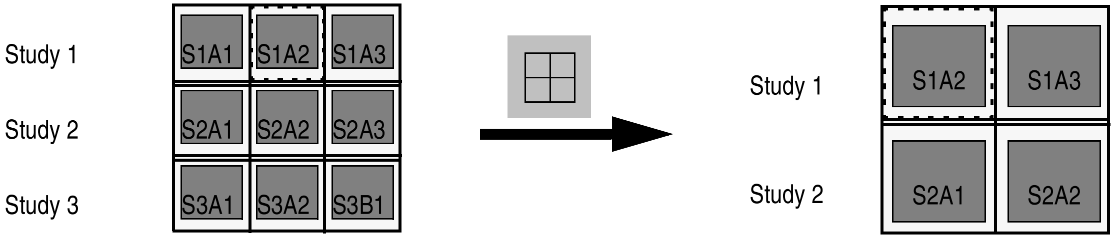
Layout change for image-stripe display



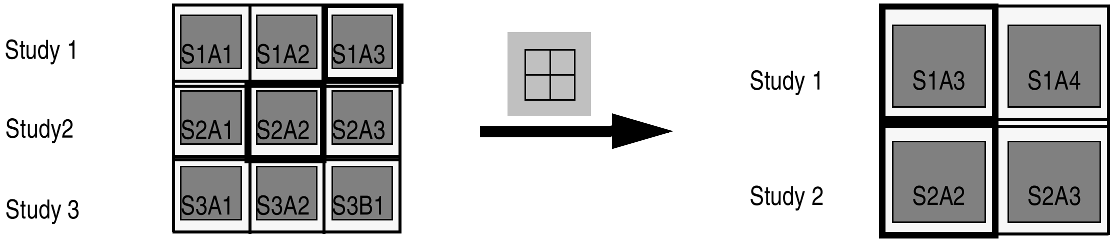
Layout change in normal mode without explicitly selected image
(with input focus)



Layout change in normal mode with explicitly selected image
Last selection A3 (no input focus)

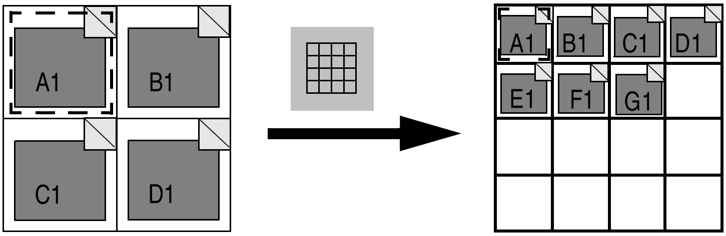


Layout change in study comparison mode without explicitly selected image (with input focus)

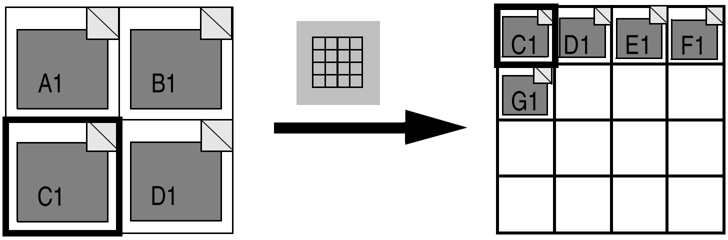


Layout change in study comparison mode after explicit selection of images (without input focus)

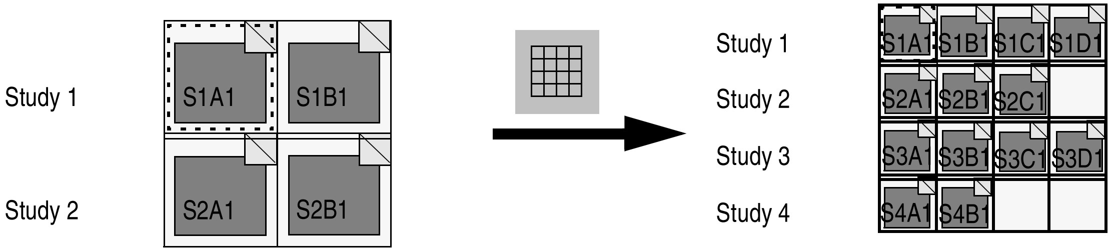
Layout change for stack display



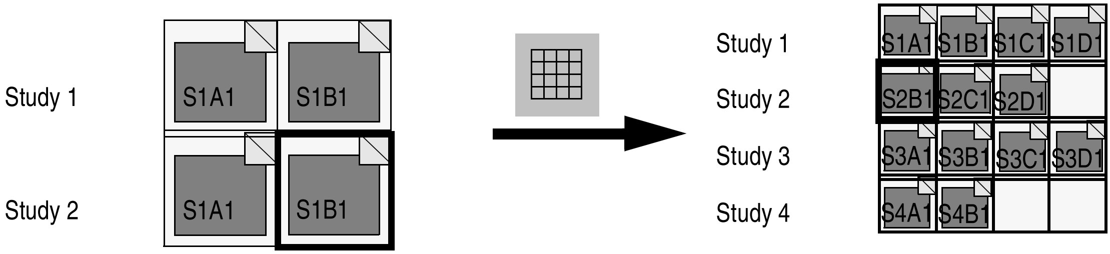
Layout change in normal mode without explicitly selected image



Layout change in normal mode with explicitly selected image (no input focus)



Layout change in study comparison mode with input focus



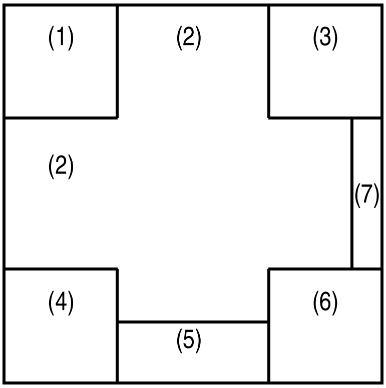
Layout change in study comparison mode with explicitly selected series

Showing and hiding image text

Patient and study-specific information and image settings can also be displayed on the images making it easier to identify each image. The image text can also be filmed/printed so that the information can be used for documentation.

Text blocks

The information displayed is arranged in blocks around the edge of the image according to its content.



(1) Patient data and zoom factor
(2) Orientation labels
→ Page E.1–6, *Image orientation*
(3) Hospital / system information
(4) Acquisition-specific settings
(5) Image comment
(6) Window values and (for images from **3D**) orientation cube
(7) Scale bar (CT, MR images only)

Hiding image text

Especially with a small division layout, the images can become cluttered by image text. You can then decide whether you want to have the image text shown in the image or not.

⇨ You cannot hide orientation labels.

✧ Call up **View > All text** in the main menu if you want to display all image texts.

Or

✧ Select **View > No Text** to hide all image texts except for the orientation marks.

Or

✧ Call up **View > Customized text** if you only want to display the most important image information.

⇨ Using the **Image Text Editor** on the configuration platform you can select which text information is to be displayed with the **Customized text** option.
→ Page A.2–8, *Configuring image text*

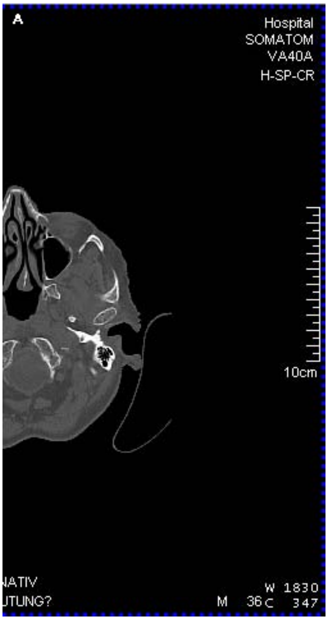
Showing and hiding the scale bar

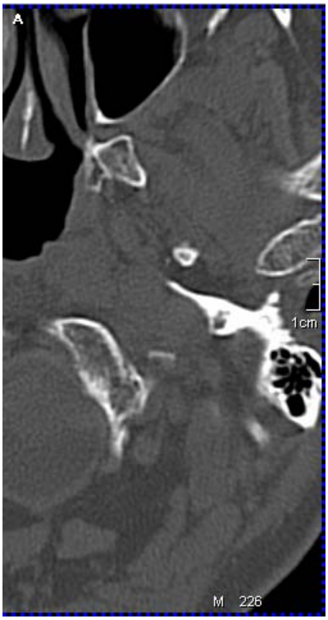
A scale bar is displayed along the right-hand edge of each segment indicating the scale of the image in cm (CT/MR only).

The size of the scale bar changes to match the current zoom settings.

✧ Call up **View > Scalebar On** to view or hide the scale bar, and the checkmark in front of the menu item is set or removed.

➩ If the scale bar would cover image text, it is not shown.





CHAPTER E.3

Scrolling and Selecting Images

You will usually have loaded more images and series of a patient onto the **Viewing** task card than can be displayed in the image area at once. All the images that cannot be displayed due to lack of space are placed in the background.

You can scroll through the loaded images of a patient to obtain an overview and to select images that you then want to process and evaluate.

The **Viewing** task card provides you not only with an option for manual scrolling, but also with an automatic, fast scrolling function. This gives you the impression of a movie being played back. The **Movie** function provides special advantages for viewing dynamic series, because processes which change over time can be displayed especially clearly this way.

Scrolling

The **Viewing** task card provides you with several alternative ways of scrolling through the loaded images of different patients, studies, or series:

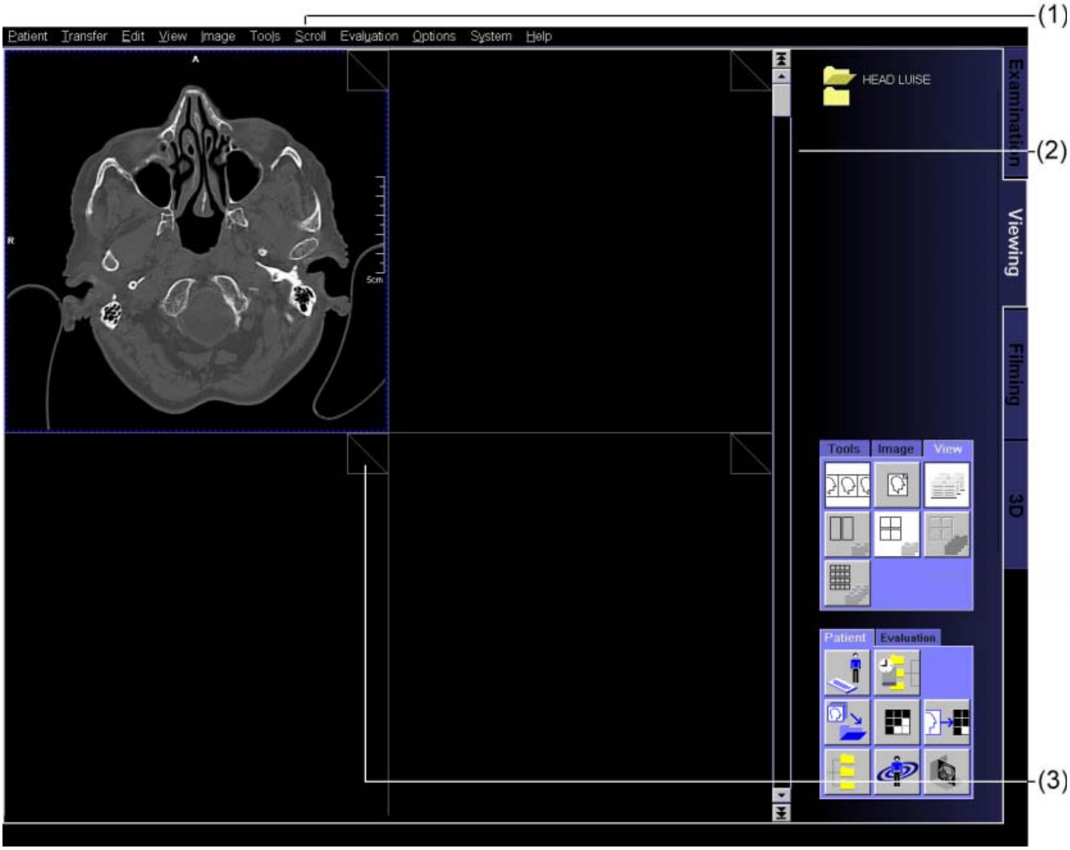
(1) **Scroll** menu

(2) Scroll bar on the right-hand or left-hand side of the image area (depending on the configuration).

(3) Dog ears in the top right-hand corner of the images (if you are in stack display)

⇨ You can also use the keys of your keypad for scrolling.

Depending on the processing step and the working methods you are accustomed to, you can select any of the above ways of scrolling.


(1)
(2)
(3)
Patient Transfer Edit View Image Tools Scroll Evaluation Options System Help
HEAD LUISE
Examination
Viewing
Filming
3D
Tools
Image
View
Patient
Evaluation
A
R
5cm

Scrolling image by image

Within a study, you can scroll through the loaded images and series image by image.

Scrolling image by image in image stripe display

✧ Call up **Scroll > Image Next** or **Scroll > Image Previous** to scroll forward or backward by one image.

Or

✧ Scroll with the **Image+** key (Num **2**) or the **Image-** key (Num **1**) on the symbol keypad.

➪ Explicitly selected images remain selected even if the images are moved into the background.

If you execute **Image+**, the image in the top left segment is moved into the background. All the following images are moved on by one segment. One image from the background moves into the bottom right segment. If there is no image in the background, the segment remains empty.

Image- reverses this process, moving an image from the background into the top left segment.

Scrolling image by image in a stack

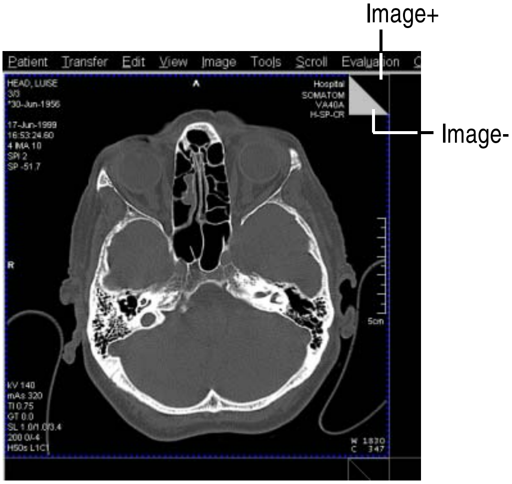
If you have selected stack display, you can scroll through a stack using all of the above methods or using the dog ears in the corner of each stack.

✧ Click on the stack through which you want to scroll with the mouse.

✧ Scroll from image to image in a stack with **Image+** or **Image-** just like in image-stripe display.

Or

✧ Click on the top or bottom of the dog ear to scroll forward or backward by one image.



➪ If you want to scroll through an image stack quickly, then click on the dog ear and hold the mouse key pressed.

➪ Explicitly selected images remain selected.

Scrolling through several stacks image by image

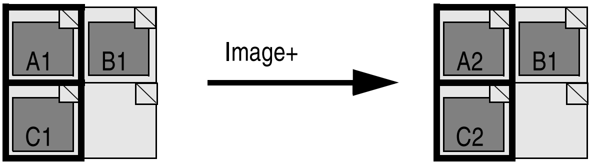
If you want to compare the images of different series, you can scroll through more than one stack simultaneously image by image.

✧ Press the **Ctrl** key and click on the stacks that you want to scroll through. If you click on a stack again, you deselect it.

✧ With the **Scroll** menu, the buttons or the symbol keypad scroll forward (**Image+**) or backward (**Image-**) through the selected stacks by one image at a time.

➪ If you have not selected a stack, you only scroll through the stack which is in the input focus.

➪ The dog ears only allow you to scroll through one stack at a time.



Scrolling page by page

A page describes the contents of the image area at a time. It can contain different numbers of segments depending on the layout selected and it may contain only images of one series or images of more than one series depending on the display mode.

You can use the menu, keyboard, or scroll bar to page through the series of a study.

Scrolling with the menu

✧ Select **Scroll > Page Down** to scroll forward by one page.

✧ Select **Scroll > Page Up** to scroll back by one page.

✧ Select **Scroll > Last Page** to jump to the last page of a study.

✧ Select **Scroll > First Page** to jump back to the first page of a study.

⇨ The first image of the series is displayed in the top left segment of the image area.

Scrolling with the keyboard

As an alternative to the menu commands, you can also scroll using the keyboard.

✧ Press the **Page Down** key to scroll forward by one page.

✧ Press the **Page Up** key to scroll back by one page.

✧ Press the **End** key to display the last page of the study.

✧ Press the **Home** key to jump to the first page of the study.

➪ The image area is filled with images. The first image of the series is displayed in the top left-hand corner of the image area.

Page-by-page scrolling with the image stripe display

In page-by-page scrolling, only the entire content of the image area is moved into the background. For example, for a 4x4 layout, four images are moved into the background at once and four images with higher image numbers moved from the background into the image area.

➪ When you reach the last page of a series, you receive the message “**At Last Page**”. The images of the last page remain displayed so that you do not have an empty image area.

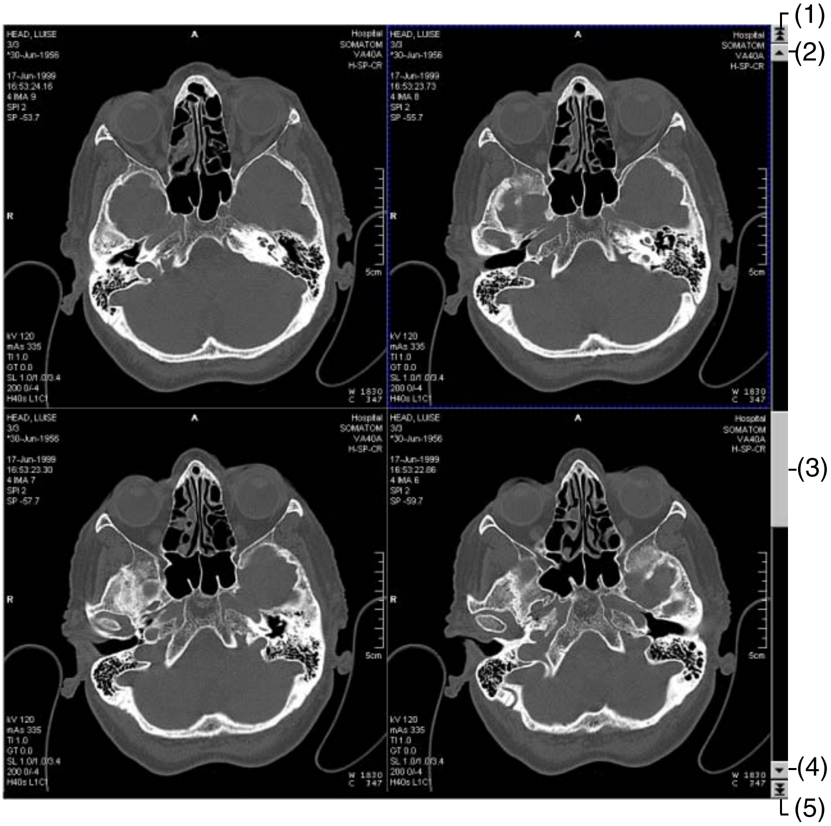
Scrolling in the stack display

In image stacks, the topmost images of all series displayed (image stacks) are moved into the background. You can then see the images of the series which follow in the image stacks displayed in the image area.

If you scroll back by one page, the preceding images in the image stacks are displayed again.

Scrolling with the scroll bar

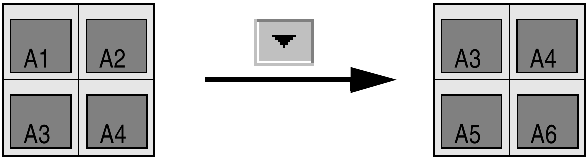
The third way of scrolling through the images and series of a study is to use the scroll bar.



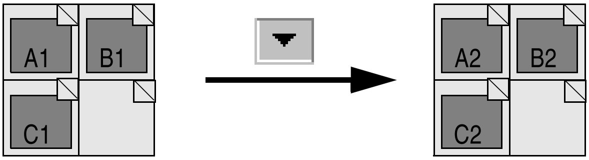
(1) Scroll arrow for first page
→ Page E.3–7, *Scrolling page by page*
(2) Scroll arrow for previous page
(3) Slider
(4) Scroll arrow for next page
(5) Scroll arrow for last page

✧ Click on the scroll arrow for the first or last page to jump to the beginning or end of the loaded series.

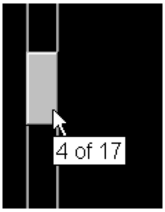
✧ Click on the scroll arrow for the next or previous row or page.



In image stripe display, the view is shifted forward or backward by one row.



In stack display, the next or previous page is displayed.



✧ Drag the slider up or down with the mouse until the page you require is displayed (the page number is also displayed).

➪ If you click the scroll bar above or below the slider, you scroll backward or forward by one page.

Scrolling from series to series

You cannot only scroll image by image or page by page, but also by entire series if you have loaded more than one series of a study into the **Viewing** task card.

✧ Call up **Scroll > Series Next** or **Scroll > Series Previous** in the main menu to scroll forward or backward by one series.

Or

✧ Press the **Series+** key (Num **5**) or the **Series-** key (Num **4**) on the symbol keypad to scroll to the next or previous series.

Which images are subsequently displayed in the image area depends on the display you select (normal mode or study mode, image stripe or stack display).

Normal mode

In **image stripe display**, the entire series of which one image fills the top left segment of the image display is moved into the background. The first image of the following series is then displayed in the top left segment and the image area is filled with images of the series.

In **stack display**, the image stack of the series that fills the top left segment is moved into the background. The image stack of the following series moves up by one segment to fill the space. If there are image stacks in the background with higher series numbers, the first image stack in the background is moved into the bottom right segment.

Study comparison mode

In study comparison mode, too, you can only scroll forwards/ backwards by a series within an examination with **Series+/ Series-**.

With **image stripe display** you scroll within the examination in which images are explicitly displayed with **Series+**. I.e. the series of which an image fills the left segment is placed in the background. The first image of the next series then replaces it. The segments of the examination series are filled with the images of the next series.

With **stack display**, the image stack of a series in the row of an examination is moved to the left into the background with **Series+**. A further series from the background replaces it from the right.

Scrolling from study to study

As many of the images of the loaded examinations and series as there are space for in a single screen are displayed in the image area of the **Viewing** task card.

As soon as you load the images, the images of the first examination are displayed starting top left.

✧ Call up **Scroll > Study Next** or **Scroll > Study Previous** in the main menu to display the series and images of the next or previous study.

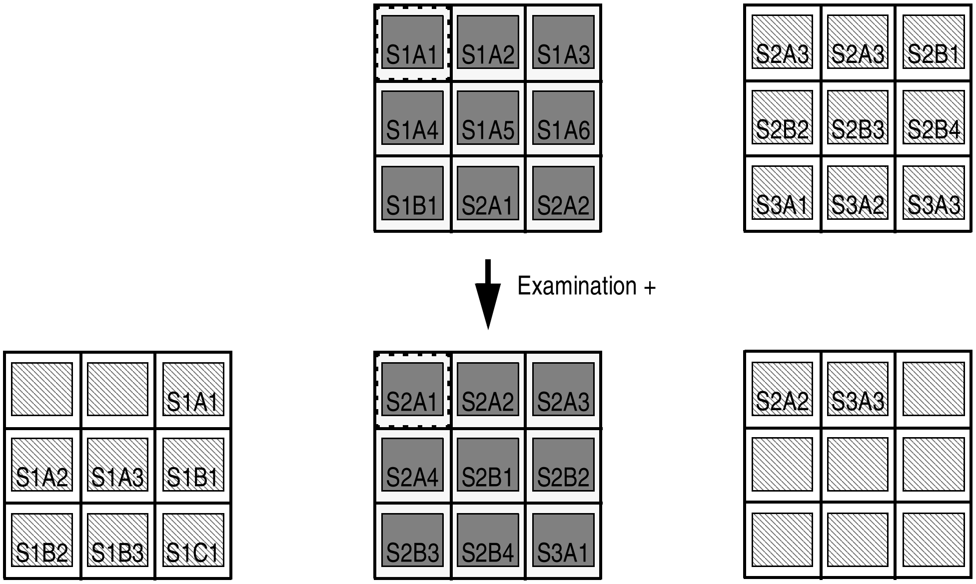
Or

✧ Scroll to another study with the **Study+** key (Num **8**) or the **Study-** key (Num **7**) on the symbol keypad.

The images of the first examination are placed in the background.

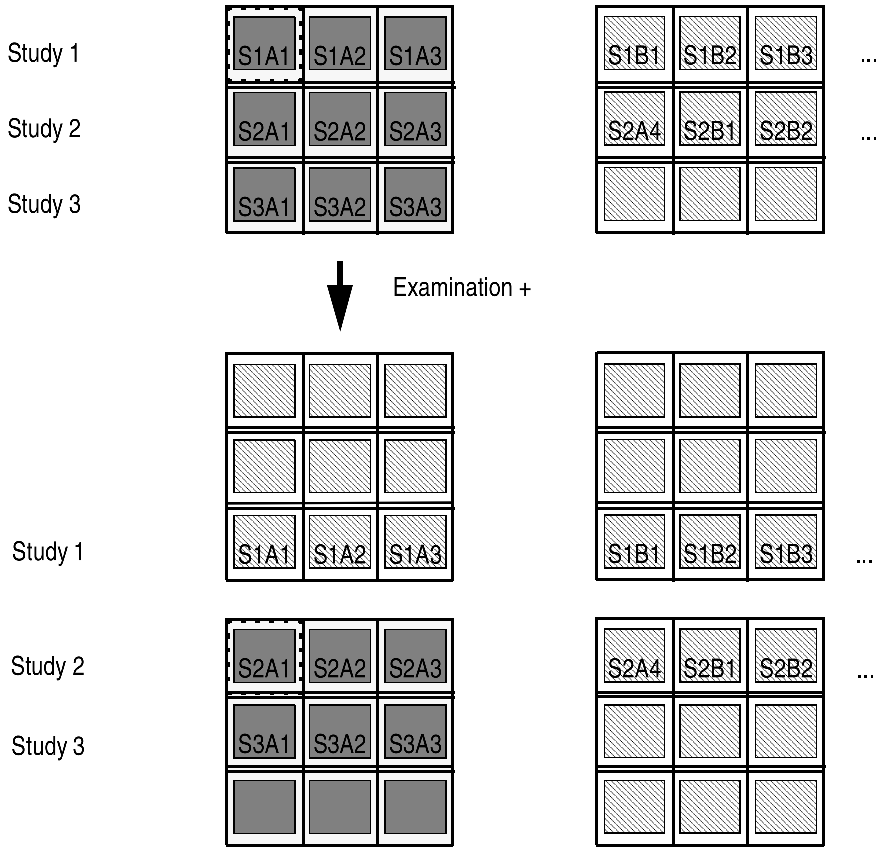
The image area display is different depending on whether you selected **normal mode** or **study comparison mode** view.

Normal mode



S1 A1 = Series A1 of Study 1
S1 A2 = Series A2 of Study 1
and so on

Study comparison mode

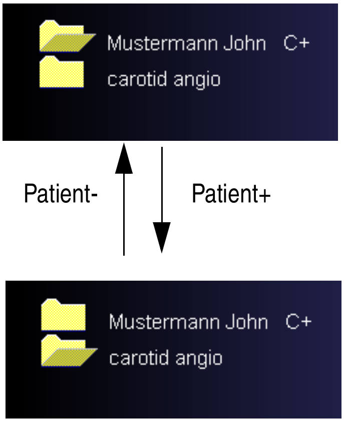


S1 A1 = Series A1 of Study 1
S1 A2 = Series A2 of Study 1
and so on

Scrolling to the next patient

Up to two patients can be loaded in the **Viewing** task card at one time. You can see whose images are currently being displayed in the image area by the opened patient folder in the patient field of the control area.

✧ Switch to the patient you require by clicking on his or her patient folder.



Animated images (Movie)

It is usually easier to recognize anomalies in processes (dynamic series) if you view the images in quick succession like a movie.

The **Movie** option allows you to scroll through the images of a series or a whole study automatically and quickly.

NOTE

While running a movie it is not advisable to activate any correct and rearrange actions.

Selecting a layout and display mode

✧ Select the stack display (**View > Stack**) if you want to view *only one* series as a movie.

Or

✧ Select the image stripe display (**View > Stripe**) if you want to view *all* the series of a study one after the other as a movie.

✧ After that, select a sufficiently large layout to be able to see all the details.

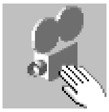
We recommend:

☐ 1 : 1
The movie takes up the whole screen.

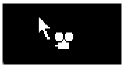
☐ 4 : 1
You can compare the movie with up to 3 “still images”.

Playing back the movie interactively

Because the left mouse key is normally used to select images and graphics, you must switch over its function to **Movie** to be able to play back images interactively.



✧ Call up **Scroll > Interactive Movie On**, or click on this button on the **Scroll** subtask card.



The mouse cursor changes shape.

Playing back the movie with the mouse

You use the mouse to start the movie and control the playback speed. The faster you move the mouse, the faster the movie will play back.

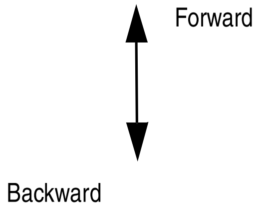
The movie segments must be selected before you start.

✧ Place the mouse cursor on the image with which you want to begin.

✧ Hold the left mouse key down and move the mouse up to playback the movie forward.

Or

✧ Hold the left mouse key down and move the mouse down to playback the movie backward.



⇨ When the movie reaches the last image of the series or study, it jumps back to the first image of the series or study and starts again (Loop).

You can interrupt the movie at any time, for example to take a better look at an image.

✧ Just release the left mouse key.

The current image is displayed in the movie segment with all its text information, drawing elements and evaluations.

In image stripe display, the images before and after the current image are displayed in the remaining segments.

✧ Click on the image area again, hold the left mouse key down, and drag the mouse over the image area to continue playback of the movie.

Ending a movie

✧ Release the left mouse key to interrupt the movie.

✧ Call up **Scroll > Interactive Movie On** again to terminate **Movie** mode and switch the function of the left mouse key back to selection mode.

Playing back the movie automatically

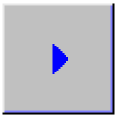
As an alternative to interactive playback of the movie using the mouse you can also run the movie automatically. This is recommended, for example, for examinations or series with a large number of images or if you want to ensure an even playback speed (e.g. for heart series).

In this mode, you can change a number of settings for movie playback.

Starting a movie

✧ Call up **Scroll > Automatic Movie On** or click on the button **Automatic Movie** on the **Scroll** subtask card.

Depending on the default settings, movie playback starts immediately or the dialog box **Movie Properties** is displayed. Here, you can change a number of settings for movie playback and then control movie playback.



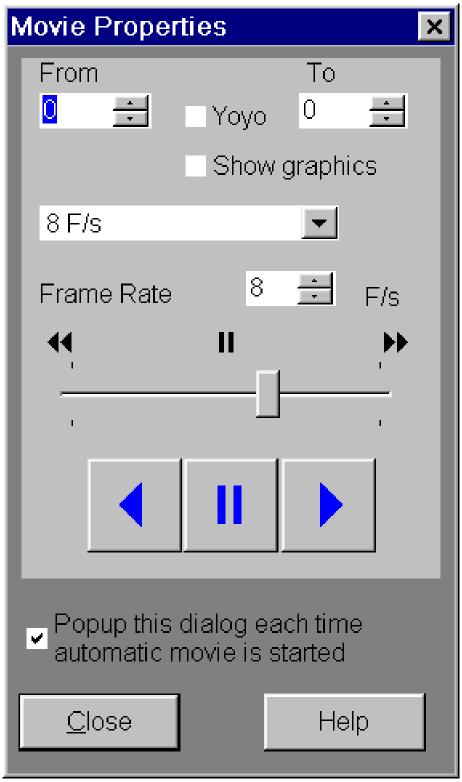
- Finally click on this button in the **Movie Properties** window to play back the movie forwards.

Changing settings for movie playback

- While a movie is being played back click into the playback segment with the right mouse key to call up a popup menu.
- Select **Movie Backward** or **Movie Forward** to change the playback direction.

Or

- Select **Scroll > Movie Properties** to open the dialog box **Movie Properties**. Press the **forward/backward** button or move slider to adapt speed.



From 0

☐ Yoyo

To 0

☐ Show graphics

8 F/s

Frame Rate 8 F/s

☑ Popup this dialog each time automatic movie is started

In the dialog box **Movie Properties** you can:

- Change the playback speed and direction
- Stop the movie and restart it
- Exclude initial and final images of little interest

Playback speed and direction

✧ Select a speed from the list.

Or

Frame Rate 25 F/s

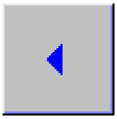
✧ Enter a playback speed via the spin box in the field **Frame Rate**.

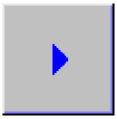
Or

✧ Select a playback speed and direction using the slider:

❑ To the extreme right - fast forward
❑ Center right - slowly forward
❑ Center position - still frame
❑ Center left - slowly backward
❑ To the extreme left - fast backward

Or





✧ Change the playback direction by clicking on the **forward/ backward** buttons.

✧ Click on the option **Yoyo**.

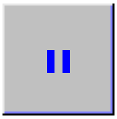
As soon as the movie has reached the last frame, it starts again backward to the first image, and from there again forward to the last image etc.

Or

✧ Deselect the option **Yoyo** to play back the movie in a loop.

When the movie reaches the last image it starts again from the first image (loop).

Stopping the movie, scrolling forwards/ backwards step by step



✧ Click on the button **Stop** to stop the movie.

Excluding initial / final images

✧ In the spin boxes **From** and **To,** specify which images are to be included in the movie playback. In this way you can exclude initial and final images of little interest.

➩ You cannot change this setting while a movie is running.

Always display the dialog box

☑ Popup this dialog each time automatic movie is started

- Select **Popup this dialog...** to display the dialog box **Movie Properties** every time you call up **Automatic Movie**.

You then always control the movie from this window.

Closing automatic movie playback

You can stop a running movie at any time automatically. This also closes **Automatic Movie** mode, but you can start it up again at any time without problem.

- Press the **Esc** key on the keyboard or click into the playback segment with the left mouse key (a single click) to terminate **Automatic Movie**.

Or

- Deselect **Scroll > Automatic Movie On** in the main menu or click on the button again.

Or

- Stop movie playback in the dialog box **Movie Properties** and close the dialog box with the **Close** button.

Synchronizing movie playback

If you are working in study comparison mode you can play back all loaded examinations and series simultaneously as movies with **Automatic Movie**.

You can synchronize playback of these movies.

✧ Call up **Scroll > Link > Acquisition Time**.

You now see images acquired at the same time in all movie segments.

Or

✧ Call up **Scroll > Link > Slice Location**.

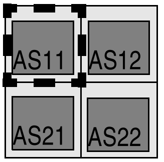
You now see images of the same slice position in all movie segments.

Or

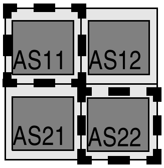
✧ Call up **Scroll > Link > Current Order** to play back the movies synchronized in the sequence in which they appear in the series.

Select the movie segments explicitly before you start.

Multiple study image stripe

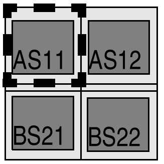


One segment is selected.
The movie contains all the images that belong to study S1.

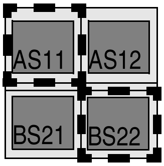


Two segments are selected.
The movie contains all the images that belong to study S1 and S2.

Multiple study compare image stripe

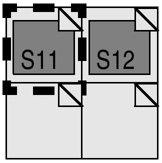


One segment is selected.
The movie contains all the images that belong to study S1.

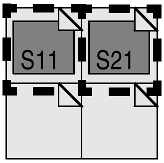


Two segments are selected, one movie for each segment. Each movie contains all the images of that series.

Multiple study series stack

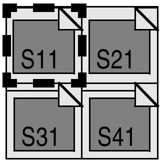


One stack is selected, one movie through series 1.

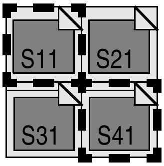


Two stacks are selected, in each case one movie in the selected segment.

Multiple study compare series stack



One stack is selected, one movie through series 1.



Two stacks are selected, in each case one movie for each selected stack.

Selecting images

On the **Viewing** task card, you can not only view images, but also process and evaluate them.

You must first select the images that you want to process.

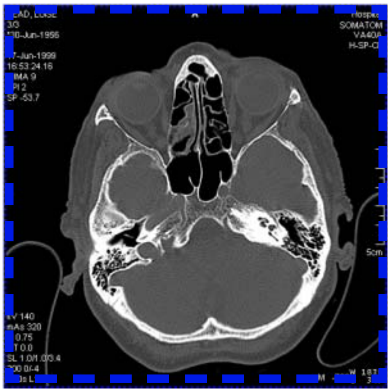
Ways of selecting images

You can select images in one of two ways:

- ❏ **explicitly** holding the **Ctrl** key down (explicitly selected images are shown with a continuous border)
- ❏ **implicitly** by working in the input focus.

Working in the input focus

The input focus shows the active segment of the image area. It is marked by a broken line border, i.e. it is selected implicitly.

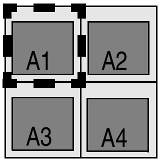


The processing steps that you execute are always applied to the image shown in the segment on which the input focus is located.

Only when you have selected images explicitly is the input focus switched off and **no** segment has a broken line border.

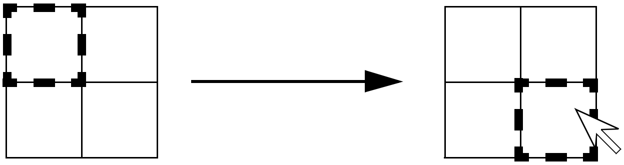
Default input focus

When you load images onto the **Viewing** task card, the input focus is in the default position in the top left segment of the image area.



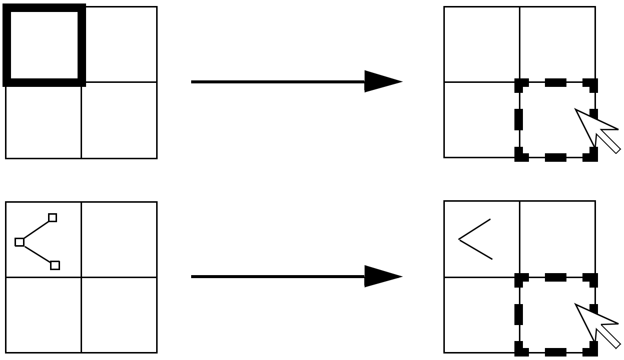
Placing the input focus with the mouse

✧ Click with the left mouse key into the segment of the image area on which you want to place the input focus.



An explicitly selected image or an explicitly selected graphic is deselected if you place the input focus on a segment even if you only click on the same segment.

Examples:



Changing the input focus using the keyboard

You can also move the input focus using the keyboard.

Use the arrow keys.

✧ Press the arrow key **left** or **right** to move the input focus to the next **column** of the image area.

Or

✧ Press the arrow key **up** or **down** to move the input focus to the next **row** of the image area.

➩ If an image or a graphic is selected explicitly, the arrow keys are not active.

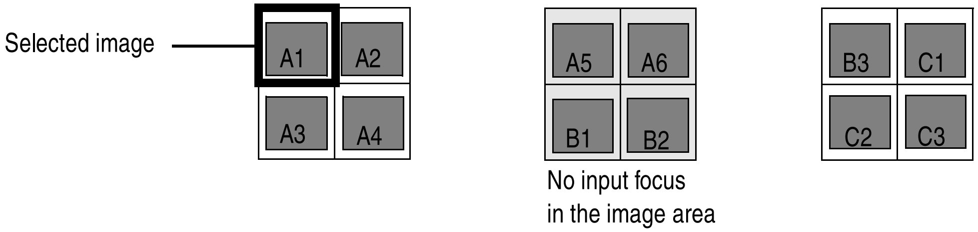
Processing an image

As long as you have not selected any images explicitly, your processing steps are applied to the image in the segment on which the input focus is located, the image with the broken line border.

✧ Place the input focus on the image that you want to process.

No input focus in the image area

If you cannot see an input focus in the image area, one or more images are explicitly selected in the background.



Your processing steps are then only applied to the explicitly selected images unless you set the input focus.

Selecting images explicitly

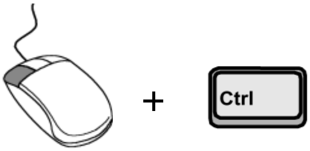
Selecting images explicitly means that you select images or series specifically and one after the other. Unlike the input focus, the explicit selection is associated with the content of the segment. Explicitly selected images **remain** selected even if you move them into the background.

All explicitly selected images have a continuous line border.

Image is not selected

Image is selected explicitly

Selecting images individually



You can explicitly select an image or more than one image one after the other.

✧ Press the **Ctrl** key **and** click on an image with the left mouse key to select it **explicitly**.

✧ Hold the **Ctrl** key down and click on **further** images if you want to extend your selection.

Selecting images explicitly up to the end of series

You want to explicitly select the image displayed and all the following images of the series.

✧ Click on the image that you want to select explicitly holding the **Ctrl** key down or set the input focus by clicking on the image.

✧ Call up **Edit > Select On Succeeding** in the main menu or **Select On Succeeding** in the popup menu (right mouse button).

The selected image and all the following images are now selected.

➪ If you have explicitly selected images of different series, the remaining images of these series are selected starting with those images.

Explicitly selecting complete series

The easiest way for you to select complete series (i.e. all images contained in them) is with **Select Series**.

➪ With **Select On Succeeding**, you would first have to select the first image of the required series.

✧ First select an image of the required series explicitly by clicking on it holding the **Ctrl** key down or place the input focus on the image by clicking on it.

✧ Call up **Edit > Select Series** from the main menu or **Select Series** from the popup menu (right mouse key).

The whole series is now selected explicitly.

Selecting more than one series explicitly

If you want to select more than one complete series, first select an image from each series and then extend your selection to the complete series.

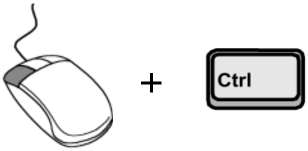
✧ Hold the **Ctrl** key down and click on individual images of the required series.

✧ Call up **Edit > Select Series** in the main menu or select **Select Series** in the popup menu.

Marking images and selecting marked images explicitly

If you have loaded a large number of images into the **Viewing** card, you might find it helpful to first page through all the images to look at them in more detail before deciding which are relevant to the next processing steps.

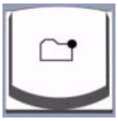
Mark an image that you want to include in your processing. Then scroll on and mark all the other relevant images one after the other.



✧ Press the **Ctrl** key and click on the image that you want to mark to select it.

✧ Then call up **Edit > Mark** in the main menu or **Mark** in the popup menu (right mouse key).

Or



✧ Press the **Mark** key (Num **3**) on the symbol keypad.

✧ Call up **Edit > Unmark** in the main menu or **Unmark** in the popup menu to undo marking of a selected image.

Or

✧ Click on the icon button or press the **Mark/Unmark** key on the symbol keypad again.

Once you have viewed all loaded images one after the other, select all marked (or all unmarked) images at once.

✧ Call up **Edit > Select Marked** to select all marked images/series explicitly.

Or

✧ Call up **Edit > Select Unmarked**, or click on the button to select all unmarked images/series at once.

Now you can edit all explicitly selected images or remove them from the **Viewing** task card.
→ Chapter E.4, *Processing Images*
→ Page E.7–15, *Closing selected images or series*

Deselecting images

If the explicit selection of images does not contain the set of images you require, you can deselect individual images or all images.

✧ Place the input focus on an unselected segment manually using the mouse by clicking on it.

Or

✧ Call up **Edit > Deselect All** in the main menu or **Deselect All** in the popup menu to deselect all selected images.

➩ After that, the standard input focus is set automatically, i.e. the top left segment is active.

Or

✧ Hold the **Ctrl** key pressed and click on an explicitly selected image again (individual image deselection).

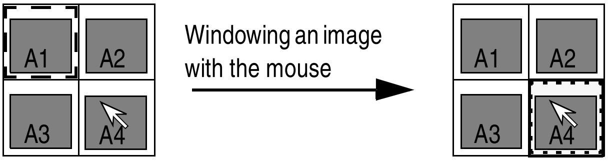
Direct image processing

Direct image processing (implicit selection) with the mouse is automatically applied to the image segment on which the mouse cursor is located.

Setting the input focus

If no images are explicitly selected, you can see the input focus in the image area. The input focus is placed on the segment on which you position the mouse cursor and perform image processing implicitly.

✧ Place the mouse cursor on an image which is not selected and process the image, for example, by zooming.

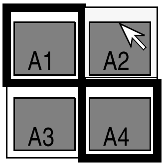


➪ If graphics were previously explicitly selected in the input focus, they remain explicitly selected.

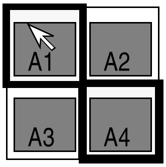
Images are explicitly selected

If images are explicitly selected, only that image is processed on which the mouse cursor is positioned, if it is not explicitly selected together with other images.

Example:
The images A1 and A4 are selected explicitly. The position of the mouse cursor defines the selection.



Only image A2 is processed
(implicit selection)



Images A1 and A4 are processed
(explicit selection)

CHAPTER

E.4 Processing Images

As soon as you have loaded all the series and/or images that you want to view and process into the **Viewing** task card, you can change the display parameters of individual images. In this way, you can emphasize areas and image contents for subsequent evaluation or reporting especially clearly.

You can adapt the window values of the loaded images or change image processing by assigning a lookup table (LUT). The images can be zoomed or ROIs can be drawn on them. You can also rotate, flip or invert images for certain diagnostic problems.

NOTE

Extreme window values may reduce the image quality.

Windowing images

Imaging methods provide diagnostic information in the form of gray scale images with up to several thousand different gray scale values. Windowing means to focus on the range of gray scales of the diagnostically relevant area and tissue type.

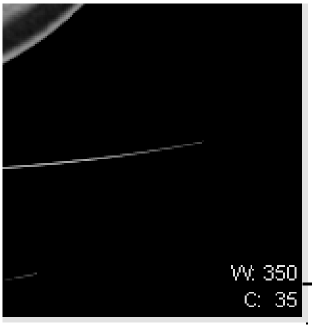
The first step in windowing is therefore to determine the center of the window, i.e. the gray scale value of the type of tissue which is central to your diagnostic problem. The smaller the window center, the brighter the image.
With the window width, you define how many gray scale values above and below the center value you want to see. The smaller the window width, the stronger the contrast.

➪ You cannot window color images.

Displaying the window values

You can see the window values set in the bottom right-hand corner of the images.

❑ W = width (contrast)
❑ C = center (brightness)



W: 350
C: 35

➩ No window values are displayed on color images.

Setting the scope

You will often need to window images several times until you have found the optimum setting for your requirements. By defining a scope, you can assign new window values to several images automatically and in a single action to simplify your work.

Windowing with a scope only applies to images that are not **explicitly** selected.

Windowing images up to the end of series

With **Windowing On Succeeding On**, you can define that windowing is to be applied to the image in the input focus (inclusive) or to the implicitly selected image and all the other following images up to the end of the series.

✧ Call up **Image > Windowing On Succeeding On** to be able to process all images up to the end of the series.

✧ Set the required window values with the keyboard, the control box, or the main menu.

The new window values are assigned to all images from the image in the input focus to the end of the series.

Or

✧ Place the mouse cursor in the **input focus** or in an image which is not selected.

✧ Window all images up to the end of the series by pressing the center mouse key and moving the mouse.

Switching between scopes

You can switch between scopes as you require.

❑ The scope **Windowing On Succeeding On** is active.

You want to window only a single image temporarily without having to select it explicitly.

✧ Press the **Ctrl** key.
The scope **Windowing On Succeeding On** is deactivated as long as you hold the **Ctrl** key down.

✧ Window an image by clicking on it with the center mouse key and move the mouse cursor holding the mouse key down.

Or

✧ Assign new window values to the image with the input focus using the main menu, keyboard, or the control box.

❑ The scope **Windowing On Succeeding On** is not active.

You want to window all images up to the end of the series temporarily.

✧ Press the **Ctrl** key and switch the scope to **Windowing On Succeeding On** while you are holding the **Ctrl** key down.

✧ Then window all images up to the end of the series as described above.

Windowing explicitly selected images

The **Windowing On Succeeding On** scope does not apply to **explicitly** selected images. If you have selected images explicitly and window them, only these images are windowed.

✧ Select one or more images explicitly and set the required window values using the main menu, the keyboard, or the control box.

Or

✧ Place the mouse cursor on an **explicitly** selected image.

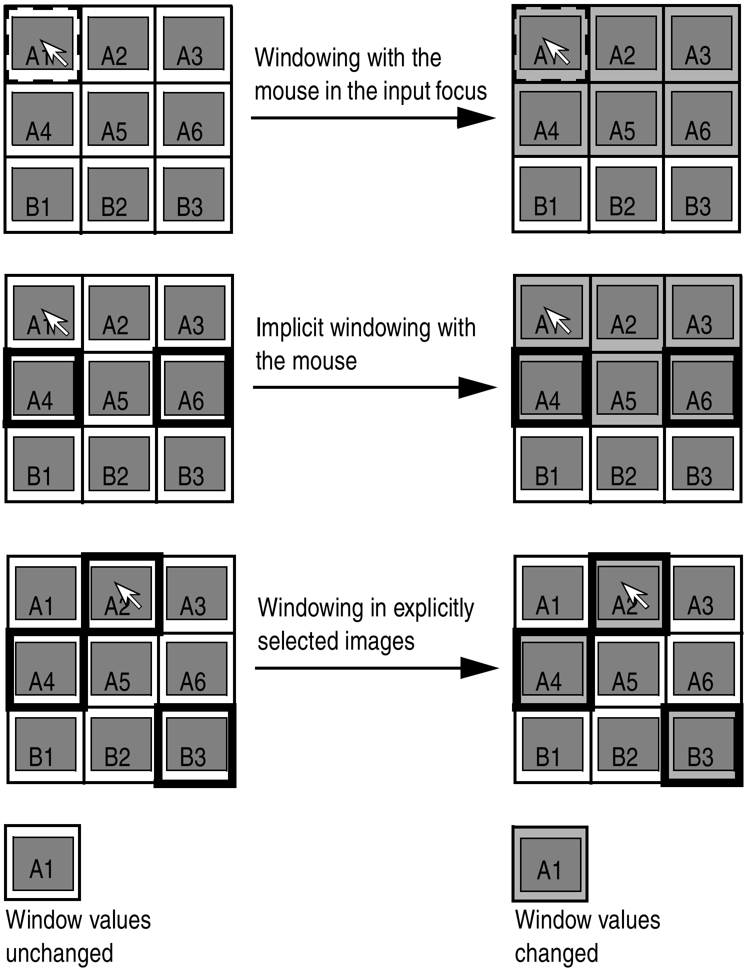
✧ Window all explicitly selected images by pressing the center mouse key and moving the mouse.

Or

✧ Execute a double-click with the center mouse key to assign preset window values automatically.

Examples:

Windowing On Succeeding On is active.

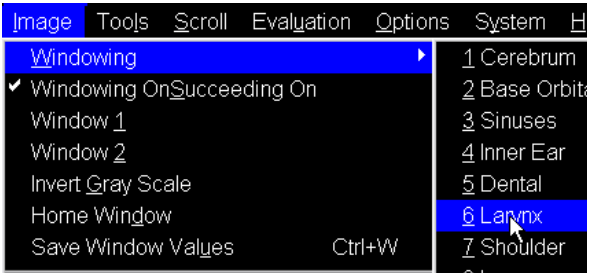


Assigning predefined window settings

A series of organ-specific, study-specific and user-specific window settings are stored in the **Viewing** task card.

Some of these window settings were made by Siemens Service. You can change them in **Viewing Configuration** and also define a few new window settings of your own.
→ Page E.8–8, *Organ-specific and user-specific window values*

✧ Select the images that you want to window, paying attention to the scope
→ Page E.4–4, *Setting the scope*



✧ Call up **Image > Windowing** to call up a submenu with all the stored window settings.

✧ Select an entry to apply these window settings to your images.

Displaying window settings one and two

For any image for which two window settings have been stored, the window value display in the bottom right-hand corner of the image indicates which window is currently active
(W1... / C1... for window 1; W2... / C2... for window 2).

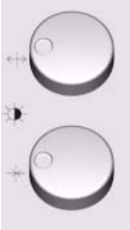
CT-Examinations will be stored with two window values. This is useful if you want to answer two diagnostic problems with one series (e.g. Window 1 for tissue, Window 2 for bone).

With the **Window 1** and **Window 2** buttons, you can switch between the two sets of window values.

✧ Select the images that you want to window.

✧ Click on the **Window 1** button or the **Window 2** button on the **Image** subtask card.

Windowing with the control box



On the control box, you will find two tuning knobs with which you can set the windowing values very finely.

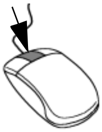
If you want to use the tuning buttons, please note:

☐ Only explicitly selected images can be windowed in this way.
☐ The left mouse key must not be pressed.

Windowing with the mouse

You can assign new window values to images using the mouse.

➩ Pay attention to the scope
→ Page E.4–4, *Setting the scope*



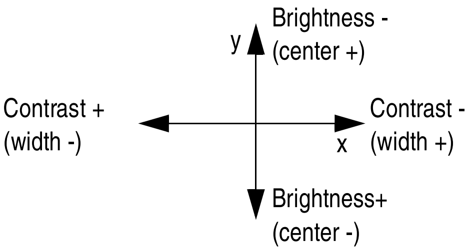
✧ Click on an image segment with the **center** mouse key and move the mouse holding the button down.

The mouse cursor disappears.

✧ Move the mouse up/down to change the window center.

Or

✧ Move the mouse right/left to change the window width.



In the image in which you are currently windowing, the changed window values are displayed immediately (interactive windowing).

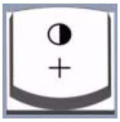
As soon as you release the mouse key, the new window values are also applied to all the other selected images or the selected scope of action.

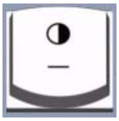
Windowing with the keyboard

For fine adjustment of the window values, you can also use the keys on the symbol keypad of the keyboard.

➪ Pay attention to the scope
→ Page E.4–4, *Setting the scope*

Setting the contrast





✧ Press the **Width+** (Num **-**) or **Width-** key (Num *****) to increase or reduce the contrast.

Setting the brightness

✧ Press the **Center+** (Num **/**) or **Center-** key (Num **Num**) to increase or reduce the brightness.

Restoring window values

You can undo your changes to the window values at any time and restore the old window settings with which you loaded the images from the database.

✧ Call up **Image > Home Window** or call up **Home Window** in the popup menu (right mouse key).

The selected image(s) is/are displayed with their original window values.

Changing the image display with LUT

Some modalities (e.g. AX, SP) produce gray scale images that cannot always be displayed optimally with windowing.

These images are stored on acquisition with a specific gray scale distribution table, called a lookup table (LUT). Depending on the default setting of the modality for images of specific examinations, more than one LUT might be stored. These images can then be stored with different LUTs depending on the diagnostic problem.

LUT instead of window values

If an image is stored with a LUT, the image is automatically displayed based on that LUT when it is loaded into the **Viewing** card. This is shown by the fact that no window values (W / C) are displayed in the bottom right-hand corner of the image.

However, you can window such an image normally (e.g. with the mouse), in which case you deactivate the LUT.

Switching over the LUT

If you window an image that was loaded with a LUT, the LUT is no longer active. However, you can call up the LUT again at any time.

If not one but several LUTs have been stored for an image, you can change the image display by selecting one of the alternative LUTs.

✧ Select the image or images that you want to display with a LUT or whose LUTs you want to change.

✧ Call up **Image > Lookup Table** and select one of the LUTs listed in the submenu.

➩ If you have loaded and selected the images for which no LUT is stored, the submenu **Image > Lookup Table** is empty and the button is dimmed.

Zooming and panning images

You can zoom in on sections of images that you are particularly interested in. If the zoomed image is too large to be displayed in the segment, you can then pan it (i.e. move it), so that the region of interest is in the center of the image again.

Displaying enlarged/reduced images

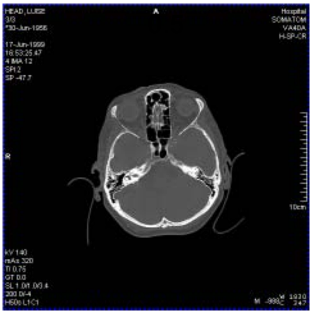
The **Viewing** task card provides you with several ways of displaying enlarged or reduced images.

Double size / half size

✧ Select the images that you want to zoom.

✧ Click on the **Minify by 0.5** or **Magnify by 2.0** buttons on the **Image** subtask card to double or half the zoom factor of an image.

0.5 2.0



Half size

Original size

Double size

Fitting an image into a segment

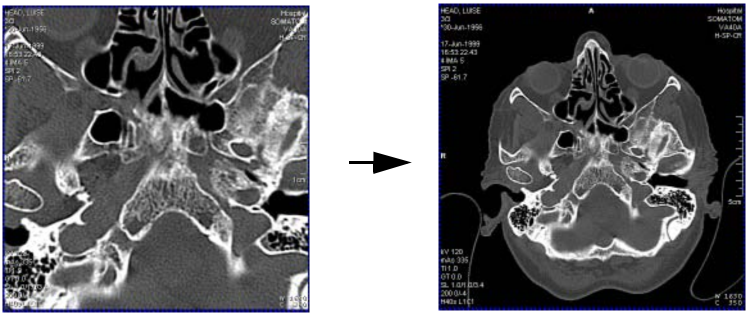
✧ Select the images that you want to process.

✧ Call up **Image > Fit to segment** to enlarge/reduce an image to the size of the segment.

Or

✧ Select **Fit to segment** with the popup menu (right mouse key).

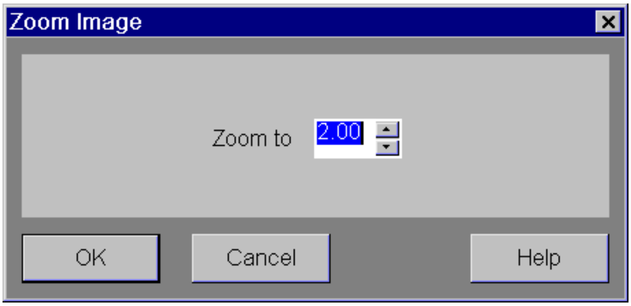
The image is displayed in such a way that it fits exactly in the segment.



Entering a zoom factor

✧ Select the images that you want to zoom.

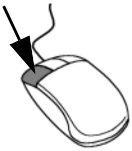
✧ Call up **Images > Zoom in/out** to open the **Zoom Image** dialog box.



✧ Enter a zoom factor and confirm with **OK.**

The image/images are enlarged/reduced by this zoom factor.

Zooming with the mouse



You usually select or deselect images and objects with the left mouse key.

You can also switch over the function of the left mouse key to perform zooming and panning.

✧ Select **Image > Zoom & Pan On**.

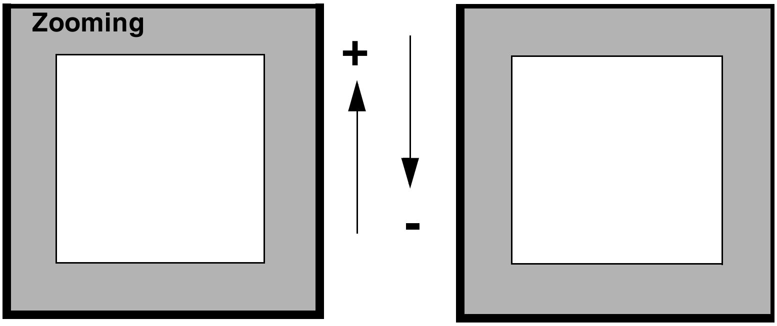
✧ Now place the mouse cursor close to the edge of an image.

The mouse cursor changes shape.

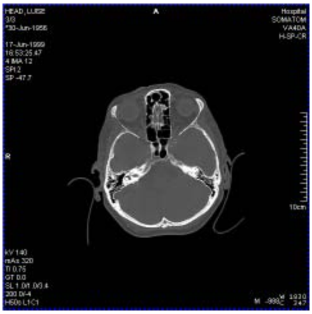
✧ Drag the mouse cursor up with the left mouse key pressed to enlarge the image.

Or

✧ Drag the mouse cursor down with the left mouse key pressed to reduce the image.



Enlarging



Reducing

As soon as you release the mouse key, the new zoom factor is applied to all the selected images or the selected scope of action.

NOTE

If the image in which you are zooming with the mouse contains graphics, make sure you do not click them by mistake. Otherwise, you will select them and enlarge/ reduce or pan them instead of zooming the image. When you press the mouse key and move the mouse cursor over the image holding the mouse key down to zoom it does not matter if you move over drawing elements.

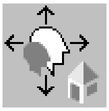
✧ Deselect **Image > Zoom & Pan On** again or click on the button to make the left mouse key available for selecting images again.

Restoring the zoom factor

You can return to the zoom factor with which the images were last stored in the database at any time.

✧ Call up **Image > Home Zoom/Pan** or call up
Home Zoom/Pan in the popup menu (right mouse key).

Or



✧ Click on the button.

Panning images

After you have zoomed the images, parts of the images might extend beyond the edge of the image segments.

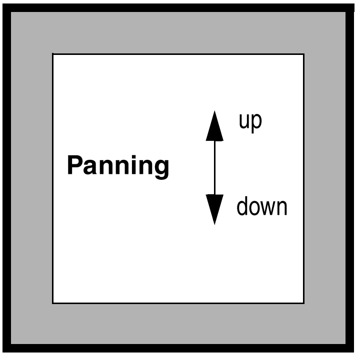
Therefore always pan the image so that the region of diagnostic interest is in the center of the segment again before storing.

✧ First select **Image > Zoom & Pan On** as you would to zoom with the mouse to switch the left mouse key function from selection to zooming/panning.

✧ Now place the mouse cursor in the center part of the image.

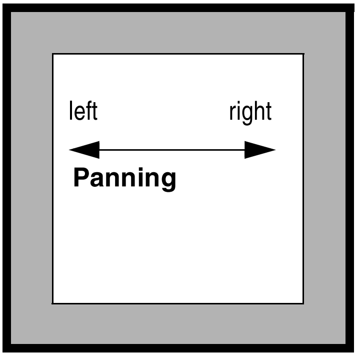
The mouse cursor changes shape.

✧ Drag the mouse up, down, right or left holding the left mouse key down to pan the image.



Up

Down



Left

Right

You can see the result of your mouse movements in the image on which the mouse cursor is located immediately.

As soon as you release the mouse key, the image content in all the selected images or all images of the selected scope of action have been panned.

NOTE

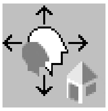
When panning, make sure you do not click on a graphic element accidentally. Otherwise, you would pan the graphic element and not the content of the image.

Restoring image display

Like with zooming, when you have panned images, you can restore the images as they were last stored in the database.

✧ Call up the popup menu (right mouse key) and select **Home Zoom/Pan**.

Or



✧ Click on the button.

Enlarging the image section

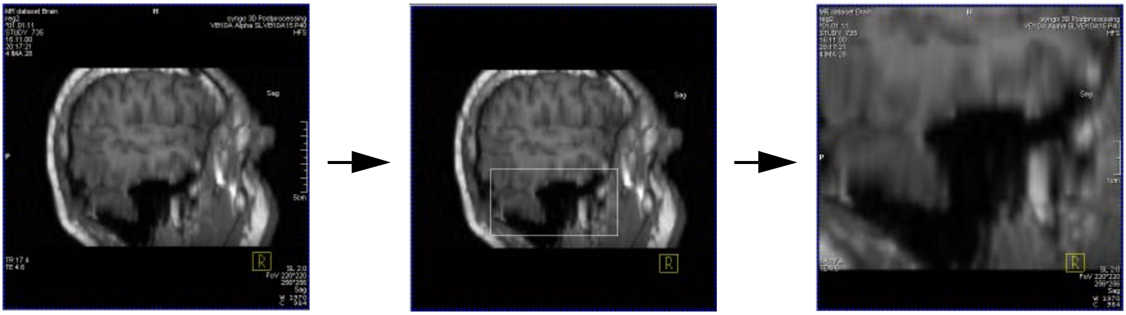
Instead of increasing the size of the image (zoom) in order to move it so that the relevant section is again located at the center of the screen (pan), you can also select explicit image sections quickly and display them at maximum size in a segment.

✧ Select the images in which you want to display an enlarged image section.

✧ Call up **Tools > Capture Area**.

✧ Click into one of the selected images with the left mouse key and drag open a square or rectangle.

As soon as you release the mouse key, that section is displayed enlarged to the total segment size in all selected images. The size ratios remain the same. The enlarging tool is now deselected again.



Rotating, flipping and inverting

Aside from the above described methods of focusing on regions of diagnostic interest in medical images the **Viewing** task card provides a number of tools with which you can change these images.

For example, you can rotate the images around any axis. You can flip images horizontally or vertically or you can invert the gray scale values of images.

These functions are useful for comparing series acquired with different patient positions, gantry inclinations or examination directions.

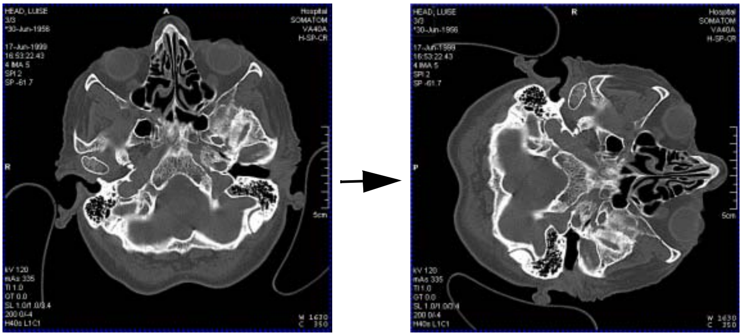
Rotating images (Rotate)

Whether you rotate images 90° or through a freehand rotation, the center is always the center of the segment.

Rotating through 90°

- Select the images that you want to rotate.
- Call up **Image > Rotate 90** or click on the **Rotate 90** button on the **Image** subtask card.

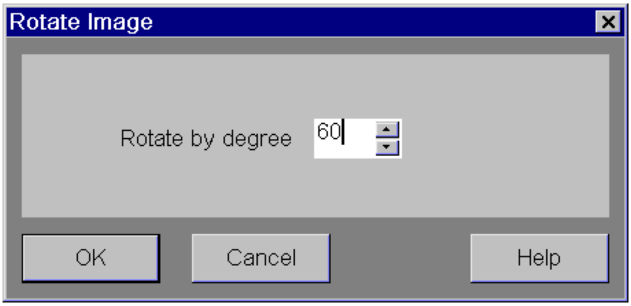
The image is rotated 90° clockwise.



Freely defined angle

✧ Call up **Image > Rotate**.

A dialog box is displayed in which you can enter an angle of rotation.


Rotate Image

Rotate by degree 60

✧ Enter a positive value to rotate the image(s) clockwise.

Or

✧ Enter a negative value to rotate the image(s) counterclockwise.

➪ You can only enter integer values.

Original image

Rotation through 120°

NOTE

Please note that any annotations and graphics you have entered will be deleted when you rotate an image.

Orientation labels are rotated together with the image.

Flipping images (Flip)

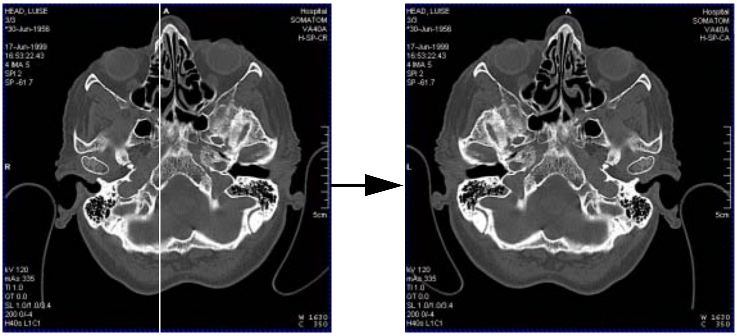
With the flip function, you can compare images of series that were taken with a different patient position or direction of examination more easily.

Flipping images vertically

✧ Select the images that you want to flip.

✧ Call up **Image > Flip Vertically** or click on the **Flip Vertically** button on the **Image** subtask card.

The image is flipped around a vertical axis.

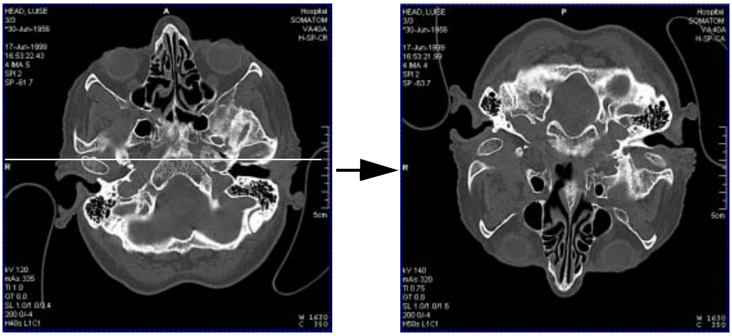


The orientation labels are changed round accordingly.

Flipping images horizontally

✧ Call up **Image > Flip Horizontally** or click on the **Flip Horizontally** button on the **Image** subtask card.

The image is flipped around a horizontal axis.



The orientation labels are changed round accordingly.

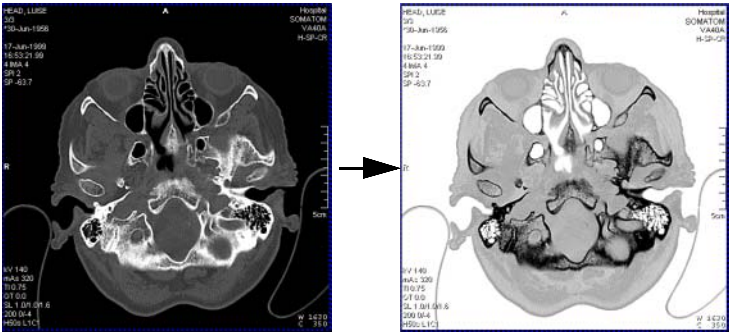
> **NOTE**
>
> Just like when you rotate images, when you flip them, all annotations and graphics are deleted from the images.

Inverting images (Invert)

When an image has been inverted, light areas are displayed dark and dark areas light. The gray scale assignment in the LUT (Look Up Table) is inverted.

✧ Select the images that you want to edit.

✧ Call up **Image > Invert Gray Scale**.



➪ To reset the original view, call up **Image > Invert Gray Scale** again.

CHAPTER
E.5 2D Evaluation

On the **Viewing** task card, you have tools for region evaluation, measuring distances, lengths, and angles, and for pixel evaluation.

You can also have a grid displayed in selected images, to allow you to estimate sizes, distances, and angles more precisely.

With a shutter, you can restrict the region of interest to what is absolutely necessary excluding all irrelevant regions.

You can annotate images with image texts in order to document your evaluation.

You can enter comment texts for the images in the database and edit existing comment texts.

CAUTION

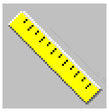
Source of danger: Distance measurements in the topogram

Consequence: Incorrect measurement values due to the projection technique used

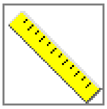
Remedy: Only perform distance measurements in the topogram in the longitudinal direction (head-foot direction)

Activating a graphic tool

You will find the tools for drawing graphics and determine pixel values in the **Tools** menu or on the **Tools** subtask card in the control area.

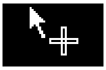


Inactive



Active

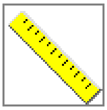
✧ Activate a graphic tool by selecting it in the menu, or click on the button.



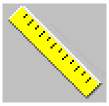
The mouse cursor becomes a graphic cursor.

You can now use the tool until you deactivate it again. For example, you can draw several regions or distances into your image one after the other.

Switching off a graphic tool



Active



Inactive

✧ Deselect the tool in the menu again.

Or

✧ Click on the button again.

Or

✧ Press the **Esc** key of your keyboard.

Or

✧ Select another graphic tool.

Paying attention to the selection

The graphic tools of the **Viewing** task card work implicitly, i.e. you do not have to select the images in which you draw the graphics explicitly. You can simply place the mouse cursor on the image. The input focus is placed on this image.

If you want to produce a graphic element on more than one image at once, you must first select these images explicitly.

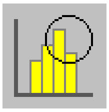
→ Page E.3–31, *Selecting images*

➩ You can only edit, i.e. resize, graphics in one image.

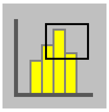
Evaluating regions

You can mark anomalies in the images and then evaluate these regions. To do this you draw a ROI graphic around the region of particular interest to you. You can now evaluate the gray scales within this ROI statistically (CT, MR only).

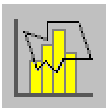
ROIs (Regions of interest) can be:



Circular



Rectangular



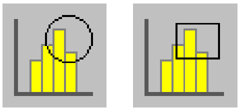
Freehand regions or polygons

Rectangular and circular ROIs

You can draw around the regions that are of special interest with a rectangle or circle and evaluate them. First select the tool.

✧ Call up **Tools > Circle** or **Tools > Rectangle**.

Or

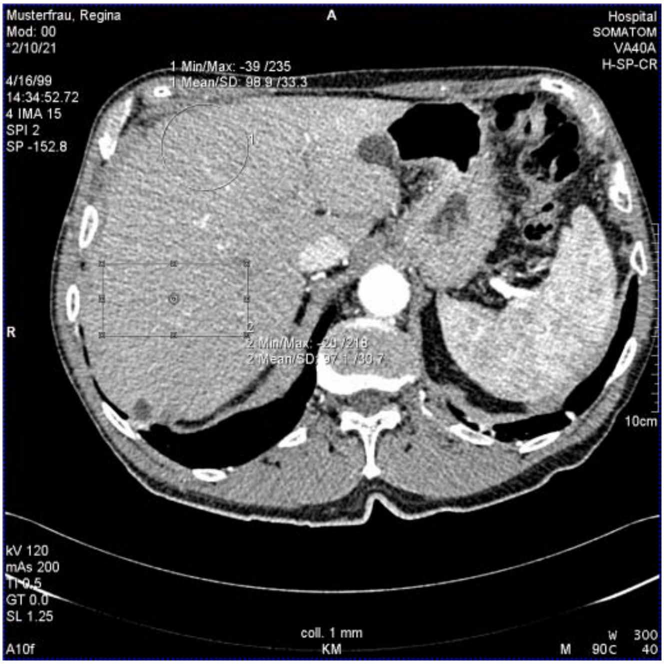


✧ Click on the **Circle** or **Rectangle** button on the **Tools** subtask card.

The mouse cursor changes shape.

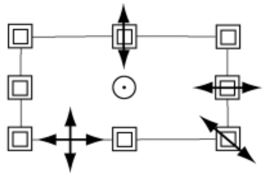
✧ Click on the image and draw the ROI (rectangle or circle) while holding the mouse key pressed.

✧ Release the mouse key as soon as the ROI has the desired size.



Resizing/moving regions

If your rectangle or circle is too small or too large or is not quite in the right position, you can still change the ROI. As soon as you move the mouse over the ROI the cursor changes shape and you can alter the graphics.



✧ Click on the border of the ROI to select it.

Or

✧ Place the mouse cursor on the border of the ROI.

✧ Enlarge or reduce the regionusing the grab handles until it meets your requirements.

Or

✧ Move the region in the image by positioning the cursor on the border line between the grab handles.

➩ You can move a small ROI easier by pressing the “Alt” key. The cursor then switches into the move mode automatically.

➩ No center is displayed for circular ROIs.

Drawing freehand ROIs

If a circle or rectangle is too imprecise to describe your ROI, you can draw a polygon or freehand region instead. This way you can draw the region that is of interest to you more precisely.

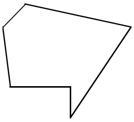
- Call up **Tools > Freehand ROI**.

Or

- Click on the **Freehand ROI** button on the **Tools** subtask card.
  The mouse cursor changes shape.

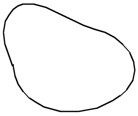
There are two methods for drawing freehand ROIs:

Drawing point to point (polygon)



- Click on the image to determine the starting point and drag a line to the first vertex (turning point) with the mouse.
- Draw the region point to point by clicking with the mouse at each change of direction (polygon definition).
- Once you double-click on the last vertex, the system closes your graphic.

Drawing a freehand region

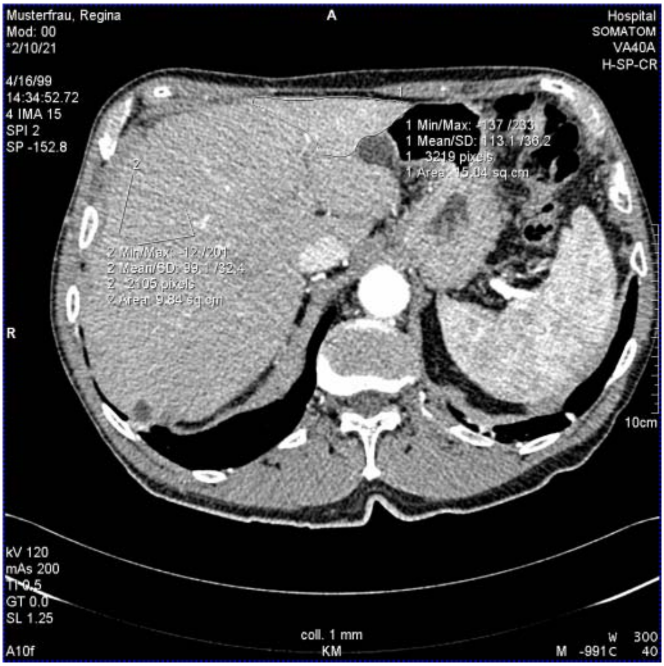


✧ Click on the image to determine a starting point.

✧ Hold the mouse key pressed and move the mouse around your region of interest.

✧ Double-click on the end point to close your region.

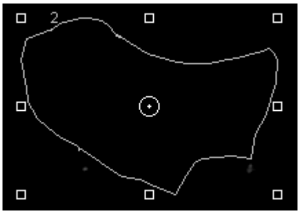
The program will connect the starting point and the end point and display the freehand ROI.



Enlarging/reducing an region

Like the rectangles and circles, you can also enlarge or reduce freehand regions or move them in the image.

✧ Select the region by clicking on it.
Grab handles will now be displayed.



✧ Change the size by dragging one of the handles.

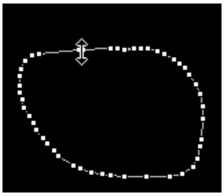
Changing the shape of the graphic

You can also change the shape of a freehand region or polygon. To do that, you activate the editing mode in which you can see a node at every change of direction of your freehand line. You can move this node in order to change the shape.

✧ First select the region (**left** mouse key).

✧ Then select **Edit** in the popup menu (**right** mouse key).

Nodes are now displayed instead of the grab handles.



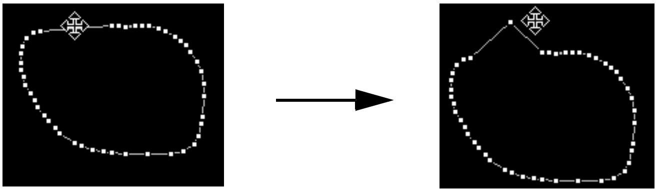
Inserting a new node

To enlarge a freehand region or a polygon or to define shapes more accurately, you can insert nodes.

✧ Click on the **polygon line** with the left mouse key, i.e. the border of the selected region, **between two nodes**.

✧ Drag the line to another position in the segment with the mouse key pressed.

A new node is added and the region remains in editing mode.



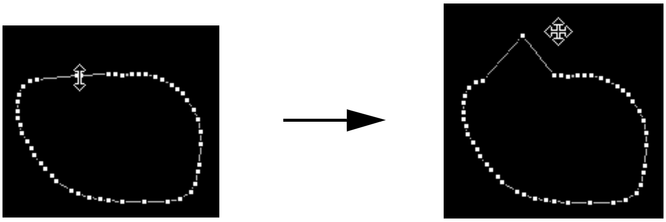
Moving a node

You can change the shape of the region by moving individual nodes.

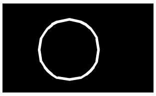
✧ Click **on one node** with the left mouse key.

✧ Drag the node to a new location holding the mouse key pressed.

The node is moved and the region remains in editing mode.



Rounding the polygon



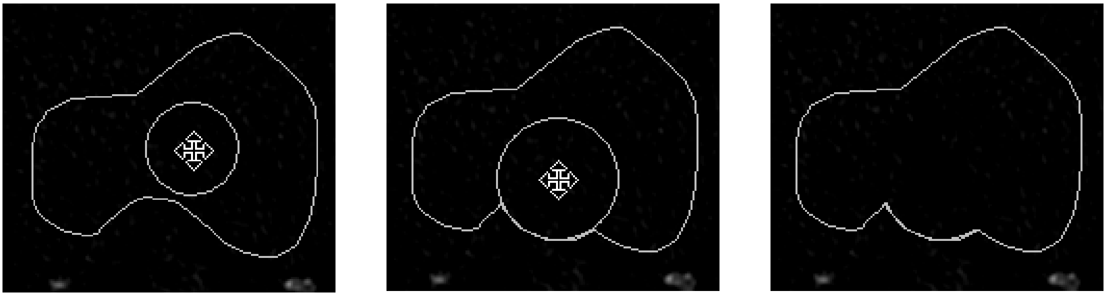
You can round off the edge of your freehand region.

✧ Select the region and call up **Edit**.

✧ Click **into the region** with the mouse cursor, but not on the polygon line or a node and hold the mouse key pressed. The mouse cursor becomes a circle.

✧ Move the circular mouse cursor to the border.

If the mouse cursor touches the line, all the nodes are moved in the direction of the movement of the mouse.



➩ The size of the mouse cursor depends on how near you click to the border of the polygon. For a precise definition, click very close to the border, for example, to obtain a very small circle.

Exiting editing mode

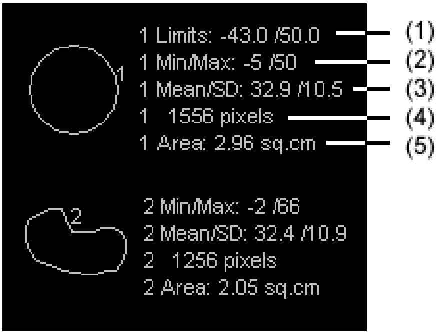
✧ Click on any point in the image with the left mouse key, but not on the edge of the ROI.

The editing mode is closed, and the region is deselected.

Evaluating ROIs

As soon as you have drawn a border around the regions of interest with a circle, rectangle or freehand line, a statistical evaluation of the ROI will be displayed.

The ROIs are now numbered. To avoid confusion, the number of a ROI is shown in front of every evaluation result.



1 Limits: -43.0 /50.0
1 Min/Max: -5 /50
1 Mean/SD: 32.9 /10.5
1 1556 pixels
1 Area: 2.96 sq.cm

2 Min/Max: -2 /66
2 Mean/SD: 32.4 /10.9
2 1256 pixels
2 Area: 2.05 sq.cm

(1) Limits
Evaluated gray scale range. The limits are taken into account in the following evaluations.

(2) Min/Max
Highest and lowest gray scale value

(3) Mean/SD
Mean value and standard deviation of the gray scales

(4) Number of pixels
Number of pixels in the ROI

(5) Area
Area of the ROI in cm^2

You can move the text block of the evaluation results to any location in the image.

✧ Click on the text block and move it with the mouse.

Showing/hiding statistical evaluations

The display of evaluation results was set up by Siemens Service during configuration of your system. The min/max and the average mode are the default settings. In **Viewing Configuration**, you can change these default settings.
→ Page E.8–2, *Displaying evaluation results*

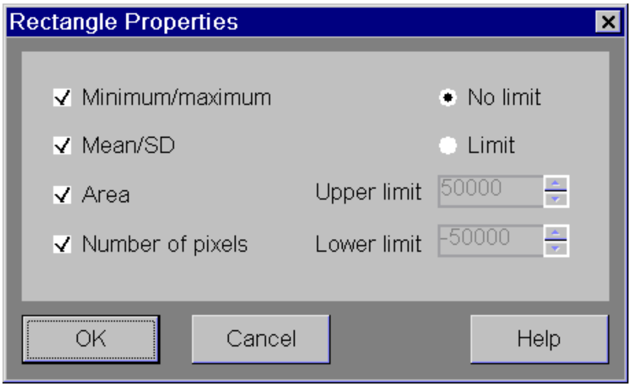
If you want to change or hide the display of evaluation results of certain ROIs only, call up the **Properties** dialog box for a particular ROI.

✧ Select the ROI.

✧ Call up **Edit > Properties** or call up **Properties** in the popup menu (right mouse key).

➪ If a ROI is not completely on the image, i.e. the black area of the border extends beyond the edge of the image, it is not possible to evaluate the region. You then obtain “???” as the area value.

A dialog box is displayed in which you can change the display of evaluation results for the selected ROI.



☑ Minimum/maximum
☑ Mean/SD
☑ Area
☑ Number of pixels

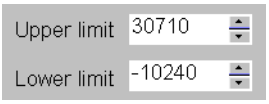
● No limit
○ Limit

Upper limit 50000
Lower limit -50000

✧ Click on the check box of individual evaluation results to show or hide these result lines.

✧ Select the **No Limit** radio button to evaluate the entire gray scale range of the ROI.

Or



Upper limit 30710
Lower limit -10240

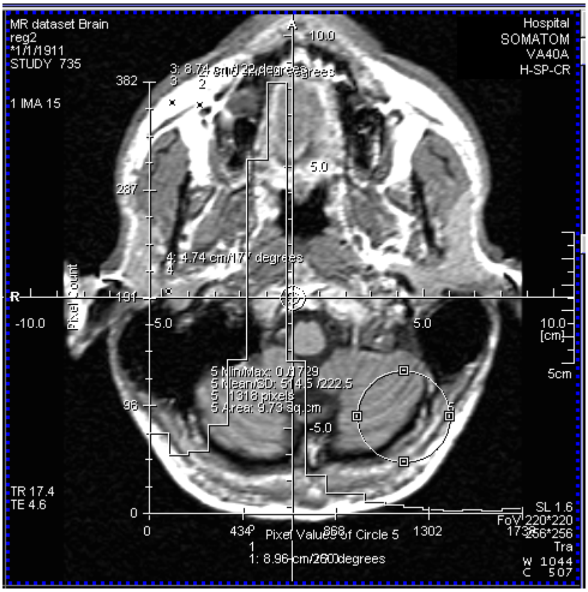
✧ Select the **Limit** radio button to evaluate only those pixels of the ROI that are within a gray scale range that you can now define.

Calculating a histogram

You can have the distribution and frequency of gray scales (or Hounsfield Unit values) calculated across the surface of a drawn in ROI.

✧ Call up **Tools > Histogram**

The histogram is placed over the image. Below the X axis label you can see which ROI the histogram belongs to (e.g. *Pixel Values of Region 1*).



➪ An image is always stored and filmed/printed out with the histogram(s) displayed on it.

Measuring distances and angles

You can measure and evaluate not only regions, but also distances and angles in images.

CAUTION

Source of danger: Distance measurements in MIP images

Consequence: False diagnosis possible

Measure: Do not use distance measurements in MIP images for diagnostic purposes.

Drawing a distance line, measuring the distance

Using a distance line, you can measure the distance between two points in an image. You can also have the statistical evaluation of the gray scales displayed for this line.

Drawing a distance line

✧ Call up **Tools > Distance**.

Or

✧ Click on the **Distance** button of the **Tools** subtask card.

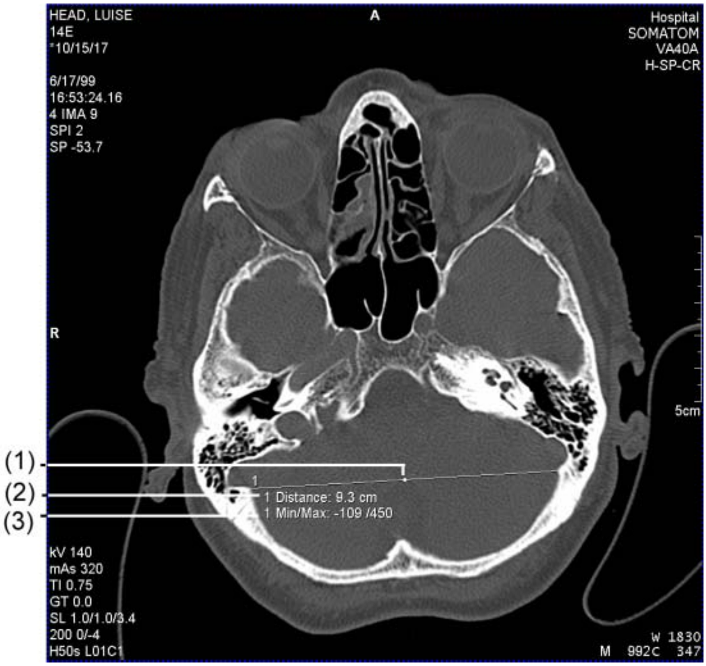
The mouse cursor changes shape.

✧ Place the mouse cursor on the starting point of the distance line.

✧ Hold the left mouse key down and drag out a line.

As soon as you move the mouse, the length of the straight line you have drawn so far is displayed.

✧ Release the mouse key to finish the line.



(1) Center
Center of the line
(2) Distance
Distance between the beginning and end point
(3) Min/Max
Minimum/maximum gray scale value on the straight line

The distance evaluation mode is the default setting.

Changing the distance line

✧ Click on a distance line with the left mouse key.

Or

✧ Place the mouse cursor on the line.

At positions at which you can edit the line, the mouse cursor changes shape.

✧ Drag the starting or end point of the line to another position.

The distance is updated as soon as you move the mouse cursor.

Or

✧ Move the entire distance line to another location.

Showing/hiding statistical evaluations

Like with regions, with distances, too, you can show or hide statistical values individually.

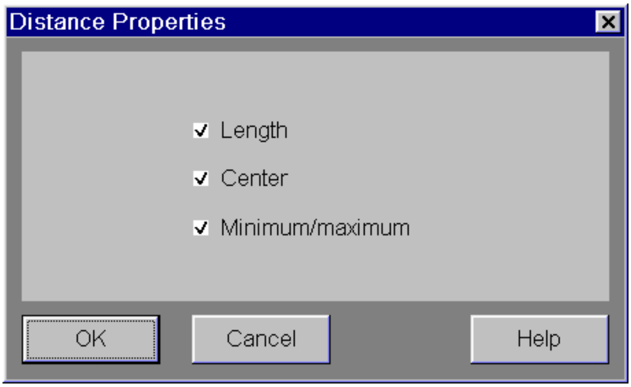
✧ Select a distance line (left mouse key).

✧ Click on a selected distance line with the right mouse key and select **Properties...** in the popup menu.

Or

✧ Click on the **Distance** button with the right mouse key, and select the **Properties...** entry in the popup menu.

The **Distance Properties** dialog box is displayed.



Distance Properties

☑ Length

☑ Center

☑ Minimum/maximum

✧ Select the evaluation results that you want displayed for your distance line.

Drawing a freehand line, measuring a distance

You can measure not only the direct distance between two points, but also the length of a structure, i.e. a blood vessel, by drawing the shape with a freehand line.

✧ Call up **Tools > Freehand Distance**.

Or

✧ Click on the **Freehand Distance** button on the **Tools** subtask card.

Point to point

✧ Place the mouse cursor in the segment and click on the starting point of your line with the left mouse key.
The mouse cursor changes shape.

✧ Click on the first point at which you want your line to change direction.

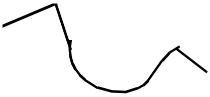
✧ Then click on the next point etc. until you have drawn the entire freehand line point by point.

✧ Double-click on the end point.

Drawing a freehand line

- ✧ Click on the starting point of your freehand line with the left mouse key.
- ✧ Draw the structure with the left mouse key pressed.
- ✧ Double-click on the end point.

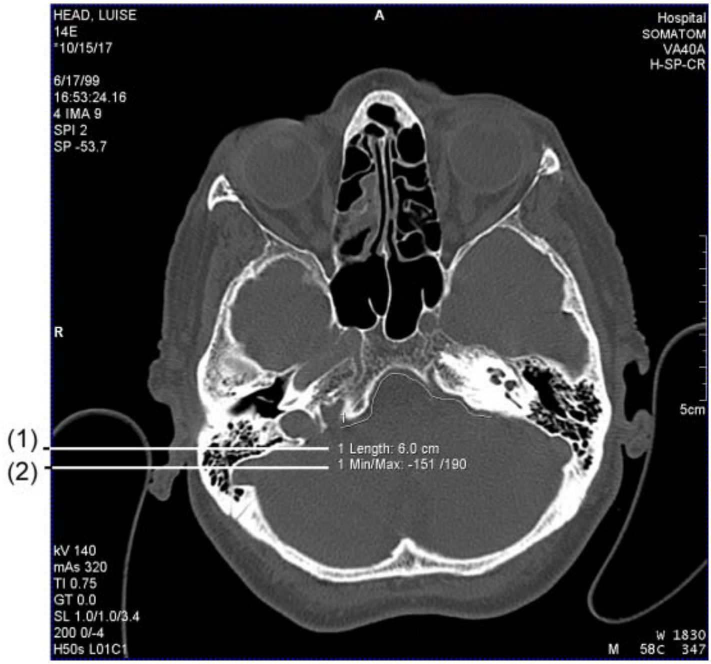
➪ Like with a freehand ROI, you can change the shape of your freehand distance line subsequently by editing its nodes.



For some applications, it might be necessary to draw a freehand line that consists of a polygon definition and a freehand line.

As long as you have not double-clicked the end point, you can mix the two methods, polygon definition and freehand line.

After you have completed your freehand line, the following values are displayed.



(1) Length
Length of the line

(2) Min/Max
Minimum and maximum gray scale value on the line

The length evaluation mode is the default setting.

Showing/hiding statistical evaluations

If you do not want to display one or more of the values about your freehand line, call up the **Open Polygon Properties** dialog box.

✧ Select the freehand line (left mouse key).

✧ Click on the selected line with the right mouse key and select the **Properties...** entry in the popup menu.

Or

✧ Click on the **Freehand Distance** button with the right mouse key and select **Properties...** in the popup menu.

☑ Length

☑ Minimum/maximum

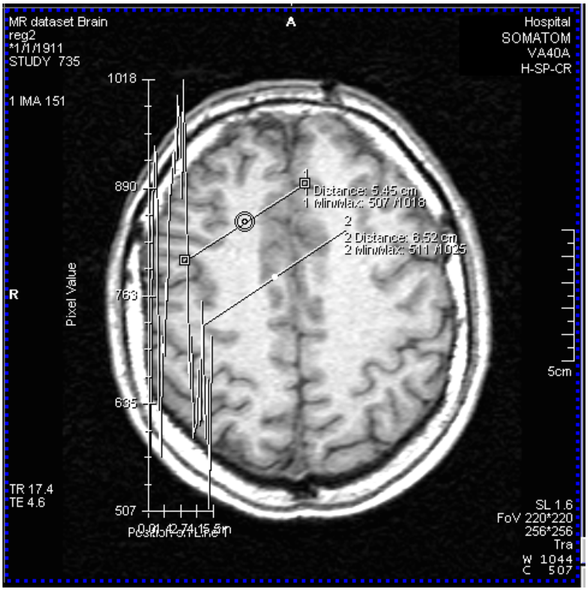
✧ Select or deselect the evaluation results that you want displayed or not displayed.

Calculating a profile

You can calculate the profile of the distribution and frequency of gray scales (or HU values) along a distance measurement or freehand line.

✧ Call up **Tools > Profile**.

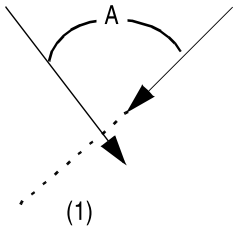
The profile is placed on the image. Below the X axis label you can see which line the profile belongs to (e.g. *Pixel Values of 1*).



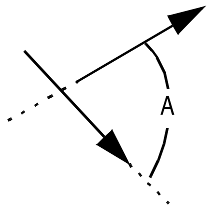
➩ An image is always stored and filmed/printed out with the profile(s) displayed on it, if applicable.

Measuring an angle

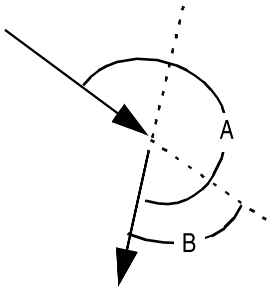
You can define an angle by two lines, the legs of the angle, that you draw on the image. The system then calculates the angle between the two lines drawn in **clockwise**. If the angle is greater than 180°, the program subtracts 180°.



(1)



(2)



(3)

The direction of the arrow indicates the direction in which you have drawn the legs of the angle.

➪ The display of the lines as arrows in the figure is for demonstration purposes, only.

(1) Both legs were drawn in the direction of the intersection. The angle A between the legs is displayed.

(2) Both legs were drawn away from the intersection. The angle A between the legs is displayed.

(3) Otherwise, the angle B (A - 180°) is displayed.

✧ Call up **Tools > Angle**.

Or

✧ Click on the **Angle** button on the **Tools** subtask card.

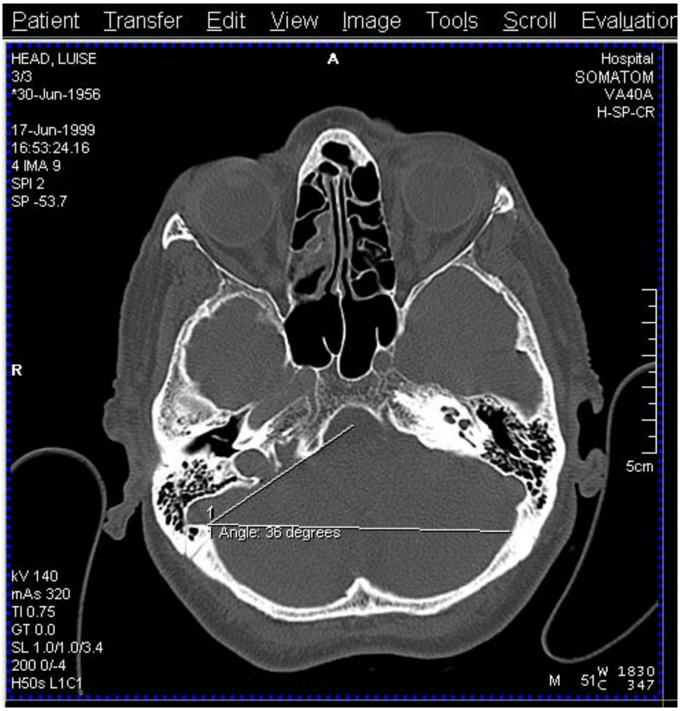
✧ Place the mouse cursor on a starting point for the first leg. The mouse cursor changes shape.

✧ Drag a line to the end point of the first leg holding the left mouse key pressed.

✧ Draw the second leg in the same way.

As soon as you start to draw the second leg, the angle size will be calculated.

➩ The two lines between which you want to measure an angle do not have to intersect in the image. The program automatically calculates the point of intersection even if you have not drawn it or if it is beyond the edge of the image.



The two legs of an angle are assigned the same number so you can distinguish several angles unambiguously.

Changing an angle

You can change the legs of an angle independently.

✧ Move the mouse cursor into the image.

At those positions at which you can change a leg of an angle, the shape of the mouse cursor changes.

✧ Move the entire line or drag an end point to another location.

The angle is constantly updated.

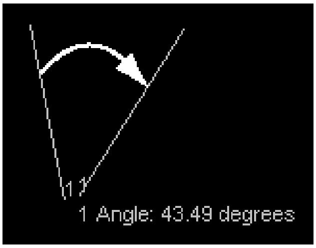
Switching the angle direction

You can also have the complementary angle displayed (180° - angle measured).

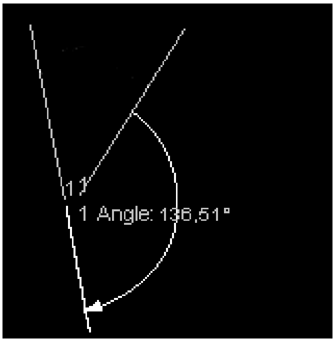
✧ Select the angle.

✧ Call up the popup menu with the right mouse key and select the entry **Other Angle**.

The angle is now measured counterclockwise and the new value displayed.



Angle between the legs



Complementary angle

NOTE

If the angle approximates to 90°, 180°, 270°, it is not clear whether the angle between the legs or the supplementary angle has been entered.

➩ Label the angle with an annotation when you display the supplementary angle.

Angle across 2 images

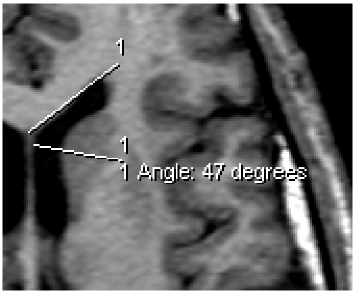
✧ Select the images.

✧ Draw an angle in one image.

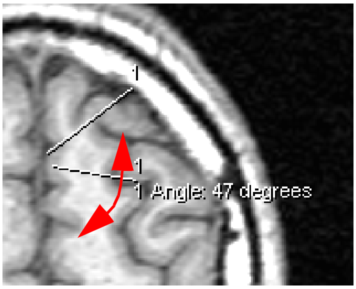
The angle is also drawn into image 2.

✧ Adjust the angle in the other image.

➪ The correction is only visible in image 2 and is not applied to image 1.



Angle in image 1



Angle in image 2

Measuring pixels with the crosshair

For stereotaxie and in radiation therapy preparation you display a crosshair to measure pixels. Using the crosshair you can determine the position of pixels and angles with reference to a starting point and two axes at right angles to each other in several images at the same time.

Displaying a crosshair

✧ Select the image or images in which you want to display the crosshair.

✧ Call up **Tools > Crosshair**

The crosshair is displayed in the selected images.

Moving the crosshair

Moving the crosshair is not possible. Wrongly positioned crosshairs must be deleted and recreated.

NOTE

This functionality ’How to Move a Crosshair’ as described in the online help is not implemented.

Measuring with the crosshair

✧ Click on the points in the image whose position you want to determine.

Depending on the setting, the coordinates of the point, or its distance from the origin and angle to the X axis are displayed.

✧ One after the other, click on all the pixels that you want to measure.

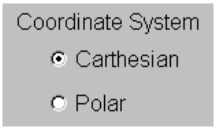
The crosshair and the measuring points are stored with the image and can be filmed and/or printed with it.

Changing the measuring method

✧ Click on one of the axes of the crosshair to select it.

✧ Call up **Edit > Properties...**, or select **Properties...** in the popup menu.

The dialog box **Crosshair Properties** is displayed.



Coordinate System

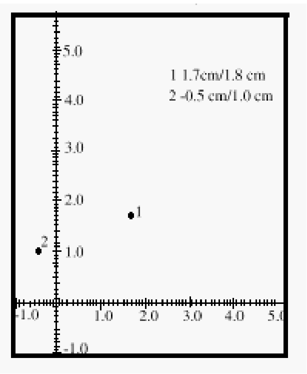
● Carthesian

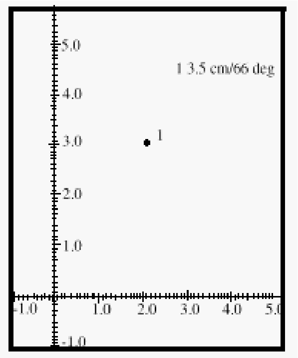
○ Polar

✧ Select the option **Carthesian** under **Coordinate System** to calculate the coordinates of pixels.

Or

✧ Click on the option **Polar** to have the distance between a measuring point and the origin, and the angle between that distance line and the X axis displayed.





✧ Confirm your selection and close the dialog box with **OK**.

✧ Now click on the other pixels to measure them by the new method.

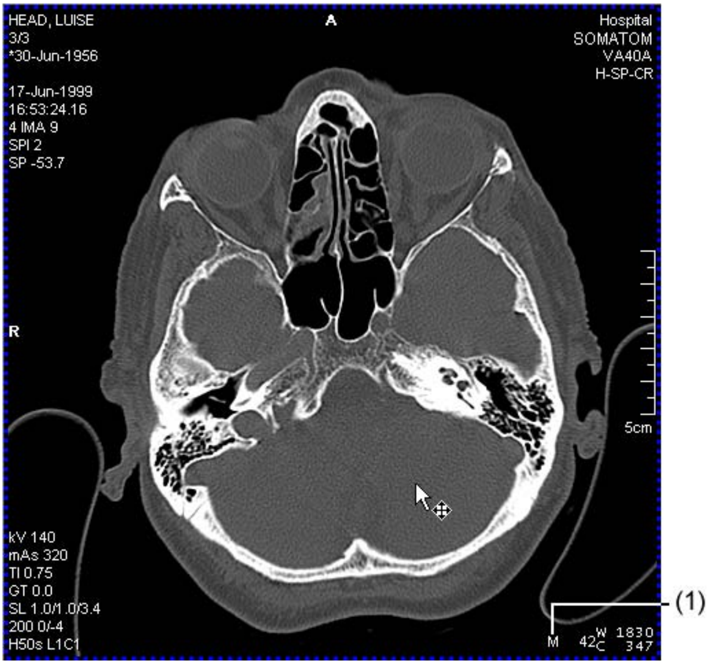
Evaluating pixels, pixel lens

With the pixel lens, you can display the average value of the gray scales (e.g. Hounsfield values for CT images) of a small area of 5× 5 pixels.

Mini Mean

The average gray scale value of the pixel lens is displayed in the bottom right-hand corner of the image next to the window values. It is formed from the values (5× 5 pixels) of the pixel lens. An M (for mean) is shown in front of the mean value. This value is determined at the current position of the mouse cursor.

If you move the mouse cursor over the image, the current pixel values are displayed in the bottom right-hand corner of the image.



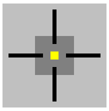
(1) Pixel value

Displaying pixel values permanently

You can have the values of pixels that are especially interesting to you displayed permanently in the image.

✧ Call up **Tools > Pixel Lense**.

Or



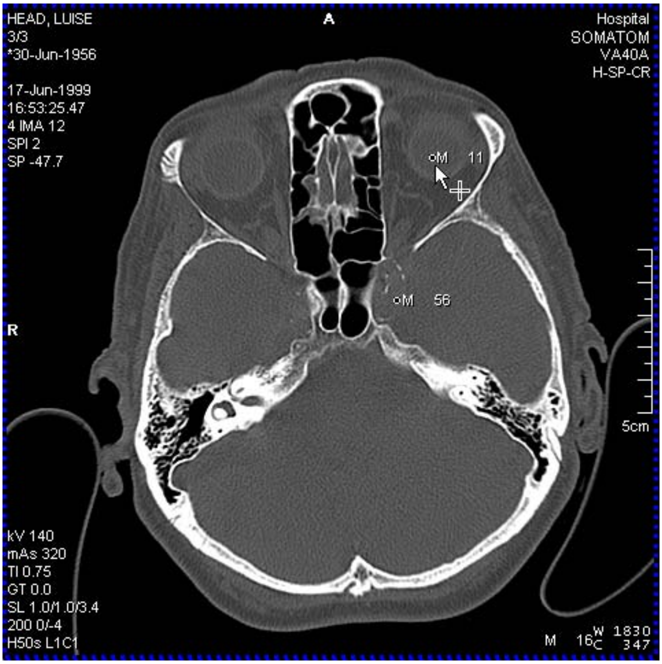
✧ Click on the **Pixel Lense** button on the **Tools** subtask card. The cursor changes shape.

✧ Click on the image with the left mouse key.

This pixel is marked, the pixel value is displayed next to the marker.

NOTE

The displayed lens area does not reflect the currently measured result, but has a constant size and is independent of the zoom factor of the image.



➪ You can also move a permanently displayed pixel marker of this type, the value is then updated.

Setting a shutter

You can hide irrelevant areas of the image. To do that, you place a shutter over the image.

After that, only the area within the shutter is displayed and all the surrounding areas are displayed black.

Setting a shutter

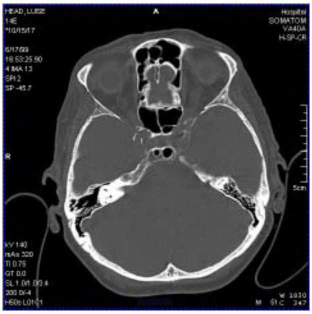
✧ Call up **Tools > Shutter**.

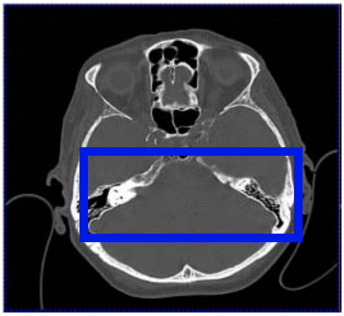
✧ Place the mouse cursor in the corner of the area of the image that you want displayed.
The mouse cursor changes shape.

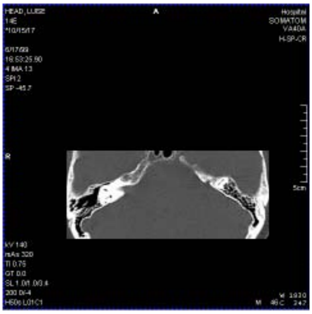
✧ Hold the left mouse key pressed and drag a rectangle open for the shutter.

➩ By clicking on the border of the image you can select a shutter which you can then move or resize.

When you release the mouse, the area outside the shutter is displayed black.







Removing the shutter

✧ Click on the border of the shutter to select it.

Or

✧ Call up **Edit > Select All Shutters In Series** if you have set several shutters within a series.

Or

✧ Call up **Edit > Select All Shutters**.

All shutter settings are now selected.

✧ Call up **Edit > Delete Graphics**, or select **Delete** in the popup menu.

Or

✧ Press the **Del** key on your keyboard to show the entire series in its original view again.

Working with grids

As an aid to orientation and estimating the sizes and angles in images, you can display a grid in selected images.

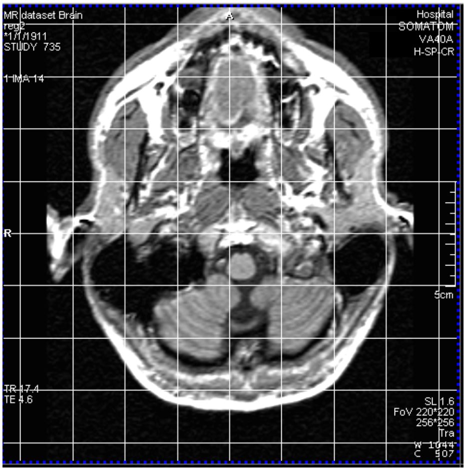
The grid consists of parallel, horizontal and vertical lines. The distance between the grid lines (grid width) can be adapted individually.

The grid and grid settings are stored together with the images.

Displaying a grid

✧ Select the image or images in which you want to display the grid.

✧ Call up **View > Scalegrid** to display the grid.

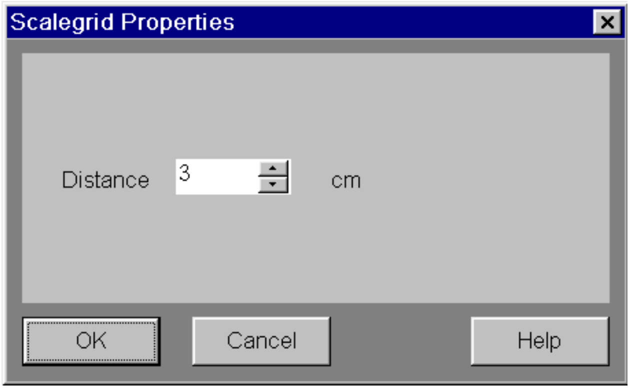


Changing grid settings

✧ Click on one of the grid lines to select the grid.

✧ Call up **Edit > Properties...** in the main menu or **Properties...** in the popup menu (right mouse key).

The dialog box **Scalegrid Properties** is displayed.



Distance 3 cm

✧ Pick a new grid distance from the spin box **Distance** to change the grid width.

✧ Click on **OK** to accept the changed grid settings and close the dialog box.

If you now zoom the images, the grid width is adapted to the new sizes. If you move the image center (panning), the grid is also moved.

Deleting the grid

✧ Select the grid again by clicking on one of the grid lines.

✧ Call up **Edit > Delete Graphics**, or select **Delete** in the popup menu.

Or

✧ Press on the **Del** key on the keyboard.

The grid is again removed from all selected images.

Text in images

You can annotate interesting or anomalous areas of the images. You can also edit annotations that you entered earlier at any time.

In some modalities, you can also store comment texts with acquisition series. These comment texts are also displayed in the images and can be altered.

Entering comment texts

You can always change image descriptions that you entered at an earlier date.

✧ Call up **Tools > Annotate**.

Or

✧ Click on the **Annotate** button on the **Tools** subtask card**.**
The mouse cursor changes shape.

✧ Click on the position in the image at which you want to insert the text with the left mouse key.

The mouse cursor becomes a text cursor (small rectangle).


Annotate

✧ Now enter your text.

You can write up to 30 characters into a line, after that, line breaks are inserted automatically. You can force a line break by pressing **Shift + Return**.

✧ Terminate text entry with the **Return** key.

Or

✧ Click into the image outside the text.


Annotate

The text is displayed white with shading.

You cannot change the font size or the alignment of the text.

NOTE

Although the text can consist of more than one line, only the line you are currently editing is displayed.

Moving text

✧ Click on the text with the left mouse key, but not on the grab handles.

✧ Drag the text to the new position.

Changing text

✧ Double-click on the text with the left mouse key to change it. The mouse cursor changes into a text cursor (rectangle) and is located on the first position of the text.

✧ Now change or add to your text.

✧ You can exit text editing by clicking into the image outside the text frame or pressing the **Return** key.

The text is displayed without a background and frame again.

Anchored annotation text

If you want to write text marked with an arrow, pull open an arrow keeping the left mouse key pressed and then write your text in the text input field (end position of the arrow).

Editing image comments

If comment texts are displayed in some or all images, you can edit them. You can add comments to images that do not have any comment texts.

➪ Comment texts are only displayed if configured in the **Image Text Editor**.
→ Page A.2–8, *Configuring image text*

✧ Place the input focus on the image whose comment you want to edit, or select the image explicitly.
→ Page E.3–31, *Selecting images*

✧ Call up **Edit > Comment** in the main menu or **Edit comment** in the popup menu.

You can now see the text cursor at the beginning of the first comment line.

✧ Overwrite, delete or add to the comment text.

After 30 characters a new line is automatically started. You can force a line break by pressing **Shift + Return**.

If your comment is longer than 2 x 30 characters it cannot fully be displayed in the image, the second comment line then ends with three periods ("...").

✧ Terminate text input by pressing the **Return** key.

Or

✧ Click into the image outside the text.

➩ The two lines of text are treated as separate entities. There is no automatic line break.

Editing graphics and image text

You can select all graphics and annotation texts (except shutter) that you have entered in evaluating the images either individually or altogether in order to delete them, or cut or copy and insert them at a new position.

Selecting/deselecting all graphics and texts

✧ Call up **Edit > Select All Graphics** to mark all graphic elements and image texts of all explicitly selected images.

Or

✧ Select **Select All Graphics** in the popup menu (right-hand mouse key at any position in the image) to mark the graphic elements and image texts of all implicitly (including input focus) or explicitly selected images.

✧ Click into a segment but not on a graphic or text to deselect the marked graphics and texts on all images.

The standard input focus is set.

➪ You cannot select images and graphics together. If you select a graphic, all images are deselected and the input focus is placed on the image associated with the graphic.

Copying, cutting and pasting graphics

You can copy or cut individual or several selected graphic and text elements from an image and insert them into another image of the same patient.

✧ Select one, more than one or all graphic and text elements in an image.

✧ Call up **Edit > Copy** or select **Copy** in the popup menu to copy the selected graphic and text elements into the clipboard.

Or

✧ Call up **Edit > Cut** or select **Cut** in the popup menu to cut out the selected graphic and text elements and place them in the clipboard.

→ Page A.1–14, *Moving or copying objects*

You can now insert the graphic and text elements from the clipboard into another image.

✧ Select an image explicitly or place the input focus on the image.

✧ Call up **Edit > Paste**.

Or

✧ Place the mouse cursor in the image into which you want to insert the graphics.

✧ Select **Paste** in the popup menu.

➩ If the zoom factors of the original image and the target image are different, the size of the graphics is adjusted in the new image.

Deleting graphics

You can delete selected graphic and text elements when you no longer require them.

✧ Select individual, several or all graphic and text elements.

✧ Call up **Edit > Delete Graphics** or select **Delete** in the popup menu

Or

✧ Press the **Del** key on your keyboard.

The selected drawing elements and annotations are deleted.

CHAPTER

E.6

Dynamic Image Postprocessing

Image manipulation generates new images by applying mathematical processes to original images and series. You can then use these for further image processing or for evaluation.

By applying arithmetic functions to the gray-scale values of images you can, for example, enhance contrasts. You can also postprocess blurred images or images with a lot of noise with a filter.

A separate dialog window is displayed for every function that you call up for postprocessing. The functions **Subtract**, **Average** and **Filter** are available.

Prerequisites for Subtract and Average

Images must fulfill the following criteria:

- ☐ The images belong to the same study.
- ☐ The images have the same field of view (FoV).
- ☐ The images have the same matrix size.
- ☐ The images have the same slice orientation.

Prerequisites for Filter

- ☐ The images are acquired at a CT scanner.
- ☐ The series are acquired with software version VA40 and higher.
- ☐ The images belong to the same study.
- ☐ None of the selected series contains a topogram.
- ☐ The images are not already filtered.

Subtracting images

In subtraction, you subtract the gray-scale values of individual or several images/series from each other. Or you subtract a constant value that you define before starting subtraction, which is subtracted from every pixel in the image or vice versa.

By image subtraction you can make the changes in an image after contrast medium administration especially clear. You subtract the gray-scale values of the images without contrast medium from the contrast medium images. You thus obtain images that only show the changes highlighted by the contrast medium.

You can subtract the following data objects (operands) from each other:

- Constant from images/series
- Images/Series from constant
- Image from image
- Series from series (one or more)
  Where series contain differing numbers of images, the number of images in the smallest series prevails.

Calling up subtraction

You execute subtraction of gray scales in the **Subtract** dialog window that you call up after you have selected your original images and series.

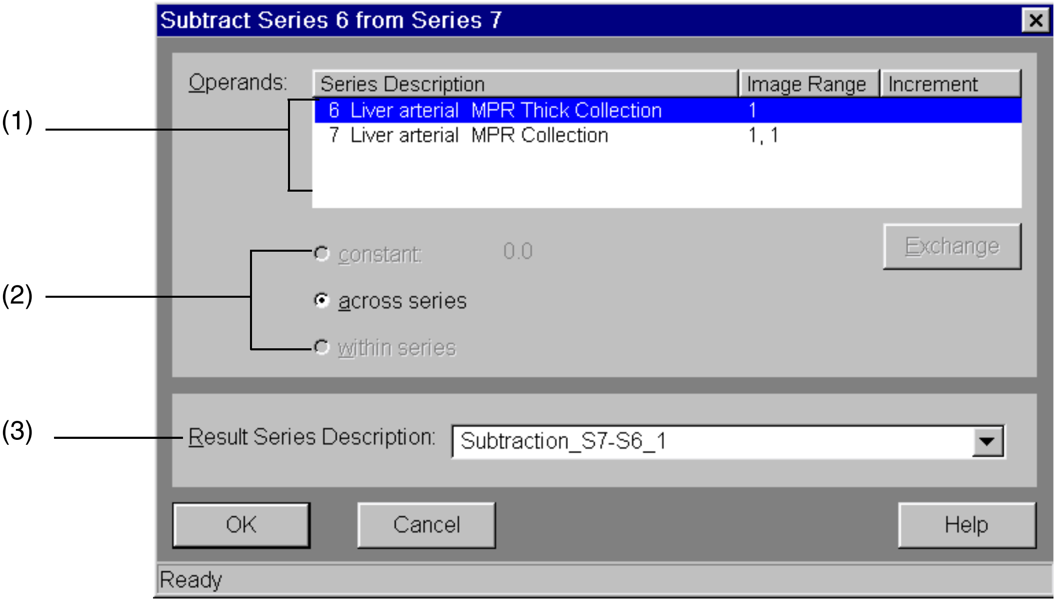
✧ Select individual images/series in the **Viewing** task card or in the **Patient Browser**.

✧ Call up **Evaluation > Subtract** in the main menu.

Or

✧ Click on **Subtract** in the **Evaluation** subtask card in **Viewing**.

The **Subtract** dialog window is displayed.



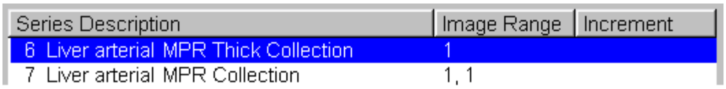
(1) Operand field with a list of loaded images and series

(2) Operation mode

(3) Name of the result series

Restricting and adding to the original images

In the upper part of the dialog window (operand field) you can see the list of operands. All selected images/series are listed in the column **Series Description** in the order in which they were acquired.



Series Description	Image Range	Increment
6 Liver arterial MPR Thick Collection	1	
7 Liver arterial MPR Collection	1, 1	

Displaying image range and increment

In the column **Image Range** you can see which images are available for evaluation.

In the column **Increment** you can specify an increment if you only want to use a subset of the existing original images for subtraction.

The following overview shows which original images are evaluated for the specified image range and increment:

Image Range	Increment	Images considered
1-n	<empty>	All images of a series
3	<empty>	3
2-5	<empty>	2, 3, 4, 5
2-10	3	2, 5, 8
2-5, 7-9	2	2,4,7,9
2-5, 7-9	3	2,5,7

Entering an increment

If you enter an increment you restrict the selection of original images.

✧ Select a series (line) in the operand field.

✧ Double-click on the selected series in the column **Increment**.

A spinbox for entering values is displayed.

Series Description	Image Range	Increment
4 Liver arterial	1-178	2

✧ Enter an increment.

✧ Complete your entry by clicking outside the spinbox with the mouse.

➩ For example, if you only want to apply subtraction to every second original image, enter the value 2 in the **Increment** column.

Adding original images

If you want to add further images to the image range displayed in the operand field, you can do that simply by drag and drop from the **Patient Browser**.

✧ In the **Patient Browser** select the next images of the series in question.

✧ Drag and drop them into the operand field.

The entries under **Image Range** are updated for the series to which you have added images from the **Patient Browser**.

Defining operands and operation modes

The type of subtraction you can apply (subtracting images or constants) will depend on the number and assignment of original images (in one or more series). Before you start subtraction, first define the sequence of operands, i.e. whether B is subtracted from A or A is subtracted from B.

Image minus constant

A constant can be subtracted from one or several images of a series. It is also possible to subtract one or more images of a series from a constant.

● constant: 100

✧ Select operation mode **constant** if you want to subtract a constant.

✧ Enter a value for the constant.

In the title bar of the dialog window you can see which operands are subtracted from each other.

If you want to subtract one or more images from a constant, reverse the operands.

✧ To do that, click on the button **Exchange**.

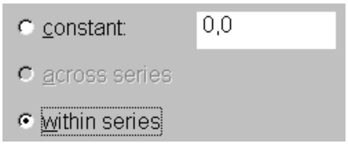
The display in the title bar is changed accordingly.

Image minus image (individual series)

If you have loaded one series with two images for subtraction, you can subtract the gray-scale values of one image from those of the other.

➪ If the series comprises more than two images, you can restrict the number of images to which subtraction will be applied to two.
→ Page E.6–6, *Entering an increment*

✧ Select operation mode **within series**.



○ constant: 0,0
○ across series
● within series

The type of subtraction is displayed on the title bar.

Image minus image (several series)

If you have selected two or more series in the operand field, the operation mode **across series** is already set. You only select the series whose images are to be subtracted from the images of the remaining series.

✧ In the operand field click on the series whose images are to be subtracted from the images of the remaining series.

Series Description	Image Range	Increment
5 Liver arterial MIP Thin Range	1-15	
6 Liver arterial MPR Thick Collection	1	
4 Liver arterial	135-1...	

NOTE

The sequence of subtraction is always remaining series - selected series.
If there are more than two series in the operand list, the selected list is subtracted from the remaining series.
A new series with the subtraction images is generated for every other series.

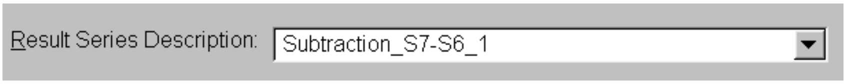
Performing a subtraction

With subtraction the results are stored in one or several new series.

Result series

The series description suggested by the system consists of the selected evaluation function (subtraction), the subsequent operand (S for series, I for image, and C for Constant) of a consecutive number.

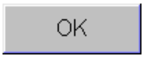
In the input field **Result Series Description** you can change the suggested name(s) for one of your own.



Result Series Description: Subtraction_S7-S6_1

✧ If necessary, enter a new name for the result series.

Starting subtraction



✧ Click on **OK** to start calculation.

The result of the calculation is an image (within a series) or a series of images (between series)

The number of result images that are stored in the database depends on the operands.

Operands:

Series Description	Image Range	Increment
5 Liver arterial MIP Thin Range	1-15	
6 Liver arterial MPR Thick Collection	1	

(1) Operand 1
(2) Operand 2

Operand1	Operand2	Mathematical operation	Number of result series	Number of images per series
constant	series1	series1-constant	1	as for series1
series1	constant	constant-series1	1	as for series1
image1 (series1)	image2 (series2)	image2-image1	1	1 image
series1	series2, ... seriesN	series2-series1...	N-1	as in smallest original series

Calculating the average

You can average out large differences in intensity from the images by calculating the average value of the gray scales. For parallel images with different slice positions, this method is equivalent to an MPR Thick display.
→ Chapter H.4, *Multiplanar Reconstruction (MPR)*

With a chronological sequence of images, averaging the images improves the signal-to-noise ratio and reduces image artifacts.

Calling up Average

You can calculate the average of the gray-scale values within the images of a series or across the images of several series. Averaging of gray-scale values is performed in the dialog window **Average** which you call up after you have selected the original images and series in the Viewing task card or in the **Patient Browser**.

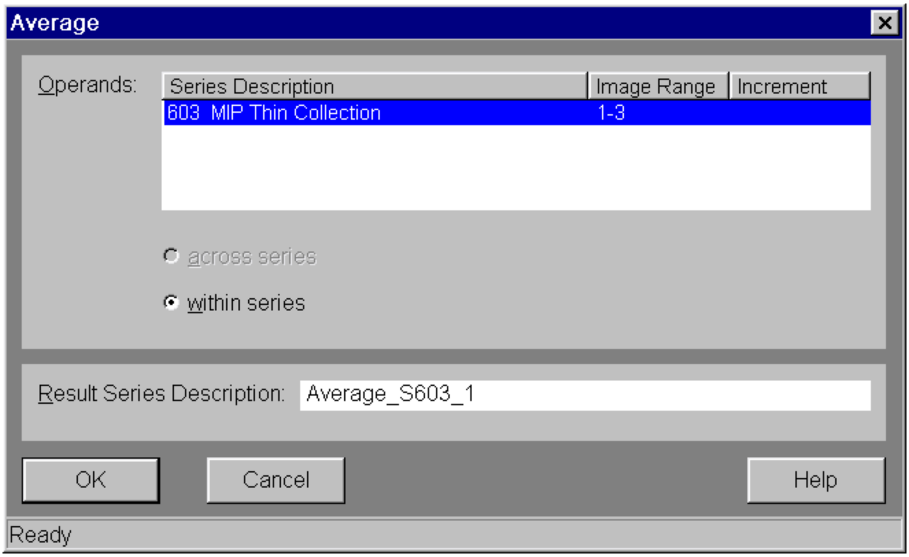
✧ Select one or several series in the **Viewing** task card or in the **Patient Browser**.

✧ Call up **Evaluation** > **Average**.

Or

✧ Click on the button Average in the **Viewing** task card/ **Evaluation** subtask card.

The **Average** dialog window is displayed.



Series Description	Image Range	Increment
603 MIP Thin Collection	1-3	

○ across series

● within series

Result Series Description: Average_S603_1

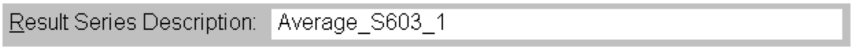
Ready

Calculating an arithmetic mean

Depending on whether you have loaded one or several series in the **Average** dialog window, either the option **within series** (one series) or **across** (several series) is preselected.

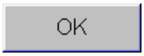
➪ You can specify an increment if you want to restrict the original images for the evaluation.
→ Page E.6–6, *Entering an increment*

Result series


Result Series Description: Average_S603_1

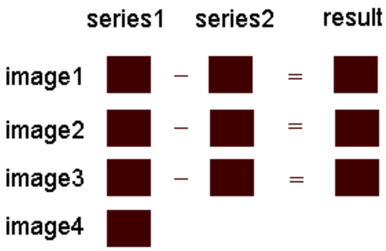
✧ If necessary, overwrite or change the suggested name for the result series.
→ Page E.6–10, *Result series*

Starting arithmetic mean



✧ Click on **OK** to start the calculation.

The result is a series with one image (within series) or a series of images (across series). Where series have different numbers of images the result series contains as many images as the smallest original series.



Filtering images

You can choose from several filter effects that subsequently optimize the image quality of the original images. For example, you can show soft tissue in close proximity to bone with greater contrast. You can also increase or reduce the contrast with preset filter values.

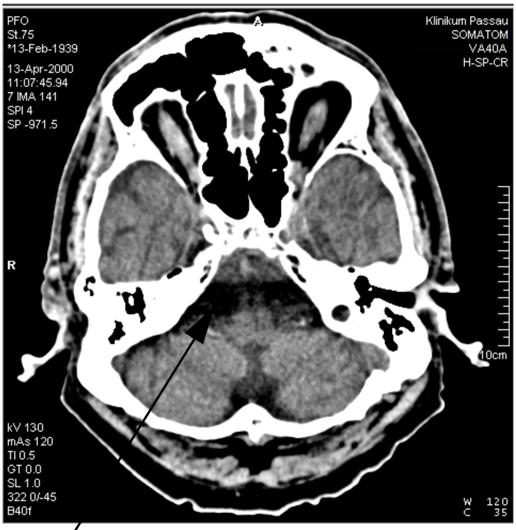


image before filtering

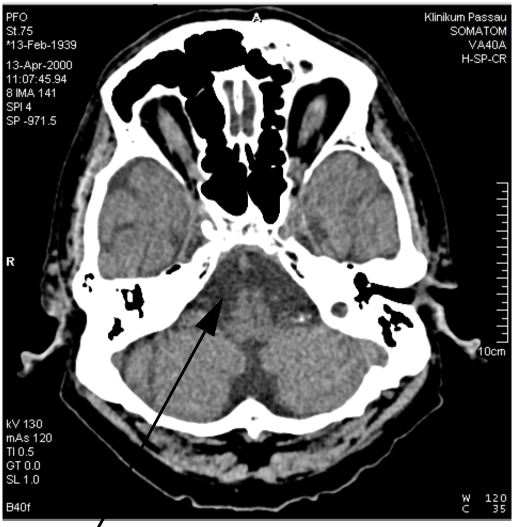


image after filtering

Calling up the filter

You will edit one original image at a time with a selected filter option. You will apply the filter to the original images in the Filter dialog window which you call up after you have selected the original image.

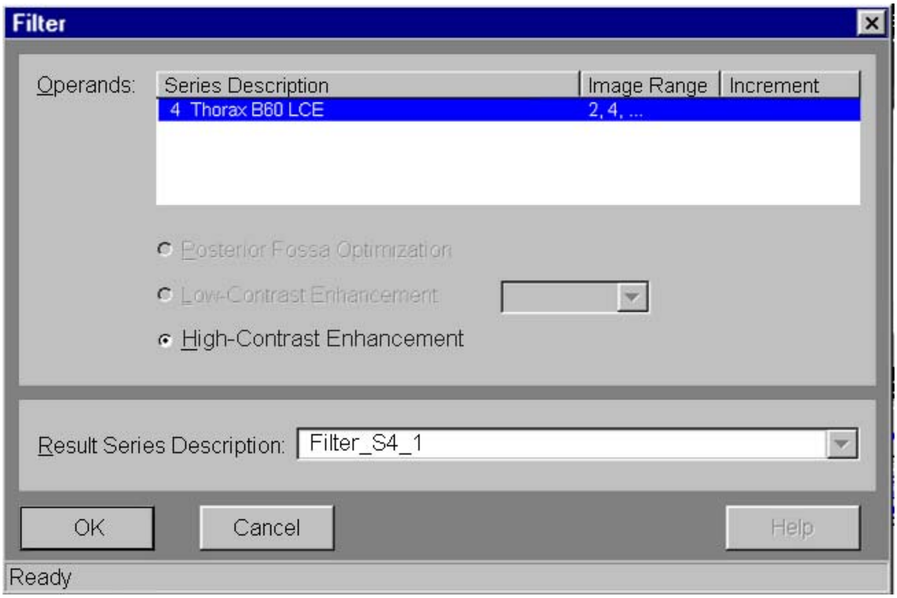
✧ Select one image or a set of images or series in the **Viewing** task card or in the **Patient Browser**.

✧ Call up **Evaluation > Filter**.

Or

✧ Click on the Filter button in the **Viewing** task card/ **Evaluation** subtask card.

The **Filter** dialog window is displayed.



Series Description	Image Range	Increment
4 Thorax B60 LCE	2, 4, ...	

○ Posterior Fossa Optimization

○ Low-Contrast Enhancement

● High-Contrast Enhancement

Result Series Description: Filter_S4_1

Ready

Filtering images

You can make your selection from three preset filter effects. The option **Low Contrast Enhancement** also offers you a listbox in which you can set four different levels of contrast from small to very strong.

Selecting a filter effect

✧ In the dialog window click on the filter option **Posterior Fossa Optimization**, **Low-Contrast Enhancement** or **High Contrast Enhancement**.

medium

✧ Select the contrast from the list box if you have selected the option **Low Contrast Enhancement**.

Result series

Result Series Description: Filter_S4_1

✧ If necessary, overwrite or change the suggested name of the result series.

→ Page E.6–10, *Result series*

Starting the filter

✧ Click on **OK** to start calculation with the set filter strengths.

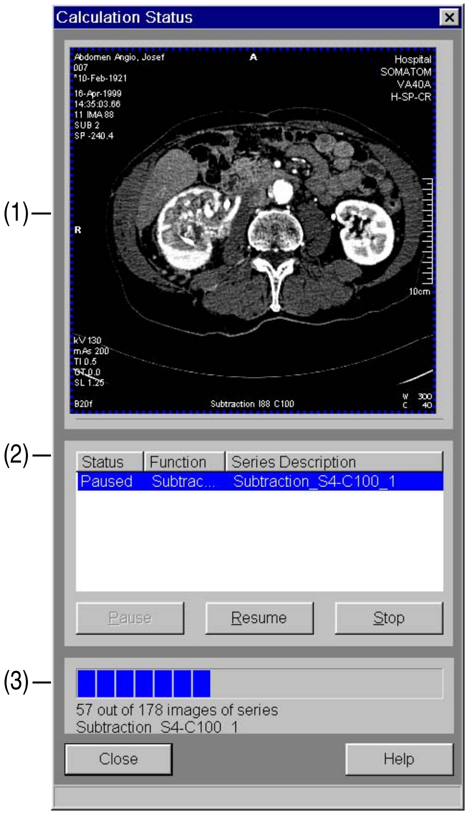
The result is a new series containing several images.

Monitoring evaluation progress

If you are evaluating a large number of extensive series, you can monitor the progress of evaluation, stop, continue, or cancel individual jobs.

✧ Click on the symbol **Image Manipulation** in the status bar.

The **Calculation Status** dialog window is displayed.



Status	Function	Series Description
Paused	Subtrac...	Subtraction_S4-C100_1

57 out of 178 images of series
Subtraction_S4-C100_1

(1) Image area
(2) Status display of evaluation jobs
(3) Progress indicator

Evaluation status

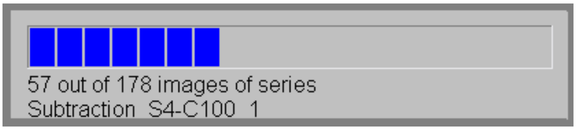
The evaluation jobs can be in one of the following processing states:

- ☐ **Active**, the job is being processed
- ☐ **Pause**, the job has been interrupted but can be continued
- ☐ **Aborted**, the job has been stopped before end of evaluation
- ☐ **Waiting**, the job is waiting to be evaluated

➩ If an active job is canceled, evaluation of the current image continues until the calculation is complete. Any images already calculated are stored in the database and can be viewed in **Viewing**.

Progress indicator

The progress indicator shows you how the current evaluation job is progressing.

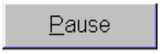


57 out of 178 images of series
Subtraction S4-C100 1

Controlling the evaluation progress

You can pause and then resume a current evaluation at any time, for example, to view an evaluated image and to check whether the evaluation meets your requirements.

Pause

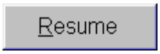


✧ Click on the **Pause** button to stop evaluation.

Calculation of the current image is completed and the status of evaluation is set to "Pause" in the image area. The **Resume** button is now no longer dimmed.

If the list contains a job with status "Waiting", it is automatically started.

Continue



✧ Click on the **Resume** button to continue a job with status "Pause".

If another job has been activated, it is placed in the queue.

Stop

You can cancel an active evaluation at any time if, for example, you notice that the evaluation does not meet your requirements.

➪ You can also cancel jobs with status "Waiting" or "Pause".

✧ To do that, click on the **Stop** button.

Calculation of the current image is completed and displayed in the image area. The status of the job switches to "Canceled".

Images that have already been calculated are stored in the database and can be displayed on the **Viewing** task card.

➪ The status display can show up to five canceled jobs. If you cancel a sixth job, the oldest canceled job is deleted.

Next job

Once a job has been processed, the images are displayed in the **Viewing** task card.

The next job with the status "Waiting" (the top one in the list) is automatically started.

Closing Calculation Status

✧ Click on the **Close** button to close the **Calculation Status** window.

Displaying the result images

The results are stored in the database under the name you have entered, and the results are displayed on the Viewing task card.

CHAPTER

E.7

Saving and Documenting Images

After image processing, when all the images have been displayed in an optimum way and have been evaluated, you can save, archive or transfer these images for further evaluation and documentation or for 3D postprocessing.

After that, you can close the images of this patient and make space in the **Viewing** task card for the images of the next patient.

Saving images

After you have completed processing and evaluation of the images, you save your results.

You can save your images in one of two ways:

☐ You can place the processed images in a new series, or
☐ You can add the images to an existing series.

Before each storage operation, the system checks whether the capacity of your hard disk is sufficient for saving these images.

If not enough free storage capacity is available, a message box is displayed.

✧ In this case, delete all the data which is **no longer required** and is already archived from your hard disk before saving your images.
→ Page D.5–16, *Deleting data*

NOTE

Graphics in medical images are not saved automatically in the same way as image text. If you want to save an image with graphics drawn in it, you must save it as a new image with **Patient** > **Save As...** .

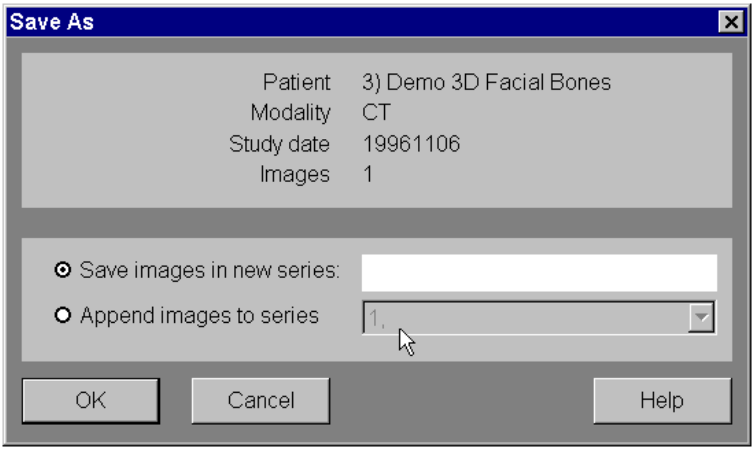
Calling up the Save As dialog box

Only images of the same study can be saved together in one series.

✧ First select the images or series that you want to save.

✧ Call up **Patient > Save As**.

The **Save As** dialog box is displayed.



Patient 3) Demo 3D Facial Bones
Modality CT
Study date 19961106
Images 1

● Save images in new series:
○ Append images to series 1.

Saving images as a new series

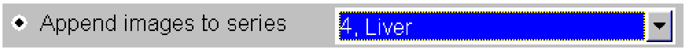
You can save all selected images in a new series. The old series remains unchanged. You can then easily compare processed and evaluated images with the original study images.

- ✧ Click on the **Save images in new series** option in the **Save As** dialog box.
- ✧ Enter the new series description in the text input field. The default is the automatically generated serial number.
- ✧ Confirm with **OK** and the images are saved in a new series.

➪ If you no longer require the original series later on, you can delete it in the **Patient Browser**.
→ Page D.5–16, *Deleting data*

Appending images to an existing series

If you do not want to create a new series for your processed and evaluated images, you can append them to an existing series.



● Append images to series 4, Liver

- ✧ Click on the **Append images to series** option in the **Save As** dialog box.
- ✧ Select the series in the selection list using the serial number and serial description.
- ✧ Confirm with **OK.**

➪ As the default setting, you will find the series in the selection list that was last used with **Save As**.
If you are using **Save As** for the first time and have selected the images of different series, the series which is entered as a default is that which contains the image last selected in the image area.

Saving window values

If you have changed the window values of your images during image processing, you can save only the new window values.

✧ Call up **Image > Save Window Values**.

Or

✧ Call up the popup menu (right mouse key) and select **Save Window Values**.

The new window values are saved for the selected images.

Archiving, passing on, or filming images

After an examination or postprocessing, the images are stored in the local database from where they can be called up for reporting or documentation, for example.

➪ A detailed description is to be found in:
→ Part F.

Archiving images

With the function **Archive To...**, you can save patient and examination data to local exchangeable data media (to MOD = magneto optical disk or CD-R = CD recordable) or to an archive via the network.
→ Chapter F.2, *Archiving data*

Inserting an MOD or CD-R

✧ Insert the required medium into the drive.
→ Page F.2–3, *Inserting and ejecting media*

✧ If necessary, format and rename a new MOD.
→ Page F.2–7, *Formatting an MOD*

✧ Select the images that you want to archive.

Standard MOD

✧ Call up **Transfer > Archive To MOD**.

Or

✧ Click on the icon button.

The data are archived on the default MOD drive.
→ Page F.2–11, *Archiving to MOD*

Standard CD-R

✧ Call up **Transfer > Archive To CD-R**.

Or

✧ Click on the icon button.

The data are selected for archiving on CD-R.
→ Page F.2–15, *Archiving to a single session CD-R*
→ Page F.2–22, *Archiving to multi session CD-R*

Or

Selecting a destination (MOD, CD-R, or archive)

✧ Execute **Transfer > Archive To...**.

Or

✧ Click on the icon button.

✧ Select your archive destination in the dialog box **Archive To**.

Archive

✧ Click on **Archive** to archive the data to the selected destination.
→ Page F.2–27, *Selecting a destination and then archiving*
→ Page F.2–29, *Archiving in the network*

Burning a CD-R

The actual storage process on CD-R, burning the CD-R either starts automatically or can be started manually.
→ Page F.2–18, *Starting the write operation automatically*
→ Page F.2–19, *Starting the write operation manually*

Passing on data

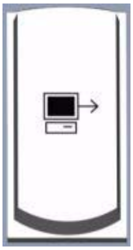
If your system is connected to a network, you can send patient and examination data to other workstations via the network with the **Send To...** function.

If your system is not connected to a network, you can write data to a data medium (MOD or CD-R) with the function **Export To...** in order to pass them on.
→ Chapter F.3, *Exchanging data*

Sending data

✧ Select the data that you want to send.

✧ Press the **Send To Node 1** key on the symbol keypad.

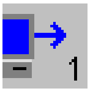


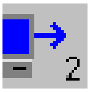
Or

✧ Call up **Transfer > Send To Node 1** or **Transfer > Send To Node 2**.

Or

✧ Click on the relevant icon button.





The data are sent to the selected address.
→ Page F.3–2, *Sending data to a standard address*

Or

✧ Execute **Transfer > Send To...**.

Or

✧ Click on the icon button.

✧ Select the network address(es) you require in the **Send To** dialog box.

Send

✧ Click on **Send** to send the selected data to the required address(es).
→ Page F.3–3, *Sending data to another address in the network*

Exporting

✧ Execute **Transfer > Export To...**.

✧ Select the data medium you require in the **Export To** dialog box.

Export

✧ Click on **Export** to archive the data on the selected data medium.
→ Page F.3–5, *Exporting to data medium*

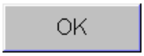
Exporting images to the file system

If you want to process or otherwise use images with other programs, you can export them to a specific directory on the system hard disk in several image formats (**Export To Off-line**).
→ Chapter F.4, *Exporting and importing images*

✧ Execute **Transfer > Export to Off-line**.

✧ Select the required directory in the **Export to Off-line** dialog box.

✧ Select the required image format (DICOM, TIFF, bitmap, or JPEG).



✧ Click on **OK** to save the selected images as individual files.
→ Page F.4–2, *Exporting images to the file system*

Filming/printing images

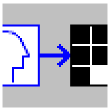
You can also use the **Viewing** task card to select images and copy them to **Filming** or **Film Preview**.

Transferring images for filming/printing

✧ Select the images in the image area of the **Viewing** task card.

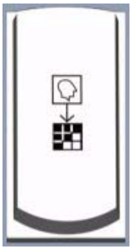
✧ Call up **Patient > Copy to Film Sheet.**

Or



✧ Click on this button on the **Patient** subtask card.

Or



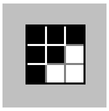
✧ Press the **Copy to Film Sheet** key on the symbol keypad.

All the selected images are transferred to the “virtual film sheet“ (**Filming** task card or **Film Preview** window). There you activate the **Auto Expose** option and the images are exposed on film or printed on paper as soon as the film sheet has been filled, or they are first collected in a film job.
→ Chapter G.2, *Automatic/Manual Filming*

Film preview

✧ Call up **Patient > Film Preview** in the main menu to have a preview displayed showing how the transferred images will be filmed/printed.
→ Page G.3–2, *Film Preview*

Or



✧ Click on this button on the **Patient** subtask card.

Printing images/exposing images on film

You can print/expose a patient's images that you have collected in a film job from the **Viewing** task card. You do not have to switch to the **Filming** task card first.

✧ Call up **Patient > Expose Film Task** to transfer all images of that film job to the camera or printer.

➩ If you have transferred images of more than one patient to the **Filming** task card so that more than one film job exists, a dialog box is displayed where you can select the film job that you require.

Filming multiframe images

You can film and print multiframe images only from the **Viewing** task card.

Transferring images to 3D

In the **Viewing** task card, you can transfer images to the **3D** task card for three-dimensional processing.

✧ Select the images or series on the **Viewing** task card that you want to process three-dimensionally.

Or

✧ Select **no** images if you want to transfer the entire content of the opened patient folder (all images of the patient displayed).

✧ Call up **Patient > MPR**, **Patient > MIP** or **Patient > SSD** depending on the 3D method with which you want to process your images.

Or

✧ Click on the **3D MPR** button on the **Patient** subtask card.

The images are checked for suitability for 3D reconstruction and transferred to the **Series List** dialog box.
→ Page H.2–5, *Series List*

⇨ If you select only one or two images, the entire series to which the selected images belong are transferred, because **3D** requires a minimum number of images for processing. If you select four or more images, only the selected images are transferred.

Closing images, series, studies, and patients

You can terminate processing of images on the **Viewing** task card by closing the images, the associated series, or the patient and thus removing them from the **Viewing** task card.

The images are still saved in the local database.

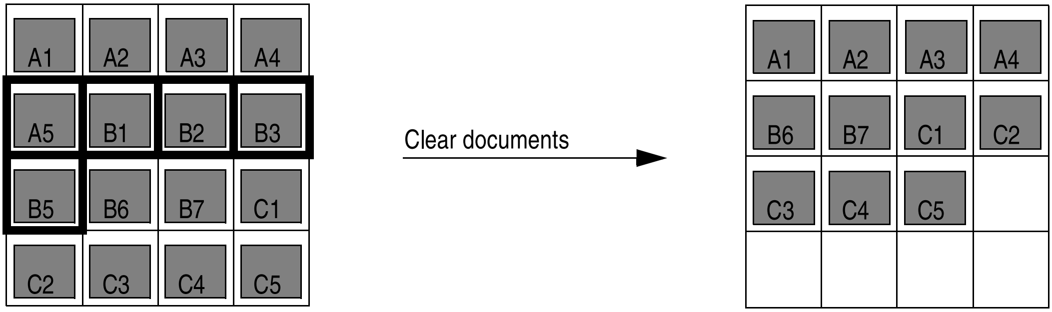
Closing selected images or series

It is sometimes helpful to close individual images of a series, for example, because some of the images are not relevant for diagnosis. If you then save the remaining images as a new series, it only contains the really relevant images. You can also close the series of a study that you no longer want to process.

✧ Select the images or series that you want to close.

✧ Call up **Edit > Clear Document(s)**.

Example: You want to close images A5 and B1 - B5.



The other images move up and the gap will be closed.

Closing patients

You can also close all images, series, and studies of the patient whose images are currently displayed.

✧ Call up **Patient > Close Patient**.

All the images of the patient are closed and removed from the **Viewing** task card, the patient folder in the control area is cleared.

➪ Changes in images, except for window values, are **not** saved.

CHAPTER
E.8

Configuring the Viewing Task Card

In **Viewing Configuration**, you can adapt the user interface and program operation of the **Viewing** task card to your method of working.

You can change and make the following settings:

❑ Display of statistical evaluation results

❑ Whether series/studies remain on the **Viewing** task card when you load new series/studies

❑ Organ-specific and user-specific window values

✧ Call up the **Configuration Panel** (**Options > Configuration...** in the main menu).

✧ Select the configuration window of the **Viewing** task card.

Viewing

The **Viewing Configuration** window is displayed with the **Graphic Tools, Administration** and **Evaluation General** tab cards.

➪ In the Basics part of this manual you can read how to call up and exit configuration windows, save changes, or reset settings back to the as-delivered state.
→ Chapter A.2, *Configuring the User Interface*

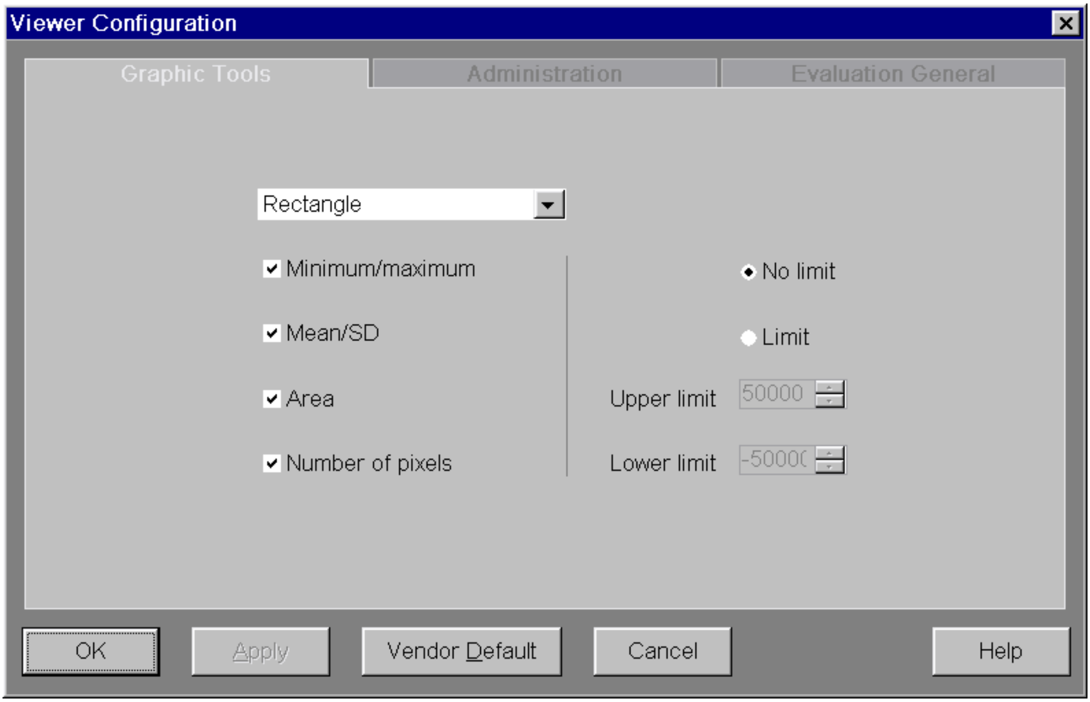
Displaying evaluation results

When you draw ROIs and distance lines, the program evaluates the areas and lines statistically.
→ Page E.5–4, *Evaluating regions*,
→ Page E.5–17, *Measuring distances and angles*

On the **Graphic Tools** tab card, you can set what evaluation results are to be displayed in the images for each ROI or line type.

You can also make settings for the **Scalegrid** and **Crosshair** evaluation tools on the **Graphic Tools** card.

✧ Click the **Graphic Tools** tab card into the foreground.



Rectangle

☑ Minimum/maximum
☑ Mean/SD
☑ Area
☑ Number of pixels

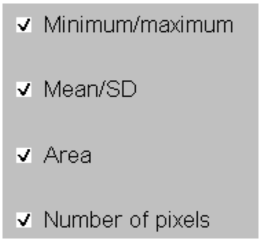
● No limit
○ Limit
Upper limit 50000
Lower limit -5000

Selecting a graphic tool

Rectangle

✧ First select for which ROI or line type you want to change the display of evaluation results.

Displaying evaluation results



☑ Minimum/maximum

☑ Mean/SD

☑ Area

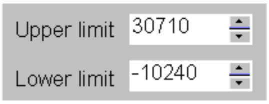
☑ Number of pixels

✧ Select or deselect the display of evaluation results by clicking or deselecting the corresponding check box.

Gray scale range

✧ Select the **No Limit** radio button to evaluate the entire gray scale range of the ROI.

Or



Upper limit 30710

Lower limit -10240

✧ Select the **Limit** radio button to evaluate only those pixels of the ROI that are within a gray scale range that you can now define.

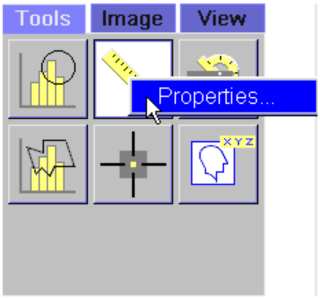
Changing the settings on the task card

You can change all the settings for the various graphic tools not only on the configuration platform but also directly on the **Viewing** task card.

✧ To do that, place the cursor on the icon button of the graphic tool whose settings you want to change on the task card stack.

✧ Call up **Properties...** in the popup menu (right mouse key).

A dialog box for defining the properties of this graphic tool is displayed. You can now change the settings for this graphic tool. This setting will be used whenever you call this graphic tool in the future.



NOTE

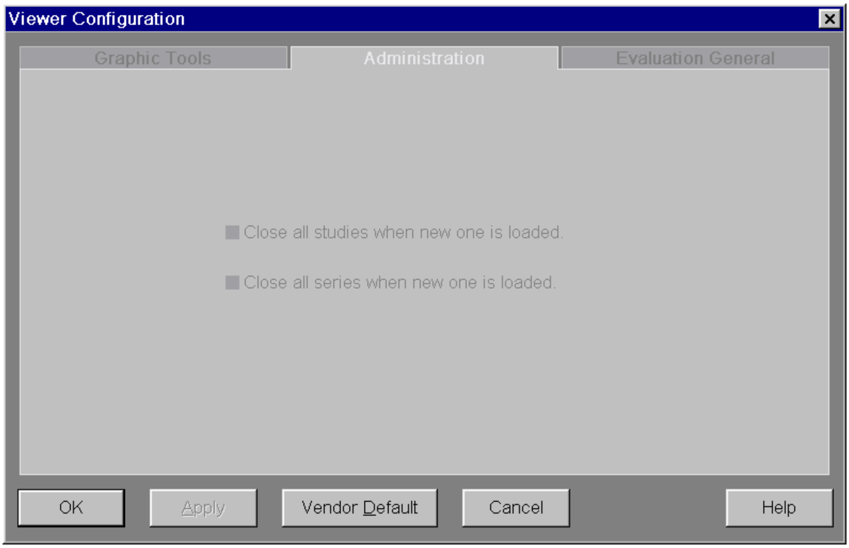
If, however, you select a *drawing element in an image* and then call up **Edit > Properties...** (or **Properties...** in the popup menu), the settings that you can make in the dialog box now displayed apply to the selected drawing element only.

Closing of series/studies in the Viewing task card

On the **Administration** card, you can see whether series or studies of a patient that are already on the **Viewing** task card are removed from **Viewing** if you load a new series/study of this patient.

➪ These settings are defined by your system administrator or Siemens Service.

✧ Click the **Administration** tab card into the foreground.



☐ Close all studies when new one is loaded.

☐ Close all series when new one is loaded.

☐ Close all studies when new one is loaded.

If the option is selected, all studies of a patient loaded on the **Viewing** task card are removed as soon as a new study of this patient is loaded.

☐ Close all series when new one is loaded.

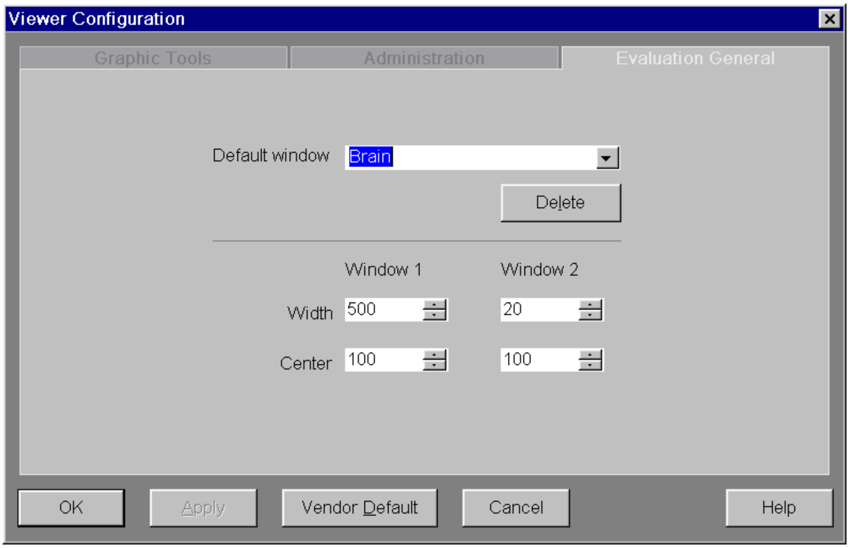
If the option is selected, all series of a study currently loaded are removed from the **Viewing** task card as soon as a new series of this study is loaded.

Organ-specific and user-specific window values

On the **Viewing** task card, you can window the images by assigning them predefined organ-specific and user-specific window values.
→ Page E.4–9, *Assigning predefined window settings*

On the **Evaluation General** tab card, you can create window values of this type, assign a name to them (e.g. organ designation or user name), and change or delete window values already created.

✧ Click the **Evaluation General** tab card into the foreground.



Default window: Brain

	Window 1	Window 2
Width	500	20
Center	100	100

Selecting a name

✧ Enter a name in the combo box to create a new organ-specific or user-specific set of window values.

Or

✧ Select a name from the list to edit window values or delete it.

Deleting window values

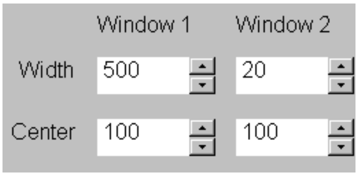
The selection list can contain up to 30 entries. If you want to define new window values when the list is full, you must first delete an existing entry.

✧ Select an entry.

✧ Click on the **Delete** button to delete the entry.

➪ Delete entries which are no longer required from time to time in the **Default window** list to keep the **Windowing** submenu clearer.

Entering or changing window values



	Window 1	Window 2
Width	500	20
Center	100	100

If you have entered a new name in the **Default window** field, the input fields for the window values are initially empty.

✧ Enter the new window values in the spin boxes.

If you have chosen a name that already exists in the **Default window** field, you can now change the window value stored under this name.

PART
F

Archiving and Sending

F.1 Introduction

F.2 Archiving data

F.3 Exchanging data

F.4 *Exporting and importing images*

F.5 *Checking data transfer*

F.6 *Configuring data transmission*

CHAPTER
F.1

Introduction

After an examination or postprocessing, the images are stored in a local database from where they can be called up for reporting or filmed for documentation.

In this section, we explain how to save images and patient data from the local database to other media, send them within the network, and how to transfer them to data media or through the network.

The following options are available to you:

Archiving

With the function **Archive To...** you can save patient and examination data to local exchangeable data media (to MOD = magneto optical disk or CD-R = CD recordable) or to an archive via network.
→ Chapter F.2, *Archiving data*

Archiving prevents data loss and is used for long-term storage of patient and examination data.

➩ You should archive patient and examination data as a routine at regular intervals.

As soon as you are sure that the data have been archived, you can delete the data from the local database to keep it manageable.
→ Page D.5–16, *Deleting data*

Sending and exporting data

If your system is connected to a network, you can send patient and examination data to other workstations via the network with the function **Send To...**.

If no network connection exists, you can write your data to a data medium (MOD or CD-R) with the function **Export To...** to pass it on.
→ Chapter F.3, *Exchanging data*

You can make examination data available to another physician for postprocessing or for reporting.

Importing

If you need archived data again at a later date, you can reimport them with the **Patient Browser**.
→ Page D.2–24, *Reading data from archive media*

Automatic archiving and sending

To make your working routine more effective, you can also have your patient and examination data automatically written to data media that you have defined, or sent to specific addresses in the network.

You can define the rules by and time at which automatic data transmission is to take place.
→ Page F.6–2, *Automatic data transfer*

Exporting and importing images

If you want to process or use images with other programs, you can export them in several image formats to a particular directory on the system hard disk (**Export To Off-line**).

In the same way, you can import images generated or processed in other programs to your application (**Import From Off-line**).
→ Chapter F.4, *Exporting and importing images*

NOTE

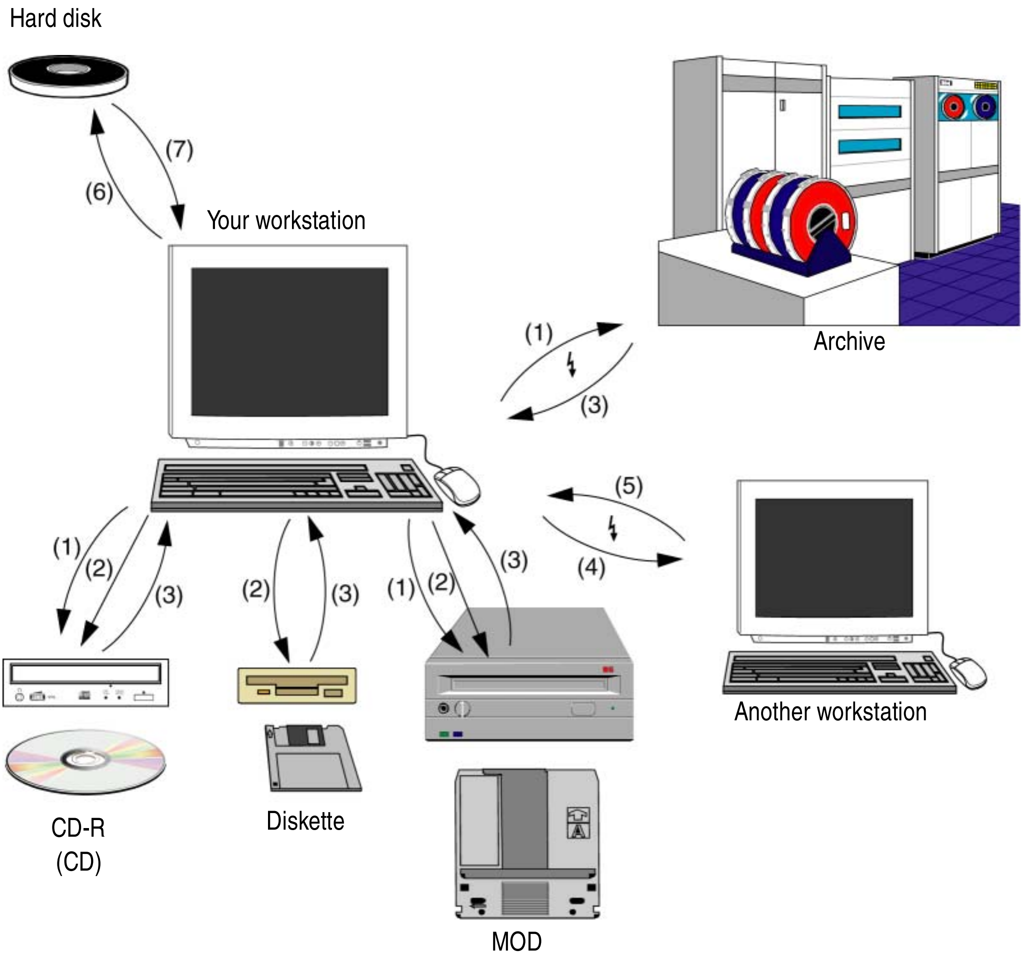
There are (statutory) regulations governing the archiving period, data availability, and data security (data integrity, incorruptibility), and recommendations concerning fire protection or water damage for the archiving of image data. The operator of the archive is responsible for observing these requirements.

NOTE

Because of constantly advancing technical developments, it might not be possible to implement storage and access for the required archiving period with a single storage technology and type of medium. Migration of the data will therefore be necessary to a greater or lesser degree under the responsibility of the operator of the digital archive.

Transfer options

The figure below shows the data backup and transfer options available to you.



(1) Archiving on CD-R, MOD or into archive
(**Archive To...**)

(2) Exporting to CD-R, MOD or diskette
(**Export To...**)

(3) Transferring from CD-R, MOD, diskette or from archive

(4) Sending to other workstations
(**Send To...**)

(5) Receiving from other workstations

(6) Exporting to a directory on the local hard disk
(**Export to Off-line**)

(7) Importing from a directory on the local hard disk
(**Import from Off-line**)

➪ Please remember that not all transfer options may be available on your system. The drives and network connections available depends on the individual configuration of your system and the options installed.

Selecting data for transfer

Before you start transfer, select the relevant data objects.

➪ You can only archive, export, or send objects that are stored in the local database. If data are to be transferred from one data medium to another, they must first be imported into the main database.

Patient Browser

If you want to archive or transfer patient or examination data, you usually select them from the local database of the **Patient Browser**.
→ Chapter D.2, *Searching for and Displaying Patient Data*

Task cards

You can also select individual objects on the task cards to start transfer.

☐ **Viewing** task card:
  → Page E.3–31, *Selecting images*

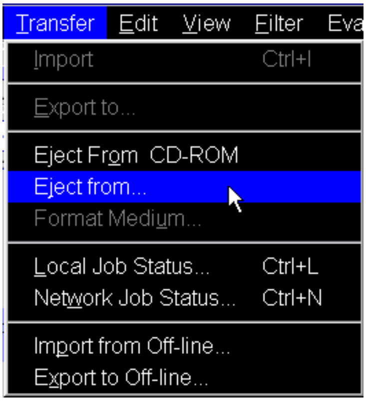
☐ **3D** task card:
  → Page H.8–2, *Selecting images and 3D graphics*

Starting transfer

You can call up archiving, data transfer within the network, and export and import either from a menu or from icon buttons.

Transfer menu

You can start archiving and transmission of data from the **Transfer** menu on several task cards and in the **Patient Browser** window.

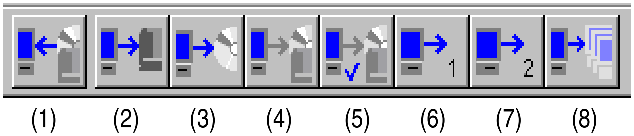


➪ Names such as **MOD** and **Node 1** are only examples of drive and network names. The names actually used depend on the configuration of your system.

Icon buttons

Depending on your configuration, you will find different icon buttons for starting transfer quickly and easily in the control area of your task cards.

You will also find a series of icon buttons in the toolbar of the **Patient Browser** with which you can start transfers.



The icon buttons have the following functions (from left to right):

(1) Import data

(2) Archive data to defined default MOD

(3) Export data to defined default CD-R

(4) Export data to selectable local data medium (MOD or CD-R)

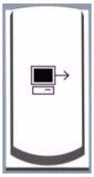
(5) Export data to a default device (MOD or CD-R)

(6) Send data to first default network destination

(7) Send data to second default network destination

(8) Send data to selectable network destination

Key



You can also start transfer to the first default network destination with the key **Send to default Node 1** on the symbol keypad or **+** on the numerical keypad of the keyboard.

CHAPTER
F.2

Archiving data

To archive, you copy selected patient and examination data to an external data medium or to the central archive. You can transfer archived data back to your local database whenever you need them.

Archiving/data backup

Depending on the routine you use, one or several drives for external data media (e.g. MOD or CD-R) will be connected to your system as an archive drive for data backup. Alternatively, an archive server can be addressed across the network.

➩ In contrast, exporting is only used for data exchange. The export procedure itself is performed in a similar way.
→ Page F.3–5, *Exporting to data medium*

In this chapter you will find out how to save data to different data media or to an archive server.

NOTE

Archiving of raw data is possible only if no examination is running.

Backup on local data media

Before you start archiving or exporting, you should find out which archiving method is used in your system and whether you have suitable data media.

Data medium

The following data medium types are supported by the system for archiving:

- 5.25" MOD (magneto optical disk)
- CD-R (CD Recordable)
- 3.5" diskettes

➪ You can only save specific small data volumes onto diskette.

➪ Data is archived to a central archive via the network. The archive can use other data media.

Handling of data media

✧ Please follow individual manufacturers' instructions when handling and storing MODs, CD-Rs, and diskettes.

Drives

Any of the following drives might be connected to your system for archiving:

- One or several MOD drive(s)
- One CD drive

Inserting and ejecting media

In order to archive or export data, you must insert a suitable MOD or CD-R in the correct drive.

➩ In the **Patient Browser**, you can see which medium has been inserted.
→ Page D.2–24, *Reading data from archive media*

➩ In **Transfer Configuration**, you can define how the data of a patient are to be written to a medium (memory utilization and compression).
→ Page F.6–9, *Archiving and exporting*

Inserting an MOD

MODs can be written to on both sides (sides A and B).

✧ Make sure that the side on and from which you want to store and read data points upwards.

✧ Insert the MOD into the drive.

The MOD is drawn in.

Inserting a CD

CDs can only be written to on one side.

✧ Press the eject button on the drive.

✧ Place the CD into the drawer with the label facing upwards.

✧ Press the eject button on the drive again.

The drawer with the CD is drawn in.

Inserting a diskette

✧ Push the diskette into the diskette drive until it slots into place.

Write protection

MODs and diskettes can be write protected by moving a small slider.

Depending on whether you want to protect data that have already been written to a MOD or diskette or whether you want to write data to one or the other you either apply or remove the write protection.

✧ Move the slider in the relevant direction.

When you insert the data medium the write protection status is displayed in the status bar.

➪ CD-Rs are automatically write protected. In single session mode this occurs after the first and only write action, in multi session mode after completing the last session.

Ejecting a medium

In order to remove a medium (MOD or CD-R) it must be ejected from the drive.

> **NOTE**
>
> Always use the menu **Transfer** to remove the MOD and never the eject button on the drive.

✧ Open the menu **Transfer**.

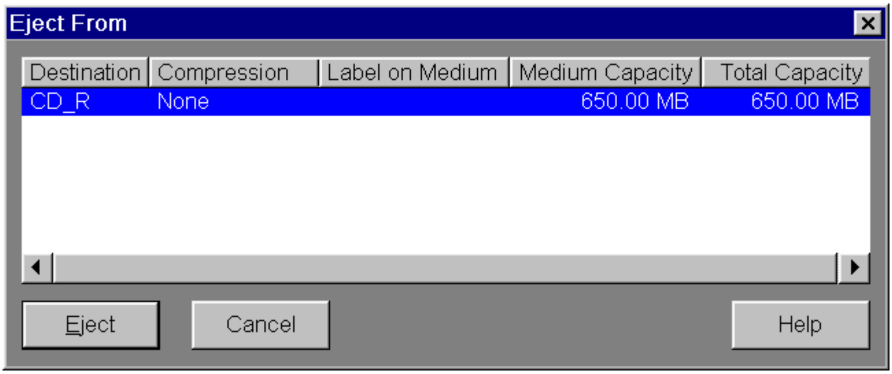
There, you will find one or more entries **Eject from <drive name>** depending on your drive configuration.

✧ Select the entry of the required drive.

Or

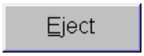
✧ Select **Eject from...**.

The dialog box **Eject From** appears.



Eject From

Destination	Compression	Label on Medium	Medium Capacity	Total Capacity
CD_R	None		650.00 MB	650.00 MB



✧ Select the drive you want and confirm with **Eject**.

➪ You can select several drives to eject the media in all of them simultaneously.

➪ If one of the data media is currently being used by the system (read or write process), the data medium cannot be ejected.

The medium or media is/are moved out of the drive(s). You can now replace them with another.

Removing a diskette

You should only ever remove a diskette from the drive when it is not being accessed by the computer.

✧ If necessary, wait until the display on the diskette drive goes out.

✧ Press the button on the diskette drive and remove the diskette.

Formatting an MOD

If you want to archive or export the data to a new MOD, you must first format it.

➪ Diskettes must be formatted and named on another PC.

If a MOD contains data *all of which* you no longer need, you can also reformat that MOD to make use of its full storage capacity again.

➪ Please note that you can only delete the entire side of an MOD (formatting) and not individual data objects (images or series).

CAUTION

Source of danger: Formatting an MOD

Consequence: Irretrievable deletion of all data stored on the MOD

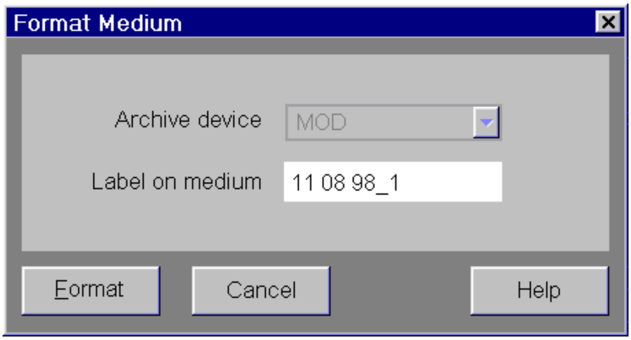
Remedy: Ensure that no important data are stored on the MOD before formatting it.

✧ Insert the MOD to be formatted in one of your MOD drives.

✧ If a MOD is already been written to and you want to delete it, call up **Transfer > Format Medium**.

Labeling an MOD

The dialog box **Format Medium** is displayed. If you insert a new MOD, this dialog box appears automatically.



Label on medium: 11 08 98_1

➪ If your system has several MOD drives, you can select the drive you want from the selection list **Archive device**.

✧ Enter a *unique* name in the input field **Label on medium** or accept the suggested name.

➪ The name can consist of letters A to Z, numbers 0 to 9, and underscores (lower case letters are automatically converted to upper case letters). The name can be between three and eleven characters long.

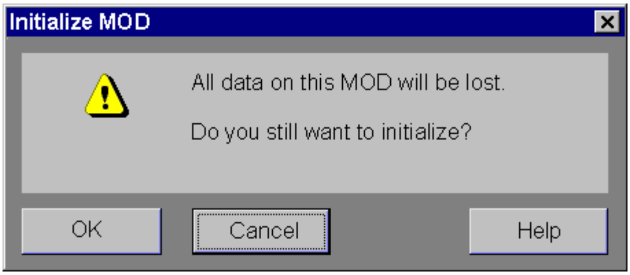
This name is permanently assigned to the MOD and is always displayed when you insert a MOD. To avoid confusion, make sure that you never assign the same MOD name twice.

Formatting a MOD

Format

✧ Click on **Format** to start formatting of an MOD.

If you have inserted an MOD with data on it, a dialog box appears.



All data on this MOD will be lost.

Do you still want to initialize?

✧ Confirm with **OK** to start formatting.

Cancel

➪ If you select **Cancel**, formatting is not performed.

Notes on saving to MOD

You can write and copy data to an MOD several times before it is full. Old MODs containing data that you no longer need can be reformatted and then used again.

Saving to MOD is performed in the background so that you can continue to work on your system at the same time.

CAUTION

Source of danger: Switching off the MOD drive while writing to MOD

Consequence: Loss of data and damage to MOD possible

Measure:.Never switch off the MOD drive while writing to MOD.

Archiving to MOD

After you have inserted an MOD with free storage capacity into the drive, select the data you wish to archive (e.g. in the **Patient Browser**). After that, archive the data onto the MOD.

➪ You can also archive patient and examination data that you have previously imported from the MOD and processed. When you store the data again, you can decide in a dialog box whether you want to overwrite the old version or not.

Archiving on the standard drive

✧ Select the data that you want to archive.

✧ Call up **Transfer > Archive To MOD**.

Or

✧ Click on this button.

The selected data are transferred to the standard MOD drive and archived there.

➪ If the patient data is incomplete, a message to that effect is displayed. Enter the missing data in the **Correct** dialog window.
→ Chapter D.4, *Correcting Data*

MOD not formatted

When exporting data to a new (unformatted) MOD or to an MOD that was formatted differently, your system automatically displays the dialog box **Format Medium**.
→ Page F.2–7, *Formatting an MOD*

CAUTION

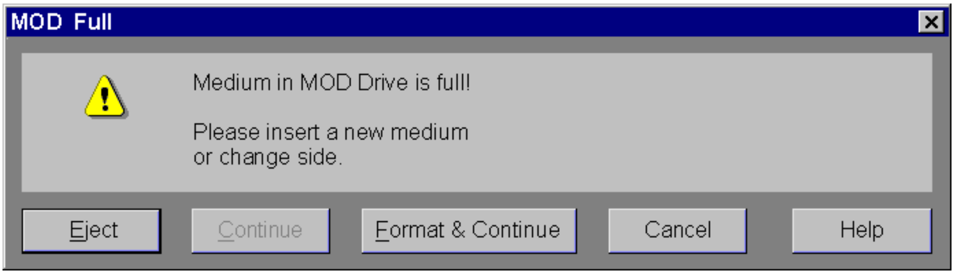
Source of danger: Format of an MOD not recognized by the system

Consequence: Loss of data possible

Remedy: Select **Cancel** in the **Format Medium** dialog box if the MOD might contain important data. Use MODs written on other systems only write protected.

MOD full

When the MOD that you have inserted is full, a window appears.



Medium in MOD Drive is full!

Please insert a new medium
or change side.

✧ Click on **Eject** and insert a new MOD into the drive, or turn over the MOD you have inserted if the other side still has space.

✧ If you insert another MOD wait a moment and then click on **Continue**.

If the MOD that you have inserted is new or has to be deleted, you must first format it:

✧ Click on **Format & Continue**, to continue archiving.

➩ If you want to cancel the whole procedure, click on **Cancel**.

Notes on saving to CD-R

CD-Rs are suitable for long-term storage and transfer of your data.

Single or multi session

CD-Rs can be written to in one step (single session) or several steps (multi session).

The method you choose depends on the configuration of your system.

Collecting and archiving data

In single session mode, you must first collect data before you write them to your CD-R.

For example, you select the examination data of a patient and select them for archiving to CD-R. You can then add the examination data of another patient, or add additional images of the same patient to your selected data.

> **NOTE**
>
> To minimize the risk of loss of data, only use CD-Rs approved by Siemens and classified as 'medical' for archiving purposes.
>
> Medical grade CD-Rs are available through your Siemens representative.

Archiving to a single session CD-R

If your system is configured for single session, you can only save data to new unwritten CD-Rs. Once a CD-R has been written to, it cannot be changed. As soon as the first write session is completed, it is no longer possible to add additional data, even if there is theoretically space for them.

You must therefore first collect all the data you want to put on a CD-R so that you can then write it to the new CD-R in one step. As soon as you have collected enough data to fill a CD-R, the system informs you of that fact.

Selecting data for storage on CD-R

✧ Select the data that you want to archive.

✧ Select **Transfer > Archive To CD-R**.

Or

✧ Click on the icon button.

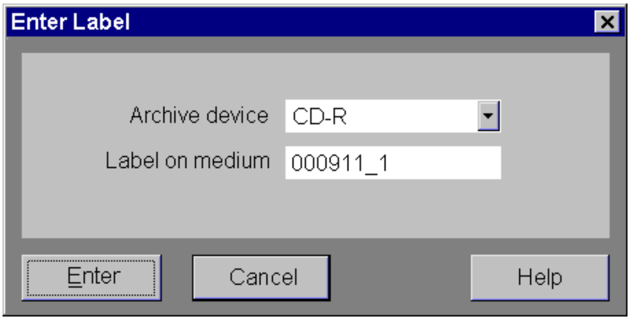
Or

✧ Call up **Transfer > Archive To...** and select the CD recorder.
→ Page F.2–27, *Selecting a destination and then archiving*

➪ If the patient data are not yet complete, a message informs you of such. Enter the missing data in the dialog box **Correct**.
→ Chapter D.4, *Correcting Data*

Labeling a CD-R

When you select data for a new CD-R for the first time, the dialog box **Enter Label** is displayed.



Archive device CD-R

Label on medium 000911_1

✧ Enter a *unique* name for the CD-R, for example, a serial number and the date, or accept the suggested name.

➪ The name can consist of letters A to Z, numbers 0 to 9, and underscores (lower case letters are automatically converted to upper case letters). The name can be between three and eleven characters long.

✧ Click on **Enter** to confirm the action.

Selecting further data

✧ Select additional data that you want to archive.

✧ Execute **Transfer > Archive To CD-R**.

Or

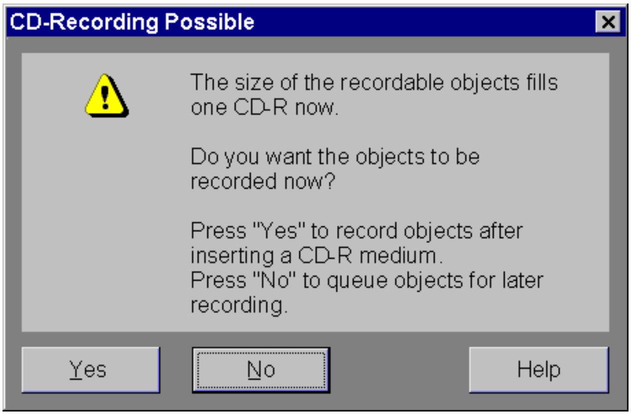
✧ Click on the icon button.

✧ In this way, select all the data records that you want to save.

➪ The window **Local Job Status** lists all the data selected for storage to CD-R.
→ Page F.5–4, *Controlling local jobs*

Starting the write operation automatically

As soon as you have collected enough data to fill a CD-R, a dialog box appears.



The size of the recordable objects fills one CD-R now.

Do you want the objects to be recorded now?

Press "Yes" to record objects after inserting a CD-R medium.
Press "No" to queue objects for later recording.

✧ Make sure you have put a new CD-R in the CD recorder.
→ Page F.2–3, *Inserting and ejecting media*

✧ Select **Yes** to start writing.

➩ If you select **No**, writing is stopped and the archiving procedure canceled. To continue at a later date, you will have to start the procedure manually.
→ Chapter F.5, *Checking data transfer*

No CD-R

If you selected **Yes** but there is no CD recorder in the CD-R, another dialog box appears.

✧ Insert a new CD-R, wait a short time and then confirm with **OK**.

Starting the write operation manually

If your system allows CD burning in the background, you can write all data so far selected to a CD-R at any time.

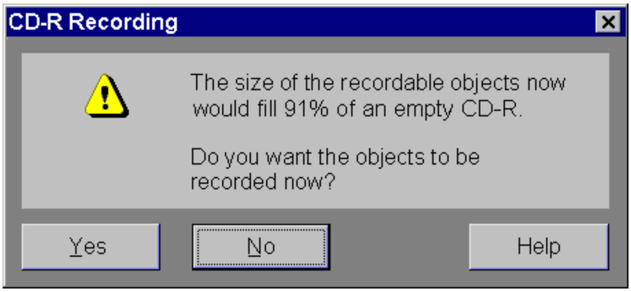
✧ Select **Transfer > Record To CD-R**.

Or

✧ Click on the icon button.

⇨ On some systems, CD burning is not possible, for example, during acquisition.
In that case, recording to CD-R is not possible.

A dialog box appears informing you about storage capacity utilization of the CD-R.



The size of the recordable objects now would fill 91% of an empty CD-R.

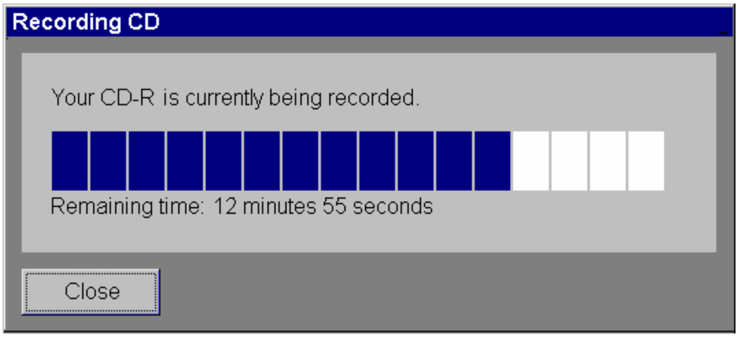
Do you want the objects to be recorded now?

✧ Confirm with **Yes** to start the write operation.
→ Page F.2–18, *No CD-R*

⇨ With **No** you postpone the operation, e.g. to a time when more data have been collected.

Write operation

A dialog box appears showing you how the write operation is progressing.



Recording CD

Your CD-R is currently being recorded.

Remaining time: 12 minutes 55 seconds

Here you can see how long the storage procedure will take. The progress bar display shows you how much storage space has now been used on the CD-R.

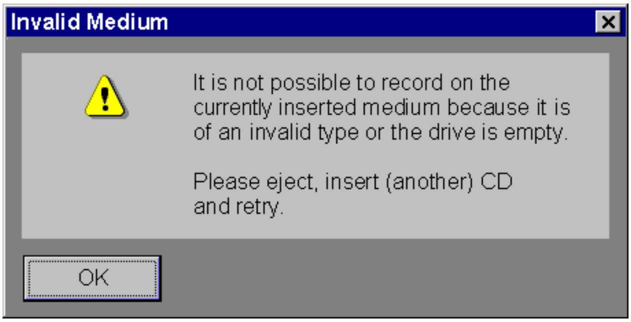
Burning in the background

The actual burning operation runs in the background. You can close the dialog box and, for example, postprocess images. The active burning operation is indicated in the status bar by a symbol.
→ Page F.5–2, *Display in the status bar*

After you have completed the burning operation, you can remove the CD-R and label it with a soft, permanent felt-tip on the upper side and then archive it or pass it on.

Wrong CD

If you insert a written or damaged CD by mistake, the following dialog box appears.



It is not possible to record on the currently inserted medium because it is of an invalid type or the drive is empty.

Please eject, insert (another) CD and retry.

✧ Confirm with **OK.**

✧ Replace the CD-R.
→ Page F.2–3, *Inserting and ejecting media*

Archiving to multi session CD-R

If your system is configured for multi session, you can store your data to new, unrecorded CDs, or CDs that have already been written to once or several times. The other data on the CD-R is not lost, the new data is simply added.

CAUTION

Source of danger: Recording on a CD-R in multi session mode interrupted by an error

Consequence: Previously stored data can no longer be read.

Measure: Only delete the data that you have archived on a CD-R from the local database *after* you have completed the session.

⇨ Previous sessions of a multi session CD-R are always preserved.

Inserting a CD-R

Before a system can select data for archiving, the storage capacity must be known.

✧ Therefore make sure that the CD-R in question is in the CD recorder.
→ Page F.2–3, *Inserting and ejecting media*

➪ In **Transfer Configuration**, you can define how the data of a patient are to be written to a CD-R (memory utilization and compression).
→ Page F.6–9, *Archiving and exporting*

Selecting data for recording onto CD-R

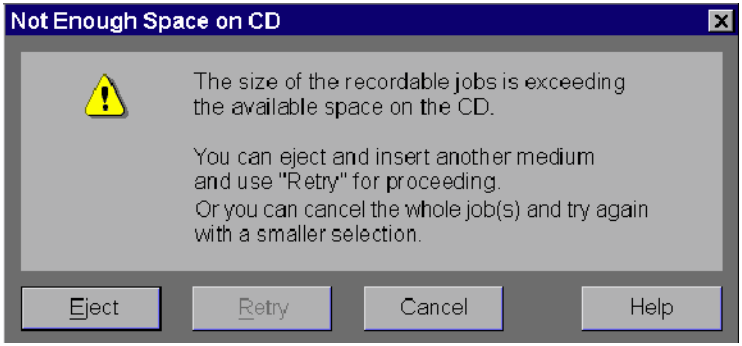
✧ Proceed as described under single session.

→ Page F.2–15, *Selecting data for storage on CD-R*
→ Page F.2–16, *Labeling a CD-R*
→ Page F.2–17, *Selecting further data*

The system checks the memory space required for the selected data and data that are available on the CD-R.

Not enough memory space

If the memory space on the CD-R is not sufficient, a dialog box appears.



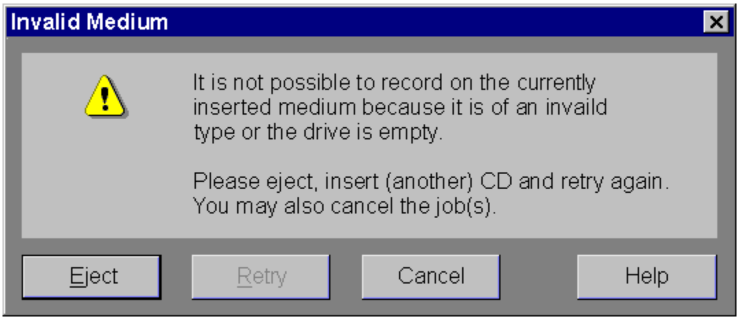
The size of the recordable jobs is exceeding
the available space on the CD.

You can eject and insert another medium
and use "Retry" for proceeding.
Or you can cancel the whole job(s) and try again
with a smaller selection.

✧ If you want to change the CD-R (for example, to insert a new, unrecorded CD-R), click on **Eject**.

Wrong CD

If you have inserted a full or damaged CD by mistake, the following dialog box appears.



It is not possible to record on the currently
inserted medium because it is of an invaild
type or the drive is empty.

Please eject, insert (another) CD and retry again.
You may also cancel the job(s).

✧ Click on **Eject**.

Continuing with another CD-R

✧ When you insert another CD-R, wait a moment and then click on **Retry**.

The system now checks whether there is enough space on the CD-R you have inserted, and if so, continues with the write operation.

➪ You can cancel the entire procedure with **Cancel**.

Write procedure

✧ Proceed as described under Single session.
→ Page F.2–19, *Starting the write operation manually*
→ Page F.2–20, *Burning in the background*

Recovering previous sessions of a multi session CD-R

In case an error (e.g. power loss) occurs during multi session writing to CD-R, all data previously stored on that CD-R might get lost as well. The software package offers a service tool to restore the previous sessions.

✧ Insert the corrupted CD-R into the CD-recorder.

✧ Call up the **Local Service** and enter the service key.
→ Page A.3–4, *Local Service*

✧ Call up the **Utilities** option.

✧ Enter “csaImaRestoreTool R:”
(if the drive letter of the CD-recorder is “R”).

If the restoration is successful, the message *“CD-R restored successfully”* is prompted.

✧ Insert the CD-R into the CD-ROM drive and check the contents within the **Patient Browser**.

➩ If it is not possible to restore the medium, the message *“Writing to CD-R failed: Cannot restore CD”* or other error messages are returned.

Selecting a destination and then archiving

If you want to select a destination and would like to have more information displayed about the inserted data media or the archiving destination, you can use this method.

✧ Insert the required data media.
→ Page F.2–3, *Inserting and ejecting media*

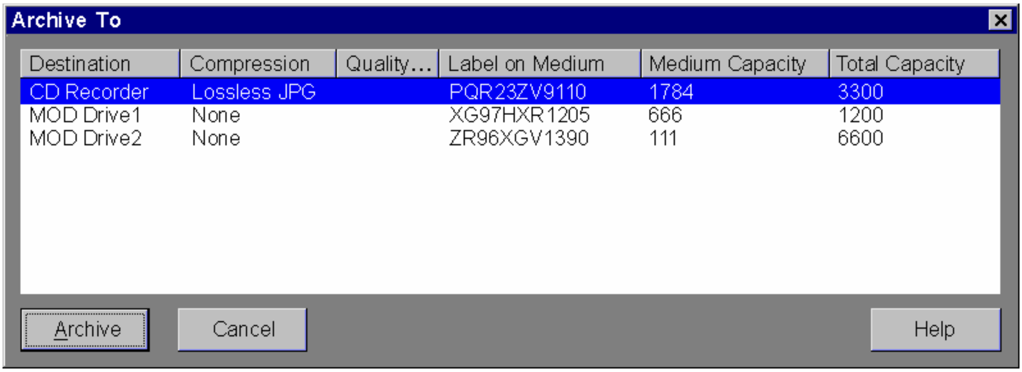
✧ Select the data that you want to archive.

✧ Select **Transfer > Archive To...**.

Or

✧ Click on the icon button.

The dialog box **Archive To** is displayed.



Destination	Compression	Quality...	Label on Medium	Medium Capacity	Total Capacity
CD Recorder	Lossless JPG		PQR23ZV9110	1784	3300
MOD Drive1	None		XG97HXR1205	666	1200
MOD Drive2	None		ZR96XGV1390	111	6600

⇨ Only those drives that contain media (with the exception of single session CD-Rs) are listed.

This list contains the following information:

❑ **Destination**
Name of the drive that contains an MOD or CD.

❑ **Compression**
Method with which data to be archived in this drive are compressed.
→ Page F.6–10, *Setting data compression*

❑ **Quality Factor**
Quality factor with which the data are compressed.

➪ In **Transfer Configuration**, you can set for each drive whether and by what method data are compressed during archiving.
→ Page F.6–9, *Archiving and exporting*

❑ **Label on Medium**
Allocated data medium name.

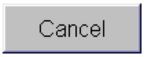
❑ **Medium Capacity**
Remaining free memory space on the data medium.

❑ **Total Capacity**
Total memory space on the data medium.

✧ Select the required drive from the list. Take the free storage capacity and the set compression into account.

✧ Click on **Archive** to archive the data on the selected drive.

Or



✧ Click on **Cancel** to cancel the operation.

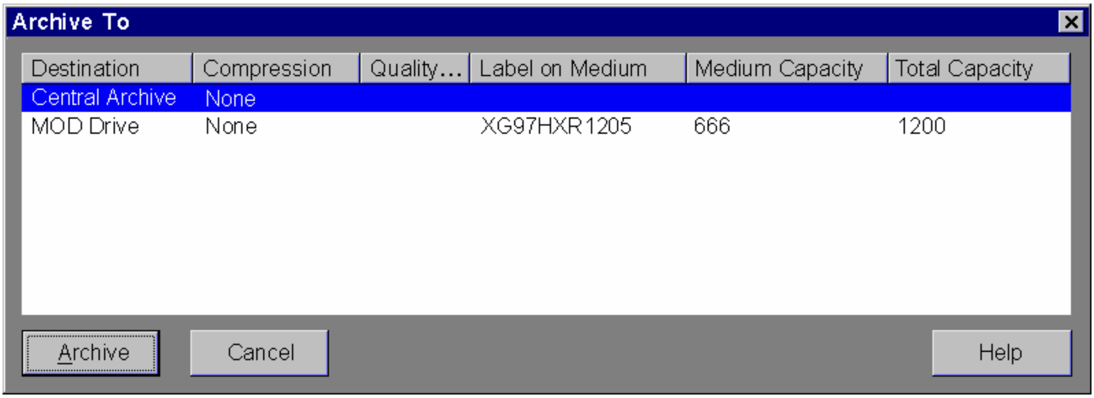
Archiving in the network

If your system is connected to a central archive, use it to archive your patient and examination data.

✧ Select the data that you want to archive.

✧ Select **Transfer > Archive To...**.

The dialog box **Archive To** is displayed. The available archive nodes and drives are displayed.



Destination	Compression	Quality...	Label on Medium	Medium Capacity	Total Capacity
Central Archive	None				
MOD Drive	None		XG97HXR1205	666	1200

The following information is of relevance for archive nodes:

☐ **Destination**
Name of the archive

☐ **Compression**
Method by which data are compressed.

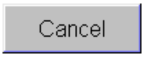
☐ **Quality Factor**
Quality factor, with which data are compressed.

➪ In the dialog box **Transfer Configuration** you can set whether and by what method data are compressed on archiving.
→ Page F.6–16, *Setting data compression*

✧ Select the required archive from the list.

✧ Click on **Archive** to transfer the data to the selected archive.

Or



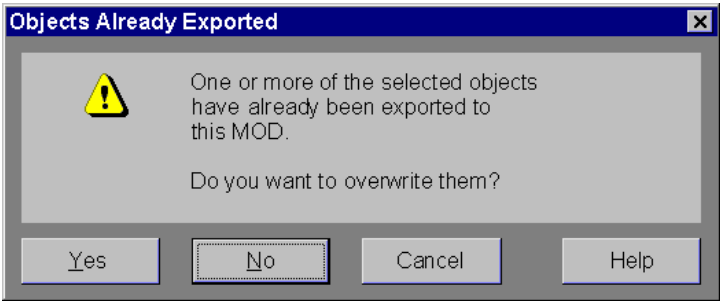
✧ Click on **Cancel** to cancel the procedure.

Errors during saving

As soon as you have started archiving or exporting, the system checks whether certain conditions have been met.

Objects already on the data medium

If an object already exists on the data medium (MOD, diskette or image file for CD-R), a message box appears.



Objects Already Exported

One or more of the selected objects have already been exported to this MOD.

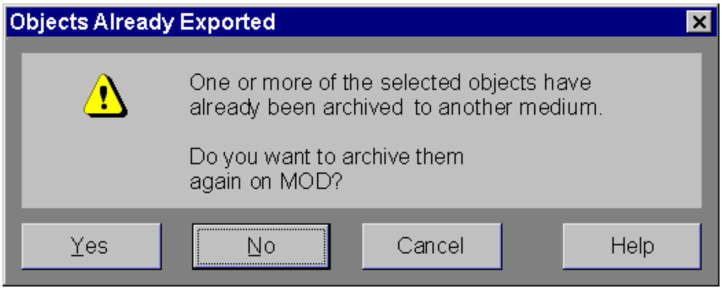
Do you want to overwrite them?

- ✧ If you want to overwrite the existing objects, click on **Yes**.
- ✧ If you want to leave the objects on the data medium untouched but want to add the objects that are missing, click on **No**.
- ✧ If you want to cancel the procedure, click on **Cancel**. In that case, no data are exported/archived.

Objects already archived

If one or more of the selected objects have already been archived, another message box appears.

➪ The system does not check whether objects have been queued several times for a transfer.


Objects Already Exported

One or more of the selected objects have already been archived to another medium.

Do you want to archive them again on MOD?

✧ If you want to save objects again that have already been saved, click on **Yes**.

✧ If you want to skip objects that have already been saved but want to add the objects that are missing, click on **No**.

✧ If you want to cancel the procedure, click on **Cancel**. In that case, no data is exported/archived.

CHAPTER
F.3 Exchanging data

You can exchange your patient and examination data with others by two methods: Via network or physically by data medium.

DICOM format

In a medical environment, this is done by a uniform format, the DICOM format (Digital Imaging and Communications in Medicine).

➪ This system conforms to DICOM. A declaration of conformity can be obtained from your service partner.

Sending/Archiving

If your system is connected to a computer network (DICOM), you can send patient and examination data from your workstation to other workstations or archive them on a remote node.

Receiving

Other workstations can send patient or examination data to you. Data are received in the background automatically. As soon as the process is complete, the data can be accessed in the **Patient Browser**.

Exporting/Archiving

If the necessary drives are installed on your system, you can also archive data to a data medium (MOD or CD-R, sometimes even diskette).

Importing

You can import the archived data with the **Patient Browser** at the same or another workstation.
→ Page D.2–24, *Reading data from archive media*

Sending in the network

If your system is connected to and configured in a network, you can select patient and examination data from your local database and send it to other users on your network whenever necessary.

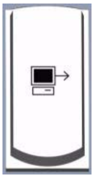
In the network, one or more workstations are set up as standard connections. You can either send your data directly to one of these standard addresses or select a network connection yourself.

➪ You can only send an image to the same network node once, even if graphics or text contained in the image has been changed since it was last sent.

Sending data to a standard address

During installation, Siemens Service sets up various network connections (e.g. **Node 1** and **Node 2**) as standard addresses in the network.

✧ Select the data that you want to send.

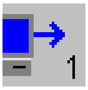


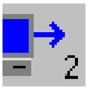
✧ Press the **Send To Node 1** key on the symbol keypad.

Or

✧ Call up **Transfer > Send To Node 1** or **Transfer > Send To Node 2**.

Or





✧ Click on the relevant button.

The data will be sent to the selected address.

Sending data to another address in the network

If you want to send data to an address other than the standard addresses or want to send data to more than one user in the network simultaneously, select the network connection(s) from a list.

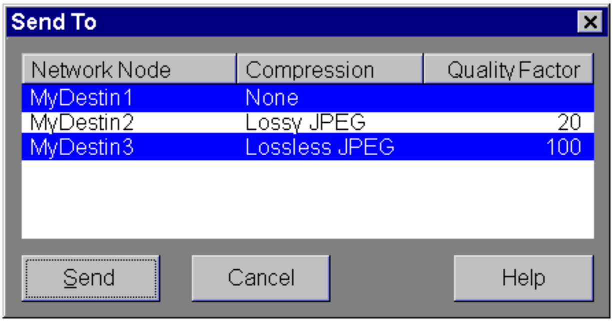
✧ First select the data that you want to send.

✧ Call up **Transfer > Send To....**

Or

✧ Click on this button.

The **Send To** dialog box is displayed with a list of all available network addresses.



Network Node	Compression	Quality Factor
MyDestin1	None	
MyDestin2	Lossy JPEG	20
MyDestin3	Lossless JPEG	100

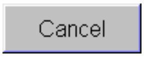
This list contains the following information:

- **Network Node**
  Name of the network connection (receiver name).
- **Compression**
  Compression method by which the data are prepared for faster transfer.
  You define in **Transfer Configuration** whether and by what method data are compressed for sending.
  → Page F.6–15, *Setting sending*
- **Quality Factor**
  The quality factor states the image quality of the compressed data compared with the original data.
  → Page F.6–16, *Setting data compression*

✧ Select one or more network connections.

✧ Click on **Send**, to send the selected data to this or these address(es).

Or



✧ Click on **Cancel** to cancel the operation.

Exporting to data medium

When you save patient and examination data in DICOM format to a data medium, always use the **Export To...** function. This function is used in exactly the same way as the **Archive To...** function.
→ Page F.2–27, *Selecting a destination and then archiving*

However, unlike the archiving function, the exporting function does not check previous archiving actions, markings or work status.

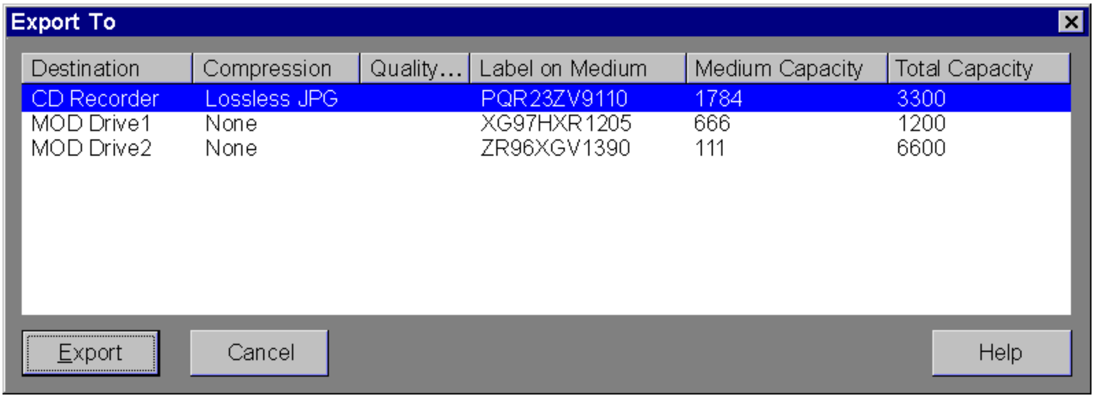
Exporting

✧ Insert the correct medium.
→ Page F.2–3, *Inserting and ejecting media*

✧ Select the data that you want to export.

✧ Call up **Transfer > Export To...**.

The dialog box **Export To** is displayed.
The available drives are listed.



Destination	Compression	Quality...	Label on Medium	Medium Capacity	Total Capacity
CD Recorder	Lossless JPG		PQR23ZV9110	1784	3300
MOD Drive1	None		XG97HXR1205	666	1200
MOD Drive2	None		ZR96XGV1390	111	6600

➪ With MODs, only those drives are listed in which formatted and named files are to be found.

✧ Select the required drive from the list. Check the remaining storage capacity and the set compression.

Export

✧ Click on **Export** to archive the data from the selected drive.

Or

Cancel

✧ Click on **Cancel** to cancel the procedure.

➪ Refer also to:
→ Page F.2–27, *Selecting a destination and then archiving*
→ Page F.2–31, *Errors during saving*

CHAPTER F.4 Exporting and importing images

If you want to use and process images in other applications, too, you can copy them from the local database to a directory on your hard disk or on a remote computer. You can also read the images from a directory on the hard disk into the system.

Image formats

The following formats are supported:

- ❑ DICOM format (*.ima)
- ❑ Tiff (*.tif) and JEPG (*.jpg)
- ❑ Windows Bitmap (*.bmp)

> **NOTE**
>
> It is not possible to import images in Windows bitmap format.

The images are stored as individual files in a directory on the system hard disk. Specific directories are enabled for this purpose (e.g. C:\Temp).

From there, you can then import the images via the network, for example.

Exporting images to the file system

You can copy one or several images to specific enabled directories of the system hard disk or within the network.

➪ You can only export data to a network drive if a network link has been configured and it is active.

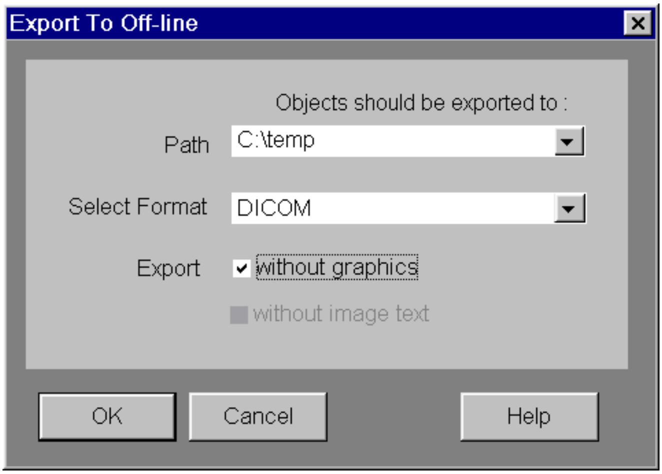
Exporting

✧ Select the images to be exported.

➪ With multiframe images, the representative is used. You can select individual images in the **Viewing** task card.

✧ Call up **Transfer > Export to Off-line**.

The dialog box **Export To Off-line** is displayed.



Objects should be exported to :

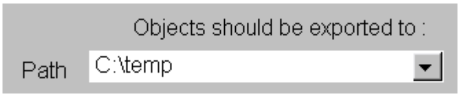
Path: C:\temp

Select Format: DICOM

Export: ☑ without graphics

☐ without image text

Path


Objects should be exported to :
Path C:\temp

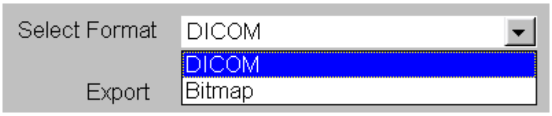
✧ Select the required drive and directory from the selection list **Path**.

✧ If necessary, extend the path.

➪ If you want to select or create a new subdirectory, add the subdirectory path separated by a "\" to the path (up to 8 subdirectory levels from the main directory are possible).

➪ You can also select a directory on another computer in the network.
If configured to do that enter "\\RemoteNode\RemoteDir".

Image format

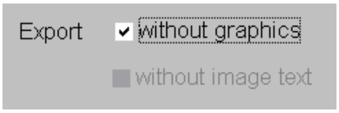

Select Format DICOM
Export

✧ Select the required image format from the selection list **Select Format** (Default setting: DICOM).

➪ Depending on the image type in question, images are exported with 8 bit/256 gray scales or 24 bit/RGB.

➪ If you have selected a multiframe image in the **Patient Browser**, only the representative image is exported.

Image text



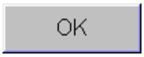
Export ☑ without graphics

☐ without image text

✧ Decide whether the image text is to be "burnt into" the image and exported with it (Default setting: without).

➩ If you have selected DICOM format, the image text is also exported as it is included in DICOM format.

Starting export



✧ Confirm with **OK**.

The selected image data are stored as individual files.

File names

File names follow the following scheme:

Last name of the patient.modality.study description.series number.image number.timestamp.internal number.image format

The timestamp follows the following format:
yyyy.MM.DD.hh.mm.ss.dddddd

yyyy: Year e.g. 2000
MM: Month e.g. 09
DD: Day e.g. 10
hh: Hour e.g. 15
mm: Minute e.g. 35
ss: Second e.g. 13
dddddd: Decimal points e.g. 123456

→ Page F.4–1, *Image formats*

Example:
Miller.CT.Liver.2.13.2000.04.10.15.35.13.123456.ima

➩ In the Japanese version, the patient name and examination are omitted from the file name.

Importing images from the file system

You can read in individual images from specific released directories of the system hard disk or read them into your local database across the network.

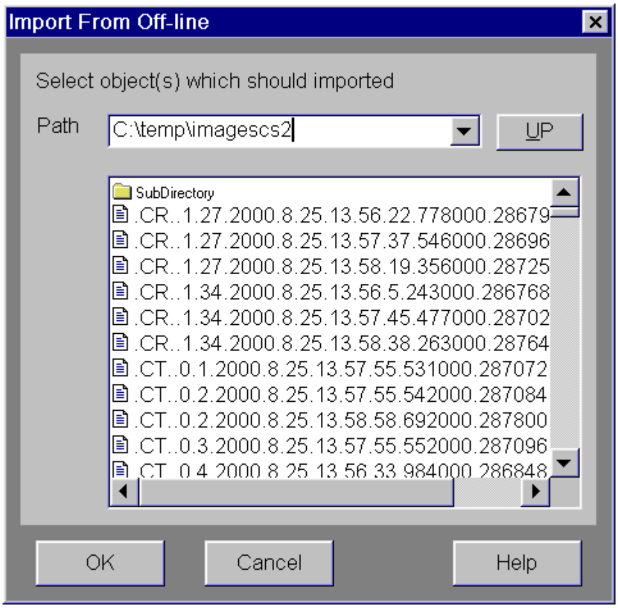
⇨ You can only import data from a network directory if a network link has been configured, the link is active, and the directory released.

⇨ You cannot read directly from a CD. For that, you must first copy the images into an enabled directory.

Importing

✧ Call up **Transfer > Import from Off-line**.

The dialog box **Import From Off-line** is displayed.

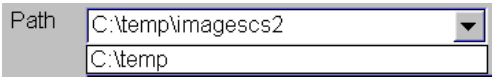


Select object(s) which should imported

Path C:\temp\imagescs2

```
SubDirectory
.CR..1.27.2000.8.25.13.56.22.778000.28679
.CR..1.27.2000.8.25.13.57.37.546000.28696
.CR..1.27.2000.8.25.13.58.19.356000.28725
.CR..1.34.2000.8.25.13.56.5.243000.286768
.CR..1.34.2000.8.25.13.57.45.477000.28702
.CR..1.34.2000.8.25.13.58.38.263000.28764
.CT..0.1.2000.8.25.13.57.55.531000.287072
.CT..0.2.2000.8.25.13.57.55.542000.287084
.CT..0.2.2000.8.25.13.58.58.692000.287800
.CT..0.3.2000.8.25.13.57.55.552000.287096
.CT..0.4.2000.8.25.13.56.33.984000.286848
```

Selecting (a) file(s)



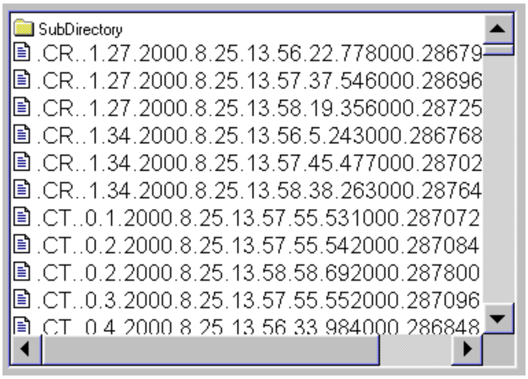
Path C:\temp\imagescs2

C:\temp

✧ Select the required drive and directory from the selection list **Path** or enter the required path and, if necessary, the file name.

➩ You can select several files at once using the standard Windows wildcard "*".

Or



SubDirectory
.CR..1.27.2000.8.25.13.56.22.778000.28679
.CR..1.27.2000.8.25.13.57.37.546000.28696
.CR..1.27.2000.8.25.13.58.19.356000.28725
.CR..1.34.2000.8.25.13.56.5.243000.286768
.CR..1.34.2000.8.25.13.57.45.477000.28702
.CR..1.34.2000.8.25.13.58.38.263000.28764
.CT..0.1.2000.8.25.13.57.55.531000.287072
.CT..0.2.2000.8.25.13.57.55.542000.287084
.CT..0.2.2000.8.25.13.58.58.692000.287800
.CT..0.3.2000.8.25.13.57.55.552000.287096
.CT..0.4.2000.8.25.13.56.33.984000.286848

✧ Select the file(s) in question from the directory.

➩ You can select several files at once with the left mouse key using **Shift** and **Ctrl**.

UP

✧ If necessary, navigate through the directory tree by double-clicking on a folder and using the "up" button.

➩ All directories starting with the configured root directory are accessible.

OK

✧ Confirm with **OK** to read the selected image files into your local database.

Or

✧ Double-click on the relevant file.

CHAPTER
F.5

Checking data transfer

All the jobs for archiving, sending or exporting data are executed one after the other.

You can check which jobs have been completed, which one is being executed and which jobs are waiting to be executed in the queue at any time.

You can classify some jobs as urgent, stop jobs, repeat jobs or delete jobs to influence how the queue is executed.

Checking data transmission

In the **status bar** you can see if your system is archiving, importing, sending, or receiving in the background.

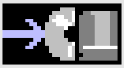
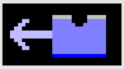
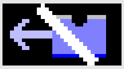
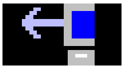
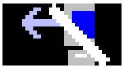
In the **Local Job Status** dialog box, you can obtain information about jobs for archiving and export or importing of data to or from your MOD and CD-R drives.

In the **Network Job Status** dialog box, you can obtain information about jobs for data exchange through the network.

Display in the status bar

During data transfer, icons are displayed in the status bar which tell you what operation is currently being executed or whether an error has occurred in at least one job.

In this way, you can observe the progress of data transfer without interrupting your work and can intervene in case of an error.

Action	Not active	Active	Error
Archiving/Exporting on data medium	no icon		
Sending/Archiving in the network	no icon		
Importing from data medium	no icon		
Receiving	no icon		

By these icons you can see if the current jobs are running without error or whether an error has occurred in at least one job.

Error messages

If an error occurs during data transfer, an error message appears on the status bar together with the appropriate icon.

Viewing and controlling the transfer jobs

The display in the status bar provides you with brief information about the progress of data transfer. You can obtain more detailed information than in the status list in the **Local Job Status** and **Network Job Status** dialog boxes. There, you can stop individual jobs or correct errors.

Whether your system is sending or receiving patient and examination data or not, you can call up the job status dialog boxes in the **Transfer** menu at any time to obtain information about the jobs in the queue.

As soon as data are transferred in the background, you can call up these dialog boxes using the icons on the status bar. This is a good idea, for example, if transfer errors occur. Then you can see immediately which data and which operation are affected and take action accordingly.

Controlling local jobs

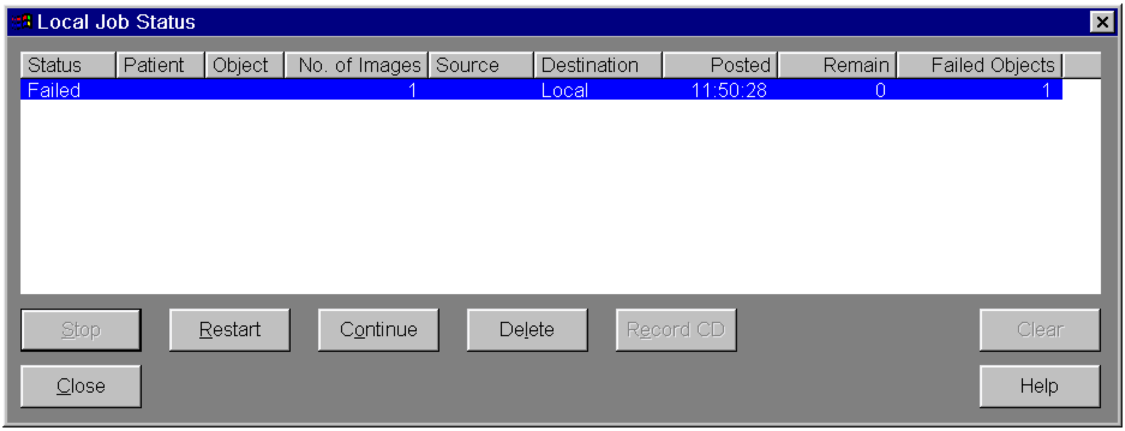
If you want to know which data are currently being written to or imported from local data media or are pending for archiving or export, call up the **Local Job Status** dialog box.

✧ Call up **Transfer > Local Job Status**.

Or

✧ Click on the status bar on an icon for local data transfer.

The **Local Job Status** dialog box is displayed.



Status	Patient	Object	No. of Images	Source	Destination	Posted	Remain	Failed Objects
Failed			1		Local	11:50:28	0	1

Controlling network jobs

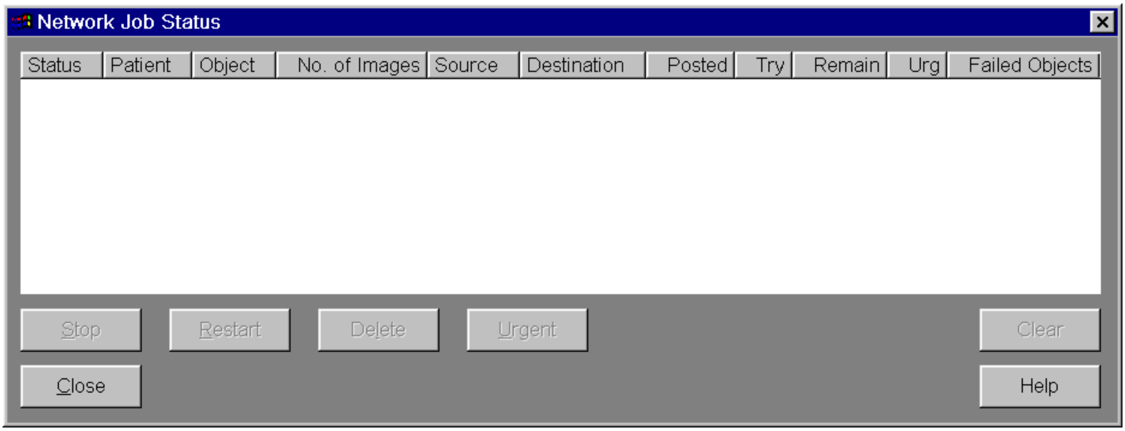
In the **Network Job Status** dialog box, you can obtain information about the data being transferred in the network or sent from the network to your system.

✧ Call up **Transfer > Network Job Status**.

Or

✧ Click on an icon for data transfer in the network on the status bar.

The **Network Job Status** dialog box is displayed.



Information in the Job Status dialog boxes

The **Local Job Status** or **Network Job Status** dialog boxes contain job lists with the following information:

☐ **Status**
Processing status of the jobs
→ Page F.5–8, *Status of a data transfer*

☐ **Patient**
Name of the patient whose data is being transferred

☐ **Object**
Type and extent of the data transferred

☐ **No. of images**
Number of images to be transferred in the job

⇨ If your system is closed down during an archiving job, the number of images displayed in the Job Status dialog boxes may be incorrect when you restart the system.

☐ **Source**
Source address, i.e. name of the data medium or the network address or your local database

☐ **Destination**
Destination address, i.e. name of the storage medium or the network address or your local database

❑ **Posted**
Time at which the data transfer was initiated (for data received via the network, the time is placed in brackets)

❑ **Try** (only in the **Network Job Status** dialog box)
Number of tries to reach the destination address until the job has been successfully processed.

❑ **Remain**
Number of images that still have to be transferred

➪ If your system is closed down during an archiving job, the number of remaining images displayed in the Job Status dialog boxes may be incorrect when you restart the system.

❑ **Urg** (only in the **Network Job Status** dialog box)
Classification as urgent

❑ **Failed Objects**
The number of objects that could not be transferred.
A message indicating this is displayed on the status bar.

Status of a data transfer

The status of a data transfer indicates to what extent this job has already been executed:

- **Queued**
  The job is still waiting to be processed.
- **Active**
  The job is currently being processed.
- **Waiting**
  A network job is waiting for confirmation that the data have arrived.
- **Stopped**
  Processing of the job has been stopped by the user.
- **Completed**
  The job has been processed completely. All data have been transferred without error.
- **Failed**
  An error occurred during processing of the job. It was therefore not possible to execute it completely.
- **Recordable**
  This job contains data that has been preselected for recording on CD-R. It has not yet been written onto CD-R.
  → Page F.2–2, *Backup on local data media*
- **Recording**
  Data are being recorded on CD-R.
- **Rec. Failed**
  During recording on CD-R an error has occurred.

- ☐ **Receiving**
  Data are being received via the network as part of this job.
- ☐ **Received**
  Receiving via the network has been completed.
- ☐ **Spooling**
  The job is being prepared for transfer.
- ☐ **Error**
  It was not possible to prepare the job for transfer (error during spooling).

➩ Jobs with the status "Error", "Receiving" (or "Import"), or "Spooling" are no longer displayed when you restart.

Manipulating data transfer

You can select transfer jobs in the **Local Job Status** or **Network Job Status** dialog boxes and process them using the buttons.

The steps that you can perform and therefore the buttons that are active depend on the status of a job.

Stopping jobs

You can stop jobs with the status “Active“ and “Queued“ at any time, for example, if you want to change the MOD or CD-R for archiving before processing.

✧ Select one or more jobs with the status “Queued“ and click on **Stop**.

The selected jobs and all other jobs with the same destination address are now no longer started automatically. These jobs now have the “Stopped“ status.

Resuming jobs

You can resume a job with the status “Stopped“ or “Failed“ at the point at which it was stopped (only for archiving and importing processes that are executed in the **Local Job Status** window).

✧ Select one or more jobs with the status “Stopped“ or “Failed“ and click on **Continue**.

Jobs with the same destination address as the selected jobs are also resumed. The status of the jobs affected is now “Active“ or “Queued“.

Restarting jobs

If you have stopped jobs or if errors occurred in jobs, you can start them again from the beginning. You can also repeat a job which has already been completed.

✧ Select one or more jobs with the status “Stopped“, “Failed“ or “Completed“ and click on **Restart**.

The jobs are restarted, their status is now “Active“ or “Queued“.

➪ You cannot restart an import job from an MOD if you removed and reinserted the MOD during the import process.

➪ If a job fails when writing to a single session CD-R, do not restart or continue this job. Archive or export it again.

Starting recording on CD-R

Jobs with the status “Recordable“ are items that you have preselected for archiving on CD-R.

✧ Make sure that you have selected either *no* job or a job with the status “Recordable“.

✧ Click on **Record CD**.

All the items that you have preselected for archiving on CD-R so far and that have the status “Recordable“ are now written onto the inserted CD-R.

While data is being recorded onto CD-R, the **Recording CD** dialog box is displayed.
→ Page F.2–20, *Write operation*

Deleting jobs

You can delete jobs that are listed in the job status windows if they do not have the status “Active”, “Receiving”, “Recording” or “Spooling”.

✧ Select one or more jobs and click on **Delete**.

These jobs will no longer be executed and they will be removed from the job list.

➩ For technical reasons, large jobs are still shown in the job list for a while after they have been deleted. Do not restart or continue such a job.

Changing the priority of send jobs

Send jobs that should be processed first are classified as “urgent“ in the **Network Job Status** dialog box.

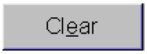
✧ Select one send job that is to be executed first and click on **Urgent**.

If several jobs are classified as “urgent“, they are executed in the sequence in which they are listed. For each destination address, it is possible to classify only one send job in the queue as “urgent”. It is then started immediately after the active jobs.

✧ If you want to cancel the classification as “urgent“, select the job or jobs and click on **Urgent** again.

Clearing a job list

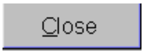
You can remove those entries from the job list that have the status "completed", "received", or "error".



✧ Click on **Clear**.

These jobs are removed from the job list.

Closing the window



✧ Click on **Close**.

CHAPTER
F.6

Configuring data transmission

In the **Transfer Configuration** window, you can define how archive, export and send jobs are executed by your system.

You can make or change the following settings here:

☐ Automatic archiving and sending of examination data

☐ Compression of data during archiving, export and sending

☐ Work status required for archiving data and whether to make optimum use of the storage capacity on the data media

✧ Call up the **Configuration Panel**
(**Options > Configuration** in the main menu).

➪ In the **Basics** part of this manual you can read how to call up and exit configuration windows, save changes, or reset settings back to the as-delivered state.
→ Chapter A.2, *Configuring the User Interface*

Transfer

✧ Select the **Transfer** configuration window.

The **Transfer Configuration** window is displayed with the **Auto Transfer**, **Exporting** and **Sending** tab cards.

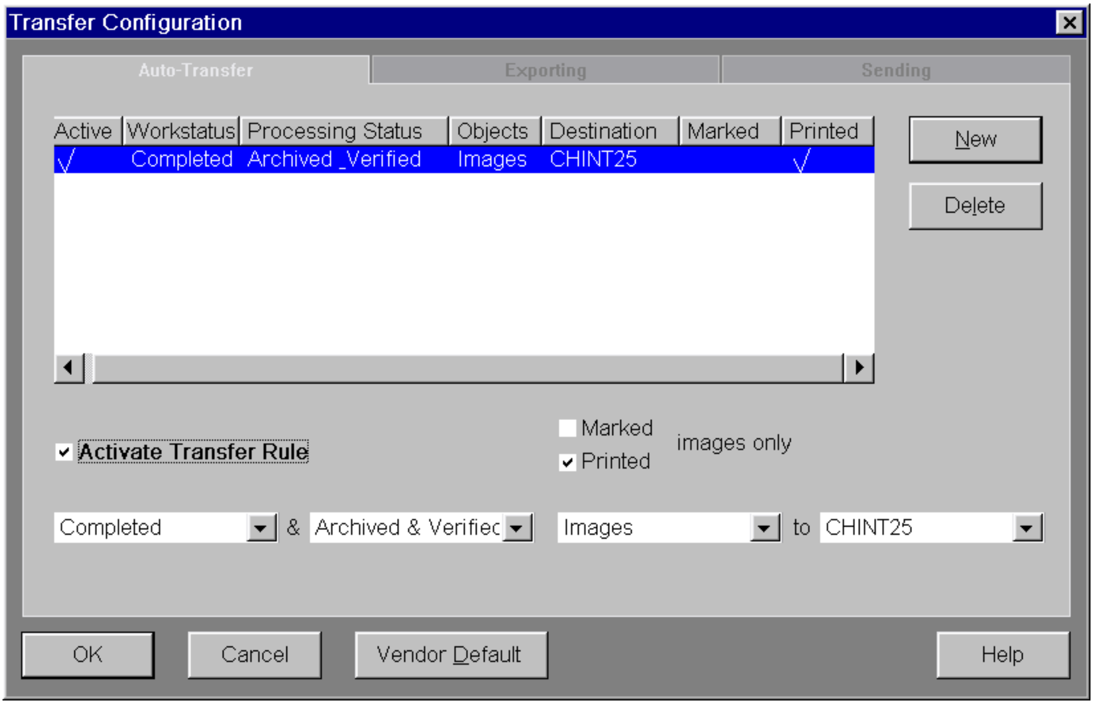
Automatic data transfer

On the **Auto Transfer** tab card, you can define whether and by what rules patient and examination data are automatically archived or sent in the network.

➪ When emergency registration is performed, automatic data transfer is deactivated (indicated in the status bar). After normal registration automatic data transfer is reactivated.

➪ You can check and change automatically started data transfer jobs in the Job Status dialog boxes in exactly the same way as manually started archiving and send jobs.
→ Page G.5–3, *Viewing and manipulating film jobs*

✧ Click the **Auto Transfer** tab card into the foreground.



Active	Workstatus	Processing Status	Objects	Destination	Marked	Printed
√	Completed	Archived _Verified	Images	CHINT25		√

☑ Activate Transfer Rule

☐ Marked
☑ Printed
images only

Completed & Archived & Verifiec Images to CHINT25

Rules for automatic data transfer

The list on the **Auto Transfer** tab card informs you what data with what work status will automatically be transferred by your system to what destination.

Each line of this list contains a rule for automatic data transfer. These rules consist of the following conditions:

❑ **Active**
A checkmark in the first column indicates that this rule is currently active.

❑ **Work status**
The data selected for transfer that have reached the work status specified here are automatically archived or sent in the network.

➪ You will find information about the work status of patient and examination data in the **Patient Browser** part.
→ Page D.5–2, *Defining the work status*

❑ **Processing Status**
Data that have reached the status stated here are automatically archived or sent via the network.

❑ **Objects**
Here you can see to what kind of data the rules refer, i.e. whether individual images, series or studies are transferred this way.

- **Destination**
  In this column, you can see to which archiving drive or to which network address the data are automatically transferred.
- **Marked**
  A checkmark in this column indicates that only marked data are automatically transferred.
- **Printed**
  A checkmark in this column indicates that only printed data are automatically transferred.

➪ You will find information about marking patient and examination data in the **Patient Browser** part.
→ Page D.5–6, *Marking examination data*

Creating, editing and deleting rules

Underneath the list, you will find input fields in which you can edit the existing rules for automatic data transfer or create new rules.

☑ Activate Transfer Rule

☐ Marked

☑ Printed

images only

Completed & Archived & Verifiec Images to CHINT25

Creating new rules and editing rules

You can create up to ten rules.

✧ Select a rule for editing from the list.

Or

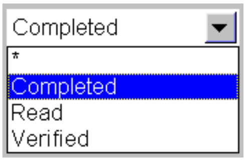
New

✧ Click on **New** to create a new rule.

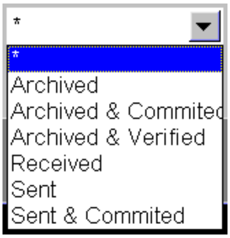
Rules

✧ Activate or deactivate the rule with the first checkbox.

✧ With the **Marked** or **Printed** checkbox define whether only marked and/or only filmed/printed images are to be used.

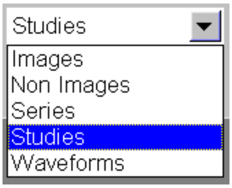


✧ With the first two selection lists define the conditions for the work status. Only data in the work status stated are considered for automatic data transmission.



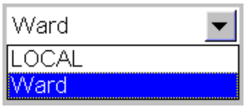
➪ Selecting * in these selection lists means that the work status is not relevant to the rule.

➪ Please note that you can also assign the “completed” status manually in the **Patient Browser** and in this way initiate automatic data transmission if necessary.
→ Page D.5–2, *Defining the work status*



✧ Define in the third selection list whether you want each individual image, complete series, or only whole studies to be transmitted given the appropriate work status.

➩ Automatic data transfer should always be configured at the instance level.



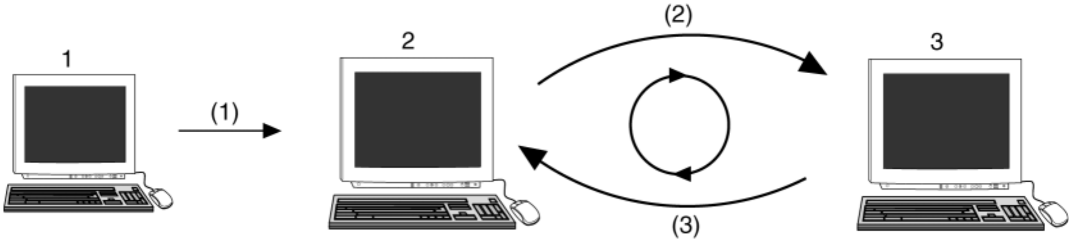
✧ Select the destination address in the fourth entry field.

➩ For example, select “Ward” as the destination address to have the examination data of a patient automatically transferred to the ward where that patient is located and which you entered during patient registration. This is, of course, only possible if the name of this ward has been set up as an address in the data network of your hospital.

Infinite loops

Make sure that you **do not create** any infinite loops with rules!

Here is an example of an unfortunate configuration with an endless loop:



(1) Computer 1 sends data to computer 2.

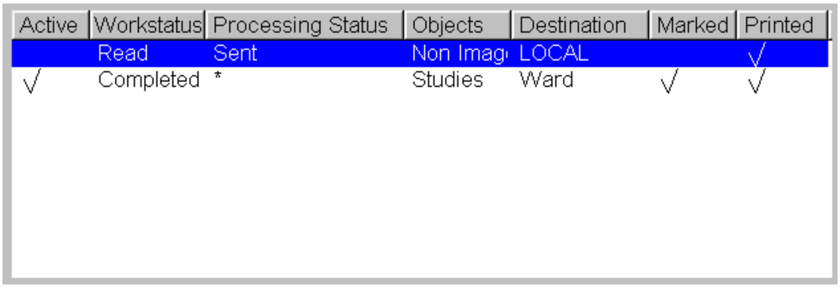
(2) Rule on computer 2: Send all data received to computer 3.

(3) Rule on computer 3: Send all data received to computer 2.

As soon as computer 2 has received data for the first time, this data is sent back and forth in a loop between computers 2 and 3.

Deleting rules

You can delete rules that you will no longer need for data transmission in the future instead of just deactivating them.



Active	Workstatus	Processing Status	Objects	Destination	Marked	Printed
	Read	Sent	Non Imag	LOCAL		√
√	Completed	*	Studies	Ward	√	√

✧ Select the rule that you want to delete from the list.

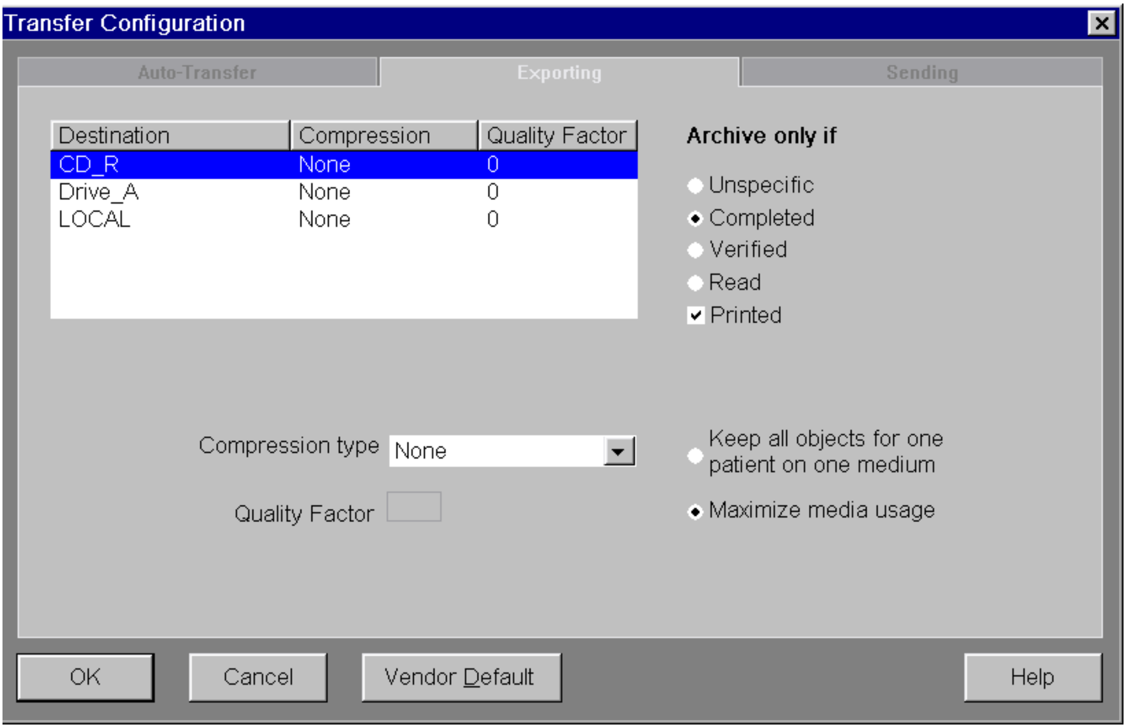
✧ Click on **Delete**.
The rule is removed from the list.

Archiving and exporting

On the **Exporting** tab card, you define the default settings for archiving and exporting data on the data media.

You can state for individual drives how the storage capacity of a data media to be used and whether data are to be stored there compressed or uncompressed. You can also define rules for the work status.

✧ Click the **Exporting** tab card into the foreground.



Destination	Compression	Quality Factor
CD_R	None	0
Drive_A	None	0
LOCAL	None	0

Archive only if

○ Unspecific
● Completed
○ Verified
○ Read
☑ Printed

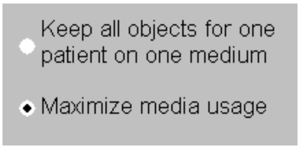
Compression type None

Quality Factor

○ Keep all objects for one patient on one medium
● Maximize media usage

Defining the use of storage capacity

If you require more than one data medium for archiving or exporting, you can define whether the data of one patient can be distributed over two data media or not (if possible).


○ Keep all objects for one patient on one medium

● Maximize media usage

✧ Click on the radio button **Keep all objects...** to have the data of one patient always stored contiguously.

Or

✧ Click on the radio button **Maximize media usage** to allow examination data of one patient to be distributed over two or more data media. This will make optimum use of the storage capacity of the data medium.

Setting data compression

Patient and examination data can be archived or exported compressed or uncompressed.

Data that has been compressed before transfer takes up less storage space and is transferred more quickly.

✧ Select a drive for which you want to define data compression.

Compression type Lossy JPEG

✧ Select under **Compression type** whether and how the data are to be compressed.

The following settings are possible:

❑ **None**
The images are not compressed.

❑ **Lossless JPEG**
The images are not compressed so small (compression factor 2 to 3) but without loss and can be imported with the original image quality (quality factor 100%).

❑ **Lossy JPEG**
The images are compressed very small but information is lost. So the quality of the images becomes worse (quality factor < 100%).

➪ It is only possible to archive images that have been stored compressed with loss of quality in your database with the same quality factor.

Quality Factor 45

The **Quality Factor** describes the degree of compression of an image.

100 percent means that the image quality has not been reduced. Values below 100% mean that the image has permanently lost image quality.

Only with the setting **Lossy JPEG** you can set the quality factor. Which quality factor is acceptable to you will depend on your requirements.

✧ If you have selected **Lossy JPEG** as the compression method, state under **Quality Factor** (0-100) the remaining image quality in % as compared with the original material.

CAUTION

Source of danger: Compression method is set to irreversible compression (Lossy JPG).

Consequence: The resulting images are no longer completely identical to the original images. Information of medical relevance may be lost.

Remedy: Lossy compressed images should not be used for primary diagnosis.

Standard setting for compression for data exchange

On data media you can exchange archived data with other systems. Standards regarding the choice of storage media and compression must be observed when archiving, which depend on the modality and data type (DICOM application profiles).

Modality / data type	**Compression**	**Storage medium** (default)
General	Uncompressed	CD-R
Angiographic images	Lossless JPEG and uncompressed	CD-R
Angiographic images (1024x1024x12 bits)	Lossless JPEG	CD-R
Angiographic secondary captures	Uncompressed	CD-R
CT and MR images and secondary captures	Lossless JPEG and uncompressed	MOD and CD-R
Waveforms (e.g. ECG and pressure curves)	Uncompressed	Floppy disk
Ultrasonic images and Ultrasonic multiframe images	Uncompressed	MOD and CD-R

Defining the necessary work status

Here you can select what work status patient and examination data must have reached before archiving. If this work status is not reached, a warning is displayed before storage.

Archive only if

○ Unspecific
● Completed
○ Verified
○ Read
☑ Printed

✧ Use the radio buttons to define the required work status to be the condition for archiving.

➩ The options **Verified** and **Read** apply to the levels Examination and Series only.

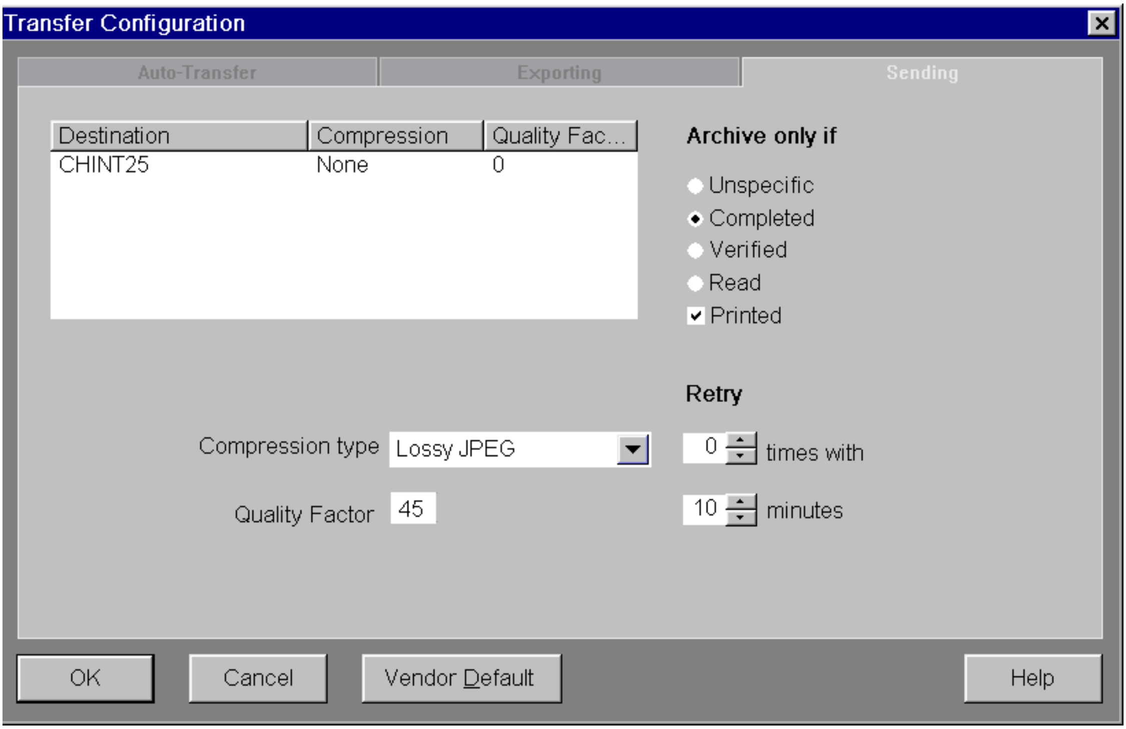
➩ If you select the **Unspecific** radio button, archiving is possible for any work status without confirmation.

✧ Also click on the **Printed** check box if you want to make sure that images have been filmed/printed before you allow them to be archived.

Setting sending

On the **Sending** tab card, you can define the default settings for sending data in the network. You can specify a type of compression and a quality factor and rules for repeated send attempts and the work status for each network address.

✧ Click the **Sending** tab card into the foreground.



Transfer Configuration

Destination	Compression	Quality Fac...
CHINT25	None	0

Archive only if

○ Unspecific
● Completed
○ Verified
○ Read
☑ Printed

Retry

Compression type: Lossy JPEG

Quality Factor: 45

0 times with

10 minutes

Setting data compression

Just like for archiving or exporting data on external data media, you can activate data compression for sending patient and examination data through the network (depending on the configuration of your system).

✧ Select a network address to which you want to send data compressed or for which you want to cancel data compression.

✧ Select whether and how you want the data compressed.
→ Page F.6–10, *Setting data compression*

You can choose between:

❏ **No** compression

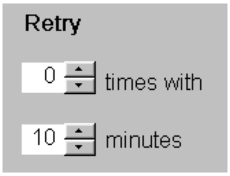
❏ **Lossless JPEG**

❏ **Lossy JPEG**

✧ Also specify a quality factor.
→ Page F.6–10, *Setting data compression*

Setting retries

If errors occur during data transmission in the network, they can often be remedied with a repeated attempt. You can set how many times and at what interval attempts are to be repeated.



Retry

0 times with

10 minutes

✧ Enter the number of retries or click on the arrows. (Possible values: 0 to 5; default: 0)

✧ Enter the time interval between the attempts or click on the arrows.
(Possible values: 5 to 60 min; default: 10 min)

➪ The number of new attempts is displayed in the window **Network Job Status**.
→ Page F.5–6, *Information in the Job Status dialog boxes*

Defining the necessary work status

Here you can select what work status patient and examination data must have reached in case of archiving. If this work status is not reached, a warning is displayed before storage.

Archive only if

○ Unspecific
● Completed
○ Verified
○ Read
☑ Printed

✧ With the radio buttons, define the work status required for sending.

➪ If you select the radio button **Unspecific**, archiving is possible in any work status without confirmation.

✧ Select the checkbox **Printed**, too, if you want to film or print the images at least once before they are sent.

PART G

Filming

G.1 Introduction

G.2 Automatic/Manual Filming

G.3 Viewing and Processing Film Sheets and Images

G.4 *Changing Film Settings for a Film Job*

G.5 *Checking Film Jobs*

G.6 *Camera Test*

G.7 *Configuring Filming Layout*

CHAPTER
G.1 Introduction

You can expose the images of an examination on film or print for documentation and reporting.

Depending on your examination schedule and on the current examination situation, you can have image material exposed on film or printed automatically. Images are then passed on to a preset camera or printer parallel to the examination.
Otherwise you can start filming manually and select which images you want to print or expose on film.

CAUTION

Source of danger: Use of paper printouts for diagnosis

Consequence: Wrong diagnosis

Remedy: Only use images on film for diagnostic purpose.

Procedure for filming

Image material is filmed/printed in two steps:

- ❏ First define on one of the task cards or in the **Patient Browser** window which images or series you want to print or expose on film. You then transfer this preselection to the **Filming** task card (virtual film sheet).
- ❏ From the virtual film sheet, you send your selected images either directly to a camera/printer or you can perform a few processing steps first. You can view the selected images using the **Film Preview** dialog box or the **Filming** task card (virtual film sheet), postprocess them to some extent, make a more precise selection, determine the film sheet layout, and reselect a camera/printer.

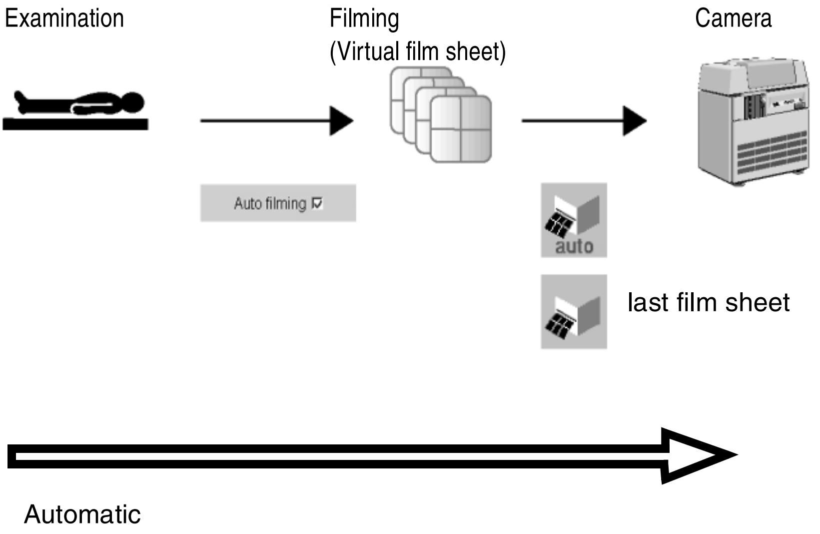
Fully automatic filming

Depending on your examination schedule, it can be useful to make image material available on film or paper for reporting as quickly as possible and without manual intervention.

To do that, activate **Auto filming** and **Auto Expose** to have the two filming steps run fully automatically.

During the examination, all the generated images are automatically transferred to the virtual film sheet and are immediately passed on from there to a preset camera or printer as soon as a film sheet is completely filled.

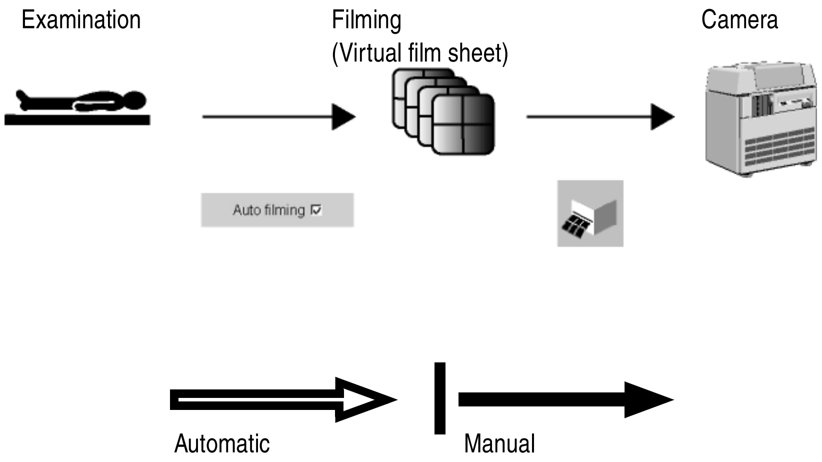
➪ The last film sheet has to be exposed manually.



Semi-automatic filming

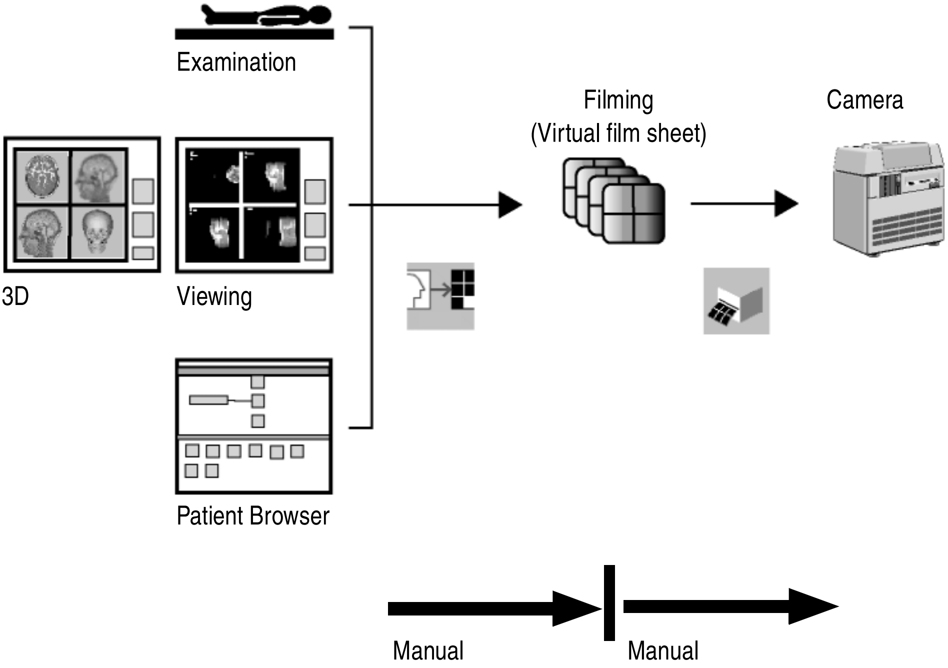
Of course, in some situations, it may be helpful to combine automatic and manual filming.

For example, activate **Auto filming** and deactivate **Auto Expose** if you want the images of your current examination to be held back before filming/printing in order to check them on the **Filming** task card and process them if necessary.



Manual filming

You can initiate transfer of images to the virtual film sheet and onto an camera or printer manually. In this way, you can divide up the work in an optimum way and only film or print those images that you really need for the diagnosis.



Manual filming with Auto Expose

If you are certain that the preselected film settings and the image order are correct you can activate **Auto Expose**.

Activate **Auto Expose** if you want all images to be immediately passed on to a preset camera as soon as a film sheet is filled.

Terms

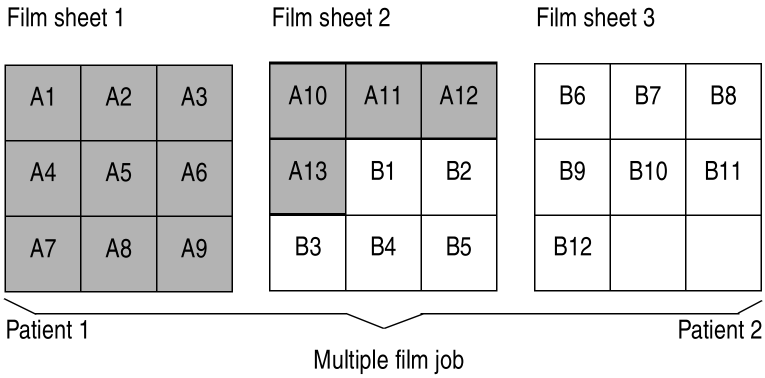
In the following chapters, you will come across several terms to do with filming that you should be familiar with.

Film job

Selected images, series and studies that you have sent for filming are managed and executed by the system as film jobs.

Multiple film job

Usually, the images of different patients are processed in different film jobs. However, you can permit images of different patients to be grouped together to form a multiple film job. The images are then processed as follows, for example:



Film Job Status	You can also obtain information about the extent to which film jobs in the camera/printer queue have been executed in the **Film Job Status** dialog box and intervene in the sequence of execution.
Virtual film sheet	All images in film jobs are not necessarily printed or exposed on film immediately but are first held in a virtual film sheet (represented by the **Filming** task card or the **Film Preview** dialog box). In the virtual film sheet, you can see how the images will later be arranged on the exposed film or print-out.

Layouts and settings

All film settings such as the layout of the film sheet or the selected camera/printer are defined in so called film layouts.

Standard layout

If you do not make any changes to the default film settings you are always working with the standard film layout (so called **Layout General Default**) which can be modified by the user.

Changing the film settings for the current film job

If you are not satisfied with the default film settings (standard layout), then you change individual film settings in the **Filming** task card. The current film job is then processed with your new settings. On the next film job, the system again accesses the defaults.

Study-specific layouts

In **Option** > **Configuration/ Filming Study Layout** you can define special film settings for individual studies. Whenever you film or print images of a study with the same study description, the system automatically accesses this study-specific layout.

CHAPTER
G.2

Automatic/Manual Filming

As explained in the introduction, filming and printing examination images is performed in two steps:

❏ Transfer of images to the virtual film sheet.

❏ Passing on the images from the virtual film sheet to a camera or printer where they will be exposed on film or printed on paper.

Both steps can be made to run automatically. This is advisable if large volumes of data resulting from a high patient throughput have to be dealt with and therefore large volumes of image material have to be made available for reporting as quickly as possible.

As an alternative, you can control filming either partially or completely manually. In this way, you can make sure that only those images are printed or being exposed on film that you really need for diagnosis or documentation.

NOTE

Please note if you want to control filming manually completely or partially:

Only up to 3 film jobs can ever be managed simultaneously in the virtual film sheet. A message appears if you exceed this number.
→ Page G.2–12, *Virtual film sheet full*

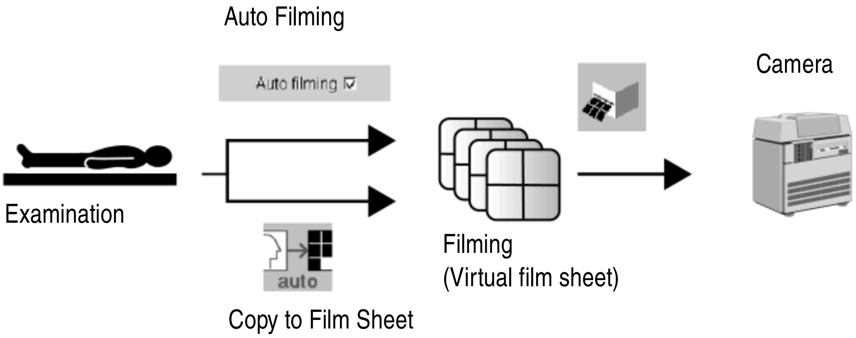
Transferring images to the virtual film sheet

In the first step, you decide on the task cards **Viewing**, **3D** or in the **Patient Browser** window which images you want to transfer to the virtual film sheet.

Examination task card

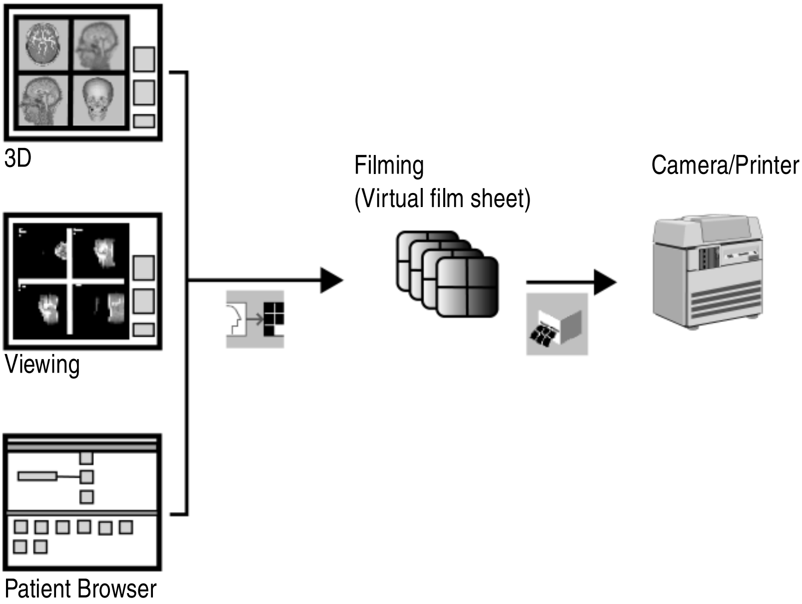
In the **Examination** task card, you can initiate automatic filming of all images after reconstruction of a series.

✧ Click on the **Auto filming** checkbox to activate automatic filming.
→ Page C.2–19, *Automatic Filming*



Viewing, 3D task cards and the Patient Browser window

You can film or print images stored in your local database from the **Patient Browser** or from the task cards. In this way, you can also send images for filming that you have evaluated with the **Viewing** card or generated in **3D**.



From **Viewing**, **3D** or **Patient Browser**, you always transfer images or series to the virtual film sheet manually.

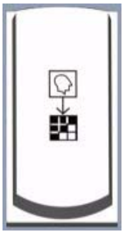
✧ First select the images that you want to film/print in the **Patient Browser**, on the **Viewing** or **3D** task card.

✧ Call up **Patient > Copy to Film Sheet**.

Or

✧ Click on the **Copy to Film Sheet** button.

Or



✧ Press the **Copy to Film Sheet** key on the symbol keypad.

All the selected images are transferred to the virtual film sheet on the **Filming** task card.

Per drag & drop

From the **Patient Browser**, you can also transfer images directly to the **Filming** task card by drag & drop.

✧ Select one or more images.

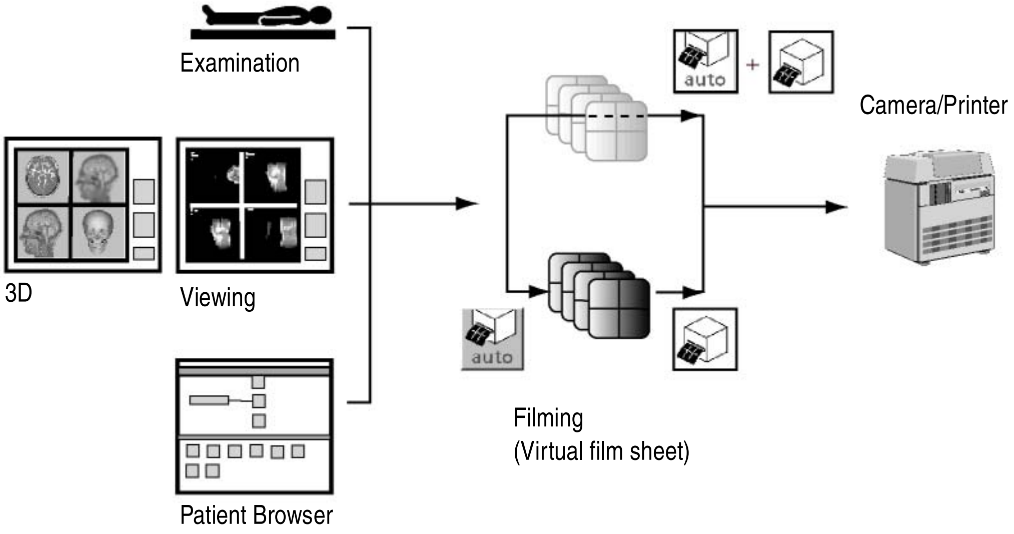
✧ Drag the images onto a segment of the **Filming** task card holding the left mouse key down.

A new film job or a multiple film job is created and the images are displayed on the virtual film sheet.

➪ If the task card is not in the foreground you can also drag the images from the **Browser** onto the corresponding tab. The task card moves into the foreground and the images are loaded into the image area.

Transferring images from the virtual film sheet to the camera/printer

Every time you want to transfer images, series or whole studies to the virtual film sheet automatically or manually, a film job is created. From the virtual film sheet, it is possible to transfer the individual film jobs to the camera/printer either automatically or manually.



Auto Expose

After a film job has been transferred completely to the virtual film sheet, it can be passed on to the camera/printer immediately and automatically.

You can define this setting at any time on the task cards or in the **Film Preview** window. It is then applied to the opened film jobs and all following film jobs.
→ Page G.3–2, *Film Preview*

Activating Auto Expose

✧ Call up **Options > Auto Expose**.

Or

✧ Activate the option via the **Auto Expose** button on the **Filming** task card or in the **Film Preview** window.

The film sheets of the **opened** film job and all following film jobs which are filled are automatically sent to the camera or printer and exposed or printed.

➩ The last partially filled film sheet must be sent manually to the camera with **Expose Film Task**.

➩ It is possible to have film jobs exposed automatically when **End Exam** is performed. Please ask your service for configuration in the **Local Service** dialog window.

Deactivating Auto Expose

If **Auto Expose** has been activated on the **Filming** task card or in the film preview, you can deactivate it at any time.

✧ Deselect **Options > Auto Expose**.

Or

✧ Click on the button on the **Filming** task card or the film preview again.

Interrupting Auto Expose

If errors occur during automatic filming, or you notice that useless images have been filmed/printed, you can interrupt automatic filming at any time.

✧ Deselect **Options > Auto Expose**.

Or

✧ Click on the button on the **Filming** task card or in the film preview again.

The sheet that is being processed will be completed. All the other film sheets are then retained in the virtual film sheet.

✧ Remedy the error or delete the useless images from the virtual film sheet.

✧ Reactivate **Auto Expose** or transfer the remaining sheets to the camera/printer manually.

Transferring images manually

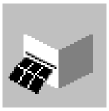
If you want to determine the time at which jobs are filmed or printed freely or if you want to view the images once more before filming, then deactivate the **Auto Expose** option.

All film jobs that you transfer from the task cards or from the **Patient Browser** are first collected in the virtual film sheet on the **Filming** task card.

Exposing a film job

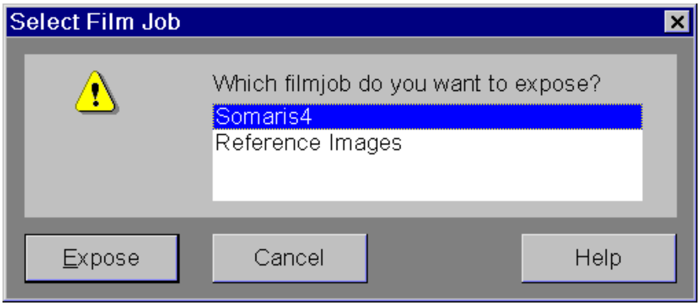
✧ Call up **Patient > Expose Film Task** as soon as you want to expose one of the film jobs in the queue

Or



✧ Click on the **Expose Film Task** button to transfer all images of this film job to the camera/printer.

The **Select Film Job** dialog box is opened, if more than one film task exist, in which you can select the job that you want to transfer to a preselected camera/printer.



Expose

✧ Select a job and click on **Expose**.

Or

Cancel

✧ Click on **Cancel** and switch to the **Filming** task card or call up **Film Preview** (**Patient > Film Preview...**).

✧ Select a film job.
→ Page G.4–4, *Selecting images and film sheets*

✧ Call up **Film > Expose Film Task**.

Or

✧ Click on the **Expose Film Task** button to transfer all images of this film job to the camera/printer.

Exposing/printing a film sheet

✧ Switch to the **Filming** task card or call up the **Film Preview** (**Patient > Film Preview...**).

✧ Select one film sheet.
→ Page G.3–15, *Selecting film sheets and images*
→ Page G.3–3, *The Film Preview window*

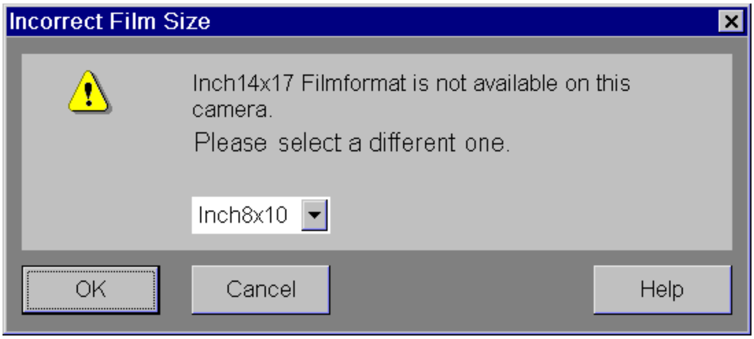
✧ Call up **Film > Expose Film Sheet**.

Only the selected film sheet(s) is/are processed.

Incorrect film size

If a film size which your camera does not support is set for the film sheet waiting to be exposed on film, the **Incorrect Film Size** dialog box is displayed.

➪ No corresponding error message is displayed when a paper printer is used.



Incorrect Film Size

Inch14x17 Filmformat is not available on this camera.
Please select a different one.

Inch8x10

✧ Select another film size and confirm with **OK** to resume filming.

Virtual film sheet full

No more than 3 film jobs can be managed in the virtual film sheet at one time. If a fourth film job is transferred to it, a message box appears. You must first expose/print one of the film jobs in the queue or delete it before a new film job can be accepted.

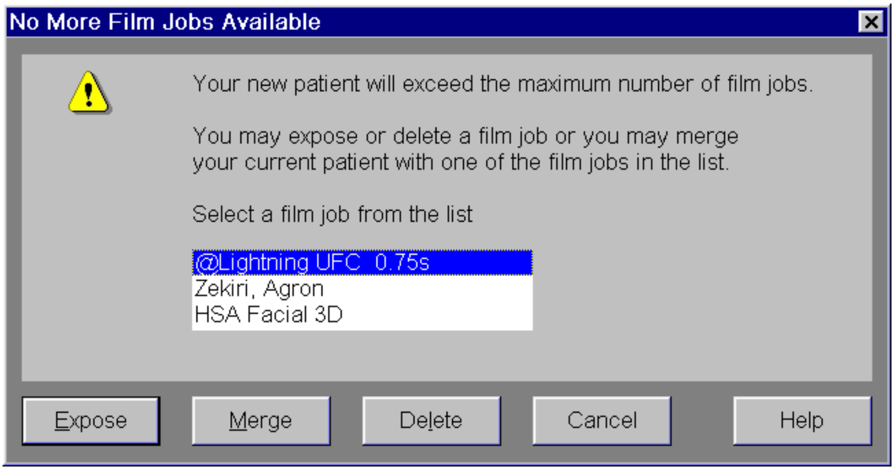
➩ This situation can usually only occur if the **Auto Expose** option is deactivated for the film jobs. The film jobs are only kept in the virtual film sheet until they are sent for filming manually and are therefore completed.

If a fourth film job is transferred, your system first checks whether it can be combined with one of the other film jobs to form a multiple film job.
→ Page G.1–6, *Multiple film job*

If this is not the case, the **No More Film Jobs Available** dialog box is displayed and you must remedy the situation.

No More Film Jobs Available

In the **No More Film Jobs Available** dialog box, you decide what film jobs are to be exposed, merged or deleted to make space for a new film job.



No More Film Jobs Available

Your new patient will exceed the maximum number of film jobs.

You may expose or delete a film job or you may merge your current patient with one of the film jobs in the list.

Select a film job from the list

@Lightning UFC 0.75s
Zekiri, Agron
HSA Facial 3D

✧ Select one of the film jobs listed.

✧ Click on **Expose** to transfer the selected job to the preselected camera/printer.

The selected job is filmed and the new job is placed in its position in the virtual film sheet.

Or

✧ Click on **Delete** to delete the selected job and place a new film job in its position.

Or

✧ Click on **Merge** to append the images of the new film job to the end of this old film job.

The film job remains in the virtual film sheet as a **multiple** film job until you transfer it to the camera or printer.
→ Page G.1–6, *Multiple film job*

Or

✧ Click on **Cancel** to cancel the new film job.

✧ Now switch to the **Filming** task card or open the **Film Preview** to expose or delete film jobs before loading the new film job.

CHAPTER
G.3

Viewing and Processing Film Sheets and Images

During manual filming, i.e. when you have deactivated the **Auto Expose** option, you can view and process the film sheets again before finally printing them or exposing them on film.
→ Page G.2–6, *Auto Expose*

Film preview

If you want to obtain a quick overview of the film jobs in the queue that have not yet been sent to the camera or printer, you can use the **Film Preview** window.

Filming task card

If you want to organize individual film sheets of the jobs in the queue more efficiently and clearly or if you want to process the images again before filming, switch to the **Filming** task card.

Film Preview

In the **Film Preview**, you can obtain information about how the images of the current film job will be arranged on the film sheets. Here, you can also call up some important functions to do with filming without having to switch to the **Filming** task card.

Calling up the film preview

✧ Call up **Patient > Film Preview** to call up the **Film Preview**.

Or

✧ Click on the **Film Preview** button on the **Viewing** task card or in the **Patient Browser**.

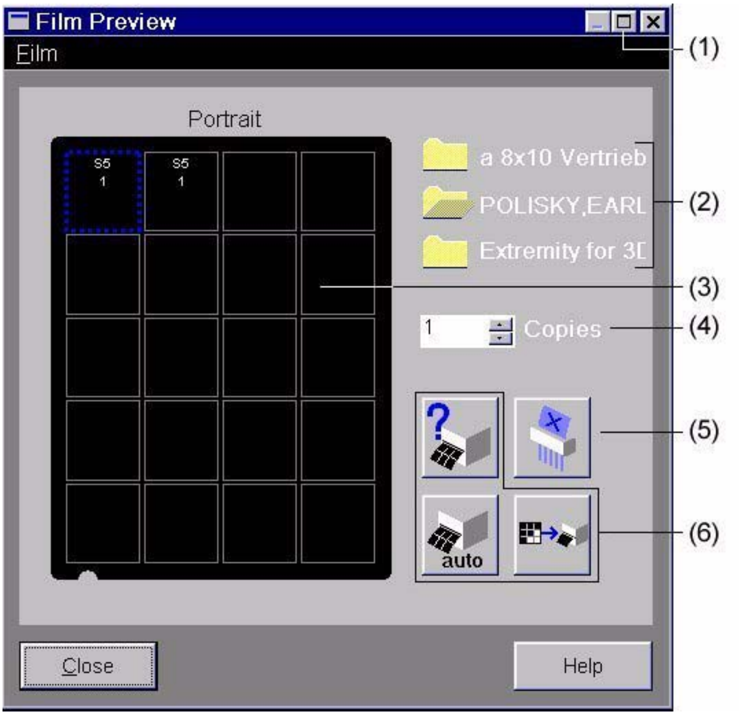
Closing the film preview

Close

✧ Click on the **Close** button to close the **Film Preview** again.

The Film Preview window

After you have called up the **Film Preview**, the **Film Preview** window will appear in front of the application you are currently working on.



(1) Maximize to Filming task card
(2) Film jobs
(3) Display of film sheet
(4) Spin box for selecting the number of copies
(5) Delete button
(6) Buttons for film control

Film jobs

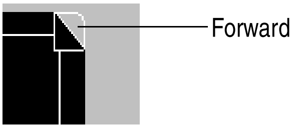
Here you can see all the film jobs listed that are in the virtual film sheet for transfer to a camera/printer. To process one film job or check the arrangement of images, you first have to open the film job.

✧ Click on a film job to open it.

Film sheets

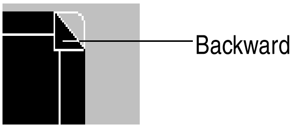
In the display area for the film sheets, you can see the last film sheet of the film job which is open.

With the dog ears in the top right hand corner, you can scroll through all the film sheets of the film job. The film sheet is subdivided into segments in which the series and image numbers of the images to be exposed or printed are displayed.



✧ Click on the top of the dog ear once to scroll forward by one film sheet.

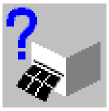
Or



✧ Click once on the bottom of the dog ear to scroll backward by one film sheet.

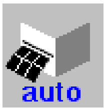
Control area

In the control area, you can call up a few important functions that have to do with filming.

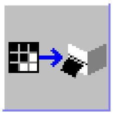


✧ Click on this button to open the **Film Job Status** dialog box.

There you can see the queue with the film jobs waiting to be transferred to the camera/printer.
→ Page G.5–1, *Checking Film Jobs*



✧ Click on the **Auto Expose** button or call up **Film > Auto Expose** to select or deselect this option.
→ Page G.2–6, *Auto Expose*



✧ Click on the **Expose** button or call up **Film > Expose Film Task** to transfer the opened film job to a camera/printer.
→ Page G.2–9, *Exposing a film job*

➪ If you do not want to film the entire film job but only the film sheet displayed, then call up **Film > Expose Film Sheet**.
→ Page G.2–11, *Exposing/printing a film sheet*

Changing default settings

By default a layout has already been defined for every film job in the virtual film sheet and a camera or printer has been selected.

You can change these film settings of a film job in the **Film Preview** dialog box or in the **Filming** task card itself.

To change settings in the **Film Preview**, proceed as follows:

Selecting a camera or printer

✧ Call up **Film > Change Camera** if you want to have the film job or film sheet displayed exposed with another camera or printed on another printer.

A dialog box is opened in which you can select a new camera/ printer.
→ Page G.4–2, *Selecting a camera or printer*

Changing film properties

✧ Click in a segment or on the border of the film sheet. In this way, you can select a single image or an entire film sheet.

Or

✧ Open and select the film job to change the film settings for the entire film job.

✧ Call up **Film > Properties** to change the film settings.

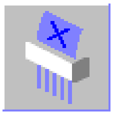
The **Film Properties** dialog box is opened in which you can change a series of layout settings for filming.
→ Page G.4–4, *Layout of the film sheet*

Processing a film sheet

In the **Film Preview**, a series of functions is available for reorganizing film sheets. These can be useful if you have opened the **Film Preview** from the **3D** or **Viewing** task card or the **Patient Browser**.

Deleting segments

If you can see that one of the images in the tomo segment of the **Examination** task card is useless (e.g. an image with motion artifacts), click on this image in the **Film Preview** (you can identify the image by its series and image number).



✧ Click on the **Delete** button in the control area to delete the selected segment.

The following images move up so that no empty segments are left behind.

Or

✧ Call up **Film > Clear Document(s)**.

The image will be cleared. The following images do *not* move up.

If you have cleared several segments in this way, your film sheets will contain a number of empty segments.

✧ Call up **Film > Repack** to make more efficient use of your film material.

Adding images

If you have opened the **Film Preview** from the **Patient Browser** window, you can add further images to a film job.

In this way, for example, you can also film images of earlier studies of a patient for comparison.

✧ Call up **Film > New Film Sheet** to add an empty film sheet to the end of the film job.

✧ Now fill this film sheet with selected images from the **Patient Browser** by **drag & drop**.

Or

✧ Send further images to **Filming** with **Copy to Filmsheet**.

These images are also appended to the end of the film job.Processing film jobs and film sheets.

Processing film jobs and film sheets

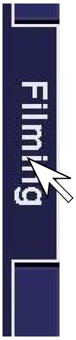
In addition to the simple processing steps in the **Film Preview**, you can also make complex and extensive changes to film jobs in **Filming**. In this way, you can make sure that you will only print or expose those images on film that you really need for reporting.

Moreover, you can process images or series of individual images or entire series in order to obtain an optimum output result on film.

For example, you can delete individual images or several images, reorganize or rearrange film sheets.

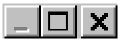
Calling up the Filming task card

You can process the film sheets of current film jobs on the **Filming** task card.



✧ Click on the **Filming** tab.

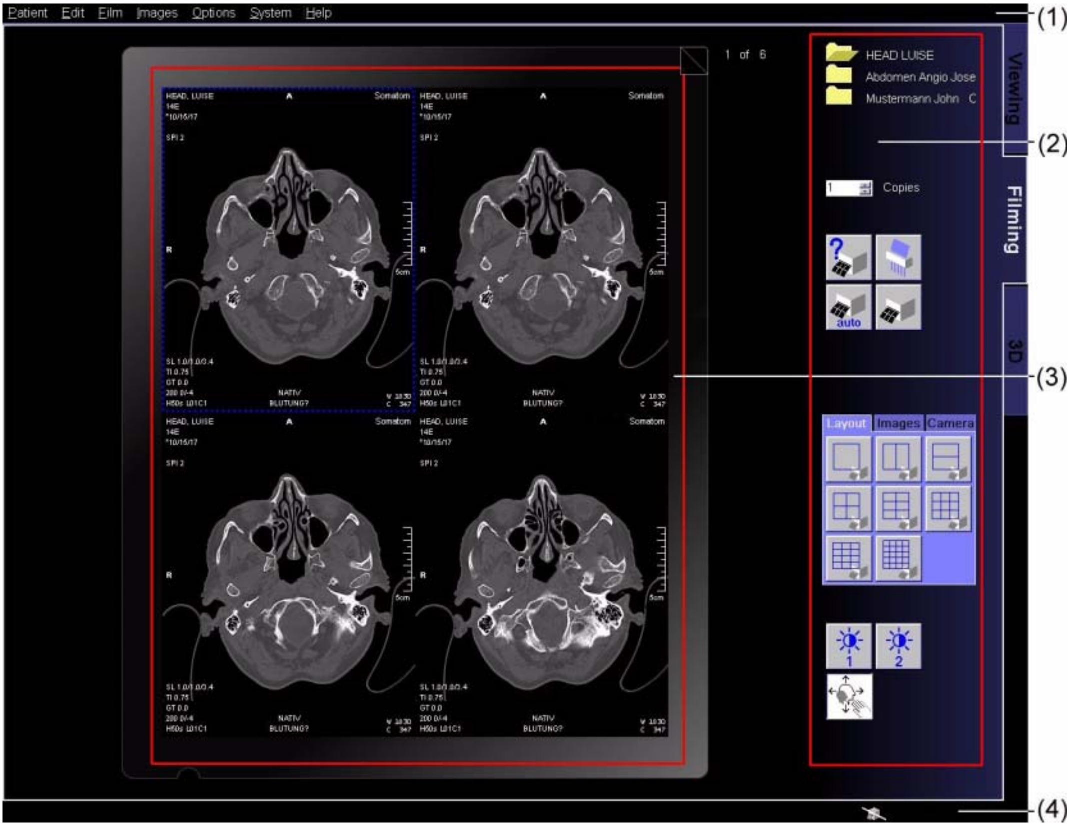
Or



✧ Maximize the **Film Preview** window.

The **Filming** task card is placed in the foreground.

The **Filming** task card is subdivided into the following areas:



(1) Menu bar with filming-specific menu entries
(2) Control area for easy call-up of processing functions
(3) Film sheet display (virtual film sheet)
(4) Status bar for system messages

Selecting a film job

By the patient folders in the upper part of the control area, you can see which film jobs are currently waiting to be transferred to a camera/printer.

Designations

These jobs have one of the following designations:

❑ **Patient name**
A film job that contains the images of a patient.

❑ **Multiple**
A film job that contains the images of several patients.
→ Page G.1–7, *Virtual film sheet*

⇨ If there is no film job in the virtual film sheet, a patient folder with the designation **New** is displayed.

Opening a film job

✧ Click on a film job to open it.

The patient folder opens up and the color of the folder remains unchanged.

The images of the opened film job are displayed on the film sheet in the left hand part of the task card.

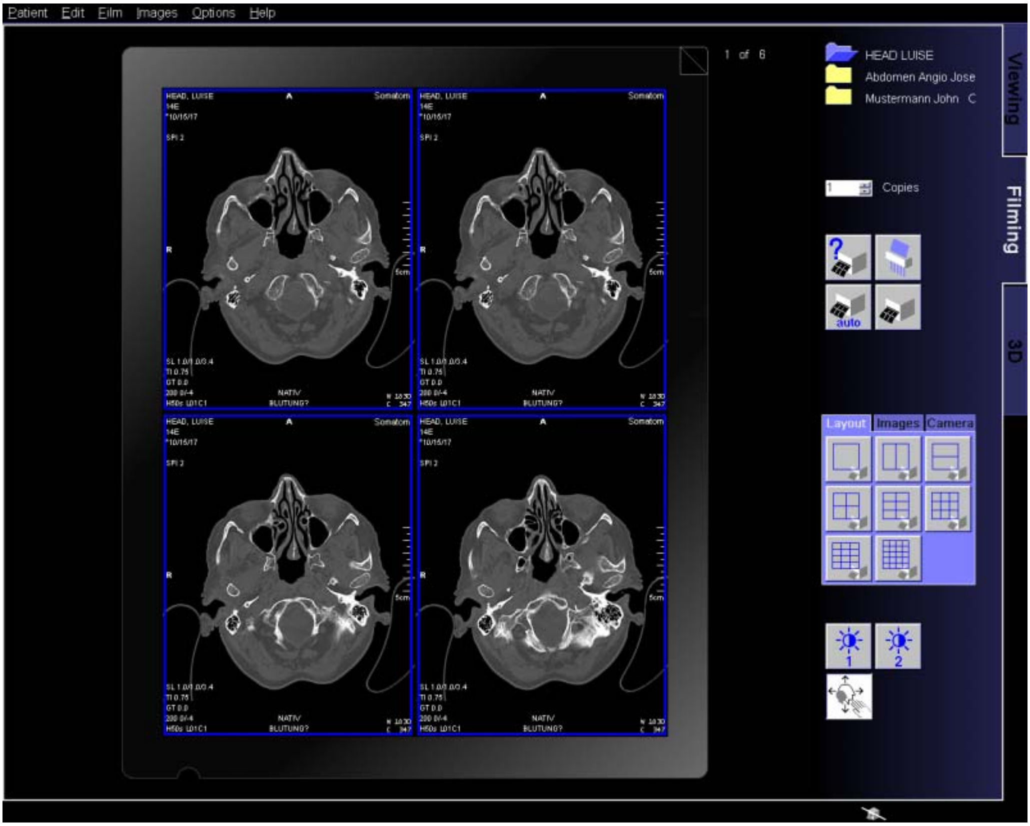
You can now page through the film sheets of this job and select and process one or more film sheets or images.
→ Page G.3–15, *Selecting film sheets and images*

Selecting an entire film job

If you want to process all the film sheets and images of a film job, you not only have to open this job but also select it explicitly.

✧ Click again on the opened film job to select all the film sheets with all images of this job.

The folder icon is now highlighted (blue), and all the images of this job will be shown with a bold border in the film sheet display and are therefore selected.



Number of copies of a film job

On the **Filming** task card or in the **Film Preview** window, you can also set how many times a job is to be exposed or printed.


1 Copies

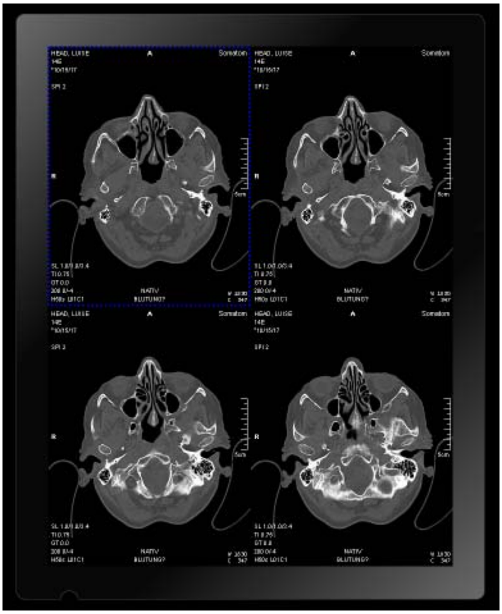
✧ Select the number of copies with the spin box or enter the required number with the keyboard.

Selecting film sheets and images

After you have opened a film job, its images are displayed in the left-hand part of the **Filming** task card.

Several film sheets

If a job contains so many images that they fill several film sheets, the sheet number and the total number of film sheets are displayed at the upper right border of each sheet, and in the top right hand corner you will find dog ears for paging.



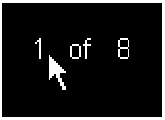
Job only extends over one film sheet

Job extends over more than one film sheet

Paging

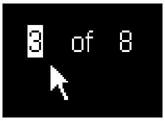
✧ Page through the film sheets using the dog ears.
→ Page G.3–4, *Film sheets*

Or


1 of 8

✧ Double-click on the number of the current film sheet.

The display field becomes an input field.


8 of 8

✧ Overwrite the number displayed with the number of the sheet that you want to go to and press **Return**.

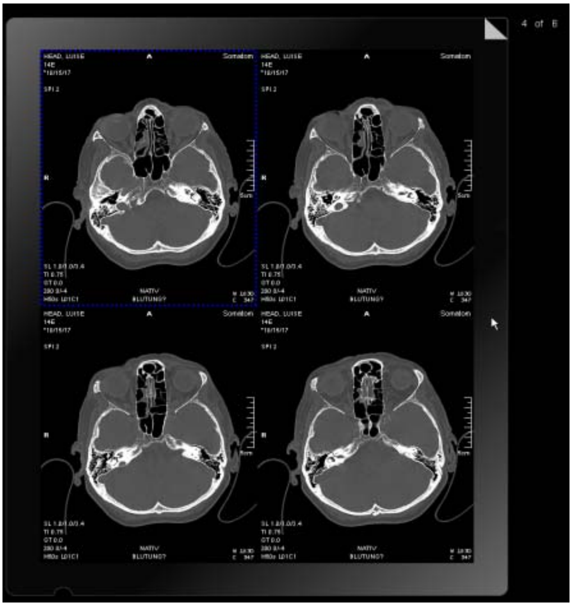
The film sheet you have entered will be displayed.

➪ If you want to scroll through a stack of images very fast, click on the dog ear and hold the mouse key down.

Selecting a film sheet

✧ Click on the border of the film sheet to select all the images it contains.

All the segments of the film sheet are now shown with a bold border.



Deselecting a film sheet

✧ Click outside the film sheet with the left mouse key.

Or

✧ Select a single image, another film sheet or another film job to cancel your selection.

Multiple selection

You can also select more than one film sheet at once.

✧ Click on the border of the first film sheet of your choice holding the **Ctrl** key down.

✧ Page to another film sheet.

✧ Hold the **Ctrl** key pressed to extend your selection by a single film sheet.

Or

✧ Hold the **Shift** key pressed to select all the film sheets from the first to the last selected film sheet including all their images.

⇨ When you have selected a film sheet, all images have a broken line border.

Selecting segments

You can not only select whole film sheets, but also individual images of a film job.

The **Input Focus** indicates the active segment of the image area. It is indicated by a broken line border and is shown so that it is always clear which image is being processed.

The processing steps that you execute are always applied to the segment on which the input focus is located.

Only if you have explicitly selected images, film sheets, or film jobs is the input focus deactivated and **no** segment has a broken line border.

✧ Click on another image with the left mouse key to place the input focus on another segment.

Or

✧ Move the input focus using the arrow keys on the keyboard.
→ Page E.3–32, *Working in the input focus*

The image is marked by a broken line border.

Selecting one or more images explicitly

You can select images explicitly one after the other like film sheets.

✧ Click into a segment holding the **Ctrl** key down.

The segment is marked with a broken line border.

➩ Like film sheets, you can also expand your selection for segments by clicking on further segments holding the Ctrl or Shift key down.
→ Page G.3–18, *Multiple selection*

Selecting images explicitly up to the end of a series

You want to select the image displayed and all the following images explicitly.

✧ Click on the image that you want to select explicitly holding the **Ctrl** key down or use the input focus.

✧ Call up **Edit > Select On Succeeding** in the main menu or **Select On Succeeding** in the popup menu.

The selected image and all the following images are now selected.

➩ If you have selected images of different series explicitly, all the remaining images in the series starting with these images are selected.

Selecting complete series explicitly

The simplest way for you to select entire series (e.g. all the images contained in them) is with **Select Series**.

✧ Click on the image of the series that you want to select holding the **Ctrl** key down or use the input focus.

✧ Call up **Edit > Select Series** in the main menu or **Select Series** in the popup menu.

The entire series is now selected explicitly.

➩ If you have selected images of different series, all the images of these series are selected.

Deselecting images

If the explicit selection does not contain the set of images that you require, you can deselect images individually or altogether.

✧ Hold the **Ctrl** key down and click on an explicitly selected image again. It is now deselected.

Or

✧ Call up **Edit > Deselect All** in the main menu to deselect all selected images again.

After that, the default input focus is set automatically, i.e. the top left segment is the destination of the next action.

Reorganizing film sheets

Using the **Filming** task card, you can reorganize film jobs in such a way that only those images are exposed or printed that you really need for a diagnosis.

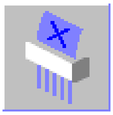
Deleting images or film sheets

You can delete image material that is useless for reporting from a film job.

✧ Select one or more images or film sheet or use the input focus.

✧ Call up **Edit > Delete** in the main menu.

Or



✧ Delete the image(s)/film sheet(s) with this button or with the **Del** key on the keyboard.

The image(s)/film sheet(s) will be removed from the film job completely. Empty segments are removed, too.

Or

✧ Call up **Film > Clear Document(s)** in the main menu or **Clear Document(s)** in the popup menu.

The images are deleted, the segments in the film job remain empty.

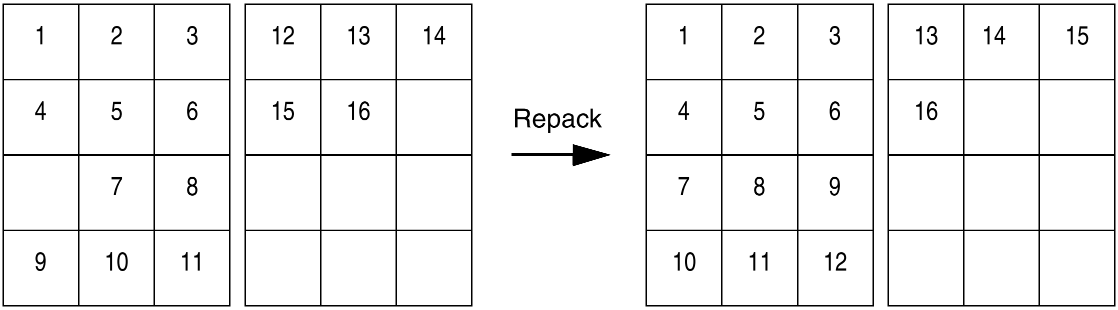
➪ The popup menu is context-sensitive, i.e. the content of the menu depends on whether you have selected an image, a film sheet, a film job or nothing.

Filling empty segments

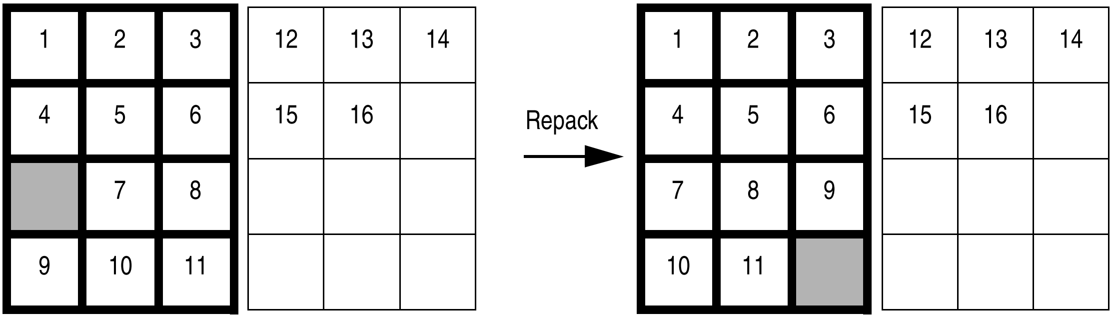
If you have deleted several images in a film job using **Clear Document(s)**, the job will contain several film sheets with empty segments. Before you send the film job to a camera/ printer, you should reorganize the film sheets to make better use of the film material.

✧ Select the entire film job.
→ Page G.3–13, *Selecting an entire film job*

✧ Select **Film > Repack** from the main menu or **Repack** in the popup menu (film jobs only) to fill the gaps again.



You can also use **Repack** during your processing to reorganize a single film sheet. In that case, only select one film sheet. Only the images of this one film sheet are reorganized.



Copying images or film sheets

If you want a film job to include images or entire film sheets more than once, you need to copy these images or film sheets first.

✧ Select the image(s)/film sheet(s) that you want to copy or copy the image that is in the input focus.

✧ Call up **Edit > Copy** in the main menu or **Copy** in the popup menu.

Or

✧ Copy the film objects with the Windows short-cut **Ctrl + C**.

Now select the image **in front of which** you want to insert the copies or work in the input focus.

✧ Call up **Edit > Paste** in the main menu or **Paste** in the popup menu.

Or

✧ Insert the images with the Windows short-cut **Ctrl + V**.

All the copied images are inserted in front of the selected segment. The image of this segment is moved back in the film job.

⇨ In **Filming Configuration**, you can define special layouts so that copies are produced automatically when images are transferred to the virtual film sheet.
→ Page G.7–9, *Configuring film sheets*

Moving images or film sheets

You can move images within a film job or from one film job to another by first cutting them and then pasting them at a new position.

✧ Select the image or the images that you want to move or work in the input focus.

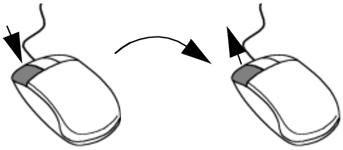
✧ Call up **Edit > Cut** in the main menu or **Cut** in the popup menu.

Or

✧ Cut the images with the Windows short-cut **Ctrl + X**.

✧ Select the segment in front of which you want to move the cut-out images.

✧ Insert the images in front of this segment with **Edit > Paste**, **Paste** or **Ctrl + V**.



➪ If you only want to move images within a film sheet, you can also do that very easily by **drag & drop**. Empty segments may result which can be filled with **Repack**

Appending a new film sheet

If the last film sheet of your job is already full and you want to copy or move images to the end of your film job, you must first append a new film sheet.

✧ Call up **Film > New Film Sheet** at any point in the film job.

A new (empty) film sheet is appended to the end of the film job.

✧ Then insert the copied or cut images into this sheet.

Appending images

From the task cards, you can only transfer images to **Filming** with **Patient > Copy to Film Sheet**.

If you transfer the images of the same patient to the virtual film sheet, they are always appended to the same film job. If you copy images of different patients onto the virtual film sheet, a new film job is created for each patient, unless your system has been configured to allow so-called multiple film jobs.
→ Page G.7–7, *One patient or more than one patient per film job*

Inserting images from the Patient Browser

If you want to insert images from the **Patient Browser** to a film job, you can do that by drag & drop.

✧ Open the **Patient Browser** (**Patient > Browser**).

The **Patient Browser** window will appear in front of the **Filming** with **Patient > Copy to Film Sheet**.

✧ Select the image, the images, or entire series or studies.

✧ Drag these images into a segment of a film sheet.

The images are inserted into the film job into this segment. The film job is called a **multiple** job if it contains the images of more than one patient now.

Processing images

In addition to the arrangement of film sheets, you can also change the display parameters of the images on the **Filming** task card to obtain an optimum output result.

Windowing

On the **Filming** task card, images are loaded with the window values with which they were last saved. If you have transferred images from the **Viewing** task card, the images are displayed with the window values last used in the **Viewing** card.

In **Filming**, you can change these window values before exposure.

➩ For color images, the window values are not displayed in the segment.

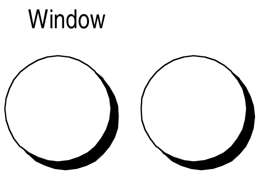
You have the following options:

Window 1 or Window 2

✧ Select one or more images, or work in the input focus.

✧ Click on **Window 1** or **Window 2** to assign the values of the first or second window stored in the **Examination** task card together with the images.

Windowing with the control box



✧ Select one or more images, or work in the input focus.

✧ Set the window values using the tuning knobs on the control box. In this way, you can adjust the window values very finely.

Windowing with the keyboard

For fine adjustment of the windowing values, you can also use the keys on the symbol keypad of the keyboard.

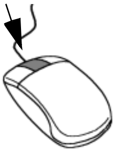
❑ Setting the contrast

✧ Press the **Width+** (Num **-**) or **Width-** (Num *****) key to increase or reduce the contrast.

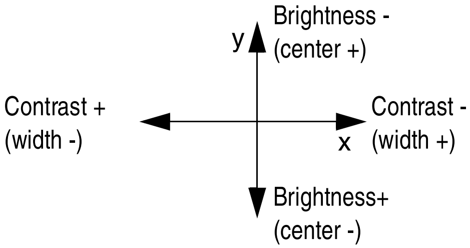
❑ Setting the brightness

Press the **Center+** (Num **/**) or **Center-** (Num **Num**) key to increase or reduce the brightness.

Windowing with the mouse



✧ Place the mouse cursor in the image and move the mouse holding the center mouse key pressed.



For more information about windowing images, see → Page E.4–2, *Windowing images*

Enlarging and reducing images

You can enlarge the image to view an area which is of special interest to you (zooming). If the enlarged image then no longer fits in the segment, you can pan or move it until the relevant area is in the center of the segment again.

You can use the following functions to zoom and pan images.

Images > Zoom in/out

✧ Select one or more images.

✧ Call up **Images > Zoom in/out** in the menu to open the **Zoom Image** dialog box. Enter a zoom factor for the selected images.

Zooming/panning with the mouse

✧ Click on the **Zoom & Pan On** button or select **Image > Zoom & Pan On** in the menu.

The function of the left mouse key is now switched from **Select** to **Zoom & Pan On**.

✧ Place the mouse cursor on an image (it need not be selected first).

✧ Now click near the edge of the image and hold the left mouse key down while moving the mouse cursor up to enlarge the image.

Or

✧ Click on the center of the image and pan the image holding the left mouse key down.

✧ Deselect **Images > Zoom & Pan On** or click on the button again to make the left mouse key available for selecting film objects again.

For more information about zooming/panning images, see
→ Page E.4–16, *Zooming and panning images*

CHAPTER G.4

Changing Film Settings for a Film Job

A standard film layout was defined during configuration of your system. This layout contains all the settings required for filming. You can also store special film settings for individual studies. These are called study-specific layouts.

All the necessary settings have therefore already been made for each new film job. If you are happy with these settings, you can start filming images without any further intervention.

If these presettings are not suitable, you can change the following settings on the **Filming** task card or in the film preview:

❑ Select another camera or printer

❑ Change the number of copies

❑ Change the arrangement of the film sheets

❑ Change the image, text and graphic display

All these settings then **only** apply to the current film job. For the next film job, the system returns to the standard layout or the default study-specific layout.

Selecting a camera or printer

If you do not want to expose or print your current film job with the default camera, then select another camera/printer for this job.

✧ Click the **Camera** subtask card on the **Filming** task card into the foreground.

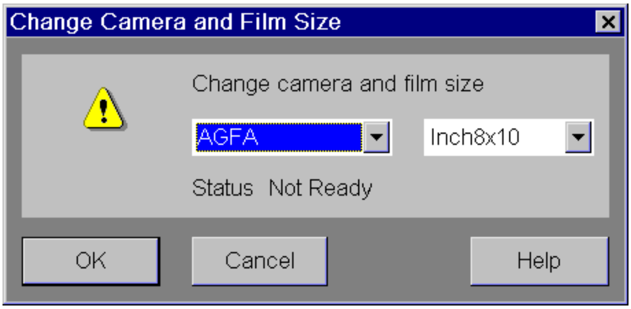
Camera
Camera2

Status: Not Ready

Film Size
Inch8x10

Or

✧ Select **Film > Change Camera** to call up the **Change Camera and Film Size** dialog box.



Change camera and film size

AGFA

Inch8x10

Status Not Ready

✧ Select a camera or printer from the list. This selection list contains all the cameras and printers connected to your system.

➩ The newly selected camera or printer is used as the default camera that is always used when no other device is selected.

In the **Status** display, you can see whether the selected camera/printer is switched on and is therefore available.

✧ Select the film format under **Film Size**.

Layout of the film sheet

With the layout of the film sheet, you can define the division of the film sheet and the size of each image.

Switch, for example, to a larger format with fewer images per film sheet, if you want to see diagnostic details on the exposed/printed images.

Selecting images and film sheets

Set the film sheet layout for selected images of a film job.

✧ Select an entire film job to change the layout for all sheets of this job.

Or

✧ Select an individual film sheet to change the layout of this sheet only.

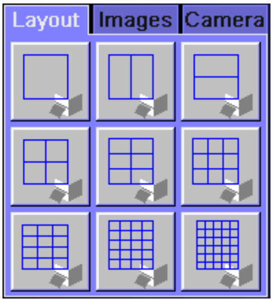
Or

✧ Select individual images or you work in the input focus to display only these images in a larger or smaller format on the same film sheet.

➩ When you change the layout of individually selected images or a film sheet, a new film sheet is created and appended at the end of the film job.
→ Page G.4–7, *Example*

Changing the layout

✧ Click the **Layout** subtask card on the **Filming** task card into the foreground.

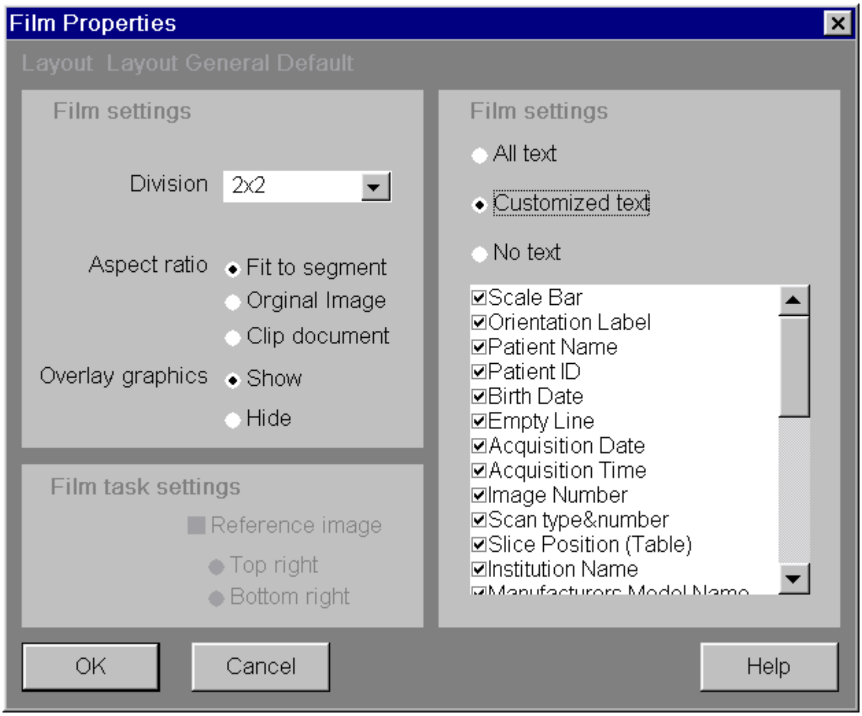


✧ Click on the button for a film layout to display the selected images in this format.

Or

✧ Call up **Film > Properties...** in the main menu or **Properties...** in the popup menu.

The **Film Properties** dialog box is opened.



Division: 2x2

Aspect ratio:
● Fit to segment
○ Orginal Image
○ Clip document

Overlay graphics:
● Show
○ Hide

☐ Reference image
○ Top right
○ Bottom right

○ All text
● Customized text
○ No text

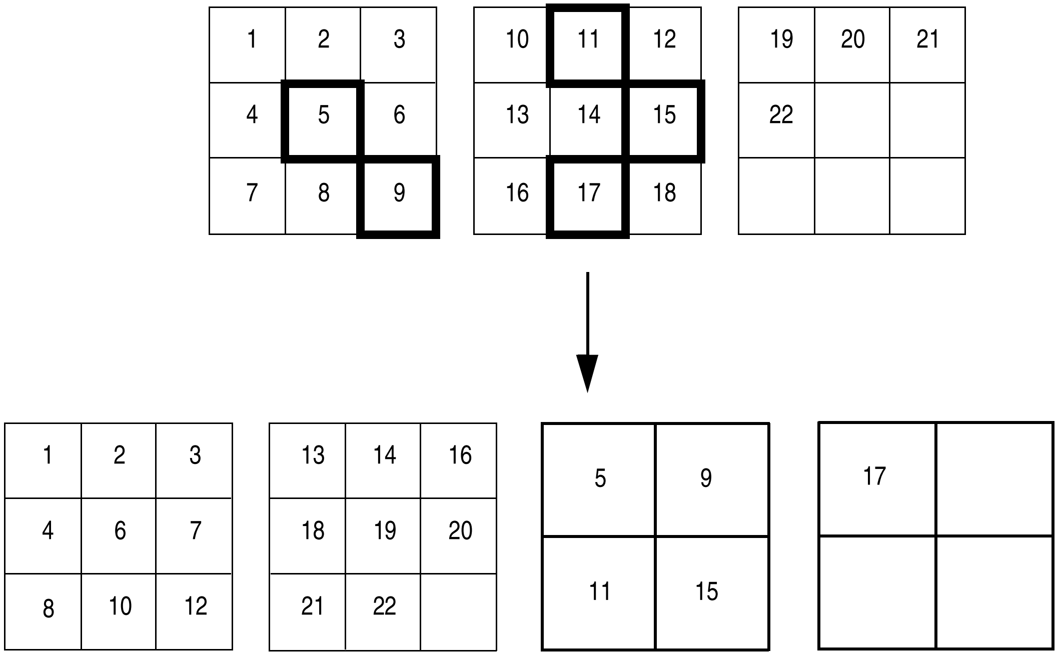
☑ Scale Bar
☑ Orientation Label
☑ Patient Name
☑ Patient ID
☑ Birth Date
☑ Empty Line
☑ Acquisition Date
☑ Acquisition Time
☑ Image Number
☑ Scan type&number
☑ Slice Position (Table)
☑ Institution Name
☑ Manufacturers Model Name

✧ Select a division in the **Division** selection list.

➪ If the film sheet division is different for the selected images or film sheets, the **Division** selection list is empty.

Example

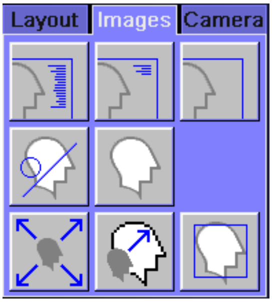
If you have only selected some images or film sheets, they are shifted to the end of the film job and displayed in the new format there. The remaining images of the film job are still displayed in the old layout.



Image, text and graphic display

The layout of the film sheet defines the number and size of the segments on a film sheet. With the **Film Preview** window and the **Filming** task card, you can change the aspect ratio of individual images in your segments and define whether and how text and graphics are to be printed or exposed on film, too.

✧ Click the **Images** subtask card on the **Filming** task card into the foreground.



Or

✧ Call up the **Film Properties** dialog box.

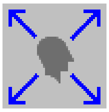
➪ You can see the settings of the currently selected images displayed. The dots in the radio buttons are displayed gray if the settings of the images are different.

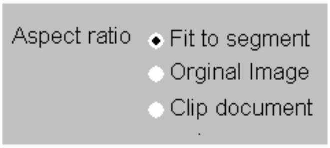
Fit to segment

- Select the image(s) whose aspect ratio you want to change.

Or

- Select the entire film job if you want to change the aspect ratio of all images.





Aspect ratio
● Fit to segment
○ Orginal Image
○ Clip document

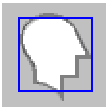
- Click on the **Fit to segment** button on the **Images** subtask card.

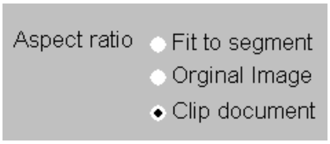
Or

- Select the option **Fit to segment** in the **Film Properties** dialog box.

The images are displayed as large as possible in the segment without any parts of the image being cut off.

Clip document





Aspect ratio
○ Fit to segment
○ Orginal Image
● Clip document

- Select an image, several images or the entire film job.
- Click on the **Clip document** button on the **Images** subtask card.

Or

- Select the **Clip document** option in the **Film Properties** dialog box.

Rectangular images can be increased so that the shorter side of the image fills the segment. Parts of the longer side of the image are cut off (upper and lower edge of the image or the sides of the image).

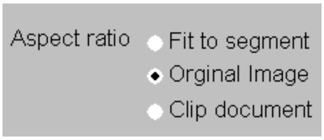
➩ For square segments **Clip document** leads to the same result as **Fit to segment**.

Original Image

✧ Select an image, several images, or the entire film job.

✧ Click on the **Original Image** button on the **Images** subtask card.

Or

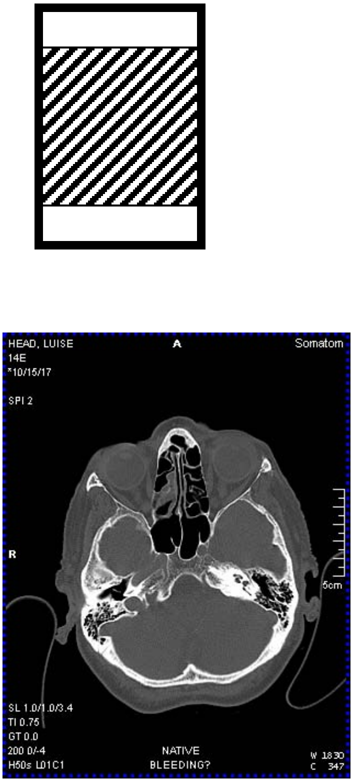


Aspect ratio
○ Fit to segment
● Orginal Image
○ Clip document

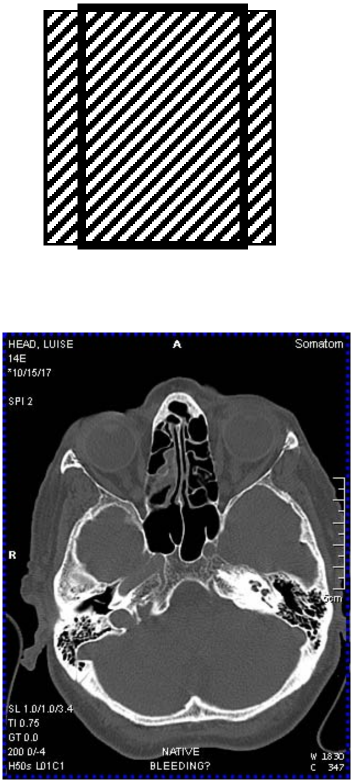
✧ Select the **Orginal Image** option in the **Film Properties** dialog box.

The images are displayed in the segment in their original size (tolerance 3 % max.).

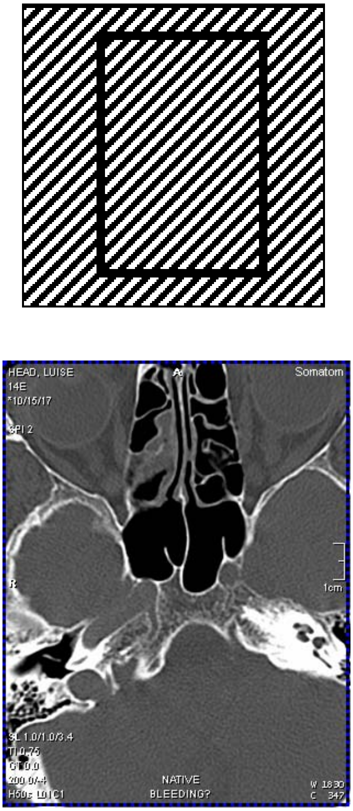
If it is not possible to display images in the **Original Image** aspect ratio (1:1 scale), a message is displayed and the **Fit to segment** option is selected instead.



Fit to segment



Clip Document



Original Image

Display image text

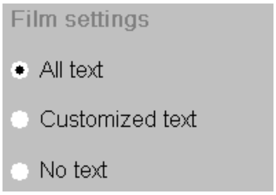
In the film settings, you can select whether text information about the images is also to be printed/exposed on film or not.

➪ Settings about filming text always apply to the entire film job and not only to selected images.

✧ Click on the **All text** button on the **Images** subtask card to have all text information about the images displayed in the segments and filmed or printed together with the images later on.

Or

✧ Select the **All text** option in the **Film Properties** dialog box.



Film settings

● All text

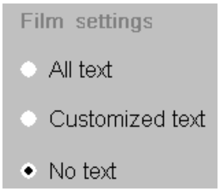
○ Customized text

○ No text

✧ Click on the **No text** button on the **Images** subtask card to hide all text information in the segments.

Or

✧ Select the **No text** option in the **Film Properties** dialog box.



Film settings

○ All text

○ Customized text

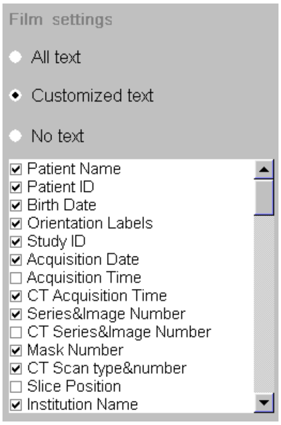
● No text

✧ Click on the **Customized text** button on the **Images** subtask card to have only part of the text information displayed and exposed on film or printed.

➪ If you select **Customized text** with the button on the **Images** subtask card, the system accesses the settings you have made during configuration.
→ Page A.2–8, *Configuring image text*

Or

✧ Select the **Customized text** option in the **Film Properties** dialog box.


Film settings

○ All text

● Customized text

○ No text

☑ Patient Name
☑ Patient ID
☑ Birth Date
☑ Orientation Labels
☑ Study ID
☑ Acquisition Date
☐ Acquisition Time
☑ CT Acquisition Time
☑ Series&Image Number
☐ CT Series&Image Number
☑ Mask Number
☑ CT Scan type&number
☐ Slice Position
☑ Institution Name

In the **Film Properties** dialog box, you can now select which text information is to be displayed if the **Customized text** option is selected.

✧ Click on the check box with the mouse to have each item of information either displayed or hidden.

All text

Customized text

No text

Displaying/hiding graphics and annotations

In the same way as text information, you can have graphics (e.g. ROIs) and annotations displayed or hidden.

✧ Click the **Show Graphics** button on the **Images** subtask card to display graphics (e.g. ROIs) and annotations.

Or


Overlay graphics ● Show ○ Hide

✧ Select the **Show** option in the **Film Properties** dialog box.

✧ Click the **Hide Graphics** button on the **Images** subtask card to hide graphics (e.g. ROIs) and annotations.

Or


Overlay graphics ○ Show ● Hide

✧ Select the **Hide** option in the **Film Properties** dialog box.


Show Graphics


Hide Graphics

CHAPTER

G.5 Checking Film Jobs

If you transfer film jobs from the virtual film sheet to a camera or printer, a queue of jobs waiting to be executed will be formed for each camera or printer.

You can obtain information about which and how many film jobs are currently being executed, are waiting to be executed or have been completed at any time. You can stop the entire queue, or repeat or delete individual film jobs and thus intervene in the execution of the queue.

In the **Film Job Status** dialog box, you can obtain information about film jobs that are waiting to be executed in the queues for each camera and printer.

On the status bar below the control area, you can see whether your system is currently exposing images on film in the background and whether exposure is progressing without error.

Display on the status bar

During film exposure, icons are displayed on the status bar which tell you whether the process is progressing without error or whether errors have occurred.

➩ The status of the printer is not shown on the status bar.

You can follow the course of film exposure without interrupting your work and intervene immediately in the event of an error.

Camera in operation

As long as the camera is working, i.e. exposing film sheets, the camera icon is displayed on the status bar.

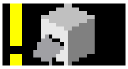
Film exposure interrupted

If errors occur during film exposure, the camera icon on the status bar is crossed out.

✧ Double-click on this camera icon to open the **Film Job Status** dialog box.

There you can see the cause of the fault.

Warning message



This symbol indicates that the camera has output a warning message.

Viewing and manipulating film jobs

The display on the status bar shows concise information about the progress of film exposure.

➩ For print jobs, no information is displayed in the status bar.

You can obtain detailed information in the **Film Job Status** dialog box. There you can stop the entire queue, trigger it again and repeat or delete individual film jobs.

Calling up the Film Job Status

Regardless of whether your system is currently printing/exposing films or not, you can call up the **Film Job Status** window via the main menu or a button at any time and from any task card. There, you can obtain information about the film jobs in the queues.

Once film exposure in the background has started, you can also display the dialog box by clicking on the icons in the status bar. That is useful if transmission errors occur. You can then immediately see which film job and which camera are affected and take appropriate action.

✧ Click on the **Film Task Status** button on the **Viewing** or **3D** task cards or in the **Patient Browser**.

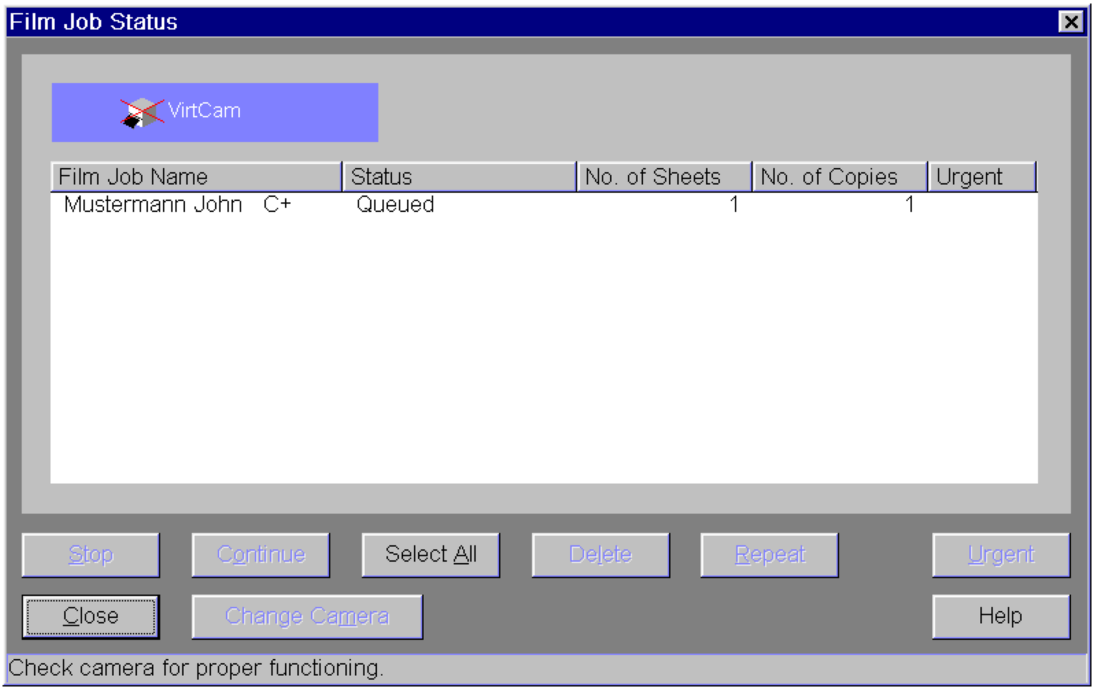
Or

✧ Call up **Patient > Film Task Status**.

Or

✧ Double-click on the camera icon on the status bar.

The **Film Job Status** dialog box is displayed.

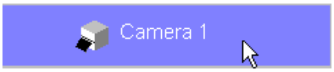


Film Job Name	Status	No. of Sheets	No. of Copies	Urgent
Mustermann John C+	Queued	1	1	

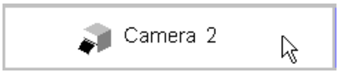
Check camera for proper functioning.

Camera

In the upper part of the dialog box, all the cameras and printers are displayed that are connected to your system.



The camera whose queue is being displayed is highlighted in a different color.

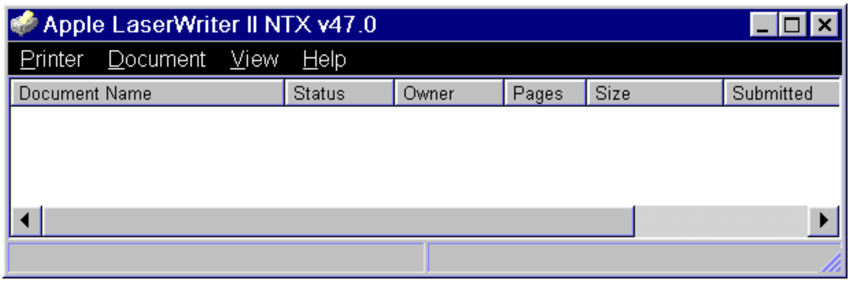


✧ Click on one of the other camera icons if you want to view the queue for another camera.

Printer

✧ Click on one of the printer icons if you want to view the queue for the respective printer.

The Windows NT print job control box is displayed. Here you can manipulate the print jobs for the selected printer by using the menu entries of the Windows NT operating system.



✧ Close the Windows NT print job control box to return to the **Film Job Status** dialog box.

Information in the Film Job Status box

The **Film Job Status** dialog box contains a job list with the following information:

Film Job Name	Name of the film job (*patient name*, if a film job contains the images of only one patient, or *multiple*, if the job contains images of more than one patient)
Status	Processing status of the film job: ❏ *Printed* The job is completed, all images have been sent to the camera. ❏ *Active* The job is currently being sent to the camera. ❏ *Queued* The job is in the queue and will be sent to the camera as soon as it is free. ❏ *Stopped* The job has been stopped. ❏ *Aborted* The job was aborted and is treated as completed.
No. of Sheets	Number of film sheets that the film job contains.
No. of Copies	Number of copies
Urgent	A job is classified as urgent.

If the list contains more film jobs than can be displayed in the content window, you can page through the queue of film jobs using the scroll bar. When you open the window, the first job with “Active” status (or “Queued”) is displayed in the list.

✧ Scroll the display up to view jobs already exposed on film (“Printed”).

Manipulating film jobs

In the **Film Job Status** dialog box, you can select film jobs and influence them by clicking buttons.

The status of a job determines how you can influence its execution and therefore what buttons are active.

➩ Only film jobs sent to a camera can be modified in the **Film Job Status** dialog box.

Stopping jobs

You can stop jobs with the status “Queued” or “Active” at any time, for example to insert a new film.

✧ Click on the **Stop** button.

All film jobs of this queue are stopped (status “Stopped”). In the job which is being exposed, a sheet which has been started is first completed. All the following film sheets are then no longer processed.

Resuming jobs

Once your camera is ready again, you can resume execution of the queue.

✧ Click on the **Continue** button.

All the jobs in the queue return to their original status. Film exposure is resumed. The job that was being exposed when you clicked **Stop** is resumed at the point at which you stopped the camera.

Repeating jobs

You can repeat a film job that has already been exposed and is therefore completed as long as it is still in the queue.

✧ Select the film job already exposed on film (status “Printed”).

✧ Click on the **Repeat** button.

The job is assigned the “Queued” status and is copied to the end of the queue.

➪ If the images of the job have already been deleted from the database, an error message is displayed.

Deleting jobs

You can delete film jobs that are listed in a queue regardless of their status.

✧ Select the job(s) that you want to delete (multiple selection using the **Ctrl** or **Shift** key).

Or

✧ Click on **Select All** if you want to delete all the jobs in the queue.

✧ Click on the **Delete** button to delete the selected job(s).

➩ If you delete a job that is being exposed, the sheet that has been started will be completed. All the following sheets will not be exposed on film.

Changing the priority of film jobs

Set the film jobs that you want to process first as “urgent”.

✧ Select one or more film jobs with the “Queued” status and click on **Urgent**.

This job moves to the first position amongst the jobs with the “Queued” status.

If more than one job is classified as “urgent”, they are executed in the order in which they are listed.

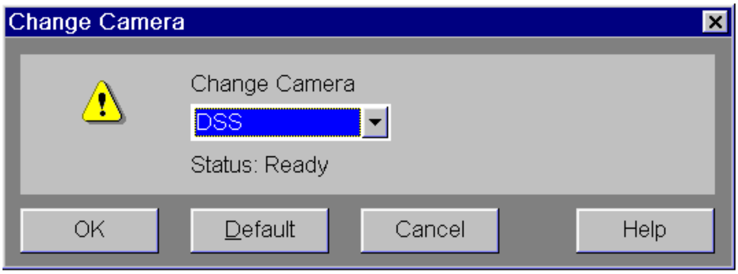
Selecting another camera

You can select a new camera for one or more film jobs.

➪ Redirecting film jobs from a camera to a printer is not possible.

✧ Select one or more film jobs.

✧ Click on the **Change Camera** button to open the **Change Camera** dialog box.



Change Camera
DSS
Status: Ready

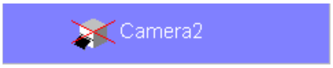
✧ Select a new camera from the selection list.

➪ You cannot redirect film jobs that are being exposed (“Active” status) to another camera.

Redirecting jobs from an inaccessible camera

If one of your cameras is defective or switched off this is indicated by a crossed-out camera icon in the header bar of the **Film Job Status** dialog box.

You can redirect the queue or even individual film jobs for this camera to another camera.



✧ Click on the camera icon.

The queue of the camera is displayed.

✧ Click on the **Change Camera** button to open the **Change Camera** dialog box.

✧ Select a substitute camera from the selection list.

✧ Close the **Change Camera** box.

The queue of the camera is redirected to the substitute camera. The redirected queue is marked with the note “**redirect**” in the header bar of the dialog box.

All film jobs whose film size is not supported by the destination camera remain in the queue for the original camera. These jobs are assigned the status “**queued**”, but do not block the following film jobs so that these can be redirected to another camera.
You can send these film jobs again when the fault has been remedied or you can redirect them to a camera that supports the required film sizes.

As soon as the defective camera has been repaired again, you can cancel the camera redirection.

✧ Click on the camera with the note “redirect” to display the redirected queue.

✧ Click on **Change Camera** to call up the **Change Camera** dialog box again.

✧ Click on the **Default** button in the **Change Camera** box.

The queue is now assigned to the original camera again. The original device designation is again displayed in the header bar of the **Film Job Status** dialog box.

Reactivating a queue after system restart

Sometimes it is necessary to shut down the system before all the film jobs in a queue have been executed.

This does not delete the queue. After rebooting the system, the film jobs are displayed in their old status again.

They are then started automatically.

CHAPTER
G.6 *Camera Test*

In the camera test, the image quality and the camera settings are checked.

You can also film test images of the quality measurement in order to meet requirements for documentation and archiving.

Image quality of the camera

The camera was set for optimum image quality during installation and should not be changed.

✧ Please note the following points:

☐ Use the correct film type (emulsion number).
☐ Keep the developer bath at a constant temperature.
☐ Use the correct chemicals.
☐ Follow the development instructions supplied by the film manufacturer.

Test film

After installation, a test film is recorded and evaluated. The results are summarized in a table. These values are used as reference values for the daily quality check of the camera.

NOTE

If the equipment or the emulsion number of the film is changed, the camera must be readjusted by a customer service technician who is authorized to do so.
After this, another camera test is required.

Test report of the camera

At the end of this chapter you will find a form for the test report.

Testing the camera

With the camera test (**Film Demo**), you can check the settings of the camera by filming the images of the “Reference Images” Patient.

➩ The reference images can be imported with **Import from Offline** in the **Patient Browser** main menu. Use the source directory “C:\Somaris\service\ReferenceImage\”.

You also have the option of filming the images of a previous constancy test to check the camera settings (**Film Quality**).

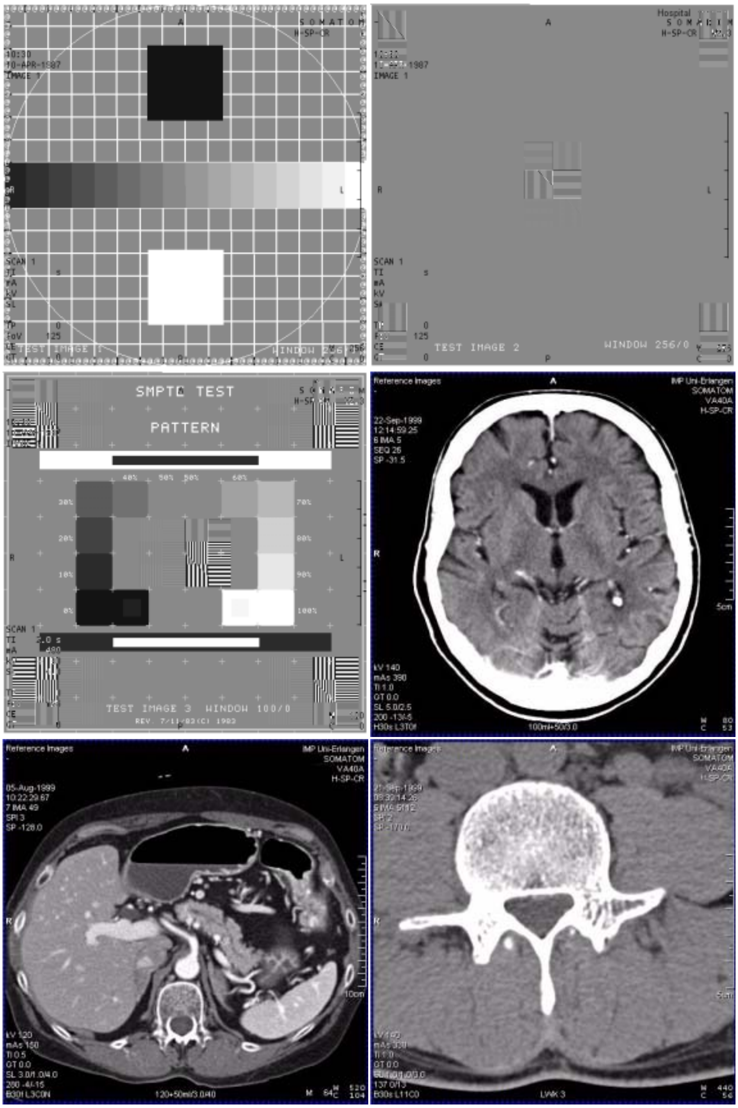
Starting the camera test

You start the camera test in the **Viewing** task card.

✧ In the **Patient Browser**, transfer the test images of the “Reference Images” Patient to the **Viewing** task card.
→ Page D.3–3, *Viewing and processing images*

✧ In the **Viewing** task card, film the test images of the “Quality Assurance Patient”.
→ Page E.7–12, *Filming/printing images*

Examples of test images

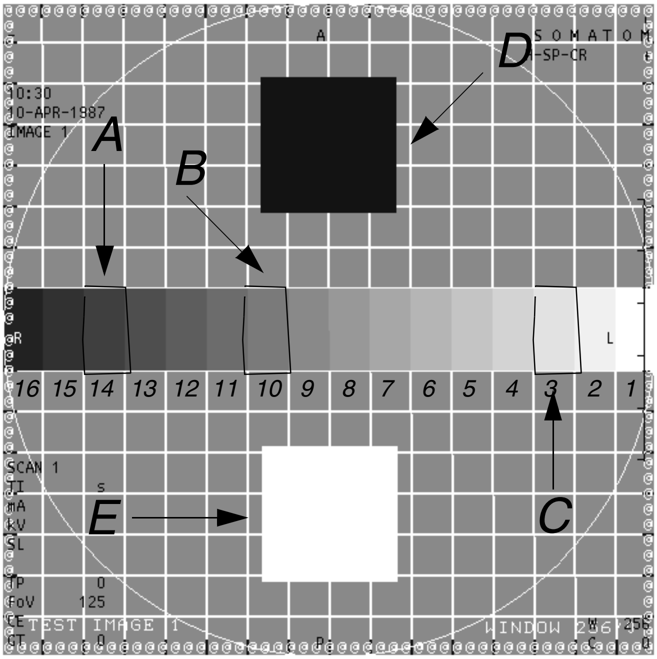


Reference values

✧ Compare the test results with the reference values.

✧ Measure the fields marked in the first test image with the densitometer X-RITE 331.

Here is an example of test image 1 with measurement fields marked by the technician:



✧ Enter the measured values in the constancy test report.

➪ If the values are outside the tolerance range, contact Siemens Customer Service.

Year: Month: Day:	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31
Density values +0.20 **Meas. field A** 1.88 −0.20 Field No.:14																															
+0.15 **Meas. field B** 1.04 −0.15 Field No.: 10.....																															
+0.05 **Meas. field C** 0.28 −0.05 Field No.: .3....																															
+25% **Meas. field D** 2.08 −25% (black)																															
+25% **Meas. field E** 0.20 −25% (white)																															
Developer temperature:																															
Replenishment Developer																															
Replenishment Fixer																															

Clinic:

Department:

Camera type:

Developing machine:

Film type:

Emulsion number:

Developer:

Fixer:

Year: Month: Day:	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31
Density values +0.20 **Meas. field A** 1.88 −0.20 Field No.:14																															
+0.15 **Meas. field B** 1.04 −0.15 Field No.: 10.....																															
+0.05 **Meas. field C** 0.28 −0.05 Field No.: 3.....																															
+25 % **Meas. field D** 2.08 −25 % (black)																															
+25 % **Meas. field E** 0.20 −25 % (white)																															
Developer temperature:																															
Replenishment Developer																															
Replenishment Fixer																															

Clinic:

Department:

Camera type:

Developing machine:

Film type:

Emulsion number:

Developer:

Fixer:

CHAPTER
G.7

Configuring Filming Layout

You can adapt the filming and printing of images to your requirements in a flexible and individual way.

The **Configuration Panel** contains two configuration windows for setting up the film function:

Filming Layout

In the **Filming Layout** configuration window, you can adapt the standard layout and create new layouts that are tailored to individual studies.

Filming Study Layout

In the **Filming Study Layout** configuration window, you can assign specific layouts to individual studies.

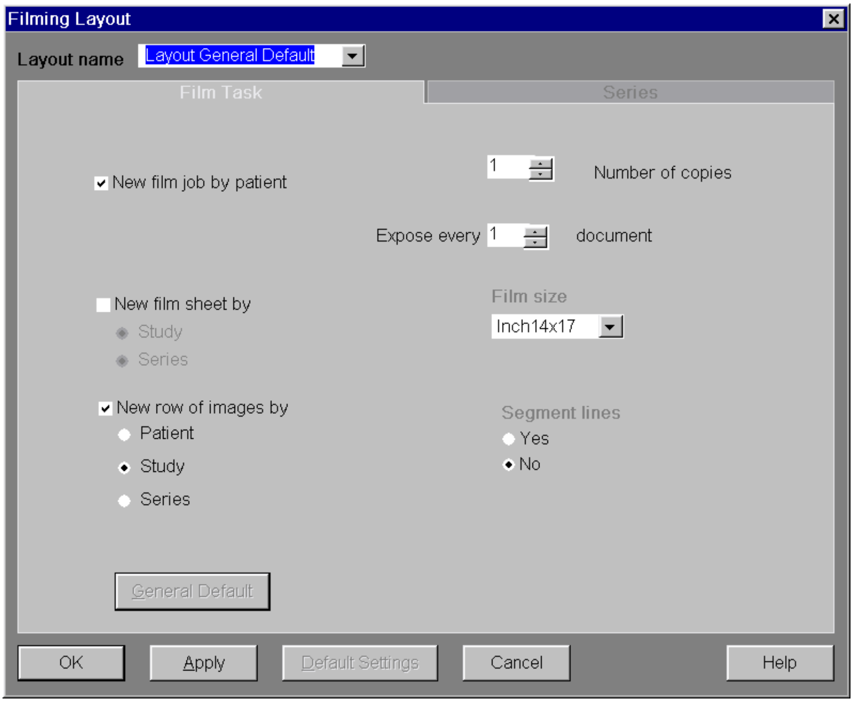
✧ Call up the **Configuration Panel**
(**Options > Configuration** in the main menu).

✧ Call up the configuration window in which you want to make settings.

➪ In the **Basics** part of this manual, you can read how to call up and exit configuration windows, save changes or reset the settings back to the as-delivered state.
→ Chapter A.2, *Configuring the User Interface*

Configuring film layouts

You can change and create film layouts using the **Film Task** and the **Series** tab cards in the **Filming Layout** window.



Filming Layout

Layout name: Layout General Default

☑ New film job by patient

Number of copies: 1

Expose every 1 document

☐ New film sheet by
● Study
● Series

Film size: Inch14x17

☑ New row of images by
○ Patient
● Study
○ Series

Segment lines
○ Yes
● No

Selecting a layout to change

In the **Filming Layout** configuration window, you can define new filming layouts, modify existing layouts or modify the **Layout General Default**.

In the **Layout name** selection list, you can specify which layout you want to change.

Changing the standard layout

The **standard layout** is used for filming/printing if no study-specific layout is assigned to the images and you have not changed the film layout in the virtual film sheet manually.

Layout name Layout General Default

Defining/modifying a study-specific layout

During installation of your system, study-specific layouts are also installed and assigned to individual studies or series.

This has the advantage that a suitable film layout is always used for these images.

You can adapt the default settings to your requirements by creating a new study-specific layout and assigning it to an study or changing an existing layout.

NOTE

Do not change the **Dental** layout settings.

(Real size, Division 1)

Layout name layout new

✧ Select the layout name that you want to change.

Or

✧ Enter a new layout name to define a new layout.

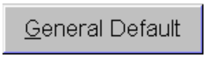
NOTE

Your system can manage up to 30 layouts. If you attempt to create a 31st layout, an error message is displayed. You must then delete an existing layout.

→ Page G.7–18, *Deleting a layout*

The standard layout as the initial setting

When creating a new layout, you can base it on the settings of the standard layout in the **Film Job** or **Series** tab cards and change it to meet your requirements. This is advisable, for example, if the new layout differs only slightly from the standard layout in one or more tab cards.



✧ Click on the **General Default** button on the **Film Task** or **Series** tab card.

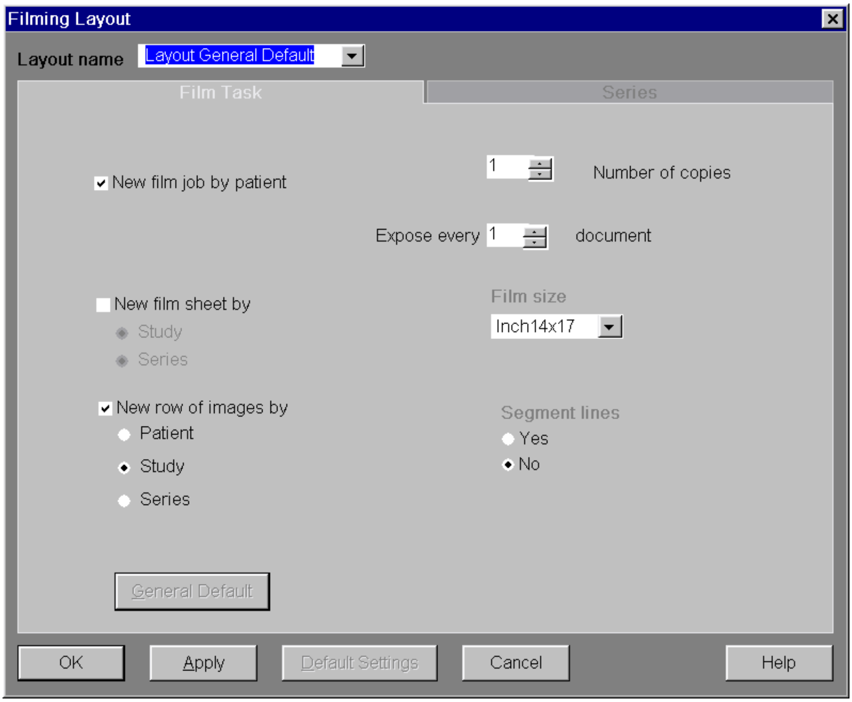
The standard settings are entered in gray in the radio buttons and checkboxes of the tab cards in question. Settings that you have changed are shown black so that you can distinguish them from the default settings,e.g.:


☑ New row of images by
○ Patient
● Study
○ Series

Configuring film job settings

On the **Film Task** tab card, you can define all the settings that determine the structure and execution of a film job.

✧ Click the **Film Task** tab card into the foreground, if necessary.



Layout name: Layout General Default

☑ New film job by patient

1 Number of copies

Expose every 1 document

☐ New film sheet by
○ Study
○ Series

Film size
Inch14x17

☑ New row of images by
○ Patient
● Study
○ Series

Segment lines
○ Yes
● No

One patient or more than one patient per film job


☑ New film job by patient

✧ Click the **New film job by patient** option if you want a film job only to contain the images of a patient.

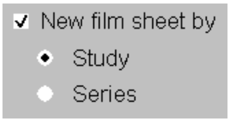
Or


☐ New film job by patient

✧ Deselect the **New film job by patient** option to permit one **multiple film job**.
→ Page G.1–6, *Multiple film job*

All images that are transfered for filming will be collected in one film job.

New film sheet


☑ New film sheet by
● Study
○ Series

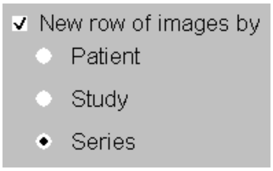
✧ Click on the **New film sheet by** option if you want to permit empty rows in film sheets.

✧ Here you define whether you want to create a new film sheet for each study or each series.

Or

✧ Deselect the **New film sheet by** option to avoid empty lines in the film sheets.

New line in the film sheet



☑ New row of images by
○ Patient
○ Study
● Series

- Click on the **New row of images by** option if you want to permit empty fields in the film sheet.
- Here you define whether a new line is to be started in the film sheet for each patient, each study, or each series.

Or

- Deselect the **New row of images by** option to avoid empty fields on the film sheet.

Filming a partial selection

Expose every 1 document

- Use the spin buttons to set whether every nth image or all images (n=1) of a film job are to be copied in the virtual film sheet and therefore exposed/printed.

Number of copies

1 Number of copies

- Define the number of copies.

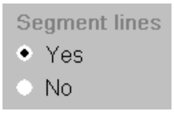
Film size

Film size
Inch14x17

- Select a film size from the **Film size** selection list.

➪ The entries offered depend on the cameras and printers.

Separator lines between segments



Segment lines
● Yes
○ No

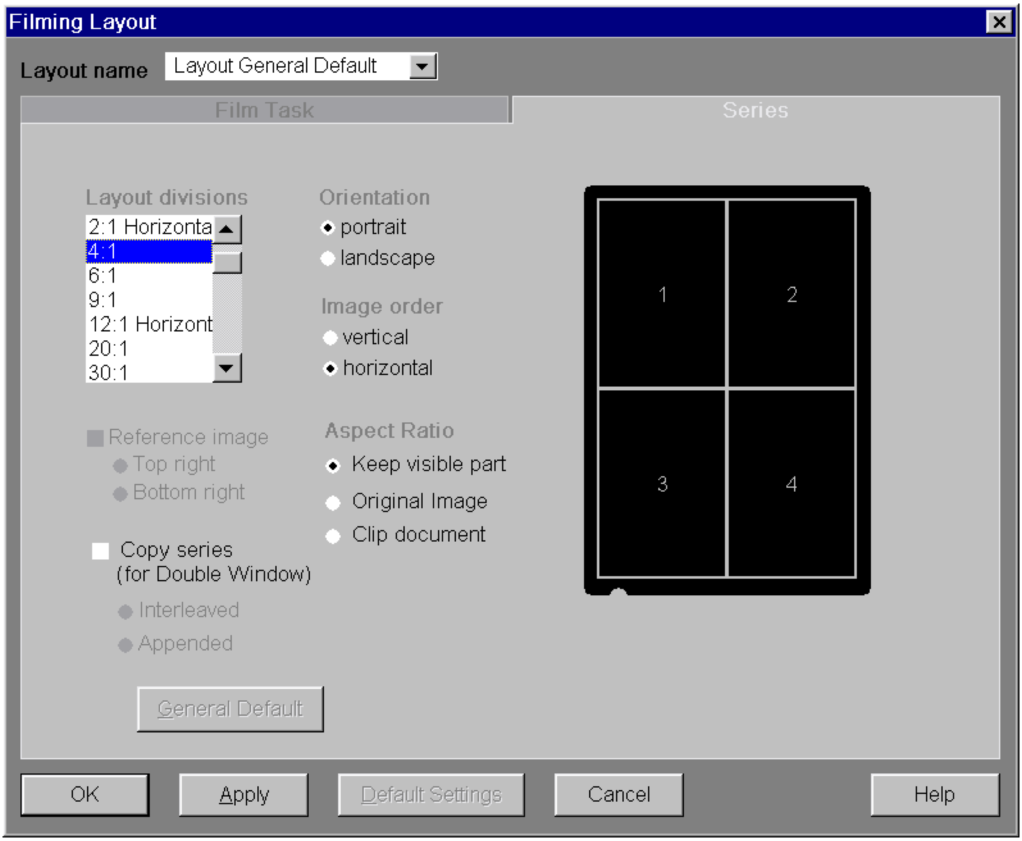
- Set the **Segment lines** option to separate the images with lines on the film sheets.

Configuring film sheets

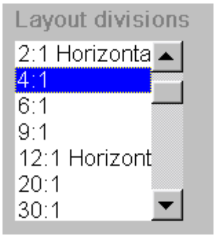
On the **Film Sheet** tab card, you define the settings a film sheet is exposed or printed.

➩ You can only print/expose film sheets in portrait format.

✧ Click the **Series** tab card into the foreground.

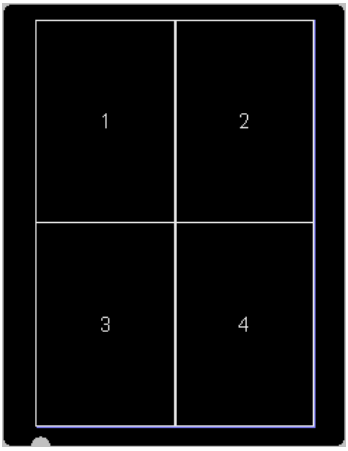


Film sheet division

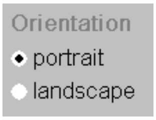


✧ Define in the **Layout divisions** selection list how many columns and rows a film sheet has.

The division is shown in a diagram in the display window.



Portrait/landscape



✧ Select **portrait** or **landscape** for exposing on film (not for postscript printer).

Filling the film sheet

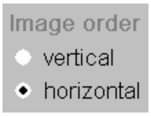
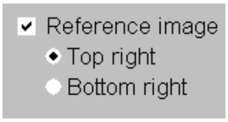


Image order
○ vertical
● horizontal

✧ Define whether the images are to be arranged from left to right (horizontally) or from top to bottom (vertically) on the film sheet.

Reference Image

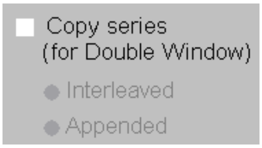


☑ Reference image
● Top right
○ Bottom right

✧ Activate the option **Reference image** to display a reference image associated with the image (e.g. a topogram in CT) **Top right** or **Bottom right**.

Depending on the modularity of the images, a preset reference image is displayed. If no reference image is displayed or you want to select another reference image, you can do so by **drag & drop**.

Series with copy on film sheet



☐ Copy series (for Double Window)

● Interleaved

● Appended

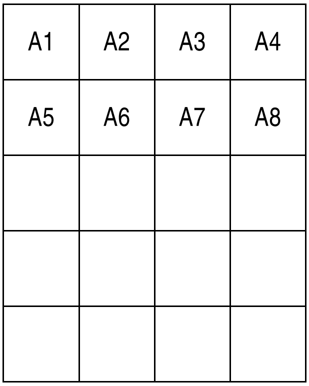
You can have a copy generated automatically when you transfer a series to the virtual film sheet and then process the copy before filming or printing.

✧ Click on the **Copy series** option if you want to make copies of the series.

✧ Set how the original images and their copies are to be arranged on the film sheet (**Interleaved** or **Appended**).

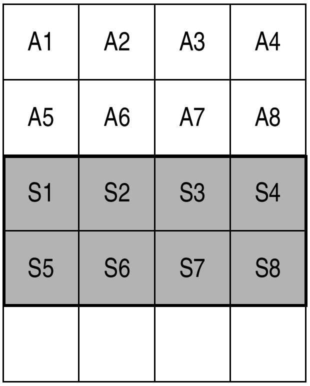
Or

✧ Deselect the **Copy series** option to deactivate automatic copying of the images.



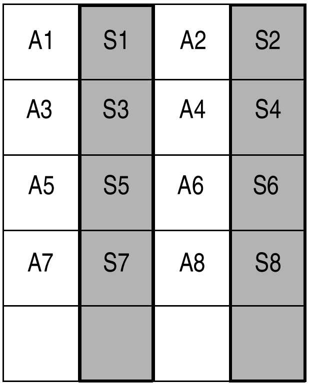
A1	A2	A3	A4
A5	A6	A7	A8

Series is loaded without copy



A1	A2	A3	A4
A5	A6	A7	A8
S1	S2	S3	S4
S5	S6	S7	S8

Copied series is appended to the end (**Appended**)



A1	S1	A2	S2
A3	S3	A4	S4
A5	S5	A6	S6
A7	S7	A8	S8

Copied series is inserted (**Interleaved**)

Series A: original series
Series S: copied series

➪ If you have created the film job by **drag & drop**, no copies of the series are created.

Aspect Ratio


Aspect Ratio

● Keep visible part

○ Original Image

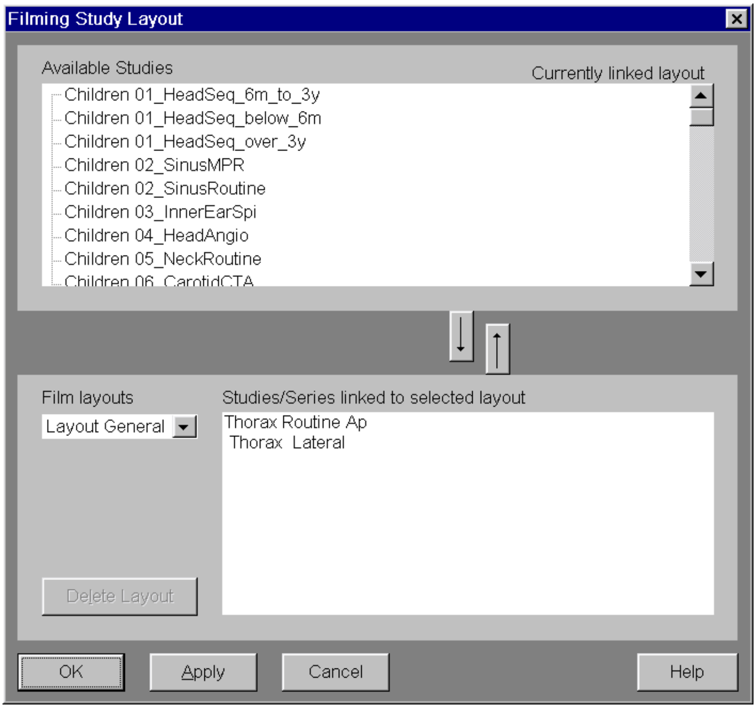
○ Clip document

✧ Define the size with which you want the images to be displayed in the segments:

- ❑ **Keep visible part**: The image is displayed in the segment with maximum size, without being cropped. This is the default.
  → Page G.4–9, *Fit to segment*
- ❑ **Original Image**: The image is displayed in its original size. Depending on the original size, the image might be cropped or displayed too small in the segment.
  → Page G.4–10, *Original Image*
- ❑ **Clip document**: The image is enlarged so that it fills the entire segment. The overlapping edges are cropped accordingly.
  → Page G.4–9, *Clip document*

Associating layouts with a study or series

In the **Filming Study Layout** window, you can assign a specific layout to a study. This can either be a layout you have created yourself or one that has been created by the Siemens Service during configuration of your system.



Children 01_HeadSeq_6m_to_3y
Children 01_HeadSeq_below_6m
Children 01_HeadSeq_over_3y
Children 02_SinusMPR
Children 02_SinusRoutine
Children 03_InnerEarSpi
Children 04_HeadAngio
Children 05_NeckRoutine
Children 06_CarotidCTA

Studies/Series linked to selected layout
Thorax Routine Ap
Thorax Lateral

Assigning film layouts

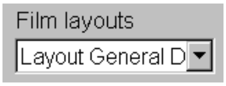
You can only assign one specific layout to each available study. This layout is then automatically used for filming the images with the specific study description.

You can assign a layout by selecting an available study stored on your system and the layout required and then linking the two.

➪ If a layout other than the standard layout is already assigned to a study or series, you must first cancel this link before you can assign a new study-specific layout.
→ Page G.7–18, *Canceling a layout assignment*

In the **Film layouts** selection list, you will find a list of the available layouts.

Selecting a film layout



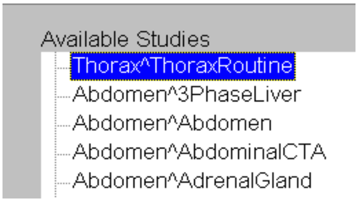
Film layouts

Layout General D

✧ Select the required film layout.

Selecting an available study

In the **Available Studies** area, you can see a list of the studies with their series. For example, for the scan protocol “ThoraxRoutine” in the region “Thorax”, the corresponding study description is Thorax^ThoraxRoutine.



Available Studies
- Thorax^ThoraxRoutine
- Abdomen^3PhaseLiver
- Abdomen^Abdomen
- Abdomen^AbdominalCTA
- Abdomen^AdrenalGland

✧ Click on the ⊞ - symbol in front of a study to display the series associated with it.

➪ You can only select entire studies if they are not subdivided into series. In such cases, the ⊞ - or ⊟ - symbol in front of the entry is missing.

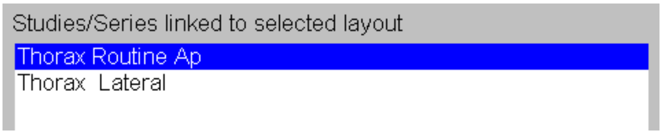
✧ Click a series or study to select it.

Linking the layout

✧ Click on the **Down arrow** button to assign the layout to the selected study or series.

Displaying the layout assignment

As soon as you have assigned an study-specific layout, the corresponding study or series is entered in the **Studies/Series linked to selected layout** list.
Here you can see for what studies or series the displayed layout is set.

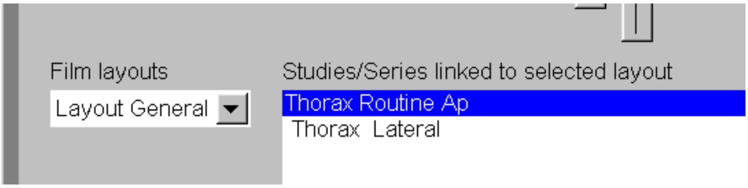


Studies/Series linked to selected layout

Thorax Routine Ap

Thorax Lateral

In the **Currently linked layout** column in the **Available Studies** area, you can see which layout is linked with a certain study.



Film layouts

Layout General

Studies/Series linked to selected layout

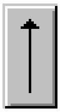
Thorax Routine Ap

Thorax Lateral

Canceling a layout assignment

If you want to assign a different study-specific film layout to an study or series, you must first cancel the old layout assignment.

✧ Select the study or series in question in the **Studies/Series linked to selected layout** list.



✧ Click on the **Up arrow** button.

The standard layout is now assigned to the study or series again and you can assign a new study-specific layout.

Deleting a layout

Your system can store and manage up to 30 layouts. Therefore you should regularly delete those film layouts that you no longer require to make space for new study-specific layouts that you create on the **Filming Layout** tab cards.

✧ Select a layout that you no longer require from the **Film layouts** selection list.

✧ Click on the **Delete Layout** button.

The entry will be deleted from the list.

➪ You cannot delete the **standard layout**.

PART
H

3D Evaluation

H.1 *Introduction*

H.2 *Transferring Images to 3D*

H.3 *Working in 3D*

H.4 *Multiplanar Reconstruction (MPR)*

H.5 *Maximum Intensity Projection (MIP)*

H.6 *Reconstructing Shaded Surfaces (SSD)*

H.7 *Volume Rendering Technique (VRT)*

H.8 *Selecting and Processing Images*

H.9 *3D Editor*

H.10 *Fusion*

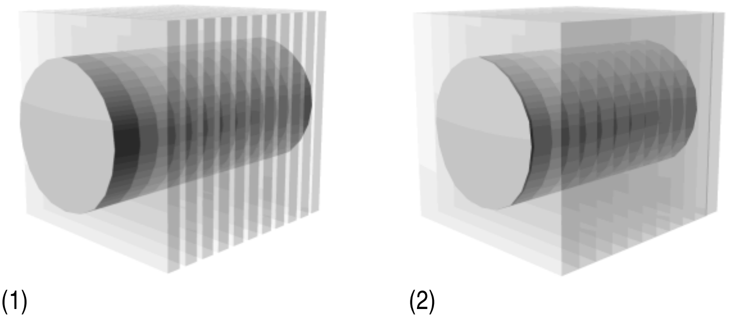
H.11 *Saving 3D Series and Images*

H.12 *Filming, Evaluating and Sending 3D images*

H.13 *3D Configuration*

CHAPTER
H.1 Introduction

The result of a tomographic examination is a sequence of images through a solid volume under examination.
By combining two-dimensional images, it is possible to obtain a three-dimensional display of the region of interest.



(1) 2D tomographic images
(2) Volume data set

In this three-dimensional display, you can work just like in a three-dimensional model. For example, you can generate any new images, cut out individual regions and apply a range of evaluation functions for special diagnostic problems.

Your system provides you with a number of alternative procedures for working with three-dimensional images.
You decide with what method you want to begin as soon as you load images into the **3D** task card.

On the **3D** task card, you then prepare your image material by the selected method, or you start another image processing procedure.

3D evaluation method

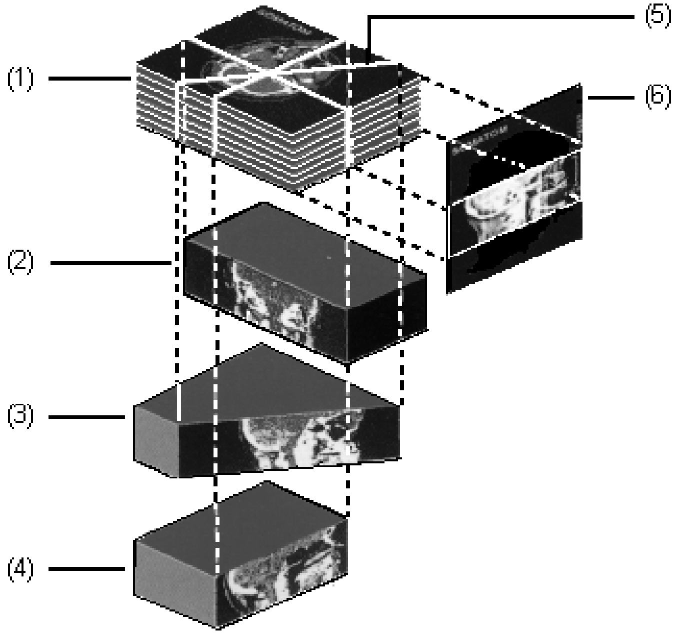
Your system provides you with the following methods for combining two-dimensional images to form three-dimensional views:

- Multiplanar reconstruction (MPR) is used to place the slices in various orientations through the region of interest. The resulting images are two-dimensional.
- You can use the maximum intensity projection (MIP) for the display of contrast medium examinations or especially for angiography.
- You can use the surface shaded display (SSD) method, for example, to evaluate bone and vascular examinations that you want to display with virtual three-dimensionality.
- Volume rendering technique (VRT) is used, for example, to differentiate between organs and tissue structures, and for colored, three-dimensional display of bone, tissue, and organs.

Multiplanar reconstruction (MPR)

With **m**ulti**p**lanar **r**econstruction you can calculate secondary images of any planes from the volume, for example sagittal, coronal, or any curved views.

You can reconstruct both single images and series of images.

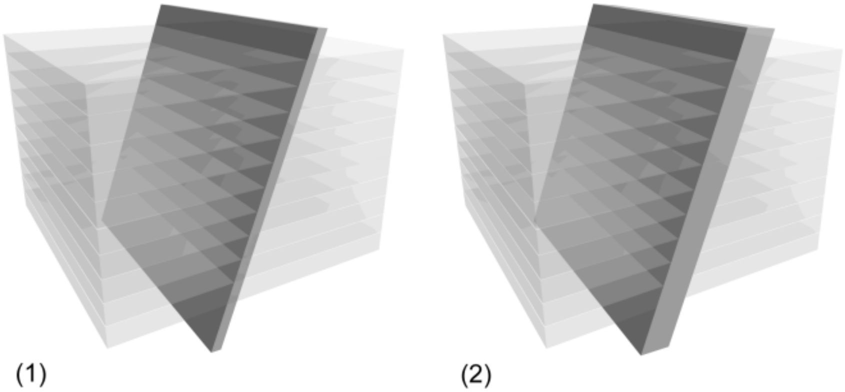


(1) Transversal/axial
(2) Coronal
(3) Paraxial
(4) Sagittal
(5) Paraxial
(6) Sagittal

In MPR, two-dimensional images are always calculated from the "volume". However, you can move through the representation quickly using the 3D cross-hair or mouse to gain a three-dimensional impression.

The smaller the distance between the slices or the larger the degree of overlap of the original images, the greater the resolution in the examination direction.

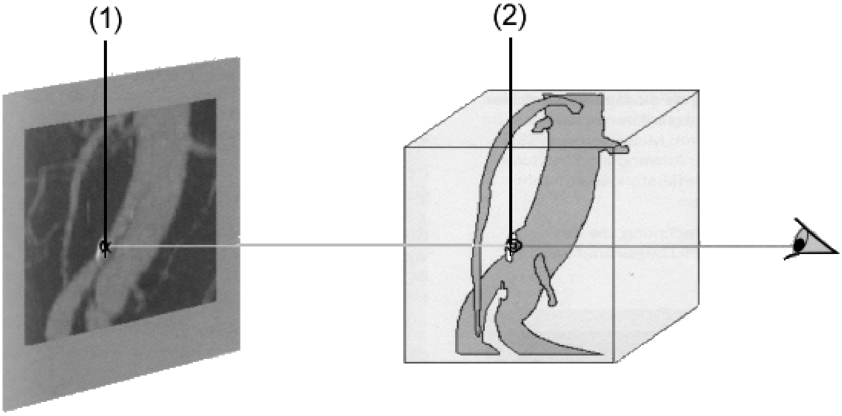
The minimum slice thickness of an MPR image is one voxel. But you can generate thicker slices (MPR Thick). The gray-scale mean values are calculated for voxels located one behind the other.



(1) MPR slice (1 voxel slice thickness)
(2) MPR Thick (slice thickness settable)

Maximum intensity projection (MIP)

In the selected view through the volume elements (called voxels) with the greatest intensity are determined and projected onto a surface irrespective of whether they are at the front or further back in the stack. This gives you the maximum intensity projection.
You can use this method, for example, to exploit the fact that blood vessels are always displayed in the volume as the structures with the most intensive gray-scale values.



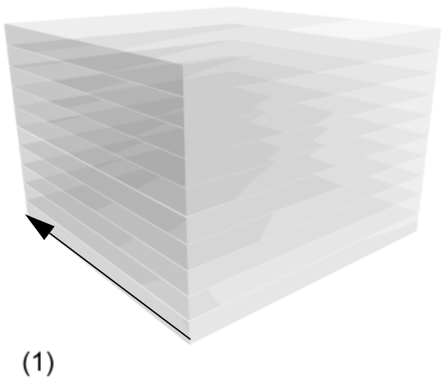
(1) Voxels in MIP images
(2) Most intensive gray scale value

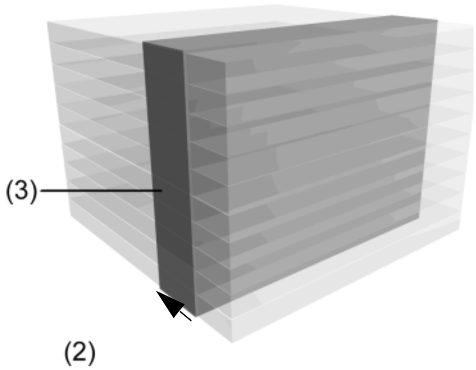
The voxel with the maximum intensity is displayed in the MIP image.

In order to gain a three-dimensional impression you can generate several MIP images from different viewing directions or rotate the projection using the mouse or the 3D cross-hair.

Some structures, especially bones, cause interference in the projections. Where bones and blood vessels are superimposed on one another on the MIP projection, the voxels of the (denser) bones can cover the voxels of the blood vessels. In this case, reduce the target volume using the VOIs (Volumes of Interest) until it only contains the vessels to be projected.

You can limit the volume for a projection to a partial area of the volume data set. In the output type MIP Thin you define which expansion the volume used for the projection should have.

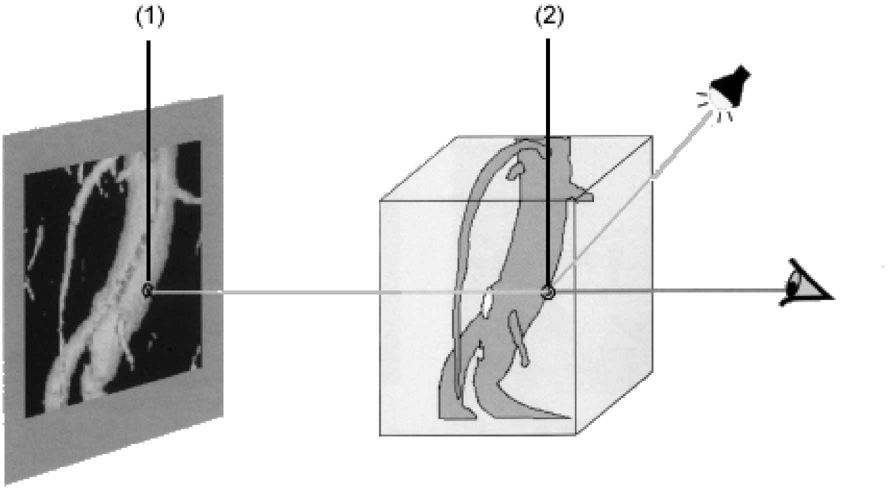




(1) Normal MIP, whole volume
(2) MIP Thin, only partial volume (slice) is used for projection
(3) Part used

Surface shaded display (SSD)

With this method, you reconstruct the surfaces of volumes. These volumes consist of voxels (volume voxels) whose gray-scales are in a range defined by two limit values, an upper and a lower gray-scale limit. This method is especially suitable for displaying bone structures or blood vessels filled with contrast medium.



(1) Voxels in the SSD image
(2) Foremost surface voxel volume data set

The foremost voxel of the volume range that is within a defined gray-scale range is displayed in the SSD image.

You can change the viewing direction in real time with the mouse or 3D cross hair. You can also generate series of views taken from different viewing angles.

You can, for example, cut out any structures to expose areas of special interest.

The gray-scales that are shown on the display are no longer the measured values. They are only intended to give a three-dimensional impression.

A fine distinction in the density of the tissue is no longer possible, for example, calcification and contrast medium in the vessels can no longer be distinguished by their density in SSD.

Volume rendering technique (VRT)

The **volume rendering technique (VRT)** is a way of creating color images in which a 3D effect is achieved with such parameters as transparency, shading, and color transition.

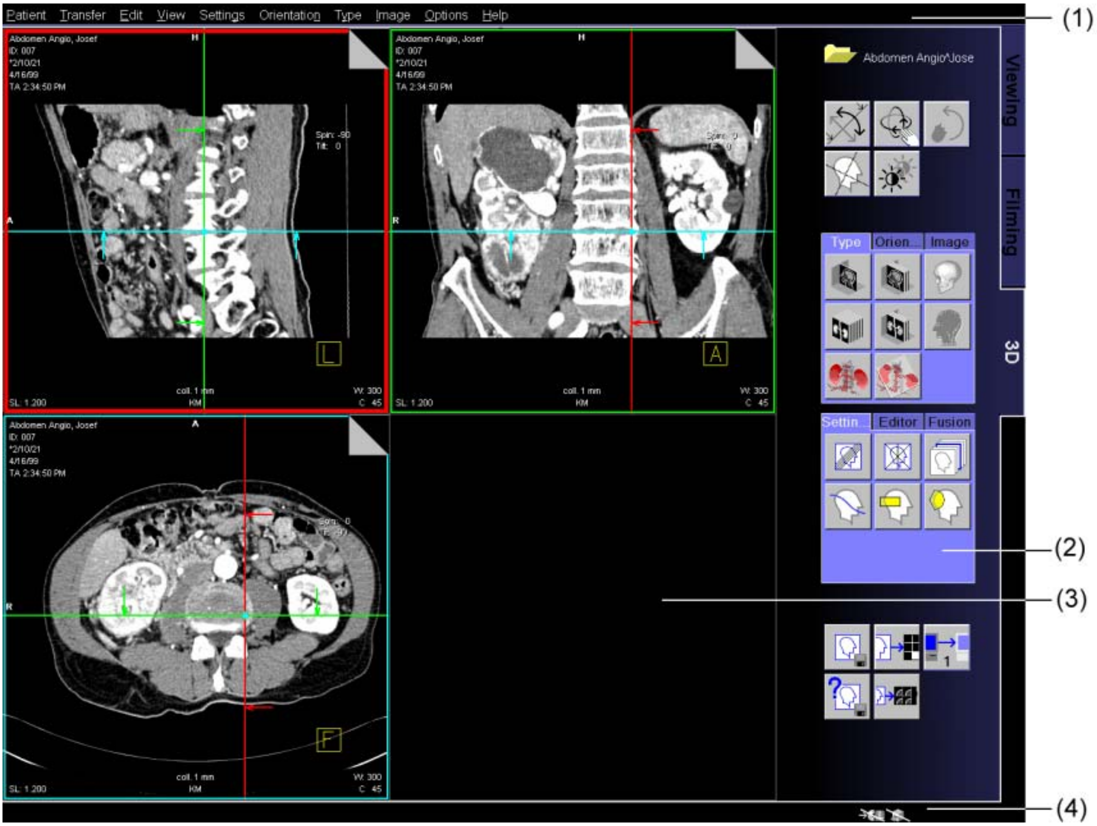
The entire volume data set is included in the image. Areas of interest such as bone and blood vessels can be emphasized interactively by assigning appropriate color and transparency values.

The VRT method is based on the idea that defined rendering properties (color, brightness, contrast, and transparency) are assigned to the voxels of the volume data set depending on the initial pixel value (HU value or MR signal value). In practice, pixel input value ranges are assigned to specific tissue classes.

The 3D task card

You process your three-dimensional images on the **3D** task card.

The task card is subdivided into the following main areas:



(1) Main menu, extended by 3D-specific items
(2) Control area for easy call-up of functions
(3) Image area, subdivided into four segments
(4) Status bar for feedback and error messages

CHAPTER

H.2 Transferring Images to 3D

For three-dimensional image processing, you use examination images that are stored in the local database of your system or in the archive.

If your system is integrated into a hospital network, you can receive image data from other departments and wards and then evaluate it three-dimensionally on your system.

In the **Patient Browser** window, you have access to this data. There you can search for patients, studies, series, or individual images and transfer them to the **3D** task card.

You can also transfer images from the **Viewing** to the **3D** task card.

Starting 3D evaluation

You call up 3D processing and load a 3D model in three steps:

Selecting images/series for processing

First select the images or series that you want to display in three dimensions in the **Patient Browser** or on the **Viewing** task card.

In this step, you can select more than one series of one patient for 3D processing.

Selecting a 3D display method

After that, select a 3D method and transfer the images/series selected to the **3D** task card.
→ Page E.7–14, *Transferring images to 3D*
Or

Drag & drop from the Patient Browser

✧ Transfer the images selected in the **Patient Browser** as an MPR by dragging & dropping them onto the **3D** task card.

➩ If the task card is not in the foreground you can also drag the images from the **Browser** onto the corresponding tab. The task card moves into the foreground and the images are loaded into the image area.

When transferring them, the system checks whether the images and series that you selected are suitable for 3D postprocessing. If necessary, the system displays a message box pointing out inconsistencies within the series.

A selection of images that are to be displayed in three dimensions must at least fulfill the following criteria:

- ❑ All images must originate from one patient and from one study.
- ❑ At least 3 images must have been loaded to process 3D.
- ❑ All images must be parallel and be located on one axis.

If you have selected only one series which also fulfills all the above criteria, the images will be transferred to the **3D** task card and you can start processing them immediately.

In that case, turn straight to
→ Page H.4–1, *Multiplanar Reconstruction (MPR)*
→ Page H.5–1, *Maximum Intensity Projection (MIP)*
→ Page H.6–1, *Reconstructing Shaded Surfaces (SSD)*
→ Page H.7–1, *Volume Rendering Technique (VRT)*

If you select several series or an unsuitable series, the **Series List** is displayed.
→ Page H.2–5, *Series List*

Displaying a series from the Series List in three dimensions

The last step is to select a series from the **Series List** and transfer it to the **3D** task card.

On the **3D** task card, the selected series is displayed in three dimensions in the selected method. You can now evaluate the display.

➩ You can only ever process one series at a time on the **3D** task card.

Calling the 3D task card

As soon as you have loaded images into the **3D** task card you can switch to other tasks and then return to the **3D** task card to continue processing the images.

✧ Click on the card tab to return to the **3D** task card.

The **3D** task card is placed at the front in the same status you have left the card.

Series List

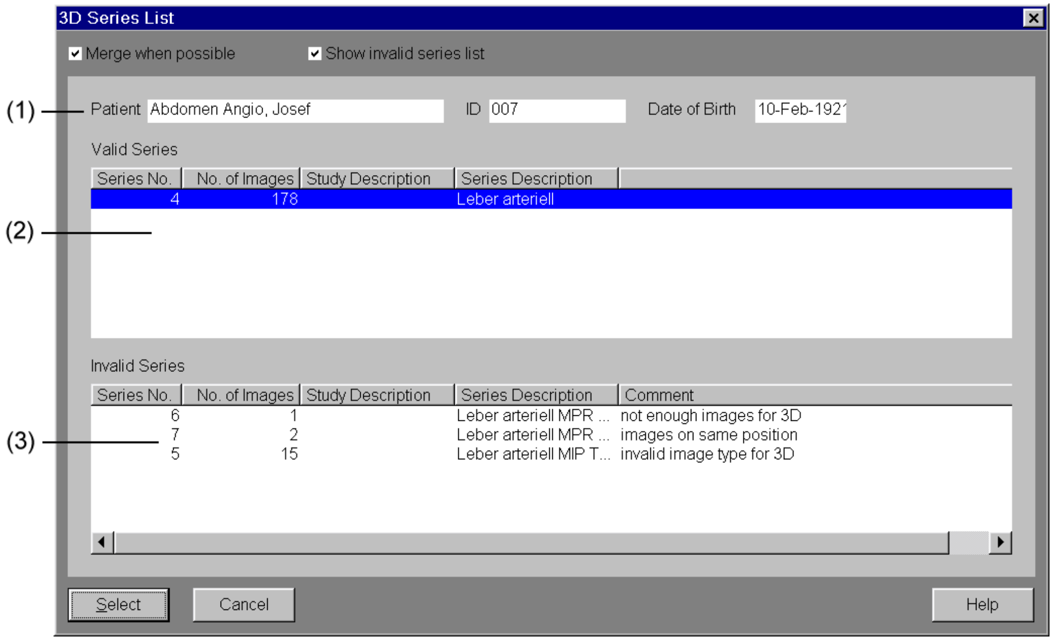
If the series you selected is not suitable for 3D display or if you have selected more than one series for processing, you can see the results of the selection check in the **Series List** dialog box.

Open Series List

You can also open the **Series List** explicitly, for example, to load another series into the **3D** task card.
→ Page H.2–11, *Other series from the Series List*

✧ Call **Patient > Open Series List...** in the main menu of the **3D** task card.

The dialog window **Series List** is displayed. It is divided into the following fields:



☑ Merge when possible ☑ Show invalid series list

Patient Abdomen Angio, Josef ID 007 Date of Birth 10-Feb-192

Valid Series

Series No.	No. of Images	Study Description	Series Description	
4	178		Leber arteriell	

Invalid Series

Series No.	No. of Images	Study Description	Series Description	Comment
6	1		Leber arteriell MPR ...	not enough images for 3D
7	2		Leber arteriell MPR ...	images on same position
5	15		Leber arteriell MIP T...	invalid image type for 3D

(1) Patient data
(2) Series suitable for 3D display (valid list)
(3) Series unsuitable for 3D display (invalid list)

Valid list

All the series suitable for a 3D reconstruction are shown in the top list (valid list). Depending on how many series you have selected, several lists might be displayed, from which, however, you can only select and transfer one.

Invalid List

All the series unsuitable for 3D reconstruction are displayed in the lower list (**Invalid series**). Displayed next to the series data you will also see a comment which gives a more detailed reason for rejection.

➪ Your computer system only has a limited storage capacity. So you cannot select an unlimited number of images for 3D display. In the **Series List** box, you will find the images that it was not possible to load in the **Invalid Series** list.

Hiding the Invalid Series list

You can hide the **Invalid Series** list to keep the **Series List** dialog box clear.

✧ Click on the **Show invalid series list** check box to remove the checkmark and deselect the option.

The screen display is updated immediately, the Valid Series list is displayed larger. The **Invalid Series** list is no longer displayed.

➪ If none of the series you selected is suitable for 3D display, so that the Valid Series list is empty, you cannot hide the **Invalid Series** list.

Merging series

If you have selected a series for 3D display whose examination ranges overlap, you can decide in the **Series List** whether you want these series to be merged to form a single series for your 3D model. In this way, it is possible to enlarge the volumes displayed or the image quality is improved.

➩ The series that you want to merge must have been acquired within 30 minutes of each other.

☑ Merge when possible

✧ Select the **Merge when possible** option if you want to merge suitable series.

The screen display is updated immediately.

➩ If a CT image has been acquired twice in the same position, the latest image is always used, or if series were acquired by different scanning methods (sequence, spiral), the spiral acquisition is always used.

☐ Merge when possible

✧ Deselect **Merge when possible**, if you want to separate merged series again.

Transferring series to 3D

If the list of Valid Series contains more than one series which is suitable for 3D display, you have to decide which series you want to display and evaluate in three dimensions.

➪ You can only ever display and process one series at a time on the **3D** task card.

➪ Only medical images can be transferred into the **3D** task card.

✧ Double-click in the list of Valid Series on the series that you want to process first.

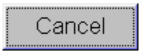
Or

✧ Select the series in the list and click on the button.

The series is passed on to the **3D** task card and the **Series List** dialog box is closed.

Close without transfer

Once you have transferred images to the **Series List** you can stop processing, for example, to process images.

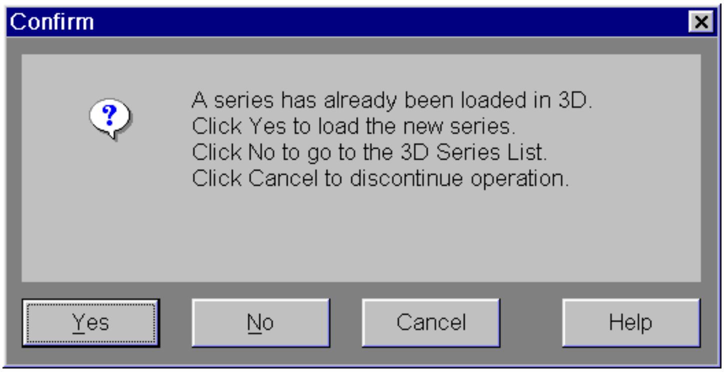


✧ Click on **Cancel** to close the **Series List** dialog box.

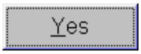
You return to the **Viewing** task card or the **Patient Browser**.

3D task card already busy

If you are processing another series on the **3D** task card, the **Confirm** dialog box is displayed.

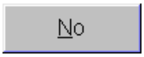


A series has already been loaded in 3D.
Click Yes to load the new series.
Click No to go to the 3D Series List.
Click Cancel to discontinue operation.



✧ Confirm with **Yes** to load the new series onto the **3D** task card and close the old series.

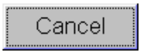
Or



✧ Click on **No** if you want to continue processing the old series on the **3D** task card.

The new list is not transferred. The dialog window **Series List** is displayed from which you can select a different list, for example.

Or



✧ To cancel transfer of the new series, click on the button.

You return to the **Patient Browser** or to the **Viewing** task card.

Other series from the Series List

At any time, you can also access the other series that you had preselected for processing in the **Series List** from the **3D** task card.

✧ Call up the **Series List** dialog box with **Patient > Open Series List...**.

✧ Select another series and transfer it by clicking on the **Select** button.

The series previously loaded is closed.

CHAPTER
H.3 Working in 3D

Your data exists as a volume data set. A large variety of options are available to you for generating and processing two-dimensional images.

Various orientation aids, e.g., the orientation cube, guide you through the volume. They refer to a patient coordinate system that displays the viewing direction or the image orientation.

You can move around the volume to find the images relevant to your diagnosis. To do that, use the 3D cross-hair, the dog ears, or rotate the image data set using the mouse.

Once you have generated a reference image you can reconstruct entire series in the view you want with the set output types.

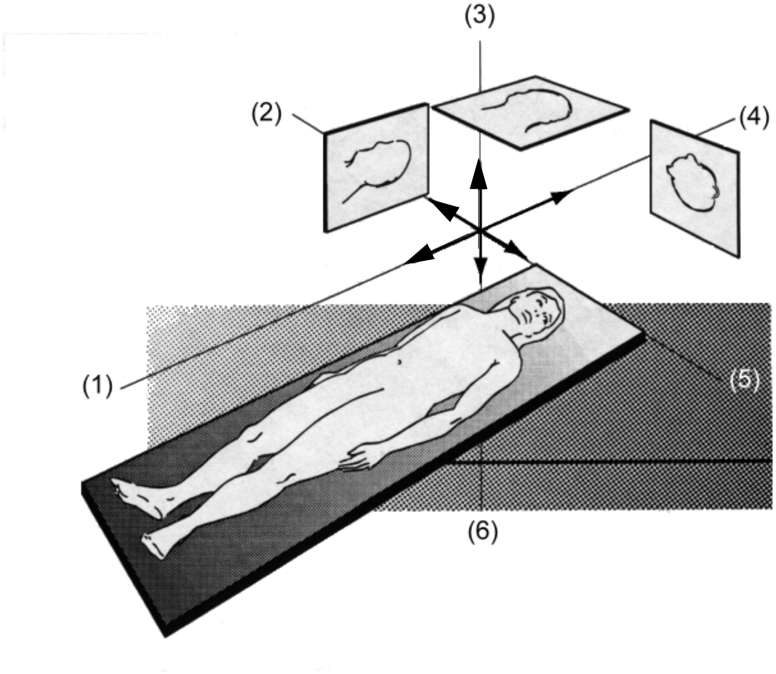
You first generate an image in the orientation that you need. This is the reference image on which all subsequent working steps are based (either the orientation or the viewing direction). Then you select the output type, i.e. either MPR, MIP, SSD or VRT, or use the type already set.

The patient coordinate system

The orientation of the images is stated by a patient-related coordinate system. In each image, this data tells you the direction from which you are looking at the patient (3D) and how a slice (2D) is positioned in the region of interest.

Directions

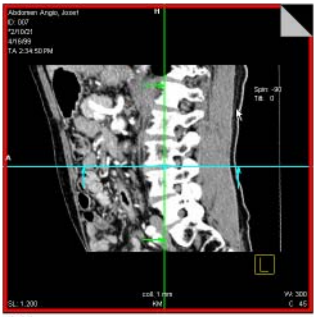
Directions are described as follows in the patient coordinate system:



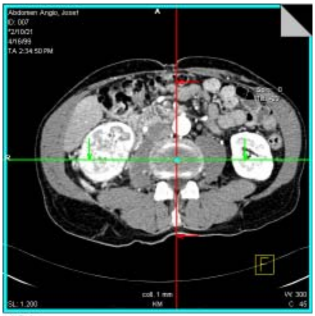
(1) F for feet (from the feet to the head)
(2) R for right (from the right to the left)
(3) A for anterior (from anterior to posterior)
(4) H for head (from the head to the feet)
(5) L for left (from the left the right)
(6) P for posterior (from posterior to anterior)

The directions are displayed as orientation labels in the images.
→ Page H.3–6, *Orientation labels*

Anatomical standard views Viewing directions along one of the axes of the patient coordinate system are called anatomical standard views. The slices which you look at in such views are designated:



(1)



(2)

(3)

(1) Sagittal slice
(2) Transversal slice
(3) Coronal slice

Orientation aids in the image

Various aids are displayed for orientation in the image. They show you from what direction you are looking at the image.

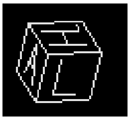
Orientation description

Spin: -90
Tilt: 0

For CT images, an angle of rotation and tilt with reference to the standard views is displayed to describe the orientation.

The orientation description is also filmed and stored.

Orientation cube



The orientation cube is displayed on all images. It indicates the position of the layer displayed with reference to the patient coordinate system.
→ Page H.3–2, *The patient coordinate system*

The cube is also filmed and saved together with the images.

Orientation labels

The orientation labels show you the orientation of the patient in the image. They are identical with the directions in the patient coordinate system and are not annotations that you can edit. This text is always displayed in the center of the top and left edge of the image.

- **L**, **R** - left, right
  Viewing direction sagittal from left or right
- **A**, **P** - anterior, posterior
  Viewing direction coronal from anterior or posterior
- **H**, **F** - head, feet
  Viewing direction transversal from head or feet

→ Page H.3–27, *Setting standard views*

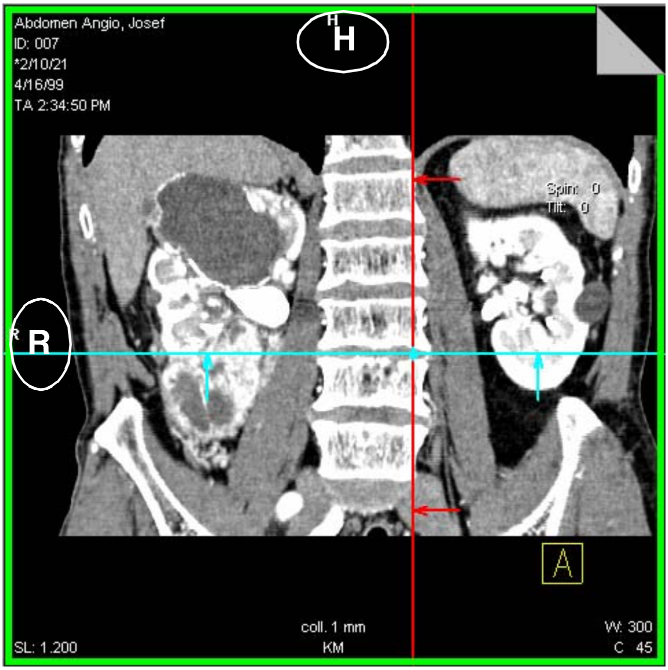


Image representation in 3D

The image area on the **3D** task card is divided into four segments. The segments have different functions depending on which mode you happen to be working in.

Image area in reference mode

The first three segments are reference segments, the fourth segment is an output segment.

Reference segments

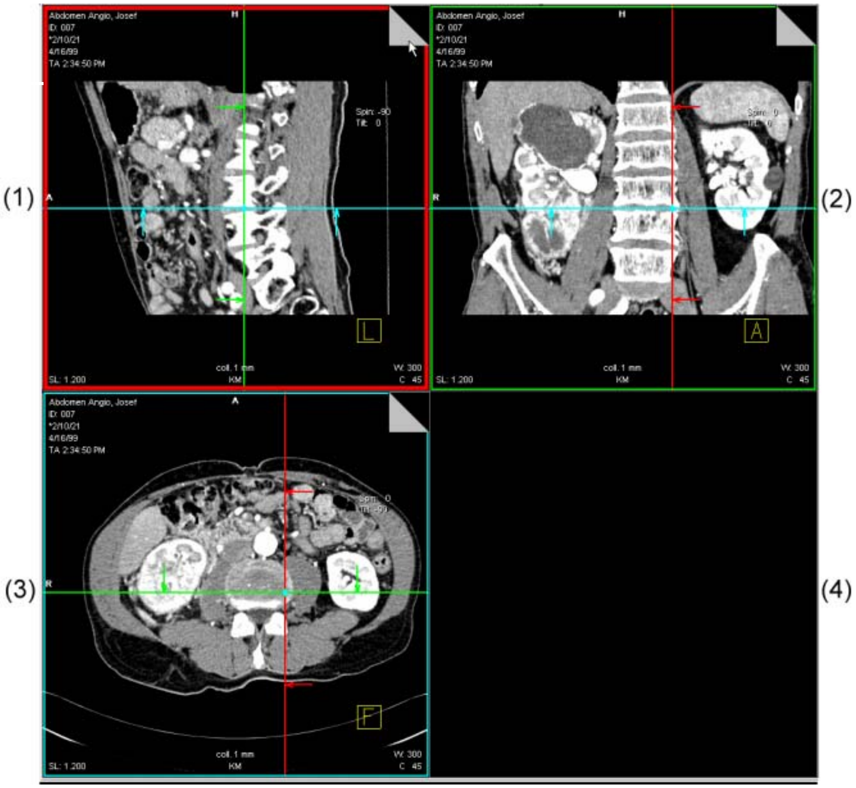
In the three reference segments the images are first shown in the views that are parallel and perpendicular to the direction of scanning.

By turning and moving the views you can define the position and orientation of the plane that is to be used as the reference image for the reconstruction of images or series.

The reference segments are used to **display** different views of the volume data set, while the reference display (the view) is used as a **reference** for a 3D-reconstruction.

Output segment

The images and series generated by various tools on the basis of the reference image are displayed in the output segment.



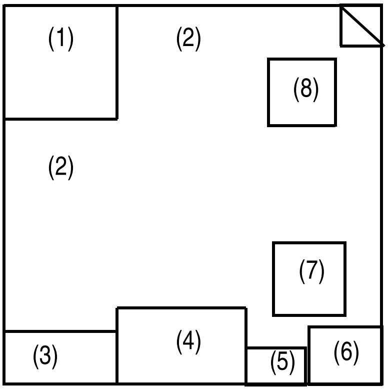
(1) Reference segment (sagittal view)
(2) Reference segment (coronal view)
(3) Reference segment (transversal view)
(4) Output segment

Image information

Information about the patient, the examination and image data are shown on the images.

➩ You can configure which image text is to be displayed.
  → Page A.2–8, *Configuring image text*

The image information displayed is always given in the same place as shown in the figure below:



(1) Patient data
(2) Orientation labels
  → Page H.3–6, *Orientation labels*
(3) Slice thickness (only MPR, MPR Thick, MIP Thin)
(4) Image comment
(5) Automatic values of the pixel lens
(6) Window values
(7) Orientation cube
  → Page H.3–5, *Orientation cube*
(8) Orientation description
  → Page H.3–5, *Orientation description*

Of the standard text elements, the following elements are not displayed:

- ❑ Scan-specific settings (e.g. gantry tilt)
  (normally in the bottom left corner)
- ❑ Hospital / system information
  (normally in the top right corner)
- ❑ Scale
  (on the right edge)

➪ You can have the image comment and orientation description displayed or not by making configuration settings.
→ Page H.13–2, *Configuring image information*

Setting views in the volume data set

Three-dimensional image processing allows you to create images in any orientations and positions within the data volume. You "move" through the volume and can rotate it in any direction. Depending on the method you are using, various aids are available to you.

Setting the reference image

Once you have loaded the images in the **3D** task card you can move through the 3D model using the aids provided on this task card. First generate a view you require. You can use this view as reference image as the basis for further processing. For example, you can reconstruct parallel slice images on it.

✧ First generate a view you require.

✧ Click on the “reference segment” of the required view.

You can use this view as a reference image as the basis for further processing. The segment is now displayed with a thick border.

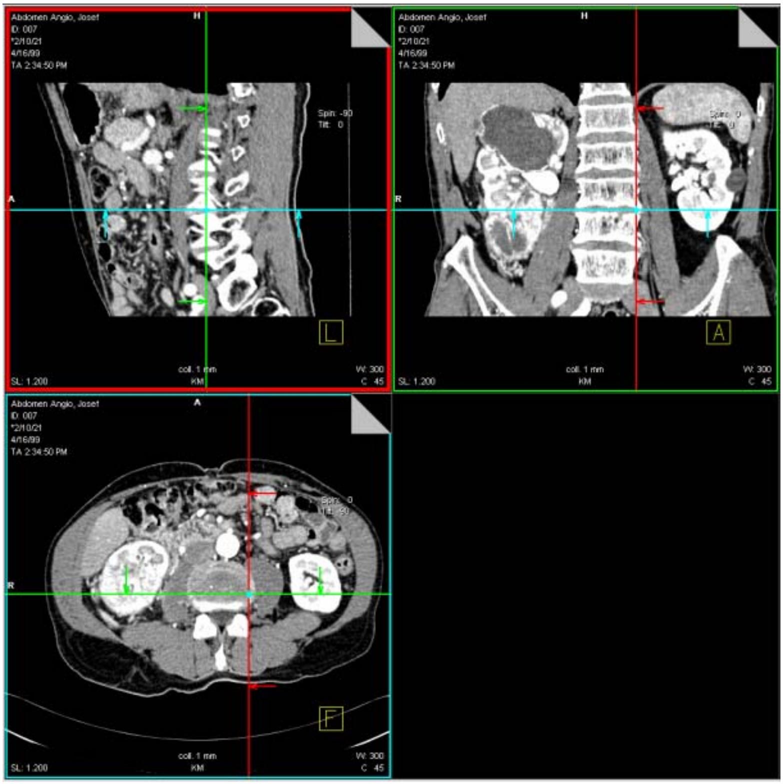
For example, you can reconstruct parallel slice images on it.

Selecting a reference image

Set the view in which you want to perform subsequent 3D evaluation in one of the three reference segments. This view is then your reference image.

✧ Click on the segment in question to select the image.

The image is displayed with a thick border. In the example below, it is the top left-hand segment.

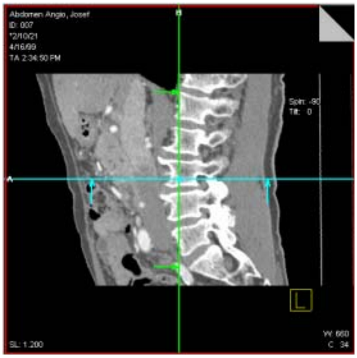


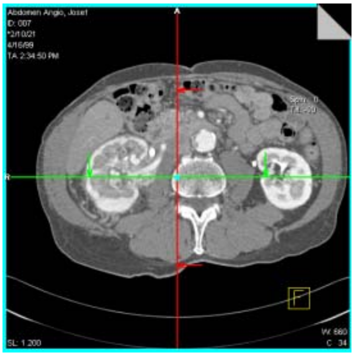
Using the 3D cross hair

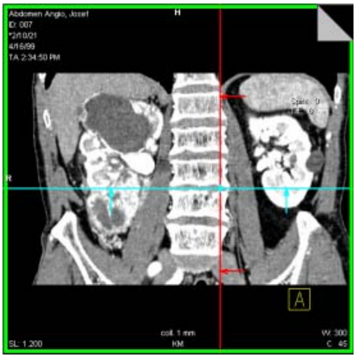
The lines through the cross hair (reference lines) indicate the position of two slice planes that are perpendicular to each other in the standard view (the lines represent the cut lines). The two planes are displayed in the two other reference segments.

You can recognize which slice image belongs to which cut lines in the segment in question by the color of the reference lines and the frame around the reference segments.

The top left-hand segment is surrounded by a red border. The position of the corresponding image in the volume data set is indicated in the two other reference segments by a red line. Correspondingly, the position of the image in a blue border is indicated by blue lines and that of the image in the green frame by green lines.







The arrows indicate the viewing direction from which you view a plane.

Broken lines indicate planes that are **not perpendicular** to the view displayed.

Moving reference lines

You can now move through the views of the reference segments in any direction using the lines.

✧ Click on a line and move it holding the left mouse key down.

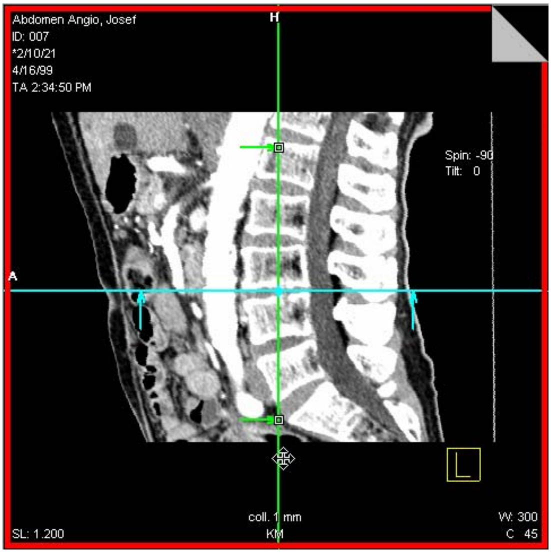
Or

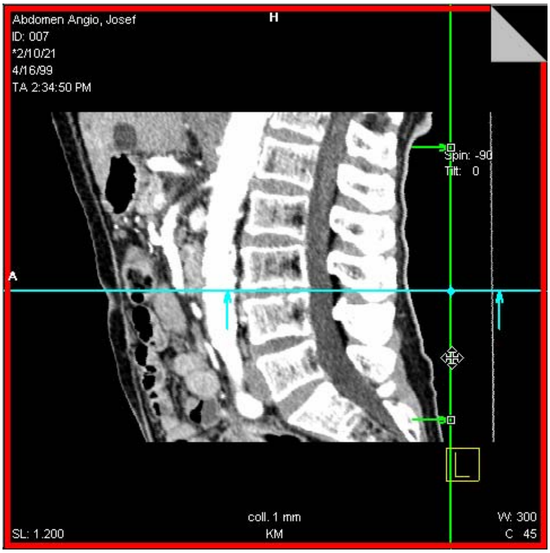
✧ Click on the intersection of the lines to move both lines at the same time.

As an alternative, you can move the reference lines to a target position in jumps by mouse click.

✧ Click a line to select it and then click the target position with the left mouse key.

The reference line is moved there immediately.

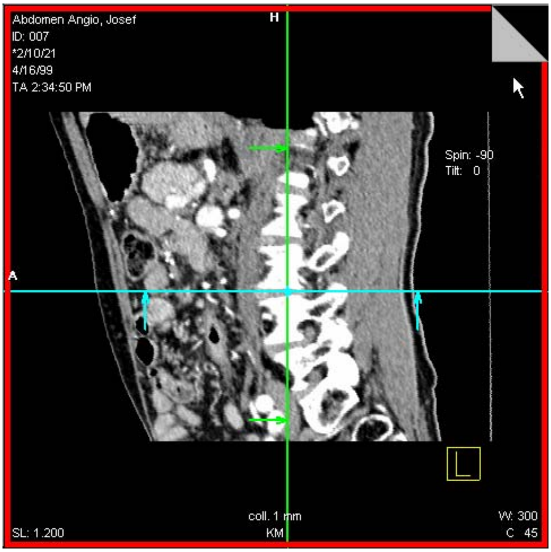




Or

✧ Select the entire reference image and click the target position with the left mouse key (no reference line selected).

Both lines are moved in such a way that the intersection is now at the position you clicked.



Rotating by cross hair

You can change the view in a reference segment by turning the corresponding line of the cross hair in one of the other two segments.

Enable rotation of the lines first by disabling fixed mode and **Free Mode**.

✧ Select **Free Mode** to activate free mode.

✧ Now rotate the lines about the displayed point of rotation.

In this way, you create oblique planes (only one line is oblique) or double-oblique planes (both lines are oblique).

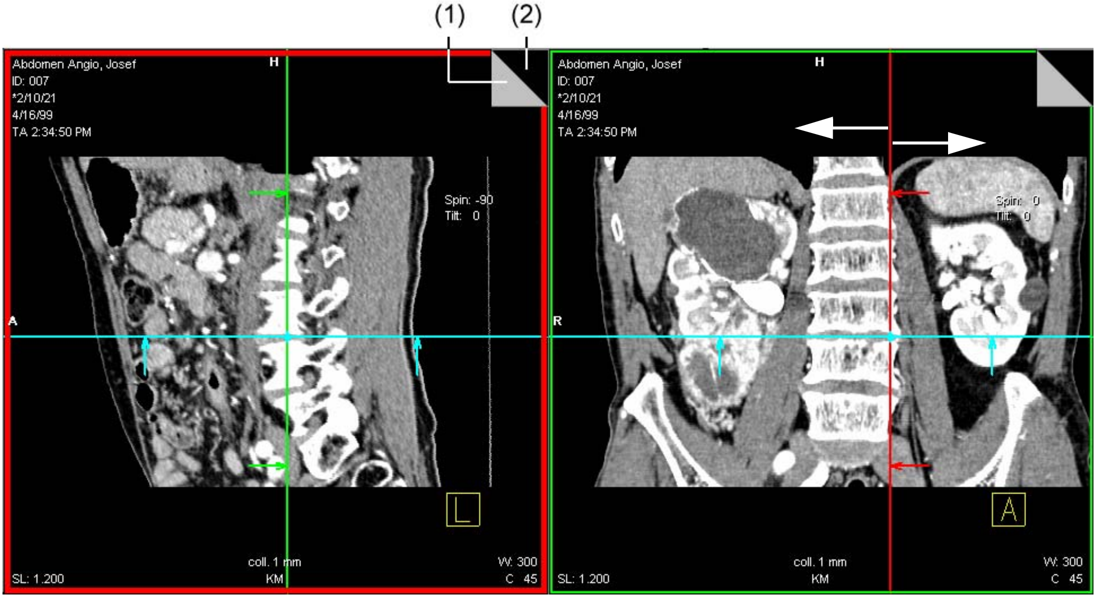
If you want to freeze an angle, you can deselect the **Free Mode** option again.

✧ To do that, click on the active button.

Paging with the dog ears

When you set the output types MPR, MPR Thick or MIP Thin, you will see dog ears in the top right-hand corner of the reference segments.

You can move slice by slice forwards or backwards through the volume using the dog ears. The corresponding line of the cross hair in another segment moves in parallel.



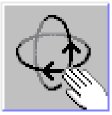
(1) Page backwards
(2) Page forwards

Rotating the volume with the mouse

You can also create oblique and double-oblique images by rotating the image display in one of the segments with the mouse.

✧ Call up **Orientation > Rotate Images**.

Or



✧ Click on the button in the upper part of the control area.

✧ When you position the mouse cursor on the segment, the cursor changes shape.

✧ Move the mouse cursor keeping the left mouse key pressed down.

❑ Moving the mouse from the center of the segment to the top, bottom, left, or right tilts the object in the corresponding direction.

❑ Moving the mouse from the border of the segment to the left, right, top, or bottom tilts along the segment border spins the object in the corresponding direction.

➪ If activated, you have to switch off the zoom/pan mode first.

Rotating around one axes (oblique cut planes)

For oblique slices, you rotate a slice about **one** axis of the patient coordinate system starting from the standard view.

The orientation is displayed in the image as a combination of two orientation labels. This designation is comparable with the designations used on a compass, e.g. NW for north-west.

One of the two reference lines in the image is now dotted. The corresponding plane is therefore oblique in relation to the displayed image.

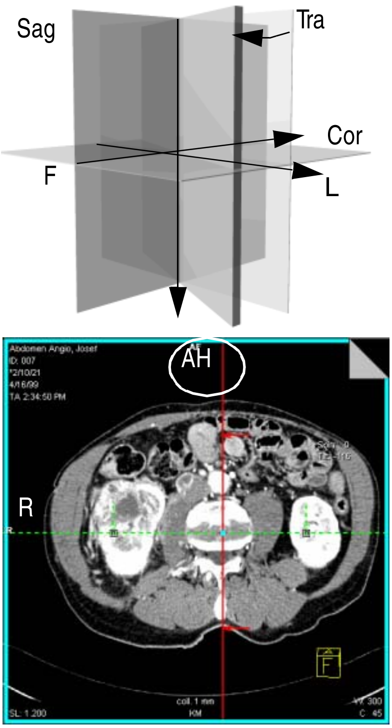
Two different directions of rotation (around an axis) exist for each standard view, each of which are explained graphically in the following examples.

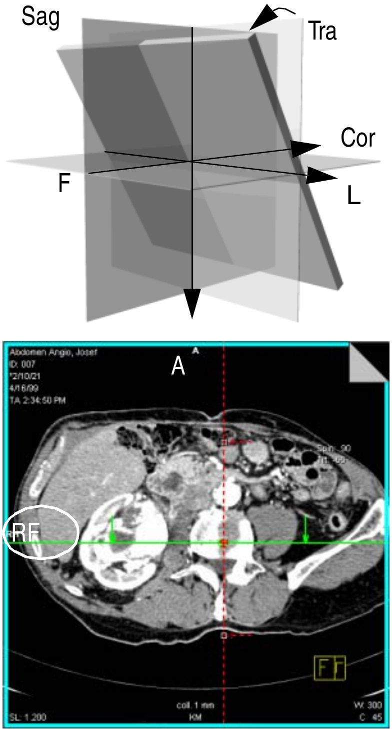
➩ In the following examples, the patient is positioned head first, supine.

Transversal slice

You can rotate a transversal slice toward the coronal or sagittal plane.

- ❑ Rotation of the transversal slice toward the sagittal slice (left example)
- ❑ Rotation of the transversal slice toward the coronal slice (right example)





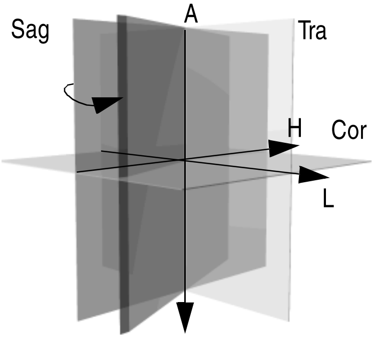
Depending on the direction of rotation, further combinations of orientation labels are displayed, e.g. RH, LF, AH, PF.

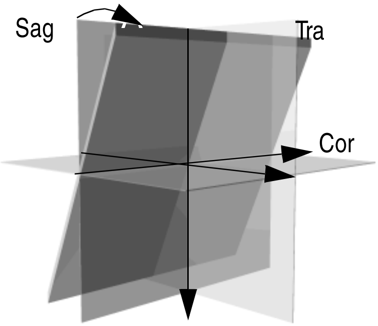
Sagittal slice

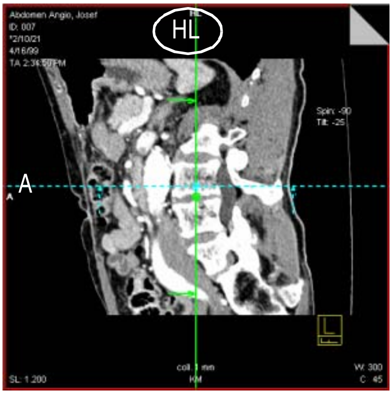
You can rotate a sagittal slice toward the transversal or coronal plane.

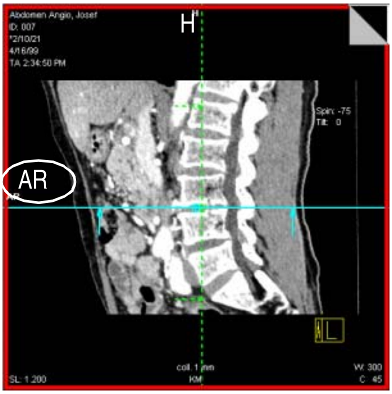
❑ Rotation of the sagittal slice toward the transversal slice (left example)

❑ Rotation of the sagittal slice toward the coronal slice (right example)







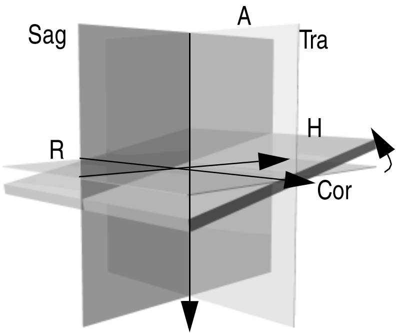


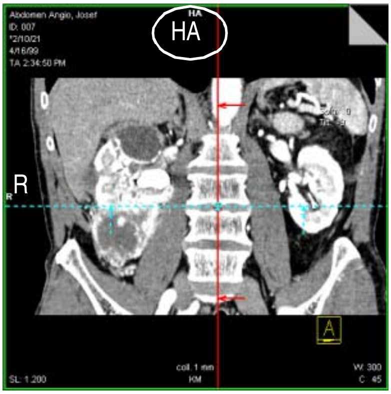
Depending on the direction of rotation, other combinations of orientation labels such as AL, PR, HR or PL can also result.

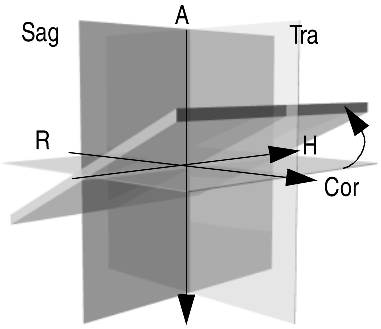
Coronal slice

You can rotate a coronal slice toward the transversal or sagittal plane.

- Rotation of the coronal slice toward the transversal slice (left example)
- Rotation of the coronal slice toward the sagittal slice (right example)



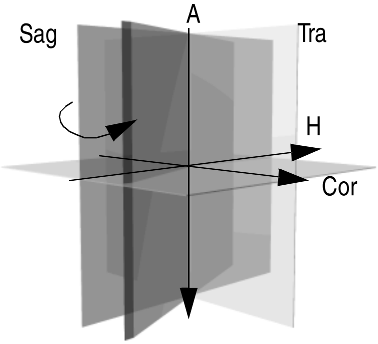




Depending on the direction of rotation, other combinations of orientation labels such as RH, HP, FA or LF can result.

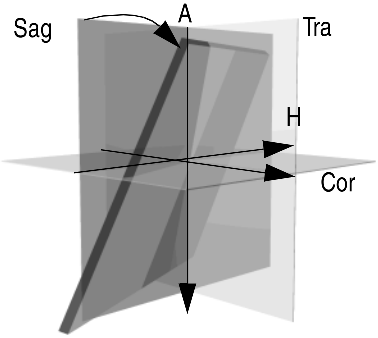
Rotating around two axes (double-oblique cut planes)

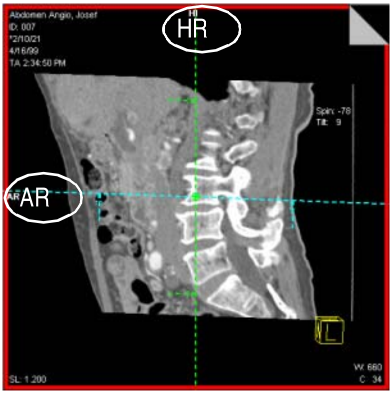
You obtain cut planes in two axes whenever you rotate one slice around *two* different patient coordinate axes one after the other. The plane is then no longer perpendicular to either of the coordinate axes. The image orientation is displayed as a combination of three orientation labels.



(1)

(2)





(3)

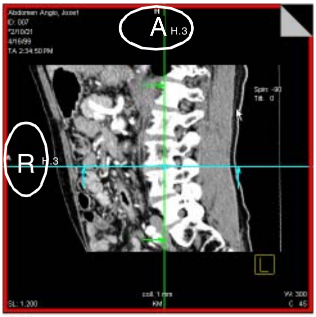
(1) Rotation of the sagittal slice toward transversal slice
(2) Rotation of the Sag/Tra slice toward coronal
(3) Resulting view

Controlling image orientation

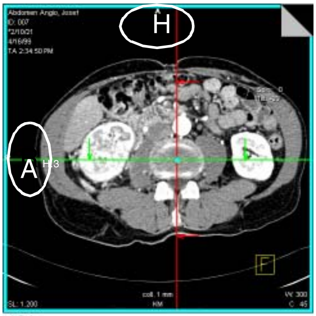
If you rotate the image in a reference segment, the viewing angle changes. To make orientation easier for you in such images, orientation markers are displayed in the images.
→ Page H.3–6, *Orientation labels*

Preferred directions

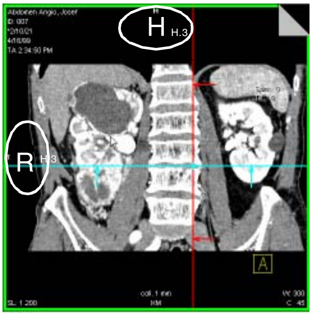
The program also uses the following **preferred directions** for image orientation/rotation within the selected cut plane:



(1)



(2)

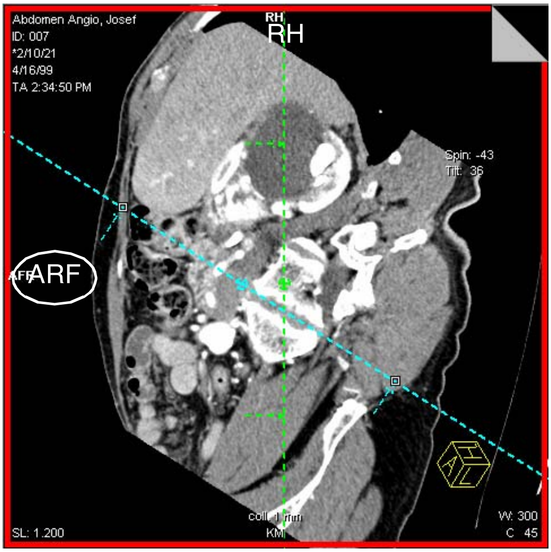


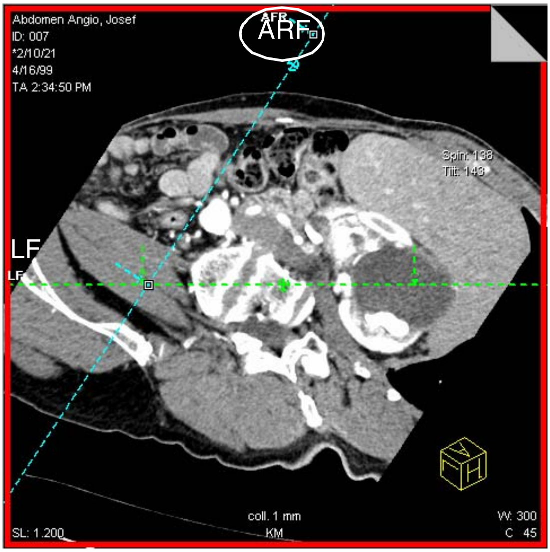
(3)

1. (1) In a **sagittal** view, the images are displayed **anterior-head** (front of the patient left and head up). The orientation label **H** is at the top.
2. (2) In a **transversal** view, the images are **right-anterior** (front up, viewing direction towards the head). The orientation label **A** is at the top.
3. (3) In a **coronal** view, the images are **right-head** (front front, head up). The orientation label **H** is at the top.

Automatic orientation control

If you rotate and tip an image from the sagittal plane towards the transversal plane, for example, you eventually find yourself in the transversal view. The program then rotates the image by another 90° to display it in a preferred direction again, i.e. from **anterior-head** to **right-anterior**.





✧ Call up **Orientation > Orientation Control** to activate this orientation control.

Or

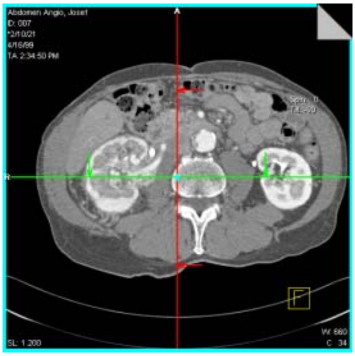
✧ Activate the **Orientation Control** option with the button in the upper part of the control area.

Setting standard views

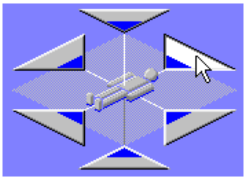
The standard views are used as a starting point for processing images on the **3D** task card.

You can set views for individual segments independently. For example, you can select a different view for each segment or define the same view in all segments.

Transversal view



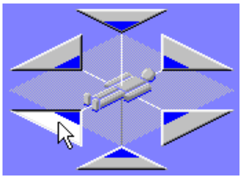
In the transversal view you view the tomographic images of the patient perpendicular to the patient axis (axis that runs from the head to the feet of the patient).
Your viewing direction is therefore from top or from bottom, i.e. cranio-caudal or caudo-cranial.



✧ Call up **Orientation > Head to Feet**, or click on the button on the **Orientation** tool card.

The viewing direction changes to *transversal, cranio > caudal*, i.e. from head to feet.

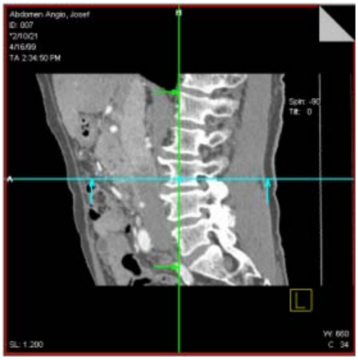
Or



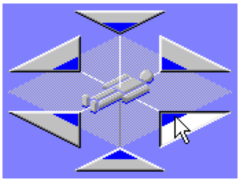
✧ Call up **Orientation > Feet to Head** or click on the button on the **Orientation** tool card.

The viewing direction changes to *transversal, caudo > cranial*, i.e. from feet to head.

Sagittal view



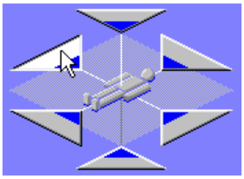
In the sagittal view, you view the patient from the side (from the left or from the right).



✧ Call up **Orientation > Left to Right** or click on the button on the **Orientation** tool card.

The viewing direction changes to *sagittal left*. You view the patient from the left side.

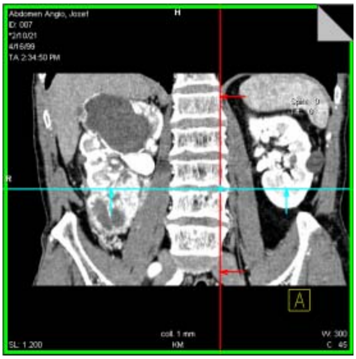
Or



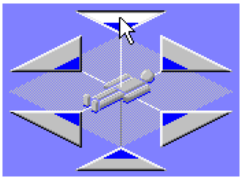
✧ Call up **Orientation > Right to Left** or click on the button on the **Orientation** tool card.

The viewing direction changes to *sagittal right*. You view the patient from the right-hand side.

Coronal view



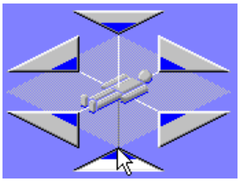
In the coronal view, you view the patient from the front or the rear.



✧ Call up **Orientation > Front to Back** or click on the button on the **Orientation** tool card**.**

The viewing angle changes to *anterior coronal*. You view the patient from the front.

Or



✧ Call up **Orientation > Back to Front** or click on the button on the **Orientation** tool card.

The viewing angle changes to *posterior coronal*. You view the patient from the rear.

Restoring the standard view

The standard views serve as orientation aids. You can return to the standard view from any other view and start your processing again.

✧ Call up **Orientation > Reset** to restore the view set at the beginning of processing.

Or

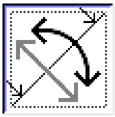
✧ Click on the **Reset** button on the **Orientation** tool card.

Fixing the angle

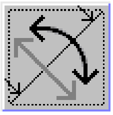
As soon as you have set a view to a particular viewing angle, you can set that angle. After that, you can no longer rotate the reference lines, only move them.

✧ Call **Orientation > Free Mode** (checkmark disappears) to move the lines in parallel only.

Or



Active

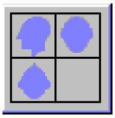


Not active

✧ Click on the active button **Free Mode** in the upper part of the control area to deselect the option.

Setting orthogonal views

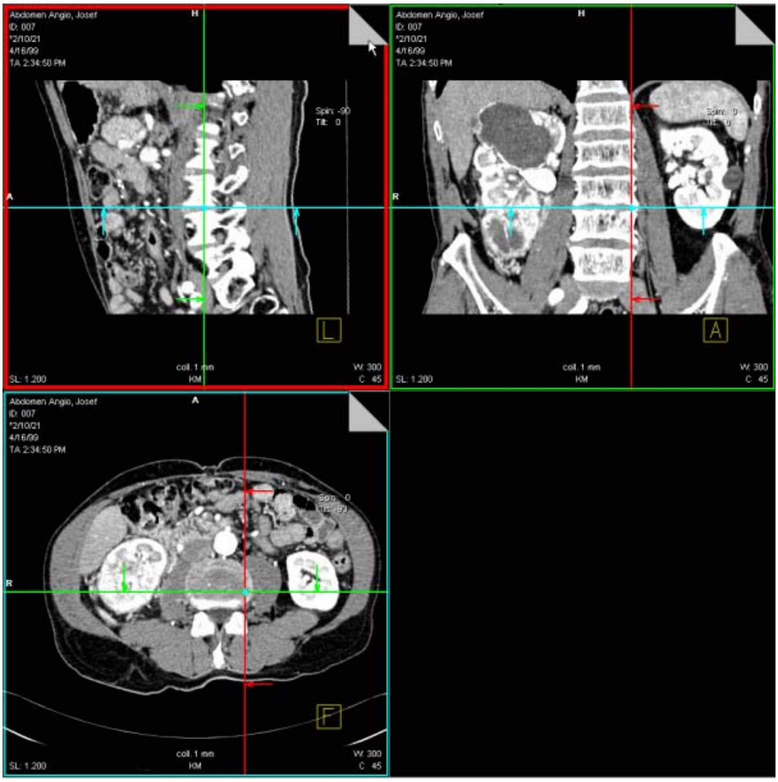
If you want all the images of the three reference segments to be at right-angles to each other, deselect the option **Free Mode**.



✧ First click on the **Reset** button, all views are now perpendicular to each other in the standard view.

✧ Then deselect the option **Free Mode** to fix the right angle.

The angle between the reference lines remains constant. The reference lines now show the standard view.

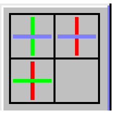


View perpendicular to reference image (Ortho Sync)

Usually, you activate the orthogonal view to display slices along the main axis of an organ, e.g. the heart. In order to do this you first set the view in the reference image.

✧ Call up **Orientation > Ortho Sync**.

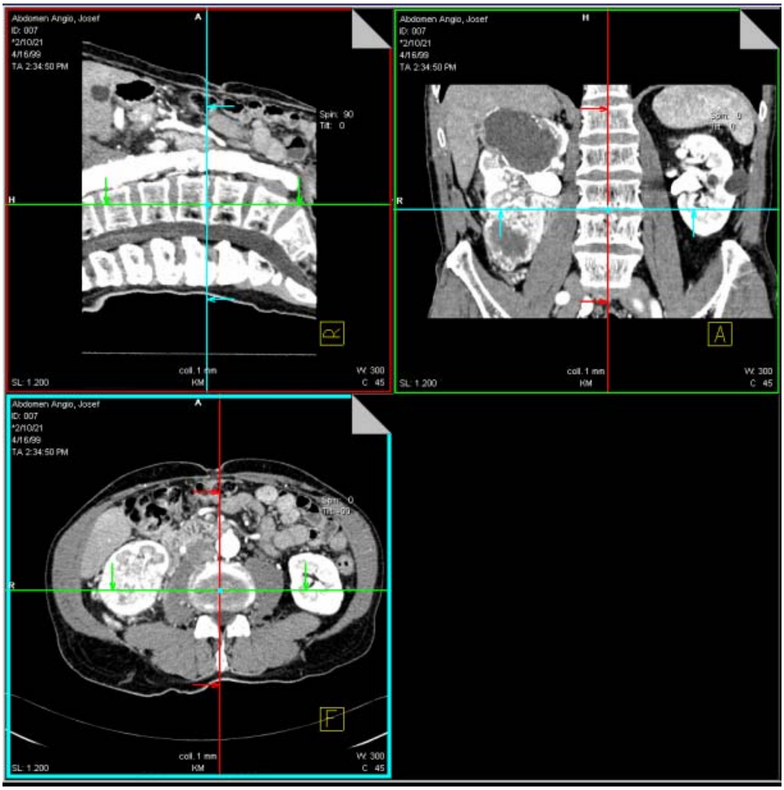
Or



✧ Click on the **Ortho Sync** button in the upper part of the control area.

Views are now displayed in the other reference segments which are perpendicular to the reference image, in the example below the top left-hand image.

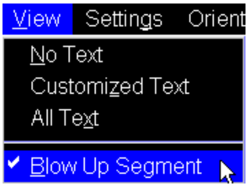
➩ These images do not have to be perpendicular to the patient coordinate system.



Blow Up Segment

You can blow up each of the reference segments for a detailed evaluation. Instead of the four image segments, a single view of the selected segment is displayed.

Activating Blow Up

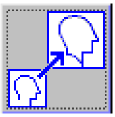


✧ To do that, call up **View > Blow Up Segment**.

Or

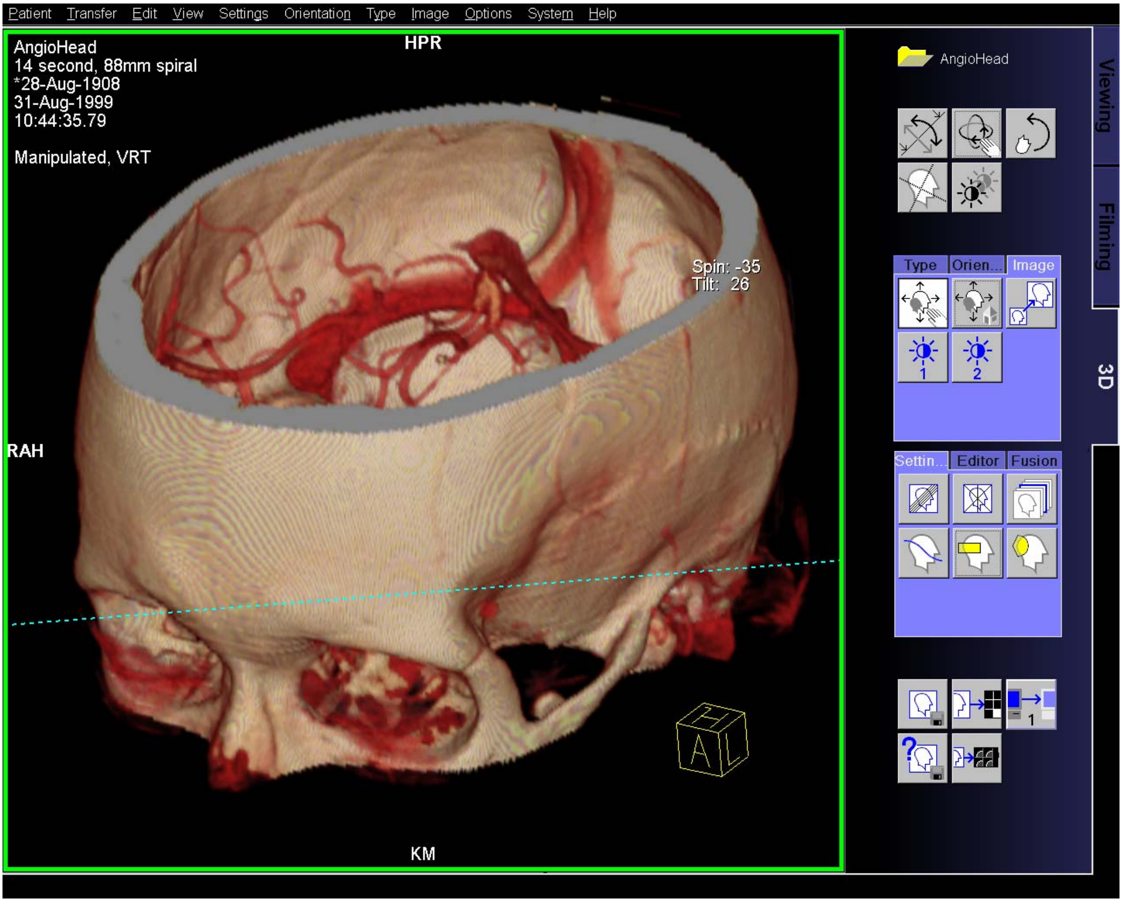
✧ Double-click on the selected segment.

Or



✧ Click on the inactive button **Blow Up** on subtask card **Image**.

The single view of the selected segment is now displayed.



You can apply the same functions to the enlarged display as to the 2:2 division.

Deactivating Blow Up

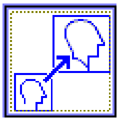
If you want to return to the normal view, deactivate the option **Blow Up** again.

✧ Call up **View > Blow Up Segment** in the main menu again.

Or

✧ Double-click on the single view.

Or



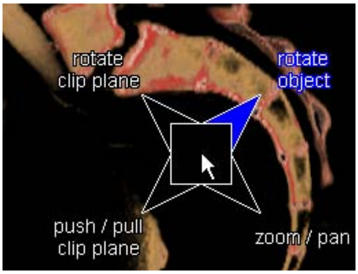
✧ To do that, click on the active button **Blow Up** on the subtask card **Image**.

Smart Selection

In **VRT Clip** mode you can switch functions directly in the image segment without calling up the relevant menus.

✧ Place the mouse cursor in the segment and keep the right mouse button pressed.

A graphical popup menu is displayed.



✧ Drag the mouse cursor onto the menu item and then release the mouse key again.

You can now apply the selected mouse function in the usual way with the left mouse key.

➪ If you are already familiar with the special function **Smart Selection** you do not need to call up the popup menu. You can simply drag the mouse in the required direction keeping the right mouse key pressed in order to switch over the mouse function.

Defining output types

You can change the output type for a segment at any time, i.e. from multiplanar reconstruction (MPR) to maximum intensity projection (MIP), to surface shaded display (SSD), or to volume rendering technique (VRT).

Depending on your working method, you will first generate a reference image, for example, in MPR in the desired view and then switch to MIP, SSD or VRT display.

✧ Click on the segment for which you want to change the output type.

➩ If you want to switch over all segments, you must select and switch over each one separately, one after the other.

Setting MPR

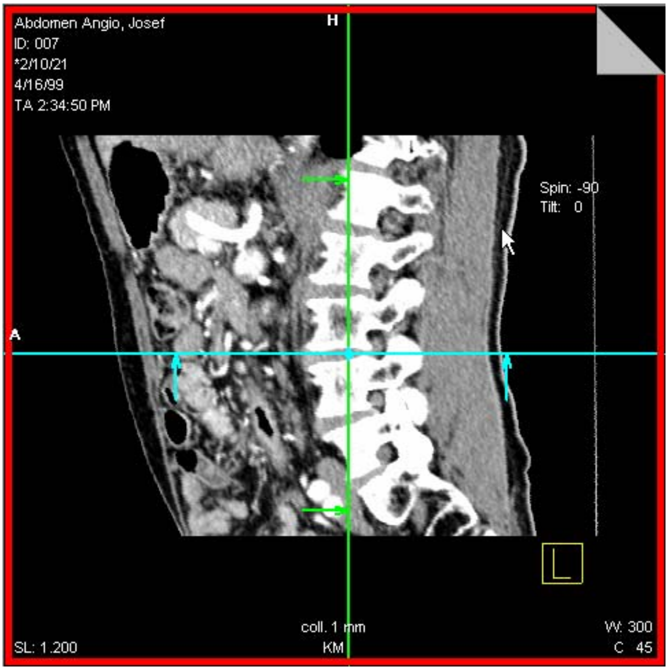
With multiplanar reconstruction you can generate tomographic images in a view and position that you define in the volume data set.

✧ Call up **Type > MPR** or click on the **MPR** button on subtask card **Type**.

Or

Transfer the images directly from the **Patient Browser** or the **Viewing** task card to **MPR** mode.

✧ Call up **Patient > MPR** or click on the button **MPR**.



Abdomen Angio, Josef
ID: 007
*2/10/21
4/16/99
TA 2:34:50 PM

Spin: -90
Tilt: 0

SL: 1.200
coll. 1 mm
KM
W: 300
C 45

Setting MIP

The maximum intensity projection uses the most intensive gray-scale values of the images for reconstruction. For example, in contrast medium examinations, that blood vessels are those structures that have the most intensive values. The system takes these voxels. The MIP display is therefore especially suitable for vascular examinations.

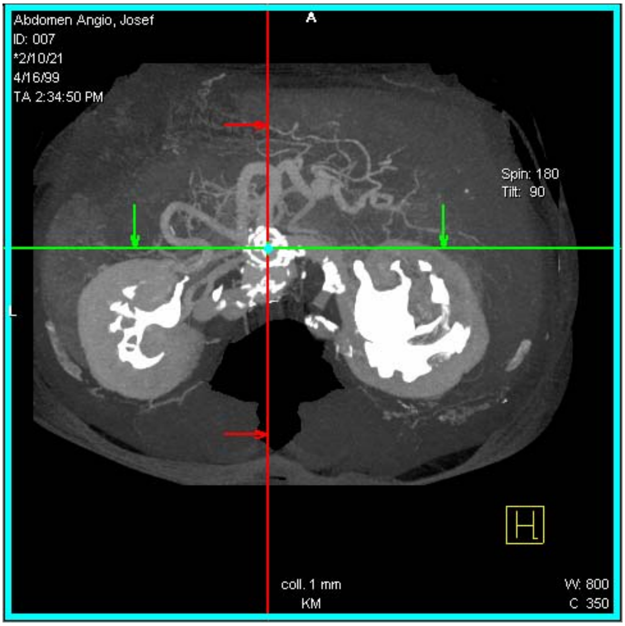
✧ Call up **Type > MIP** or click on the **MIP** button on subtask card **Type**.

The output type in the selected segment is switched over.

Or

Transfer the images directly from the **Patient Browser** or the **Viewing** task card to **MIP** mode.

✧ To do that, call **Patient > MIP**.



Abdomen Angio, Josef
ID: 007
*2/10/21
4/16/99
TA 2:34:50 PM

Spin: 180
Tilt: 90

coll. 1 mm
KM

W: 800
C 350

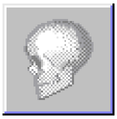
Setting SSD

After you have generated a reference image, you can also generate a surface structure in this view.
→ Page H.3–11, *Setting the reference image*

➩ You can display both complete volume data sets and previously defined partial volumes (VOIs, volumes of interest) in SSD display.
→ Page H.5–4, *Extracting a volume of interest (VOI)*

✧ Call up **Type > SSD**.

Or



✧ Click on the **SSD** button on the **Type** tool card.

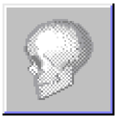
A surface view is generated in the selected segment. Your system uses modality-specific default gray-scale values as threshold values to extract the surface.

Or

Transfer the images directly from the **Patient Browser** or the **Viewing** task card to SSD mode.

✧ To do that, call **Patient > SSD**.

Or

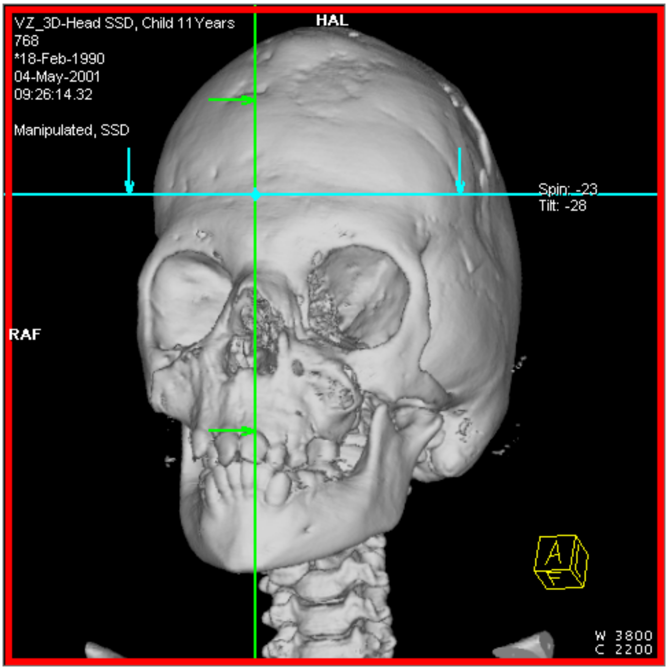


✧ Open the **Threshold** dialog window by calling up **Type > SSD Definition** in the main menu or clicking on the button with the right mouse key.

The **Threshold** dialog box is displayed.

There you can enter threshold values yourself and start SSD extraction.

→ Page H.6–5, *SSD reconstruction with changed thresholds*



Setting VRT

With the volume rendering technique you can generate true color images in which the entire volume data set is displayed. The **VRT** display provides the most information about the examined volume data set.

In the 3D card

✧ Call up **Type > VRT** or click on the **VRT** button on subtask card **Type.**

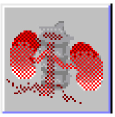
A three-dimensional image is generated in the selected segment. The system uses the preset parameter data sets for the display.

➩ The **VRT Gallery** is supplied with a series of predefined parameter data sets. You can change these parameter data sets.
→ Page H.7–11, *VRT Definition*

In the Viewing or Patient Browser card

Transfer the images directly from the **Patient Browser** or the **Viewing** task card to **VRT** mode.

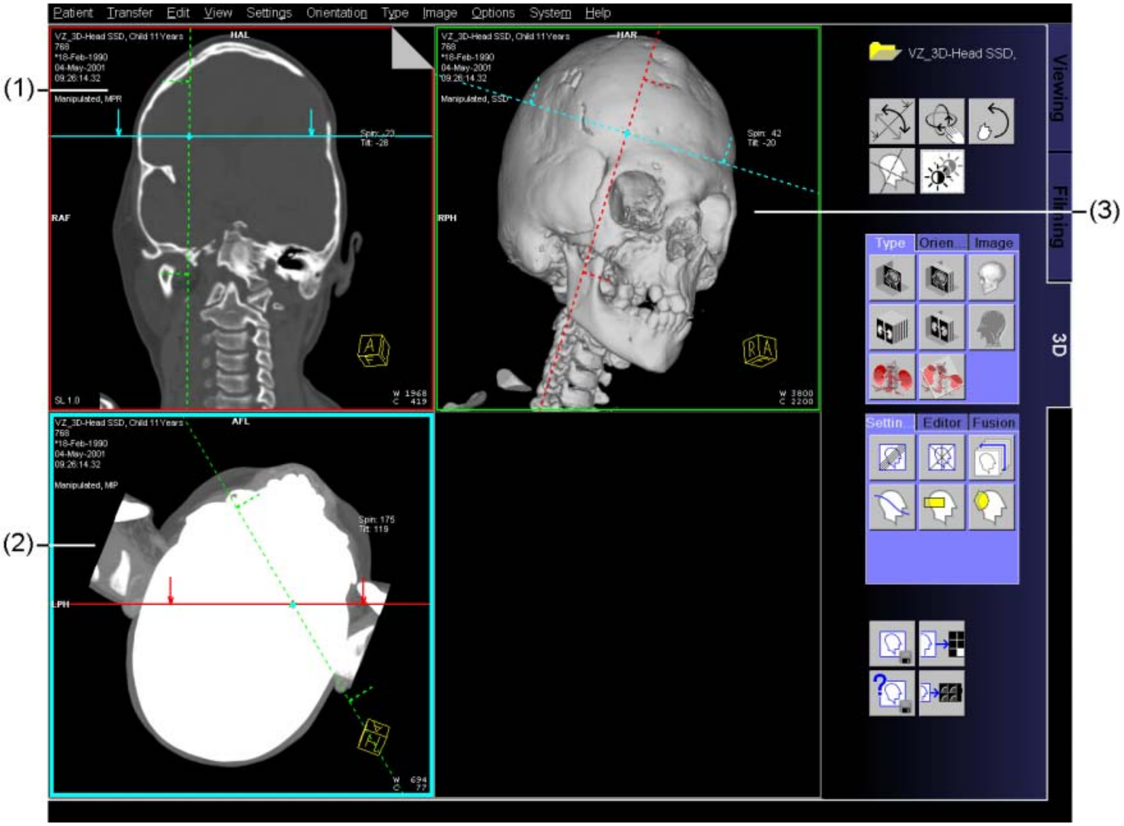
✧ Select the examination or series that you want to edit in 3D.



✧ Call up **Patient > VRT** or click on the button.

3D task card with mixed output types

You can set the three output types independently of each other in the three reference segments.



(1) MPR image
(2) MIP image
(3) SSD image

Generating series from 3D images

In most cases, the result of your 3D evaluation will be the reconstruction of entire series of images. To do that, first select a reference image in the view that you require.
→ Page H.3–12, *Selecting a reference image*

Depending on the output type you are using, the following options will be available to you:

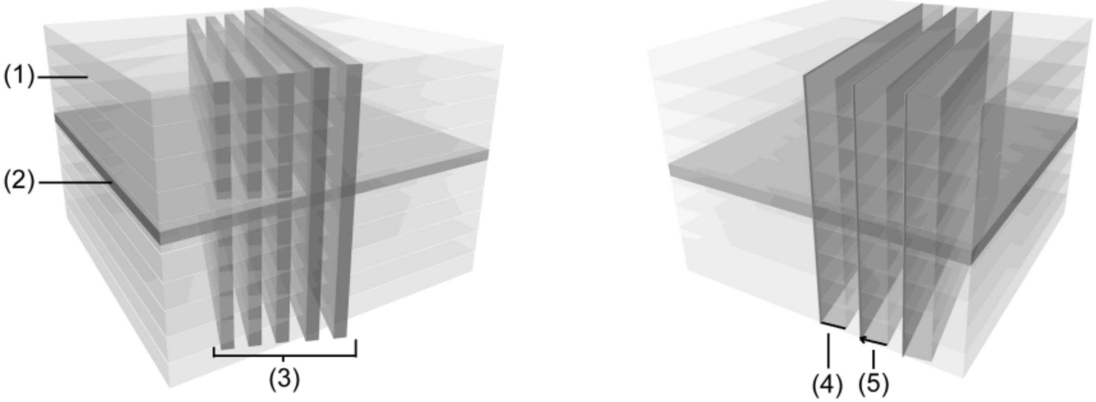
❏ Series of parallel tomographic images

❏ Radial series

❏ Expanded ranges

Series of parallel tomographic images

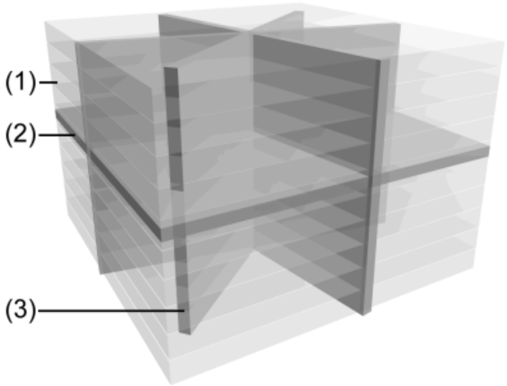
With this option you generate series of cut images that are parallel to one another and perpendicular to the reference image for the output types MPR, MPR Thick and MIP Thin.



(1) Volume data set
(2) Reference image
(3) Parallel tomographic images
(4) Volume used for projection (MIP Thin)
(5) Direction of projection (MIP Thin)

Radial series

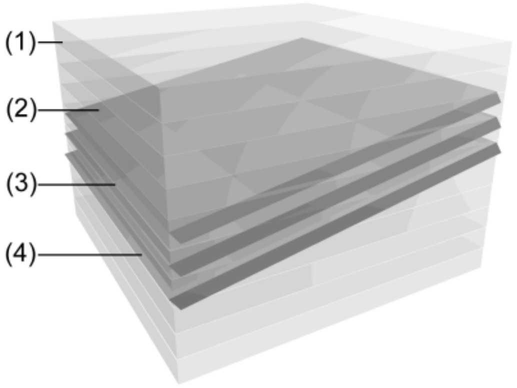
For output types MPR, MPR Thick and MIP Thin you generate a series of cut images arranged in a star shape. For output types MIP, SSD and VRT you generate a series of projections and views of the volume each rotated around a defined angle.



(1) Volume data set
(2) Reference image
(3) Radial tomographic

Expanded ranges

With this option you generate tomographic images that are located in front of or behind the reference image. This option, too, is only available for output types MPR, MPR Thick or MIP Thin.



(1) Volume data set
(2) Range in front the target image
(3) Target image
(4) Range behind the target image

Generating parallel images

In a series of parallel tomographic images, you generate images that are parallel and a defined distance apart, and perpendicular to the reference image. This is equivalent to a step-by-step offset of a reference line of the 3D cross hair.

✧ Select a continuous reference line to define the position of the reconstructed images with that line.

➪ The reference line that you select represents an image in one of the two other reference segments. This image must be of the required output type, i.e. MPR, MPR Thick or MIP Thin.
→ Page H.3–13, *Using the 3D cross hair*

➪ The presets or the last selected settings are used if no continuous reference line is selected.

Calling up Parallel Ranges

✧ Call up **Settings > Parallel Ranges**.

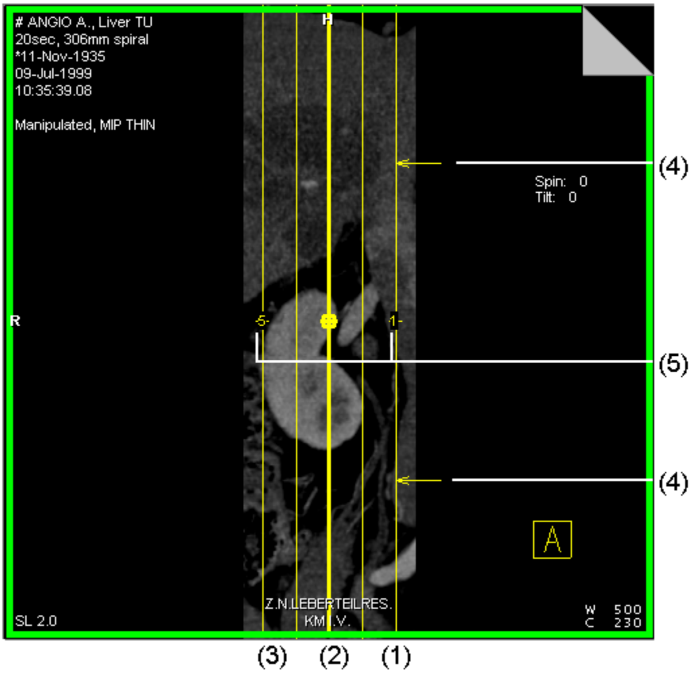
Or

✧ Click on the **Parallel Ranges** button on the **Settings** tool card.

In the reference segment, the positions of the parallel tomographic images are shown graphically. The tomographic image of the selected reference line (preview) is displayed in the output segment.

Graphic display of the new series

The lines in the output segment show the position of the individual images. The arrows indicate the viewing direction.

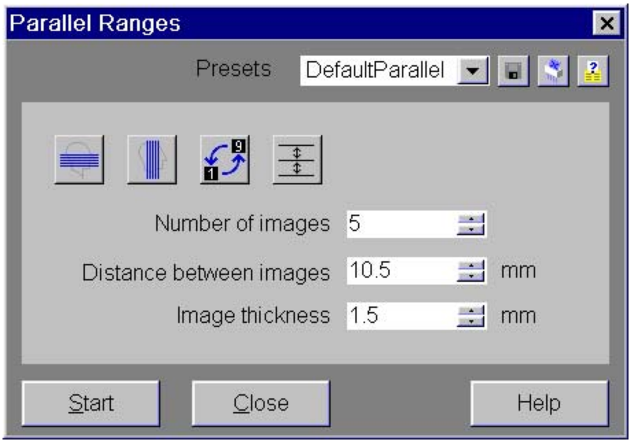


(1) Start line (marked by number 1)
(2) Reference line
(3) End line
(4) Arrows indicate the viewing direction
(5) Image numbers in one series

➪ If the series is made up of many images, not all the lines are displayed in the graphic. The inside lines are then displayed in green.

Parallel Ranges dialog box

The dialog box **Parallel Ranges** is displayed as soon as you called up **Settings > Parallel Ranges...**.



Presets DefaultParallel

Number of images 5

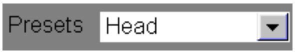
Distance between images 10.5 mm

Image thickness 1.5 mm

Loading default settings

Default parameter settings with individual designations for generating parallel series are stored in your system. You can access these parameters with the selection button **Presets** and call up a parameter setting adapted to your requirements.

➩ If no parameter set exists that is suitable for your diagnostic problem, load a similar parameter set and then edit it.



Presets Head

✧ Select the parameter set you want from the selection list.

Changing a range numerically


Number of images 5

✧ Enter the required number of parallel tomographic images using the spin box or the input field.

➪ Enter at least three images.


Distance between images 21.9 mm

✧ Enter the distance between the individual images in the input field and confirm your entry with the **Return** key.


Image thickness 1.3 mm

✧ Enter the slice thickness of the result image and confirm your entry with the **Return** key.
→ Page H.4–3, *Changing the slice thickness (MPR Thick)*

✧ Click on the **Horizontal Ranges** button.

This is how you generate a series whose intersection planes are horizontal in the center of the reference image.

Or

✧ Click on the button **Vertical Ranges**.

This is how you generate a series whose intersection planes are vertical in the center of the reference image.

✧ Click on the button **Swap Range Order** to reverse the existing image numbering of the series.

The graphic display of the series on the reference segment changes according to your settings. A new preview image is reconstructed in the output segment.

Changing the range with the mouse

You can also increase or reduce the area of a series calculation by moving the starting line or end line with the mouse. The image that corresponds to the line you have just processed is displayed in the output segment.
→ Page H.3–52, *Graphic display of the new series*

✧ Click on the starting or end line and move the line holding the left mouse key down.

The number of images changes accordingly (is increased or decreased). The distance between the cut images remains the **same**.

Or

✧ Click on the **Keep No. of Images Constant** icon and move the starting or end line holding the left mouse key down.

The distance between the cut images changes accordingly (is increased or decreased). The number of images remains the **same**.

➪ The values in the **Parallel Ranges** dialog box change in accordance with the changes in the graphic display.

✧ Move the entire range by clicking on the point of rotation of the reference line and moving the mouse with the left mouse key pressed.

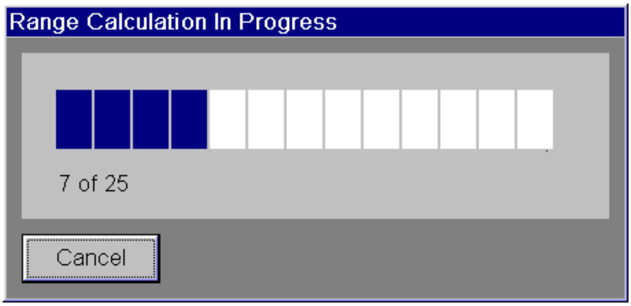
✧ Rotate the entire range by clicking on the reference line and moving the mouse cursor around the point of rotation with the mouse key pressed.

Starting reconstruction

If all the settings are as you require them, you can start reconstruction.

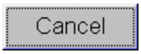
✧ Click on the **Start** button to create the series of parallel tomographic images.

A message box is displayed in which you are informed about the progress of reconstruction. Each image is displayed in the output segment as soon as it has been calculated.


Range Calculation In Progress

7 of 25

Canceling reconstruction



You can cancel reconstruction at any time.

✧ Click on **Cancel** in the progress box.

All the images already reconstructed are displayed in the output segment.

➪ Even if you have pressed **Cancel**, all the images you have so far reconstructed are saved if the **auto-store** function is active.
→ Page H.13–6, *Activating automatic storage*

Terminating reconstruction

After reconstruction has been completed, the last image of the range, i.e. the image of the end line, is displayed in the output segment.

➪ Each image of the series is assigned automatically an image number.

➪ Click on the dog ear in the top right-hand corner of the output segment and page through the stack to display another image of the new series.

Saving a series

When the series meets your requirements:

✧ Save your new series.
→ Page H.11–2, *Storing 3D images manually*

➪ If the option **Enable auto-store** has been activated in the configuration, the series is automatically saved.
→ Page H.13–6, *Activating automatic storage*

Saving a parameter set

If you want use the parameter set again in the future, we recommend that you store it in the system.

✧ Click on the **Link Preset** button to have a suitable suggestion for the name of the series entered.


Presets Head

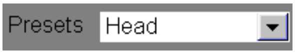
✧ Shorten the **Presets** in a useful way in order to keep the assignment general and confirm with the **Return** key.

✧ Click on the button to save the parameter set.

The next time you load, the presets are assigned to the series that contain the name entered as the first part of their name.

Deleting a parameter set

You can delete parameter sets that you no longer require for editing parallel series from the selection list **Presets**.


Presets Head

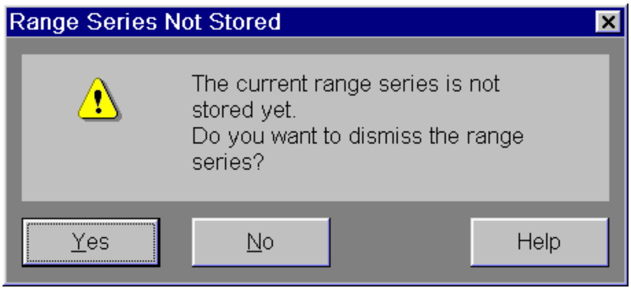
✧ Select the existing parameter set from the selection list.

✧ Click on the button to delete the parameter data set.

Close

✧ When you have finished editing, click on this button to return to the original mode.

If you have not stored the reconstructed series, the following dialog box is displayed:


Range Series Not Stored

The current range series is not stored yet.
Do you want to dismiss the range series?

Yes

✧ Click on **Yes** to reject the series.

The **Parallel Ranges** dialog box is closed.

Or

No

✧ Click on **No** to continue processing the series.

Postprocessing series of parallel images

If the reconstructed range of the series is not as you require it, you can adapt it either graphically or in the **Parallel Ranges** dialog box.

➩ If you generate a new series by changing the values, a query appears asking whether you want to store or reject the old series.

Generating an expanded range

Use the expanded range if you want to generate a series of images that are located in front of or behind the reference image. In this way, you simulate scrolling through the image stack with the dog ears.

It is not possible to define an expanded range graphically with the mouse. You can only define it using standard values in the **Expand Ranges** dialog box.

✧ First select a reference image that contains the view of your choice.
  → Page H.3–12, *Selecting a reference image*

Output type MPR, MPR Thick or MIP Thin must be set in this reference segment.

✧ Call up **Settings > Expand Ranges**.

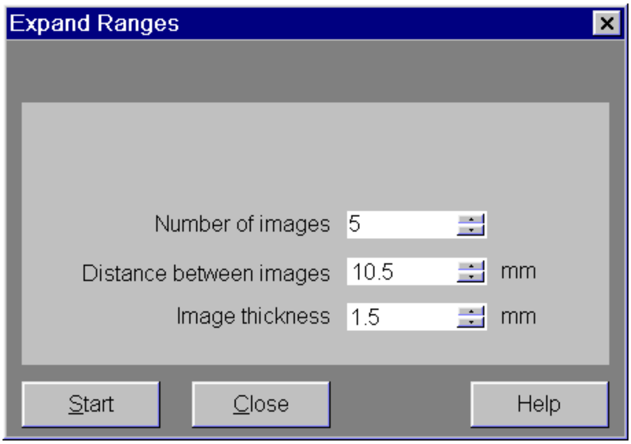
Or

✧ Click on the **Expand Ranges** button on the **Settings** tool card.

A preview of the expanded range is displayed in the output segment. The 3D cross hairs in the reference segment are now no longer visible.

Expand Ranges dialog box

The **Expand Ranges** dialog box is displayed.



Number of images 5

Distance between images 10.5 mm

Image thickness 1.5 mm

5

✧ Enter how many images you want reconstructed in the input field.

Distance between images: 13.8 mm

✧ Enter the distance between the images in the input field.

Image thickness 0.8 mm

✧ Enter the slice thickness in the input field (only possible for **MPR Thick** and **MIP Thin**) and confirm with the **Return** key.

The new reference image is displayed in the output segment.

✧ Start reconstruction by clicking on the **Start** button.

The images of an expanded series are displayed in the output segment. They are parallel to the reference image. The last image of the series is displayed.

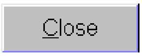
✧ Use the dog ears in the top right-hand corner of the output segment to page through the series.

If you want to change the range, you must enter new values in the **Expand Ranges** dialog box.

If the new series is as you require it:

✧ Save your new series.

⇨ If the **Enable auto-store** option was activated during configuration, the series is stored automatically.
→ Page H.13–6, *Activating automatic storage*



✧ Then click on **Close** to return to the original mode.

If the series does not yet provide the views you want, change the range settings in the dialog window **Expand Ranges** and reconstruct again.
→ Page H.3–61, *Expand Ranges dialog box*

Generating radial images

You generate radial tomographic images to be able to view a range from different angles. In this way, you simulate step-by-step rotation of a reference line. A number of tomographic images, depending on the angle, are generated from the volume data set.

✧ Select a broken reference line or a reference image to generate a series whose intersection plane covers a quadrant in the reference image and is perpendicular to the reference image.
→ Page H.3–12, *Selecting a reference image*

➪ The selected reference line represents an image in one of the two other reference segments. That image must be in the required output type, i.e. MPR, MPR Thick or MIP Thin. How to generate series of radial projections (MIP, SSD, VRT) you find on:
→ Page H.3–71, *Series of radial projections and views*

Or

✧ Select a continuous reference line to define the position of the reconstructed images with the reference line.

Calling up Radial Ranges

✧ Call up **Settings > Radial Ranges**.

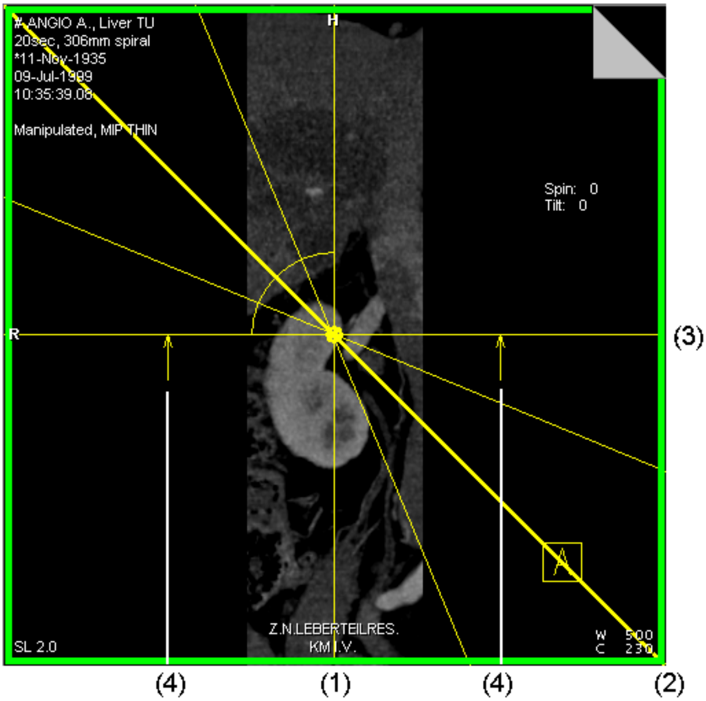
Or

✧ Click on the **Radial Ranges** button on the **Settings** tool card.

Graphic display of the radial series

The radial segments are displayed as lines in the reference segment. The lines have a common point of intersection and are distributed with a constant angle between them (default 22.5°).

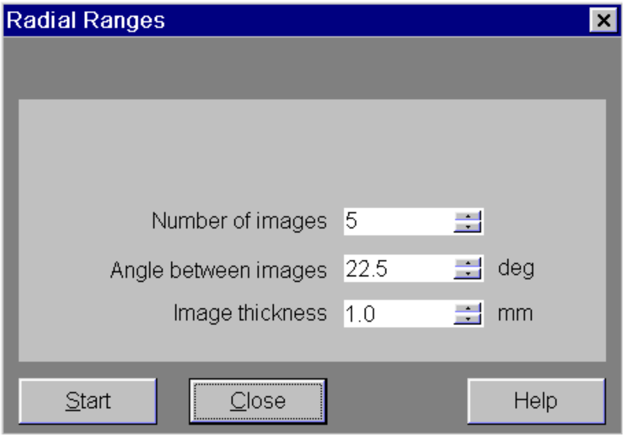
The image of the reference line is reconstructed and displayed in the output segment. You can see the direction of viewing of the resulting images by the arrows drawn in the reference segment.



(1) End line
(2) Reference line
(3) Starting line (marked by arrows)
(4) Viewing direction arrow

Radial Ranges dialog box

The **Radial Ranges** dialog box is displayed.



Number of images: 5

Angle between images: 22.5 deg

Image thickness: 1.0 mm

The settings you first see are the default settings. You can change them according to your requirements.


Angle between images: 22.5 deg

✧ Enter the required angle between the images in the input field and confirm with the **Return** key.

The position of the starting and end line remains identical. If you enter a new angle between the images, the number of images is changed accordingly.

Number of images 5

✧ Set a new number of images to be reconstructed in the spin box or the input field.

The angle between the images changes accordingly.

Image thickness 0.8 mm

✧ Enter the slice thickness (for **MPR Thick** and **MIP Thin** only) and confirm your entry with the **Return** key.

✧ The graphic display of the series in the reference segment changes according to the settings. A new preview image is reconstructed in the output segment.

Changing the range with the mouse

✧ Place the mouse cursor on the starting line, the center line, or the end line.

✧ Rotate the selected line around the rotation point holding down the mouse button.

By rotating the center line you also rotate all the other lines around the rotation point. Turning the starting line and end line changes the angle of aperture.

➪ If you rotate the starting line over the end line, angle measurement restarts at 0° again.

Or

✧ Move the entire range by moving the point of rotation with the mouse key pressed.

The image corresponding to the line being processed is displayed in the output segment. The values in the **Radial Ranges** dialog box change in accordance with the changes made to the graphic display.

⇨ If you change the range by rotating the start or end line, the number of images remains constant. Only the angle between the images changes.

Starting reconstruction

If all the settings are as you require them, you can start reconstruction.

✧ Click on the **Start** button to start reconstruction of the range.

A message box shows the progress of reconstruction and allows you to cancel reconstruction.

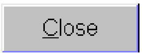
The reconstructed images are displayed as a stack of images in the output segment. The upper image corresponds to the end line in the graphic display.

Using the dog ears in the top right-hand corner of the images, you can page through the stack.

If the radial series is as you require it:

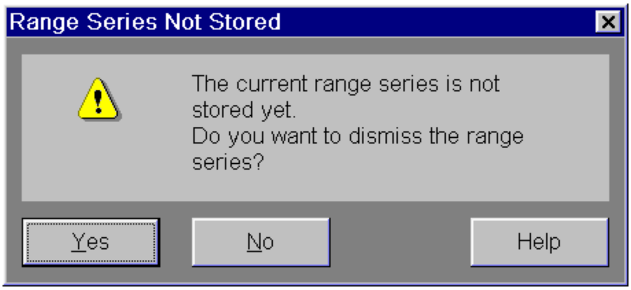
✧ Save your new series.
→ Page H.11–2, *Storing 3D images manually*

⇨ If the **Enable auto-store** option was activated during configuration, the series is stored automatically.
→ Page H.13–6, *Activating automatic storage*



✧ Click on **Close** to return to the original mode.

If you have not stored the reconstructed series, the following dialog box is displayed:



Range Series Not Stored

The current range series is not stored yet.
Do you want to dismiss the range series?

Yes

✧ Click on **Yes** to reject the series.

The **Radial Ranges** dialog box is closed.

Or

No

✧ Click on **No** to continue processing the series.

Postprocessing a radial range

You can rotate the starting and end line of the range in order to change the range and the angle between the result images.

➩ If you generate a new series by changing the values, a prompt appears asking you whether you want to save or reject the old series.

Series of radial projections and views

You do not reconstruct tomographic images for output types MIP, SSD and VRT, but series of projections and views.

Defining view directions

The future position of the projections/views is displayed graphically by projection arrows on the reference image. The reconstructed images are at right angles to these arrows. The arrows therefore indicate the direction in which you generate the projection. You can define the orientation of these arrows as follows:

✧ Select a broken reference line or a reference image.

➩ The image of this segment must be of the same output type.

The projections of the series describe a quadrant within the reference image.

Or

✧ Select a continuous reference line in your reference image to define the direction of viewing graphically.

➪ The reference line that you select represents an image in one or both of the other reference segments. This image must be in the required output type, i.e. MIP, SSD or VRT.

The selected reference line is at right angles to the center projection arrow of the series 3d graphics. All other projections are obtained by rotating this reference line clockwise or counterclockwise.

Setting radial projections and views

You can generate radial projections in radial range mode in the same way as radial cut images in output type MPR, MPR Thick or MIP Thin. The images of this series simulate step-by-step rotation of a reference line.

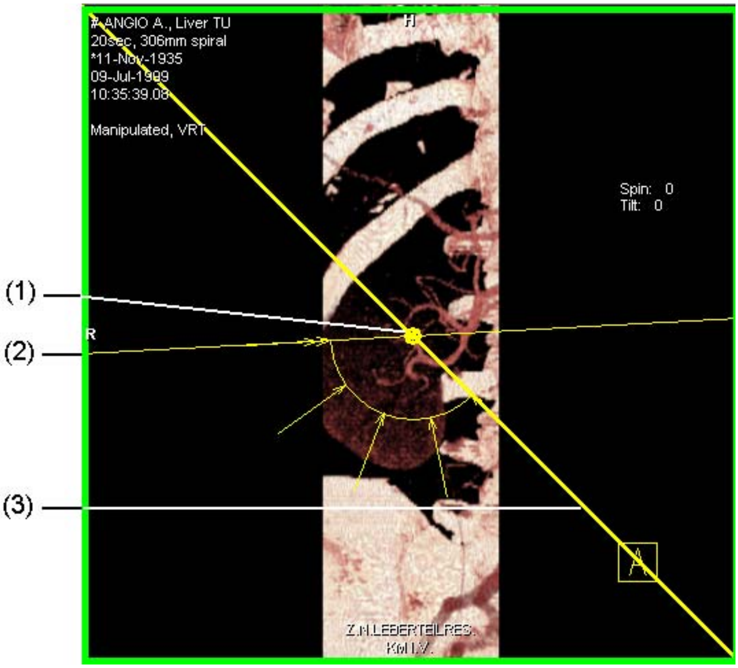
✧ Call **Settings > Radial Ranges**.

Or

✧ Click on the button **Radial Ranges** on the tool card **Settings**.

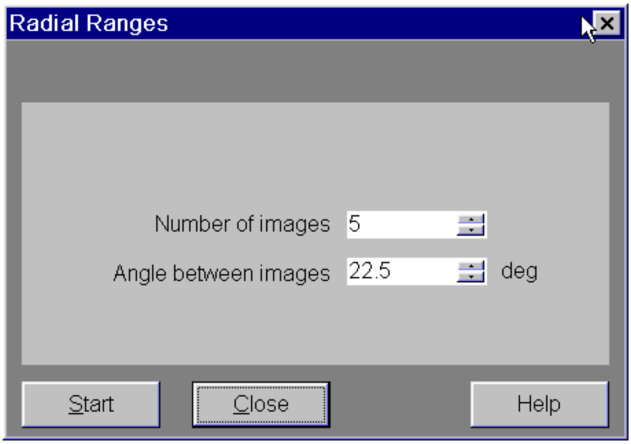
The range of the new series is marked in the reference image.

The arrows indicate the direction of the projections.



(1) Rotation point
(2) Start arrow (double arrow)
(3) End arrow

The dialog box **Radial Ranges** is displayed.



Number of images 5

Angle between images 22.5 deg

With the exception of the slice thickness, you now select all other settings for the radial series in the dialog box **Radial Ranges** or with the mouse in the reference image as you do for the reconstruction of radial cuts.
→ Page H.3–64, *Generating radial images*

CHAPTER H.4

Multiplanar Reconstruction (MPR)

In multiplanar reconstruction you can create parallel, radial, expanded series, or individual curved cuts from a selected view.

The multiplanar reconstruction is first displayed in the views that are parallel and perpendicular to the direction of scanning.

You can then move through the volume using the functions of the **3D** task card such as the 3D cross hair or mouse in order to generate the views which are important for you.

Transfer as MPR to 3D

You have selected a series of images for display in **MPR** in the **Patient Browser** or the **Viewing** task card and then transferred them possibly (or from the **Series List** dialog box) to the **3D** task card.

The series will be loaded and shown in MPR display mode.

➪ If you have already loaded images onto the **3D** task card and have only switched back to another application temporarily, switch back to **3D** by clicking the tab.
→ Page H.2–4, *Calling the 3D task card*

➪ If you have finished processing your first 3D series and saved it, you can load the next marked series directly from the **Series List** (**Patient > Open Series List...**). If the last patient to have been processed is in 3D, a dialog box appears in which you can specify whether you wish to continue processing or load the new series.
→ Page H.2–11, *Other series from the Series List*

Changing the slice thickness (MPR Thick)

With the MPR for thick slices, you can define the thickness of the original slice from which the image is to be reconstructed. The program calculates an average from several gray-scale values and uses these averages to build up the image.

✧ Call up **Type > MPR Thick** to set the output type **MPR Thick**.

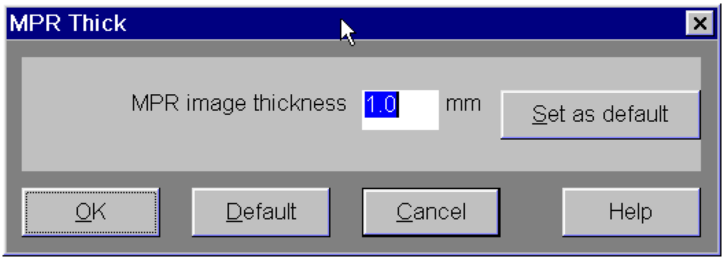
Or

✧ Click on the **MPR Thick** button on the **Type** tool card.

✧ Call up **Type > MPR Thickness** to display the **MPR Thick** dialog box for setting the slice thickness.

Or

✧ Click the **MPR Thick** button on the **Type** tool card with the *right* mouse key.



MPR Thick

MPR image thickness 1.0 mm

✧ Enter an image thickness (in mm).

OK

✧ Confirm your entry with **OK**.

Or

Default

✧ Click on **Default** to set the preset image thickness.

The selected setting is applied to all **MPR Thick** reconstructions.

➪ The value for **MPR image thickness** is displayed in the image and always also filmed and stored.

Changing the default setting

Set as default

✧ Click on **Set as default** to store a new preset value for the image thickness.

➪ When you load a new data set, the stored preset value is used.

Generating series of images

With the facility to generate images with any interval and direction, you can simulate examinations independently of the scanning direction.

You can save images reconstructed in this way as new series and, for example, transfer them to the **Viewing** task card for 2D evaluation.

Parallel ranges

In this mode, parallel tomographic images are generated a defined distance apart. The images are then perpendicular to the reference image.

✧ Generate and process series of parallel tomographic images as described in the following chapters:

→ Page H.3–51, *Generating parallel images*
→ Page H.3–59, *Postprocessing series of parallel images*

Radial ranges

The images are always arranged in a star and are a defined angle apart. They are perpendicular to the reference image.

✧ Generate and process series of radial tomographic images as described in the following chapters:

→ Page H.3–64, *Generating radial images*
→ Page H.3–70, *Postprocessing a radial range*

Expanded ranges

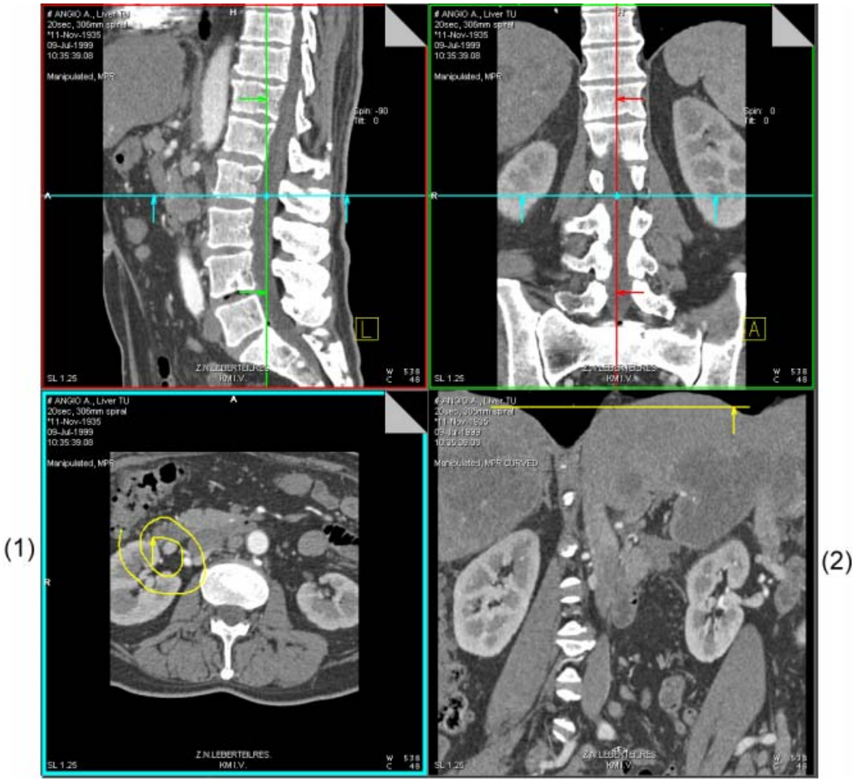
An expanded range consists of a series of parallel slices that are a defined distance apart and parallel to the reference image. You usually use this mode if you want to obtain a range in front of and behind the target image (reference image) as a series.

✧ Generate and process series of an expanded range as described in the following chapter:

→ Page H.3–60, *Generating an expanded range*

Generating curved slices

If you want to view subareas that cannot be obtained by planar, i.e. flat images, you can draw in a cut line with any curvature freehand. You can then display this cut as an image in the output segment.



(1) Working segment
(2) Output segment

Drawing curves

In reference mode, you have already generated a view which is important to you.

➪ You can set any output type, e.g. also SSD, in the working segment.

✧ Select the segment that contains your reference image.

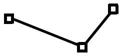
✧ Call up **Settings > Curved Mode**.

Or

✧ Activate the curve mode by clicking the **Curved Mode** button on the **Settings** tool card.

The program is in drawing mode and the cursor changes shape.

Polygon definition as the cut line



You can draw a cut line by entering several vertices.

✧ Click into the working segment (selected segment) with the left mouse key to define the beginning of the cut line.

✧ Define further points along the cut line by clicking each position at which you want the direction to change with the left mouse key.

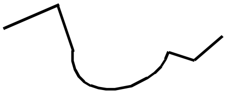
✧ Finish off the line by double-clicking with the left mouse key.

Drawing a line freehand

As an alternative, you can also draw structures freehand.

✧ Open up a curve by moving the mouse cursor over the image with the left mouse key pressed.

✧ Finish off the freehand line by double-clicking with the left mouse key.



For some applications, it can be necessary to connect a polygon definition with a freehand line and vice versa.

As long as you have not double-clicked the end point, you can mix the two methods, polygon definition and freehand line.

➪ The way the image is reconstructed depends on the direction in which the line is drawn. For example, if you draw the spinal canal starting from the top and moving downwards, the image that you produce is different to the one you produce when you draw the line from the bottom to the top (opposite way round).

Displaying images

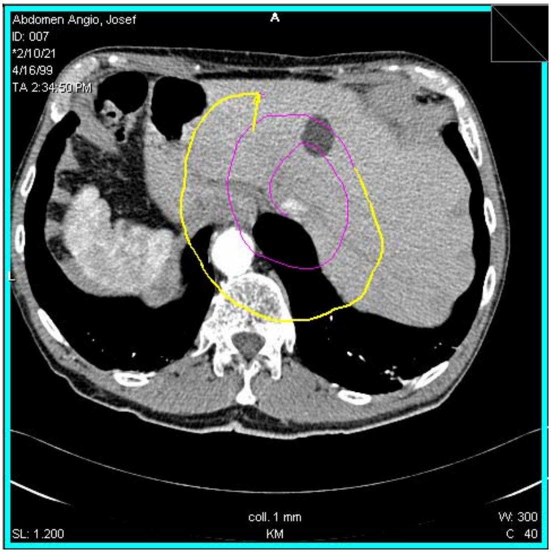
After you have completed your cut line, a new image is reconstructed in the output segment. In the reference image (working segment), the starting point of this image is marked by an arrow.

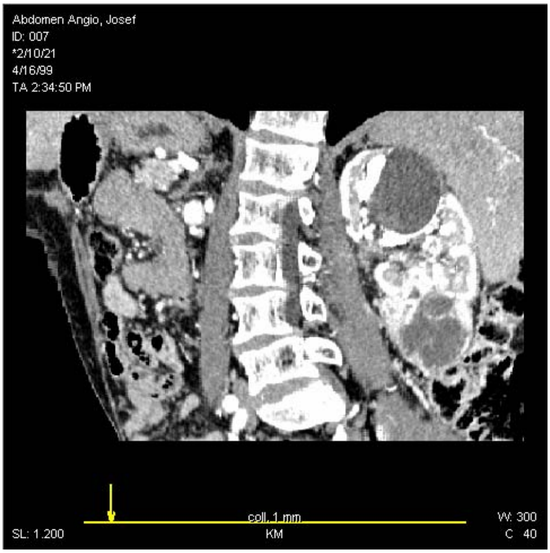
⇨ The orientation mark and the cutline are displayed as orientation aids.

Long cut lines

If you have drawn a very long cut line, it might not be possible to display the entire image in the output segment. Then, only the first part of the line is used to generate an image. This part is then highlighted in the working segment.

The starting point of the display is marked by an arrow.





CAUTION

Source of danger: Less orientation aids possible than in planar slice images

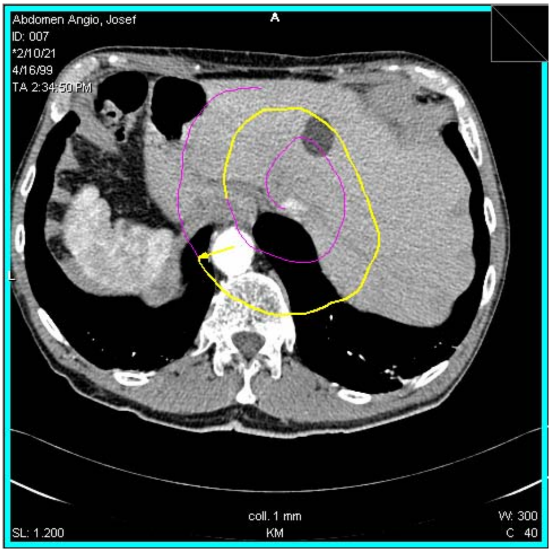
Consequence: wrong diagnosis

Remedy: The physician conducting the examination is responsible for the professional and correct interpretation of the reconstructed image.

Moving the displayed part of the line

✧ Move the starting point in the working segment to display further parts of the cut line by moving the arrow along the line with the mouse.

A new image is generated. In this way, you can draw the structures bit by bit over their entire extent.



Moving the entire line

Sometimes, you might want to move a curved cutline in the working segment to a new location.

✧ Place the mouse cursor on the line.

The mouse cursor changes shape.

✧ Move the entire line holding the left mouse key down.

A new image is displayed in the output segment.

➪ Delete a line by pressing the **Del** key.

➪ The direction in which you have drawn the curve into the working image is shown by an arrow on the resulting image

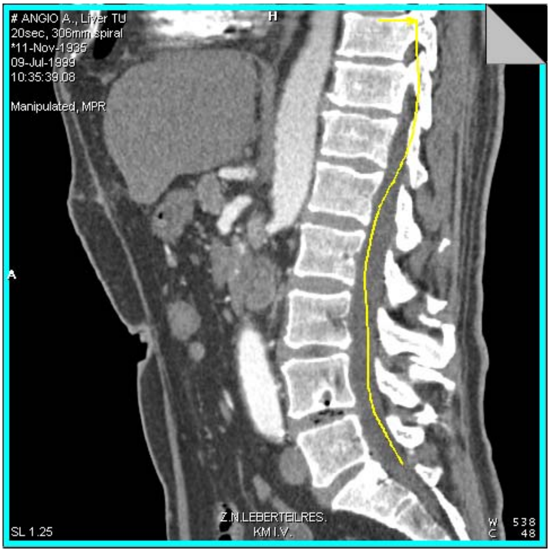
Moving a curve within the volume with the dog ear

While drawing you can also move the cutline within the volume data set layer by layer by paging with the dog ear of the working segment.

✧ Click on the outside field of the dog ear to move forwards.

Or

✧ Click on the inner field of the dog hear to move backwards.



Rotating images

✧ Call up **Image > Rotate Curved 90° +**, to rotate the image clockwise.
→ Page E.4–27, *Rotating images (Rotate)*

Or

✧ Call up **Image > Rotate Curved 90° -**, to rotate the image anti-clockwise.

Flipping images

✧ Call up **Image > Flip Curved Vertically**, to flip the image around a vertical axis.
→ Page E.4–30, *Flipping images (Flip)*

Or

✧ Call up **Image > Flip Curved Horizontally**, to flip the image around a horizontal axis.

CHAPTER
H.5

Maximum Intensity Projection (MIP)

The maximum intensity projection is often used for angiography, for example, to display the course of a blood vessel or a contrast medium injection. It is also used to punch (i.e. extract) volumes of interest (VOIs).

If other structures are obstructing the volumes of interest to you, it is useful to extract a VOI (volume of interest).

You can also create radial series in maximum intensity projection (MIP) from the reference mode.

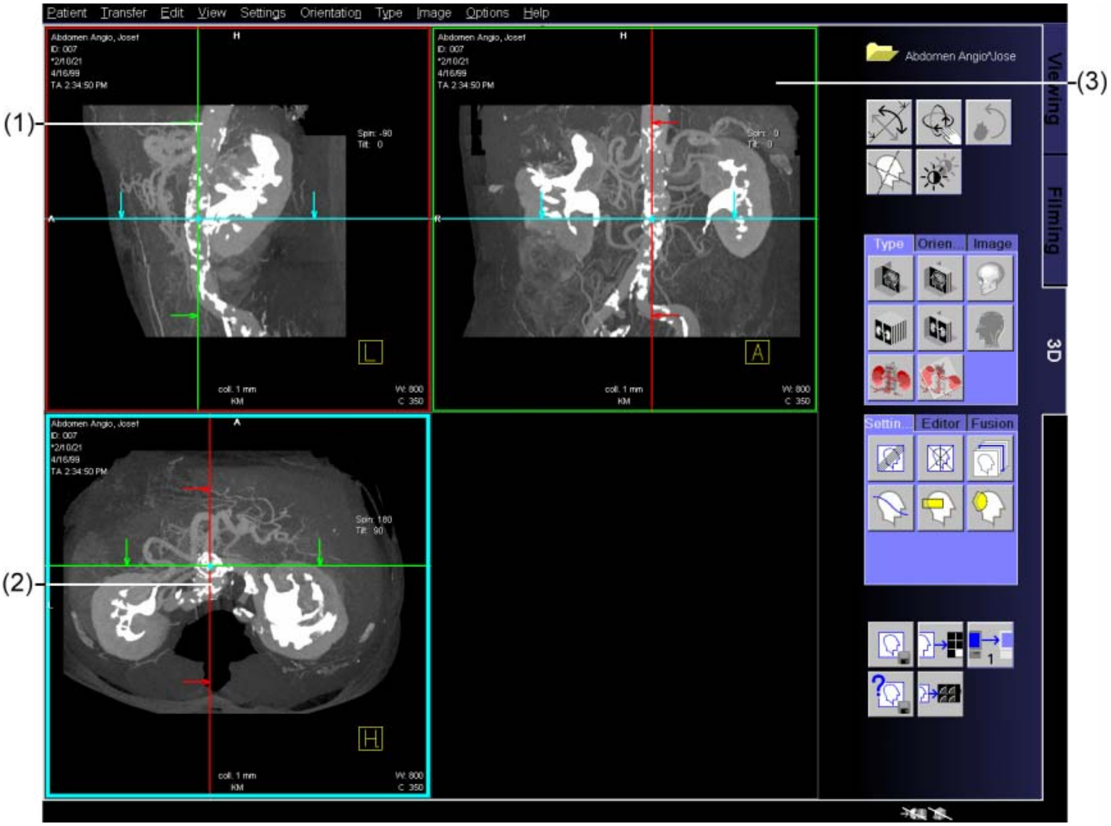
Transfer as MIP to 3D

You have selected a series of images for display in **MIP** and transferred them to the **3D** task card.

The series will shown in MIP display mode.

➩ If you have already loaded images onto the **3D** task card and have only switched back to another application temporarily, switch back to **3D** by clicking the tab.
→ Page H.2–4, *Calling the 3D task card*

➩ If you have finished processing your first 3D series and saved it, you can load the next marked series directly from the **Series List** (**Patient > Open Series List...**). If the last patient to have been processed is in 3D, a dialog box appears in which you can specify whether you wish to continue processing or load the new series.
→ Page H.2–11, *Other series from the Series List*



(1) Sagittal view
(2) Transversal view
(3) Coronal view

Extracting a volume of interest (VOI)

With a **volume of interest (VOI)**, you extract a volume of diagnostic interest to you, thus limiting the volume to be reconstructed to a partial volume.

You can extract a VOI (volume of interest) in one of the following ways:

❏ Position and delimit a cuboid VOI (**VOI Clipbox**)

❏ Draw a freehand VOI (**VOI Punch Mode**)

Using the VOI clipbox

If you are in reference mode you must activate VOI clipbox mode.

✧ Call up **Settings > VOI Clipbox** to access VOI mode.

Or

✧ Click on the button **VOI Clipbox** on the **Settings** subtask card.

The entire data set with the default VOI delimitation appears in the output segment. The rectangle shows the preset delimitation of the VOI.

Changing the size

In the bottom right-hand segment, you initially see a predefined cuboid VOI. You can use this for processing or changing its size and position as required.

✧ You can change the size by clicking on one of the boundary lines and moving the grab handles while holding the mouse key down.

Moving the VOI

✧ Change the position of the VOI by placing the mouse pointer on the border around the selected VOI, not on a handle.

✧ Move the VOI while holding down the left mouse button.

Setting standard views

You can change the default views in the three segments in any possible way. This way you control the position of the VOI along all three axes.

✧ Select the result segment.

✧ Select the required standard view using the buttons on the **Orientation** tool card or in the **Orientation** menu.
→ Page H.3–27, *Setting standard views*

➩ The views are perpendicular or parallel to the scan direction of the data set, but might not be perpendicular to the patient coordinate system.

Rotating the VOI

✧ Click on the **Rotate Images** button on the **VOI Definition** dialog box to activate rotation mode.

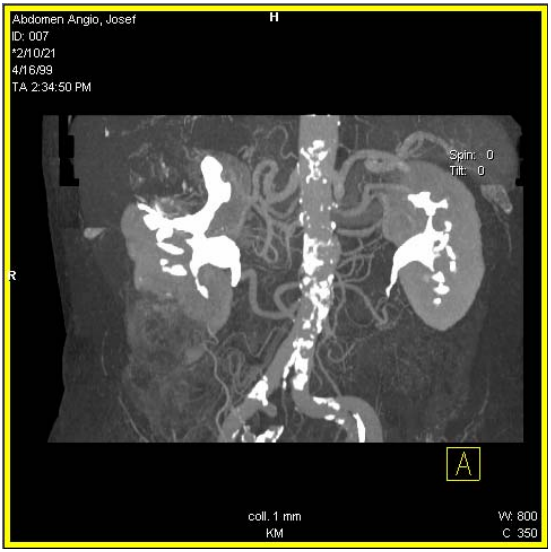
✧ Place the mouse cursor in the bottom right-hand segment.

The mouse point changes shape.

✧ Move the mouse cursor holding the left mouse key down and rotate the VOI.

❑ Moving the mouse up or down tilts the object in 90°-steps.

❑ Moving the mouse to the left or right rotates the object in 90°-steps.



Activating VOI punch mode

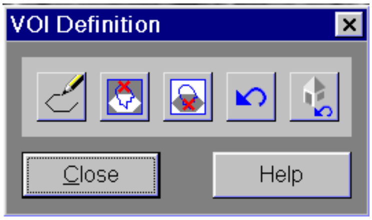
Once you have positioned and delimited the VOI using the **VOI Clipbox**, switch to **VOI Punch Mode**.

✧ Call up **Settings > VOI Punch Mode** to access VOI punch mode.

Or

✧ Click on button **VOI Punch Mode** on subtask card **Settings**.

The dialog box **VOI Definition** appears in the output segment.



In this dialog box, you will find a number of buttons which you can use to extract and process a freehand VOI.

The individual buttons perform the following functions (from left to right):

❑ Drawing a freehand VOI
→ Page H.5–11, *Drawing a freehand line*

❑ Punching a freehand VOI
→ Page H.5–12, *Punching a freehand VOI*

❑ Cutting out a freehand VOI
→ Page H.5–14, *Cutting out a freehand VOI*

❑ Undoing last command
→ Page H.5–17, *Undo Last Step*

❑ Undoing all
→ Page H.5–17, *Undo All*

Defining a freehand VOI

If you have adapted the view and size of the rectangular VOI to your requirements, you can draw a freehand curve (polygon) in it. With this irregular VOI you can define the contours along which you can later cut out or reveal parts of images.

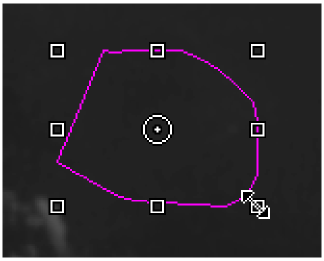
✧ Select the reference segment in which you want to define the freehand VOI.

Drawing a freehand line

- Click on **Draw New** in the **VOI Definition** dialog box to activate the drawing mode.
- Click on the required starting point of the line with the left mouse key.
- Click on any other point in the image at which you want the curve to change direction.

Or

- Draw a continuous line by dragging the mouse cursor over the image holding the left mouse key down.
- Complete your line with a double-click.



The starting and end point of the line are connected. The line thus becomes a closed polygon definition and includes an area. You can now select the curve and change its position and size.

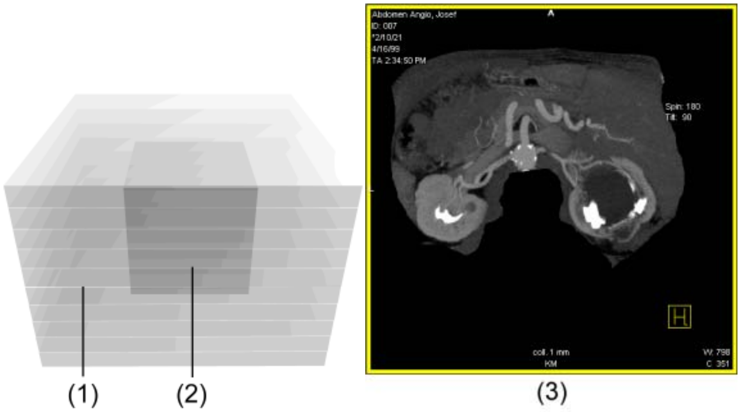
Punching a freehand VOI

In angiography, it is often of diagnostic interest only to display the highlighted blood vessels in the image, because other details can obstruct the projection.

✧ Draw a freehand VOI around the volume of interest to you.

✧ Click on the **Keep Inside** button.

All volume areas of the rectangular VOI *outside* the freehand VOI are deleted.



(1) Volume data set
(2) Rectangular VOI
(3) Punched freehand VOI

The inside of the rectangular VOI is processed, not the volume data set that surrounds the VOI. The VOI is used as a sort of protection for the remaining volume, because you can only work within the rectangular VOI.

➩ Once you have cut out the contour, the program automatically switches to drawing mode.
→ Page H.5–10, *Defining a freehand VOI*

Cutting out a freehand VOI

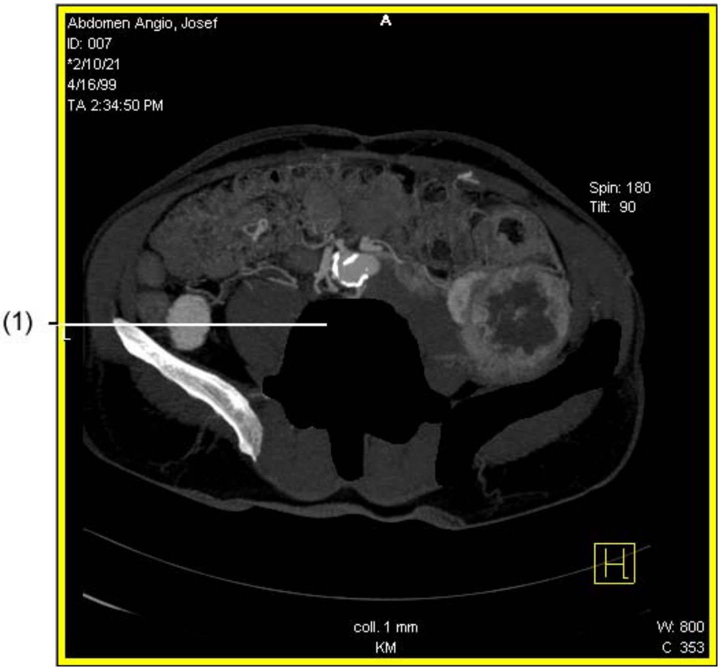
You can also proceed in the opposite manner and expose the VOI by cutting out the uninteresting parts of the volume.

To do this, you will usually proceed in small steps, cutting out as many small areas as necessary until only those structures remain that are of interest to you.

✧ Draw a freehand VOI around the area that you want to remove.

✧ Click on the **Remove Inside** button.

The area *inside* the polygon is cut out and removed.



(1) The freehand VOIs cut through the volume of the rectangular VOI in the viewing direction

Deleting a freehand line

You can delete freehand lines that are not as you require them.

✧ Select the line by clicking on it.

✧ Delete the line by pressing the **Del** key on your keyboard.

The program is switched back to drawing mode.

Undoing deletion of VOIs

If you accidentally cut out too much when working on a VOI, you can undo your processing steps (only **Keep Inside** and **Remove Inside**).

Undo Last Step

✧ Click on the **Undo Last Step** button in the **VOI Definition** dialog box.

Undo All

✧ Click on the **Undo All** button in the **VOI Definition** dialog box.

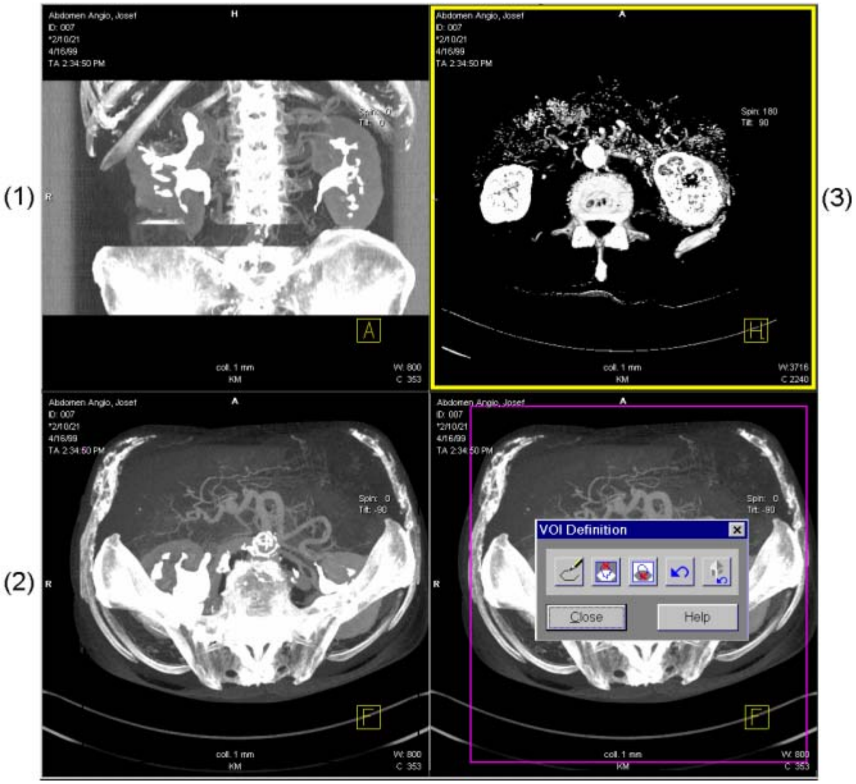
The graphic is reset to the state in which you found it before processing.

All steps performed so for are undone.

Combining the MIP and SSD output types

When extracting VOIs, you can combine the output types **MIP** and **SSD** (surface shaded display) in different segments to extract and reveal the volume of interest especially clearly.

For example, select the **MIP** display in the two left-hand segments to define the size and position of your VOI in these images and then have the result displayed in the top right-hand segment in surface shaded display.
→ Page H.3–39, *Defining output types*



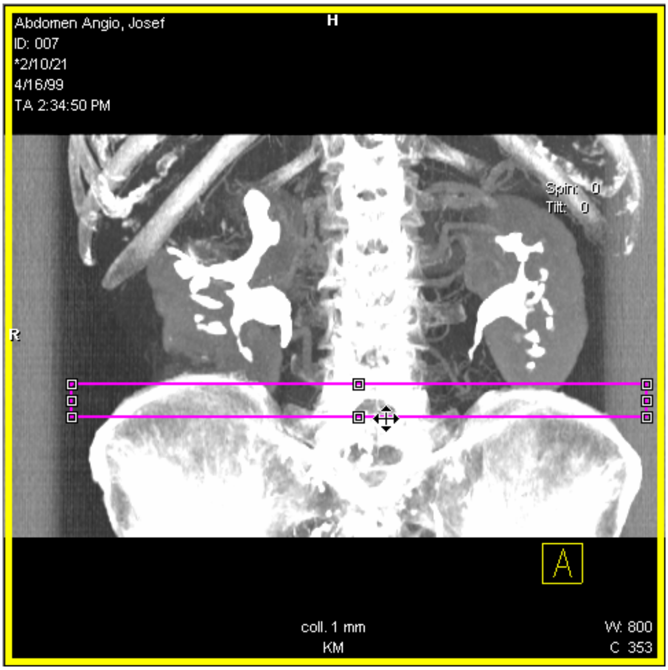
(1) MIP type
(2) MIP type
(3) SSD type

Generating complex VOIs

If you want to punch very complex structures that extend through the entire reconstructible volume in an irregular shape, you combine cuboid and freehand VOIs in several substeps.

In each step you select a rectangular VOI and then punch the relevant structure in this VOI. This way you proceed through the entire reconstructible volume. In the end you have the system put the various segments of the complex VOI structure together.

✧ First define a relatively narrow cuboid VOI in the bottom right-hand image area.



Abdomen Angio, Josef
ID: 007
*2/10/21
4/16/99
TA 2:34:50 PM

Spin: 0
Tilt: 0

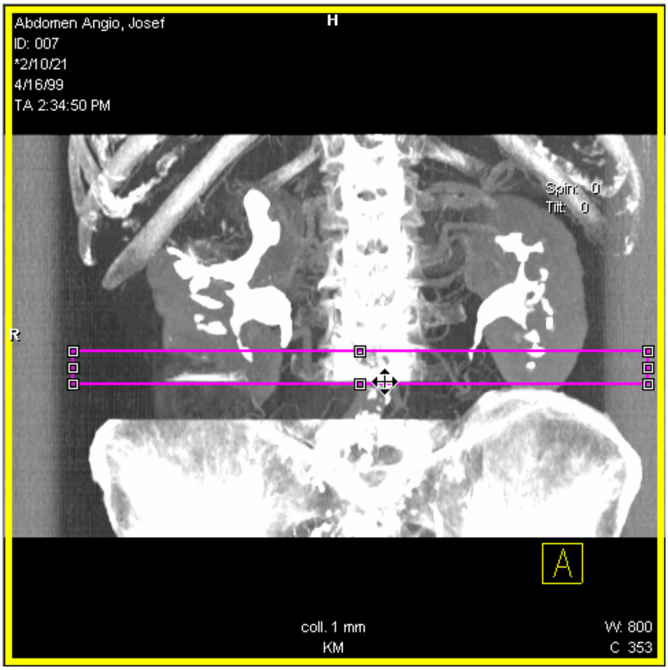
coll. 1 mm
KM

W: 800
C 353

This VOI is displayed in the other segments of the screen.

✧ Punch the structures of interest to you for the VOI freehand in an other image segment.
→ Page H.5–12, *Punching a freehand VOI*

✧ Now move the rectangles in the lower right image segment.

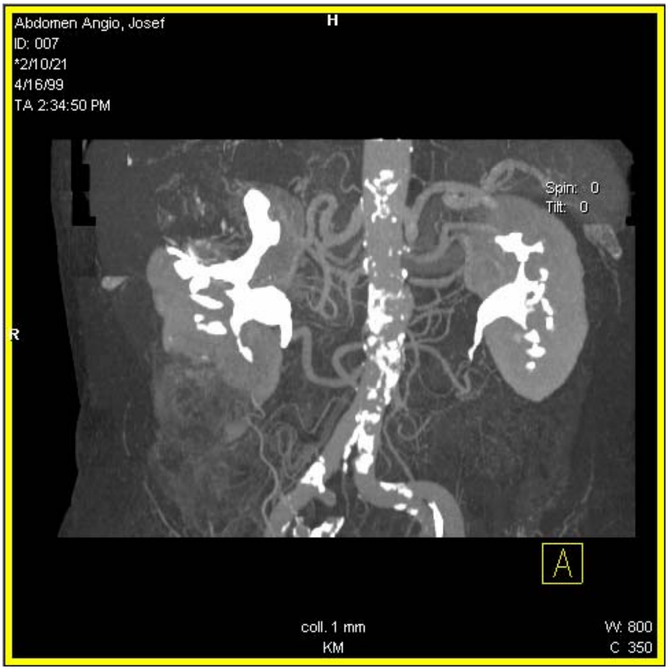


✧ Also punch the structure you require in this second rectangular VOI in freehand technique.

✧ Continue until you have processed the entire volume of interest to you.

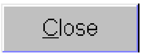
✧ Now drag the rectangle in the lower right image segment out to a size suitable for your diagnostic problem again.

All your freehand VOIs are now combined.



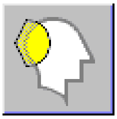
Exiting VOI mode

When you have finished punching your VOI, return to reference mode.



✧ Click on the **Close** button in the **VOI Definition** dialog box.

Or



✧ Click on the button on the **Settings** subtask card.

VOI mode is terminated. The effective VOI, i.e. the last status of your VOI, is saved.

Generating a radial series from MIP displays

Using radial projections, you can view the volume of interest to you from various angles.

Once you have generated a sufficient number of images in a complete circle, you can play them back as a movie on the **Viewing** task card as if you were “walking round” the volume or partial volume of interest. You can achieve the same effect by clicking on the dog ear in the output segment while keeping the mouse button pressed.
→ Page E.3–18, *Animated images (Movie)*

Generating radial series

For a description of how to generate radial series of MIP projections, please see the following chapters:

→ Page H.3–72, *Setting radial projections and views*

➪ On the basis of the MIP display, you can also generate parallel images or curved sections. However, the results are always displayed as MPR images. Generation of parallel series and curved sections is therefore described in the following chapters:

→ Page H.3–51, *Generating parallel images*
→ Page H.4–7, *Generating curved slices*

Defining the MIP slice thickness (MIP Thin)

For maximum intensity projection, the entire volume of the data set is normally used. Sometimes you will only want to use a part of the volume for the projection. For example, you may want to cut out interfering structures.

Selecting a reference image

In the reference segment, you can define the view of your reference image.

✧ First select a reference segment.

✧ Change the position of the image until it meets your requirements.

Starting MIP Thin

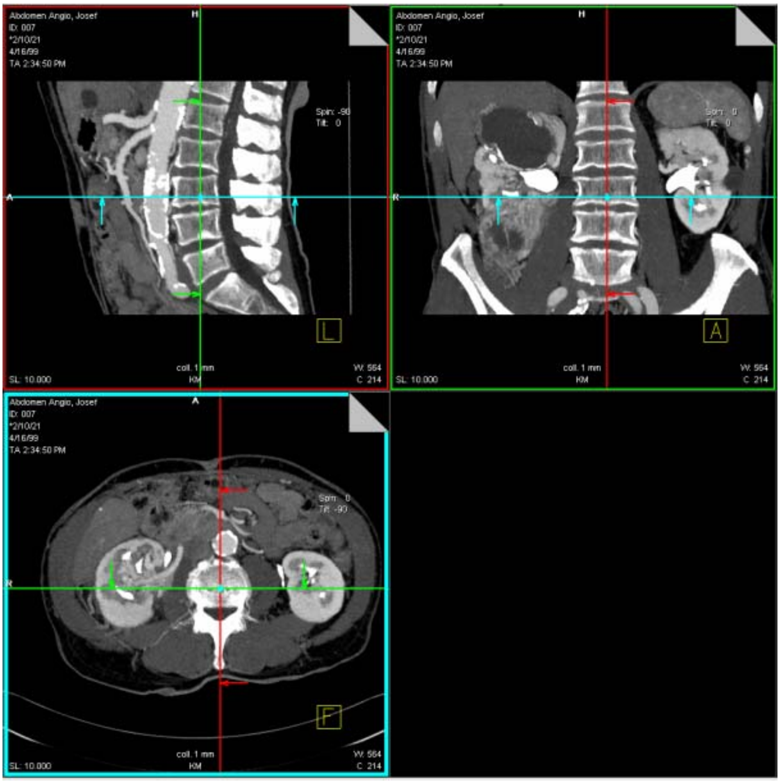
You can set **MIP Thin** in one, two, or all three reference segments.

✧ Call up **Type > MIP Thin** to set MIP Thin output type.

Or

✧ Click on the **MIP Thin** button on the **Type** tool card.

In the reference segment, an MIP Thin display is shown with the standard settings.

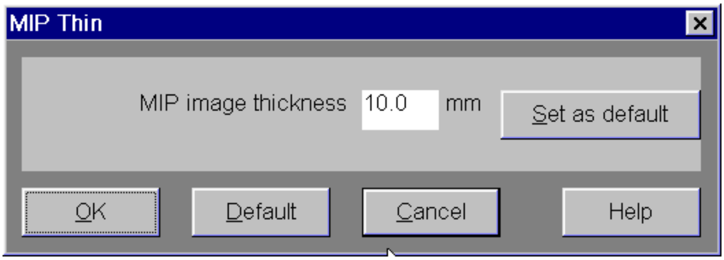


Changing slice thickness

✧ Call up **Type > MIP Thickness** to display the **MIP Thin** dialog box to set the slice thickness.

Or

✧ Click on the **MIP Thin** button on the **Type** subtask card with the *right* mouse button.



MIP Thin

MIP image thickness 10.0 mm

✧ Enter the thickness of the initial slice to be used for the projection in mm.

OK

✧ Confirm your entry with **OK**.

Or

Default

✧ Click on **Default** to set the default value (10 mm) for **Image thickness**.

⇨ The selected setting is applied to *all subsequent* MIP thin slice reconstructions. Only when you reconstruct a new series is a new slice thickness used.

The value for the **MIP image thickness** is always filmed and stored with the image.

✧ Click on **Set as default** to store a new default value.

✧ When you load a new data set, the stored default value is used.

Generating series of MIP Thin images

For the MIP Thin output type too, you can generate parallel, radial, and expanded series of images. In this way, you divide the volume data set into partial volumes with a predefined thickness. MIP Thin images are then reconstructed from these partial volumes.

Parallel MIP Thin series

The structures (bones) that might be an obstruction in a maximum intensity projection usually only extend over a small part of the volume data set. With parallel MIP images, you can, for example, ascertain where the obstructing structures end and where you can generate usable MIP images in the volume data set.

✧ Generate and process images of parallel MIP Thin series as described in the following chapters:

→ Page H.3–51, *Generating parallel images*
→ Page H.3–59, *Postprocessing series of parallel images*

Radial MIP Thin series

✧ Generate and process images of radial MIP Thin series as described in the following chapters:

→ Page H.3–64, *Generating radial images*
→ Page H.3–70, *Postprocessing a radial range*

Generating an expanded MIP Thin range

✧ Generate and process images of parallel MIP Thin images of an expanded range as described in the following chapters:

→ Page H.3–60, *Generating an expanded range*

CHAPTER
H.6

Reconstructing Shaded Surfaces (SSD)

Surface shaded display (SSD) is based on the extraction of gray scales between two predefined thresholds. The SSD output type reconstructs surface shaded structures and displays them in three dimensions.

SSD images are especially suitable for displaying bone structures and blood vessels filled with contrast medium.

As threshold values for surface extraction in SSD, modality-specific defaults stored in your system are commonly used.

If these defaults are not appropriate for your diagnostic problem, you can adapt them individually. In this way, you can display the structures of interest to you in an optimum way.

Same as with multiplanar reconstruction (MPR) and maximum intensity projection (MIP), you can generate a new radial series on the basis of SSD displays and save these images for further processing.

⇨ SSD images only have one window level.

Transferring as SSD to 3D

You have selected a series of images for display in **MPR** and transferred them to the **3D** task card.

The series will be loaded and shown in SSD display mode.

⇨ If you have already loaded images onto the **3D** task card and have only switched back to another application temporarily, switch back to **3D** by clicking the tab.
→ Page H.2–4, *Calling the 3D task card*

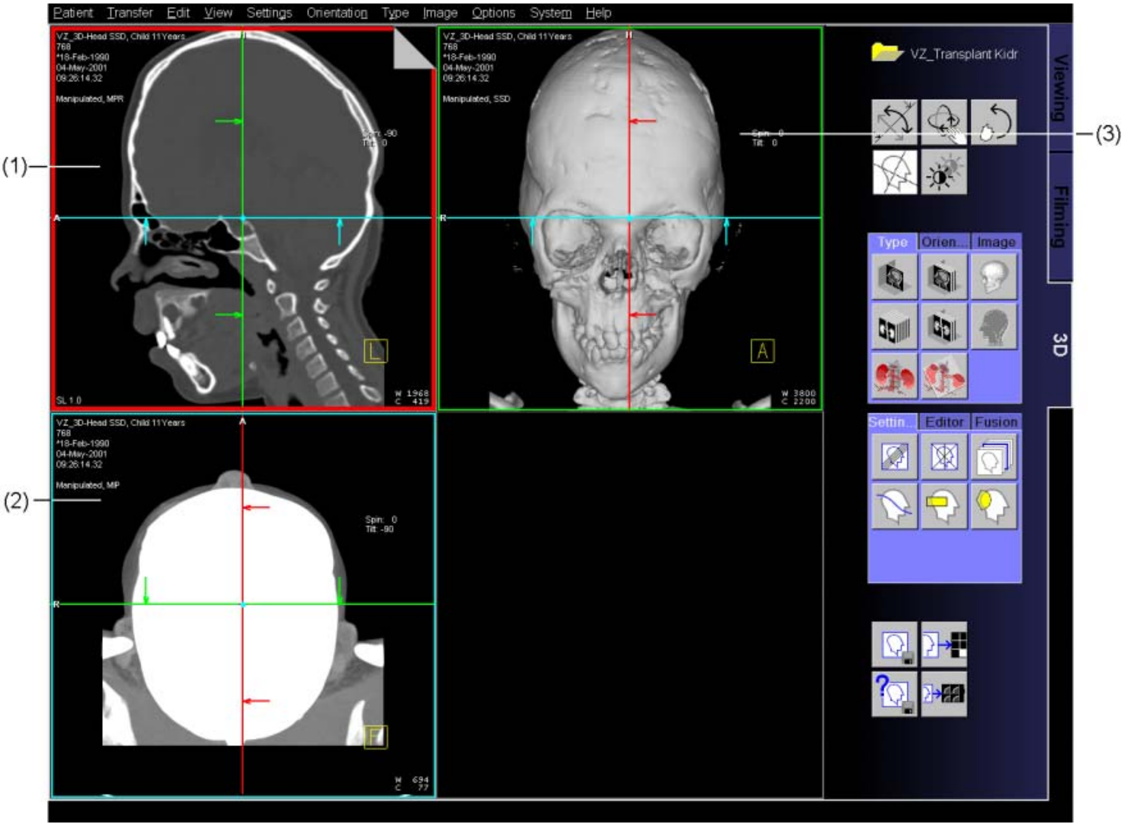
⇨ If you have finished processing your first 3D series and saved it, you can load the next marked series directly from the **Series List** (**Patient > Open Series List...**). If the last patient to have been processed is in 3D, a dialog box appears in which you can specify whether you wish to continue processing or load the new series.
→ Page H.2–11, *Other series from the Series List*

A message box informs you of the progress of surface reconstruction. This progress display is only displayed the first time you call up SSD and whenever you have changed the threshold values. If you do not change the threshold values, the SSD images are reconstructed immediately.

As long as the message box is displayed you can cancel the operation with the **Cancel** button.

Once reconstruction has been completed, surface shaded display is shown in the all segments in the set viewing direction.

In each of the three reference segments, an SSD display is shown in the standard view.



(1) Sagittal view
(2) Transversal view
(3) Coronal view

SSD reconstruction with changed thresholds

If the SSD reconstruction based on the default threshold values in the system is not appropriate for your diagnostic problem, you can adapt these values. You can then reconstruct your surface image again.

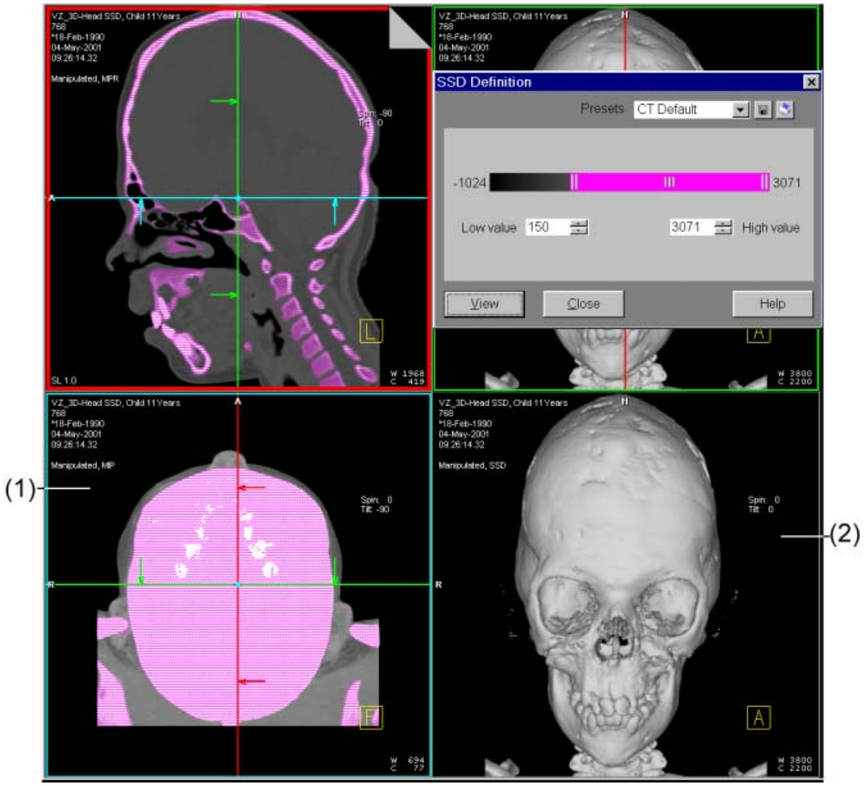
✧ Call up **Type > SSD Definition...** to switch to threshold mode.

Or

✧ Click on button **SSD** on subtask card **Type** with the right mouse key.

Areas within the set threshold values are marked in all images of output type MPR or MIP.

In the output segment, an SSD image is displayed with reduced quality which is based on the last extraction or the default threshold values.



SSD Definition

Presets: CT Default

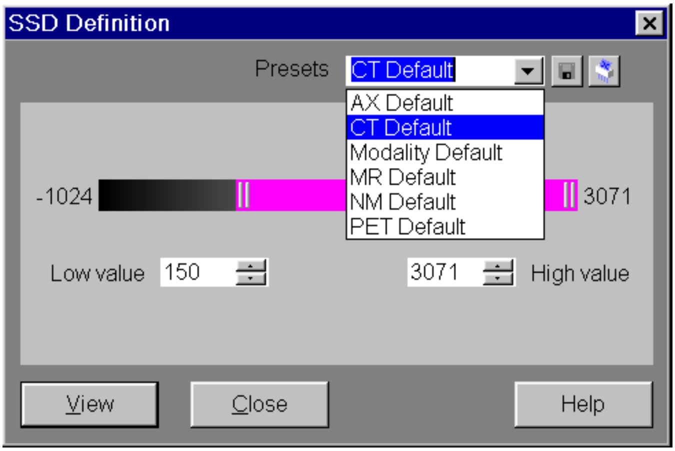
-1024 … 3071

Low value: 150

High value: 3071

(1) Highlighted pixels
(2) SSD image

The **Threshold** dialog box is displayed.



SSD Definition

Presets: CT Default

Low value: 150

High value: 3071

In the **Threshold** dialog box, the preset or last used threshold values are displayed for **SSD** extraction.

3071 High value

Low value 150

✧ Enter new threshold values in the input fields and confirm with the **Return** key.

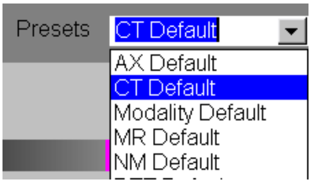
The threshold values entered are applied to the displays in the reference segments.

Another way to change the threshold values is:

✧ Click on the slider with the left mouse key and drag the marker to the right or to the left to increase or reduce the threshold value.

The new threshold values are immediately applied whenever they are changed with the slider or arrow keys and appear in the **Upper** or **Lower Threshold** fields.

Assigning threshold values

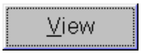


You can see predefined lower and upper threshold values in the **Presets** list.

✧ Select the threshold value that is appropriate for your diagnostic problem by clicking on the entry in the list.

The values of the list entry are displayed in the **Lower** and **Upper Threshold** fields. The pixels that are within the threshold values are highlighted in color in the reference segments.

➪ For how to generate predefined threshold values, see:
→ Page H.6–10, *Creating and processing predefined threshold values*



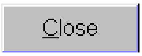
✧ Click on the **View** button after you have found the desired threshold values.

The SSD display in the output segment is now recalculated. A process indicator tells you how extraction is progressing.

When the procedure is complete an SSD image based on your new threshold values is displayed in the output segment.

➪ You can rotate and move the resulting image in any way you wish.

Returning to reference mode



If the new surface display is as you require it, close the **Threshold** dialog box and return to reference mode.

✧ Click on the **Close** button.

In reference mode, all reference segments are shown in the display last saved before you started threshold mode.

Now select output type SSD for one of these reference segments. You can see a surface shaded image based on your new threshold values.

Creating and processing predefined threshold values

With predefined lower and upper threshold values, you can store optimized threshold values for different diagnostic problems.

Creating new threshold values

The lower and upper threshold values are listed under their designation in the **Presets** list in the **Threshold** dialog box.

Bone

The upper field of the **Presets** list is initially empty or contains the last entry selected from the **Presets** list.

✧ Overwrite the old designation or enter a new designation in the empty field.

✧ Press the **Return** key to apply the new designation.

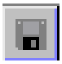
The overwritten designation is still also in the **Presets** list.

✧ Now adapt the values with the sliders or the arrow keys for the upper or lower threshold values.

Or

✧ Enter the threshold values in the **Upper** and **Lower Threshold** value input fields.

✧ Confirm the numerical values you have entered by pressing the **Return** key on your keyboard to check whether the values meet your requirements.



✧ Save the new threshold values by clicking on the button.

Processing threshold values

If a pair of threshold values no longer meets your requirements, you can change the two values at any time.

✧ First select a pair of threshold values by clicking on it in the **Presets** list.

The values are displayed in the **Lower** and **Upper Threshold** fields.

✧ Adapt the threshold values to your requirements with the sliders.

Or

✧ Enter the values in the **Lower** and **Upper Threshold** input fields.

✧ Apply the settings by pressing the **Return** key.

✧ Save the new threshold values by clicking on the button.

Deleting a pair of threshold values

You should delete lower and upper threshold values that you will no longer require in future. In this way, you keep your threshold value list down to a manageable size.

✧ First select a pair of threshold values by clicking on it in the **Presets** list in the **Threshold** dialog box.

✧ Click on the button.

The entry is deleted.

➩ You cannot delete the modality-specific default entries.

Generating a radial series of SSD displays

Using radial projections, you can generate views of your surface structure from different angles.

You can generate radial series based either on the entire volume data set or on a partial volume (VOI, volume of interest) that you have extracted earlier.
→ Page H.5–4, *Extracting a volume of interest (VOI)*

If you generate enough images forming a complete circle, you can play them back as a movie on the **Viewing** task card and, in this way, you can “walk around” your surface structure.
→ Page E.3–18, *Animated images (Movie)*

Generating radial series

You will find a description of how to generate radial series from SSD projections in the following chapters:

→ Page H.3–71, *Series of radial projections and views*

Parallel tomographic images and curved sections

On the basis of the SSD display, you can also generate parallel images and curved sections. However, the results are always displayed as MPR images. Generation of parallel series and curved sections is therefore described in the following chapters:

→ Page H.3–51, *Generating parallel images*
→ Page H.4–7, *Generating curved slices*

CHAPTER H.7

Volume Rendering Technique (VRT)

You will use the **Volume Rendering Technique (VRT)** to obtain more precise representation and separation of tissue types. In that way you can obtain a three-dimensional representation.

To highlight certain aspects of the anatomical region, you can change the color, brightness, and transparency of different areas.

As display parameters for the **VRT** view, customary default settings are stored on your system in the **VRT Gallery**.

If the default settings are not appropriate for your diagnostic problem, you can alter them individually. In that way you can emphasize the structures of interest in an optimum way.

➩ The Volume Rendering Technique is only possible if the depth of color of your system is at least 24 bits.

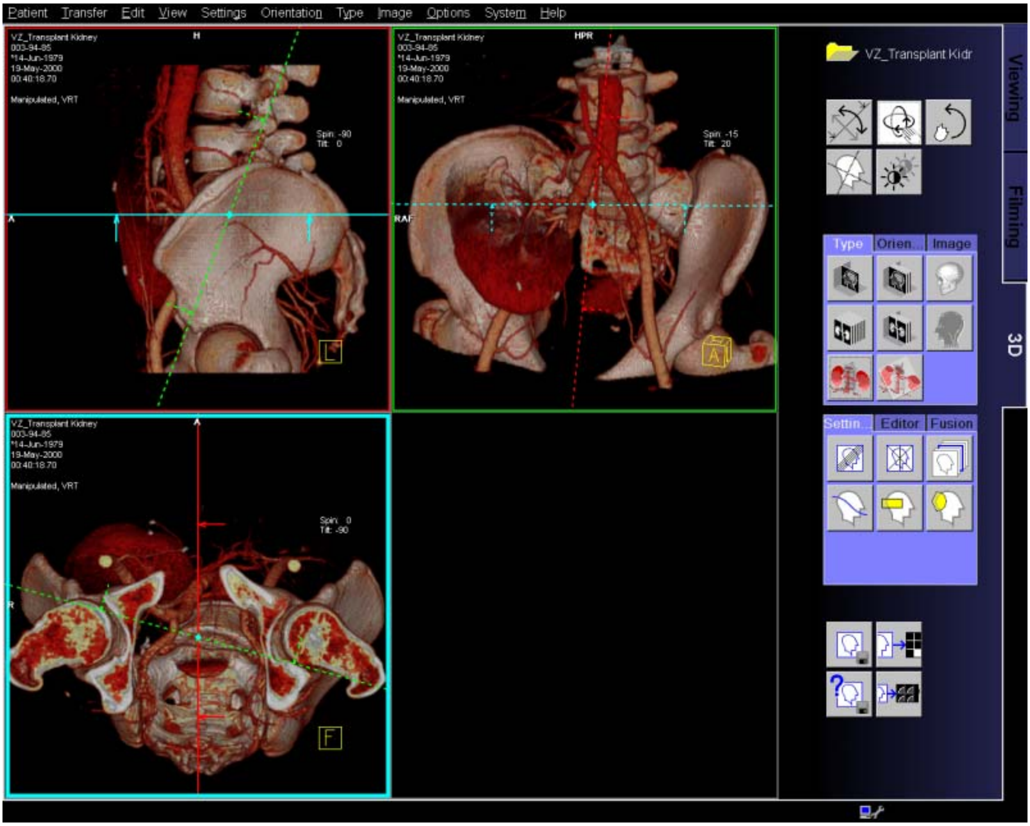
Transferring to 3D as VRT

You have transferred a series of images to the **3D** task card from the **Patient Browser,** the **Viewer** task card, or the **Series List** dialog box in **VRT** mode.

The **3D** task card is displayed in the **VRT** view.

➪ If you have already loaded images into the **3D** task card and had only switched to another application temporarily, you can now switch back to **3D** by clicking on the card’s tab.
→ Page H.2–4, *Calling the 3D task card*

➪ If you have completed processing and storage of your first 3D series, you can load the next preregistered series directly from the **3D** task card (**Patient > Open Series List...**). If the patient to have been processed last is still in **3D**, a dialog box is displayed. In it you can decide whether to go ahead with processing or to load the new series.
→ Page H.2–11, *Other series from the Series List*


Patient Transfer Edit View Settings Orientation Type Image Options System Help
VZ_Transplant Kidney
003-94-85
*14-Jun-1979
19-May-2000
00:40:18.70
Manipulated, VRT
H
Spin: -90
Tilt: 0
L
HPR
Spin: -15
Tilt: 20
RAF
A
Spin: 0
Tilt: -90
R
F
VZ_Transplant Kidr
Viewing
Filming
3D
Type
Orien...
Image
Settin...
Editor
Fusion

Assigning parameter sets

In the **Volume Rendering Technique**, display of a volume data set is defined by the properties color, brightness, and transparency. The color and the brightness determine the light emitted by the object. With the transparency you can define how the object absorbs and reflects light.

The way in which an object absorbs, emits, or reflects light depends on the properties of the data set. These can be different within three-dimensional space.

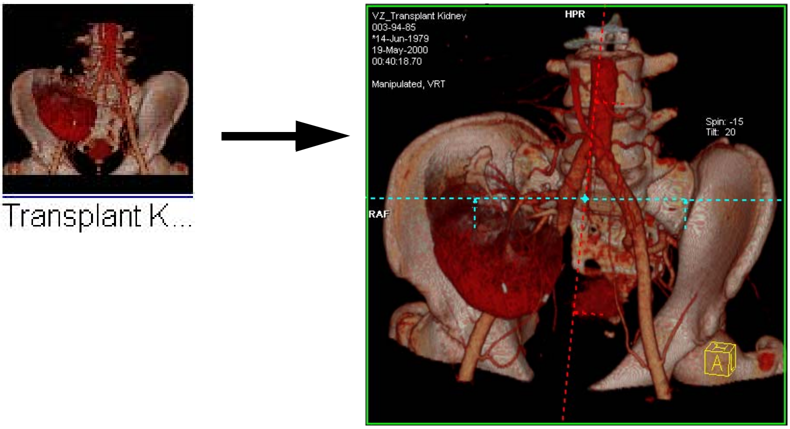
Information about the color, brightness, and light are not contained in the original data sets. The CT value or MR signal value must therefore be assigned to the properties used in **VRT** mode. This is done by subdividing value ranges into tissue classes to which certain display properties are assigned.

The tissue classes and their representation are defined in parameter sets that are stored in the **VRT Gallery**. These parameter sets are automatically or manually assigned to the original data set in **VRT** mode.

Automatic assignment of the parameter set

Each parameter set is assigned a name.

As soon as you load the images into **VRT** mode, the system will look for a parameter set with the same name (e.g. head) in the **VRT Gallery**. If a parameter set is found, the preset tissue classes are transferred to the image.



If there is no appropriate parameter set in the **VRT Gallery**, the **VRT** image is displayed with the last parameter set to have been selected from the **VRT Gallery**.

Assigning a parameter set manually

If the **VRT** display with the automatically assigned parameter set does not meet your expectations, select another parameter set from the **VRT Gallery**.

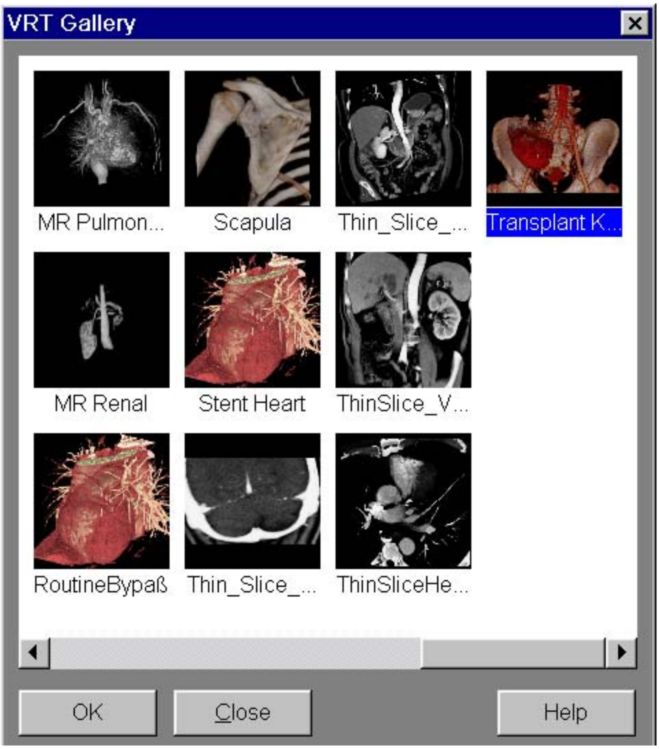
Opening the VRT Gallery

✧ Call up **Type > VRT Gallery...** to display the **VRT Gallery** dialog box.

Or

✧ Click on the **VRT** button on the **Type** subtask card with the right mouse key.

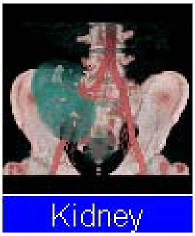
The **VRT Gallery** dialog box is displayed. Within the **VRT Gallery** the parameter data sets are arranged alphabetically from top left to bottom right.

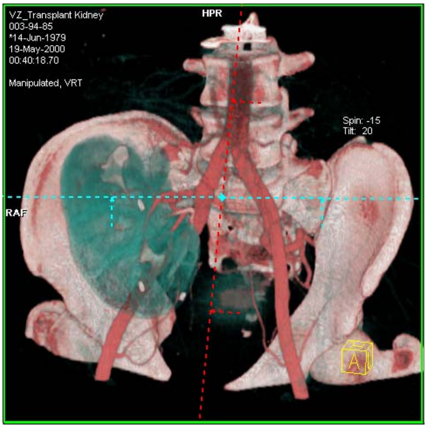


➪ If the content of the window is not displayed in its entirety, you can have the other parameter data sets displayed along the bottom edge of the window with the scroll bar.

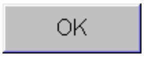
Assigning a parameter set

✧ Click on a parameter set with the left mouse key to transfer the predefined tissue classes to the current **VRT** display.





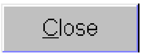
Closing the VRT Gallery



✧ Close the dialog box with the **OK** button.

The **VRT** image is displayed with the selected parameter set.

Or



✧ Press the **Close** button**.**

The **VRT Gallery** is closed. The **VRT** display remains unchanged.

Creating and editing parameter sets

The **VRT Gallery** provides various parameter sets for different types of image data sets. With the **VRT Definition** you can create additional parameter sets and edit existing parameter sets. In that way, you can expand the **VRT Gallery** considerably and will easily be able to assign parameter settings that are tailored to your diagnostic problem.

Dialog box VRT Definition

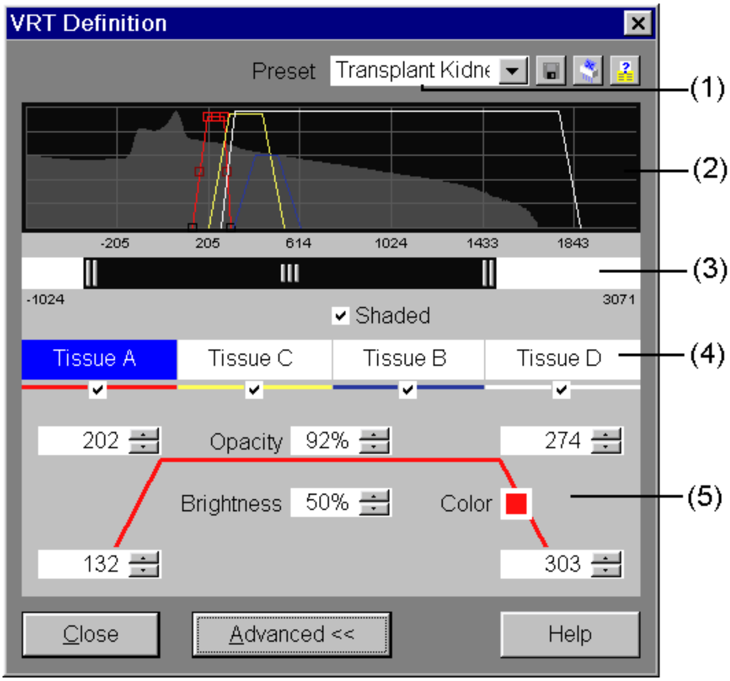
The **VRT Gallery** contains a number of predefined parameter data sets. Each parameter set corresponds to a special tissue class that you can define individually in the **VRT Definition**.

Calling up VRT Definition

✧ Call up **Type > VRT Definition...** to switch to the **VRT Definition** dialog box.

➪ You can have both dialog boxes **VRT Definition** and **VRT Gallery** open at the same time.
Changes made in the **VRT Definition** are applied in the **VRT Gallery** immediately.

VRT Definition



(1) List of parameter sets

(2) Graphic setting of the transfer function in the histogram

(3) Slider for zooming the histogram area in or out

(4) Tissue classes

(5) Numerical setting of the transfer functions (transparency, color, brightness)

Displaying the numerical setting range

It is possible to process the parameter sets both graphically in the histogram and numerically. For numerical input you can display the numerical setting area, if it was not already displayed when you called up the **VRT Definition**.

✧ Click on the **Advanced >>** button.

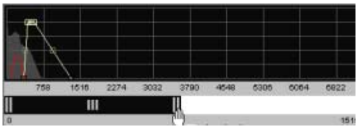
The **VRT Definition** dialog box is enlarged so you can edit the input fields for numerical processing.

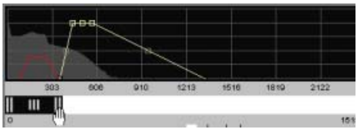
➩ If you want to hide the numerical setting area, simply click on the **Advanced <<** button again.

Adapt the graphic setting area

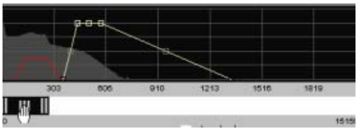
Depending on the modality, the examination data only covers a limited pixel range that is then evaluated in **VRT** mode. In the histogram window, the complete value range is initially displayed. Using the slider you can zoom the range of examination data and center it in the histogram. In that way, you can make graphic processing of the parameter set easier using the displayed trapezoids that are assigned to each tissue class.

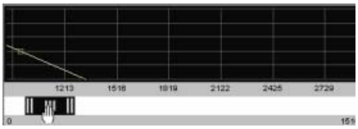
✧ To enlarge or reduce the histogram range drag the outer border of the slider with the mouse.





✧ Slide the central mark of the slider to change the position of the histogram.





Editing a parameter set

You can edit the parameter set by setting the following properties for various tissue classes:

☐ Transparency
☐ Brightness
☐ Color
☐ Signal intensity /HU values

➩ When you enter a new transparency value, brightness value, or a new color, the **VRT** display also changes immediately.

In a parameter set you can define up to four different tissue classes.

Selecting a parameter set

First select the parameter set that you want to edit or whose settings are very similar to the new parameter set you want to create.

✧ Select a parameter set from the selection list.

✧ Overwrite the name of the parameter set with another designation if you want to created a new parameter data set.

Selecting tissue classes

In a parameter set, you can define up to four different tissue classes.

✧ Select the required number of tissue classes using the check boxes.

For each tissue class, a trapezoid is displayed in the histogram.

To delete a tissue class, simply deselect it.

In the **VRT** image, this tissue class is then no longer displayed.

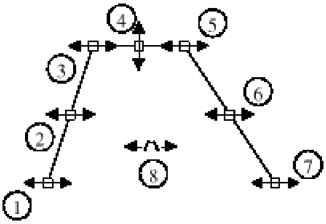
✧ Then click on the tissue class whose display you want to change.

Or

✧ Click on the trapezoid associated with it in the histogram.

Setting a value range

By changing the corner values of the trapezoid in the histogram, you can alter the position and size of the value range that is assigned to a tissue class. This is comparable with setting window values (center, wide).

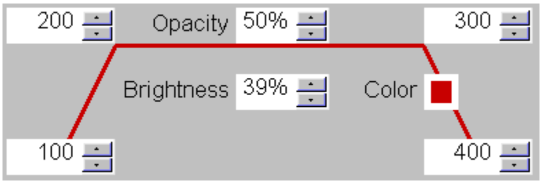


✧ Click on a trapezoid with the left mouse key.

✧ Slide one of the handles to the side (but not 4) with the mouse key.

Or

✧ Enter the value you require in the relevant spin box.



200

Opacity 50%

300

Brightness 39%

Color 🟥

100

400

➩ If the values in the spin box change, display of the trapezoid also changes.

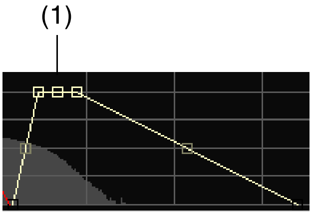
Transparency


Opacity 50%

✧ Set the transparency that you want the tissue to have using the spin box.

➩ You can enter values from 0% (transparent) to 100% (opaque).

Or



✧ Slide the center handle (1) of the trapezoid up or down in the histogram.

Brightness


Brightness 39%

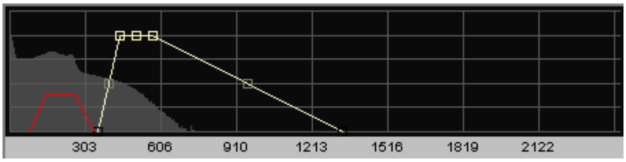
✧ Use the spin box to set the brightness you want the tissue to have.

➩ The brightness control defines the gray scale value of the tissue displayed. It ranges from 0% (black) to 100% (white).

Color

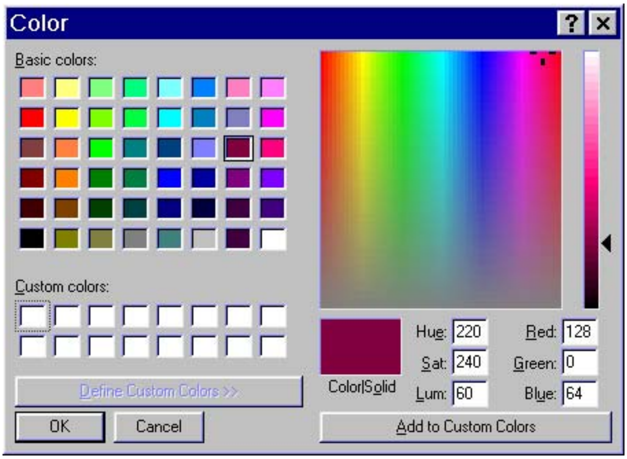
✧ Click on the **Color** field in the numerical input area with the left mouse key.

Or

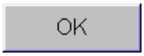


✧ Click into of the trapezoid in the histogram with the right mouse key.

The color palette is displayed.



Hue: 220
Sat: 240
Lum: 60
Red: 128
Green: 0
Blue: 64

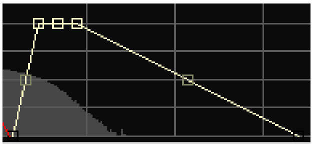


✧ Select the required color and confirm with **OK**.

The object appears in the result segment with the new color.

Color transition for tissue class

You can assign a color to each handle in the histogram. In that way, you can set a color transition for display of the tissue class. The colors of the handles define the corners of the transition.



✧ Click on a handle with the right mouse key to change its color.

➪ The color of handles 1 and 7 are always set to black in the original mode.

➪ The color is interpolated linearly between handles 1 and 3 and handles 5 and 7.

Setting shading

☑ Shaded

✧ Click on the option **Shaded** to create a shaded display.

➪ If the option **Shaded** is activated, the **VRT** display is processed with a shading algorithm, and a simulated light source casts a shadow in the image. This way a three-dimensional view is achieved.

Saving a parameter set

If you want use the parameter set again in the future, we recommend that you store it in the system.

✧ Click on the **Link preset** button to have a suitable suggestion for the name of the series entered.

✧ Shorten the **Preset** in a useful way in order to keep the assignment general and confirm with the **Return** key.

✧ Click on the button **Save Preset** to save the parameter set.

The next time you load, the presets are assigned to the series that contain the name entered as the first part of their name.

Deleting a parameter set

You can remove each parameter set from the **VRT Gallery**.

✧ Click on the **Delete Preset** button to delete a parameter set from the selection list.

As soon as you delete a parameter set from the selection list, the image icon will also disappear from the **VRT Gallery** dialog box.

Finishing VRT Definition

After you have saved all the required settings in the dialog box for **VRT Definition**, you can close the dialog box.

Close

✧ Click on **Close** to close the **VRT Definition** dialog window.

Or

✕

✧ Press on the button.

Defining a VRT slice thickness (VRT Clip)

To achieve maximum intensity projection, the entire volume of the data set is normally used. However, sometimes it is useful to use only part of the volume for projection. The subarea is defined by the two parallel intersection planes ("separation plane"). The distance between these planes is the slice thickness to be defined. For example, you can avoid cutting out interfering structures.

Selecting a reference image

In the reference segment, you can define the view of the reference image.

✧ First select a reference segment.

✧ Change display of the image until it meets your requirements.

Starting VRT Clip

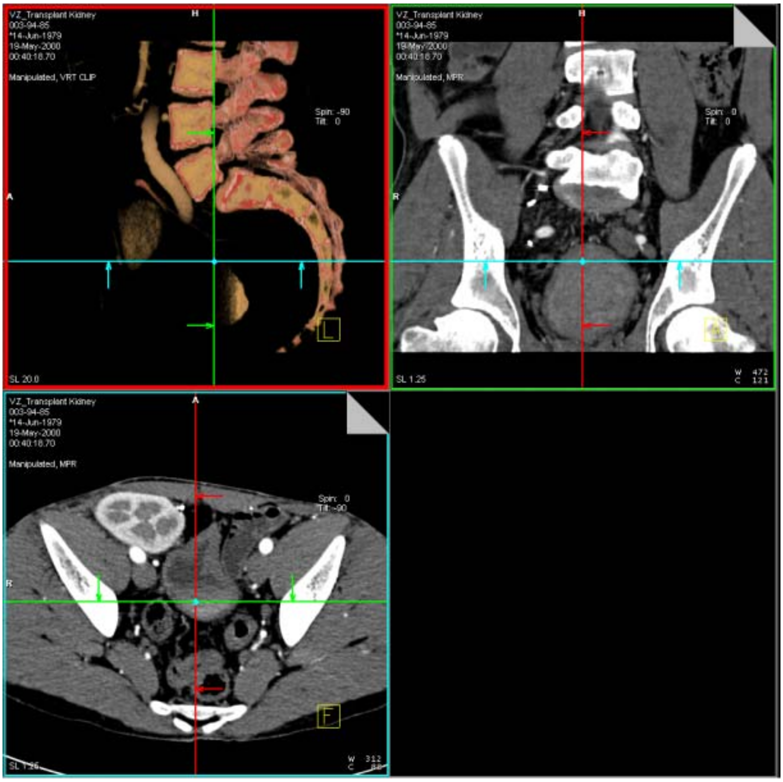
You can set VRT Clip in one, in two, or in all three reference segments.

✧ Call up **Type > VRT Clip** to set the output type VRT Clip.

Or

✧ Click on the **VRT Clip** button on the **Type** subtask card.

A VRT Clip display appears in the selected segment with the standard settings.



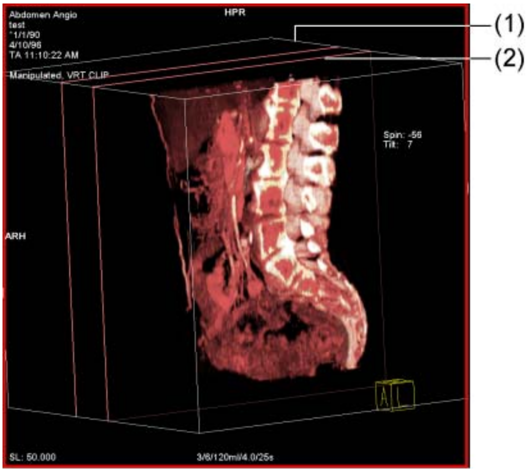
Orientation aids

As an aid to orientation when rotating the volume and changing the clip plane, you can call up auxiliary lines. The clip box surrounds the entire volume displayed, the clip plane indicates the position of the defined intersection plane.

✧ Call up the **Edit** menu.

✧ Deselect **hide Clip Box Graphics**, to display the Clip Box.

✧ Deselect **hide Clip Plane Graphics**, to display the Clip Plane.

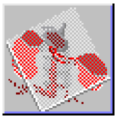


(1) Clip Box
(2) Clip Plane

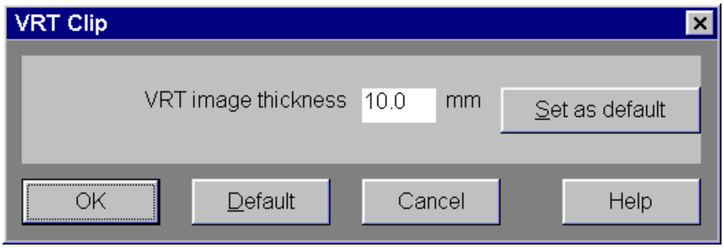
Changing the slice thickness

✧ Call up the **Type > VRT Thickness** to display the **VRT Clip** dialog box for setting the slice thickness.

Or

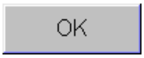


✧ Click on the **VRT Clip** button on the **Type** subtask card with the *right* mouse key.



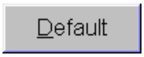
VRT image thickness 10.0 mm

✧ Enter the thickness that you want to use for projection in mm.



✧ Confirm your input with **OK**.

Or



✧ Click on **Default** to set the default value (10 mm) for the image thickness.

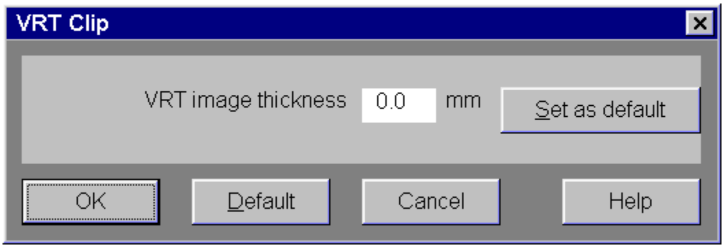
➪ The selected setting is applied to *all* VRT Clip reconstructions.

✧ Click on **Set as default** to store the displayed settings as new default value.

➪ When you load a new data set, the stored default value is applied.

Slice thickness 0 mm

The use of slice thickness 0 mm is a special case of the **VRT** display. A separation plane is created from intersection planes, normally two, to delimit the visible area. This plane separates the visible area from the hidden area.


VRT Clip

VRT image thickness 0.0 mm

✧ Set a slice thickness of 0 mm and confirm with **OK**.

➩ You can position the separation plane freely in three-dimensional space (e.g. with **Smart Selection**) and, in that way, hide the area you do not require.
→ Page H.3–38, *Smart Selection*

CHAPTER
H.8

Selecting and Processing Images

After you have transferred a volume data set to the **3D** task card, you can optimize the display of the images in the segments.

For the images loaded, you can adapt the window values. You can display the sections enlarged and place areas of interest in the center of the image.

Selecting images and 3D graphics

You must first select the images or 3D graphics that you want to process or with which you want to work.

On the **3D** task card, a distinction is made between images that are displayed in the reference segments and series that are located in the output segment.

Selecting the reference segment

In a reference segment, you can only ever select one reference image.

✧ Click on the image that you want to process with the left mouse key.

The segment is now displayed with a thick border.

Selecting the output segment

The reconstructed series is displayed in the output segment (bottom right).

✧ Click on the output segment to select all images of the reconstructed series.

Selecting 3D graphics

Graphic displays, e.g. graphic display of a parallel series, are usually displayed in the images of the reference segments.

✧ Click on a line of such a display with the left mouse key to select it.

Handles and a rotation point are then displayed on the 3D graphics.

Processing images and 3D graphics directly

You can execute many processing steps without having to select images or 3D graphics explicitly.

✧ Place the mouse cursor on the image or graphic and start operation immediately by pressing a mouse key.

For example, you can now window the image or move the reference line of the 3D cross hair.

Showing and hiding reference lines

The 3D cross hair can sometimes be an obstruction when you want to look at details in the image.

You can hide these graphic elements and show them again as required.

✧ Click on the **Hide Reference Lines** button in the upper part of the control area to hide the reference lines.

➩ If you now want to change the views of the images, use the mouse.

✧ Click on the **Hide Reference Lines** to display the reference lines again.

Windowing images

When transferring the volume data set to the **3D** task card, the images are displayed with the window values with which they were last stored.

In order to make diagnostically relevant details clearer, it is often necessary to assign new window values to the images.

➩ On SSD images you can regulate the brightness and shadows on the surface.

➩ For details about windowing, see also
→ Page E.4–2, *Windowing images*

Defining the scope of action (Single Windowing)

In the default setting, all images of the same output type e.g. MPR are assigned the same window values.

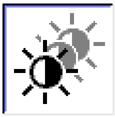
If you want to assign window values only to individual images, you must activate the **Single Windowing** option.

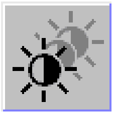
Windowing an image

✧ Call up **Image > Single Windowing** to select the option. The menu item is shown with a checkmark.

Or

✧ Click on the **Single Windowing** button in the control area to set **Single Windowing**.


Single


Multi

Processing an image view

You can enlarge image sections that are of particular interest to you (zooming). If the zoomed image no longer fits in the segment, you can move it so as to place the relevant section in the center of the image again (panning).
You will find a detailed description of how to set the image view in:
→ Page E.4–1, *Processing Images*

CHAPTER

H.9 3D Editor

A common problem in evaluating medical images is that areas relevant to an examination are hidden by other structures, especially bones. The necessary image information is contained in the volume data set but must be made visible with suitable editing steps.

In simpler cases you can solve the problem by post-editing in VOI mode. You can delimit concealing structures manually and cut them out of the data set.

In more complex cases, this method will require greater effort if you want to separate areas relevant to the diagnosis from concealing structures cleanly. In that case we recommend using the **3D Editor** which provides tools for marking and isolating structures of interest semi-automatically in three-dimensional space. These structures are referred to as “objects”.

Functions of the 3D editor

With the **3D Editor** you can perform the following operations:

- Object generation with **Region Growing**
- Object management in the object list
- Object editing with **Object Punching** and **Morphological Operations**

Region Growing

Normally in the first step you will generate one or more "objects" from the volume data set originally loaded in **3D**. By specifying a limited voxel value range you extract only a section of the voxels from the original data set. In this way, you generate an object in the result segment.

Instead of extracting globally from the entire volume data set you can also proceed "slice by slice" (in 3D blocks) using the **Slab Editor**.

You can also set **Seed Points** in the original data set, thus limiting the creation of an object to defined regions which are also connected to one another in the specified voxel area.

Object Punching

Like editing volume data sets in VOI mode, you can use the **3D Editor**, too. You are provided with tools for cutting out structures from an object that you have previously generated.

Using the **Slab Editor** you can define your own cutting depth.

Morphological Operations

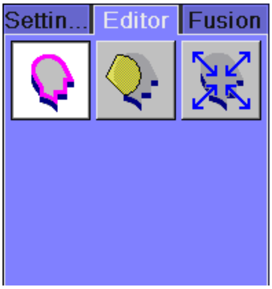
In some cases it will not be simple to separate the structures of an object using the cutting tools. Here we recommend *eroding*, or *shrinking*, the areas of the object by a specified surface thickness until the obscuring structures are no longer contained in the object. You can subsequently dilate, or blow up, the remaining object areas by a defined surface thickness. As a result, the irrelevant areas contained at the outset are now removed from the representation. If you perform the same operations in reverse order, small cavities in the object will be filled.

NOTE

With **Morphological Operations** you can eliminate small structures and fill cavities but you will also change the structures of the target object.

Calling up the 3D editor

You can edit the volume data set using the **3D Editor** in the dialog box **Object Editor** which you call up as soon as you have transferred the volume data set to the **3D** card in any representation (MPR; MIP; SSD, etc.).



✧ Place the **Editor** subtask card in the foreground.

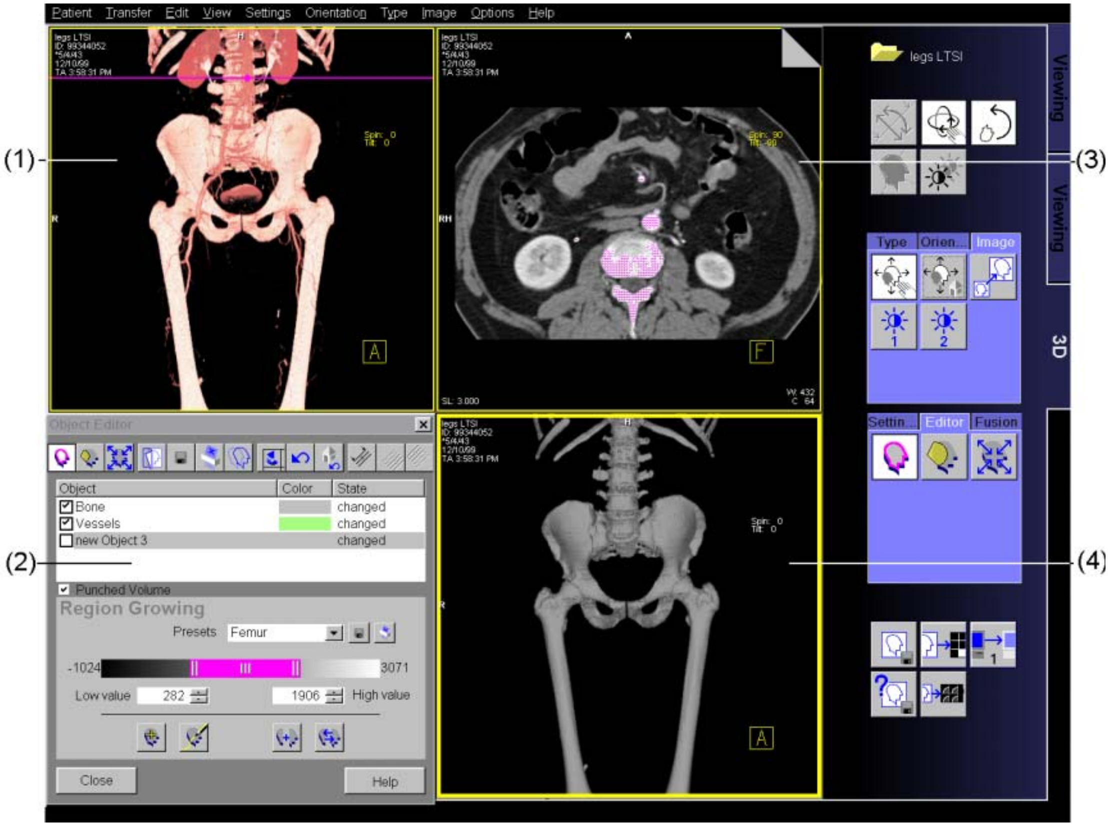
✧ Click on the **Region Growing** button.

The dialog box **Object Editor** is opened in **Region Growing** mode. The segments of the **3D** card are repositioned for editing in the **3D Editor**.

➩ You can also call up the **3D Editor** via the two buttons **Object Punching** (center) and **Morphological Operations** (right). This takes you straight to the mode for object editing.

3D card in editor mode

When you call up the **3D Editor**, the image area of the **3D** card is subdivided into the following segments:



Object	Color	State
☑ Bone		changed
☑ Vessels	🟩	changed
☐ new Object 3		changed

☑ Punched Volume

Region Growing

Presets: Femur

-1024 … 3071

Low value: 282

High value: 1906

(1) Slab segment for defining the slice to be edited and representing the resulting series

(2) 3D editor window

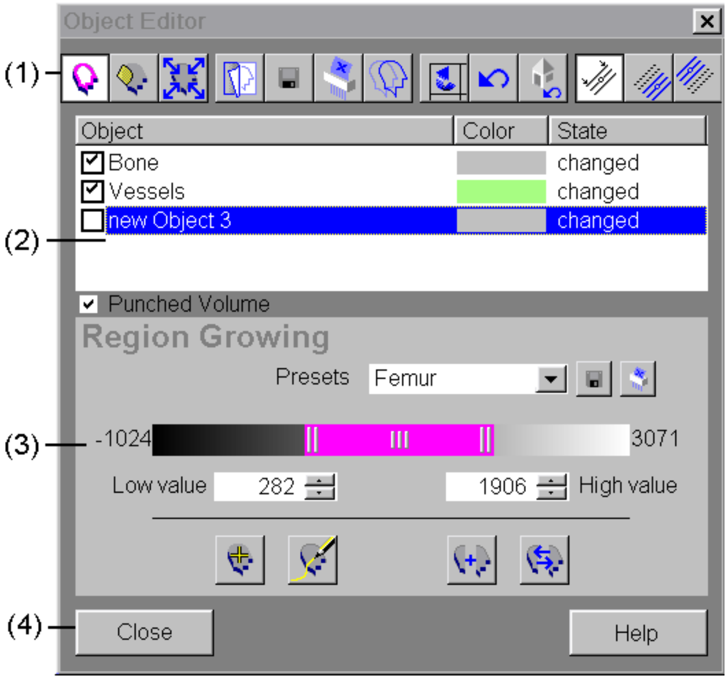
(3) Working segment (MPR or MIP Thin)

(4) Result segment (SSD)

Dialog box Object Editor

The dialog box **Object Editor** always appears in the bottom left-hand (empty) segment and does not therefore hide any of the working or result segments.

It contains the following areas:



Object	Color	State
☑ Bone	▨	changed
☑ Vessels	🟩	changed
☐ new Object 3	▨	changed

☑ Punched Volume

Presets: Femur

-1024 3071

Low value: 282

High value: 1906

(1) Tool bar

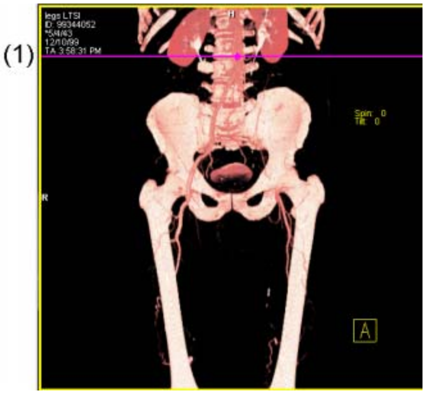
(2) Object list

(3) Mode-specific tools

(4) General buttons (close 3D editor)

The slab editor

When you call up the **3D Editor**, the loaded series of the last view to be set appears in the slab segment in the selected display mode. Usually you see a sagittal tomogram as an MPR image. In this example you will see a transversal tomogram in the working segment whose position in the slab segment is indicated by a navigation line.



(1) Navigation line

The navigation line always indicates the current tomogram position when you are scrolling through the image stack with the dog ears. Conversely you can change the position and orientation of the tomographic image in the working segment with the navigation line as you do with the reference lines.
→ Page H.3–13, *Using the 3D cross hair*

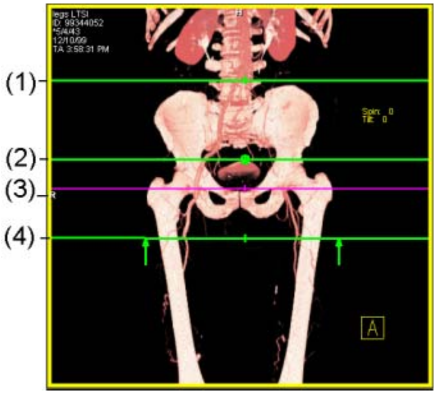
Switching on the slab editor

Select the area of interest from the loaded volume data set as a 3D block. From this 3D block generate and edit the 3D objects using the editor functions.

✧ Click on the button **Use Slab** in to tool bar of the dialog box **Object Editor** to activate slab mode.

➪ To deactivate slab mode, click again on the **Use Slab** button.

The slab lines are displayed in the slab segment.

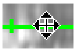


(1) Upper boundary line of the 3D block
(2) Center line of the 3D block
(3) Navigation line
(4) Lower boundary line of the 3D block

Changing a 3D block

All editing operations that you perform in the 3D editor only affect the structures in the 3D block (*within* the boundary lines). You therefore still have to adjust the position, extent, and orientation of the 3D block.

Enlarging/reducing a 3D block



You can enlarge or reduce a 3D block by moving the boundary lines with the mouse.

✧ Move the upper boundary line away from the center line keeping the mouse key pressed to increase the size of the 3D block.

Or

✧ Drag the boundary line toward the center line to reduce the size of the 3D block.

⇨ The same applies to moving the lower boundary line.

In each case, the center line is moved toward the new center of the enlarged or reduced 3D block. The other boundary line remains unchanged.

Moving a 3D block

You can move the 3D block within the slab segment using the center line.

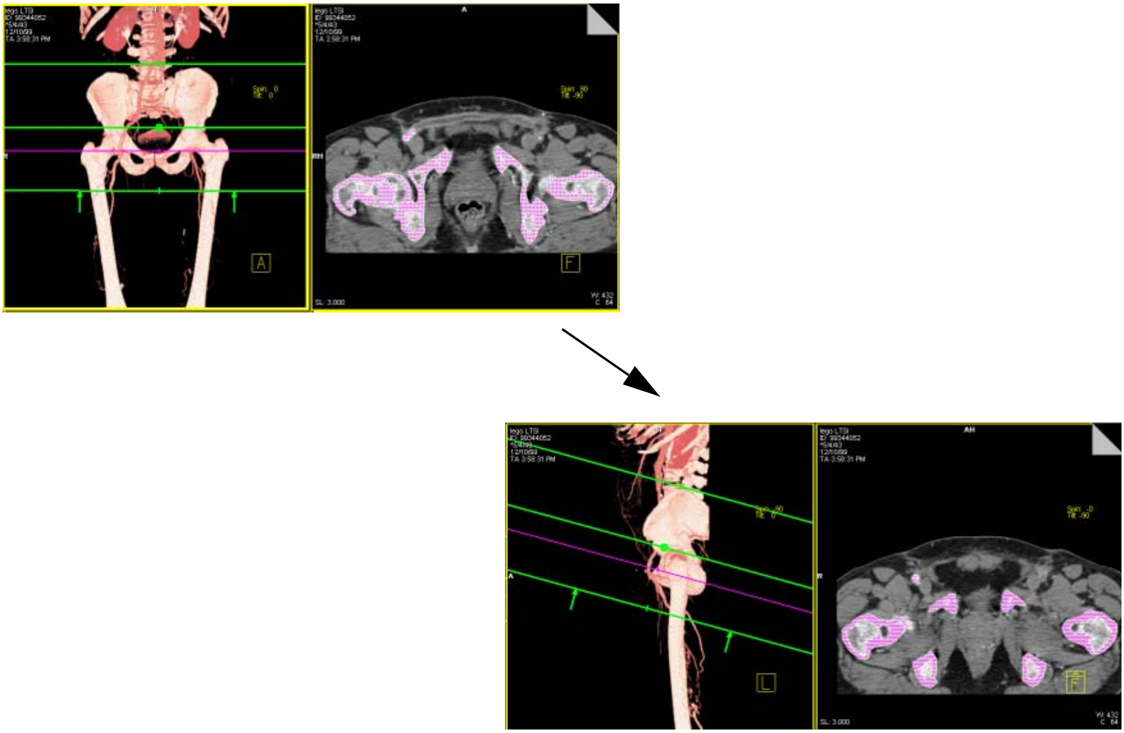
✧ Pull the center line at its center point to the desired position keeping the mouse button pressed.

Rotating a 3D block

You can change the orientation of a 3D block by tilting the center line or turning the tomographic images.

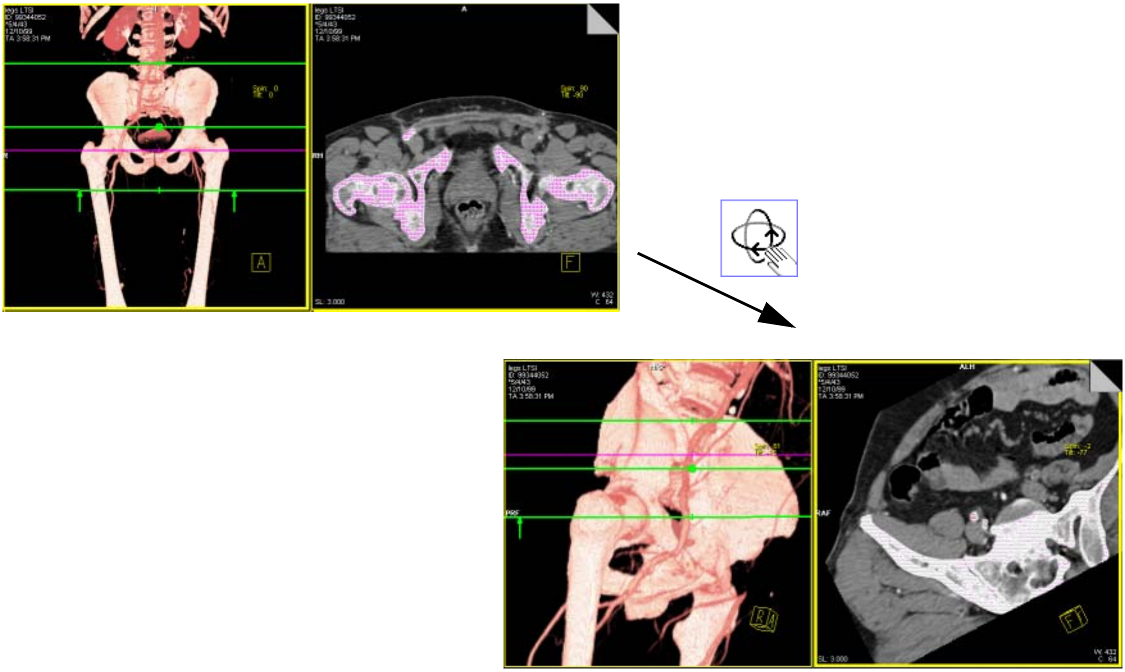
✧ Click on the center line (*not* on the center point) and rotate the center line in the desired direction keeping the mouse button pressed.

The entire 3D block is moved together with the navigation line in the corresponding direction.



Or

✧ Click on the working segment or slab segment and change the orientation of the tomographic image using the menu commands and screen buttons.
→ Page H.3–11, *Setting views in the volume data set*



Block by block editing with the slab editor

When generating and postprocessing objects you can successively extract structures from blocks of the original data set. To do that, you first define a 3D block and then position it at one end of the volume. When you have extracted the voxels, move the 3D block within the volume so that it joins on to the end position of the first block. Then start the next extraction and continue in this way until you have covered the entire volume.

In this procedure you move the 3D block equidistantly up or down by one block thickness

✧ Click on the **Move Slab +** button to move the 3D block in the opposite direction to the slab arrow by the amount of its thickness.

Or

✧ Click on the **Move Slab -** button to move the 3D block equidistantly in the direction of the slab arrows.

Or

✧ Move the navigation line beyond the upper or lower boundary line of the 3D block.

When you have moved the 3D block, the previous upper boundary line is now the lower line of delimitation and vice versa.

Creating 3D objects

By extracting particular voxels from the volume data set you create objects with the **3D Editor** representing organs and structures, e.g. blood vessels, bones, and soft tissue.

With **Region Growing** you create an object from the voxels of the original data set that are located within a prescribed value range. You can subsequently expand the objects by adding voxels from other value ranges.

The use of **Seed Points** and **Blocker** allows you to define as an object only the regions that you have selected and which are spatially connected, taking the specified threshold range into account.

➩ In the slab segment (top left) you can apply the creation of objects to an entire volume data set or limit it to one 3D block.
→ Page H.9–7, *The slab editor*

Creating an object with threshold

You usually create new objects with **Region Growing** mode.

✧ Call up **Settings > Editor Region Growing...**.

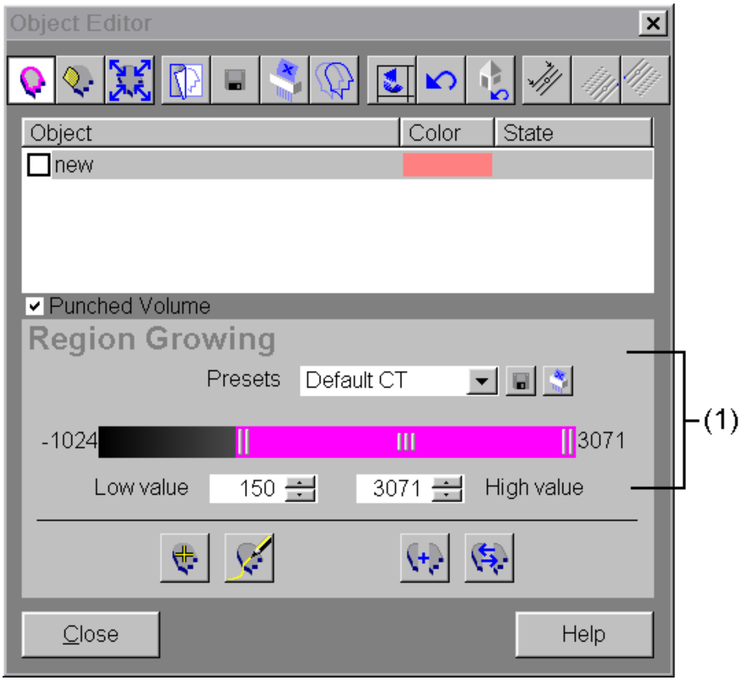
Or

✧ Click on the button **Region Growing**.

Or

✧ Click on the button **Region Growing** on the tool bar of the dialog box **Object Editor**.

The tools for thresholding are now displayed in the dialog box **Object Editor**.



☐ new

☑ Punched Volume

Presets: Default CT

Low value: 150

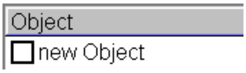
High value: 3071

(1) Tools for thresholding

Selecting a new object

The list of objects that have been created for the loaded volume data set is displayed in the central area of the dialog box **Object Editor**. When you edit the list for the first time it contains the entry "*New object*".

➪ If objects have already been defined for the volume data set, you can now select them from the object list and postprocess them.
→ Page H.9–24, *Working with the object list*

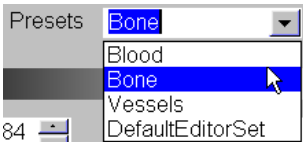


✧ Click on **new Object** to define a new object.

Setting a threshold

In the dialog box **Object Editor** you will first see the default or last threshold values to have been used to reconstruct an object. The associated areas are highlighted in color in the working segment (top right).

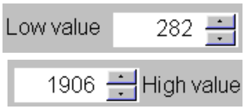
You can use predefined threshold value pairs or define new threshold value ranges to create new objects.



Presets Bone

✧ Select the threshold value suitable for your diagnostic problem from the **Presets** list.

Or



Low value 282

High value 1906

✧ Enter new threshold values in the spin box and confirm them with the **Enter** key.

Or

✧ Set a threshold value with the slider.

☐ Drag the end boundaries of the slider with the mouse to increase or decrease the threshold range.

☐ Move the center mark of the slider to change the position of the threshold value range.

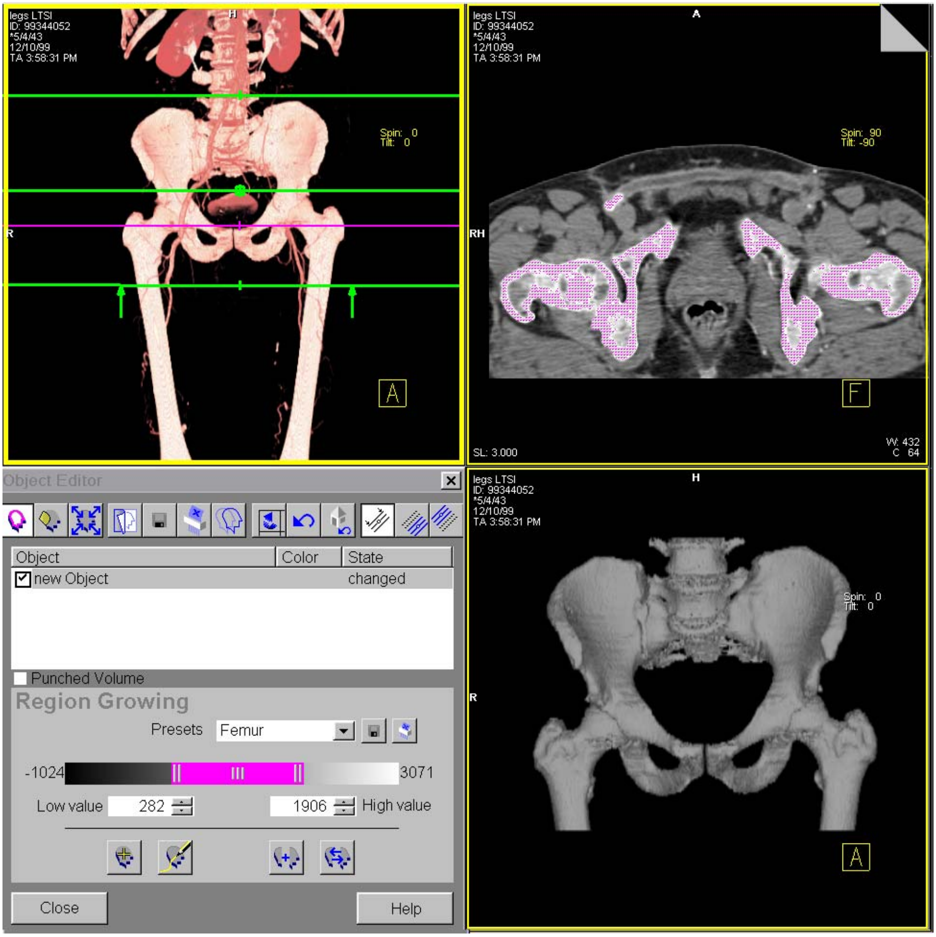
The threshold values you enter are applied to the representation in the working segment.

Displaying an object

As soon as you have set the threshold values start reconstruction of the object.

✧ To do that click on the button **Add to Object**.

The reconstructed object appears in the result segment.



Object	Color	State
☑ new Object		changed

☐ Punched Volume

Region Growing

Presets: Femur

-1024 … 3071

Low value: 282

High value: 1906

Undo

You can undo the last task, e.g. **Add to Object**, if the entries you have made are incorrect.

✧ To do that click on the button **Undo Last Step**.

Saving presets

When you have found suitable threshold value pairs you can store them under a new name in the preset list.
→ Page H.6–10, *Creating and processing predefined threshold values*

Presets Bone

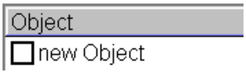
✧ Overwrite the original name with a name of your choice.

✧ Store the new threshold values by clicking the button.

Creating an object with Region Growing

Once you have created an object by defining the threshold values, you limit the size of the object with the functions **Define Seed Points** and **Draw Blocker**.

Selecting an object



Object

☐ new Object

✧ Click on the object in the object list.

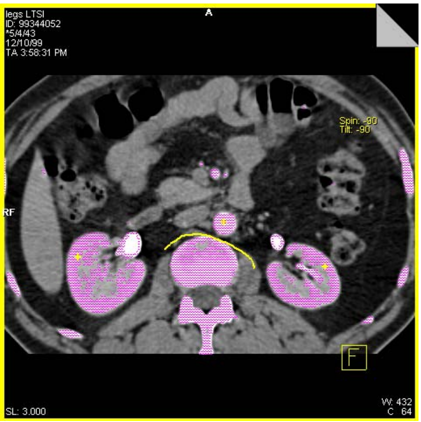
Setting Seed Points

In the working segment you can see the selected object within the defined threshold values.

✧ Click on the button **Define Seed Points** in the **Region Growing** window area.

The mouse cursor changes shape.

✧ Click on the relevant points in the working segment with the left mouse key to set the **Seed Points**.



➪ You can set any number of **Seed Points** and move them by clicking on them and dragging them with the mouse.

Deleting seed points

If you have set too many **Seed Points** you can delete them again.

✧ Click with the left mouse key on the **Seed Point** and then press the **Del** key on your keyboard.

Setting a blocker

With blockers you can limit growing of the voxel areas starting from the seed points. To do that you define boundary lines beyond which the voxel areas are not allowed to grow.

✧ Switch to MIP display in the working segment.

➩ If necessary, use the **Slab Editor**.
→ Page H.9–7, *The slab editor*

✧ Click on the button **Draw Blocker** in the window area **Region Growing**.

The mouse cursor changes shape.

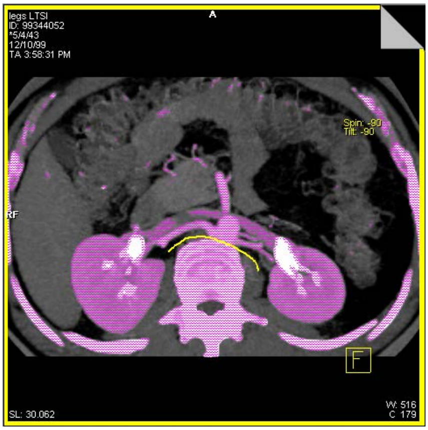
✧ Click with the left mouse key on the required starting point of the boundary line in the working segment.

✧ Click on any other point in the image at which the direction of the curve must change.

Or

✧ Draw a continuous line by dragging the mouse cursor across the image keeping the left mouse key pressed.

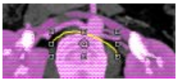
✧ Terminate the line with a double-click.



➪ You can draw one or several freehand curves into your working segment.

Removing a blocker

You can remove any freehand curves that you no longer need at any time.



✧ Click with the left mouse key on the **Blocker** that you want to delete and then press the **Del** key.

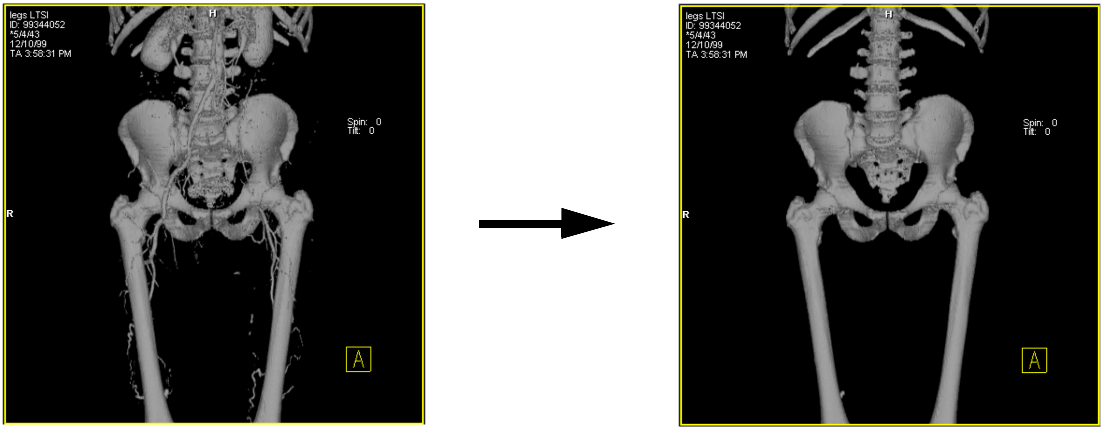
Displaying an object

Once you have set the **Seed Points** and drawn in any **Blockers** you require you can start reconstruction of the object.

✧ To do that click on the button **Replace Object**.

➪ You can also set a threshold value range from the beginning and use **Seed Points** and **Blockers**. You can generate a new object with **Add to Object**.

The edited object appears in the result segment.



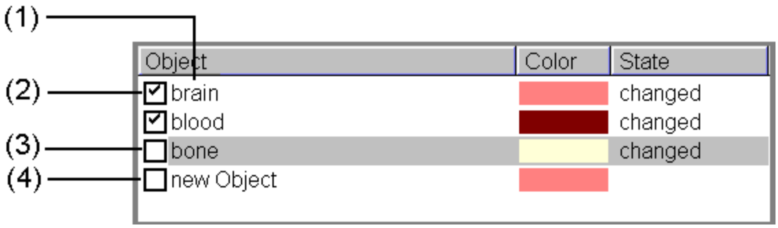
Undo

You can undo the last step, e.g. **Replace Object**, if entries are incorrect.

✧ To do that click on the button **Undo Last Step**.

Working with the object list

The object list appears as soon as the **Object Editor** is opened. All predefined and new objects are displayed in the list.



Object	Color	State
☑ brain	🟥	changed
☑ blood	🟥	changed
☐ bone	🟨	changed
☐ new Object	🟥	

(1) Name of object

(2) Check box to display the object in the slab segment.

(3) Selected object for display in the result segment

(4) New (empty) object

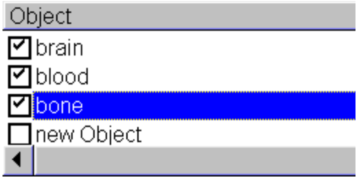
You can select one or several objects simultaneously in the object list. The selected objects are displayed in the result segment.

In the object list you can see the name, color, visibility, and status of the object (marked blue). As soon as you change a predefined object in the working segment, the status "changed" is entered in the list.

Selecting objects

When you open the dialog box Object Editor, the existing objects of the loaded volume data set appear in the object list. The list is updated every time an object is updated.

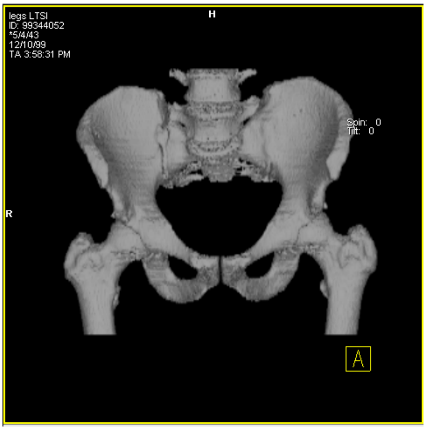
Individual object



Object
☑ brain
☑ blood
☑ bone
☐ new Object

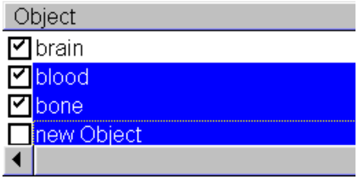
✧ Click on an object in the object list.

The selected object appears in the result segment.



➪ The selected object does not appear in the slab segment until you activate it in the object list via the check box.

Several objects



Object
☑ brain
☑ blood
☑ bone
☐ new Object

✧ Check several objects one after the other while keeping the **Ctrl** key pressed.

All the selected objects are displayed in the result segment in the color assigned to them.

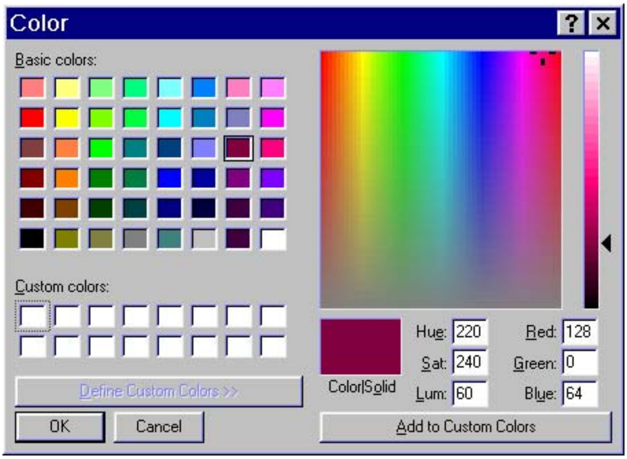
Changing object properties

You can change the color of objects in the result segment to provide a more realistic representation of the structure. You can keep your object list understandable by assigned appropriate names (e.g. Bone for bone structure).

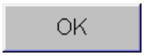
Assigning a color

✧ Double-click with the left mouse key on the field **Color** of the selected object.

The color palette is displayed.



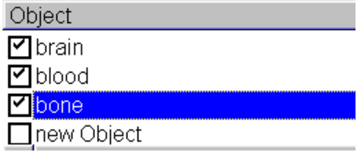
Hue: 220
Sat: 240
Lum: 60
Red: 128
Green: 0
Blue: 64



✧ Select the required color and confirm with **OK**.

The object appears in the result segment with the new color.

Changing an object name



Object

☑ brain

☑ blood

☑ bone

☐ new Object

✧ Select an object from the object list with the mouse.

✧ Click again on the entry keeping the mouse pressed for a short time.

A text input field is displayed.

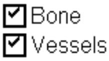
☑ bone1

✧ Enter a name for the new object via the keyboard and confirm it with the **Return** key.

Displaying objects in the slab segment

The objects contained in the object list can be hidden or revealed individually in the slab segment. In that way you determine which areas are to be stored as a new series for further processing.

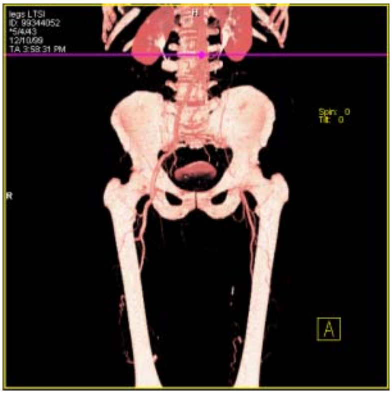
Displaying objects



☑ Bone

☑ Vessels

✧ Check the check boxes of the objects to be displayed in the slab segment.



Hiding an object

☐ Bone
☑ Vessels

✧ Uncheck the check box of the relevant object again.

Displaying the complement area

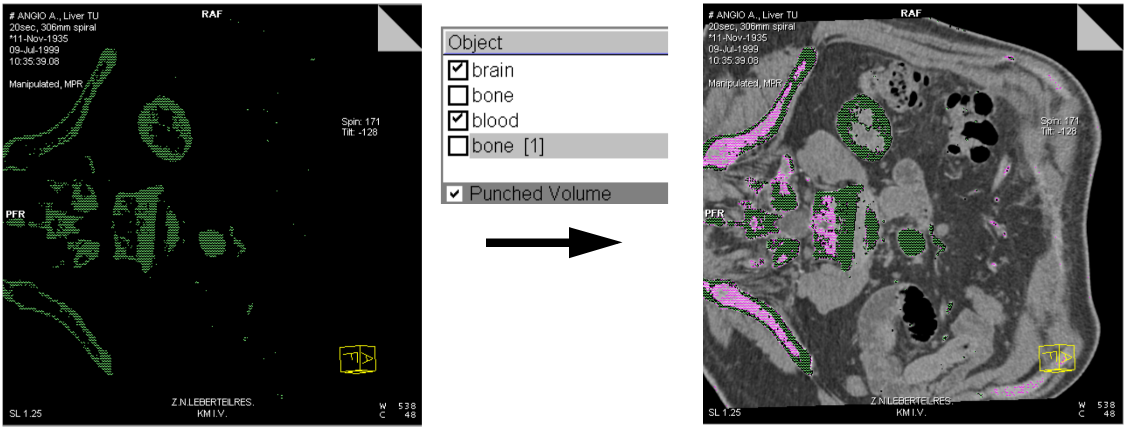
☑ Punched Volume

The **Punched Volume** contains all the voxels of the original data set not yet contained in objects.

✧ Activate **Punched Volume** to display the residual data set.

The **Punched Volume** and all objects activated in the object list are displayed.

➩ If, for example, you only want to hide the bones in the data set, deselect the bone objects from the list and activate all the remaining objects as well as **Punched Volume**.



Object
☑ brain
☐ bone
☑ blood
☐ bone [1]
☑ Punched Volume

Updating the display

Whenever you create or change objects you must update the views. Only then are the changes made to objects activated. For example, an object hidden in an object list is not removed from the display in the two upper segments until the display is updated.

✧ Click on **Update Masking** to apply the changes of your object editing.

Saving, adding, deleting objects

You can manage existing objects or objects you have just created with the object list. It is recommended that you save intermediate versions while you are working which you can restore whenever necessary. If you want to keep a particular version of an object but want to continue working on it, simply create a duplicate.

Delete any objects that you no longer require from the object list. This keeps the object list and the database in which the objects are stored to a manageable size.

Storing an intermediate version of the object

✧ With the mouse select the objects in the object list for which you want to store an intermediate version

✧ Click on the button **Save Selected Objects**.

Restoring an object version

You have continued working on an object for which you created in intermediate version and would like to restore the previous version.

✧ Select the object in question from the object list with the mouse.

✧ Click on the button **Reload Selected Objects**.

NOTE

Any changes you have made to an object after you stored an intermediate version of it are lost if you restore that version.

Duplicating an object

During your work on an object you have arrived at a version that you do not want to lose by continued work on it. Duplicate this object and then continue work on the new duplicated objects. In this way, you can make several versions of an object by producing further duplicates.

✧ With the mouse select the object from the object list that you want to duplicate.

✧ Click on the button **Duplicate Selected Object**.

The new object is stored under the same name but with the extension **1** (or **2**, **3**,... for further duplicates of this object) to the end of the object list.

Creating a new object

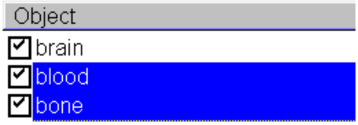
Create a new object for each new extraction of voxels from the volume data set.

✧ To do that click on the button **New Object**.

A new object with the name **new Object 1** (or **new Object 2**, **new Object 3**,...) is appended to the end of the object list.

Deleting an object

You can remove any objects that you no longer require from the object list.



Object

☑ brain

☑ blood

☑ bone

✧ With the mouse select the objects that you want to delete from the object list.

✧ Click on the button **Delete Selected Objects**.

✧ Confirm deletion of the selected objects in the dialog box displayed.

Postprocessing objects

The 3D editor offers you the functions **Object Punching** and **Morphological Operations** for fine editing of objects.

With these functions you can edit existing objects that you can access from the object list.

Cutting out structures

With **Object Punching** mode you can cut freely definable areas out of the object.

Activating Object Punching

✧ Call up **Settings > Editor Object Punching...** .

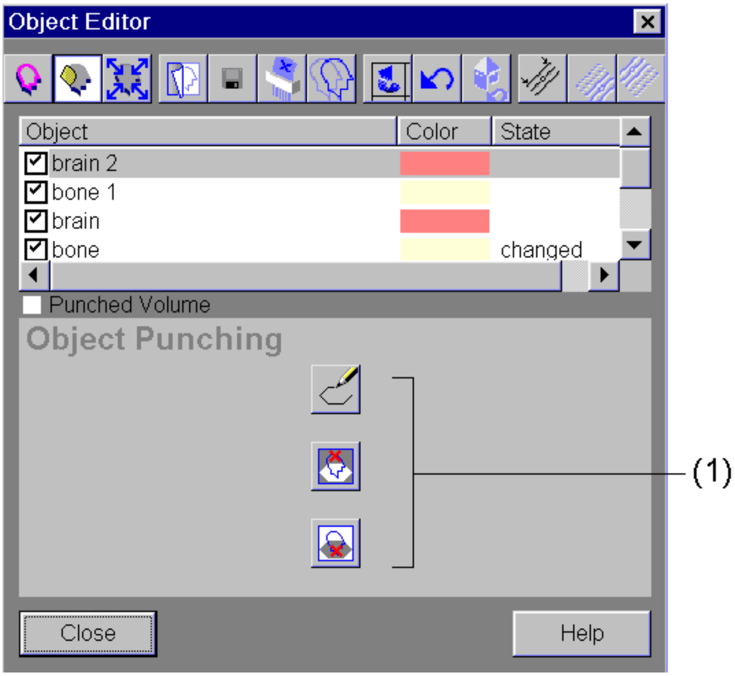
Or

✧ Click on the button **Object Punching** in the subtask card **Editor**.

Or

✧ Click on the button **Object Punching** in the tool bar of the dialog box **Object Editor**.

The tools of **Object Punching** mode are displayed in the bottom half of the dialog box **Object Editor**.



Object	Color	State
☑ brain 2	🟥	
☑ bone 1	🟨	
☑ brain	🟥	
☑ bone	🟨	changed

☐ Punched Volume

(1) Tools of **Object Punching** mode.

Defining a cutting depth

You can extend the cutting out of structures to the entire volume data set or limit it to one 3D block (**Slab**). If you work in slab mode, the cutting depth is limited by the size of the 3D block.

✧ Click on **Use Slab** to hide or reveal the 3D block in the slab segment.

✧ If necessary, set the required position, extent, and orientation of the 3D block.
→ Page H.9–7, *The slab editor*

Drawing in a cut line

Now draw a contour around the object structures that you want to cut out in the result segment.

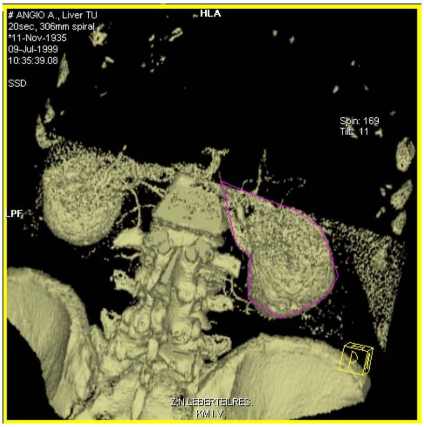
✧ Click on the button **Draw Contour**.

The mouse cursor changes shape.

✧ Set the starting point of your contour with a mouse click.

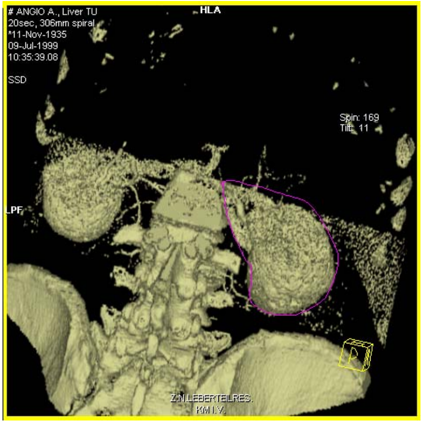
✧ Set further contour points with the mouse.

The individual contour points are joined up by the straight line.



Or

✧ Draw a continuous line around the required structure while keeping the left mouse pressed.

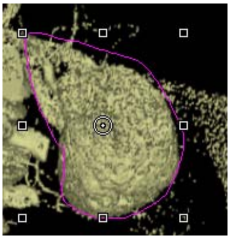


✧ Close each contour in question with a double click.

Editing cut lines

You can lengthen, shorten, and move the cut lines that you have drawn using handles.

✧ Click on a cut line with the mouse to show the handles.



✧ Change the length and orientation of the cut line using the lateral handles.

✧ Move the cut line using the center graphic marker.

Removing cut lines

If the contour that you have drawn does not meet your requirements, simply delete the line.

✧ Click on the line with the mouse to mark it.

✧ Press the **Del** key on your keyboard to delete the cut line.

Cutting out structures

Once you have drawn in a contour and adapted its position and extent, you can reveal or delete the structures in the contour.

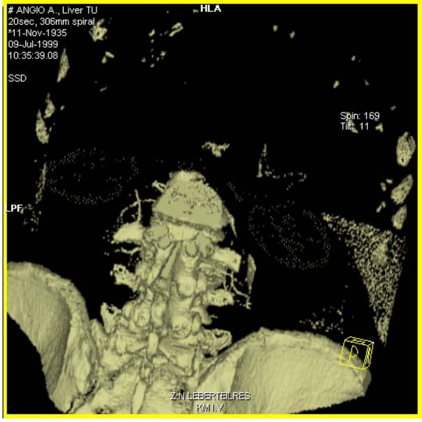
✧ Click on the button **Keep Inside**.

The structures *outside* the contour are deleted.

Or

✧ Click on the button **Remove Inside**.

The structures *inside* the contour are removed.



➪ With the tools **Draw Contour** and **Remove Inside** you can successively remove structures from the object and gradually adapt the object to its most important structures.

Undo

If you remove any structures accidentally you can undo the last step.

✧ To do that click on **Undo Last Step**.

Morphological editing

You apply morphological operations if structures inside the object cannot be separated simply with the cutting tools. You can remove edge areas in the representation by eroding, or shrinking, and then dilating, or blowing up, an object. If you perform the same operations in reverse order, small cavities in the object will be filled.

➪ With the **Morphological Operations**, you can also produce softer transitions for **VRT** display, for example.

Activating Morphological Operations

✧ Call up **Settings > Editor Morphological Operations...** .

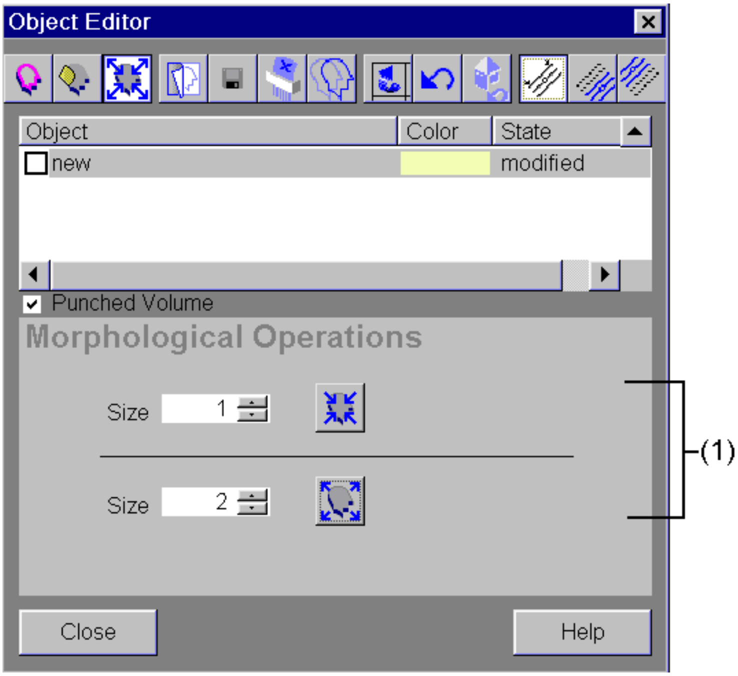
Or

✧ Click on the button **Morphological Operations** in the **Editor** subtask card.

Or

✧ Click on the button **Morphological Operations** in the tool bar of the dialog box **Object Editor**.

The tools for the Morphological Operations are displayed in the lower half of the dialog box **Object Editor**.



(1) Tools of **Morphological Operations** mode

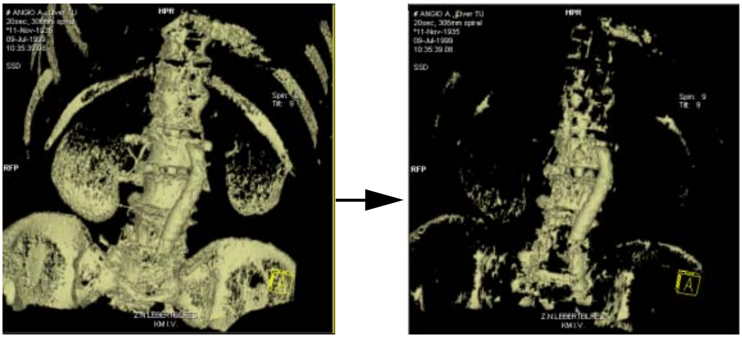
Eroding an object

Size 1

✧ Enter the surface thickness via the spin box by which the object is to be eroded or shrunk.

✧ Then click on the **Erode Object** button.

The eroded object appears in the result segment.



If there are still structures concealing the object you can enter a new surface thickness and erode the object again.

Undo

If the result is unsatisfactory you can undo the last step.

✧ To do that click on **Undo Last Step**.

Dilating an object

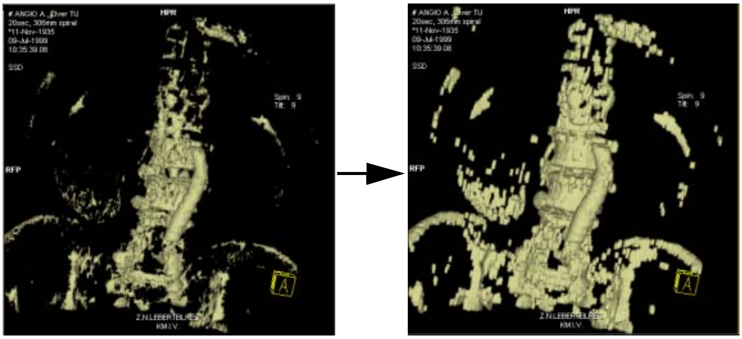
You have eroded the object so far that it no longer contains concealing structures. Now dilate, or blow up, the object to the desired size.

Size 2

✧ Enter the surface thickness via the spin box by which the object is to be dilated.

✧ Then click on the **Dilate Object** button.

The object is displayed with the relevant areas in the result segment.



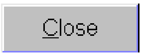
➪ Use the **Undo** function if you have used the incorrect surface thickness to dilate the object.

Closing the 3D editor

Once you have defined and evaluated as objects all the structures to be displayed, you can close down the **3D Editor**.

When you close the **3D Editor** the objects are saved to your local database together with the original series.

Closing the 3D Editor



✧ Click on the button **Close** in the dialog box **Object Editor** to close the **3D Editor**.

Or

✧ Click on the **Close** button.

CHAPTER H.10 Fusion

The function Fusion allows you to combine the results of different acquisition techniques or acquisitions performed at different times by overlaying them.

Two image series are loaded in **3D** and then aligned spatially and overlaid with **Fusion**. The initial data sets are merged to a new data set. In this data set, matching image pairs from the two loaded series are linked and can then be displayed for diagnostic purposes like two slides one on top of the other.

Functions of Fusion

To perform an evaluation with Fusion, you must execute the three following steps:

☐ Loading two different image series of a patient

☐ Overlay the two image series

☐ Edit the overlaid image data sets

Loading

In the first step you load two volume data sets in **3D**, one *reference series* and one *model series*.

The *reference series* serves as an anchor for subsequent overlaying of the two image data sets.

The *model series* is aligned spatially on the reference series.

Overlaying

In the overlaying step, the data of the model and reference series are merged with one another.

You can overlay the two image series either by assigning points (landmarks) or by shifting the model series visually (visual alignment).

Editing the Fusion image data set

Once you have successfully overlaid the image data sets you can edit them in order to display them more clearly. You can window individual image series and change the field of view and color display of the Fusion images. You can then apply the whole range of 3D functions to the merged image data set.

→ Page H.3–39, *Defining output types*

Calling up Fusion

To perform the function **Fusion** you require two volume data sets, the reference series and the model series.

Both image series must cover the same examination range.

➪ If you select a data set that has already been edited with **Fusion**, it is loaded in **3D** together with the overlay parameters already used. It is then not necessary to realign the overlaid series.

Loading image data sets

In normal operation, you select the two image series for your Fusion evaluation in the **Patient Browser** and transfer them one after the other to the **3D** task card.

If you had already edited the reference series in **3D** with another function (e.g. editor), you can load the missing model series from the **Patient Browser**.

CAUTION

Source of danger: Loading image data sets of different patients

Consequence: Mix-up of patients and incorrect diagnosis possible

Measure: When loading reference and model series, take care that you select the data of the correct patient.

Loading a new series

✧ Call up **Patient Browser** (**Patient > Patient Browser**).

✧ Select the series that you want to use as reference images in the navigation or content area.
→ Page D.2–6, *Scrolling through and selecting patient data*

✧ Call up **Patient > 3D MPR** from the main menu or click on the **3D MPR** button on the toolbar of the **Patient Browser**.

➪ If you have activated the function **Close after loading**, the **Patient Browser** dialog box is closed as soon as the images are loaded.

✧ Select the series that you want to use as model images in the navigation or content area of the **Patient Browser**.

✧ Call up **Patient > Fusion** from the main menu or click on the **Fusion** button on the toolbar of the **Patient Browser**.

➪ When you apply the function **Fusion** only whole volumes of the image data sets are used, previously defined VOIs are ignored.

Loading the model series subsequently

You have already loaded an image data into the **3D** task card and now want to overlay another task image data set on top of it.

✧ Call up **Patient Browser (Patient > Patient Browser)**.

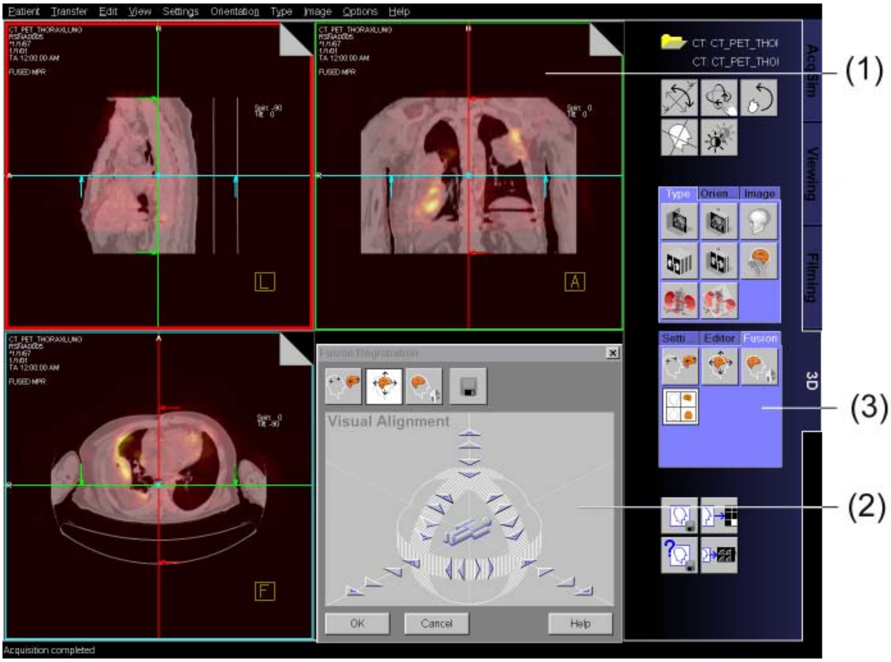
✧ Select the series that you want to use for the model images in the navigation or content area of the **Patient Browser**.

✧ Call up **Patient > Fusion** from the main menu or click on the **Fusion** button on the toolbar of the **Patient Browser**.

3D card in Fusion mode

The images of the loaded reference and model series are displayed overlaid in the first three segments.

In the fourth segment, a dialog box is displayed which supports you with the alignment of the images in the reference and model series.



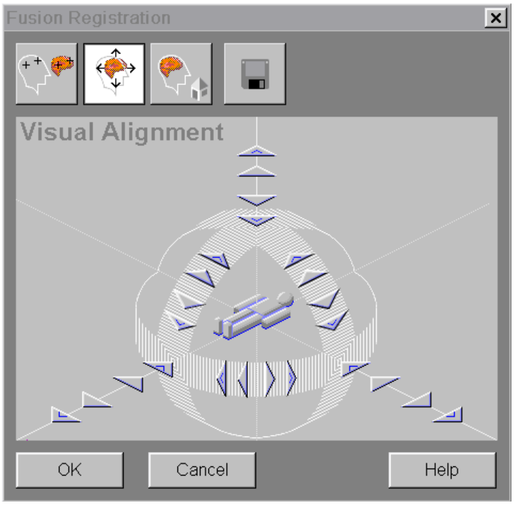
(1) **Image area**
three orthogonal views of the loaded images.

(2) **Dialog box Fusion Registration**
operating elements for overlaying images.

(3) **Fusion subtask card**
buttons for overlaying and displaying images.

Overlaying image series

As soon as you have loaded the image series for processing with **Fusion** you can align them in orientation and rotation. You perform these steps with the help of dialog box **Fusion Registration**.



The dialog box **Fusion Registration** contains the following functions:

☐ **Landmarks** (optional)
Both loaded image series are made to match using suitable reference points.

☐ **Visual Alignment**
The two loaded image series are made to match visually.

☐ **Reset**
Here you can reset individual steps that you have already executed.

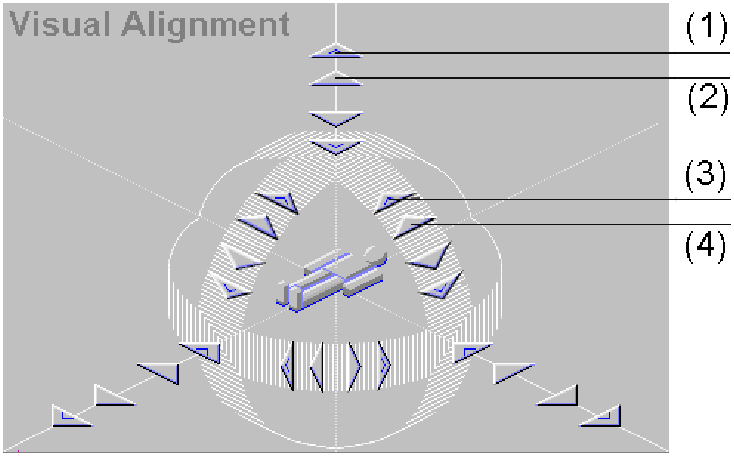
Aligning images visually

With Visual Alignment you make the reference and model series match by aligning the model images in the three segments step by step with the reference images.

✧ Click on the button **Visual Alignment** to display the functions of **Visual Alignment** in the dialog box **Fusion Registration**.

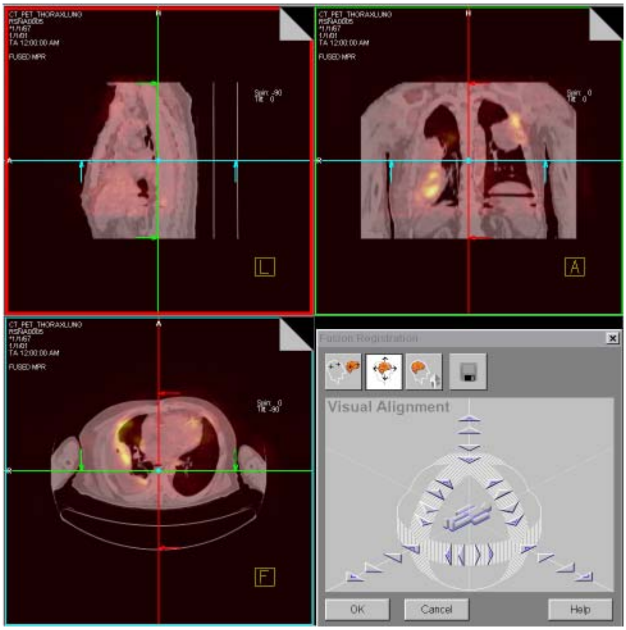
Or

✧ Call up **Settings > Fusion Visual Alignment** in the main menu.

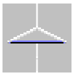


(1) Double direction arrow
for large image movements
(2) Single direction arrow
for small image movements
(3) Double rotation arrow
for large image rotations
(4) Single rotation arrow
for small image rotations

The two image series are displayed overlaid. In three segments of the image area you can see the reference and model images in three orthogonal views. To help you distinguish between them they are displayed in different colors.



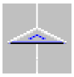
Moving a model series



✧ Click on a single direction arrow in the overview drawing of the function window **Visual Alignment**.

The model series moves by 1 mm in the selected direction.

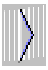
Or



✧ Click on a double direction arrow.

The model series moves by 10 mm in the selected direction.

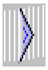
Turning a model series



✧ Click on a single rotation arrow in the overview drawing of the function window **Visual Alignment**.

The model series turns in steps of 1° in the selected direction.

Or



✧ Click on a double rotation arrow.

The model series turns in the selected direction in steps of 10°.

Saving overlaid images

Last Saved

You can intermediately save any promising alignments you have performed. You can call up these versions whenever you need them with the **Last Saved** button.

> **NOTE**
>
> Whenever you make an improvement by turning and moving the images, you should save the new alignment to the buffer. You can then return to a previous result if the two series start to drift apart again.

✧ Click on the **Save** button to save the current overlaid images.

➩ You can save the alignment as often you want. The previous result is then overwritten by the new one.

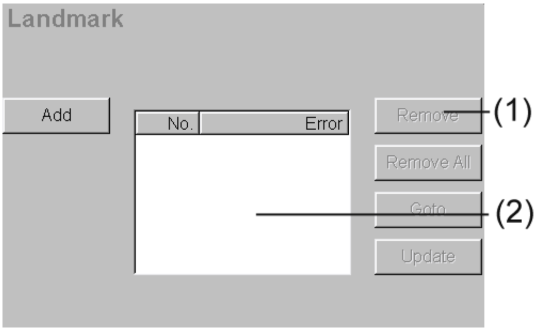
*Aligning images with reference points (the **Landmarks** function is optional)*

Alignment of image series with reference points is an optional function. You apply this method if you have detected distinguishing structures in both data sets.

✧ Click on the **Landmarks** button to display the functions of **Landmarks** in the dialog box **Fusion Registration**.

Or

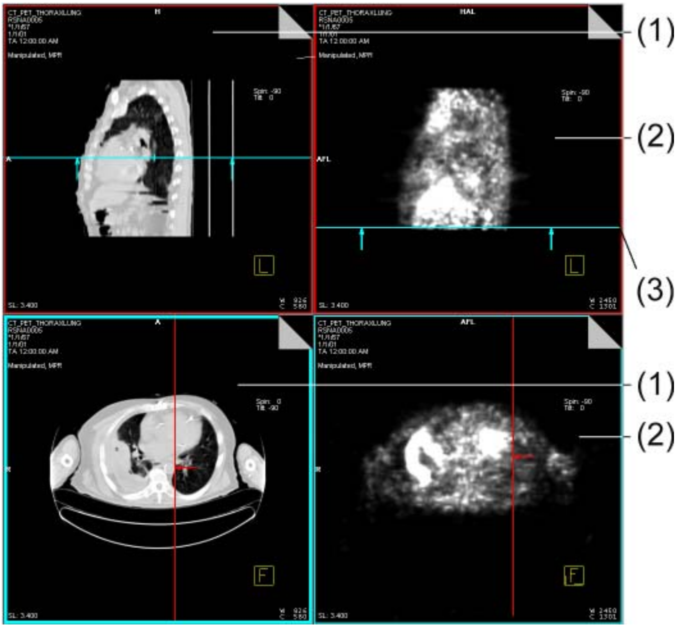
✧ Call up **Settings > Fusion Landmarks** in the main menu.



(1) **Buttons**
for setting and editing reference points.

(2) **List of reference points**
with deviation from the current alignment (when there are at least three defined reference point pairs)

The reference series is displayed in the two left segments and the model series in the right segments of the image area. You can address all the image segments separately.



(1) **Reference images**
Sattigal view above, axial view below

(2) **Model images**
Sattigal view above, axial view below

(3) **Reference *lines***
on all images

Defining reference points

You first define a reference point at a distinguishing location in the volume. Then you place the associated second reference point at the relevant position in the other series. The result is a reference point pair on which your system for aligning a model series to a reference series is based.

✧ Set the views in the reference segments in which you can clearly see the position for the reference point.

✧ Move the crosshair in one of the reference segments to the desired reference point position keeping the left mouse key pressed.

✧ In the other reference segment check whether the crosshair is located at the correct position and move it, if necessary.

✧ Now define the associated reference point on the model side in the same way.

✧ Click on the button **Add** to apply the reference point pair.

The new reference point is numbered and entered in the list of reference points. Your system now anchors the model series at the defined reference points with the reference series.

➩ The more points you define, the more precise the overlaying of the two image series. You must define at least three reference points to determine the spatial alignment of the series.

Displaying a reference point

- Click on the line in the list that refers to the reference point.
- Click on the **Goto** button.

Or

- Double-click on the relevant line.

The crosshair for the reference point is displayed in the image segments. The displayed reference point is displayed in the table with a blue background.

Moving a reference point

- Display one of the reference points.
- Move the crosshairs in both series to the required position keeping the left mouse key pressed.

- Click on the **Update** button.

Deleting a reference point

- Display one of the reference points.
- Click on the **Remove** button.

The marked reference point is deleted.

Saving overlaid images

Last Saved

You can intermediately save any promising alignments you have performed. You can call up these versions whenever you need them with the **Last Saved** button.

> **NOTE**
>
> Whenever you make an improvement by turning and moving the images, you should save the new alignment to the buffer. You can then return to a previous result if the two series start to drift apart again.

💾

✧ Click on the **Save** button to save the current overlaid images.

➪ You can save the alignment as often you want. The previous result is then overwritten by the new one.

Deleting all reference points

✧ Click on the **Remove All** button if you want to delete all defined reference points.

NOTE

When you click on the **Remove All** button all the reference points you set are deleted without a safety query.

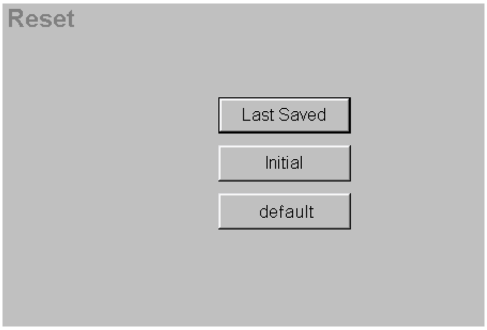
Resetting editing steps

If you want to restart overlaying from the beginning or from an intermediate stage you have saved, call up the **Reset** functions in the dialog box **Fusion Registration**.

✧ Click on the button **Reset**.

Or

✧ Call up **Settings > Fusion Reset** in the main menu.



Last Saved

If the overlaying state has deteriorated during the course of your work, you can return to the step you saved.

✧ Click on the **Last Saved** button to call up the last overlaying version that you stored with **Save**.

Initial position

If the last overlaying that you saved is unsuitable, you can return to the initial position.

✧ To do that, click on the **Initial** button.

Default setting

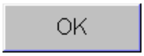
If you are working on a combination device (e.g. CT-PET scanner) you have an additional option; i.e. calling up a default overlaying stored in the system and applying it to the alignment of a reference and model series.

✧ To do that, click on the **default** button.

Closing alignment

If you have overlaid the model series and reference series with sufficient precision you can store the overlaying in the local database.

Applying overlaying



✧ Click on the **OK** button to merge the reference series and the model series into a single image data set.

Canceling overlaying

✧ Click on **Cancel** if you want to cancel your alignment of the images.

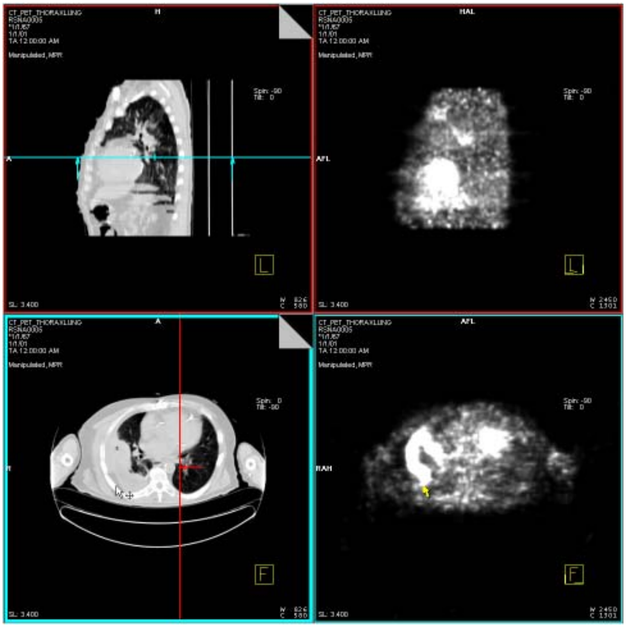
Displaying overlaid images

Once you have aligned the image data sets and confirmed overlaying, you can display the image data sets both next to one another (Side-by-Side) and overlaid (Fusion).

Side-by-Side-mode

In Side-by-Side mode, both image data sets are displayed side by side in separate segments.

✧ Click on the button **Side-by-Side** on the **Fusion** subtask card to activate the Side-by-Side display.



The left image area is used to display the reference images and the right for the model images. To assist assignment in space, two coupled mouse pointers are displayed that move across both data sets synchronously. The coupled mouse pointer is marked in a color.

Setting the view

In Side-by-Side mode, you move through the image stack on the reference segment. The corresponding image is automatically displayed on the model segment. You can change the view of the merged data set by one of the following methods:

- **Paging**
  → Page H.3–17, *Paging with the dog ears*
- **Rotating the volume with the mouse**
  → Page H.3–18, *Rotating the volume with the mouse*
- **Setting standard views**
  → Page H.3–27, *Setting standard views*
- **Using a crosshair**
  → Page H.3–13, *Using the 3D cross hair*

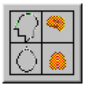
Setting the display mode

In Side-by-Side mode, the following display modes are possible:

- MPR
- MIP Thin
- Fusion

✧ Click on the relevant button on the **Type** subtask card.

Closing Side-by-Side



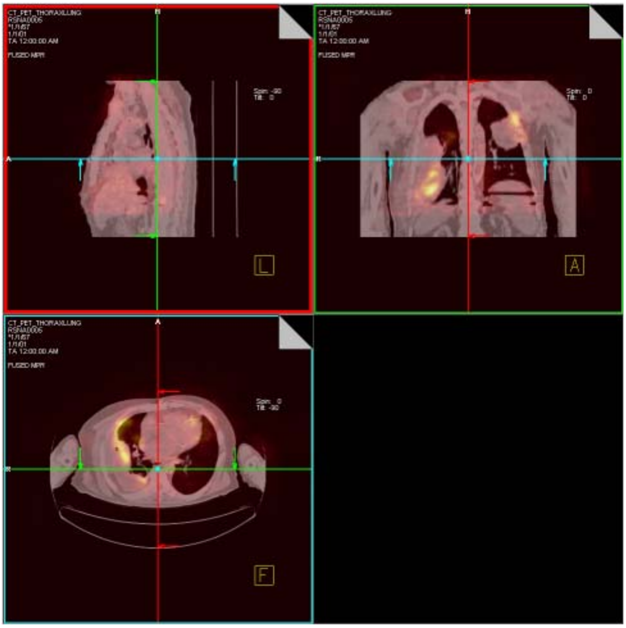
✧ Click on the button **Side-by-Side** to close the Side-by-Side view.

The merged data set is now displayed in fusion mode.

Fusion-mode

In fusion mode, both image data sets are displayed like two slides placed on top of each other.

✧ Click on the **Fusion** button on the **Type** subtask card to switch to fusion mode.



The two image data sets are displayed in different colors to help you distinguish between them. The overlaid image data set is displayed as it is for **Visual Alignment** in three orthogonal displays in three segments.

Setting the view

In fusion mode you move through the image stack in each segment. You can change the view of the merged data set by one of the following methods:

- ❏ **Paging**
  → Page H.3–17, *Paging with the dog ears*
- ❏ **Rotating the volume with the mouse**
  → Page H.3–18, *Rotating the volume with the mouse*
- ❏ **Setting standard views**
  → Page H.3–27, *Setting standard views*
- ❏ **Using a crosshair**
  → Page H.3–13, *Using the 3D cross hair*

NOTE

Creating curved cuts, 3D editor objects, and VOI punchings affects the reference series only

Changing the display

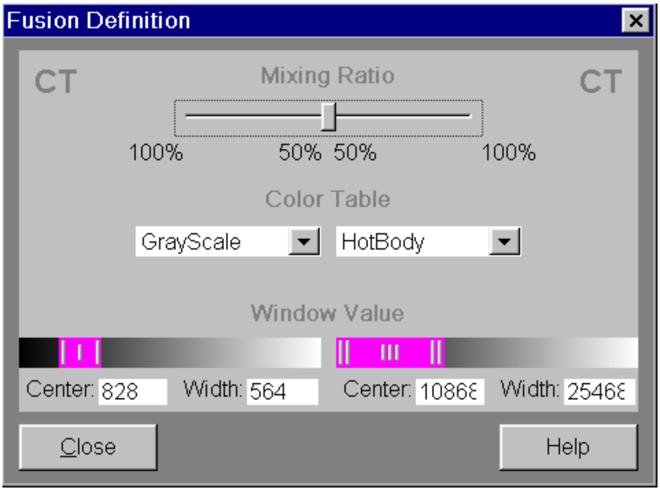
Once you have successfully overlaid your images, you can optimize the window values, the mixing ratio, and display of the images so that you can recognize the structures of individual image data sets for diagnostic evaluation more easily.

✧ To do that click on the **Fusion** button with the right mouse button.

Or

✧ Call up **Type > Fusion Definition** from the main menu.

The dialog box **Fusion Definition** is displayed.

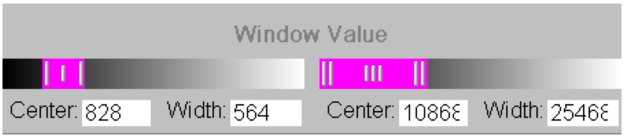


GrayScale

HotBody

Center: 828 Width: 564 Center: 10868 Width: 25468

Windowing



Center: 828 Width: 564 Center: 10868 Width: 25468

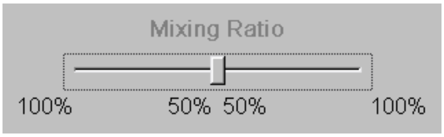
- Move the slider for the data set in question using the left mouse key to change the window position (brightness).
- Move the right or left edge of the slide with the left mouse key to change the window width (contrast).

Or

- Enter the window values numerically into the edit fields and confirm with the **Enter** key.

Mixing ratio

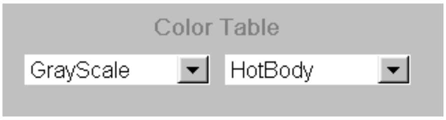
To emphasize certain information of one of the two image data sets, increase its relative importance in the fused image.



- Pull the slider with the left mouse key in the direction of the data set whose intensity you want to increase.

Display

In order to delimit the reference and model series more precisely you can change the color marking of the image data sets.



✧ Select the color representation you want in the selection list for the reference or model data set (LUT, Look Up Table).

CHAPTER H.11

Saving 3D Series and Images

You can store series of images or projections that you have generated on the **3D** task card for documentation purposes.

You can either store the images quickly in a series that already exists or store the images in new series.

You can store reconstructed series automatically as new series after reconstruction.

Storing 3D images manually

Once you have generated a new series of parallel, radial or expand images or projections on the **3D** task card, you can store them in your main database.

➪ In **Configure 3D**, you can set whether you also want to store the reference image of a series or not.
→ Page H.13–6, *Configuring storage*

Saving with the default settings

If you want use the defaults when saving images or series, simply click on the **Save** button.

➪ When you use the save button, the settings that you made in the **Save as** dialog are valid.

✧ Click on the output segment and select an image, several images or an entire series.

✧ Call up **Patient > Save**.

Or

✧ Click on the **Save** button in the lower part of the control area.

Defining setting when saving

The first time you save a reconstructed series you should first make a few default settings.

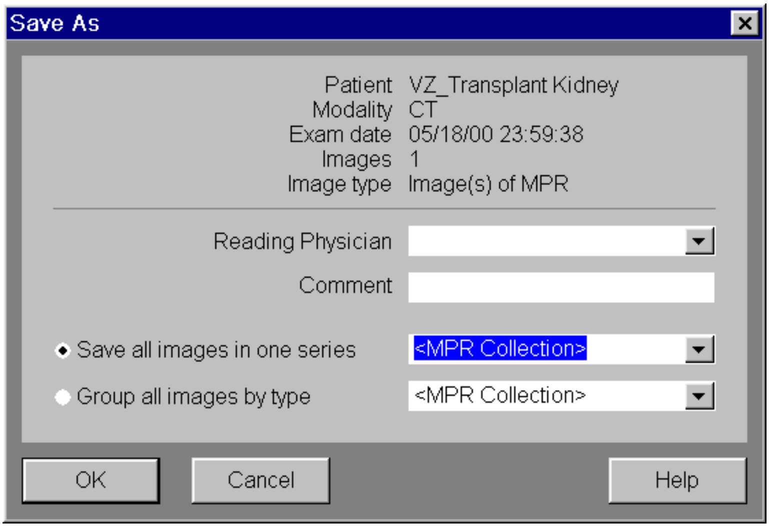
✧ Select an image in a reference segment or the images in the output segment.

✧ Call up **Patient > Save As...**

Or

✧ Click on the **Save As...** button.

The **Save As** dialog box is displayed.



Save As

Patient VZ_Transplant Kidney
Modality CT
Exam date 05/18/00 23:59:38
Images 1
Image type Image(s) of MPR

Reading Physician
Comment

● Save all images in one series <MPR Collection>
○ Group all images by type <MPR Collection>

Image information

You can see this image information in the upper part of the dialog box:

- Patient name
- Imaging method (modality)
- Exam date
- Number of images
- 3D output type (MIP, MIP Thin, MPR, MPR Thick, MPR Curved, VRT, VRT Clip, SSD)

This information is saved together with the series.

Reading physician

✧ Enter the name of the physician to whom you want to provide the series of a patient.

Comments

You can comment on a series. These comments are then saved together with the images.

✧ Enter a comment text.

➩ The input field contains a default comment text which is the comment saved together with the original images. If various original images had different comments, then there will be no default comment text.

Saving images in a series

If you want to save all the images that you generate from a set of volume data in one series, select the **Save all images in one series** option.

All the images are now saved with the same series name in your main database regardless of the 3D output type they were generated with (MPR, MPR Thick, MPR Curved, MIP, MIP Thin, VRT, VRT Clip or SSD).

✧ Click on the **Save all images in one series** option.

✧ Enter a series name or select a name from the selection list.

Every time you generate and save images in **3D** from your original set of data, they are appended to the series entered here.

Grouping images by output type

If you generate images with different output types (MIP, MPR, MPR Thick, MPR Curved, VRT, VRT Clip or SSD) during processing of your original set of data, you can save them in your database sorted by the output type.

● Group all images by type abdomen/KIDNEY_ISO_1

✧ Click on the **Group all images by type** option.

✧ Enter a series name or select a name from the selection list.

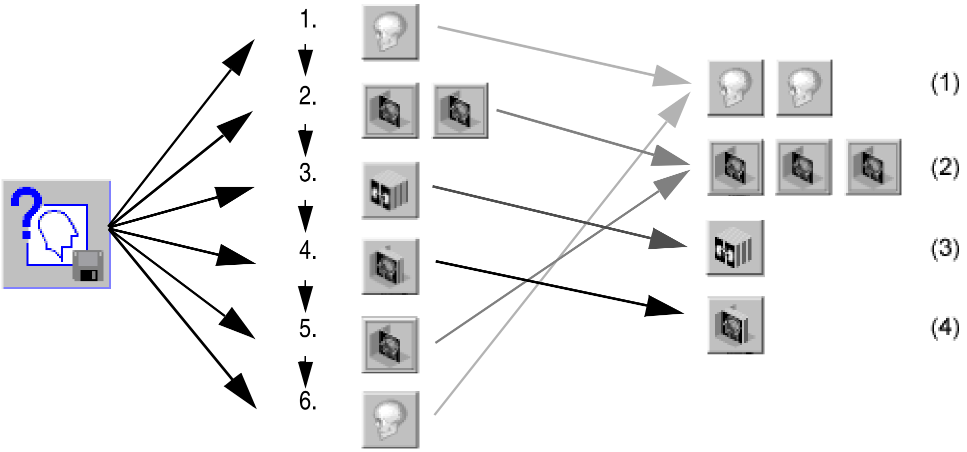
All images that you generate from this original set of data are now saved under this series name and the designation of the output type.

➩ If you generate an entire series of images, these images are always saved with a different series name.
→ Page H.11–8, *Saving 3D-series*

Example

You enter “name” as the series name for your grouped images. You then save 1 SSD image, 2 MPR images, 1 MIP image, 1 MPR Thick image, 1 MPR image, and another 1 SSD image one after the other.

In this way, you generate four series:



(1) name SSD Collection
(2) name MPR Collection
(3) name MIP Collection
(4) name MPR Thick Collection

OK

✧ Save your series by clicking on **OK**.

Or

Cancel

✧ Reject your inputs by clicking on **Cancel**.

Saving 3D-series

You can also save images that you have reconstructed, for example, as parallel images with a comment.

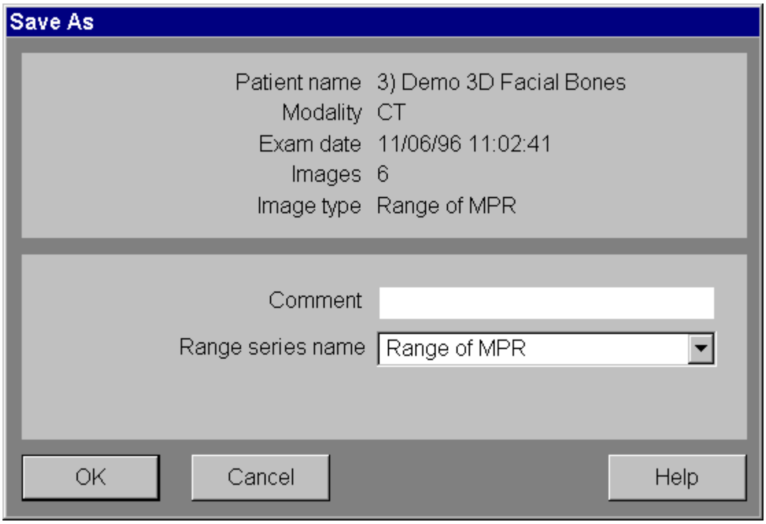
✧ First select the series in the output segment.

✧ Call up **Patient > Save As...**.

Or

✧ Click on the **Save As...** button.

The **Save As** dialog box is displayed.



Patient name 3) Demo 3D Facial Bones
Modality CT
Exam date 11/06/96 11:02:41
Images 6
Image type Range of MPR

Comment
Range series name Range of MPR

Entering series name

Range series name abdomen/KIDNEY_ISO_1

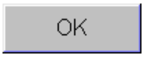
✧ Enter a series name in the combo box.

Or

✧ Select a series name from the selection list.

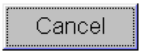
Comments You can enter a comment for a series. These comments are then saved together with the images.

✧ Enter a comment text.



✧ Save your series by clicking on **OK**.

Or



✧ Reject your inputs by clicking on **Cancel**.

Storing series automatically

If you want to store the reconstructed series as quickly and easily as possible, you can have them stored automatically during reconstruction.

✧ Click on the **Enable auto-store** option on the **Ranges** subtask card in **Configure 3D**.
→ Page H.13–6, *Activating automatic storage*

All series are then automatically stored after reconstruction.

➪ In **Configure 3D** you can define whether you want to additionally store the reference image of a series or not.
→ Page H.13–6, *Storing the reference image*

The name of an automatically stored series then consists of the following parts:

❏ the name of the original series or the name that you entered in the “**Range series name**” field in the **Save As** dialog box.

❏ the output types, e.g. MPR

❏ a serial number

➪ With **auto-store**, you can produce large volumes of data very quickly and fill up the capacity of your hard disk. Check the data stored on your hard disk at regular intervals. Archive data that you still require and delete data that you no longer require.
→ Page F.2–1, *Archiving data*

CHAPTER H.12

Filming, Evaluating and Sending 3D images

To film images, send them to the **Filming** application card from where you can send them to the camera or printer.

Or you can send data for further processing to the **Viewing** task card in order to comment new image series using text and graphic elements or to continue processing using the 2D evaluation tools that it provides.

If your system is part of a network you can send data to other workstations in the network where processing can continue.

Filming 3D images

If you want to document the images or series, you can send them to a camera or printer for exposure on film or for printing on paper.

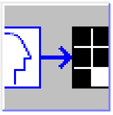
✧ Select an image in the reference segment by clicking on it.

Or

✧ Select the images in the output segment.

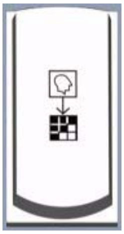
✧ Call up **Patient > Copy to Film Sheet**.

Or



✧ Click on the **Copy to Film Sheet** button in the lower part of the control area of the **3D** task card.

Or



✧ Press the **Copy to Film Sheet** key on the symbol keypad.

Depending on the settings that you have defined for the film layout, the images are transferred to the camera or printer directly or remain on the **Filming** task card for processing until you send them to the camera/printer manually.
→ Chapter G.2, *Automatic/Manual Filming*

➩ In **Configure 3D**, you can set whether you also want to film the reference image of a series or not.
→ Page H.13–7, *Configuring filming*

Transferring images to the Viewing task card

If you want to evaluate or process selected images in 2D, you need to transfer the images to the **Viewing** task card.

✧ Select an image in a reference segment by clicking on it.

Or

✧ Select the images in the output segment.

✧ Call up **Patient > Copy To Viewing**.

Or

✧ Click on the **Copy To Viewing** button in the lower part of the control area.

The images are transferred to the **Viewing** task card and you can process them there.
→ Page E.4–1, *Processing Images*
→ Page E.5–1, *2D Evaluation*

CAUTION

Source of danger: Thickness and length measurements on MIP and SSD images do not reflect the actual anatomical conditions.

Consequence: wrong diagnosis possible

Remedy: Do not perform thickness and length measurements on MIP and SSD images.

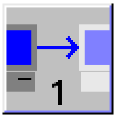
Sending images through the network and archiving

If you want to send 3D images to another location in your hospital, you can do this directly from the **3D** task card.

✧ Select an image in the reference segment by clicking on it.

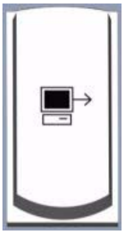
Or

✧ Select the images in the output segment.



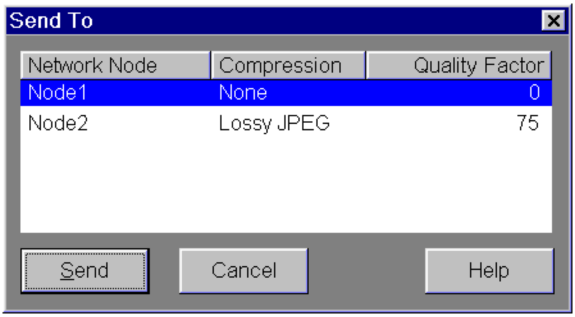
✧ Click on the **Send To Node 1** button in the control area of the **3D** task card.

Or



✧ Press the **Send To Node 1** key on the symbol keypad.

The **Send To** dialog box is only displayed if more than one network node has been configured.



Network Node	Compression	Quality Factor
Node1	None	0
Node2	Lossy JPEG	75

✧ Select the destination workstation or destination database.

✧ Click on the **Send** button to transfer the selected images.

➩ With the **Transfer** menu item, you can access further functions for archiving and sending.
For detailed information, see:
→ Page F.1–2, *Automatic archiving and sending*

CHAPTER H.13 3D Configuration

In **3D Configuration**, you can adapt several settings:

❏ Hide or show orientation description

❏ Automatic storage of series

❏ Storage with reference image

❏ Filming with reference image

❏ Automatic orientating of the reference image.

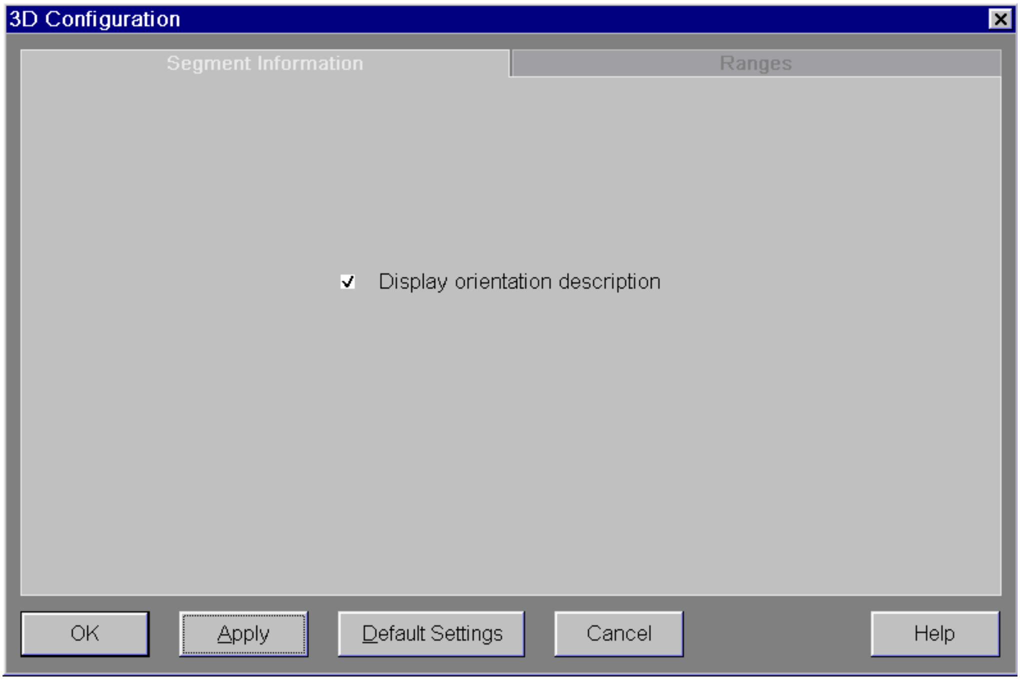
✧ Call up **Options > Configure 3D** to display the **3D Configuration** dialog box.

➪ In the Basics part of this manual, you can read how to call up the configuration window and exit it again, store changes and reset the settings to their as supplied state.
→ Chapter A.2, *Configuring the User Interface*

Configuring image information

Various orientation aids are displayed in the images which you can configure.

✧ Move the **Segment Information** card into the foreground.



☑ Display orientation description

Displaying the orientation description

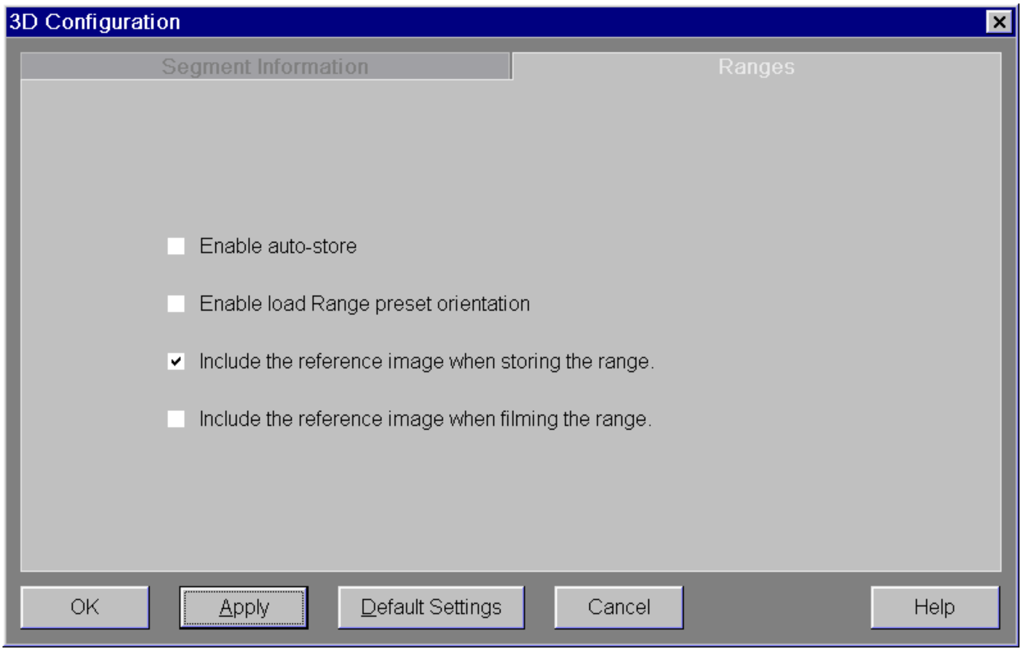
☑ Display orientation description

✧ Click on the **Display orientation description** option if you want to have the orientation description displayed.
→ Page H.3–5, *Orientation aids in the image*

Configuring processing of series

On the **Ranges** card, you can define the settings for storing and filming series. In addition, you can configure the orientation of the reference image when generating parallel ranges.

✧ Click the **Ranges** subtask card into the foreground.



☐ Enable auto-store

☐ Enable load Range preset orientation

☑ Include the reference image when storing the range.

☐ Include the reference image when filming the range.

Configuring the orientation of the reference image

When you generate parallel series using the stored defaults, you have the option of having reference image orientation set in the defaults called up automatically.

☑ Enable load Range preset orientation

✧ Just click on the **Enable load Range preset orientation** option.

When you call up the dialog for creating parallel series in future, the reference image is reoriented automatically. The orientation is used that you set for the reference image when you saved the default of the group of series in question.

Configuring storage

Reconstructed series (ranges) can be stored completely automatically with or without the reference image.

Activating automatic storage

☐ Enable auto-store

✧ Click on the **Enable auto-store** option if you want to have all reconstructed series stored automatically.

Storing the reference image

☑ Include the reference image when storing the range.

✧ Click on the option **Include the reference image when storing the range** if you want to have the reference image of the series stored, too.
→ Page H.3–47, *Generating series from 3D images*

Configuring filming

Reconstructed series can be filmed with or without the reference image.

☑ Include the reference image when filming the range.

✧ Click on the option **Include the reference image when filming the range** if you want to have the reference image of the series filmed, too.

PART
J

Osteo (Option)

J.1 Introduction

J.2 Loading and displaying images

J.3 Evaluating vertebral scans

J.4 Configuring Osteo Evaluation

CHAPTER J.1 Introduction

With the **Osteo** task card, you can quantitatively determine the bone mineral content of vertebrae with a high degree of precision.

Osteo Evaluation consists of automatic and semiautomatic procedures for defining the vertebral contours. The bone mineral densities of the vertebrae are calculated and can be used for comparison with the Siemens Standard Reference Data. The Siemens Standard Reference Data is age- and gender specific. The data results from a European multicenter study on 274 patients.

Original data for evaluation with **Osteo** are sequence data sets that were acquired with the special **Osteo** scan protocols. You can select them under **Specials** in the examination list during patient registration.

You should perform the **Osteo** scan acquisition with the Siemens Reference Phantom.
→ SOMATOM Operator Manual, page C.3–32, *Vertebrae examinations with Osteo*

NOTE

Osteo examinations should be completed with **End Exam**, otherwise some **Osteo** evaluation steps are not possible.

The evaluation results are then calibrated with the measured values of water and bone equivalent portions of the phantom. In this way, a reliable comparison of the calculated bone density with the reference data is possible.

NOTE

Osteo evaluation of examinations without a Siemens reference phantom is not recommended. However, if you do want to perform a bone density calculation for such image material, you must enter the necessary calibration values manually.
→ Page J.4–4, *Entering calibration values without a reference phantom*.

Calling up Osteo

You can call up the **Osteo** evaluation card without loading a series so that it is initially empty.

✧ Call up **Patient > Osteo** in the main menu.

The **Osteo** task card is displayed. All buttons and most menu entries are still grayed out.

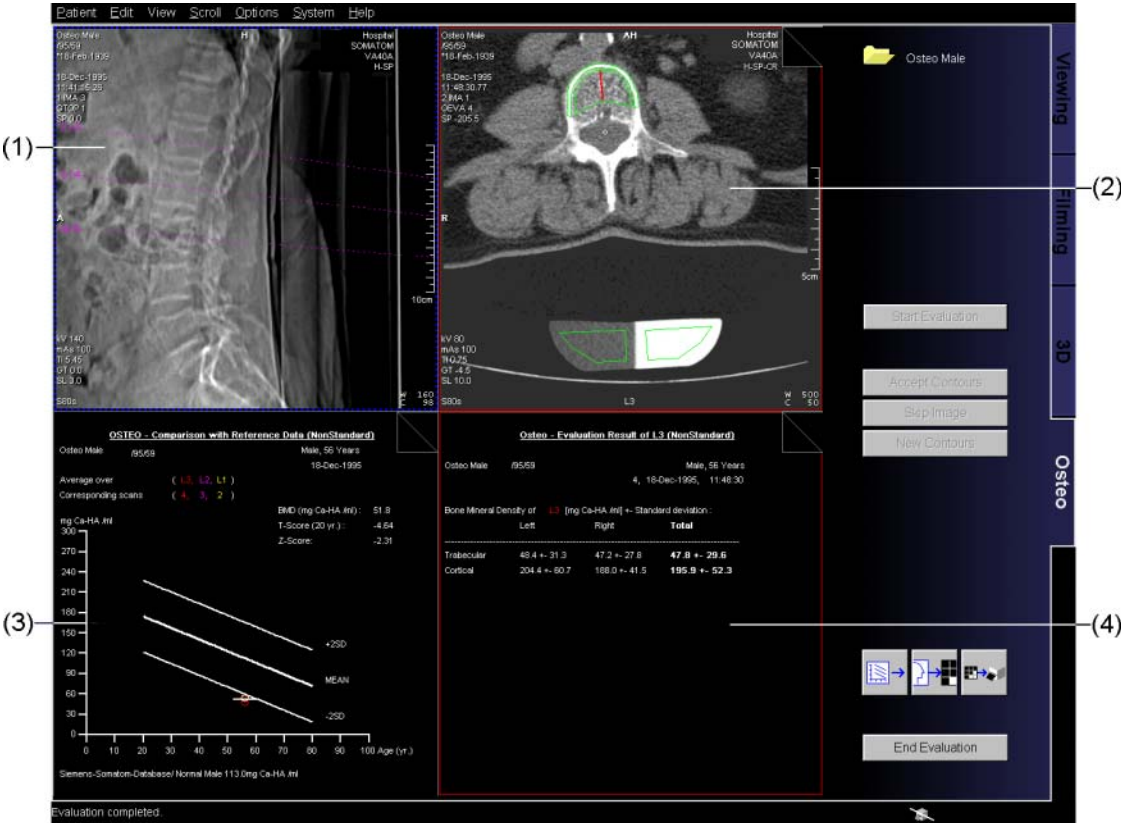
Or

✧ Click on the **Osteo** tab if you have switched to another task card in the meantime.

The **Osteo** card is subdivided into two large areas, the **control area** with the buttons, and the **image area** for displaying the original images and results.

For the result display, the image area is subdivided into four segments.

When it is first called up and during the evaluation, the image area is displayed with 1:1 layout.



OSTEO - Comparison with Reference Data (NonStandard)

Osteo Male /95/59 Male, 56 Years

18-Dec-1995

Average over (L3, L2, L1)

Corresponding scans (4, 3, 2)

BMD (mg Ca-HA /ml) : 51.8

T-Score (20 yr.) : -4.64

Z-Score: -2.31

Siemens-Somatom-Database/ Normal Male 113.0mg Ca-HA /ml

Osteo - Evaluation Result of L3 (NonStandard)

Osteo Male /95/59 Male, 56 Years

4, 18-Dec-1995, 11:48:30

Bone Mineral Density of L3 [mg Ca-HA /ml] +- Standard deviation :

	Left	Right	**Total**
Trabecular	48.4 +- 31.3	47.2 +- 27.8	**47.8 +- 29.6**
Cortical	204.4 +- 60.7	188.0 +- 41.5	**195.9 +- 52.3**

Evaluation completed.

(1) Topo segment
(2) Tomo segment
(3) Statistics segment
(4) Result segment

Closing Osteo

As soon as you no longer want to perform an Osteo evaluation, you can close the **Osteo** task card again.

✧ Call up **Patient > Close Osteo**.

The task card is closed, the **Osteo** tab disappears again.

Or

✧ Call up another task card, e.g. **Pulmo** or **Dental** and confirm the displayed dialog box with **Yes**.

The **Osteo** task card is closed and another task card is displayed instead.

CHAPTER
J.2

Loading and displaying images

On the **Osteo** task card you can perform a bone mineral density calculation of the vertebrae using the tomograms of the Osteo examination.

Prerequisites

For standardized evaluation and a standardized comparison with reference data, examination data are required that have been acquired with an Osteo scan protocol using the Siemens reference phantom.

In general, the image data set must fulfill the following conditions:

- ☐ The patient must be positioned specifically for the Osteo examination.
- ☐ The image data set must consist of 3 vertebrae L1 – L3.
- ☐ The scans must be performed with the same fixed table height of 125 mm (tolerance ± 1 mm).
- ☐ Only original or lossless compressed images must be used.
- ☐ The Osteo scan protocol must be used.

Loading original images

You can load images of the Osteo examination from the **Patient Browser** into the **Osteo** task card.

➩ Before loading onto the **Osteo** task card, your system checks whether the images you selected are suitable for an Osteo evaluation. If they are not, the **Osteo** card remains empty and all buttons are grayed out.

Transferring images with the Patient Browser

In the **Patient Browser** window you can search for the examination, series, or images that you want to load onto the **Osteo** task card.

✧ Call up the **Patient Browser** (**Patient > Patient Browser**).

✧ Select the required examination data in the navigation or content areas.
→ Page D.2–6, *Scrolling through and selecting patient data*

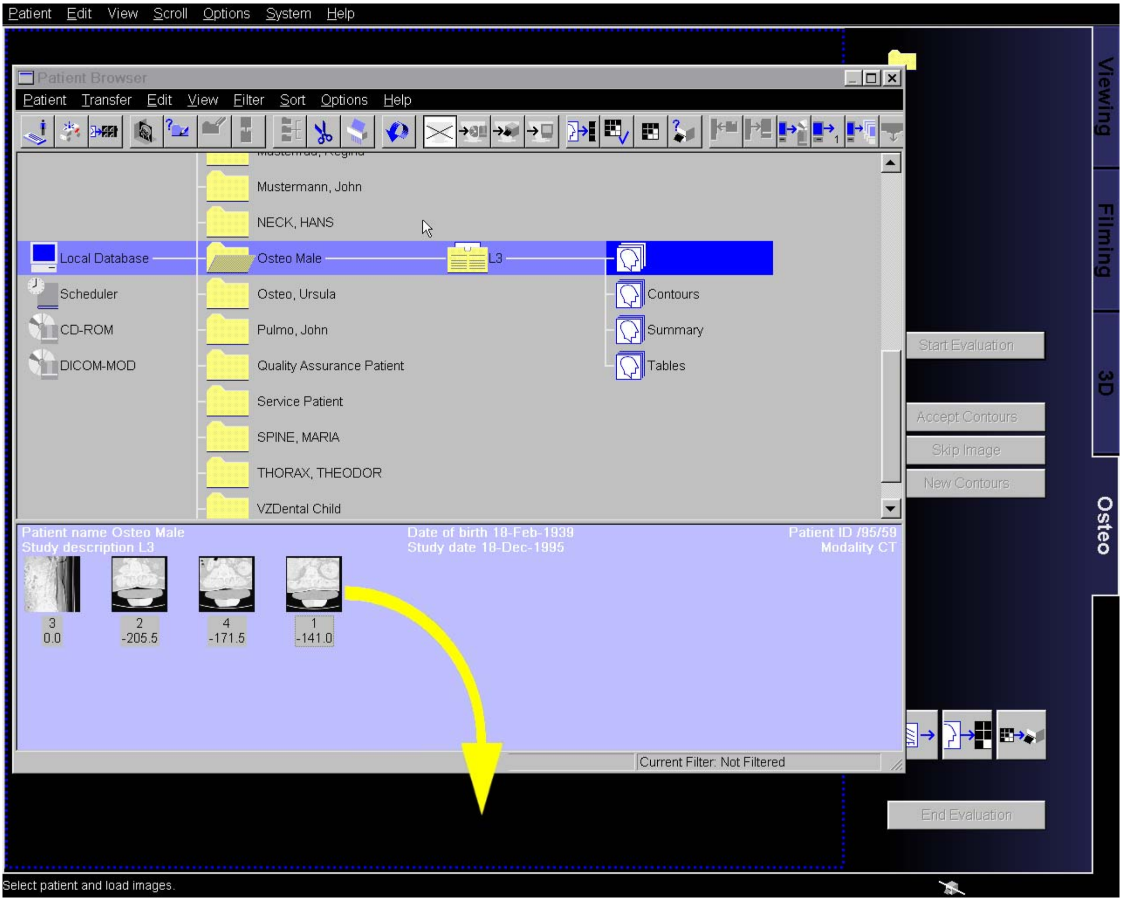
✧ Call up **Patient > Osteo** or click on the **Osteo** button on the tool bar of the **Patient Browser**.

Or

✧ Place the **Osteo** card topmost up in the stack and double-click on the required entry(ies).

Or

✧ Drag and drop your selection onto the task card **Osteo** with the mouse.



Patient name Osteo Male
Study description L3
Date of birth 18-Feb-1939
Study date 18-Dec-1995
Patient ID /95/59
Modality CT

Current Filter: Not Filtered

Select patient and load images.

➩ If **Close after Loading** is activated, the **Patient Browser** dialog box is closed as soon as the images have been loaded onto the **Osteo** task card.

Changing image settings

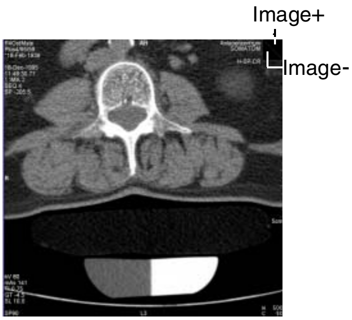
On the Osteo task card, the loaded images are displayed in 1:1 layout grouped by series.

Scrolling

If you have loaded several images for Osteo evaluation, the tomograms are displayed as a stack of images.

You can scroll through the image stack before and after the Osteo evaluation. In the latter case you can view the individual vertebra with the respective evaluation result.

Scrolling image by image



To scroll image by image:

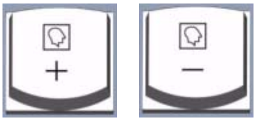
✧ Click into the outside triangle to scroll forward or on the dog-ear to scroll back by one image.

To scroll image by image within one series:

✧ With the mouse click into the stack in which you want to scroll.

✧ Call up **Scroll > Next image** or **Scroll > Previous image** to scroll forward or back by one image.

Or



✧ Scroll using the **Image+** and **Image-** keys on the symbol keypad.

Scrolling from series to series

In addition to scrolling image by image, you can also scroll whole series forward or back if you have loaded several series of an examination into the Osteo task card.

✧ Call up **Scroll > Next series** or **Scroll > Previous series** in the main menu to scroll forward or back by one series.

Or

✧ Click on the **Series+** or **Series-** key on the symbol keypad to go to the next or previous series.

Windowing images

Before you begin with the Osteo evaluation, you can change the window setting for optimum display of the images.

Windowing with the mouse

✧ Click into an image segment with the center mouse key and keep the mouse key pressed.

The mouse cursor disappears.

✧ Move the mouse up/down to vary the brightness (Center)

Or

✧ Move the mouse right/left to alter the contrast (Width).

Windowing with the control box

✧ Window the images with the tuning knobs on the control box (only Navigator).
→ Page E.4–10, *Windowing with the control box*

CHAPTER
J.3

Evaluating vertebral scans

After you have loaded images for bone density calculation onto the **Osteo** card, you can start the evaluation of the vertebral scans.

Procedure

The vertebral scans are evaluated image by image by your system. In individual tomograms you can check the delimitation of vertebral regions suggested by the system and the regions in the Siemens reference phantom and correct them if necessary.

The evaluation is performed in the following steps:

- ❑ Start evaluation with the first tomogram.
- ❑ Automatic positioning of one ROI each in the water and bone equivalent portion of the reference phantom.
- ❑ Automatic definition and drawing of the vertebral contours.
- ❑ Check and, if necessary, redefine the suggested ROIs and contour line.
- ❑ Continue evaluation with the next tomogram.

Performing an evaluation

As part of the evaluation, the Hounsfield units of water and bone equivalent portions are determined in the reference phantom. The values are later used for the correction and calculatic of the bone mineral density in the vertebral.

NOTE

Slice acquisitions with the Siemens reference phantom are a prerequisite of standardized evaluation of the vertebral scans.

Evaluation of image material without a Siemens reference phantom is not recommended. If you do want to perform bone density calculation, you must first enter the necessary calibration values.
→ Page J.4–4, *Entering calibration values without a reference phantom*.

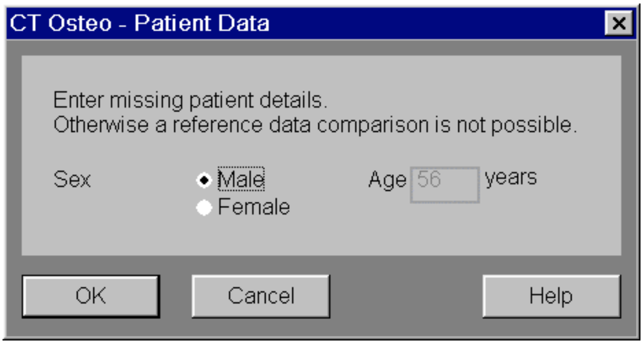
Starting evaluation

As soon as you have loaded images onto the **Osteo** task card, the **Start Evaluation** button is activated in the upper part of the control area.

✧ Click on the **Start Evaluation** button to start evaluation.

Adding missing patient data

The age and sex of the patient are taken into account in Osteo evaluation. If this information is missing, a dialog box is displayed.



CT Osteo - Patient Data

Enter missing patient details.
Otherwise a reference data comparison is not possible.

Sex ● Male ○ Female

Age 56 years

✧ Click on the appropriate radio button to enter the sex of the patient.

✧ Enter the age of the patient in the input field.

➩ Data that you have already entered during registration remains grayed out and cannot be altered.

✧ Confirm your changes with **OK**.
They will then be used for the evaluation.

Or

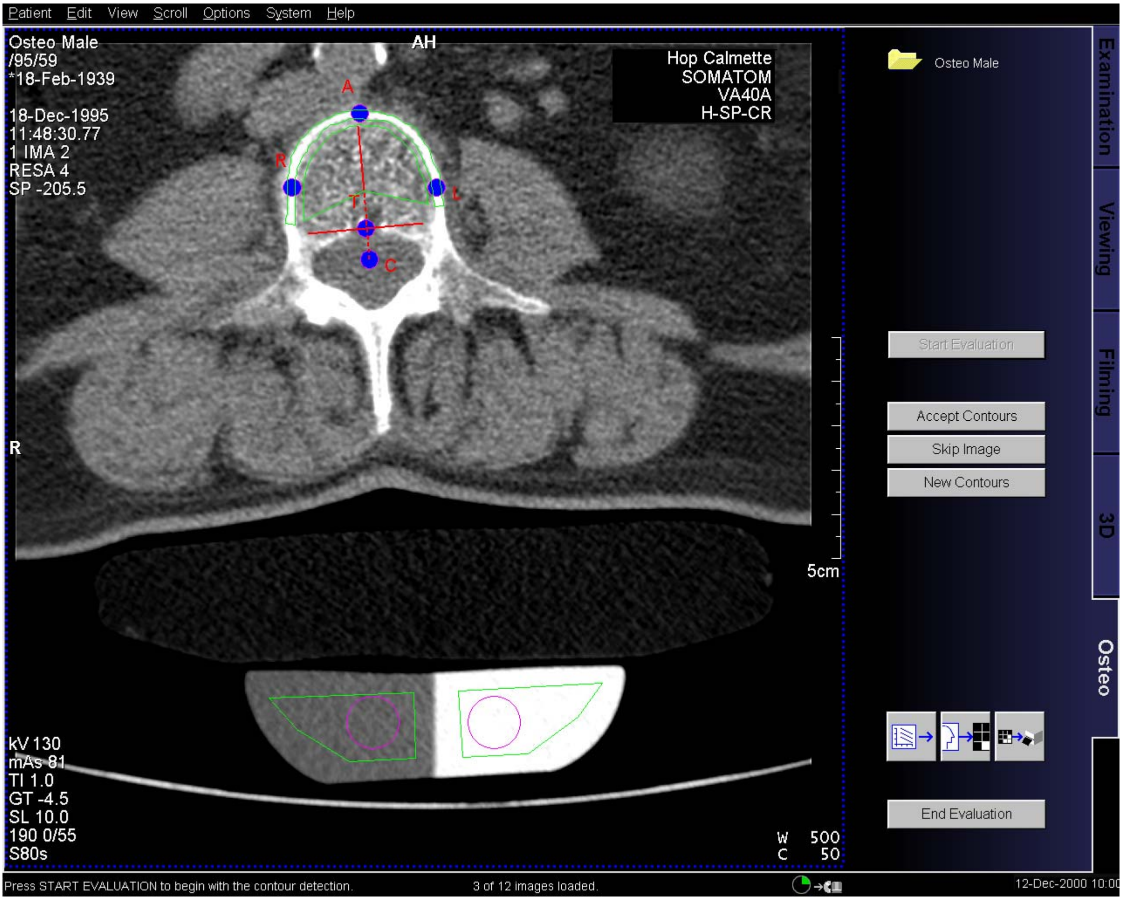
✧ Cancel input of data with **Cancel**.

➩ For patients under 20 or over 80 years of age, no Z-score comparison is displayed.

➩ For patients over 100 years no bone density values can be displayed graphically.

Automatic definition of the ROIs and contour lines

In the first loaded image, one ROI is positioned each in the bone equivalent and in the water equivalent portion. This is followed by automatic contour definition of the vertebral regions.



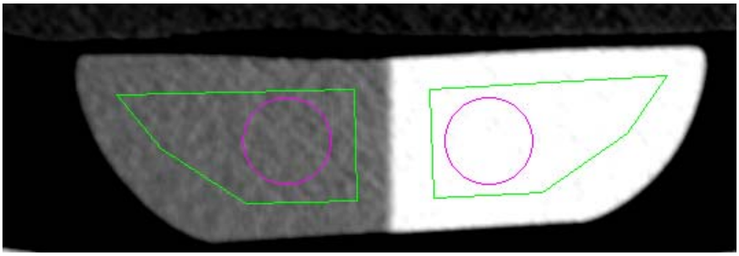
Press START EVALUATION to begin with the contour detection.

3 of 12 images loaded.

ROIs in the reference phantom

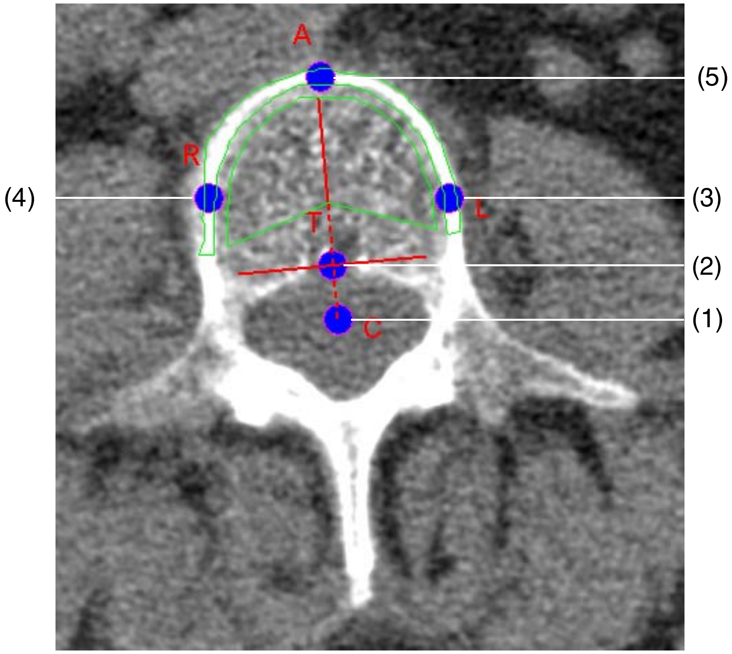
The ROIs of the reference phantom are displayed with green lines.

The circles for positioning are highlighted with purple lines and can be moved interactively.



Vertebral contour lines

The contours of the cortical substance and trabecular bone are marked by a green line. With the base points (blue) and the base line (red), you can alter the contour line if necessary.



(1) Center of the spinal canal (C)
(2) Uppermost point of the spinal canal (T)
(3) Intermediate point, on the anatomical left (L)
(4) Intermediate point, on the anatomical right (R)
(5) Uppermost point of the cortical spinal body (A)

Starting evaluation of the next tomogram

The vertebral contours and the ROIs in the reference phantom are usually positioned correctly. You can then confirm the contour definition and continue with evaluation of the next tomogram.

If the current slice image is not suitable for bone density calculation, you can skip it.

✧ Click on **Accept Contours** or press the space bar to accept the suggested contour line definition.

The contours and bone density values of the current image are then saved.

Or

✧ Click on **Skip Image** to reject the tomogram.

The system now begins with evaluation of the next tomogram.

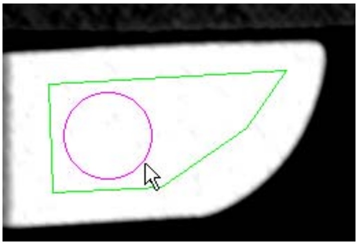
Editing ROIs and contour lines

If the ROIs in the reference phantom or the contour lines in the vertebral region are not correctly positioned, you can correct them using the mouse. If a contour line is missing, you can have it calculated by moving the base points to the correct position.

➩ The **Accept Contours** button remains grayed out if the contour lines are absent in the tomogram or if the phantom could not be detected.

Correcting phantom ROIs

If the ROIs in the reference phantom are placed in at the wrong position, correct their position with the mouse.



✧ Click on one of the two circles and move it to the correct position.

The second circle is also moved with the same action.

➩ If it is not possible to correct the ROIs or the reference phantom cannot be seen, reject the tomogram (**Skip Image**).

Editing contour lines

In general, automatic contour finding is very precise and reproducable. If you are not satisfied with the suggested contour, you can correct it manually.

You can perform correction of the contours by moving the base points.

Center of the spinal canal

As the first base point in the vertebral region you should always check the position of the center of the spinal canal and correct if necessary.

➪ In rare cases, it might not be possible to find (C). In that case you are prompted to mark the center of the spinal canal with the mouse.

✧ Click on reference point C with the mouse and move it to the correct position keeping the mouse key pressed.

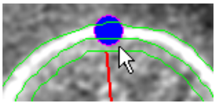
As soon as the center of the spinal canal has been moved, the system recalculates the cortical and trabecular contour lines.

➪ Base points that have already been modified are not recalculated but remain where they were.

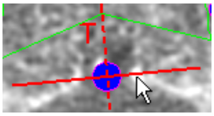
Correcting contour lines

If you move the remaining base points you can adapt the contour line marked on the vertebra.

We recommend editing base point A, then L or R and last of all, T.



✧ Click on a base point with the mouse and move it keeping the left mouse key pressed.



✧ Move the base line at T, if you want to change the position of base point T.

Contour line recalculation

If the positioning of the contour lines becomes worse after you have moved the base points, you can have all base points recalculated. In that way, you can restore the original definition of the contour lines.

✧ Click on the **New Contours** button.

✧ Then correct the position of the guidance points again starting with base point C.

Completing the contour line change

As soon as the ROIs and contour lines have been positioned correctly, you can accept the image. If it is not possible for an image, you can reject it.

✧ Click on **Accept Contours** or press the space bar as soon as the contour lines have been correctly adapted to the structure of the vertebral region.

Or

✧ Click on **Skip Image** if adaptation is not possible.

Output of evaluation results

When you have completed contour line definition in all loaded tomograms, your system switches the image area display to 4:1 layout.

The evaluation results are displayed in the two lower segments.

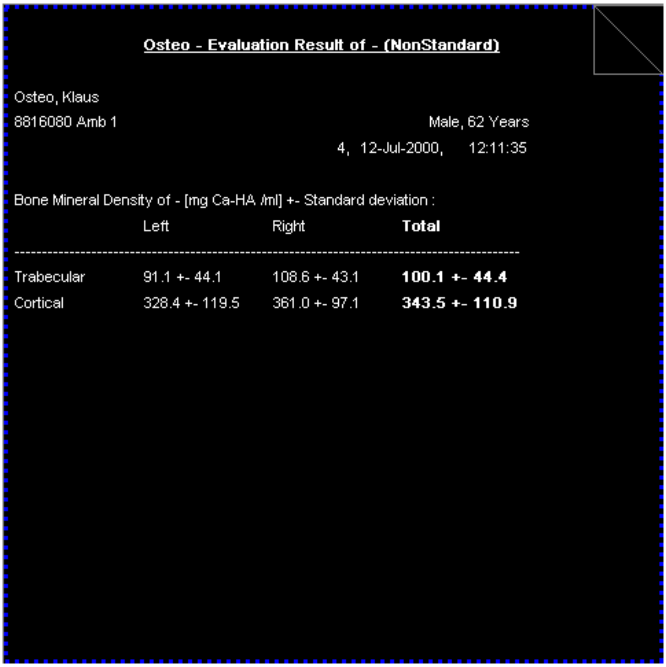
Bone density values of individual vertebrae

A table showing the bone density values appears in the result segment (bottom right) for the corresponding tomogram (top right).

The cortical and trabecular bone mineral content is specified for the anatomical right and left side and for the entire vertebral body (with standard deviation) in Ca-HA/ml (calcium hydroxy apatite).

The vertebra scanned is identified in the image title if the vertebra name is available in the image comment.

➪ We recommend to enter the name of the vertebraes as image comments (L1, L2, ...) during the examination.



Osteo - Evaluation Result of - (NonStandard)

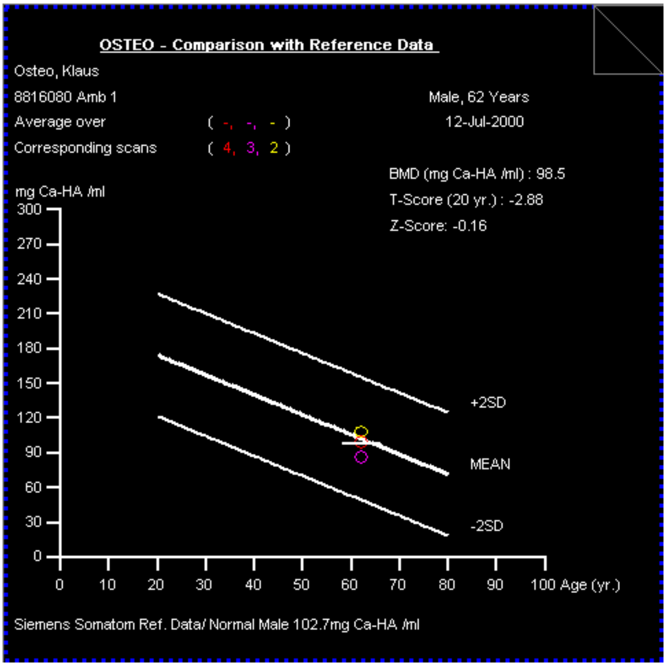
```
Osteo, Klaus
8816080 Amb 1                                              Male, 62 Years
                                           4,  12-Jul-2000,     12:11:35

Bone Mineral Density of - [mg Ca-HA /ml] +- Standard deviation :
                  Left              Right             Total
-------------------------------------------------------------------------
Trabecular        91.1 +- 44.1      108.6 +- 43.1     100.1 +- 44.4
Cortical          328.4 +- 119.5    361.0 +- 97.1     343.5 +- 110.9
```

✧ Scroll through the stack of tomograms or result images to list the bone density values of the other vertebrae.

➪ When you scroll through the tomo segment the result images are scrolled through in parallel and vice versa.

Comparison statistics

In the statistic segment (bottom left) you can see the graphic representation of the average bone mineral content of the patient as compared with the reference data.



OSTEO - Comparison with Reference Data

Osteo, Klaus

8816080 Amb 1

Male, 62 Years

Average over (-, -, -)

12-Jul-2000

Corresponding scans (4, 3, 2)

BMD (mg Ca-HA /ml) : 98.5

T-Score (20 yr.) : -2.88

Z-Score: -0.16

Siemens Somatom Ref. Data/ Normal Male 102.7mg Ca-HA /ml

The center line (MEAN) represents the bone mineral density curve for healthy persons.

The two adjacent lines correspond to twice the standard deviation upward and downward.

The average bone mineral content of the examined patient appears in the graphic as a small horizontal line, the individual vertebrae results as small colored circles.

The numeric value is given in the image text (BMD = bone mineral density).

The **T Score** value in Osteo evaluation expresses the deviation of the average bone density value of the examined patient from the average bone density value of a 20-year-old healthy control. You can configure the age of the control.
→ Page J.4–5, *Age of young controls*

The **T Score** value is normalized using the standard deviation of the reference collection.

Formula: [BMD (patient) - BMD (young healthy patient within reference group)] / SD (reference group)

The **Z Score** value is a measure of the deviation of the average bone density of the patient from the average bone density of a healthy person of the same age. The **Z Score** value is also normalized using the standard deviation of the reference collection.

Formula: [BMD (patient) - BMD (healthy patient of same age within reference group)] / SD (reference group)

SD = Standard deviation

Filming and exporting results

You can film the results of an Osteo evaluation directly from the **Osteo** task card quickly and easily. If your configuration permits it, you can store your evaluation results as a text file to diskette.

Filming

The buttons for filming become active as soon as you have completed evaluation of the tomograms.

✧ Select the images or series to be filmed with **Edit > Select All** in the main menu.

✧ Click on the button **Copy to Film Sheet** to transfer the result images to the **Filming** card.

✧ Then click on the button **Expose Film Task** to expose all images on the **Filming** card to film on a preset camera.

Exporting to diskette

You can transfer the results of your Osteo evaluation to diskette in order to process the data at another workstation, for example, with a spreadsheet program.

✧ Insert a formatted diskette in your diskette drive.

✧ Click on this button to export the results of the current examination to diskette.

➪ This button is not displayed in standard mode. You can activate this setting in the window **CT Osteo Configuration** (call up **Options Configuration** and select **CT Osteo**).
→ Page J.4–6, *Enabling export of data to diskette*

The evaluation results are written to diskette as a structured ASCII file. You can further process this data in any program that supports ASCII format.

You can append further evaluation results to the existing file.

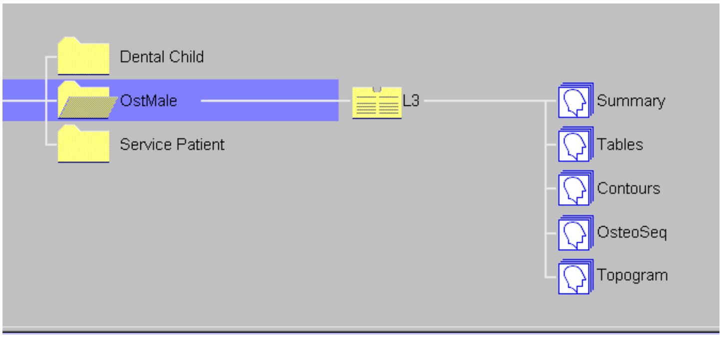
Terminating evaluation

When you have completed all the steps of the current examination, you can terminate evaluation. The **Osteo** card is then empty again and you can start the examination of another person.

✧ Click on **End Evaluation** to close the current evaluation.

All images and evaluation results are stored as new series of the examination in the local database.

You can call up, transfer, or archive these data any time via the **Patient Browser**.



CHAPTER J.4

Configuring Osteo Evaluation

In **Osteo Configuration** you adapt the evaluation functions of the **Osteo** task card to your requirements.

You can make or modify the following settings here:

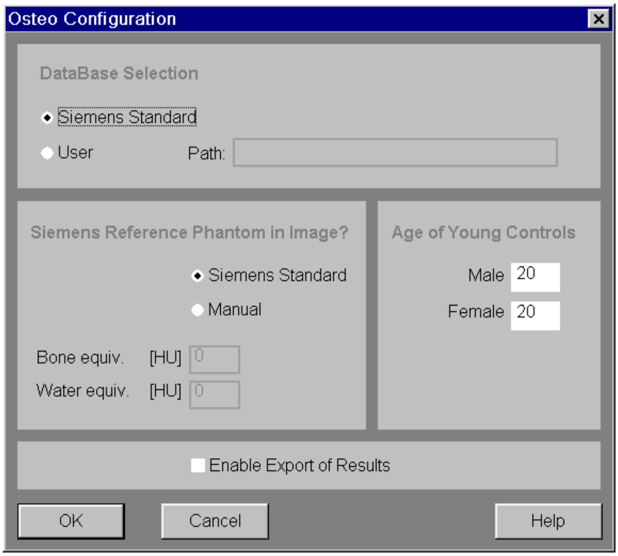
- Reference Data selection
- Calibration values without reference phantom
- Age of young controls
- Exporting results to diskette

✧ Call up the **Configuration Panel** (**Options > Configuration** in the main menu).

✧ Select the configuration window of the task card **CT Osteo**.

CT Osteo

The window **Osteo Configuration** is displayed.



Osteo Configuration

DataBase Selection

● Siemens Standard

○ User Path:

Siemens Reference Phantom in Image?

● Siemens Standard

○ Manual

Bone equiv. [HU] 0

Water equiv. [HU] 0

Age of Young Controls

Male 20

Female 20

☐ Enable Export of Results

OK

✧ Click on **OK** to save the new settings

Or

Cancel

✧ Click on **Cancel** to close the **Osteo Configuration** window without any changes.

Selecting a reference table

Comparison data from a reference table are used for the statistical comparison of the actual bone density data with data of healthy patients.

The Siemens reference table is the default table set when your system is installed.

However, you can use other reference data for your Osteo evaluation.


DataBase Selection

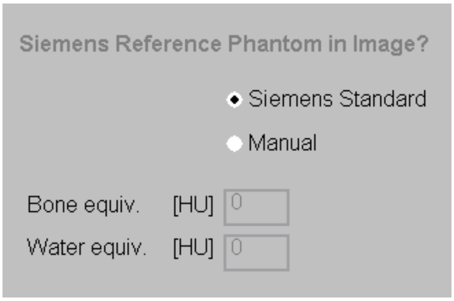
● Siemens Standard

○ User Path:

✧ Please consult Siemens Service if you want to use another reference tables.

Entering calibration values without a reference phantom

It is possible, but not recommended, to evaluate the tomograms of vertebrae without a reference phantom. In that case, you must enter the water and bone equivalent calibration values manually.



Siemens Reference Phantom in Image?

● Siemens Standard

○ Manual

Bone equiv. [HU] 0

Water equiv. [HU] 0

✧ Click on **Manual** to perform Osteo evaluation without a reference phantom.

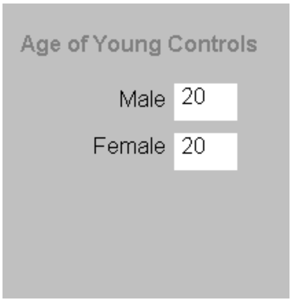
✧ In the fields **Bone equiv. [HU]** and **Water equiv. [HU]**, enter the bone and water equivalent values.

The evaluated images do not correspond to a standard evaluation and are indicated as such.

Age of young controls

In the Osteo evaluation, the **T Score** value specifies the deviation of the bone density value of the examined person from a young, healthy control, normalized using the standard deviation of the reference data. The age of the control can be configured and should be between 20 and 30 years.

✧ Enter the age of the male and female control group.



Age of Young Controls

Male: 20

Female: 20

➩ The age range of the control groups must be between 20 and 80 years.

Enabling export of data to diskette

You can save the data of your Osteo evaluation to diskette in ASCII format.

You can enable or disable this function in **CT Osteo Configuration**.

✧ Check the check box **Enable Export of Results** to allow the transfer of results to diskette.

PART
K

Pulmo (Option)

K.1 Introduction

K.2 Loading and displaying images

K.3 Pulmo Evaluation in Standard Mode

K.4 Extended functions in Pulmo

CHAPTER

K.1 Introduction

With **Pulmo** you can evaluate CT images of the lung for density and structure values.

Pulmo offers you an automatic and semi-automatic procedure to isolate the lung parenchyma, to calculate the lung density, display statistical results and compare your examination values with individual average values of healthy persons.

Comparison with reference data

The lung density of a patient varies depending on the respiratory status, i.e. if the scan is performed during full inspiration, full expiration or at a level inbetween (defined as a percentage of the vital capacity). Therefore a comparison of two scans only makes sense if the scans were performed at the same respiratory level.

NOTE

The Siemens reference data for lung-healthy individuals was acquired at 50% vital capacity. For a meaningful comparison of the current patient with the Siemens reference data, the current patient must also be scanned at 50% vital capacity.

As default, a reference comparison is switched off.

Standard mode and extended functions

With **Pulmo** you can perform lung evaluations fast and largely automatically. You use the basic configuration of the task card as set up by Siemens Service when your system was installed. **Standard mode** provides most important results for many diagnostic problems and allows you to work fast and comfortably in routine operation.

In addition to standard mode, **Pulmo** also offers you a range of **extended functions**. With these functions you can, for example, evaluate subranges of the left and right lung. You can change the HU area under consideration, threshold values for automatic contour definition, and result representation. Furthermore, a reference data comparison can be enabled.

You can activate these extended functions via a configuration platform.

Calling up Pulmo

When you call up the **Pulmo** evaluation card it is initially empty.

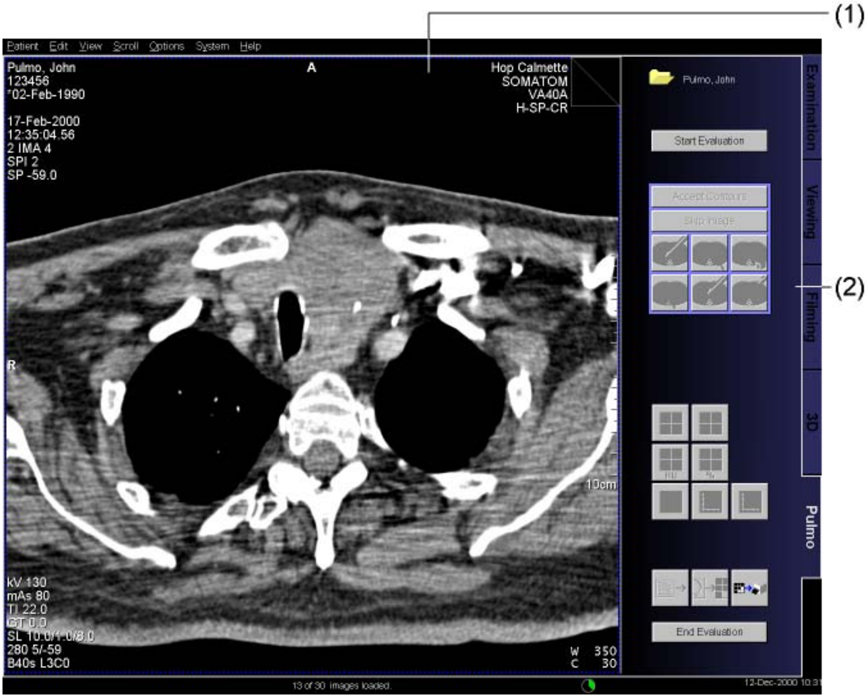
✧ Call up **Patient > Pulmo** in the main menu.

The **Pulmo** task card is now displayed. It does not yet contain any images. All the buttons and most of the menu entries are grayed out.

Or

✧ Click on the **Pulmo** tab if you changed to another task card in the meantime and now want to return to Pulmo evaluation.

The **Pulmo** card is subdivided into two large areas.



(1) **Image area**
This is where the original images are displayed and you prepare Pulmo evaluation. This is where the result tables and diagrams are then also displayed.

(2) **Control area**
Here you will find the buttons for controlling evaluation and further processing your results. The appearance of the control area depends on your configuration.
→ Page K.4–1, *Extended functions in Pulmo*

Closing Pulmo

Once you have completed **Pulmo** evaluation, you can close the Pulmo task card.

✧ Call up **Patient > Close Pulmo**.

The task card is closed, the **Pulmo** tab disappears.

Or

✧ Call up one of the other task cards, e.g. **Dental** or **Osteo** and confirm the displayed dialog box with **Yes**.

The **Pulmo** task card is closed and another task card is displayed in its place.

CHAPTER
K.2 Loading and displaying images

Pulmonary examinations with one topogram and three scans in a sequence are typically suitable for Pulmo evaluation.

Prerequisites

The lung density of a patient varies depending on the respiratory status, i.e. if the scan is performed during full inspiration, full expiration or at a level inbetween (defined as a percentage of the vital capacity). Therefore a comparison of two scans only makes sense if the scans were performed at the same respiratory level.

Original images should have been stored without compression or with lossless JPEG compression on archive media. "Lossy JPEG" compression can distort results.

NOTE

Pulmo examinations should be completed with **End Exam**, otherwise some Pulmo evaluation steps may not be possible.

System checks

When you load tomograms, the system checks whether the images have been reconstructed with a high-resolution kernel. In this case they are automatically smoothed. If details about the sex or age of the patient are missing, this information is requested.

If the tomograms that you want to load do not meet the Pulmo standard and the system is not able to adapt them, a message indicating that appears in the status line.

Loading original images

If the **Pulmo** card is not yet displayed you can call up the Pulmo task card from the **Patient Browser** and load images for evaluation in one step.

➩ A progress bar will be displayed while loading the images.

Loading images from the Patient Browser

✧ Open the **Patient Browser**.

✧ Select a suitable study or one or more series of a pulmonary examination.

> **NOTE**
>
> You can only ever load images of one patient and study in **Pulmo CT**.

✧ Then click on the **Pulmo** button in the tool bar of the **Patient Browser**.

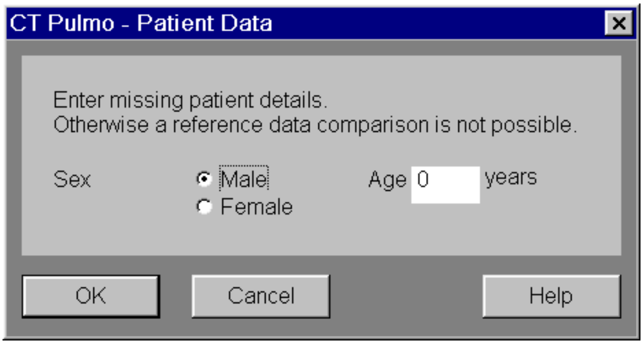
Or

✧ Call up **Patient > Pulmo** in the menu bar of the **Patient Browser**.

Missing patient information

As soon as you start the Pulmo evaluation, the system checks whether the patient data sex and age are complete.

If any of this information is missing, the dialog box **CT Pulmo - Patient Data** is displayed.



CT Pulmo - Patient Data

Enter missing patient details.
Otherwise a reference data comparison is not possible.

Sex ● Male ○ Female

Age 0 years

✧ Select the correct sex and enter the age of the patient.

✧ Confirm your entries with **OK**.

Or

✧ Click on **Cancel** if you do not want to start evaluation.

Loading images

If the **Pulmo** task card is already open because you have been performing evaluations, for example, you can also load images into that open **Pulmo** card.

✧ Call up **Patient > Patient Browser** in the main menu to open the **Patient Browser**.

✧ Select the images or series (one or more) that you want to evaluate.

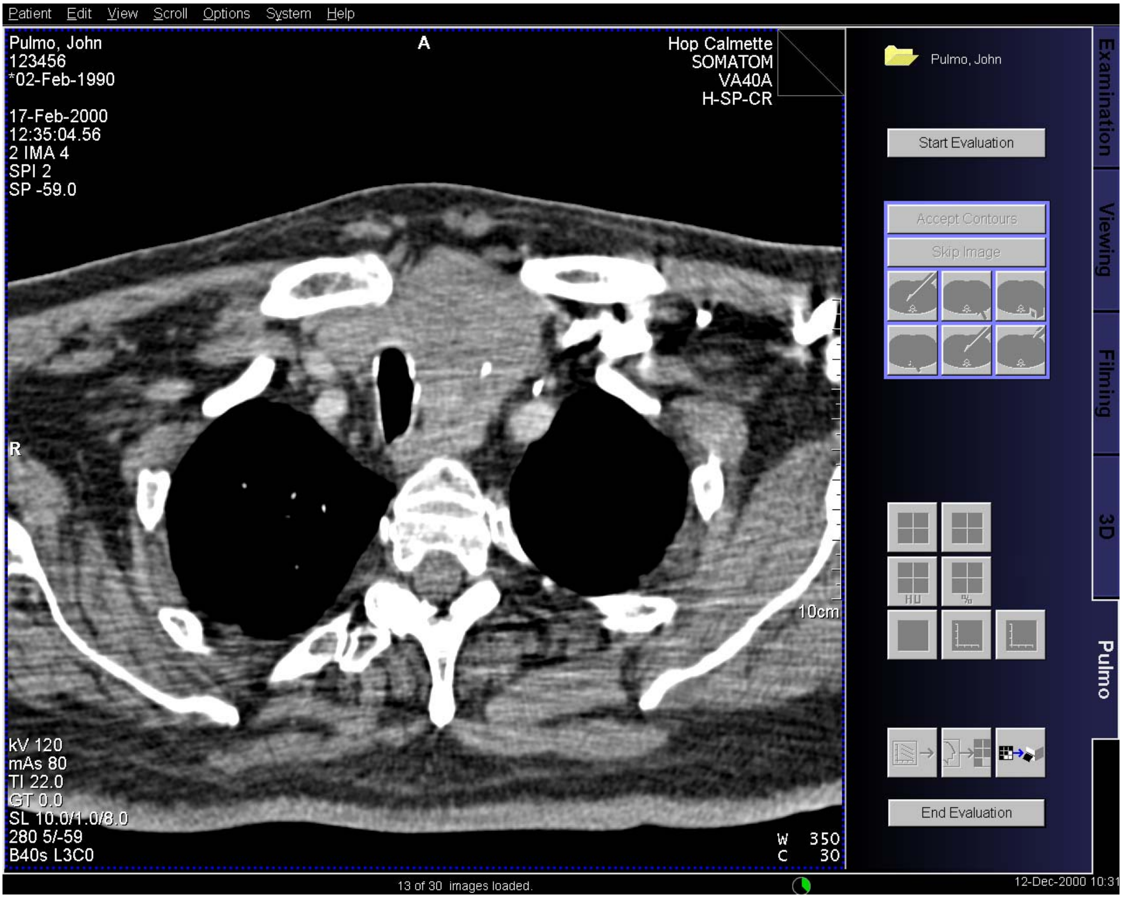
✧ Drag your image selection into the **Pulmo** task card keeping the left mouse key pressed (drag & drop).

Or

✧ Double click on your selection to load the images into **Pulmo**.

Changing the image display

The loaded tomograms are now displayed as a stack in the image area of the **Pulmo** task card. The image stack is sorted in the craniocaudal direction. The first image to be displayed is the tomogram that was measured nearest the head.



Pulmo, John
123456
*02-Feb-1990

17-Feb-2000
12:35:04.56
2 IMA 4
SPI 2
SP -59.0

Hop Calmette
SOMATOM
VA40A
H-SP-CR

kV 120
mAs 80
TI 22.0
GT 0.0
SL 10.0/1.0/8.0
280 5/-59
B40s L3C0

W 350
C 30

13 of 30 images loaded.

12-Dec-2000 10:31

Scrolling through the image stack

✧ Click on the dog-ears in the top right-hand corner of the image stack to scroll image by image.

Or

✧ Call up **Scroll > Next image** or **Previous image** in the main menu to scroll one image forward or back within a series.

Or

✧ Call up **Scroll > First page** or **Last page** to scroll to the first or last image in the image stack.

➪ If you have loaded images of several series, scroll from one series to the next with **Scroll > Next Series** or **Previous Series** and then through the images of that series with **Next Image** or **Previous Image**. Or you can use the **Image+/ Image-** and **Series+/Series-** buttons on the symbol keypad on your keyboard.

Windowing images

As in other task cards, you can window the images that you have loaded in the **Pulmo** card. You always change the window settings of all the other images behind the current image in the stack.

✧ Click into the image area with the center mouse key and pull the mouse down/up or left/right to optimize the window settings in the image stack.
→ Page E.4–11, *Windowing with the mouse*

Or

✧ Window the images with the tuning knobs on the control box (only Navigator).
→ Page E.4–10, *Windowing with the control box*

Displaying/hiding the image text display

When the original images have been loaded they are displayed together with the following image information:

❑ Patient and examination data (top left))
❑ System in which the images were measured (top right)
❑ Scan parameters (bottom left)
❑ Window values (bottom right)

You can hide image information if it covers interesting structures.

✧ Select **View > No Text** to switch off display of image text.

➩ If you want to display image text information later, just select **View > All Text**.

> **NOTE**
>
> You can only scroll through the image stack, window images, and hide/display image texts before you start evaluation.

CHAPTER
K.3

Pulmo Evaluation in Standard Mode

When **Pulmo** was installed, this task card was configured for evaluations in standard mode. With these settings, you can perform Pulmo evaluation comfortably and largely automatically.

Standard mode produces data for distribution of the HU values (Hounsfield units) in the two lung sides for each evaluated tomographic image and across all evaluated images.

Sequence of a standard evaluation

A Pulmo evaluation in standard mode comprises the following steps:

- ☐ Start evaluation via the **Start Evaluation** button.
- ☐ Automatic contour definition and the possibility of manual correction in all loaded images.
- ☐ Automatic calculation of results after confirming the lung contours in all images.
- ☐ Display results in standard layout.
- ☐ Transfer results to film camera, write results to diskette, if necessary.
- ☐ Terminate evaluation with the **End Evaluation** button, results are automatically stored in database.

Contour definition and correction

Once you have loaded the original images for your Pulmo evaluation and optimized their window settings, you can start standard evaluation.

✧ Click on the **Start Evaluation** button.

Automatic contour definition is activated as soon as you start evaluation. The first tomogram is now displayed. The program has drawn in the lung contours with a red line.

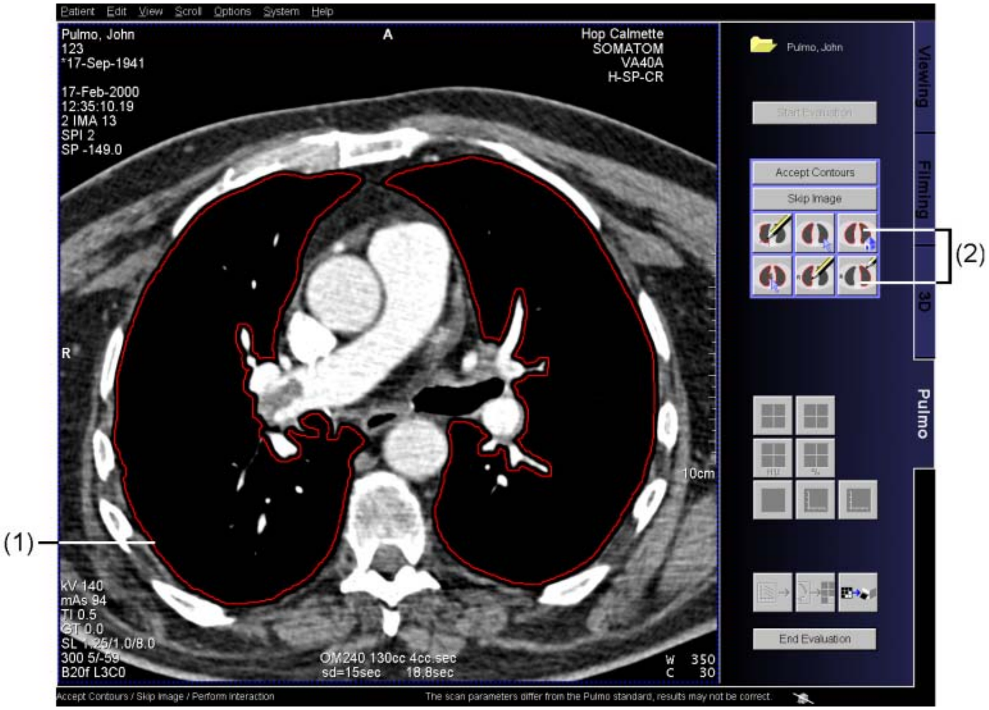
Check the automatic contour and decide how you wish to proceed in this image:

- Accept the contour (**Accept Contours**).
- Change, redraw or recalculate the contour with a different starting point (buttons in the control area).
- Reject the image (**Skip Image**)
  (i.e., skip this image and do not use it for Pulmo evaluation).

As soon as you accept the lung contours in this image with **Accept Contours**, or reject the image with **Skip Image**, the second loaded tomogram is displayed. In this image, too, an automatic contour suggestion has been made which you can confirm or change. In this way you work through this step in the evaluation, looking at each individual loaded image.

Manual correction of the lung contours

You can change the lung contours that have automatically been drawn into a tomogram. A series of buttons are activated in the control area of the **Pulmo** task card for that purpose.



Accept Contours / Skip Image / Perform Interaction

The scan parameters differ from the Pulmo standard, results may not be correct.

(1) Automatically derived lung contours

(2) Buttons for semi-automatic and manual modification of the contours.

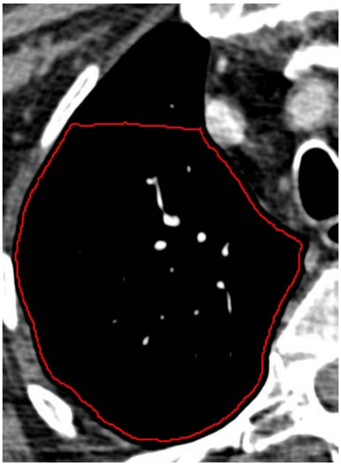
Including/excluding areas

You use the option for manual inclusion or exclusion of regions if automatic contour definition has not correctly detected the lung contours or if you only want to evaluate a specific area of a lung.

- Click on this button to activate the drawing tool for changing the contour line.

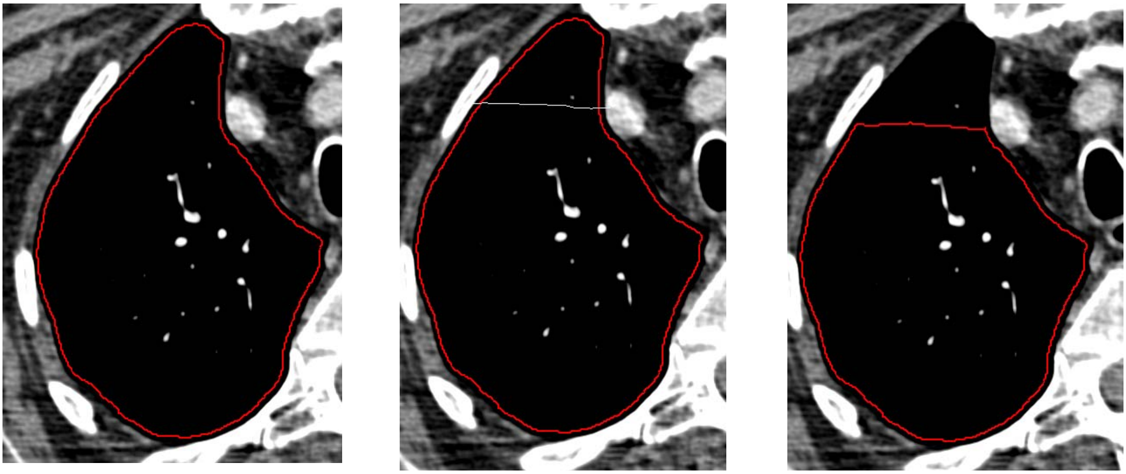
To add a region to the contour:

- Click on any point well inside the automatically generated contour with the left mouse key.
- Move the mouse right round the area outside the contour that you want to add keeping the left mouse key pressed as you do so.
- Close contour extension by releasing the left mouse key at any point well inside the automatically generated contour.



To exclude a region from the contour:

- Click on any point well outside the automatically generated contour with the left mouse key.
- Move the mouse right round the area inside the old contour that you want to exclude keeping the left mouse key pressed as you do so.
- Close contour reduction by releasing the left mouse key at any point well outside the automatically generated contour again.

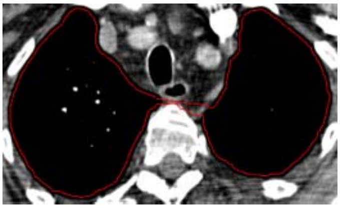


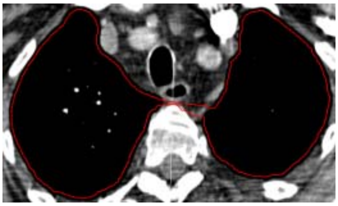
Separating the left and right lung manually

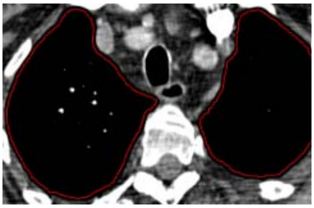
You can also use the drawing tool for changing the contour line to separate the left and right lungs from each other should that be necessary in any of your tomograms.

If you want to separate regions:

- Click on any point well outside the automatically generated contour with the left mouse key.
- Draw in a dividing line and complete it by releasing the left mouse key again at a point well outside the automatically generated contour.





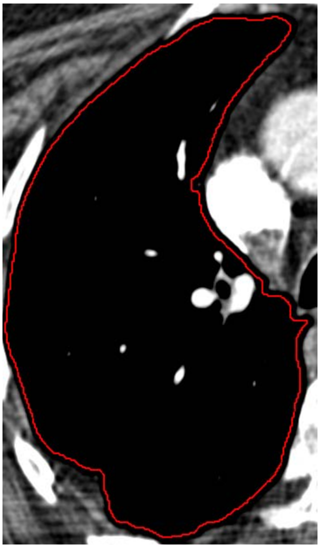


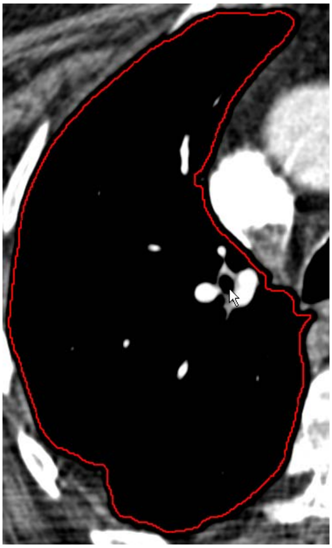
Excluding the trachea or bronchi

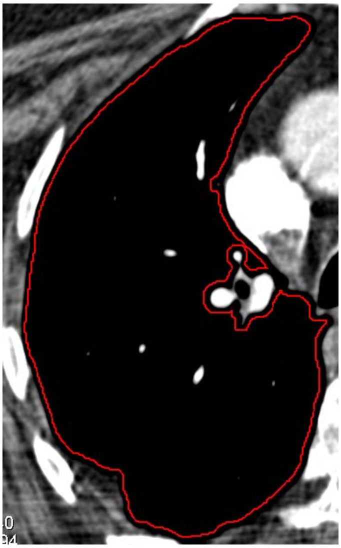
If automatic contour definition has included the trachea or bronchi but you want to exclude them, proceed as follows:

✧ Click on this button.

✧ Then click on the trachea or main bronchi with the left mouse key to exclude them.







Calculating the contours with starting point

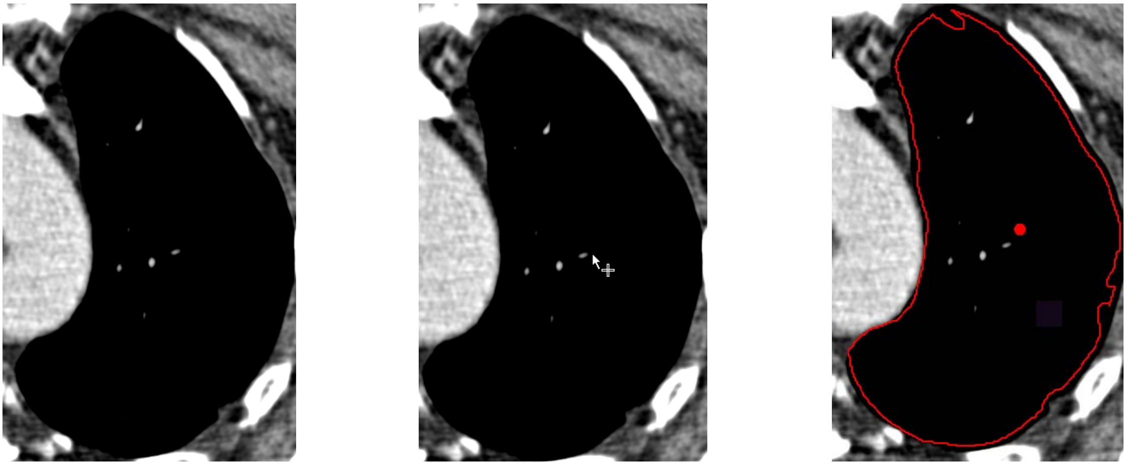
Sometimes the program is not able to recognize the left, right, or both lungs in a tomogram and cannot therefore draw in the contour lines automatically.

In such cases, use the **Define Starting Point** tool to identify the left and right lungs yourself.

✧ Click on this button.

✧ Then click onto the area of the image in which the right or left lung is visible.

Automatic contour definition is now started and a contour line is drawn in. The starting point for contour definition drawn in by the system is a small red circle.



Drawing in lung contours freehand

If you cannot produce the correct contour definition with the defined starting point, you can draw in the lung contours freehand.

✧ Click on the button **Draw Left Lung Contour** to draw the contour of the left lung freehand.

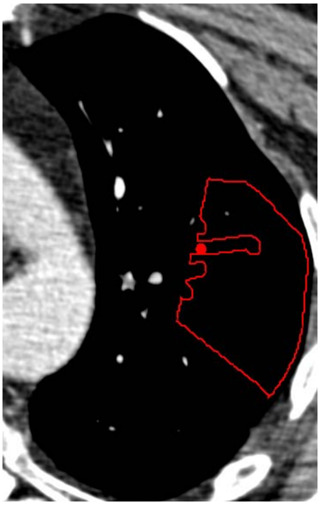
Or

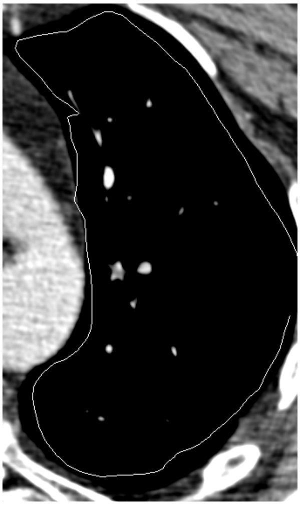
✧ Click on the button **Draw Right Lung Contour** to draw the contour of the right lung freehand.

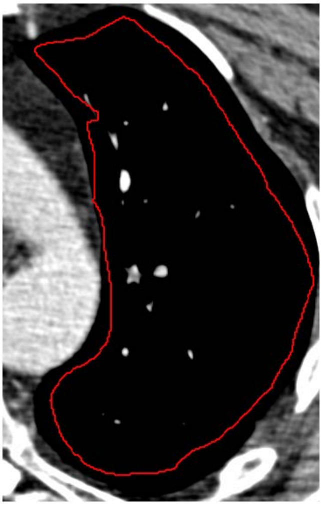
The old contours for each lung are deleted.

✧ Keep the left mouse key pressed and draw in the lung contour freehand.

✧ Release the mouse key to close the contour.







➩ You cannot change freehand lung contours with the tools **Separate/Include/Exclude**, and **Exclude Trachea/Bronchi** once you have drawn them.
If your first attempt to draw in the left or right lung was not successful, draw it again. Click again on the button **Draw Left/ Right Lung Contour** and start drawing again.

Returning to automatic contour definition

If you are not satisfied with the changes that you have made to the lung contours, you can return to automatic contour definition at any time.

✧ Click on this button to reject all changes and return to the suggestions made by automatic contour definition.

Accepting a contour or skipping an image

You can repeat manual correction of the lung contours as often as you want. If the changes you make to the contours make them worse, you can keep returning to the suggestions of the program.

Only when you have an image in which the left and right lungs are optimally displayed should you accept them.

✧ To do that, click on the button **Accept Contours**.

Or

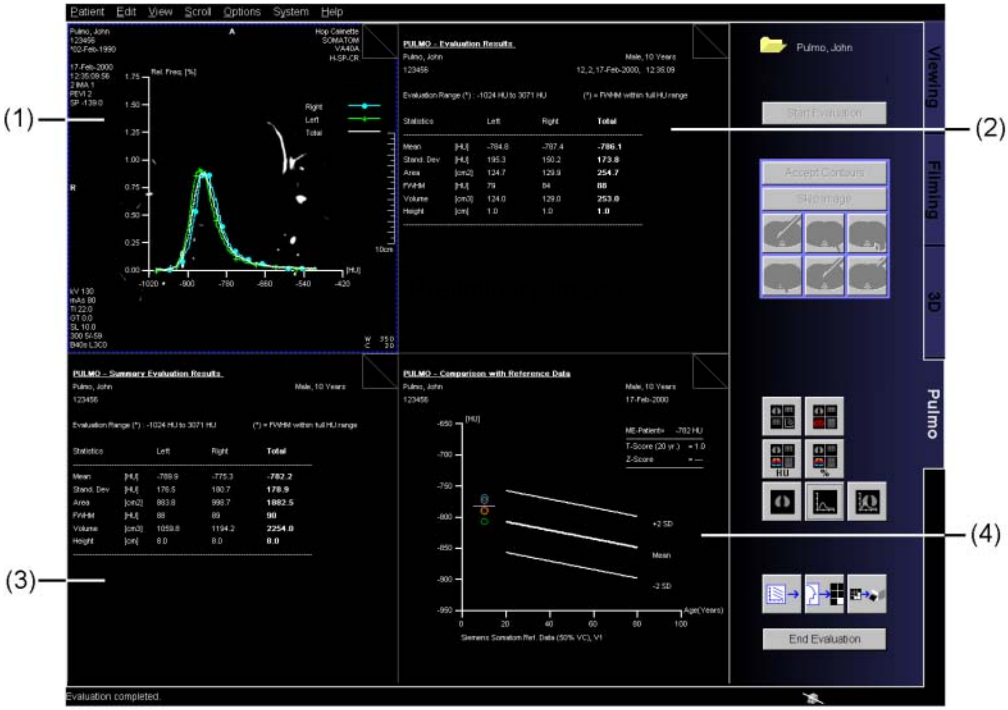
✧ Click on the button **Skip Image** to skip an image.

The image is not used for Pulmo evaluation.

Result display

As soon as you confirm the lung contours in the last image to have been loaded, result calculation starts automatically.

The original images are hidden. In their place you can see the result diagrams and tables in the image area.



PULMO - Evaluation Results

Pulmo, John   Male, 10 Years
123456   12, 2, 17-Feb-2000, 12:35:09

Evaluation Range (*) : -1024 HU to 3071 HU   (*) = FWHM within full HU range

Statistics		Left	Right	Total
Mean	[HU]	-784.8	-787.4	**-786.1**
Stand. Dev	[HU]	195.3	150.2	**173.8**
Area	[cm2]	124.7	129.9	**254.7**
FWHM	[HU]	79	84	**88**
Volume	[cm3]	124.0	129.0	**253.0**
Height	[cm]	1.0	1.0	**1.0**

PULMO - Summary Evaluation Results

Pulmo, John   Male, 10 Years
123456

Evaluation Range (*) : -1024 HU to 3071 HU   (*) = FWHM within full HU range

Statistics		Left	Right	Total
Mean	[HU]	-789.9	-775.3	**-782.2**
Stand. Dev	[HU]	176.5	180.7	**178.9**
Area	[cm2]	883.8	998.7	**1882.5**
FWHM	[HU]	88	89	**90**
Volume	[cm3]	1059.8	1194.2	**2254.0**
Height	[cm]	8.0	8.0	**8.0**

PULMO - Comparison with Reference Data

Pulmo, John   Male, 10 Years
123456   17-Feb-2000

ME-Patient= -782 HU
T-Score (20 yr.) = 1.0
Z-Score = ---

Evaluation completed.

(1) Stack of result histograms
(HU frequency distribution per tomogram)

(2) Stack of result tables
(HU value statistics for each tomogram)

(3) Result table across all tomograms

(4) Comparison with reference data

Evaluation results for each tomogram

In the two upper segments in the image area you can see the evaluation results for each tomogram loaded.

Result diagrams

The left segment shows the tomograms in an image stack where the image background is hidden and only the lung parenchyma is visible.

Each tomogram is overlaid by a histogram of the HU values in this image:

- The **white curve** shows the HU frequency distribution across both lungs.
- The **blue curve** shows the HU frequency distribution in the right lung.
- The **green curve** shows the HU frequency distribution in the left lung.

Hiding the tomogram or histogram

In order to see details more clearly, you can hide either the tomogram or the histogram in the top left segment.

✧ Click on this button in the lower half of the control area to display the lung images only.

Or

✧ Click on this button to display the diagrams only.

Or

✧ Click on this button to display the overlaid tomogram and histogram again.

Scrolling through the diagram and table synchronously

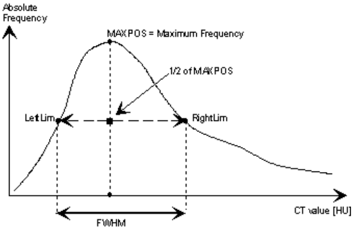
You can scroll through the result display of the individual tomograms with the dog-ears in the image stack (segment top left) or result tables (segment to right).

If you scroll by one page in the diagrams, you also scroll by one table in the table view and vice versa. You are therefore always looking at the diagram and result table of the same tomogram.

Result tables

The tables show the following evaluation results for each lung tomogram, in each case for the right, left, and for both lungs:

- ☐ **Mean**
  Average value of HU frequencies
- ☐ **Stand.Dev.**
  Standard deviation of the HU values
- ☐ **Area**
  Area of each lung or both lungs in cm^2
- ☐ **FWHM** (full width at half maximum)
  Length of the range of the measured HU values that occur at least half as often as the most frequent HU value (this value determines the histogram shape).



In the header of the table you also see the following patient and examination data:

- ☐ Patient name and patient ID
- ☐ Sex and age of the patient
- ☐ Image number, scan number, scan date and time

Sum values

In the lower left segment of the image area you can see a table of evaluation results derived for all loaded tomograms.

The table is structured in the same way as the result tables for each tomogram.

Filming and storing results

You can film the results of a Pulmo evaluation directly from the task card quickly and easily.

Filming result diagrams and tables

✧ Select the images or series that you want to film.

Or

✧ Call up **Edit > Select All** in the main menu to film all result diagrams and tables.

✧ Click on the button **Copy to Filmsheet** to pass on the results of a Pulmo evaluation to the virtual film sheet.

⇨ In the **Filming** task card, you can modify the view of the images.

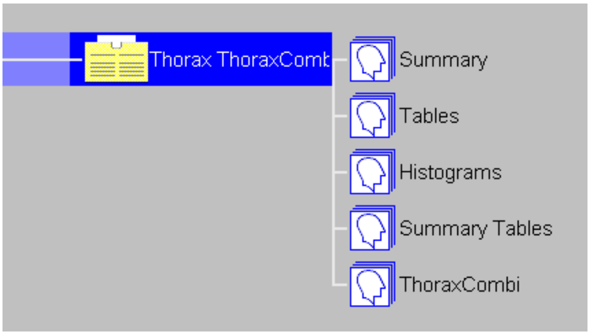
✧ Then click on the button **Expose Film Task** to expose the result diagrams and tables to film on a preset camera.

Closing evaluation
Storing results

As soon as you close Pulmo evaluation with **End Evaluation**, the results are automatically stored in the main database. The results are grouped according to output and result type and appended as new series to the study that provided the original images.

End Evaluation

✧ Click on the button **End Evaluation** to close evaluation and store the results as new series in the main database.



CHAPTER
K.4

Extended functions in Pulmo

In addition to standard Pulmo evaluation, the **Pulmo** task card also offers a range of extended functions. These extended applications allow even more detailed and precise evaluation of lung tomograms for specific diagnostic problems.

You can activate the extended functions of **Pulmo** via a configuration platform. There, you can combine various additional options with one another and optimize them for a specific problem or diagnostic problems that frequently occur in you examination practice.

As soon as you have activated an additional option and adapted its evaluation parameters, those settings remain active until such a time as you disable or change them again in the configuration platform.

If you only want to use the extended evaluation functions for one Pulmo evaluation, activate the option before you load the images or directly after (i.e. before you click on **Start Evaluation**). Deactivate the option again on the configuration panel once you have completed your evaluation (i.e. after you have clicked on **End Evaluation**).

Calling up the configuration platform

CT Pulmo

✧ Call up **Options > Configuration** to display the configuration window.

✧ In the dialog box **Configuration Panel** double click on **CT Pulmo** to call up the configuration window for this task card.

On the subtask cards of the dialog box **Pulmo Configuration** you can now activate various options for evaluating subareas of the lungs.

You can calculate distribution values for subranges (HU values) in the loaded tomograms.

You can change basic evaluation and display parameters and activate or deactivate various options for storing your results.

➪ Please refer to Section Basics to find out how to call up and close configuration windows, save changes, or restore factory settings.
→ Chapter A.2, *Configuring the User Interface*

Evaluating subareas

In segmentation, both lungs are subdivided into comparable subareas. **Pulmo** then calculates the average values and standard deviation of the HU values as well as the size (in cm^2) of these subareas. The values are calculated in the background and shown in the final result display.

The average density increase from anterior to posterior resulting from the collection of fluid in the supine position (posterior) can be represented by the HU density values calculated. Higher density values in the anterior area can have a pathological cause.

Automatic segmentation

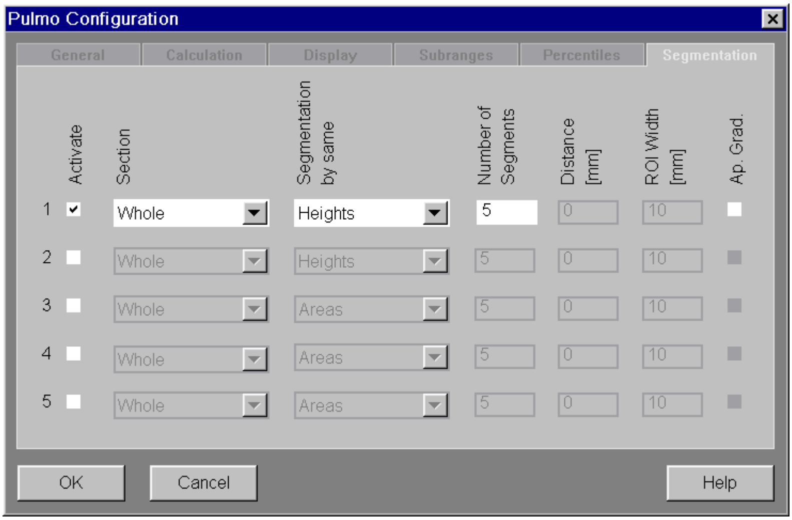
In automatic segmentation, you define a range of criteria according to which the program then divides the left and right lungs into subareas.

You can perform several segmentations simultaneously (max. 5).

For example, the left and right lungs can each be divided into 3 subareas and their HU value statistics calculated in one segmentation operation. At the same time, it is possible to divide each lung into 10 subareas for improved spatial resolution of the results.

Activating automatic segmentation

- Call up the dialog window **Pulmo Configuration** via the configuration platform.
- In it, click the **Segmentation** subtask card into the foreground.

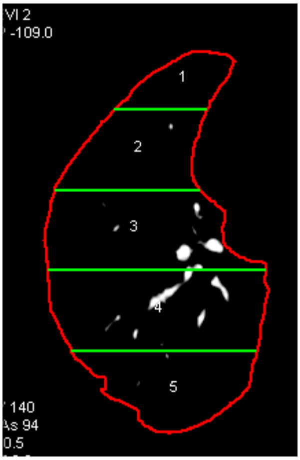


Pulmo Configuration

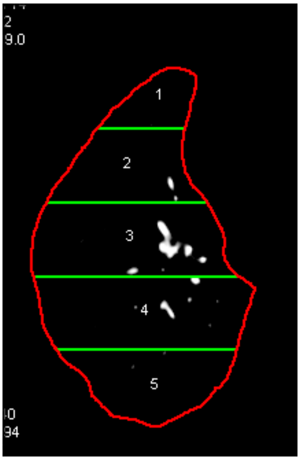
	Activate	Section	Segmentation by same	Number of Segments	Distance [mm]	ROI Width [mm]	Ap. Grad.
1	☑	Whole	Heights	5	0	10	☐
2	☐	Whole	Heights	5	0	10	☐
3	☐	Whole	Areas	5	0	10	☐
4	☐	Whole	Areas	5	0	10	☐
5	☐	Whole	Areas	5	0	10	☐

- Click on the **Activate** check box in front of the line of a segmentation to activate it.
- In the list **Section**, select the section or sections of the lung that are to be segmented:

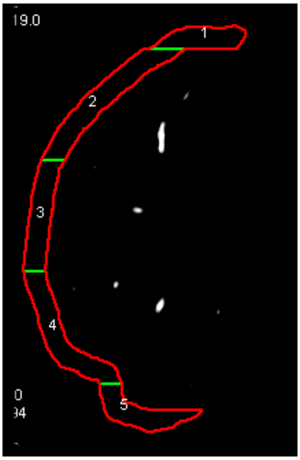
- **Whole**
  the entire lung
- **Central**
  only the central area of each lung
- **Peripheral**
  peripheral areas only
- **Central & Peripheral**
  first the central area and then the peripheral areas



Whole

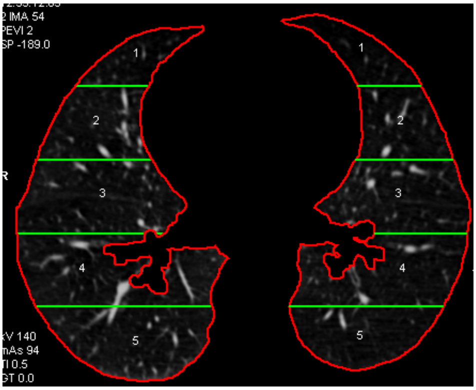


Central

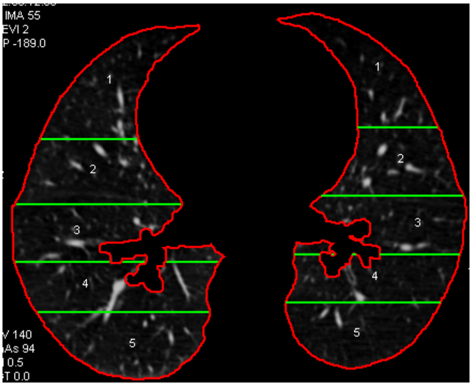


Peripheral

✧ Then select whether segments of the same anatomical **Height** or segments of approximately the same **Area** are to be generated.



Heights



Areas

✧ Under **Number of Segments**, define the number of segments each of the two lungs is to be divided into in this segmentation.

✧ Under **Distance [mm]**, enter the distance between the segments and the edge of the lung if you have selected segmentation of the peripheral areas and/or central areas.

✧ Under **ROI Width**, enter the width of the segments in the peripheral area of the left or right lung if you have selected segmentation of the peripheral areas.

✧ Check the **AP. Grad.** check box to calculate the AP gradient. (Change in the average HU values in the segments from anterior to posterior).

Result display

Once you have clicked on **Start Evaluation**, you check and correct the lung contours in the loaded tomograms in the normal way.

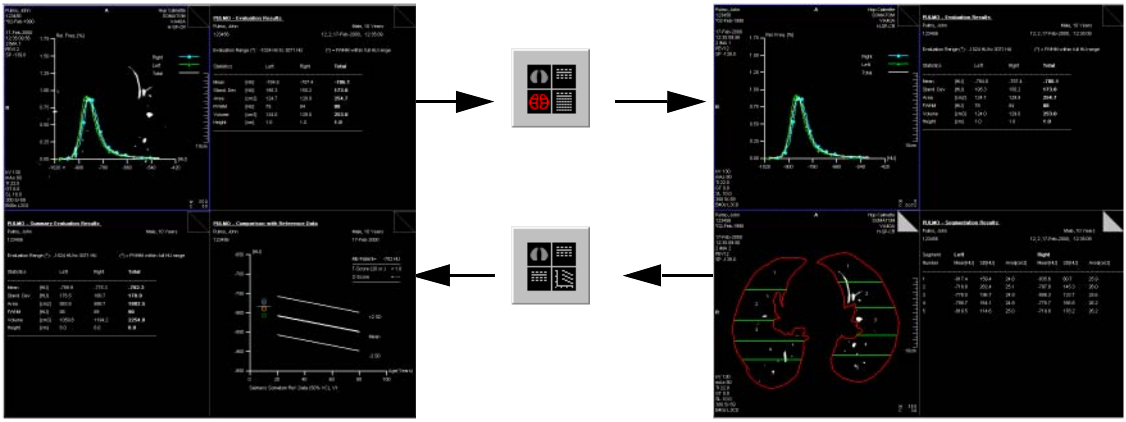
As soon as you have confirmed the contours of the last tomogram, Pulmo result display starts automatically.

When Pulmo evaluation is complete, the standard result display appears in the usual way.

✧ Click on the **Segment Results** button in the lower part of the control area to display the results of automatic segmentation.

Or

✧ Click on the **Standard Results** button to return to the standard result display.



In the lower left segment of the image area you now see the automatically calculated segmentation boundaries of the first segmentation operation in the first tomogram.

To the right, a table containing the average values and standard deviation of the HU values and area data of the individual segments for both lungs is displayed. If you selected calculation of the AP gradient for this segmentation operation, this is also displayed.

PULMO - Evaluation Results

Pulmo, John Male, 10 Years
123456 12, 2, 17-Feb-2000, 12:35:09

Evaluation Range (*) : -1024 HU to 3071 HU (*) = FWHM within full HU range

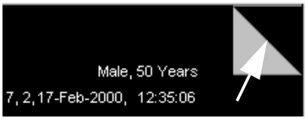
Statistics		Left	Right	**Total**
Mean	[HU]	-784.8	-787.4	**-786.1**
Stand. Dev	[HU]	195.3	150.2	**173.8**
Area	[cm2]	124.7	129.9	**254.7**
FWHM	[HU]	79	84	**88**
Volume	[cm3]	124.0	129.0	**253.0**
Height	[cm]	1.0	1.0	**1.0**

PULMO - Segmentation Results

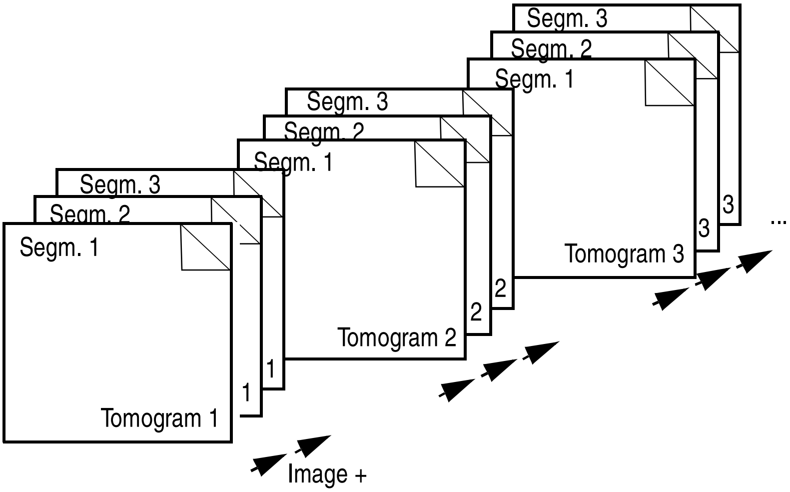
Pulmo, John Male, 10 Years
123456 12, 2, 17-Feb-2000, 12:35:09

Segment	**Left**			**Right**		
Number	Mean[HU]	SD[HU]	Area[cm2]	Mean[HU]	SD[HU]	Area[cm2]
1	-817.4	159.4	24.8	-835.6	80.7	25.9
2	-718.8	282.4	25.1	-797.8	145.3	26.0
3	-778.0	196.7	24.9	-806.3	133.7	25.6
4	-790.7	164.1	24.9	-778.7	166.8	26.2
5	-819.5	114.6	25.0	-719.8	178.2	26.2

13 of 13 images evaluated.



✧ Click on the dog-ears in the segmentation result display to scroll through all the loaded and evaluated tomograms and all segmentation operations.



➪ You scroll through the tomograms and their segments and result tables (lower left and right image segment) synchronously.

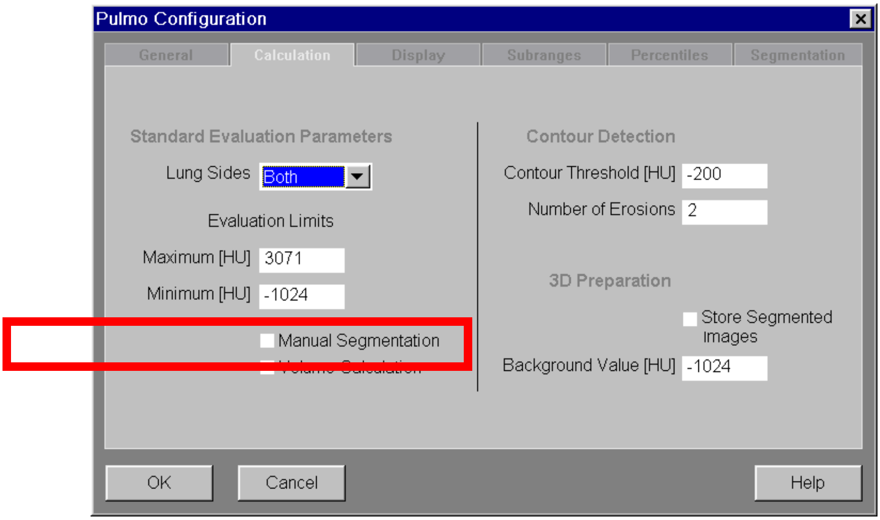
Manual segmentation

In addition to automatic segmentation, **Pulmo** also allows you to draw segment boundaries in tomograms manually. In this way, you can optimize segmentation evaluation to the anatomical situation and current diagnostic problem.

You can also combine automatic and manual segmentation, i.e. you allow the program to execute up to 5 segmentation operations according to the above criteria and calculate the corresponding segment statistics. You then draw the segment boundaries into a tomogram yourself for the next calculation.

Activating manual segmentation

✧ Call up **Pulmo Configuration** and click the card **Calculation** into the foreground.



Standard Evaluation Parameters

Lung Sides: Both

Evaluation Limits

Maximum [HU]: 3071

Minimum [HU]: -1024

☐ Manual Segmentation

☐ Volume Calculation

Contour Detection

Contour Threshold [HU]: -200

Number of Erosions: 2

3D Preparation

☐ Store Segmented images

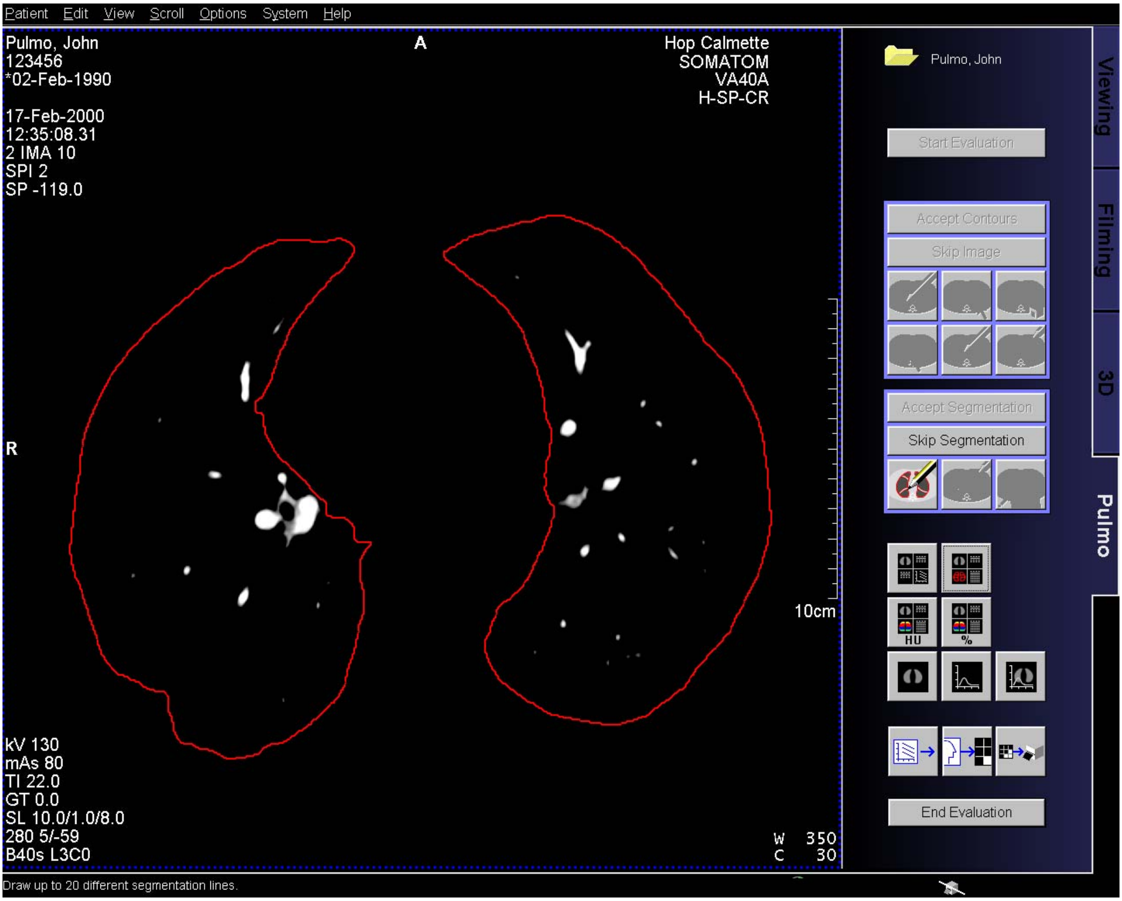
Background Value [HU]: -1024

✧ Check the **Manual Segmentation** check box to activate this option for the following Pulmo evaluations.

As soon as you activate **Manual Segmentation** and press **Start Evaluation** more buttons are displayed in the control area of the **Pulmo** task card.

In the image area you now see the first lung tomogram.

➪ After confirmation of the lung contour, the image background is hidden, only the lung parenchyma is visible.



Pulmo, John
123456
*02-Feb-1990

17-Feb-2000
12:35:08.31
2 IMA 10
SPI 2
SP -119.0

Hop Calmette
SOMATOM
VA40A
H-SP-CR

kV 130
mAs 80
TI 22.0
GT 0.0
SL 10.0/1.0/8.0
280 5/-59
B40s L3C0

W 350
C 30

Draw up to 20 different segmentation lines.

Segmenting

- Click on the button **Draw Freehand Lines** to activate drawing mode.
- Click well outside one of the lungs with the left mouse key.
- Keep the mouse key pressed to draw in a freehand segment boundary that cuts through the lung contour or other segment boundaries.
- Release the mouse key (again outside the lung) to complete the first line.
- Click again well outside the tomogram and draw the next freehand line.

Repeating segmenting

- Click on the button **Clear All** if your first attempt at drawing in the segment boundaries is not successful.
- Then click again on the button **Draw Freehand Lines** to start drawing in segment boundaries again.

Numbering segments

- When you are satisfied with all your segment boundaries, click on the button **Mark Segments**.
- Then click into the areas between the drawn segment boundaries that you want to evaluate. The segments are numbered contiguously.

Accept Segmentation

✧ Finally, click on **Accept Segmentation** to start evaluation of your manually drawn segments.

Or

Skip Segmentation

✧ Click on **Skip Segmentation** to skip manual segmentation.

Result display

↔

As in automatic segmentation, you can switch between the standard results and the results of segmentation in the result display.

You can now scroll through the stack of tomograms with the segment boundaries or through the stack of result tables to display the evaluation results of each tomogram.

Evaluation of HU value ranges in the tomograms

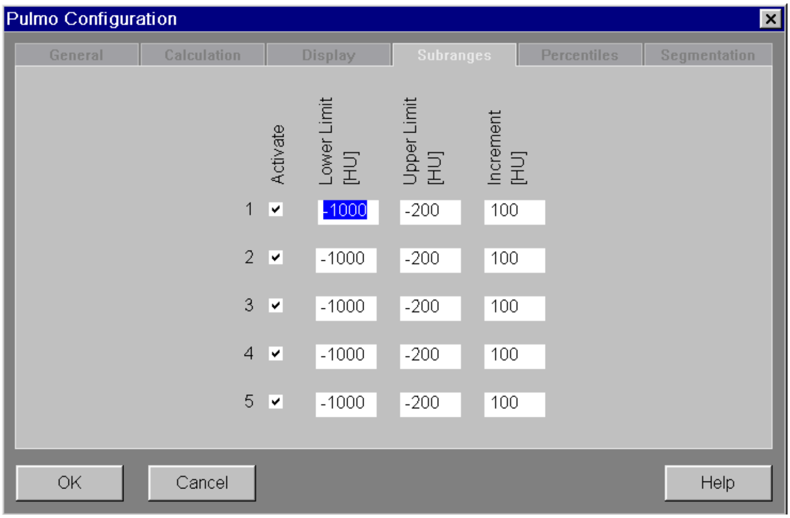
With **Pulmo** you can divide the lung into subranges (HU value ranges). In this way, you can evaluate different density ranges separately, e.g. the emphysema range from –1000 to –900 HU, normal lung tissue from –900 to –700, and densified areas (fibrosis) from –700 to –400 HU.

You can either base your evaluations directly on HU value ranges, and calculate their relative frequency in the tomograms (subranges).

Or you can base your evaluations on relative frequency classes and show which HU value intervals in the individual tomograms fall into those frequency categories (percentiles).

Activating evaluation of subranges

✧ Call up **Pulmo Configuration** and click the **Subranges** card into the foreground.



	Activate	Lower Limit [HU]	Upper Limit [HU]	Increment [HU]
1	☑	-1000	-200	100
2	☑	-1000	-200	100
3	☑	-1000	-200	100
4	☑	-1000	-200	100
5	☑	-1000	-200	100

✧ Click on the **Activate** check box in front of the line to activate it.

✧ Enter an upper and lower limit value for the HU range that you want to analyze in both fields.

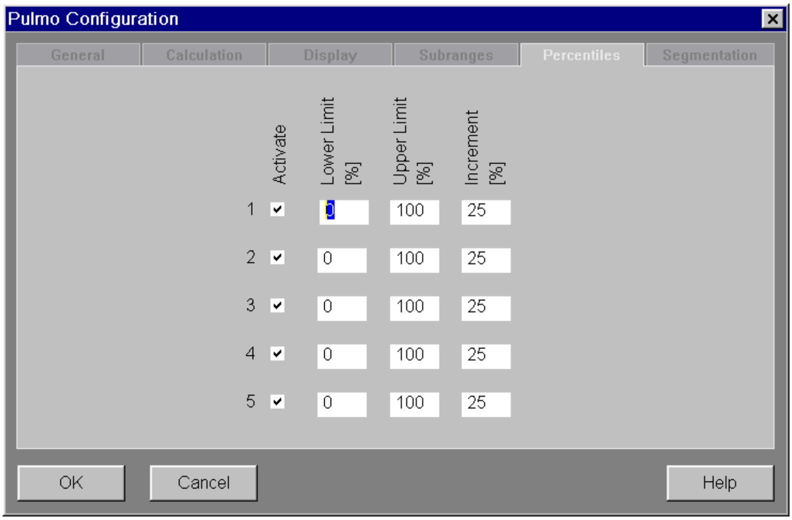
✧ Under **Increment**, specify into how many increments you want to divide the HU range.

➪ E.g. for limit values - 1000 HU and - 800 HU and increment 25 HU, the program calculates the frequency of 8 subranges as percentages.
(- 1000 HU to - 976 HU, - 975 HU to - 951 HU, etc.)

➪ E.g. for limit values - 1000 HU to - 950 HU without increment enter increment 0.

Or

✧ Call up **Pulmo Configuration** and click the card **Percentiles** into the foreground.



	Activate	Lower Limit [%]	Upper Limit [%]	Increment [%]
1	☑	0	100	25
2	☑	0	100	25
3	☑	0	100	25
4	☑	0	100	25
5	☑	0	100	25

✧ Click on the **Activate** check box in front of the line to activate it.

✧ Enter the **upper** and **lower limit** value of the percentage range that you want to analyze.

✧ Under **Increment**, enter the increments into which you want to divide the percentage range.

➪ E.g. for limit values 0% and 100%, and **Increment** 25%, the program calculates which HU ranges in the left, right, and in both lungs fall into the frequency classes 0-24%, 25-49%, 50-74%, and 75-99%.

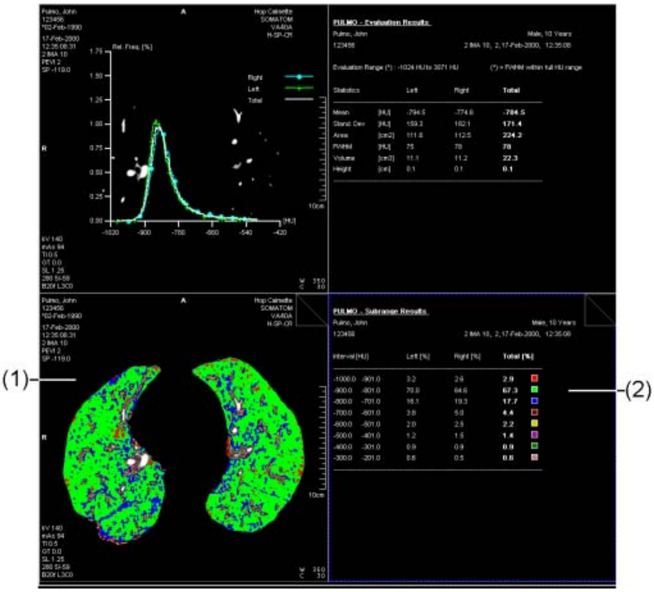
➪ E.g. for limit values 25% and 75% without increment enter **Increment** 0.

Result display

As soon as you click on **Start Evaluation** and confirm the lung contours in all tomograms, Pulmo evaluation starts automatically. The standard results and the subrange results are then calculated automatically.

As soon as Pulmo evaluation is complete the standard result display appears.

✧ Click on the **Subrange Results** button to display the results and the color highlighting of the subranges.



PULMO - Evaluation Results

Pulmo, John Male, 10 Years

123456 2 IMA 10, 2,17-Feb-2000, 12:35:08

Evaluation Range (*): -1024 HU to 3071 HU (*) = FWHM within full HU range

Statistics		Left	Right	Total
Mean	[HU]	-794.5	-774.8	**-784.5**
Stand. Dev	[HU]	159.3	182.1	**171.4**
Area	[cm2]	111.8	112.5	**224.3**
FWHM	[HU]	75	78	**78**
Volume	[cm3]	11.1	11.2	**22.3**
Height	[cm]	0.1	0.1	**0.1**

PULMO - Subrange Results

Pulmo, John Male, 10 Years

123456 2 IMA 10, 2,17-Feb-2000, 12:35:08

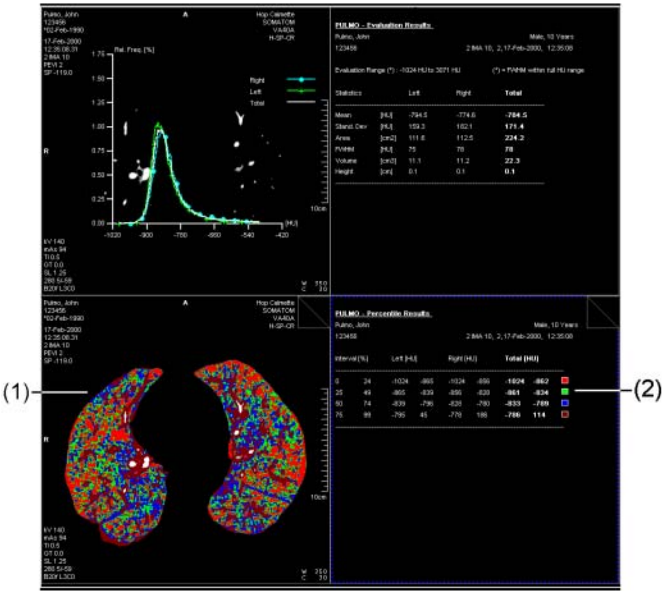
Interval [HU]		Left [%]	Right [%]	Total [%]	
-1000.0	-901.0	3.2	2.6	**2.9**	🟥
-900.0	-801.0	70.8	64.6	**67.3**	🟩
-800.0	-701.0	16.1	19.3	**17.7**	🟦
-700.0	-601.0	3.8	5.0	**4.4**	🟫
-600.0	-501.0	2.0	2.5	**2.2**	🟨
-500.0	-401.0	1.2	1.5	**1.4**	🟪
-400.0	-301.0	0.9	0.9	**0.9**	🟩
-300.0	-201.0	0.6	0.5	**0.6**	⬜

(1) Color highlighting of the subranges

(2) Result table for the HU value ranges

Or

✧ Click on the **Percentile Results** button to display the result table for the HU frequency classes.



PULMO - Evaluation Results

Pulmo, John Male, 10 Years
123456 2 IMA 10, 2,17-Feb-2000, 12:35:08

Evaluation Range (*) : -1024 HU to 3071 HU (*) = FWHM within full HU range

Statistics		Left	Right	Total
Mean	[HU]	-794.5	-774.6	**-784.5**
Stand. Dev	[HU]	159.3	162.1	**171.4**
Area	[cm2]	111.6	112.5	**224.2**
FWHM	[HU]	75	78	**78**
Volume	[cm3]	11.1	11.2	**22.3**
Height	[cm]	0.1	0.1	**0.1**

PULMO - Percentile Results

Pulmo, John Male, 10 Years
123456 2 IMA 10, 2,17-Feb-2000, 12:35:08

Interval [%]		Left [HU]		Right [HU]		Total [HU]		
0	24	-1024	-865	-1024	-856	**-1024**	**-862**	🟥
25	49	-865	-839	-856	-820	**-861**	**-834**	🟩
50	74	-839	-796	-828	-780	**-833**	**-789**	🟦
75	99	-795	45	-778	186	**-786**	**114**	🟫

(1) Color highlighting of the percentiles

(2) Result table for the frequency classes

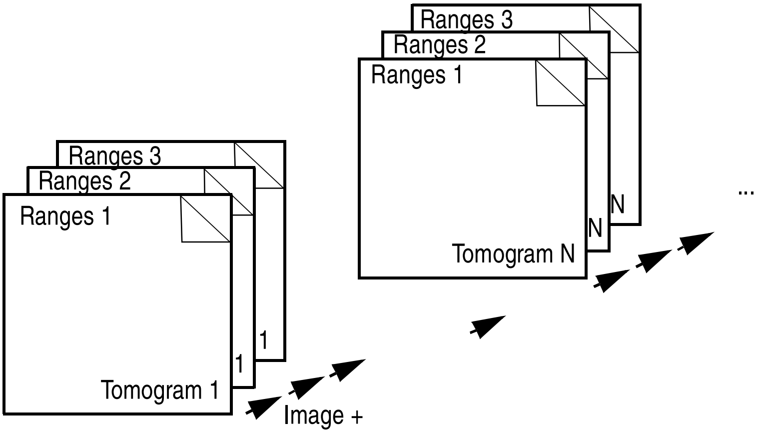
NOTE

When exporting/importing images or sending them in the network, color overlays are reduced to one color due to technical reasons.

➪ With the **Evaluation Results** button you can return to the default results display.

✧ Click on the dog ears in the lower right segment to scroll through the result displays.

You always start at the first result table of the first calculation run for the first tomogram.



Volume calculation

If your image material is suitable you can also calculate the volume of both lungs and their vertical extent in a Pulmo evaluation.

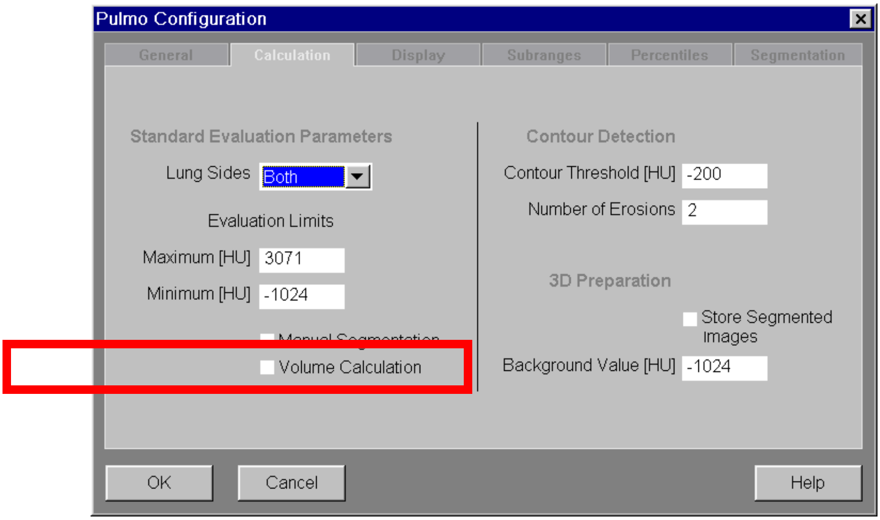
NOTE

In order to calculate the lung volume, the program requires a volume data set, i.e. the diagrams must not contain gaps of more than 1 cm.

An error message appears if there are gaps greater than 1 cm.

Activate volume calculation

✧ Call up **Pulmo Configuration** and click the **Calculation** card into the foreground.



Lung Sides: Both

Maximum [HU]: 3071

Minimum [HU]: -1024

☐ Manual Segmentation

☐ Volume Calculation

Contour Threshold [HU]: -200

Number of Erosions: 2

☐ Store Segmented images

Background Value [HU]: -1024

✧ Click on the **Volume Calculation** check box to activate this option for the following evaluations.

Result display

As soon as you have confirmed the lung contours in all images, result display starts automatically. The additional evaluation results for lung volume and height are to be found in the result tables for the tomogram in question (here you will find data about the added up volume and height of each slice). In the sum table you will then find information about the whole scanned lung volume and its vertical extent.

PULMO - Evaluation Results

Pulmo, John Male, 10 Years
123456 12, 2, 17-Feb-2000, 12:35:09

Evaluation Range (*) : -1024 HU to 3071 HU (*) = FWHM within full HU range

Statistics		Left	Right	**Total**
Mean	[HU]	-784.8	-787.4	**-786.1**
Stand. Dev	[HU]	195.3	150.2	**173.8**
Area	[cm2]	124.7	129.9	**254.7**
FWHM	[HU]	79	84	**88**
Volume	[cm3]	124.0	129.0	**253.0**
Height	[cm]	1.0	1.0	**1.0**

PULMO - Summary Evaluation Results

Pulmo, John Male, 10 Years
123456

Evaluation Range (*) : -1024 HU to 3071 HU (*) = FWHM within full HU range

Statistics		Left	Right	**Total**
Mean	[HU]	-789.9	-775.3	**-782.2**
Stand. Dev	[HU]	176.5	180.7	**178.9**
Area	[cm2]	883.8	998.7	**1882.5**
FWHM	[HU]	88	89	**90**
Volume	[cm3]	1059.8	1194.2	**2254.0**
Height	[cm]	8.0	8.0	**8.0**

PULMO - Comparison with Reference Data

Pulmo, John Male, 10 Years
123456 17-Feb-2000

ME-Patient= -782 HU
T-Score (20 yr.) = 1.0
Z-Score = ---

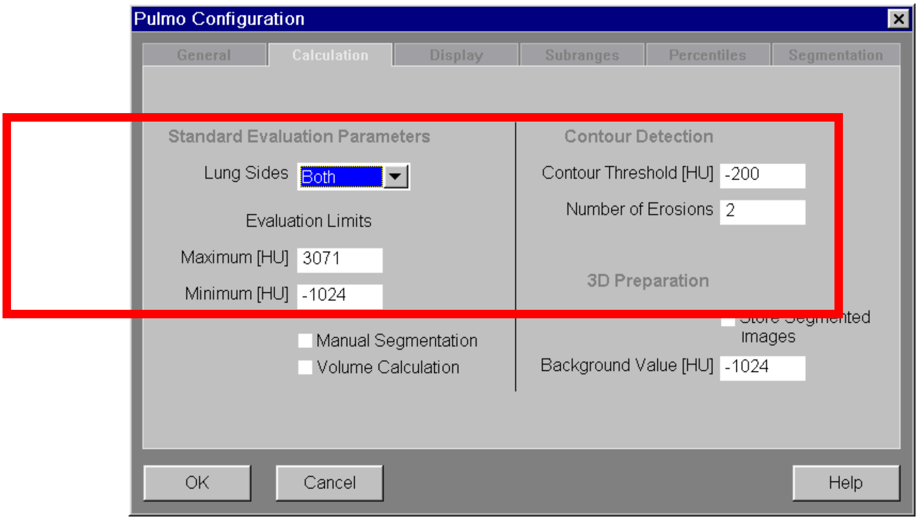
6 of 6 images evaluated.

12-Dec-2000 11:13

Changing the parameters for evaluation and contour definition

In addition to activating extended evaluation functions, the configuration window **Pulmo Configuration** also allows you to change the basic settings for Pulmo evaluations.

✧ Call up **Pulmo Configuration** and click the **Calculation** card into the foreground.



Standard Evaluation Parameters

Lung Sides: Both

Evaluation Limits

Maximum [HU]: 3071

Minimum [HU]: -1024

☐ Manual Segmentation

☐ Volume Calculation

Contour Detection

Contour Threshold [HU]: -200

Number of Erosions: 2

3D Preparation

☐ Store Segmented images

Background Value [HU]: -1024

✧ Under **Standard Evaluation Parameters**, select whether you always want to evaluate both lungs, the right lung only, or the left lung only.

✧ If necessary, under **Evaluation limits** change the HU value range to be evaluated (i.e. HU value definition of the lung)

✧ If necessary, change the parameters for automatic contour definition.

NOTE

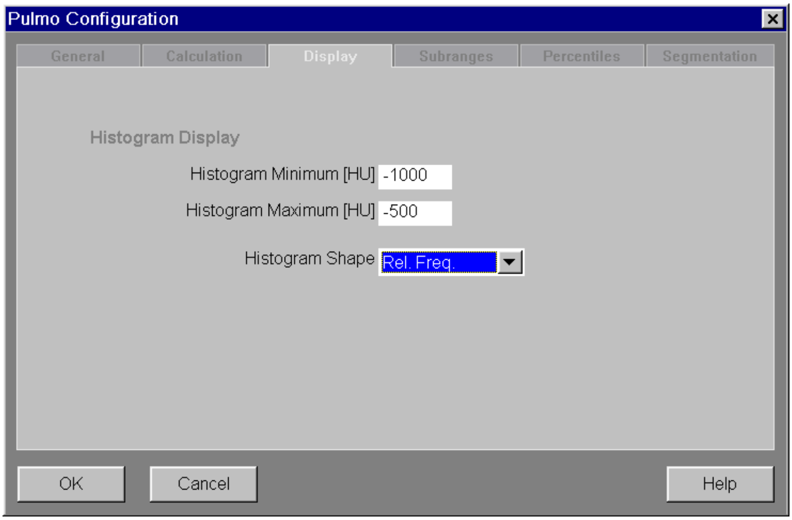
The default values for automatic contour definition are – 200 HU and 2 erosions.

Only experienced users should use settings other than these.

Adapting the histogram display

In the **Display** subtask card of the configuration window you can change the histogram display in the top left result segment.

✧ Call up **Pulmo Configuration** and click the **Display** card into the foreground.



Histogram Display

Histogram Minimum [HU] -1000

Histogram Maximum [HU] -500

Histogram Shape Rel. Freq.

✧ Select which HU value range is to be displayed in the histograms by overwriting the values for **minimum** and **maximum**.

✧ Then, in the list **Histogram Shape**, define whether the curves are to display the absolute and relative frequencies or the peak frequency.

NOTE

We recommend that you use relative frequencies. Only with relative frequencies can you compare the histogram curves of different patients. Other settings are influenced by the zoom factor.

Reference data files and reference parameters

Pulmo evaluation calculates the lung density and structure data of the examined patient and compares that information with the corresponding values of reference persons. For this, the program can access a reference data file when your system is installed.

NOTE

The Siemens reference data for lung-healthy individuals was acquired at 50% vital capacity. For a meaningful comparison of the current patient with the Siemens reference data, the current patient must also be scanned at 50% vital capacity.

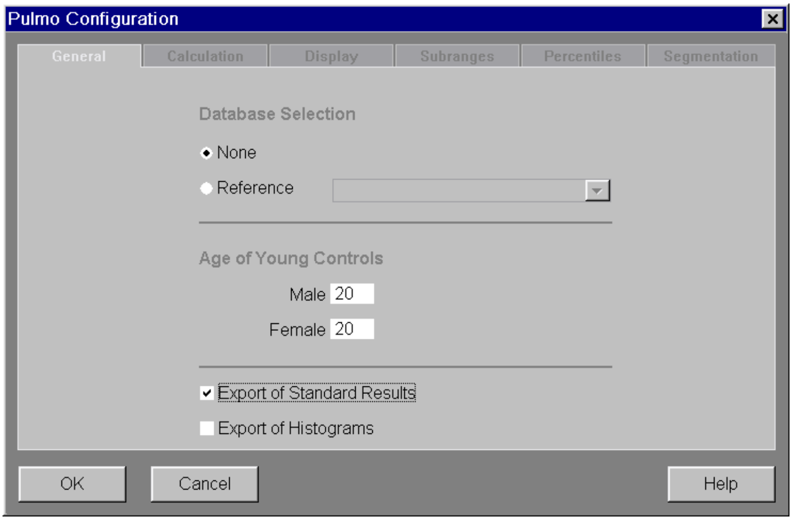
As an alternative to the Siemens standard reference data you can also use an individually created reference data file for the reference data comparison.

➩ Please consult Siemens Service if you want to use a different reference data file

Configuration of reference data comparison

In the comparison with the reference data, the system compares the results of your current examination with the values of reference persons of the same age and with the average values of younger persons.

✧ Call up **Pulmo Configuration** and click the card **General** into the foreground.



Database Selection

● None

○ Reference

Age of Young Controls

Male 20

Female 20

☑ Export of Standard Results

☐ Export of Histograms

In the input fields under **Age of Young Controls** you can specify for each sex separately which age the controls used for comparison in your evaluation should have.

✧ Overwrite the default 20 years, if necessary.

Evaluation results

The lung density of a patient varies depending on the respiratory status, i.e. if the scan is performed during full inspiration, full expiration or at a level inbetween (defined as a percentage of the vital capacity). Therefore a comparison of two scans only makes sense if the scans were performed at the same respiratory level.

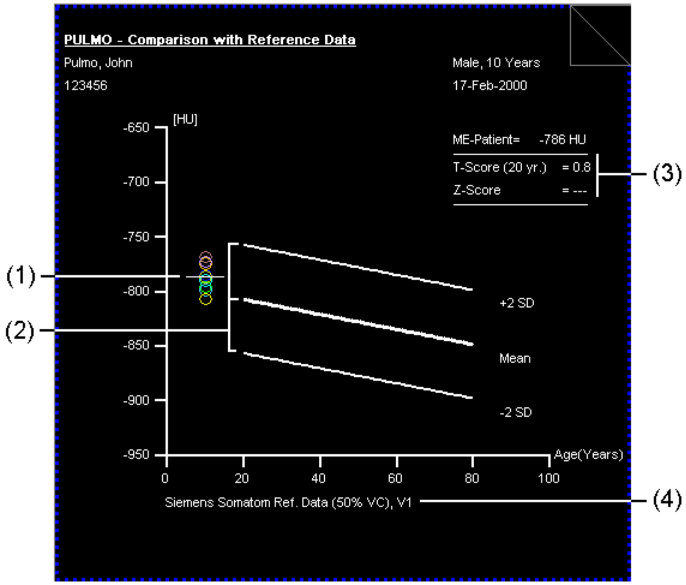
Result display

In the lower right segment of the image area you can see a comparison of the evaluation results with the reference values of healthy persons:

- **Reference data comparison as a function of the age**
  This diagram shows a comparison of the average lung density of the examined patient with the reference data of patients with healthy lungs aged between 20 and 80 years.
- **Histogram comparison**
  This diagram shows a comparison of the relative frequency of the HU values of the patient under examination with the average HU frequency distribution in the lungs of a comparable age group.

➩ Using the dog-ears (top right corner of the segment) you can scroll back and forth between the two diagrams.

Reference data comparison



PULMO - Comparison with Reference Data

Pulmo, John

123456

Male, 10 Years

17-Feb-2000

ME-Patient= -786 HU

T-Score (20 yr.) = 0.8

Z-Score = ---

Siemens Somatom Ref. Data (50% VC), V1

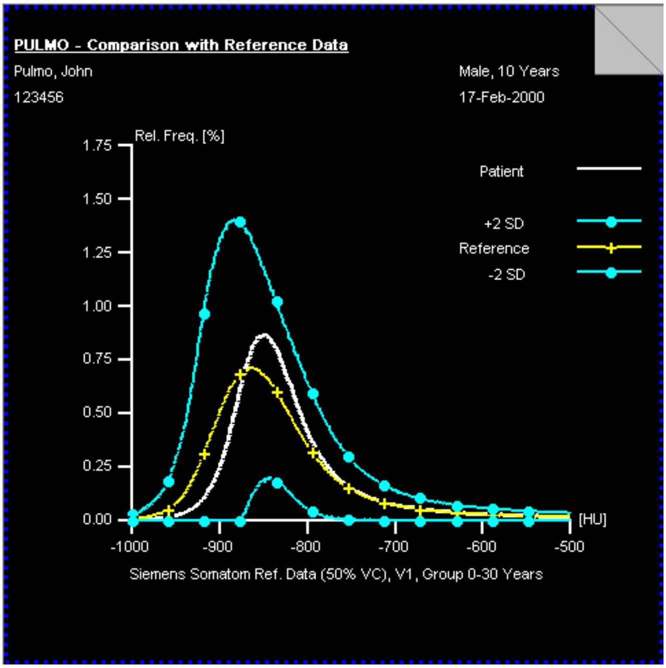
(1) Average lung density of the examined patient (small white line)

(2) Curve of the average lung density of a healthy person aged between 20 and 80 years
(as well as curve plus twice the standard deviation and curve minus twice the standard deviation)

(3) Statistics:
T-Score = Comparison of the average lung density of the patient with the average lung density of a young healthy 20-year-old (age can be configured), normalized using the standard deviation of the reference collection.
Z-Score = Comparison of average lung density of the patient with the average lung density of a healthy person of the same age normalized using the standard deviation of the reference collection.

(4) Name assigned to the reference data.

Histogram comparison



PULMO - Comparison with Reference Data

Pulmo, John

123456

Male, 10 Years

17-Feb-2000

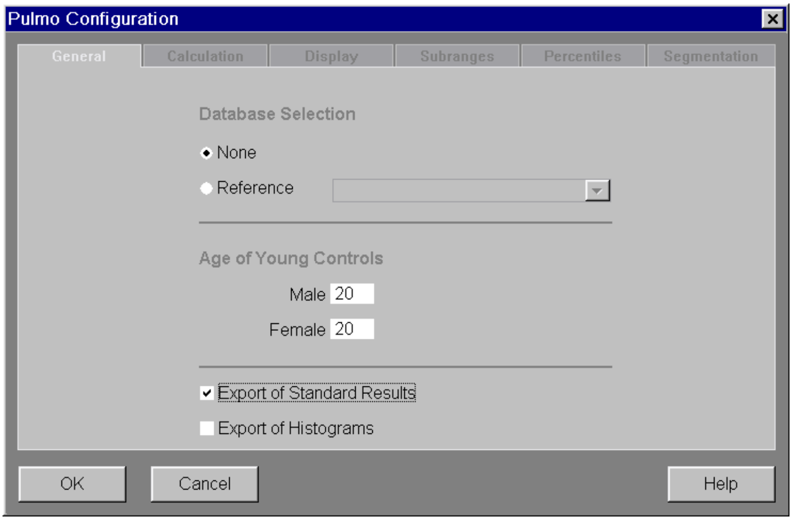
This diagram shows a comparison of the relative frequencies of the HU values (lung density values) of the patient and persons of the same age group (reference data).

The white curve shows the patient histogram. The colored curves each show a histogram with + or - 2 standard deviations for lungs of healthy patients.

Export options

After you have completed evaluation and the layout is 2 by 2, you can export the evaluation results to diskette or prepare them for further processing in 3D.

✧ Call up **Pulmo Configuration** and click the **General** card into the foreground.



Database Selection

● None

○ Reference

Age of Young Controls

Male 20

Female 20

☑ Export of Standard Results

☐ Export of Histograms

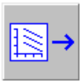
Writing your results to diskette


☑ Export of Standard Results

✧ Click on the **Enable Export of Results** check box so that you can write your evaluation results to diskette at a later stage.

If you check the check box you can write the results of your Pulmo evaluation to diskette, allowing further statistical evaluation of your data, for example, with a spreadsheet program such as MS Excel.

✧ Insert a formatted diskette in your diskette drive.



✧ When you have completed Pulmo evaluation, click on this button in the lower part of the control area to store the results of your current evaluation to diskette.

The evaluation results are written to diskette as structured ASCII data in a file called "PulmoRes.txt". You can now simply read this file into any spreadsheet or statistics program and evaluate the information further for scientific purposes, for example.

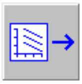
➩ If you again click on the **Save** button after having evaluated the data further, the new results are appended to the file "PulmoRes.txt".

Storing histograms

☑ Export of Histograms

✧ Click on the **Export of Histograms** checkbox so that you can store histograms on hard disk at a later stage.

If you have clicked on this checkbox, you can store the histograms on hard disk after a pulmo evaluation.

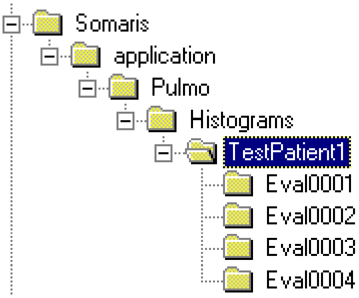


✧ Click on this button in the lower part of the control area.

Each histogram is stored as a single file in ASCII format. The filename is composed of the letter "L" (histogram of the left lung) or "R" (histogram of the right lung) + preset string "_Ser" + number of the acquisition series + preset string "_Ima" + image number, e.g. "R_Ser10_Ima5.txt".

The files are written into the subdirectory C:\Somaris\applications\Pulmo\Histograms\<PatientName>\Eval0001.

➪ If you click on the **Save** button after a further evaluation, the changed histograms are stored in a new subdirectory, e.g. "Eval0002".



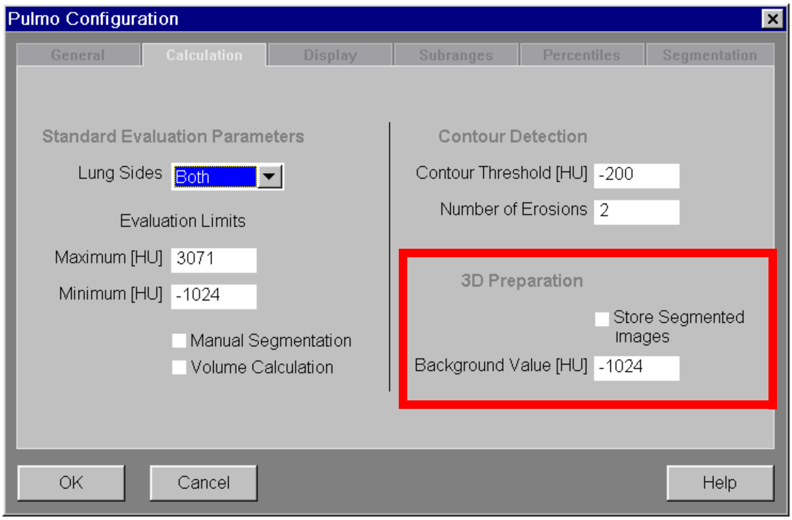
3D preparation

In contour definition the program delimits the lungs from adjacent tissue and hides it for the purposes of Pulmo evaluation. This step might also be necessary for 3D evaluations of lung examinations.

If, after Pulmo evaluation, you intend to process the examination data further with the 3D task card, you can store this intermediate step.

The system then automatically creates another series when the layout is switched to 2 by 2 (**End Evaluation**). This series contains your original images in which the surrounding tissue has a specified background value and only the lung parenchyma is differentiated in the display.

- Call up **Pulmo Configuration** and click the **Calculation** card into the foreground.



Standard Evaluation Parameters

Lung Sides: Both

Evaluation Limits

Maximum [HU]: 3071

Minimum [HU]: -1024

☐ Manual Segmentation

☐ Volume Calculation

Contour Detection

Contour Threshold [HU]: -200

Number of Erosions: 2

3D Preparation

☐ Store Segmented images

Background Value [HU]: -1024

- Check the **Store Segmented Images** check box to activate this option.
- Change the default background value, if necessary.

PART
L

Dental (Option)

L.1 *Introduction*

L.2 *Loading and displaying images*

L.3 *Calculating panoramic and paraxial images*

L.4 *Evaluating, filming, and storing result images*

CHAPTER

L.1 Introduction

The task card **Dental** provides options for 3D evaluation of orthodontic region CT images. With **Dental** you can reconstruct panoramic images and paraxial tomographic images.

Depending on the original images used, panoramic images provide either a full or partial view of the upper and lower jaw. Paraxial images are reconstructions of individual teeth and the jaw bone perpendicular to the panoramic view.

You can document these reconstructed tomograms quickly, easily, and true to scale (i.e. actual anatomical size) on film from the **Dental** task card. They are useful as a basis for planning implants and surgery in the jaw area.

Data required for evaluations with **Dental** are CT volume data sets which are usually scanned with the scan protocol **Dental-Scan**. You can select **Dental-Scan** in the scan protocol list under **Specials**. The procedure for scanning is the same as that for normal CT examinations.

NOTE

Dental result images imported from MOD or CD cannot be filmed in real size and cannot be evaluated further due to technical reasons.

Calling up Dental

You can first call up an empty evaluation card **Dental**.

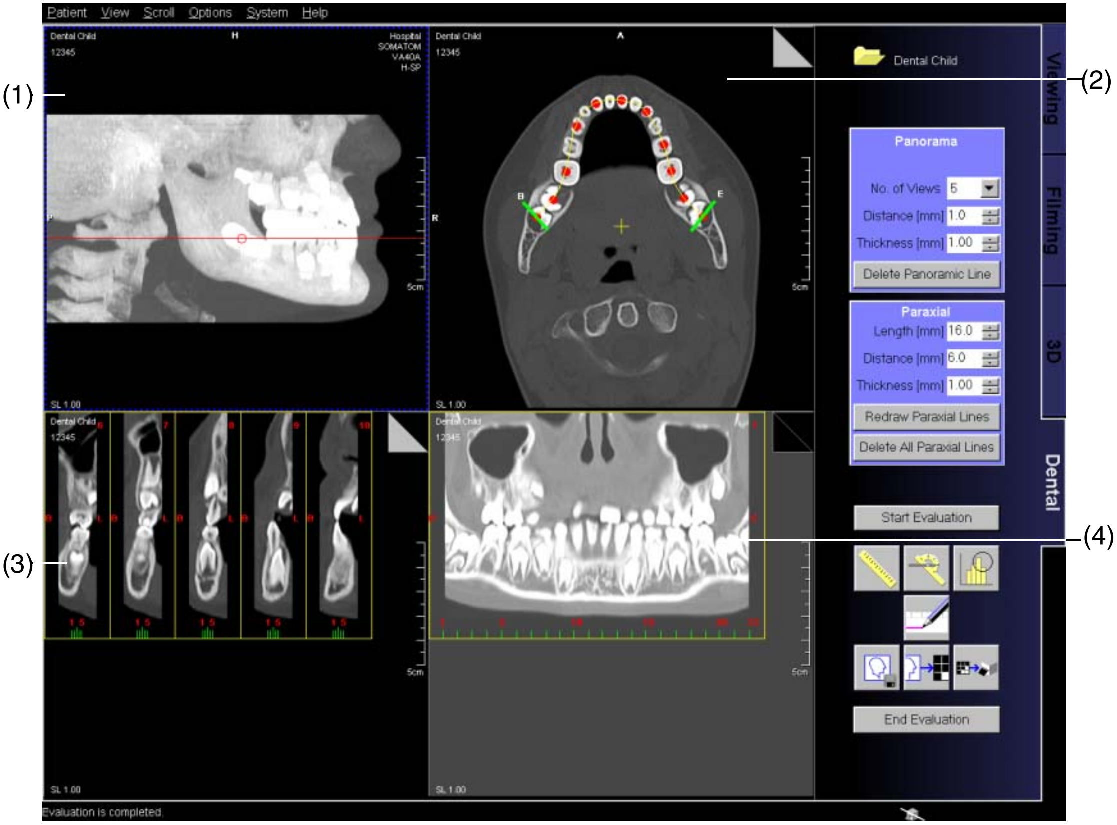
✧ Call up **Patient > Dental** in the main menu.

The **Dental** task card is displayed. No images have yet been loaded. All the buttons and most of the menu items are still grayed-out.

Or

✧ Click on the **Dental** tab if you switched to a different task card in the meantime and now want to return to dental evaluation.

The **Dental** card is subdivided into two large areas. The **control area** contains subtask cards and buttons for performing evaluations and for image postprocessing and further processing. The **image area** is used to display the original and results images. It is subdivided into four segments.



Panorama

No. of Views 5

Distance [mm] 1.0

Thickness [mm] 1.00

Paraxial

Length [mm] 16.0

Distance [mm] 6.0

Thickness [mm] 1.00

Evaluation is completed.

(1) **Overview segment**
lateral MIP view of the jaw.

(2) **Planning segment**
with a stack of MPR images.

(3) **Paraxial segment**
with a stack of reconstructed paraxial tomographic images of the teeth and the associated reference image.

(4) **Panoramic segment**
with a stack of reconstructed panoramic images of the upper and/or lower jaw and the associated reference image.

Closing dental

Once you have completed all dental evaluations, you can close the **Dental** task card again.

✧ Call up **Patient > Close Dental**.

The task card is closed, the **Dental** tab disappears.

Or

✧ Call one of the other task cards (e.g. **Pulmo** or **Osteo**) and confirm the displayed dialog box with **Yes**.

The **Dental** task card is closed and replaced by another task card.

CHAPTER
L.2 Loading and displaying images

In the **Dental** task card you can reconstruct panoramic images of the upper and lower jaw as well as paraxial tomographic images of the teeth and the adjacent jaw bone.

Original image material

Basis for these reconstructions are volume data sets of the upper and lower jaw. This CT data is usually scanned with spiral technique.
→ Navigator Operator Manual, chapter C.5, *Spiral*

NOTE

The examination must be completed with **End Exam**, otherwise Dental evaluation is not possible.

The original data set used for dental evaluation must fulfill the following conditions and have been scanned with the following parameters:

- ❏ All images must be part of a single study and must have been scanned within 1 hour.
- ❏ The scans must have been acquired at the same table height and gantry tilt.
- ❏ In the case of sequence scans (which can be a useful method in some cases) the images must have been scanned overlapping, with slices adjacent to each other, or with a maximum gap of 10 mm.
- ❏ The original images must have the same zoom factor, the same center of reconstruction, the same slice orientation and an image resolution of 512 x 512.

Loading original images

If the **Dental** task card is not yet displayed, call it up from the **Patient Browser**. At the same time load the images on which your Dental evaluation is to be based. Or open an empty **Dental** task card and load the images afterwards with **Patient > Dental**.

While loading the original images, the system generates two 3D data sets:

❑ a lateral view of the jaw region for display in the overview segment (MIP reconstruction).

❑ a set of transaxial tomographic images for display in the planning segment (MPR reconstructions).

Loading images from the Patient Browser

- Open the **Patient Browser**.
- Select a suitable study or one or several series of a CT examination (at least 4 images).
- Then click on the **Dental** button in the tool bar of the **Patient Browser**.

Or

- Call up **Patient > Dental** from the menu bar of the **Patient Browser**.

Image loading failed

If the system has not been able to load the selected images in **Dental** an error message is output.

The task card is displayed, but the planning and overview segment remains empty. All buttons, input fields, and most of the menu items are grayed-out.

Reloading images

If you were not able to load images or you have completed your first evaluation and wish to evaluate further image material, you can reload images in the open **Dental** card.

- Call up **Patient > Patient Browser** in the main menu to open the **Patient Browser**.
- There, select the images or series that you want to evaluate.

- Drag your image selection keeping the left mouse key pressed into the **Dental** task card (drag & drop).

Or

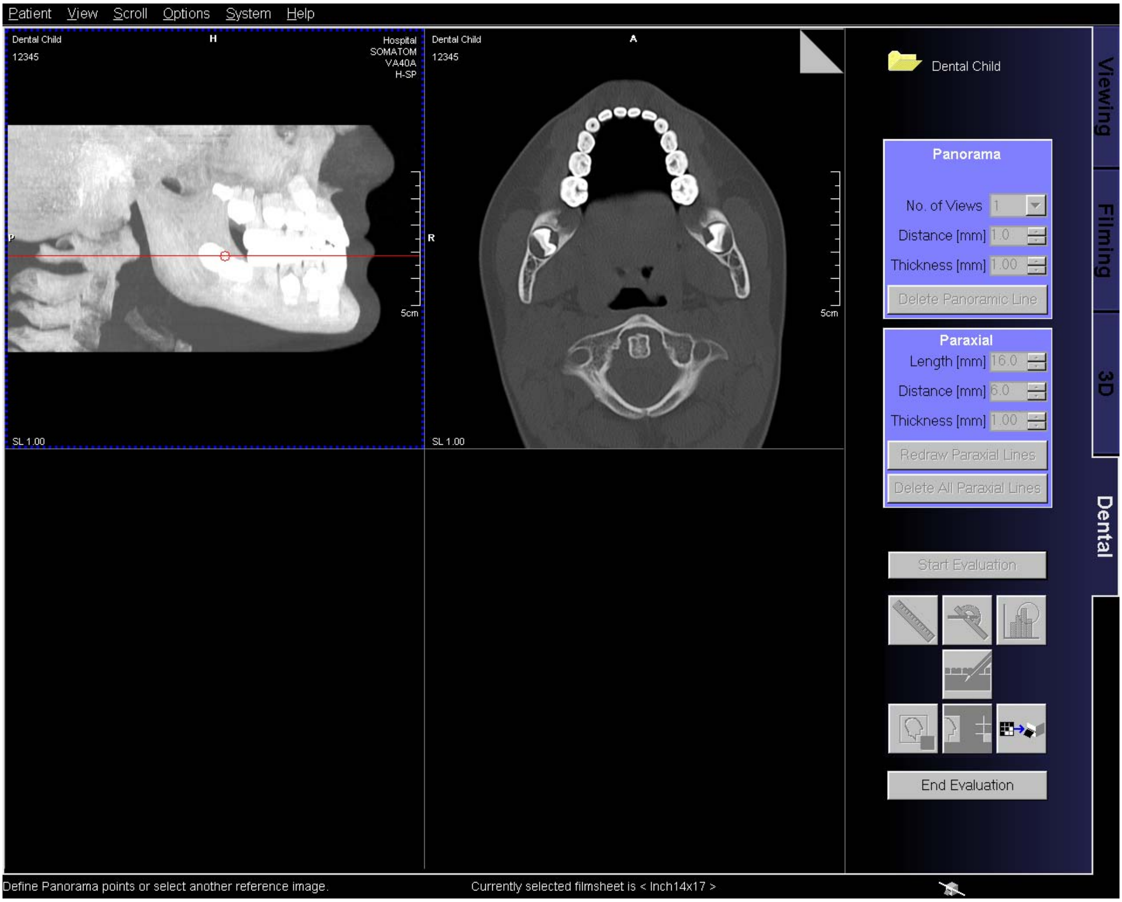
- Double-click on the selected images to load them into the **Dental** task card.

If **Dental** already contained images, they are now automatically closed. If the task card contains evaluation results that you have not yet saved, a query now appears. You can either reject your earlier evaluation results or start the loading procedure later and store these results first.

Changing the image display

Once you have loaded the original images you will see a set of transaxial tomographic images of the jaw region (MPR reconstructions) in the planning segment.

The horizontal red orientation line in the overview segment shows you which tomographic image is currently being displayed in the planning segment.



No. of Views 1

Distance [mm] 1.0

Thickness [mm] 1.00

Length [mm] 16.0

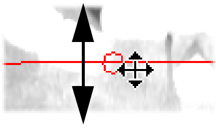
Distance [mm] 6.0

Thickness [mm] 1.00

Define Panorama points or select another reference image.

Currently selected filmsheet is < Inch14x17 >

Image selection with the orientation line



Using the orientation line you can scroll through the transaxial tomographic images. Choose an image that is most suitable for planning the panorama view of the jaw and the paraxial tomographic images of the teeth.

✧ Click on the circle of the orientation line.

✧ Keep the left mouse key pressed and pull the line up or down.

In the planning segment you can now see the tomographic image at the new position of the orientation line.

Scrolling image by image

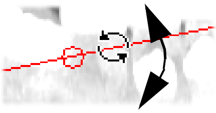
✧ Click on the dog ears in the planning segment to scroll one by one through the transaxial tomographic images.

Or

✧ Call up **Scroll > Next Image** or **Scroll** > **Previous Image** in the main menu.

The red orientation line moves along correspondingly in the overview segment.

Oblique sections in the planning segment



If none of the horizontal tomographic images in the planning segment is suitable for planning your jaw reconstructions, you can also display oblique sections in the planning segment.

✧ Click on any part of the red orientation line in the overview segment with the mouse, but not on its center.

✧ Drag the line up or down keeping the left mouse key pressed to rotate the line around its center.

➪ The angle by which the red orientation line can be rotated is limited to ±90°.

Windowing, zooming, and panning images

To make details clearer, you can window and zoom the images in the planning segment and change the image section.

➪ You can zoom, pan, and window in the same way as in the panoramic and paraxial segment, as soon as reference images or reconstructed tomographic images are displayed in it. **Zoom & Pan On** must be selected in the **Image** menu.

✧ Click into an image with the center mouse key to window and drag the mouse vertically or horizontally.
→ Page E.4–11, *Windowing with the mouse*

Or

✧ Set the required window values with the tuning knobs at the control box (only Navigator).

✧ Click into the image periphery (zooming) or in center of the image (panning) with the left mouse key (but *not* on a line that you have already drawn).

✧ Drag the image section to the required position holding the left mouse key down.
→ Page E.4–16, *Zooming and panning images*

Image text

After loading image material the following image information is displayed in the planning and overview segment:

❑ Patient name (upper left)
❑ Patient ID (upper left)
❑ Slice thickness (lower left)

As soon as images are displayed in the panoramic and paraxial segment, this image information is also displayed in both segments.

You can hide image information if it covers interesting structures.

✧ Select **View > No Text** in the main menu to switch off the image text display.

✧ If you want to display the image text information again, just select **View > All Text**.

CHAPTER
L.3

Calculating panoramic and paraxial images

With the **Dental** task card you can reconstruct views which are especially useful for planning orthodontic surgery and implants quickly and precisely from CT volume data sets of the jaw region.

You plan these views using transaxial tomographic images that are generated when you load a data set into the **Dental** card. You start in the planning segment (top right segment in the image area).

As soon as you have defined a reference line in a suitable tomographic image in the planning segment, it is also displayed as a reference image in the two lower segments of the image area.

The following applies to all subsequent steps:

- ❑ In the **Planning segment** (upper right)
  you draw the reference line and correct it if necessary.
- ❑ In the **Panoramic segment** (lower right)
  you check the parameter entries for planning your panoramic views.
- ❑ In the **Paraxial segment** (lower left)
  you draw paraxial lines and check your parameter entries for planning paraxial tomographic images.

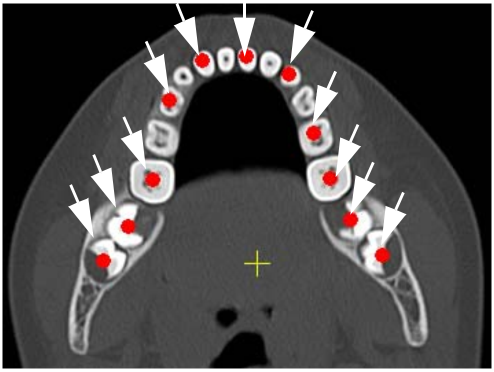
Drawing a reference line in the planning segment

Once you have loaded your original images, you use the transaxial tomographic images in the planning segment to draw in a reference line, which is used as a basis for planning your panoramic views and paraxial tomographic images.

Drawing a reference line

✧ With the left mouse key defined the position of the base points of your reference line along the jaw.

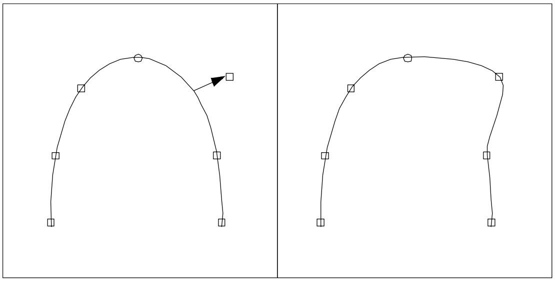
✧ Double-click into the segment to join the line.



Changing the shape of a reference line

✧ Click on *one of the base points* of the reference line in the planning segment with the mouse.

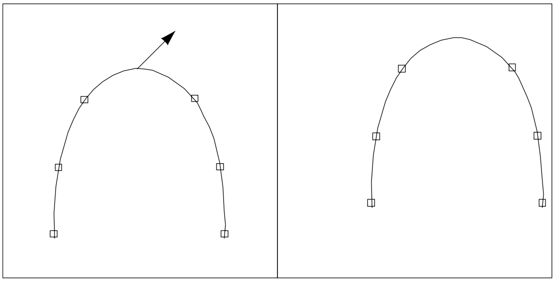
✧ Drag the cornerpoint with the left mouse key pressed to a different position to change the shape of the line.



Moving a reference line

✧ Click *on the reference line between the base points* with the mouse.

✧ Drag the line to a different position keeping the mouse key pressed to move the entire line.

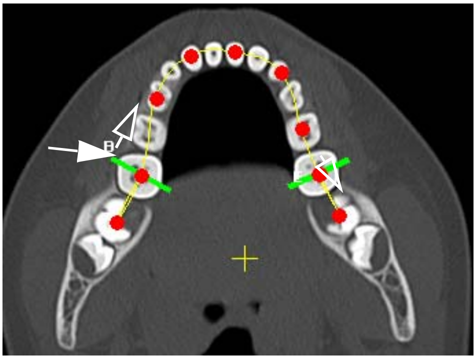


Moving a film segment

Panoramic views that are generated and filmed in the **Dental** evaluation card are output on film in their actual, anatomical size. Very rarely (depending on the film format you use), there might not be sufficient space on the film segment for the entire panoramic view (e.g. along the full length of the reference line) but only a section of it.

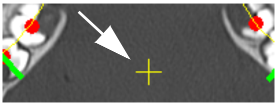
The beginning (**B**) and end (**E**) mark in the reference image shows you which panoramic section can be displayed.

✧ Click on the beginning mark (**B**) with the mouse and move it keeping the mouse key pressed along the reference line to move the section.



➩ You cannot alter the length of the line between the beginning and end mark, i.e. the width of the film section.

Positioning the direction marker



As soon as you have completed the reference line (double-click) and a reference image is displayed in all three segments, you will see a cross roughly in the center of the segment. Mark the tongue area with this cross.

This mark will later be used for reconstruction of panoramic views and paraxial tomographic images as a reference point for orientation marks (buccal or lingual).

Note

You can move the marking cross freely within the planning segment.

It is the responsibility of the user to position the cross correctly in the tongue area.

An incorrectly positioned cross will result in incorrect orientation marks in the reconstructed tomographic images!

Deleting and redrawing the reference line

You can delete and redraw the reference line at any time.

✧ Click on the **Delete Panoramic Lines** button on the **Panorama** subtask card in the control area.

Your reference line is removed from the reference image. You can now draw a new reference line.

Scrolling through the reference image stack

Scrolling in the reference image stack with drawn planning lines is useful if there are positions at which you cannot make out contours precisely enough in a reference image. The next and the preceding reference image in the image stack might provide better orientation.

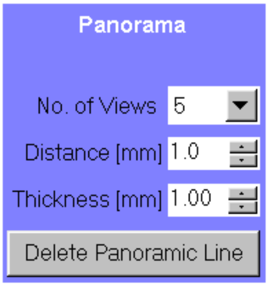
The reference line and all other planning lines in the panoramic and paraxial segments that you have drawn in remain stationary while the basic reference image (background image) continues to scroll.

Planning panoramic images

Once you have drawn in the reference line you can start to plan your panoramic views of the jaw region in detail.

You will work in the input fields of the subtask card **Panorama** and check the results in the reference image view of the Panorama segment.

➪ You cannot make any changes in the panoramic segment graphically (with the mouse).



No. of Views 5

Distance [mm] 1.0

Thickness [mm] 1.00

✧ Select the number of panoramic views you want to calculate (1, 3, 5, 7) via the spin box **Number of Views**.

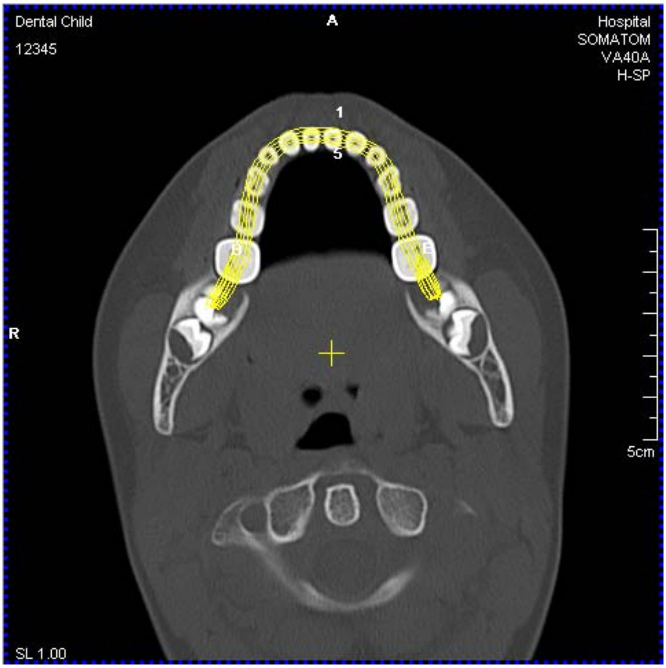
If you have selected more than one panoramic image you will see additional, parallel lines above and below the reference line that you have drawn in the reference image in the panoramic segment.

✧ Select the distance between the panoramic views via the spin box **Distance**.

If you increase the distance, the panoramic lines move apart. If you reduce the distance, the lines move together.

➩ If you have only selected one panoramic view under **Number of Views**, the field **Distance** is grayed out.

✧ Select the slice thickness for the panoramic images that you want to reconstruct via the spin box **Thickness** (up to 20 mm).



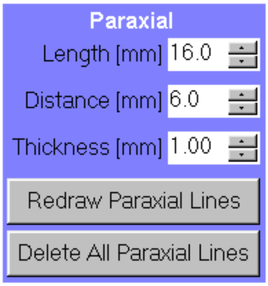
Planning paraxial cuts

As soon as you have completed a reference line in the planning segment, a reference image is also displayed in the paraxial segment. It shows your reference line together with suggestions by the program for planning paraxial cuts.

➪ In order to make it easier to assign paraxial lines in this reference image to reconstructed tomographic images at a later stage, every fifth paraxial line is numbered and shown as a thick dotted line.

Modifying paraxial lines via parameters

You can adapt these program suggestions for paraxial lines to your individual requirement by changing the parameter values on the **Paraxial** subtask card.



Paraxial

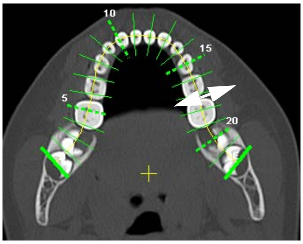
Length [mm] 16.0

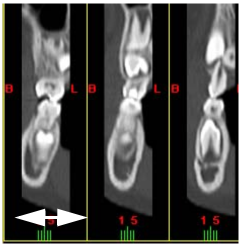
Distance [mm] 6.0

Thickness [mm] 1.00

✧ First fit the length of the paraxial lines using the **Length** spinbox.

The length of the paraxial lines will later correspond to the image width of a paraxial section in the reconstructed tomographic images.





⇨ The image height will be automatically derived from the length of the measured examination range. The program always reconstructs the paraxial tomogram as well as the panoramic views for the entire data material available.

✧ Enter the slice thickness for the planned paraxial tomograms via the spin box **Thickness**.

✧ Enter the distances between the paraxial lines via the spin box **Distance** if you want equidistant paraxial tomograms.

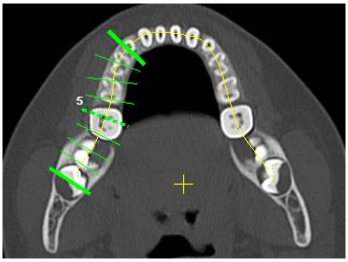
The smaller the selected distance, the larger the number of paraxial lines planned by the program. The greater the distance, the fewer the number of paraxial lines that are displayed in the reference image.

Changing paraxial lines graphically

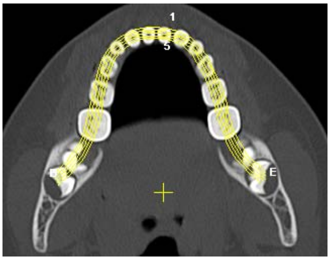
You can move, add or remove paraxial lines graphically using the mouse in the reference image of the paraxial segment.

You always do this within the beginning (**B**) and end (**E**) mark using the range end markers. They mark these sections along the line within which you want to have tomographic images reconstructed.

In the paraxial segment, too, you can move the range end markers along the reference line in order to reconstruct paraxial tomographic images in one section of the panoramic curve only, for example.
→ Page L.3–4, *Moving a film segment*



Paraxial segment



Panoramic segment

Adding a paraxial line

✧ With the left mouse key click on the reference line (between the range end markers) at the point at which you want to add a new paraxial line.

In this way you can add up to 400 paraxial tomographic images.

Moving a paraxial line

✧ Click on the paraxial line that you want to move.

✧ Drag it keeping the left mouse key pressed along the reference line to its new position.

Deleting a paraxial line

✧ Click on the paraxial line that you want to delete.

✧ Drag it over from the reference line keeping the left mouse key pressed.

When the color of the paraxial line changes from green to red and you release the mouse key, the paraxial line is deleted.

Deleting all paraxial lines

✧ Click on the **Delete All Paraxial Lines** button on the **Paraxial** subtask card if you want to remove all paraxial lines suggested by the program.

Returning to the program suggestions

If the modified paraxial lines are not satisfactory, have the system draw in equidistant paraxial lines again.

✧ Click on the **Redraw Paraxial Lines** button on the **Paraxial** card if you want to reject your graphic changes.

Starting with the equidistant paraxial lines you can make the change you require using the mouse and the parameter card.

You can define the distance between this lines and the number in the film segment using the **Distance** spinbox.

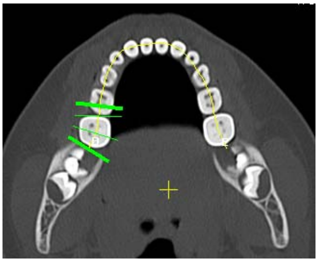
Grouping paraxial lines

To reconstruct paraxial images only from individual teeth, group paraxial lines in the reference image of the paraxial segment and copy them to an other position on the reference line. The original paraxial lines remain unchanged.

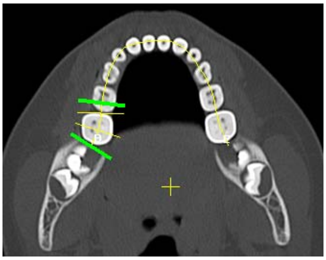
✧ Limit the paraxial lines to one or a few teeth only.

✧ Call up **Cluster** from the popup menu (right mouse key).

The system automatically groups all existing intersection lines in the paraxial segment. The intersection lines are displayed yellow.



Paraxial lines

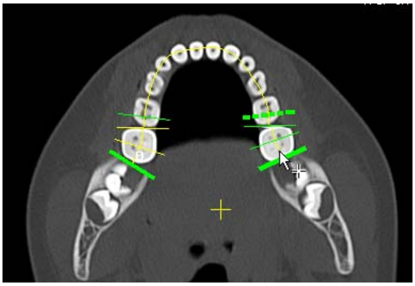


Grouped paraxial lines

⇨ In the popup menu, the item **Cluster** changes to **End Cluster**.

Copying grouped paraxial lines

✧ Click with the left mouse key at the position on the reference line to which you want to copy the grouped intersection lines.



➩ The inserted paraxial lines must have sufficient space on the reference line (at least the same length) and must not overlap the existing intersection lines.

Deleting grouped paraxial lines

If you no longer require the copy of the grouped paraxial lines, delete then using the popup menu.

✧ Call up **Undo** from the popup menu (right mouse key).

The paraxial lines last copied are removed.

Canceling the grouping

After you have copied the grouped paraxial lines to the required position, cancel the grouping.

✧ Call up **End Cluster** from the popup menu.

You can now postprocess the paraxial lines again using the mouse or the parameter cards.

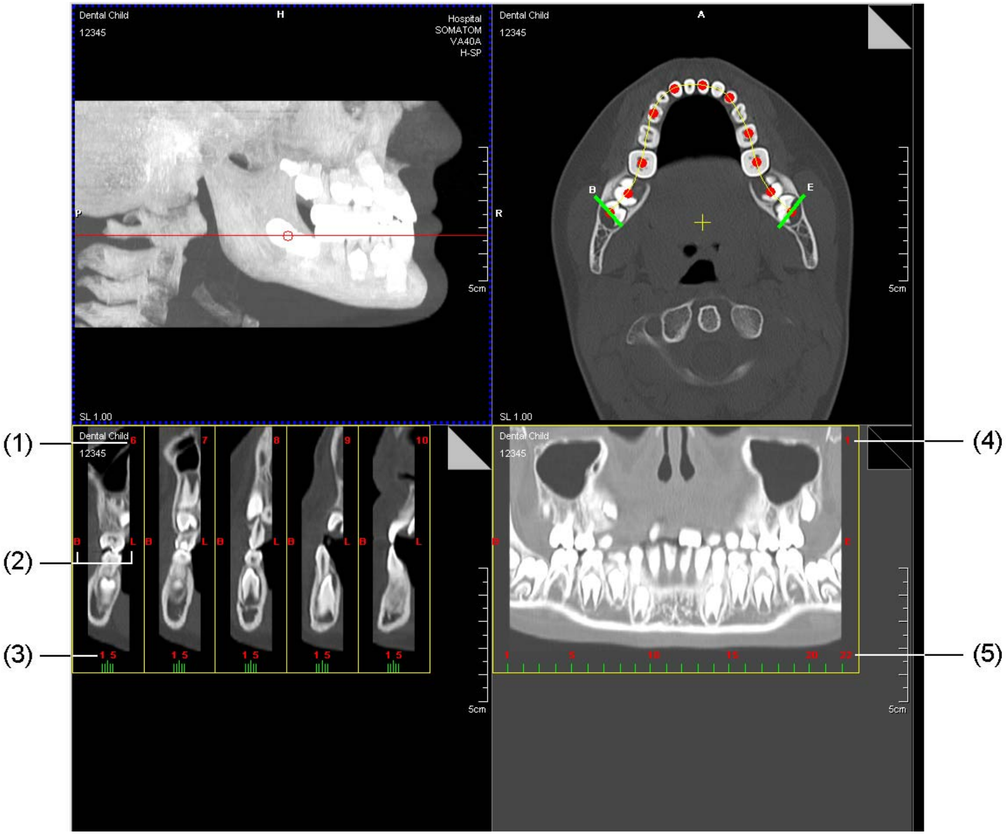
Starting reconstruction

Once you have completed your preparations you can start reconstruction of your panoramic views and paraxial tomographic images.

Start Evaluation

✧ Click on the button **Start Evaluation** below subtask cards in the control area.

The panoramic and paraxial images are calculated and displayed in the appropriate image segments.



(1) Reformat number of paraxial image
(2) Orientation labels (B = Buccal, L = Lingual)
(3) Reformat numbers of the corresponding panoramic images (at the position indicated by the tick mark)
(4) Reformat number of panoramic image
(5) Reformat numbers of the corresponding paraxial images (at the position indicated by the tick mark)

You can scroll through the stack of result images in the panoramic and paraxial segment with the dog ears.

➩ The image at the bottom of each stack is the reference image which you use to plan these reconstructions.

Repeating a reconstruction

If you are not happy with the result images, change the reference images and repeat the reconstruction.

You can do this via the parameter entries in the subtask cards or graphically in the reference image of the paraxial segment.

✧ Scroll through the entire panoramic or paraxial segment image stack until you get to the reference image.

✧ Change your planning of the tomographic images.

➩ Two query boxes appear as soon as you start your modification. You are asked whether you want to film and store or reject the first results.

✧ Then click on **Start Evaluation** again to have the new result images calculated.

You then see the new result images displayed in the panoramic and paraxial segment.

Marking the mandibular canal

After you have displayed the result images, you can mark the mandibular canal in all paraxial and panoramic images, but only marks made in the paraxial segment will be stored and displayed on filmsheet. You can either outline the mandibular canal manually by drawing it in the individual panoramic images, or mark and interpolate it semi-automatically in paraxial images.

All set and calculated points in the paraxial images, as well as lines that have been drawn in the panoramic images are stored in the database and can be viewed on filmsheet.

Localization of the mandibular canal in the paraxial images is necessary, for example, for planning implants.

All actions for mandibular canal made in the panoramic images result in **support points** in the paraxial lines.

NOTE

Support points are not stored and not filmed.

Outlining the mandibular canal manually

Using freehand lines or graphic points, you can outline the mandibular canal manually.

Drawing a freehand line

You can draw the freehand line in the panoramic images.

➪ You can only draw one freehand line in a panoramic image. As soon as you draw a further line, the existing line is deleted.

✧ Click on this button to activate the drawing tool for the mandibular canal.

✧ Click in the image on the required starting point.

✧ Draw the mandibular canal from the starting point holding the left mouse key.

✧ Double-click on the end point to end the freehand line.

The outlined mandibular canal appears in the panoramic image, and support points are shown in the paraxial image.

Setting graphic points

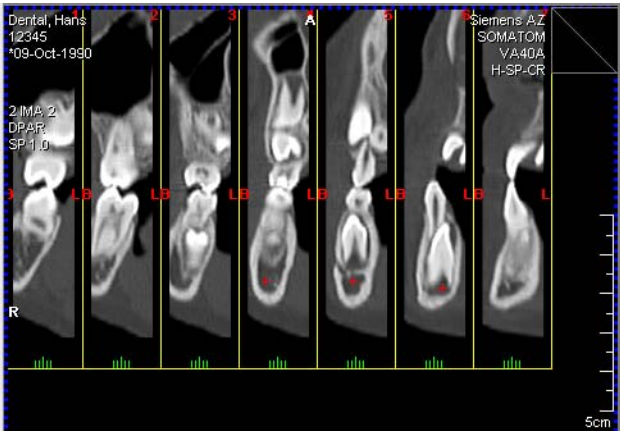
You can mark the mandibular canal using graphic points in which you set one graphic point at the position in question in each paraxial image.

➪ As soon as you set a second graphic point in the same paraxial image, the first graphic point is cleared.

✧ Click on this button to activate the drawing tool.

✧ Click with the left mouse key at the position in the image at which you want to set a graphic point.

The set graphic points appear in the paraxial image.



Interpolating the mandibular canal

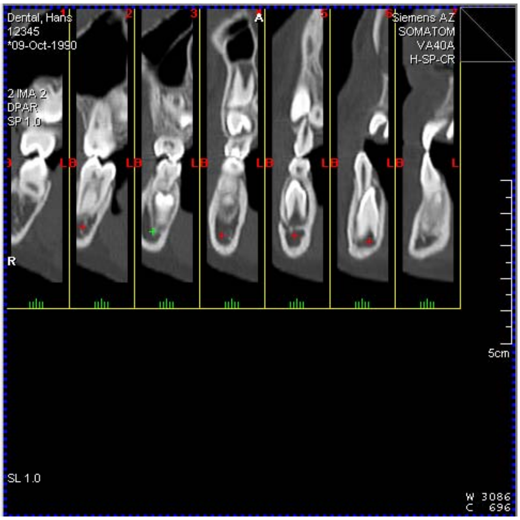
Sometimes not all paraxial images are suitable for drawing the mandibular canal. You will then draw the mandibular canal only in those images in which it can be recognized clearly. You system then interpolates the marking of the canal in the missing paraxial images.

Performing interpolation

✧ Mark the mandibular canal using a freehand line or graphic points in the suitable images.

✧ Call up **Start Calculation** from the popup menu (right mouse key) to start interpolation.

In the paraxial images, the interpolated graphic points are displayed.



➩ All interpolation points are shown in a different color from the points you have set.

Undoing interpolation

If the mandibular canal is not correctly shown by the interpolation, undo calculation of the interpolation points.

✧ Call up **Undo Calculation** from the popup menu (right mouse key).

You can now continue by drawing the freehand lines or setting the graphic points.

Closing mandibular canal definition

✧ Click on the mandibular canal button again to deactivate it and confirm the popup message.

CHAPTER L.4

Evaluating, filming, and storing result images

You can continue to evaluate panoramic views of the jaw and paraxial tomographic images of the teeth that you reconstructed in the **Dental** task card here.

You can then film these reconstructions from **Dental** easily and in their actual size and store them as result series.

Evaluating result images

In the result images of a dental evaluation, you can measure distances and angles and draw a ROI for area calculation.

For more comprehensive image evaluation store your result series and then load them in the **Viewing** task card. It is not possible, however, to film images in real size from the **Viewing** task card.

Measuring lengths and angles

✧ Scroll through the panoramic segment and/or paraxial segment using the dog ears to the tomographic image that you want to measure.

✧ Click on the button **Distance** in the lower part of the control area if you want to measure distances.

Or

✧ Click on the button **Angle** if you want to measure angles.

✧ Now draw the distance line or the side of the angle that you want to measure.
→ Page E.5–17, *Measuring distances and angles*

Evaluating areas

✧ Click on the **Circle** button to draw a circular ROI.

✧ Click into the image and draw the ROI holding the mouse key down.
→ Page E.5–13, *Evaluating ROIs*

Deleting graphics

You have the option of selecting all graphic elements (distance, angle, ROI) in the result images to delete them.

Before you send the images to the filmsheet, you can delete graphic elements.

✧ Click on **Edit > Select All Graphics** from the main menu to select all graphic elements.

✧ Then delete the selected graphics with the **Del** key on your keyboard.

Filming result images

From the **Dental** task card, you can film your result images and all reference and MIP images quickly and easily or print them out on paper.

All the necessary film settings are preset.

NOTE

If you have to make the necessary settings yourself, proceed as follows:

✧ To do that, call up **Options > Configuration** in the main menu.

✧ Click on the button **Filming Layout** in the configuration panel and select the entry **Dental Layout** in the dialog box **Filming Layout** under **Layout name**.

✧ Now select the option **Original Image** under **Aspect Ratio** on the card **Series**.

✧ Select the entry **1:1** under **Layout divisions** on the card **Series**.

NOTE

While you run the **Dental** application, do not change any camera settings, except filmsheet size. Do not change from one camera to another camera.

Selecting images

Before you can transfer image material to the **Filming** task card for filming, you have to select the required images on the **Dental** card.

✧ Call up **Edit > Select All** from the main menu if you want to film all result, reference, and MIP images.

Or

✧ Call up **Edit > Select On Succeeding** to select the image displayed and all successive images.

Or

✧ Call up **Edit > Select Series** to select the entire series.

Deselect images

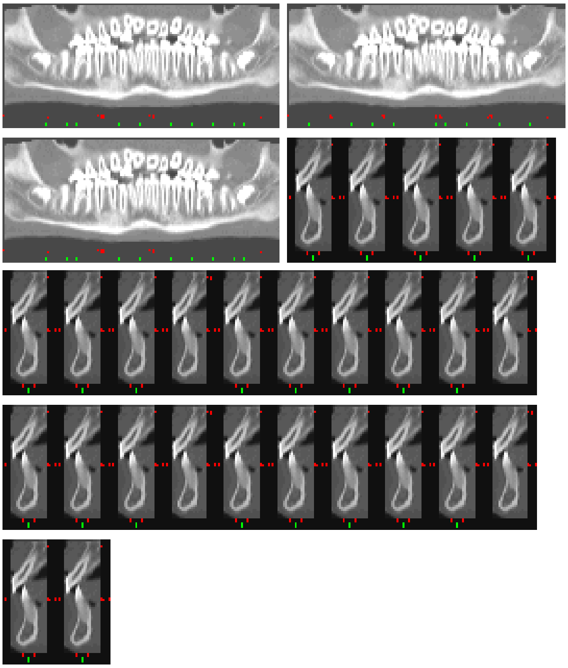
✧ Call up **Edit > Deselect All** from the main menu to deselect all selected images.

Filming images

✧ Click on the button **Copy to Film Sheet** in the control area of the **Dental** task card to send the images to the virtual film sheet first.

✧ Then click on the button **Expose Film Task** to send the images from the virtual film sheet to the default camera or the default printer.

The images of the dental evaluation are output clearly in the default film layout.



Storing result images

As soon as you store your result images they are stored as separate series together under the same study as the original images.

✧ Click on the button **Store to Disk** to store the results of your dental evaluation.

The system now creates 4 new series:

- Overview image (MIP image)
- Reference image with drawn in reference line
- Panoramic image(s)
  (the last image of this series is the reference image with the reference lines for planning the panoramic views)
- Paraxial Images
  (the last image of this series is the reference image with the reference line and the paraxial lines).

You can now load these series and images in other task cards to work on them whenever you want (e.g. the **Viewing** task card).

Closing dental evaluation

Once you have generated, filmed, and stored all the panoramic and paraxial images that you need, you can close the current dental evaluation session.

✧ Click on the button **End Evaluation** in the lower part of the control area.

All images are removed from the task card. You can now load new original images for another dental evaluation. Or you can close the task card if you do not wish to perform any further dental evaluations.
→ Page L.1–4, *Closing dental*

PART
M

Calcium Scoring (Option)

M.1 Introduction

M.2 Loading and displaying images

M.3 Performing evaluation of coronary lesions

M.4 Documenting evaluation results

M.5 Configuring CaScoring

CHAPTER

M.1 Introduction

The task card **CaScoring** allows you to estimate the amount of detected calcium in the coronary arteries.

Calcium Scoring evaluation is based on CT images which are used to calculate the number of coronary lesions, the volume and equivalent mass of detected calcium and the Agatston Score.

Calcium Scoring software is a sophisticated tool that allows the experienced physician to make the correct decision for future treatment. It provides a semi-automatic method for identifying calcium deposits in an entire volume.

Thus, Calcium Scoring greatly facilitates the screening and therapy of patients who run the risk of suffering from coronary heart disease.

CT sequence and spiral data sets that have been measured with special Calcium Scoring scan protocols are used as the basis for evaluation with Calcium Scoring.

Calling up CaScoring

You can call up the **CaScoring** evaluation card without loading a series so that it is initially empty.

✧ Call up **Patient > CaScoring** in the main menu.

The **CaScoring** task card is displayed. All buttons and most menu entries are still grayed out.

Or

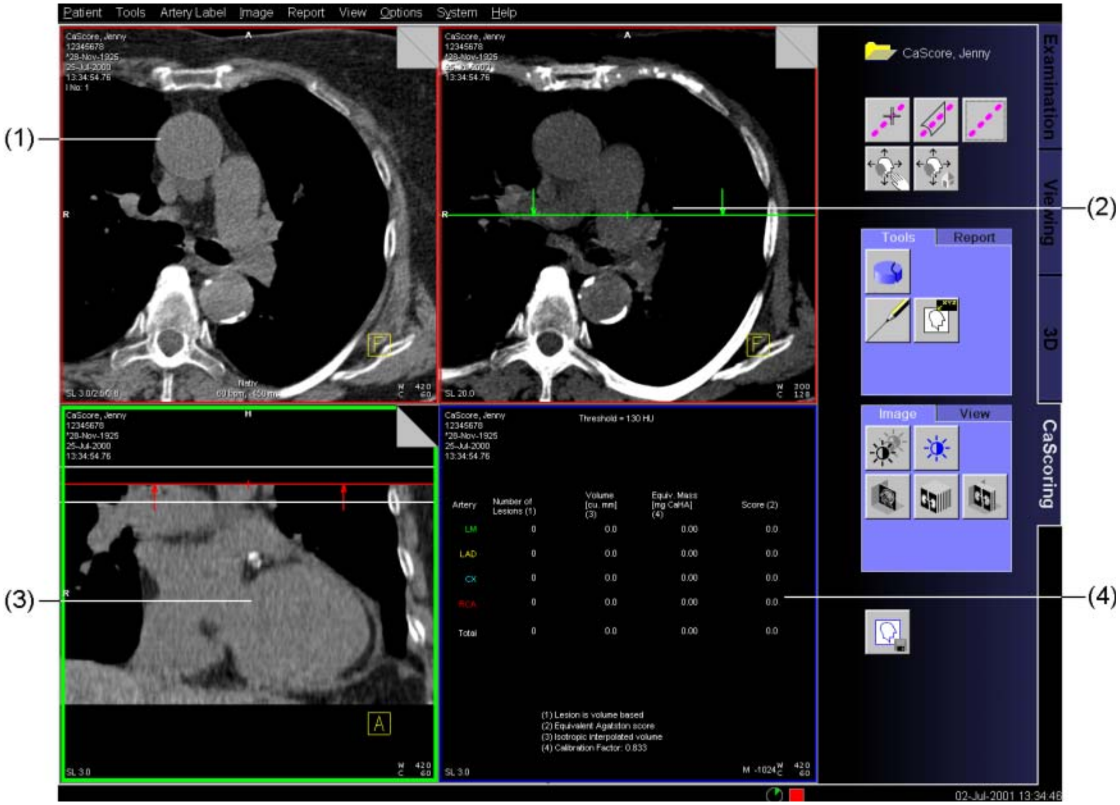
✧ Click on the **CaScoring** tab if you have switched to another task card in the meantime.

As soon as you have loaded images into the **CaScoring** task card, the task card moves into the foreground. But you can also switch to other applications at any time and resume evaluation on the **CaScoring** task card later.

The **CaScoring** task card is subdivided into two large areas.

The **control area** contains subtask cards and additional buttons for editing and documenting the image material.

The **image area** is subdivided into four segments. Here, you can view a representation of the current tomogram, all the detected calcium within the reconstructed volume, a coronal or sagittal cut through the current position in the volume, and the results of the evaluation.



Threshold = 130 HU

Artery	Number of Lesions (1)	Volume [cu. mm] (3)	Equiv. Mass [mg CaHA] (4)	Score (2)
LM	0	0.0	0.00	0.0
LAD	0	0.0	0.00	0.0
CX	0	0.0	0.00	0.0
RCA	0	0.0	0.00	0.0
Total	0	0.0	0.00	0.0

(1) Lesion is volume based
(2) Equivalent Agatston score
(3) Isotropic interpolated volume
(4) Calibration Factor: 0.833

(1) **Tomo segment**
current slice in transaxial projection (caudo-cranial direction)

(2) **Overview segment**
reconstructed volume in transaxial projection
(entire calcium detection)

(3) **Detail segment**
coronal or sagittal cut through the current position in the volume

(4) **Result segment**

Closing CaScoring

As soon as you no longer want to perform an CaScoring evaluation, you can close the **CaScoring** task card again.

✧ Call up **Patient > Close CaScoring**.

The task card is closed, the **CaScoring** tab disappears again.

Or

✧ Call up another task card, e.g. **Pulmo** or **Dental** and confirm the displayed dialog box with **Yes**.

The **CaScoring** task card is closed and another task card is displayed instead.

CHAPTER

M.2

Loading and displaying images

In the task card **CaScoring**, you can determine the amount of calcium of lesions in the coronary arteries within the entire volume.

Evaluation with Calcium Scoring is performed on tomograms that have been acquired with special Calcium Scoring scan protocols (e.g. CaScoreSeq).

Original image material

To achieve standardization of the evaluation results the image material must meet the following requirements:

- ❏ Only images of one patient must be loaded for Calcium Scoring evaluation.
- ❏ The scans must have been acquired without gantry tilt (gantry tilt = 0)
- ❏ Only original image material must be used that has neither been edited with 2D tools in the **Viewing** task card e.g. Zoom&Pan nor with 3D tools in **3D** e.g. curve.
- ❏ Only image data sets with the same slice orientation must be used.
- ❏ Only contiguously scanned and reconstructed sequence or spiral data sets with identical slice distances and identical thickness must be evaluated.
- ❏ The slices must have been scanned at different table positions.
- ❏ The data capacity of the volume must not exceed 1024 images with a matrix size of 512 x 512 pixels.

Loading original images

You can load the images of the Calcium Scoring examination from the **Patient Browser** onto the **CaScoring** task card.

➩ Before loading onto the **CaScoring** task card, your system checks whether the images you selected are suitable for a Calcium Scoring evaluation. If you select several series or an unsuitable series, the **3D Series List** is displayed.
→ Page H.2–5, *Series List*

Transferring images with the Patient Browser

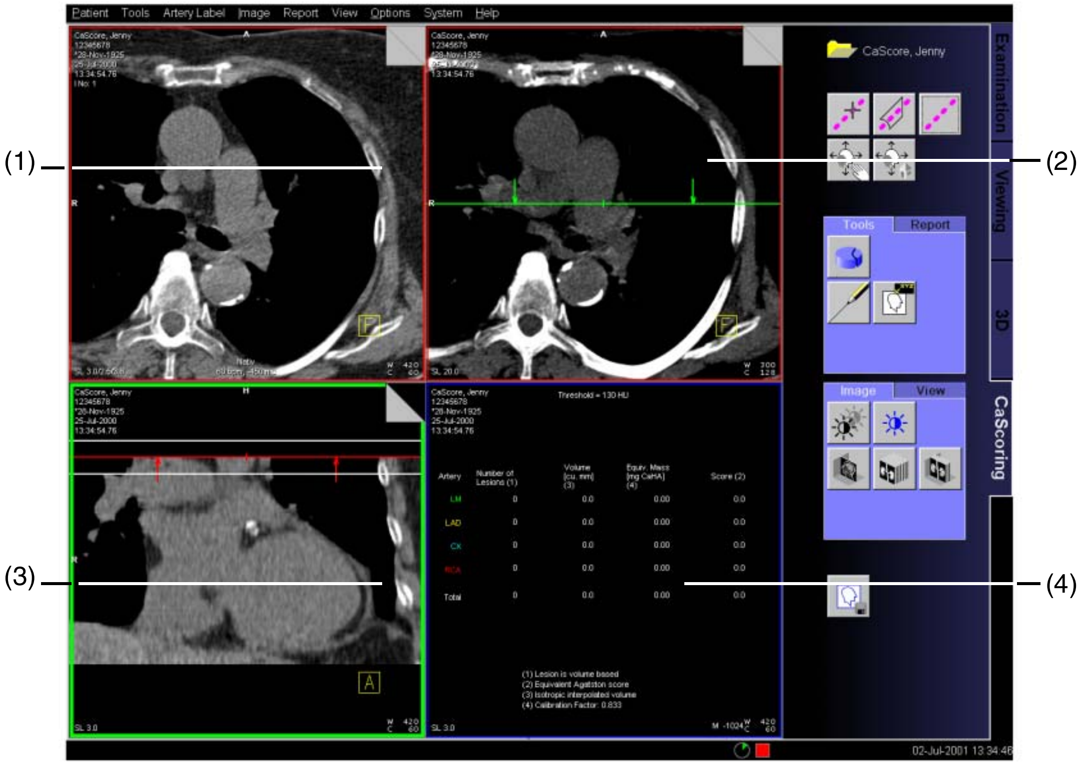
In the **Patient Browser** window you can search for the examination, series, or images that you want to load onto the **CaScoring** task card.

✧ Call up the **Patient Browser** (**Patient > Browser**).

✧ Select the required examination data in the navigation or content areas.
→ Page D.2–6, *Scrolling through and selecting patient data*

✧ Call up **Patient > Calcium Scoring** in the **Patient Browser** or click on the **Calcium Scoring** button on the tool bar of the **Patient Browser**.

➩ If you have activated **Close after Loading** the **Patient Browser** dialog box is closed as soon as the images have been loaded onto the **CaScoring** task card.



Threshold = 130 HU

Artery	Number of Lesions (1)	Volume [cu. mm] (3)	Equiv. Mass [mg CaHA] (4)	Score (2)
LM	0	0.0	0.00	0.0
LAD	0	0.0	0.00	0.0
CX	0	0.0	0.00	0.0
RCA	0	0.0	0.00	0.0
Total	0	0.0	0.00	0.0

(1) Lesion is volume based
(2) Equivalent Agatston score
(3) Isotropic interpolated volume
(4) Calibration Factor: 0.833

The loaded images are originally displayed in the following projection modes:

(1) **Tomo segment**:
Caudo-cranial projection

(2) **Overview segment**:
Sliding MIP mode in caudo-cranial projection

(3) **Detail segment**:
MPR mode in coronal projection

(4) **Result segment**

Changing image settings

In the **CaScoring** task card the loaded images are displayed grouped into series in the tomo segment, in the overview segment and in the detail segment.

Zooming and panning images

It is possible to zoom any part of the image that is of particular interest to you. If the size of the image is increased so much that it no longer fits into the segment, you can pan it so that the relevant part is again in the center of the image.

You can zoom and pan the images of your Calcium Scoring evaluation with the mouse. To do that, you must change the function of the left mouse key, as you usually select and deselect objects with it.

✧ Call up **Image > Zoom/Pan**.

Or

✧ Click on the button **Zoom/Pan** in the control area.

Zooming images

✧ Now place the mouse cursor in the **outer** area of an image.

The mouse changes shape.

✧ Drag the mouse cursor up to enlarge or down to reduce the image holding the left mouse key down.

As soon as you release the mouse key, the zoom factor is applied to the selected area.

Or

Panning images

✧ Now place the mouse cursor in the **inner** portion of the image.

The mouse changes shape.

✧ Drag the mouse up, down, right, or left holding the left mouse key down to pan the image.

✧ Deselect **Image > Zoom/Pan** again, or click on the appropriate button to make the left mouse key available for selecting images again.

You can restore the original zoom factor or the original position of the images again at any time.

✧ Call up **Image > Home Zoom/Pan** in the main menu.

Or

✧ Click on the button **Home Zoom/Pan**.

The results of the zooming and panning procedure which you have performed either in the tomo segment or in the overview segment are automatically adapted in both segments. Images are panned separately in the detail segment.

Windowing images

Before you start Calcium Scoring evaluation you can correct the window values of the loaded images to display and thus detect the individual coronary structures in an optimum way.

Windowing with the mouse

✧ Click on the center mouse key in an image and keep the mouse key pressed.

The mouse cursor disappears.

✧ Move the mouse up/down to vary the brightness (Center).

Or

✧ Move the mouse right/left to alter the contrast (Width).

Windowing with the keypad

For fine tuning of window values you can also use the keys on the symbol keypad of the keyboard.

✧ Select the image segment whose window values you want to modify.

✧ Press the **Center+** or **Center-** keys to reduce or increase the brightness.

✧ Press the **Width+** or **Width-** keys to reduce or increase the contrast.

The new window values, that you have acquired by windowing with the mouse or with the keypad are adapted for all the images of the same type in the individual segments. If you have windowed an image of the **MIP** type in one segment, for instance, all the images of this type are adapted in all other segments that contain **MIP** images. The same applies to images of the **MPR** type.

You might only want to change the window values of a single segment without affecting the display of the images in the other segments.

✧ Click on the segment whose window values you want to modify.

✧ Call up **Image > Single Windowing** in the main menu.

Or

✧ Click on the button **Single Windowing.**

Once you have activated **Single Windowing** you can modify the window values of the selected segment with the mouse or the keyboard.

Restoring window values

You can undo your changes to the window values at any time and restore the old window settings with which you loaded the images from the database.

✧ Call up **Image > Home Window** in the main menu.

Or

✧ Click on the **Home Window** button on the **Image** subtask card.

➩ If you had selected **Single Windowing**, the window values of the selected segment will be restored with **Home Window**.

➩ Otherwise the window values of all the images of the same type (**MIP**/**MPR**) as the image in the selected segment will be restored to the original window value settings.

Evaluating pixels

The average gray scale value of the pixel lense is displayed in the bottom right-hand corner of the image next to the window values. It is formed from the values (5× 5 pixels) of the pixel lense. An M (for mean) is shown in front of the mean value. This value is determined at the current position of the mouse cursor.

CHAPTER
M.3

Performing evaluation of coronary lesions

As soon as you have loaded the images of a Calcium Scoring examination onto the **CaScoring** task card, you can screen the image material for the amount of calcium of any coronary lesion there might be.

Once you have detected calcium plaque you can start evaluating the individual lesions in the coronary arteries.

Procedure

Instead of performing Calcium Scoring evaluation in individual slices you can evaluate detected lesions for the amount of calcium across the entire marked volume using **3D region growing**.

The Calcium Scoring evaluation procedure comprises the following steps:

(1) Evaluating coronary lesions including:

❑ Screening loaded images for coronary lesions with significantly increased calcification.

❑ Marking the detected lesions in the tomogram.

❑ Editing the coronary lesions in 3D or 2D.

(2) Automatic result display

(3) Creating an examination report.

Evaluating coronary lesions

Before you start Calcium Scoring evaluation you have to identify coronary arteries and lesions with significantly increased calcification in the loaded images first.

Screening loaded images for lesions with increased calcification

In the images of your Calcium Scoring examination all structures with calcium values above the set threshold value are displayed in color.

Threshold

Before you start to identify coronary arteries and specific coronary lesions you should optimize the threshold settings.

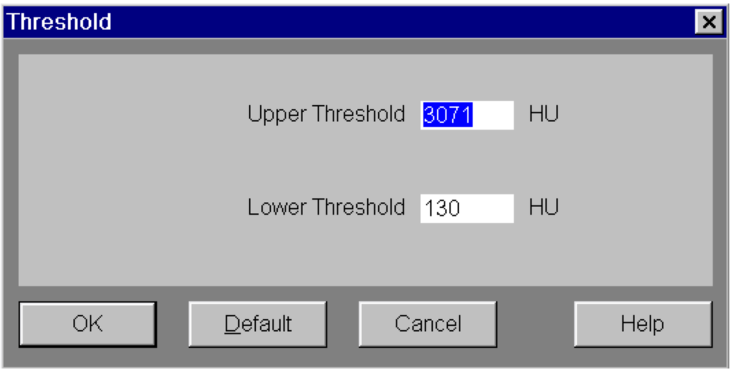
Initially, the threshold value is set to a default value of 130 HU which is an empirical value. However, you can freely configure this value yourself.

✧ Call up **Options > Threshold** in the main menu to display the **Threshold** dialog box.

Or

✧ Click on the **Highlight** button with the right mouse key.

The Threshold dialog box is displayed.



Upper Threshold 3071 HU

Lower Threshold 130 HU

✧ Enter the threshold value of your choice in the input fields **Upper Threshold** and **Lower Threshold**.

✧ Click on **OK** button to confirm your entry.

NOTE

If you change the threshold value during Calcium Scoring evaluation you will lose all the evaluation results you have obtained so far.

If you have already performed a Calcium Scoring evaluation for a particular patient and then changed the threshold values, those evaluation results are no longer valid.

You will then have to repeat the Calcium Scoring evaluation for that patient.

Gray scale image

Calcium values above the threshold value are displayed in color to facilitate fast screening of coronary structures.

However, it is possible to switch between color display and a gray scale image whenever you require.

✧ Call up **Image > Highlight** in the main menu to toggle between the color display and the gray scale image.

Or

✧ Click on the button **Highlight** in the control area to toggle between the color display and the gray scale image.

Overview segment

Overview segment

Identifying coronary arteries in the overview segment

Once you have loaded a series onto the **CaScoring** task card, you can view the entire reconstructed volume in caudo-cranial direction in the overview segment.

✧ Click into the overview segment to select it.

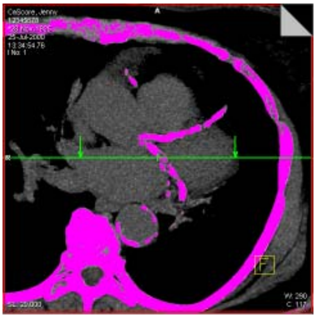
✧ Click on the button **MIP** on the **Image** subtask card with the left mouse key to switch to the **MIP** projection.

You can now view the entire reconstructed volume in the overview segment.

The **MIP** projection functions as an overview image. It allows you to easily determine all the pixels with an increased density value within the reconstructed volume irrespective of their position within the stack.

The green line in the overview segment is provided as a navigation aid. It can be moved either upwards or downwards or from left to right or from right to left in the volume depending on the projection mode in the detail segment.

The green navigation line represents the position of the current cut in the detail segment.



Overview segment

Detail segment

You can also switch to **MIP** projection in the detail segment to view the entire reconstructed volume in coronal or sagittal direction.

✧ Click into detail segment to activate it.

✧ Call up **Image > Visualization Mode** in the main menu and select **MIP** from the selection list.

Or

✧ Click on the **MIP** button to switch to that projection.

The entire volume is now displayed in **MIP** projection in coronal or sagittal direction in the detail segment.

Sliding MIP

Once you have identified calcium plaques in the coronary arteries you improve the image display in both the overview and the detail segment by switching back to the **Sliding MIP** projection.

✧ Click into the overview or the detail segment to activate it.

✧ Call up **Image > Visualization Mode** in the main menu and select **Sliding MIP** from the selection list.

Or

✧ Click on the **Sliding MIP** button to switch to this projection.

Once you have switched to the **Sliding MIP** projection you may not be able to view the detected lesion in the detail segment any longer. You can use the green navigation line in the overview segment to update the position of the current cut in the detail segment.

Slice thickness

The **Sliding MIP** projection allows you to display only one partial area of the reconstructed volume for the projection. You can configure the slice thickness of the **Sliding MIP** projection to avoid cutting out any interfering structures.

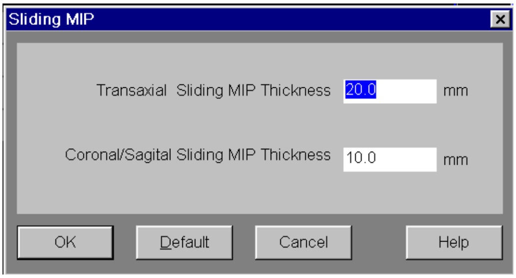
➪ The slice thickness of the **Sliding MIP** projection can be configured for the overview and the detail segments separately.

✧ Call up **Options > Sliding MIP** in the main menu.

Or

✧ Click on the button **Sliding MIP** with the right mouse key.

The **Sliding MIP** dialog box is displayed with default values for the slice thickness.



Sliding MIP

Transaxial Sliding MIP Thickness 20.0 mm

Coronal/Sagital Sliding MIP Thickness 10.0 mm

✧ Enter the desired slice thickness for the caudo-cranial projection in the overview segment or for the sagittal or coronal projection in the detail segment.

✧ Click on **OK** button to confirm your entry.

The new slice thickness of the **Sliding MIP** is automatically adapted in the corresponding segments and displayed by means of white lines in the detail segment.

You can also modify the **Sliding MIP** for the overview segment graphically in the detail segment.

✧ Close the **Sliding MIP** dialog box in case it is still displayed and click on one of the white lines in the detail segment with the cursor.

The selected line is highlighted by grab handles.

✧ Move the cursor on the grab handle in the center of the white line.

The cursor changes the shape.

✧ Drag the white line(s) to reduce or enlarge the current slice thickness.

➪ The volume data set is reconstructed with the new slice thickness in the overview segment.

NOTE

The **Sliding MIP** thickness you have set by moving the white lines in the detail segment is not displayed graphically in the overview segment.

Switching back to MIP or MPR projection

You can easily switch back to the **MIP** or **MPR** projection in the overview or in the detail segment whenever you choose.

✧ Click on the segment, to select it.

✧ Click on the button **MIP** with the left mouse key to switch to **MIP** projection.

The entire reconstructed volume is now displayed in **MIP** projection in the selected segment (overview or detail segment) again.

Or

✧ Click on the button **MPR** with the left mouse key to switch to **MPR** projection.

The reconstructed volume is now displayed in **MPR** projection in the selected segment (overview or detail segment).

Identifying coronary lesions in the detail segment

As soon as you have identified a coronary artery with increased calcification in the overview segment, you can switch to the detail segment, to have the detected lesion displayed in coronal or sagittal projection.

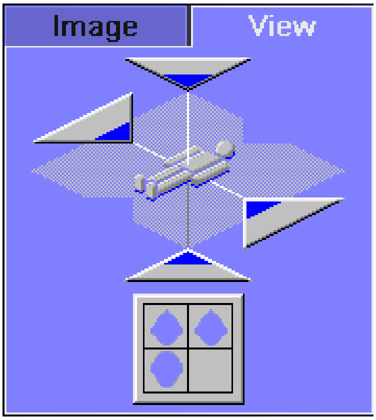
✧ Call up **View > Orientation** and select **Right to Left** or **Left to Right** to switch to the sagittal projection.

Or

✧ Call up **View > Orientation** and select **Front to Back** or **Back to Front** to switch back to the coronal projection.

Or

✧ Click the subtask card **View** to the top of the stack and select either a coronal or a sagittal orientation.



You can restore orientation settings in all segments at any time.

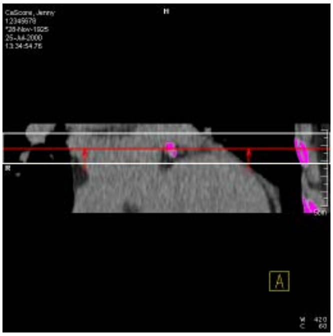
✧ Call up **View > Orientation** and select **Reset** in the selection list.

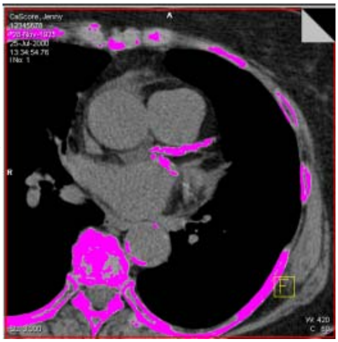
Or

✧ Click on the **Restore** button on the **View** subtask card.

The orientation are restored to the original setting with which the images were loaded in all segments. Yet, the projection mode to which you have switched in individual segments in the meantime remains unaffected.

Once you have optimized the image display in the detail segment you can move the red positioning line onto the detected lesion.


Detail segment


Tomogram

Selecting a tomogram for evaluation

As soon as you have moved the red navigation line onto a specific coronary lesion in the detail segment, this lesion is displayed in the tomogram in caudo-cranial direction.

You can scroll through the image stack of tomograms to view the detected lesion in individual slices and decide which image allows you to evaluate the lesion best.

- Click into the tomo segment to select it.
- Click into the outside triangle to scroll forward or on the dog-ear to scroll back by one image.

Tomogram

Or

- Click into the triangle and keep the left mouse key pressed. The images are scrolled like a movie.

Or

- Scroll using the **Image+** and **Image-** keys on the symbol keypad.

Marking detected lesions in the tomogram

Evaluation with Calcium Scoring is based on automatic determination of the amount of calcium in the detected coronary lesions. Evaluation must therefore be preceded by precise marking of the lesions in the individual coronary arteries.

With **3D Region Growing**, you can mark connected lesions in the individual coronary arteries over the entire volume.

You assign a lesion to a particular coronary artery by activating **3D Region Growing**, then selecting the artery and eventually marking the corresponding lesion.

Marking lesions with Seed Point

✧ Call up **Tools > Pick Seed Point** to activate seed point function for **3D Region Growing**.

Or

✧ Click on the button **Pick Seed Point**.

Marking lesions with Freehand ROI

✧ Call up **Tools > Freehand ROI** to activate seed point function for **3D Region Growing**.

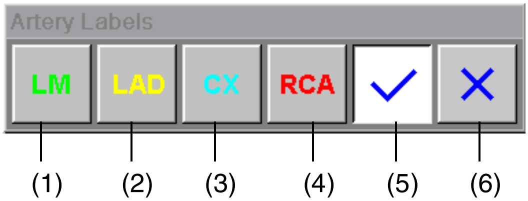
Or

✧ Click on the button **Freehand ROI**.

➪ Marking lesions with Seed Points is only possible in the tomo segment (upper left segment).

Marking coronary arteries

After you have pressed **Seed Point** or **Freehand ROI** button, the **Artery Labels** dialog box is displayed.



(1) **LM** stands for the common branch of the left coronary artery (A. coronaria sinistra)

(2) **LAD** stands for the anterior branch of the left coronary artery (A. coronaria sinistra, R. interventricularus anterior)

(3) **CX** stand for the circumflex branch of the left coronary artery (A. coronaria sinistra, R. circumflexus)

(4) **RCA** stands for the right coronary artery (A. coronaria dextra)

(5) Allows you to assign the marking **Other** to a lesion which does not pertain to the coronary arteries.
Lesions to which this marking is assigned are not included in the evaluation but merely highlighted.

(6) Allows you to delete a marking that was not correctly assigned.

✧ Click on the button **LM**, **LAD**, **CX**, or **RCA** in the **Artery Labels** dialog box to select a coronary artery.

✧ Click on the lesion in the tomogram with the left mouse key to mark the lesion directly, if you have pressed **Seed point** button.

Or

✧ Draw a freehand ROI around the lesion with the left mouse key, if you have pressed **Freehand ROI** button.

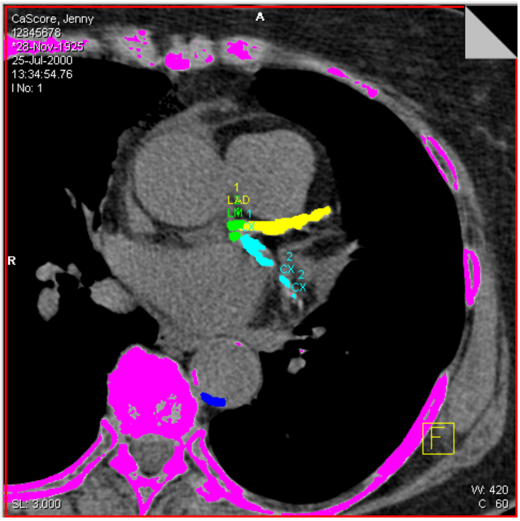
➪ The lesion is automatically assigned to the selected coronary artery across the entire volume.

All pixels inside the lesion whose HU values are above the threshold value are then automatically evaluated.

NOTE

Marking the lesions correctly is the responsibility of the physician.

The lesion is marked in color over the entire volume. The color is the same as that of the coronary artery assigned to it. The image text displayed with a lesion contains the lesion number and the name of the coronary artery associated with it.



➪ The program automatically extends this marking to all immediately adjacent pixels whose HU values are above the set threshold value **(3D Region Growing)**.

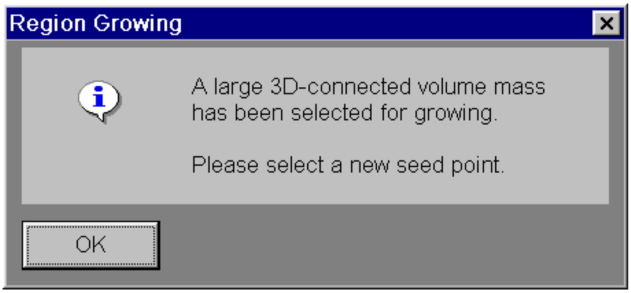
✧ Repeat the marking procedure until you have assigned markings to all the sections of the coronary arteries.

✧ Scroll through the remaining tomograms to make sure that all the detected lesions are marked correctly and set new seed points if necessary.

NOTE

The **3D Region Growing** function considerably facilitates Calcium Scoring evaluation because all adjacent pixels whose HU values are above the set threshold value are marked over the entire volume of the marked lesion.

A dialog box is displayed if you have inadvertently marked a non-coronary structure of very high density such as bone mass.



A large 3D-connected volume mass has been selected for growing.

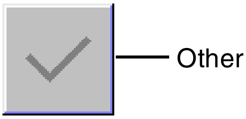
Please select a new seed point.

Marking further calcifications (in preparation)

You can also mark calcifications in color that are not located in the coronary arteries but in which you have ascertained calcification that you want to mark.

However, lesions marked in this way are not included in the Calcium Scoring evaluation.

✧ Click on button **Pick Seed Point** to activate **3D Region Growing**.



✧ Click on **Other** in the **Artery Labels** dialog box to assign this marking to the lesion in the tomogram.

✧ Click on the lesion in the tomogram with the left mouse key to mark the lesion directly.

The lesion is automatically marked in color over the entire volume.

Labelling marked lesions

Once you have assigned a specific lesion to a coronary artery you might want to label this calcification for later documentation. You can do that using graphic tools such as lines or arrows and annotation texts.

✧ Click the button **Line** on the **Tools** subtask card to select this tool.

✧ Click into the tomogram and draw a line keeping the left mouse key pressed.

NOTE

Lines and/or arrows that indicate a lesion must be started at some distance from the lesion. You can then point them to the lesion.

✧ Click the button **Annotation Text** on the **Tools** subtask card to select this tool.

✧ Click on a specific point into the tomogram to write a text comment.

Or

✧ For writing a text comment with an arrow showing a specific structure, click into the tomogram and draw an arrow while keeping the left mouse key pressed. After releasing the left mouse key you can write a text comment.

✧ Press the **Return** key to assign the label to a lesion.

Deleting labels

You can correct or delete a label that you have assigned to a calcification at any time.

✧ Click on the label you want to delete with the left mouse key to select it.

Or

✧ Call up **Tools > Select all annotations,** if you want to delete all the labels that you have previously assigned.

✧ Call up **Tools > Deselect All** if you do not want to delete all the selected labels.

✧ Call up **Tools > Delete** in the main menu to delete the selected labels.

Or

✧ Press the **Delete** key on your keyboard.

Deleting markings

You can also delete markings that you have assigned to a lesion.

✧ Click on the contour of the lesion whose marking you want to delete in the tomogram with the left mouse key.

The lesion has now been selected.

✧ Click on the **Delete** icon in the **Artery Labels** dialog box.

The marking of the selected lesion is now deleted from the tomogram.

You can also delete the marking of a lesion if the **Artery Labels** dialog box is not displayed.

✧ Click on the contour of the lesion whose marking you want to delete in the tomogram with the left mouse key.

The lesion has now been selected.

✧ Call up **Tools > Delete** from the main menu

Or

✧ Press the **Delete** key on your keyboard.

The marking of the lesion is removed.

➪ To include this lesion in the Calcium Scoring evaluation, you must assign it to a coronary artery again and mark it accordingly.

Editing coronary lesions in 3D or in 2D

You can include the entire volume of adjacent pixels of a calcification by marking the detected lesions with **3D Region Growing**.

As a result of **3D Region Growing** calcifications of an artery (e.g. **LM**) might be assigned wrong markings (e.g. **LAD**) and evaluated as a single lesion due the close proximity to that artery.

You can now edit such a lesion by scrolling to the corresponding slice and splitting it into several parts and assigning the marked parts to the corresponding arteries.

You can either edit a lesion slice by slice with **2D Edit** mode or edit the entire volume of the lesion using **3D** Edit mode. That saves you time-consuming editing of individual slices.

Editing coronary lesions in 3D mode

You can edit a lesion in any slice with **3D mode** and, in that way, assign a new marking to a part of a lesion over the entire volume in one step.

The precondition for **3D** editing is that a lesion has already been marked using the **3D Region Growing** function.

✧ Select a lesion that you want to edit in any slice in the tomogram and adapt the window values and image size if necessary.
  → Page M.2–6, *Windowing images*
  → Page M.2–4, *Zooming and panning images*

✧ Click on **Draw Freehand ROI** to draw a ROI round the part of the lesion that you want to delimit.

✧ Call up **Tools > 3D** in the main menu to switch to 3D mode.

Or

✧ Click on button **3D Edit** to activate this mode.

The **Artery Labels** dialog box is displayed.

✧ Click on the button for the coronary artery that you want to assign to the delimited part of the lesion.

✧ Draw a ROI around the part of the lesion that you want to mark again and double-click on it with the left mouse key to close the contour.

The new contour includes the lesion as in a cylinder with certain extent in the upward and downward directions.

A new marking is assigned to the new part of the lesion delimited from the original lesion over the entire volume and it is automatically included in the result table.

NOTE

A minimum volume of 1 mm^3 is configured for each lesion. If lesions are the result of 2D or 3D postprocessing, whose volume is less than the minimum volume, they are only highlighted with the colored contour of the coronary artery in question but not marked.
Such lesions are not included in the result table.

➩ Distinct lesions that are also included in the cylinder by the marking, remain unchanged.

.Editing coronary lesions in 2D mode

With **2D Edit**, you can delimit parts of lesions from each other, and assign those parts to different coronary arteries.

The precondition is that a lesion has already been marked using the **3D Region Growing** function.

✧ Scroll through the slices in the tomogram with the dog-ears until you have found the slice in which you want to perform **2D** editing.

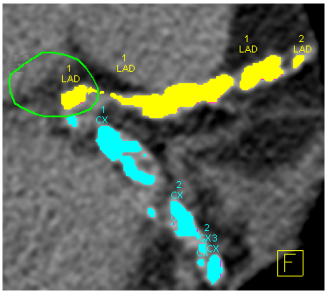
✧ If necessary, adapt the window values and image size for optimum viewing.
→ Page M.2–6, *Windowing images*
→ Page M.2–4, *Zooming and panning images*

✧ Call up **Tools > 2D Edit** in the main menu to switch to **2D Edit** mode.

The **Artery Labels** dialog box is displayed.

✧ Click on the button for the coronary artery that you want to assign to the delimited part of the lesion.

✧ Click near the lesion you want to edit holding the left mouse key pressed.



✧ Draw around the part of the lesion that you want to mark again. With a double-click you apply the changes.

The original lesion is now split into several parts within the slice and the part of the lesion delimited by the ROI is marked again (**3D Region Growing**). The result table is updated automatically.

✧ Repeat these steps in the remaining tomograms if necessary.

NOTE

It is not possible to edit two lesions with different markings with **2D Edit** by dragging a ROI around both lesions.

CHAPTER

M.4

Documenting evaluation results

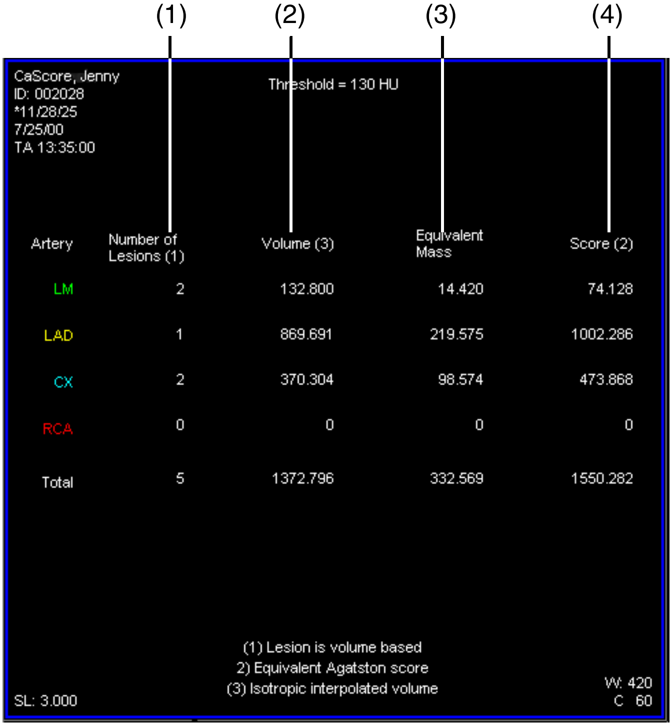
Once you have marked all lesions in which calcification has been detected by the threshold value, a complete list of results is displayed in the result table.

As a result of 3D region growing you will obtain calcium score values representing the amount of calcium detected in a coronary artery over the marked volume.

Automatic result display

With **3D region growing** evaluation, you have selected lesions over a volume and evaluated them as indicated by the markings.

The following measured values are listed in the result table:



CaScore, Jenny
ID: 002028
*11/28/25
7/25/00
TA 13:35:00

Threshold = 130 HU

Artery	Number of Lesions (1)	Volume (3)	Equivalent Mass	Score (2)
LM	2	132.800	14.420	74.128
LAD	1	869.691	219.575	1002.286
CX	2	370.304	98.574	473.868
RCA	0	0	0	0
Total	5	1372.796	332.569	1550.282

(1) Lesion is volume based
2) Equivalent Agatston score
(3) Isotropic interpolated volume

SL: 3.000

W: 420
C 60

(1) The number of lesions per coronary artery based on the evaluated volume.

(2) The volume of the marked lesions per coronary artery in mm^3, based on isotropic interpolation. This interpolation addresses the partial volume effect problem by interpolating slices in between the originally measured ones such that the voxels are cubes. The scoring algorithm is subsequently applied to these interpolated voxels.

(3) The equivalent mass per coronary artery. This is the mass of calcium in mg CaHA (calcium hydroxyapatite).
The algorithm for the calculation of the equivalent mass is scanner-specific. The calculation of the equivalent mass is calibrated for the system, on which the Calcium Scoring application software is installed and for the Calcium Scoring protocols recommended by the manufacturer.

NOTE

Using the application software only for the supported scanner in order to determine the equivalent mass is the responsibility of the physician.

(4) The Agatston score represents the amount of detected calcium in each individual coronary artery. For every slice, the area of each lesion is weighed by a factor *f* which depends on the peak CT value of this very lesion:
$f=1$ for 130 HU ≤ Peak CT value < 200 HU
$f=2$ for 200 HU ≤ Peak CT value < 300 HU
$f=3$ for 300 HU ≤ Peak CT value < 400 HU
$f=4$ for 400 HU ≤ Peak CT value
All scores of a specific artery are added for the Agatston score of this artery. All scores of all arteries are added for the total Agatston score.
The original definition of the Agatston score is based on contiguous 3mm slices. For a study which was acquired with a slice thickness different from 3mm (e.g. 2,5mm), or for overlapping slices, an equivalent Agatston score is calculated. It takes the different slice width and interslice distance into account.

Creating an examination report

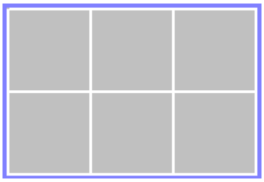
You can transfer your results to an examination report and use them to document your examination results at any time.

Including images in your report

You can include up to six images and the result table of the Calcium Scoring evaluation in your report and save them for later documentation.

- Click on the segment you wish to include in your report to select it.
- Call up **Report > Copy Image** and add an image to your report by selecting an image number from the selection list.

Or



- Move the cursor onto an **Image** field on the **Report** subtask card and click on this field with the right mouse button.
- Select **Copy Image** in the popup menu.

The selected image will be copied into your report as soon as you generate it.

If you have selected the wrong image and now want to correct your choice you can easily do so.

- Call up **Report > Delete Image** and select the number of the image you wish to delete image from your report.

Or

- Move the cursor onto the **Image** field on the **Report** subtask card containing the image you wish to delete and click on this field with the right mouse button.
- Select **Delete Image** from the popup menu.

The image is deleted from your report.

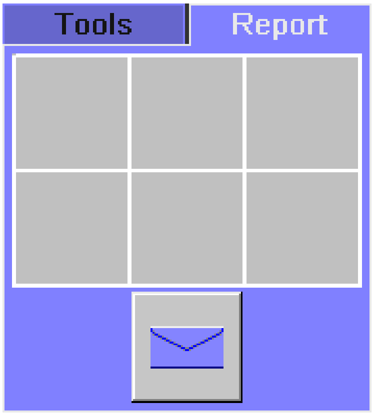
Generating the evaluation report

Once you have selected all the required images and transferred them to your report, you can start to generate the report.

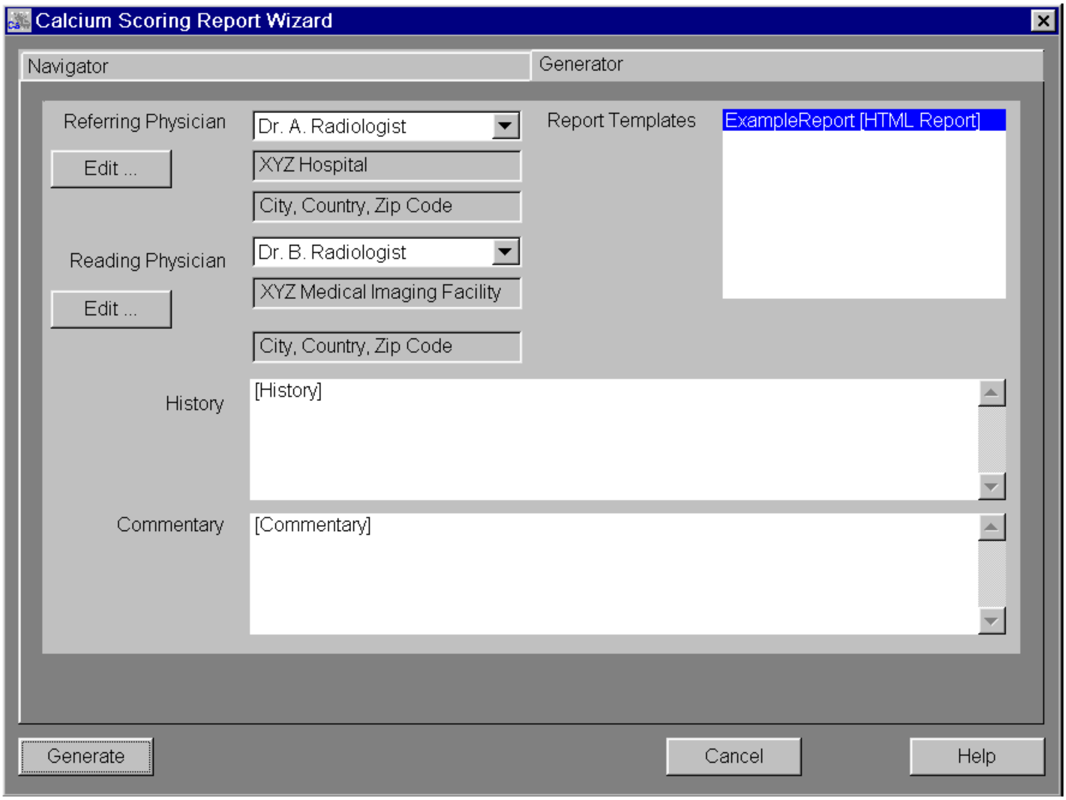
✧ Call up **Report > Report Wizard** from the main menu.

Or

✧ Click on the button **Report Wizard** on the subtask card **Report**.



The **Calcium Scoring Report Wizard** dialog box is displayed.



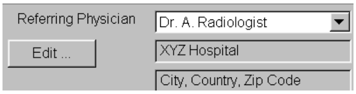
Referring Physician: Dr. A. Radiologist
XYZ Hospital
City, Country, Zip Code

Reading Physician: Dr. B. Radiologist
XYZ Medical Imaging Facility
City, Country, Zip Code

Report Templates: ExampleReport [HTML Report]

History: [History]

Commentary: [Commentary]

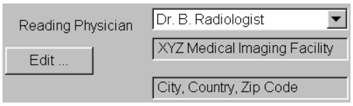


Referring Physician: Dr. A. Radiologist
XYZ Hospital
City, Country, Zip Code

✧ Select the referring physician from the selection list.

Or

✧ Click on the button **Edit** to enter either a new physician, or a new hospital or city.



Reading Physician: Dr. B. Radiologist

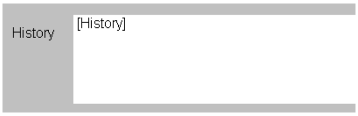
XYZ Medical Imaging Facility

City, Country, Zip Code

✧ Select the reading physician from the selection list.

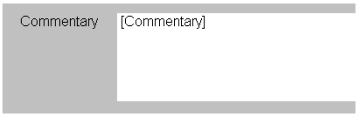
Or

✧ Click on the button **Edit** to enter either a new physician, or a new hospital or city.



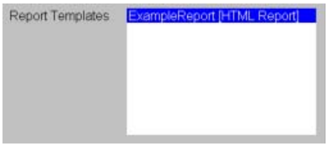
History: [History]

✧ Enter the history of the patient.



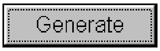
Commentary: [Commentary]

✧ Enter commentaries on the patient.

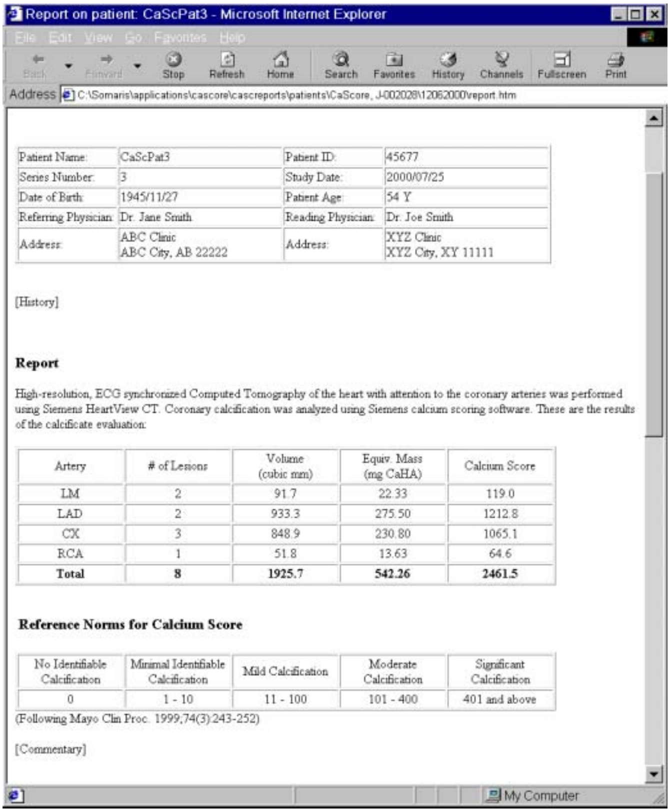


Report Templates: ExampleReport [HTML Report]

✧ Select the format in which you want the report to be created.



✧ Click on the button **Generate** to have the report of your Calcium Scoring evaluation generated and displayed automatically.



Report on patient: CaScPat3 - Microsoft Internet Explorer

C:\Somaris\applications\cascore\cascreports\patients\CaScore, J-002028\12062000\report.htm

Patient Name:	CaScPat3	Patient ID:	45677
Series Number:	3	Study Date:	2000/07/25
Date of Birth:	1945/11/27	Patient Age:	54 Y
Referring Physician:	Dr. Jane Smith	Reading Physician:	Dr. Joe Smith
Address:	ABC Clinic ABC City, AB 22222	Address:	XYZ Clinic XYZ City, XY 11111

[History]

Report

High-resolution, ECG synchronized Computed Tomography of the heart with attention to the coronary arteries was performed using Siemens HeartView CT. Coronary calcification was analyzed using Siemens calcium scoring software. These are the results of the calcificate evaluation:

Artery	# of Lesions	Volume (cubic mm)	Equiv. Mass (mg CaHA)	Calcium Score
LM	2	91.7	22.33	119.0
LAD	2	933.3	275.50	1212.8
CX	3	848.9	230.80	1065.1
RCA	1	51.8	13.63	64.6
Total	**8**	**1925.7**	**542.26**	**2461.5**

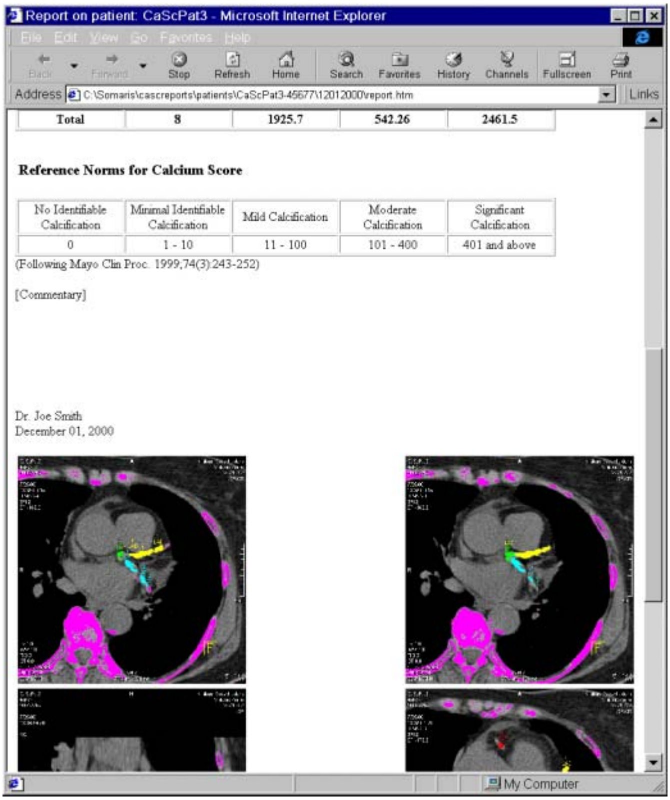
Reference Norms for Calcium Score

No Identifiable Calcification	Minimal Identifiable Calcification	Mild Calcification	Moderate Calcification	Significant Calcification
0	1 - 10	11 - 100	101 - 400	401 and above

(Following Mayo Clin Proc. 1999;74(3):243-252)

[Commentary]

✧ Scroll downwards to view the images that you have included into your report.



Total	**8**	**1925.7**	**542.26**	**2461.5**

Reference Norms for Calcium Score

No Identifiable Calcification	Minimal Identifiable Calcification	Mild Calcification	Moderate Calcification	Significant Calcification
0	1 - 10	11 - 100	101 - 400	401 and above

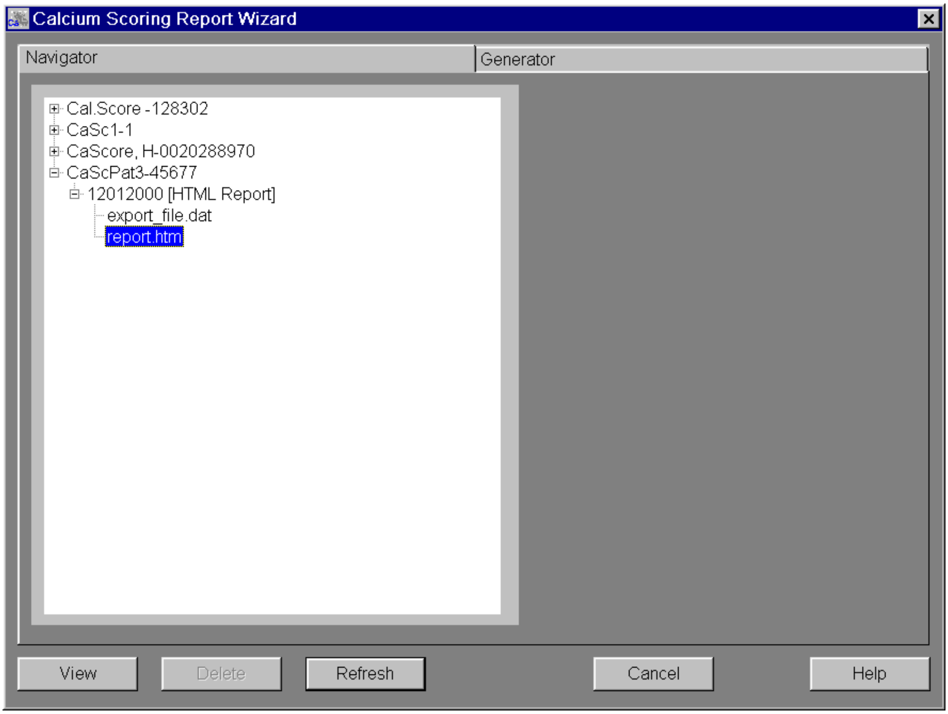
(Following Mayo Clin Proc. 1999;74(3):243-252)

[Commentary]

Dr. Joe Smith
December 01, 2000

Printing your Calcium Scoring evaluation report

Your report is automatically saved in two different formats on the **Navigator** subtask card of the **Report Wizard** as soon as you generate it.



✧ Click the **Navigator** subtask card to the top of the stack in the **Report Wizard**.

✧ Double-click on the htm-file to open your report with the **Microsoft Internet Explorer**.

➪ You can use the dat-file to generate a database with specific data belonging to this patient or for other scientific purposes.

Print

✧ Click on the **Print** icon in the tool bar of the **Microsoft Internet Explorer** to print your report on paper.

> **NOTE**
>
> The HTML Report has been designed for Microsoft Internet Explorer 4.0. It is viewed best with Medium Fonts (Western Alphabet)

Filming results

You can transfer the results of a calcium scoring evaluation to a filmsheet quickly and easily from the **CaScoring** task card.

✧ Select the segment with the image or the results to be filmed.

✧ Call up **Patient > Copy To Filmsheet** in the main menu to transfer the result image to the **Filming** card.

Or

✧ Click on the button **Copy To Filmsheet**.

Saving results

You can save the results of your Calcium Scoring evaluation in the local database.

✧ Call up **Patient > Save** from the main menu to save the selected image in the local database.

Or

✧ Click on the button **Save** in the control area.

Images can only be saved individually.

➪ The system automatically generates 3 series. The series names consist of the name of the scan protocol and the extension of the corresponding series type. The extensions used are MIP collection for MIP images, MPR collection for MPR images and result tables, MIP thin collection for sliding MIPs, CaScoring for tomograms. The images are automatically saved according to type and assigned to the corresponding series. It is not possible to rename an existing series or to add a new series to the local database.

The evaluation results are saved to the local database as secondary captures.

Terminating evaluation

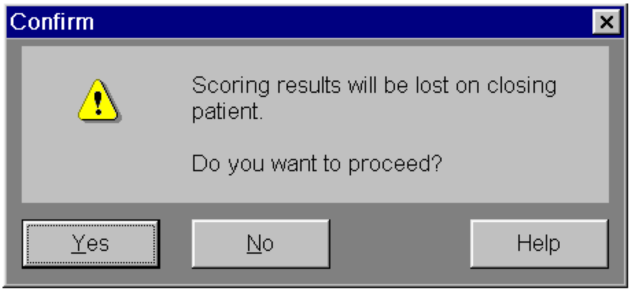
When you have completed all the steps of the current evaluation you can terminate the calcium scoring evaluation for this patient.

✧ Call up **Patient > Browser** and load a new series for evaluation in CaScoring. The current evaluation will be closed.

Or

✧ Call up **Patient > Close CaScoring** to close the current task card.

The **Confirm** message box is displayed.



Confirm

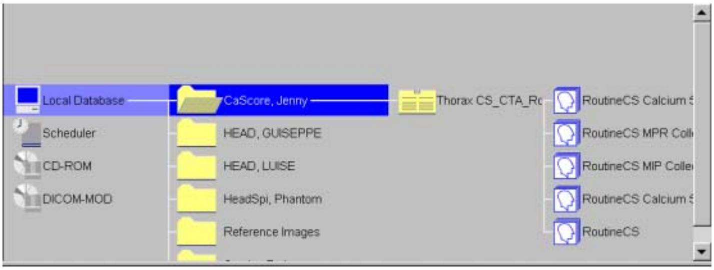
Scoring results will be lost on closing patient.

Do you want to proceed?

✧ Click on **Yes** if you want to terminate calcium scoring evaluation without saving the results.

✧ Click on **No** if you want to continue with your calcium scoring evaluation.

You can call up, transfer, or archive these data at any time via the **Patient Browser**.



CHAPTER
M.5 Configuring CaScoring

In **CS Report Configuration** you can edit the output of the CaScoring evaluation. You can do the following:

☐ Enter hospital information

☐ Set and check a template for the report

☐ Import other reference data and templates

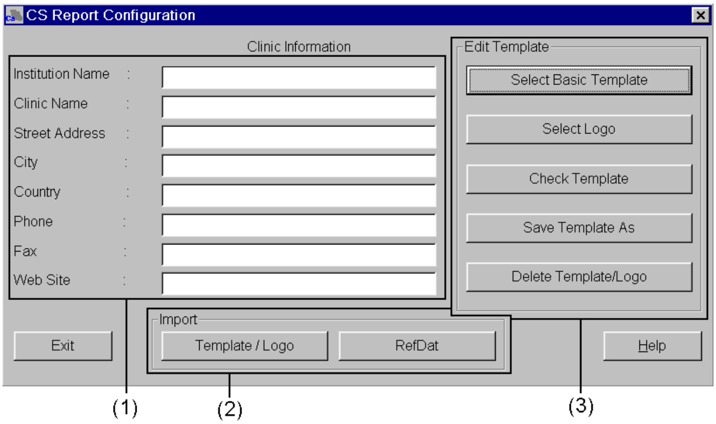
✧ Select **Options > Configuration** from the main menu.

✧ Double-click on the **Calcium Scoring** button to display the **CS Report Configuration** dialog box.

➪ In the **Basics** part of this manual you can read how to call up and exit configuration windows, save changes, or reset settings back to the as-delivered state.
→ Chapter A.2, *Configuring the User Interface*

Configuration window CS Report Configuration

The **CS Report Configuration** dialog is divided into areas for entering hospital data, for processing the report template and importing templates/data from another database.



(1) General hospital data
(2) Importing templates/reference data
(3) Editing the template

Editing templates

The template defines the structure and appearance of the examination report. You can import your own template, enter the clinic data and insert a logo.

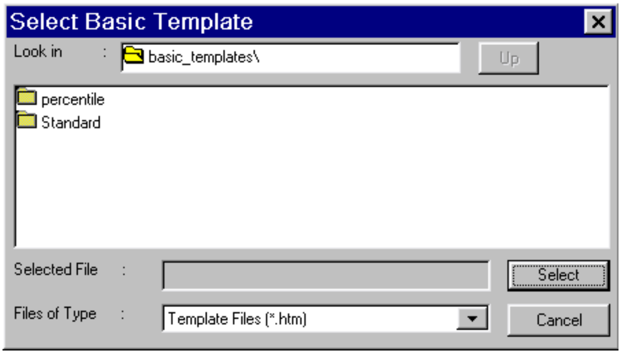
Selecting a template

You can format the CaScoring report with templates stored in the database. Your choice of template will determine whether a comparison of examination results and reference data appears in the report. If you want to use a template that you have created yourself, you must first import it into the database.

Template from the database

✧ Click on the **Select Basic Template** button.

The dialog box **Select Basic Template** is called up.



Look in : basic_templates\

percentile

Standard

Selected File :

Files of Type : Template Files (*.htm)

- Call up the **percentile** folder and select the required reference data in the required language.

Or

- Select a template in the **Standard** folder if you do not want comparison with statistical reference data..

Select

- Confirm your input with the **Select** button..

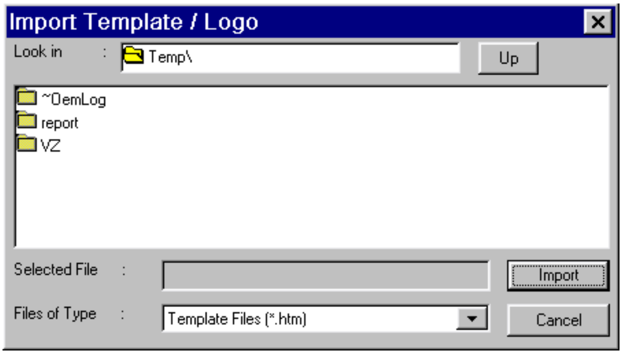
Importing your own template

If a template is to be structured in a particular way, you can store a template that you have created yourself in the database and call it up from there.

Template / Logo

- Click on the **Import Template/Logo** button.

The dialog box **Import Template/Logo** is called up.



Look in : Temp\

Files of Type : Template Files (*.htm)

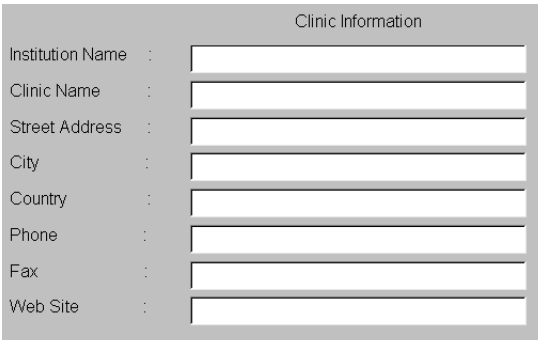
- Select the template you require from your directory structure.

Import

- Click on the button **Import**.

Entering clinic data

You can display general hospital information such as name, address, and telephone number in the header of the CaScoring report.



✧ Enter the text you require in the fields in question and confirm your entries with the **Enter** key.

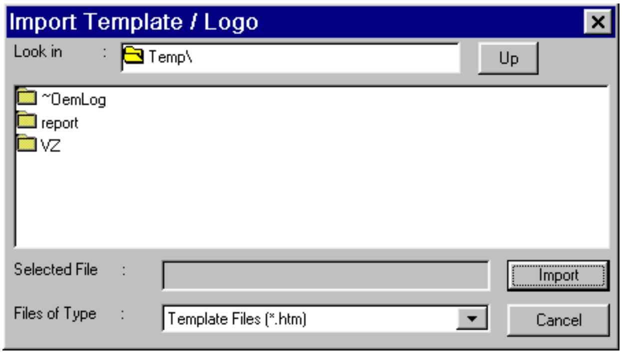
Selecting a logo

If you want to include a logo in the report header, you must assign one from the database. If you want to link in your own logo, you must first import it into the database.

Importing a logo

✧ Click on the **Import Template/Logo** button.

The dialog box **Import Template/Logo** is called up.



Look in : Temp\

~OemLog
report
VZ

Files of Type : Template Files (*.htm)

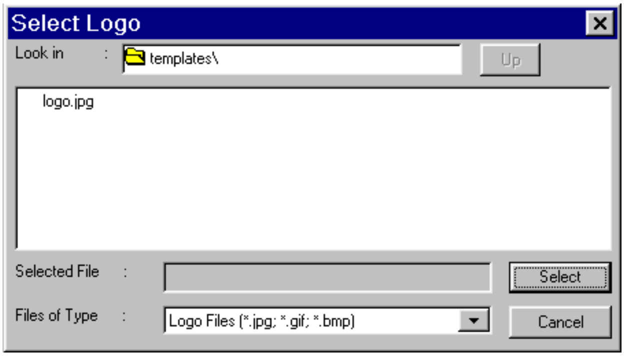
✧ Select the logo you require from your directory structure.

✧ Click on the **Import** button to import the selected logo.

Assigning a logo

✧ Click on the **Select Logo** button.

The dialog box **Select Logo** is displayed. All the logos you have loaded are listed in the templates folder.



Look in : templates\

logo.jpg

Selected File :

Files of Type : Logo Files (*.jpg; *.gif; *.bmp)

✧ Select the logo you require from the templates folder.

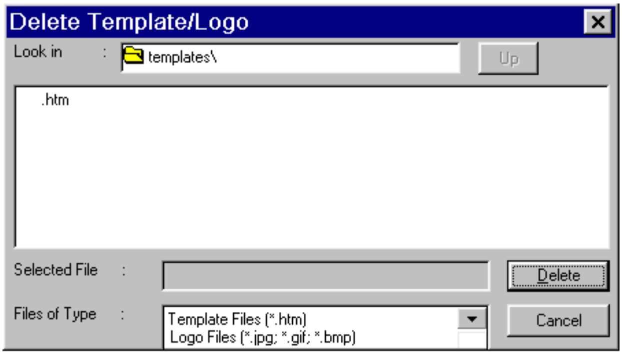
✧ Confirm your input with the button **Select**.

Deleting a logo

If you no longer require a logo you can delete it from the database.

✧ Click on the **Delete Template/Logo** button.

The **Delete Template/Logo** dialog box is called up.



Look in : templates\

.htm

Selected File :

Files of Type : Template Files (*.htm)
Logo Files (*.jpg; *.gif; *.bmp)

✧ Select the Logo you want to delete from the **templates** directory.

✧ Click on the **Delete** button.

Checking, saving, and deleting templates

Before storing templates, you can check any you have edited without printing them out first.

Checking templates

Check Template

✧ Click on the **Check Template** button.

The form that you have set is displayed in the **Check Template** window.

SIEMENS

Customer
Hospital

Phone: Phone
Fax:

StreetNo Street
City /9B20E0/ ZIP
Country

Patient Name:	---	Patient ID:	---
Series Number:	---	Study Date:	---
Date of Birth:	---	Patient Age:	---
Referring Physician:	---	Reading Physician:	---
Address:	--- ---	Address:	--- ---

Report

High-resolution, ECG synchronized Computed Tomography of the heart with attention to the coronary arteries was performed using Siemens HeartView CT. Coronary calcification was analyzed using Siemens calcium scoring software. These are the results of the calcificate evaluation:

Threshold = --- HU				
Artery	# of Lesions	Volume [mm³]	Equiv. Mass [mg CaHA]	Calcium Score
---	---	---	---	---

✧ Check the template.

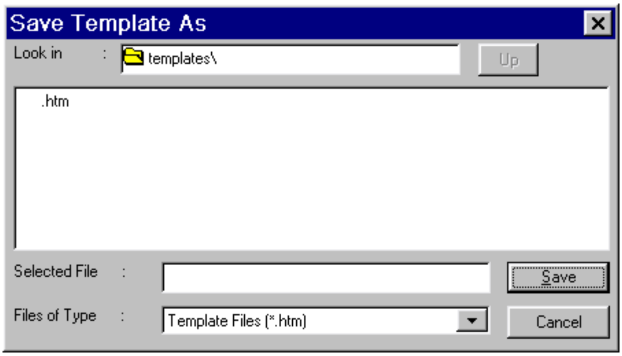
☒

✧ Close the **Check Template** window by clicking on the button.

Saving templates

✧ Click on the **Save Template As** button.

The **Save Template As** dialog box is called up. Save your template to the **templates** folder.



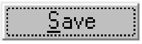
Look in : templates\

.htm

Selected File :

Files of Type : Template Files (*.htm)

✧ Enter the name of the template in the **Selected File** input field.

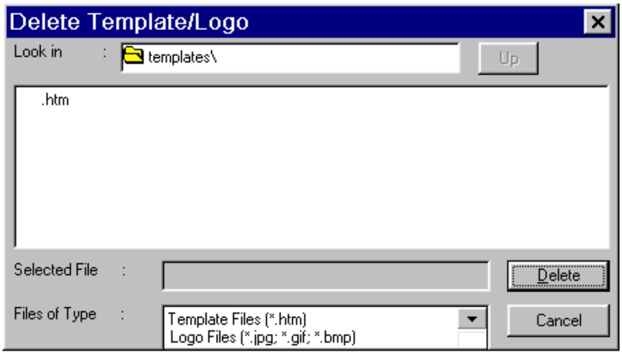


✧ Save the template by clicking on the **Save** button.

Deleting a template

✧ Click on the **Delete Template/Logo** button.

The **Delete Template/Logo** dialog box is called up.



Look in : templates\

.htm

Selected File :

Files of Type : Template Files (*.htm)
Logo Files (*.jpg; *.gif; *.bmp)

✧ Select the template you want to delete from the **templates** directory.

✧ Click on the **Delete** button to delete.

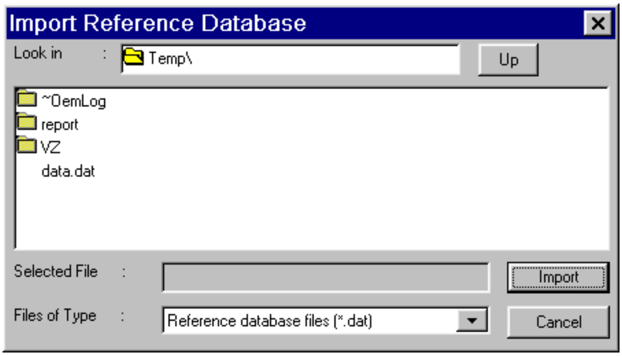
Importing reference data

You can save internal or general reference statistics to the database so that you can then link them into the templates.

RefDat

✧ Click on the **Import Reference Database** button.

The **Import Reference Database** dialog box is called up.



Look in : Temp\

~OemLog
report
VZ
data.dat

Selected File :

Files of Type : Reference database files (*.dat)

✧ Select the required reference data from your directory structure.

Import

✧ Import the data by clicking on the **Import** button.

PART
N

DynEva CT (Option)

N.1 Introduction

N.2 Loading and Displaying Images

N.3 Evaluating Images

N.4 Documenting and Closing Evaluation

N.5 Configuring DynEva

CHAPTER
N.1 Introduction

The task card **DynEva** allows you to analyze contrast enhancement in different regions (ROIs) of the examination range that you define.

In general, CT acquisitions without table feed (dynamic sequence, multiscan) are used for the dynamic evaluation. The absorption of the X-rays, which is dependent on the flow of the contrast agent, is evaluated in the individual tomographic images. The resulting enhancement curves provide information about the flow of contrast agent in the regions in question.

Calling up dynamic evaluation

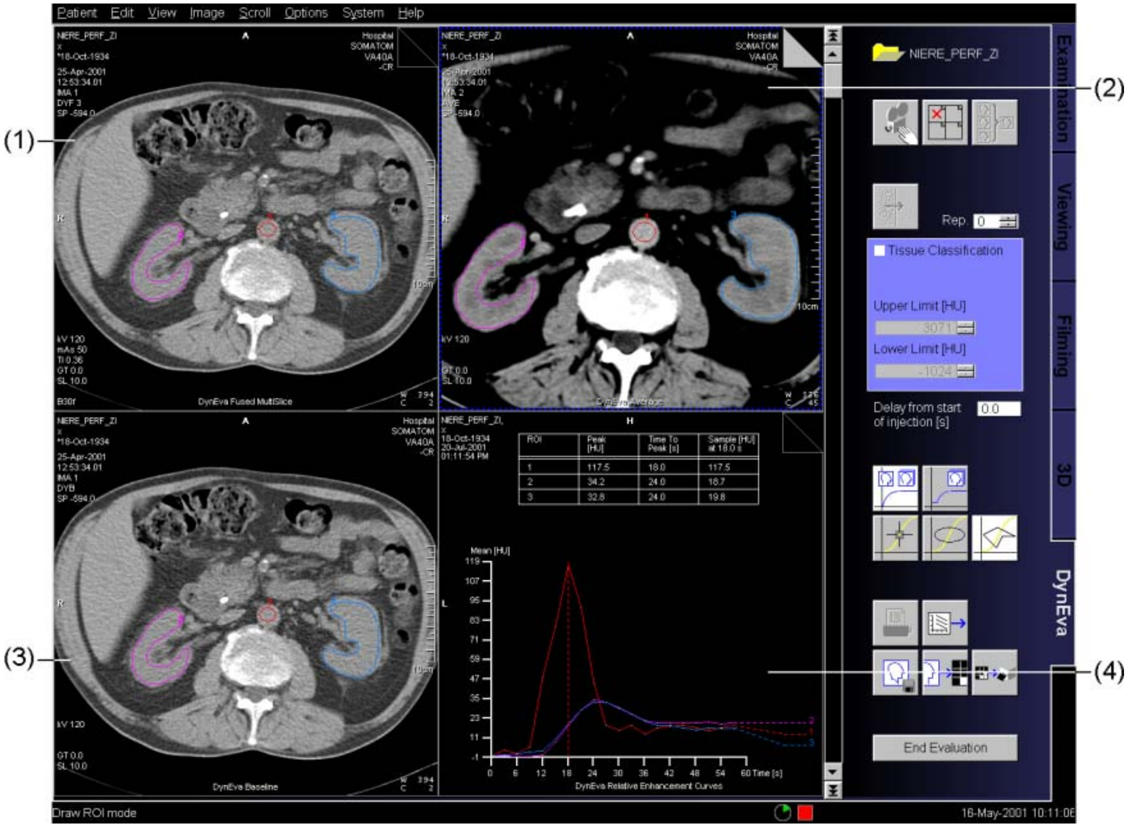
As soon as you have loaded the images into the **DynEva** task card, the task card moves to the foreground. You can also switch to other applications at any time and start evaluation on the **DynEva** task card at a later stage.

✧ If the **DynEva** task card is in the background, click on the tab to activate the task card.

The **DynEva** task card is subdivided into two large areas.

The control area contains the input-fields and the buttons for editing and documenting the loaded image material.

The image area is divided into four segments, three image segments, and one graphic result segment.



Rep. 0

☐ Tissue Classification

Upper Limit [HU] 3071

Lower Limit [HU] -1024

Delay from start of injection [s] 0.0

ROI	Peak [HU]	Time To Peak [s]	Sample [HU] at 18.0 s
1	117.5	18.0	117.5
2	34.2	24.0	18.7
3	32.8	24.0	19.8

(1) **Tomo segment**
Stack of input images to be evaluated

(2) **Parameter image segment**
Display of calculated parameter images

(3) **Baseline image segment**
Used to calculate parameter images (Time to Peak, Peak Enhancement) and Relative Enhancement curves

(4) **Result segment**
Output of the enhancement curves

CHAPTER
N.2

Loading and Displaying Images

In dynamic evaluation, images that were scanned as part of an examination with contrast agent at a constant table position are evaluated.

Rejected image material

The image material will be rejected, if one of the following conditions is not fulfilled:

❏ The images have to be CT-images.

❏ The images have to be tomographic images.

❏ The images have to be of the same image size.

NOTE

If the images have not been taken at the same table height, with the same gantry inclination, and with the same tube voltage a corresponding dialog box is displayed.

Loading images

You load the images for a dynamic evaluation from the **Patient Browser** into the **DynEva** task card.

➪ If you load series for evaluation with **DynEva** that have been scanned with a multi-row scanner you have several options to proceed with multiple slices.
→ Page N.2–3, *Slice position with multi-row scanners*

Transferring images with the Patient Browser

In the **Patient Browser** window you can access the examination data of all the patients examined in your system.

✧ Call up the **Patient Browser** (**Patient > Patient Browser**).

✧ Select the examination data in question in the navigation or content area.
→ Page D.2–6, *Scrolling through and selecting patient data*

✧ Call up **Patient > DynEva** in the main menu or click on the button **DynEva** on the toolbar of the **Patient Browser**.

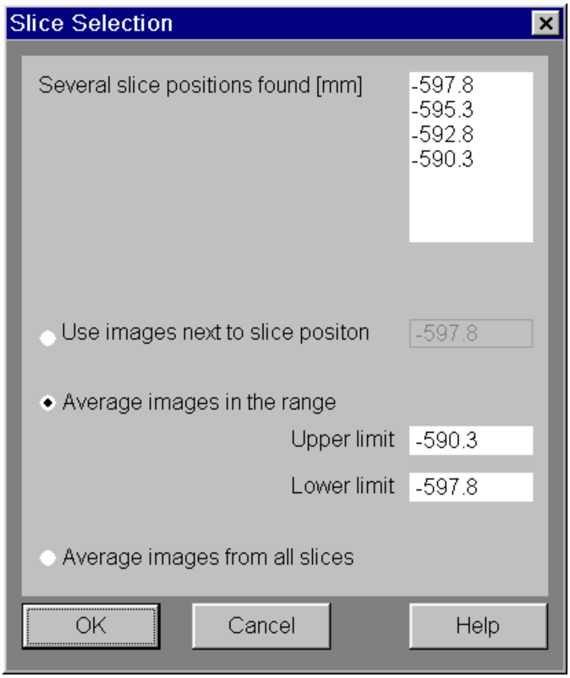
Or

✧ Place the **DynEva** task card on top of the card stack and double-click on the required data in the **Patient Browser**.

➪ If you have activated the function **Close after loading**, the **Patient Browser** window is closed as soon as you load the images into the **DynEva** task card.

Slice position with multi-row scanners

When you use a multi-row scanner several slice positions are scanned per acquisition. When you load the images, the window **Slice Selection** is displayed in which you can define the slice position to be analyzed.



Several slice positions found [mm]
-597.8
-595.3
-592.8
-590.3

○ Use images next to slice positon -597.8

● Average images in the range

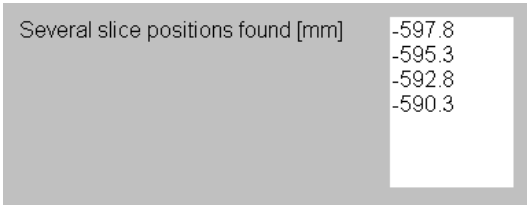
Upper limit -590.3

Lower limit -597.8

○ Average images from all slices

Overview of slices

In the upper area of the window **Slice Selection**, the slice positions of the examination are listed. You can evaluate either the examination data of a scanned or an averaged slice position.



Several slice positions found [mm]

-597.8
-595.3
-592.8
-590.3

Acquired slice position

When you select a slice position, the input value does not have to correspond with the scanned slice position. In this case, a slice position that is closest to the selected value is selected.

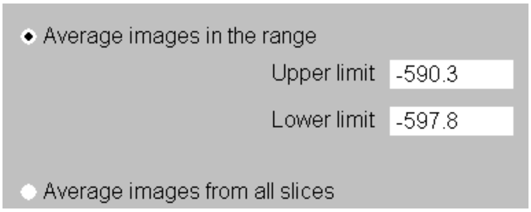
● Use images next to slice positon -597.8

- ✧ Click on the radio button **Use images next to slice position**.
- ✧ Enter the slice position in the input field.

- ✧ Click on **OK** to confirm your entry.

Averaged slice position

For the calculation of an image, the average value of the image data within specified slice positions is derived for each point in time.



● Average images in the range

Upper limit -590.3

Lower limit -597.8

○ Average images from all slices

✧ Click on the radio button **Average images in the range** and enter the upper and lower limit of the required slice range here.

Or

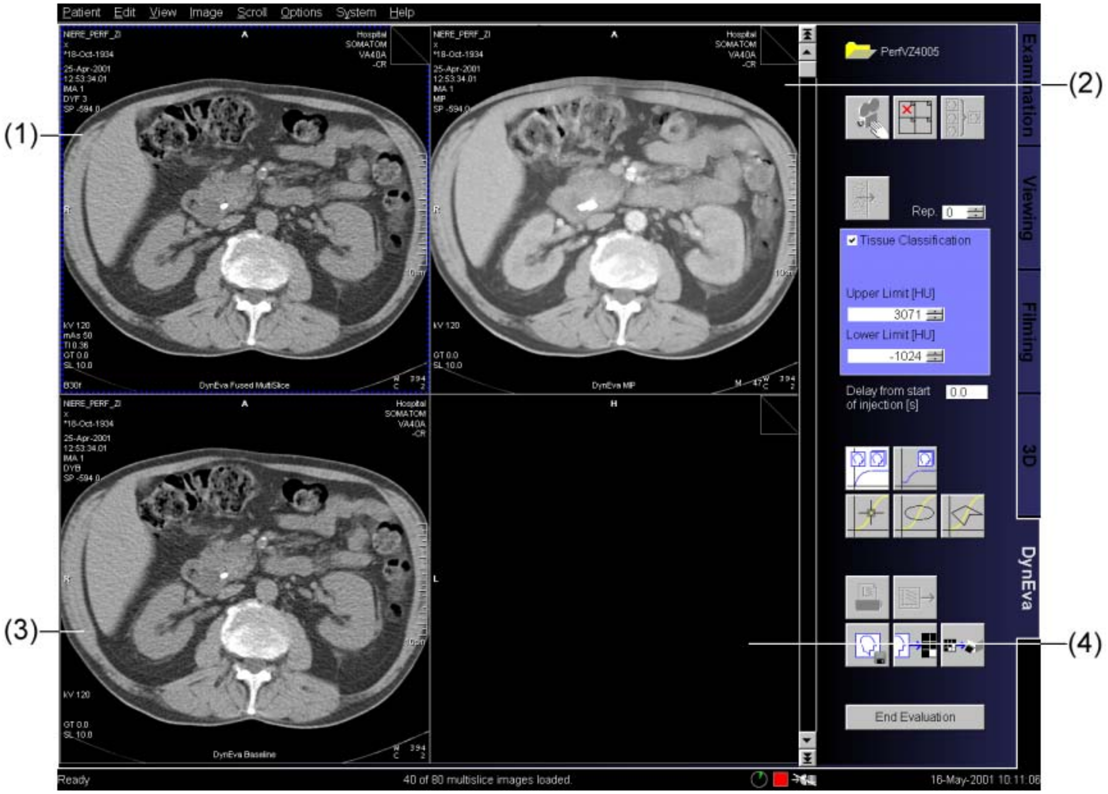
✧ Click on the radio button **Average images from all slices** if you want to average across all acquisition positions.

➪ **Average images from all slices** can be used for example to average the scanned slice positions for each point in time of a spiral scan.

✧ Click on **OK** to confirm your entry.

Display of the original images

Once the images have been loaded they are arranged in a stack in the 1st segment of the **DynEva** task card. The parameter image segment is immediately updated.



Ready 40 of 80 multislice images loaded. 16-May-2001 10:11:08

(1) **Tomo segment**
All loaded images (stack display)

(2) **Parameter image segment**

(3) **Baseline image segment**
Top stack image of tomo segment is the default baseline image

(4) **Result segment**

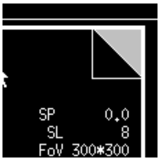
Inspecting the input images

Before you begin evaluation, optimize the display of loaded images in the tomo segment in such a way that the regions to be evaluated are clearly visible. Scroll through the image stack and remove the images that are not suitable for dynamic evaluation (e.g. when the patient has moved during scanning).

Scrolling in the image stack

In the tomo segment you can scroll image by image through the original data set or jump to the desired image within the stack.

Scrolling image by image



✧ In the tomo segment use the dog ears to page to the image in which the area to be evaluated is clearly visible.

Or

✧ Move the arrow buttons up and down along the scroll bar next to the segment.

Or

✧ Scroll with the **Image+** and **Image-** buttons on your symbol keypad through the series of acquisitions.

➪ To page you can also use the **Scroll** menu and the **Page up**, **Page down**, **Home** or **End** symbol keys.
→ Page E.3–7, *Scrolling page by page*

Movie display

Movie display allows you to display the examination range against time making it easier to detect motion-related artifacts.

✧ Click on the button to activate the movie function.

✧ Keep the left mouse key pressed and move the mouse upward/downward to run the film forward/backward.

➩ The faster you move the mouse, the faster the sequence of images in the movie display.

✧ Click on the button again to terminate the movie function.

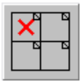
Removing input images

Any image that you do not want to use for dynamic evaluation you delete from the tomo segment.

NOTE

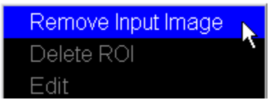
Deleting an image will remove it from the **DynEva** task card and exclude it from dynamic evaluation but will not remove the image from the local database.

✧ Select the image you want to delete in the tomo segment.



✧ Click on the button **Remove Input Image**.

Or



✧ Select **Remove Input Image** in the popup menu of the tomo segment (right mouse key).

➪ Removing input images might alter the baseline image and the images in the parameter image segment.
→ Chapter N.3, *Evaluating Images*

➪ If you delete all the images in the tomo segment, evaluation is canceled.

Windowing, zooming, panning images

You can modify the image settings to distinguish the areas of interest in the images well from the other areas. This will be of help when you come to draw the ROIs for evaluation.

Windowing

✧ Activate **Image** > **Windowing on Succeeding** in the main menu, to apply the altered window values to the current image and following images in the stack.

✧ Click into the tomo segment with the center mouse key and pull the mouse down/up or left/right to optimize the window settings in the image stack.
→ Page E.4–11, *Windowing with the mouse*

Or

✧ Window the images with the tuning knobs on the control box.
→ Page E.4–10, *Windowing with the control box*

Zooming and panning images

Once you have adapted the window values it is advisable to increase the size of the images and center the areas of interest.

✧ Call up **Image > Zoom & Pan On** in the main menu.

✧ Move the mouse cursor to the center of the image and move the image to the required position keeping the left mouse key pressed.

✧ Place the mouse cursor on the edge of the image and move the mouse keeping the left mouse key pressed to zoom the image.

➩ With **Edit > Select All** or **Edit > Select on Succeeding** you can apply the zoom and panning values to all or all subsequent images of the stack.

CHAPTER

N.3 Evaluating Images

Dynamic evaluation comprises automatic evaluation of the entire image area of the images contained in the tomo segment as well as interactive evaluation of individual regions that you define.

Procedure

Dynamic evaluation comprises the following steps:

- ❏ Definition of a baseline image
  The baseline image is considered for the calculation of parameter images and the Relative Enhancement curves
- ❏ Optional definition ot the tissue class for parameter image calculation in order to limit the CT value range
- ❏ Evaluation of ROIs
  Drawing one or several ROIs for calculation of Absolute and Relative Enhancement curves

Generation of parameter images

As soon as you load the original image material your system performs an evaluation of the entire image area. The results (parameter images) are displayed in the parameter image segment. Each time you make a change to the original data set (by removing images, and/or defining a new baseline image) your system recalculates the parameter images on the basis of the existing images.

Average image

The average image (AVE) is an averaged addition of all pixels at each pixel location across the images of the tomo segment.

MIP image

Parameter image where each pixel is the maximum value of all images at that pixel location. The image data is checked pixel by pixel. The pixels with the maximum intensity are recorded in an image (Max IP image).

→ Page H.1–5, *Maximum intensity projection (MIP)*

Time to Peak image

Parameter image where each pixel indicates the period of time (in tenths of a second) from the time when the first image was acquired (Delay = 0) or the time when the CM was injected (Delay > 0) to the time when the highest CT value is reached at that pixel location. The longer the time period until the peak CT value is reached, the brighter the pixels.

➪ The time to peak (in seconds) at the cursor position in the Time to Peak image is the CT value displayed in the lower right corner divided by 10. This relation is valid for ROI evaluations of Time to Peak images in the **Viewing** task card, too.

Peak Enhancement image

Parameter image where each pixel indicates the enhancement at that pixel location. CT value of a pixel = maximum value found at that pixel location (pixel value of the MIP image) - CT value of the baseline image at that pixel location.

➩ You can activate or deactivate calculation of the Time to Peak image and the Peak Enhancement image in the configuration.
→ Page N.5–1, *Configuring DynEva*

Creating a baseline image

The - so called - baseline image is located in the third segment. All relative results refer to this image. The top image of the image stack in the tomo stack is used as the default baseline image. If you want to use a different baseline image, proceed as follows:

✧ Scroll to the required image in the tomo segment.

✧ Click on the button **Generate baseline image** with the mouse.

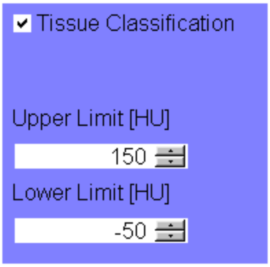
An average image is calculated from the selected and the images preceding it and used as a new baseline image.

NOTE

When you delete an image that is used to define the current baseline image, a new baseline image is calculated.

Defining the tissue range

With **Tissue Classification** you can exclude all tissue regions outside the CT-value range entered. This allows you to emphasize the organ to be examined and remove disturbing factors. HU limitation does not affect evaluation of the ROIs and only appears at the Time to Peak and the Peak Enhancement image.



☑ Tissue Classification

Upper Limit [HU]

150

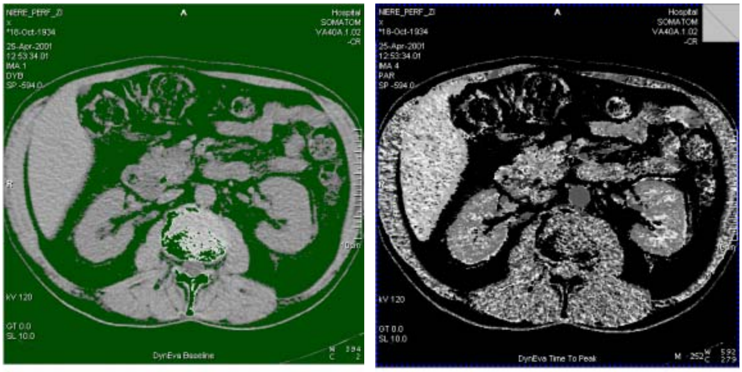
Lower Limit [HU]

-50

✧ Check the checkbox **Tissue Classification**.

✧ Enter the upper and lower limit value of the CT-value range that you want to have displayed.

The excluded tissue densities are masked by a color in the baseline image. The excluded areas are displayed black in the Time to Peak and Peak Enhancement images.



(1) (2)

(1) Baseline image

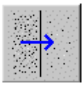
(2) Time to Peak image

Filtering

To reduce noise in the Time to Peak and Peak Enhancement image you can apply a smoothing filter.

➪ Filtering does not affect the evaluation of ROIs.

✧ Enter the number of times filter application is to be repeated, if applicable.



✧ Click on the button **Filter input images**.

➪ If you want to filter with a different repeat factor, you must click on the button **Filter input images** once more.

Evaluation of ROIs

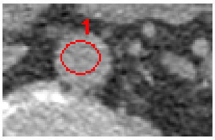
You select the image regions to be evaluated by marking them with ROIs or applying the pixel lens. An absolute/relative CT-value calculation is performed for these selected image regions.

Creating ROIs

You use ROIs (regions of interest) to mark the region in the tomographic image that you want to evaluate. You can draw either elliptical ROIs or freehand ROIs. The number of ROIs that you can define is limited to five. The ROIs that you have drawn are transferred to the other views. To aid examination, they are numbered in sequence and color coded.

Elliptical ROI

✧ Click on the button **Elliptical ROI**.

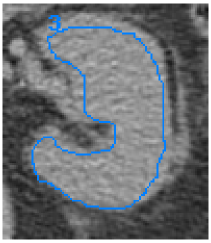


✧ Click into an image and drag open an ellipse keeping the left mouse key pressed.

➩ The elliptical ROI is always oriented horizontally or vertically.

Irregular ROI

- ✧ Click on the button **Irregular ROI**.



- ✧ Click into an image and draw your contour keeping the mouse key pressed.

Or

- ✧ Draw the ROI using vertex points, clicking the mouse key each time you change direction (polygon drawing).
- ✧ Close the ROI with a double-click.

The program links the starting point with the end point to form a ROI.

➪ You can also draw in a freehand ROI by combining both procedures (dragging with the mouse key pressed, setting vertex points).

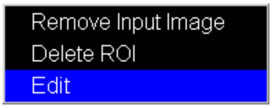
Modifying a ROI

You can modify a ROI in any image, precisely adapting it to the shape of the area of relevance to you.

- ✧ Click on the border of the ROI to display its base points for adapting the shape of the ROI.

Or

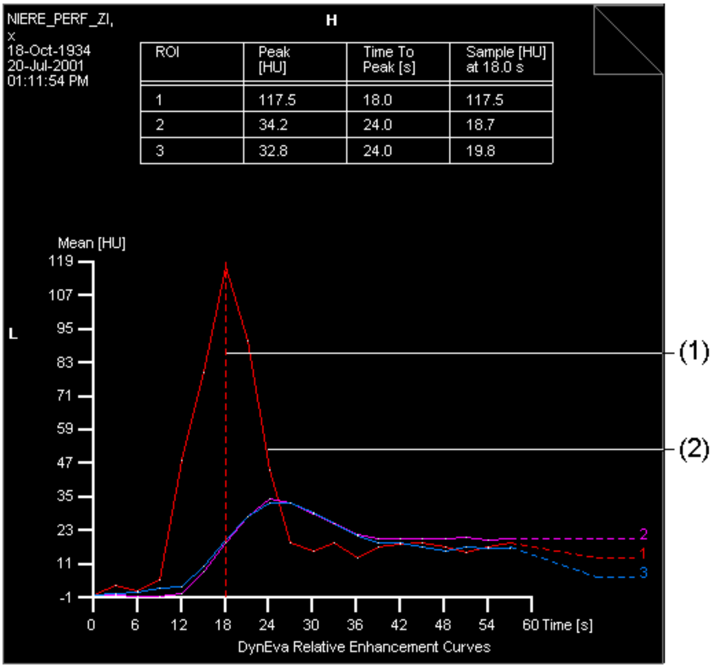
- ✧ Click into the center of the ROI to display a surrounding square for moving, resizing or deleting the ROI.



Once you have selected the ROI or inserted the base points, you can edit the ROI with the mouse or call up the relevant functions in the popup menu (right mouse key).
→ Page E.5–7, *Drawing freehand ROIs*

Enhancement curve

As soon as your have defined a ROI, an enhancement curve (time-density curve) is calculated and displayed in the fourth segment. To facilitate identification, this curve has the same color and numbering as the associated ROI. The maximum CT-value of the ROI first drawn is indicated by a dashed sampling line.



NIERE_PERF_ZI,
x
18-Oct-1934
20-Jul-2001
01:11:54 PM

ROI	Peak [HU]	Time To Peak [s]	Sample [HU] at 18.0 s
1	117.5	18.0	117.5
2	34.2	24.0	18.7
3	32.8	24.0	19.8

1) Sampling line

2) Enhancement curve

Absolute/Relative Enhancement curve

The enhancement curves are displayed as absolute or relative curves. The Absolute Enhancement curve displays the original CT-value derived at every point in time during the examination. The Relative Enhancement curve displays the variation of CT-values with reference to the CT-values in the baseline image at every point in time.
→ Page N.3–3, *Creating a baseline image*

✧ Click on the button **Absolute curve** to display the Absolute Enhancement curve.

Or

✧ Click on the button **Relative curve** to display the Relative Enhancement curve.

Moving the sampling line

If you want to evaluate the enhancement values for a different point in time, move the sampling line in the horizontal direction.

✧ Click on the sampling line with the left mouse key.

✧ Move the sampling line in the required direction keeping the left mouse key pressed.

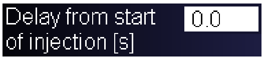
Associated tomographic image

You can display the tomographic image for the time marked by the sampling line as the top image in the tomo segment.

✧ To do that, double-click on the sampling line.

Delay of injection

You usually start the CT scans with contrast medium after a delay following contrast medium injection. You can have this offset taken into account in calculation of the Time to Peak image and enhancement curves. The results then refer to the time of contrast medium administration (zero on the time scale).



Delay from start of injection [s] 0.0

✧ Enter the delay from the start of injection of the CM to the start of the scan and confirm with the **Enter** key.

Pixel lens

You can use the pixel lens similarly to the ROI to examine the change of enhancement of a particular position.

➩ You can only draw one pixel lens.

Drawing a pixel lens

✧ Click on the button **Pixel lens** in the control area.

✧ Move the mouse cursor to the position in the image that you want to examine more closely.

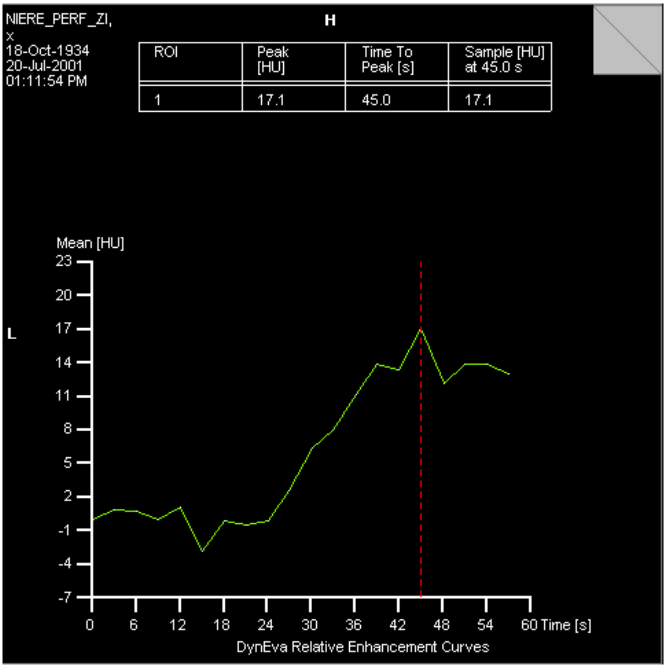
✧ Press on the left mouse key.

The pixel lens is drawn into the image and transferred to the two other image segments.

Enhancement curve

As soon as you have drawn a pixel lens, an enhancement curve is generated in the result segment for this position.

.



NIERE_PERF_ZI,
x
18-Oct-1934
20-Jul-2001
01:11:54 PM

ROI	Peak [HU]	Time To Peak [s]	Sample [HU] at 45.0 s
1	17.1	45.0	17.1

➪ The image containing the graphic evaluation of the pixel lens is on top of the stack. Deactivating the button **pixel lens** removes the pixel lens and its evaluation.

CHAPTER
N.4

Documenting and Closing Evaluation

During the course of your evaluations you will have drawn in individual regions using ROIs and had the enhancement curves and result tables generated. You can save and print out this information or store it on a diskette for further processing.

Saving your data

You can save the result images you have created to the local database as a new series, or print them out in tabular form, or store the tables on a diskette for further processing.

Saving to your local database

✧ In the four segments scroll to the images that you want to save as a new series.

✧ Click on the button **Save**.

Two new series are generated. One series contains the MIP, AVE and, if applicable, the Peak Enhancement image and Time to Peak image without ROIs.
The other series contains the images displayed in the four image segments with ROIs.

Printing tabular values

You can print out the table of the result segment together with the general patient and examination data on a connected printer. The result data are listed in the columns for the associated ROIs.

✧ Click on the button **Print Tabular Result**.

Filming tabular values

If you want to expose the result table on the filmsheet together with the tomograms, transfer the result table to the **Filming** task card.

✧ Click on the **Copy to Film Sheet** button.

Exporting tabular values

If you want to continue processing the tabular results with other programs, export the data to a floppy.

✧ Click on the button **Export Tabular Result**.

The tabular results are output in ASCII format. This allows you to load the tables in a format that can be imported into spread sheet programs.

Closing dynamic evaluation

When you have completed and documented your evaluations you can close evaluation of the loaded data set and evaluate the next data set. Or you can close the **DynEva** task card if you do not want to perform any further dynamic evaluations.

Closing evaluation

✧ Click on the button **End Evaluation** to close evaluation of the loaded data set.

If images are still loaded that you have not yet stored, a dialog box appears telling you so.

✧ Select **Yes** if you want to store the images.

Or

✧ Click on **No** if you want to end evaluation without storing the images.

Closing the task card

If you no longer require the **DynEva** task card, you can hide it.

✧ To do that select **Patient > Close DynEva** in the main menu.

✧ Select **Yes** if you want to store the images.

Or

✧ Click on **No** if you want to close evaluation without storing the images.

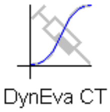
CHAPTER
N.5

Configuring DynEva

You can make the following settings in **DynEva Configuration**:

- Enable/disable the calculation and output of the Time to Peak image and of the Peak Enhancement image
- Output of the results in tabular form to printer or diskette
- Change the size of the pixel lens

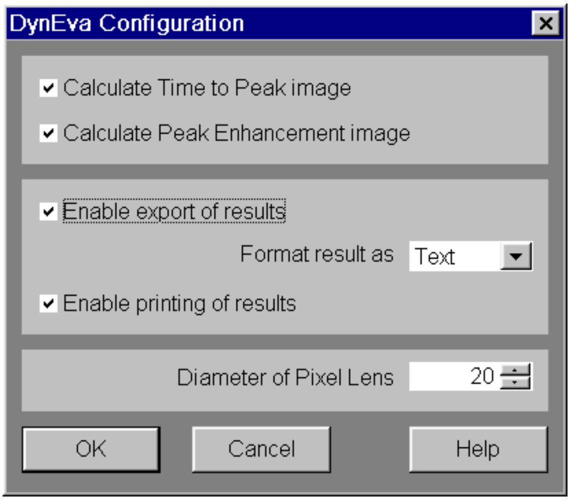
✧ Call up **Options > Configuration** in the main menu.



✧ Double-click on the button **DynEva Configuration** to display **DynEva Configuration** dialog box.

Configuration window DynEva

The **DynEva Configuration** dialog box contains areas for configuring image calculation, result output, and the pixel lens.



DynEva Configuration

☑ Calculate Time to Peak image

☑ Calculate Peak Enhancement image

☑ Enable export of results

Format result as: Text

☑ Enable printing of results

Diameter of Pixel Lens: 20

Parameter images

You can use the configuration to define the scope of evaluation of the entire image area.

You can calculate the Time to Peak and/or the Peak Enhancement image and display it in the second segment.C

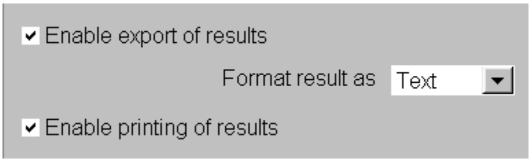
☑ Calculate Time to Peak image

☑ Calculate Peak Enhancement image

✧ Check the relevant checkbox to execute calculation and result display.

Saving/printing out

You can export the results of your evaluation to diskette in the form of a table in ASCII format or print them out. To do that, you must enable these options in the configuration.



☑ Enable export of results

Format result as Text

☑ Enable printing of results

✧ Check the relevant checkbox to activate exporting or printing out of the result table.

✧ In the menu **Format result as** define the format in which your table is to be output.

The following formats are possible:

❏ Text = (MS-WindowsText format)

❏ HTML format

Size of pixel lens

You can set a pixel lens size to suit your chosen examination size and precision.


Diameter of Pixel Lens 20

✧ Enter the diameter of the pixel lens in the field **Diameter Of Pixel Lens** using the keyboard or the spinbox.

PART O

Volume (Option)

O.1 Introduction

O.2 Loading and Displaying Images

O.3 Volume Evaluation

O.4 *Configuring Volume Evaluation*

CHAPTER
O.1 Introduction

On the **Volume** task card you can define and evaluate a volume (VOI) of any shape in a set of two-dimensional CT images.

You can define a volume interactively by drawing ROIs in various slices. The system then combines the two-dimensional ranges to form a single volume. Or you can have a VOI created automatically around a **Seed Point** that you have set.

In addition to the axial images, a sagittal, coronal, and MIP/MPR are displayed in further segments. This allows you to check complex ROIs quickly.

After you have designed the VOI you can calculate the size of the volume and have the statistical data output.

ROI (Region of Interest)	A two-dimensional region of the CT image which can be selected with respect to position, size and shape, and in which quantitative evaluations are performed.
VOI (Volume of Interest)	A three-dimensional region (block) of a CT volume dataset. With a volume of interest, you extract a volume of diagnostic interest to you, thus limiting the volume to be reconstructed to a partial volume.

Calling up Volume

You can first call up an empty task card **Volume**.

✧ Call up **Patient > Volume** in the main menu.

The **Volume** task card is displayed. No images have yet been loaded. All the buttons and most of the menu items are still grayed-out.

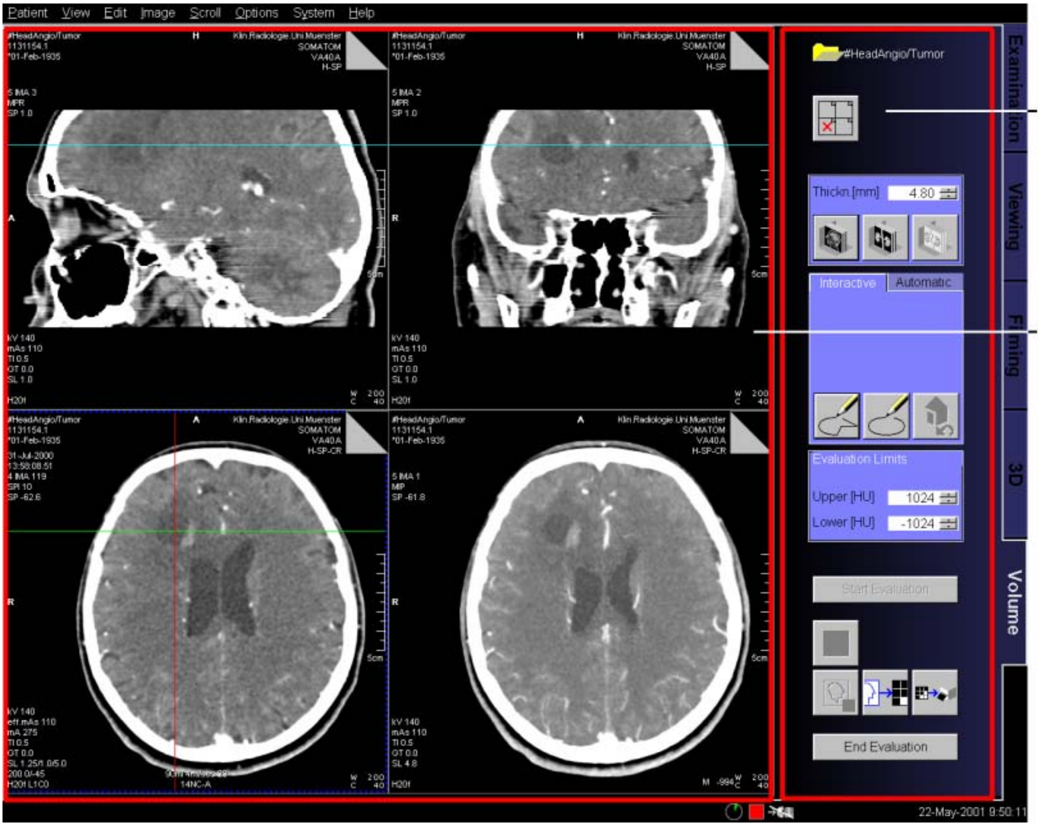
Or

✧ Click on the **Volume** tab if you switched to a different task card in the meantime and now want to return to volume evaluation.

The **Volume** task card is subdivided into two large areas.

The **control area** contains input fields and buttons for setting the various views and for defining and evaluating the VOIs.

The **image area** is subdivided into four segments. The segments show the sagittal, coronal, axial and MIP/MPR view of the image data set and the ROIs that have been drawn. The lower right segment shows the MPR, MaxIP, MinIP view of the loaded images.



(1) Control area
(2) Image area

Closing Volume

When you can completed all the volume evaluations that you want to do, close the **Volume** task card again.

✧ Call up **Patient** > **Close Volume**.

The task card is closed and the **Volume** card disappears from the main menu.

Or

✧ Call up one of the other task cards **Osteo**, **Pulmo**, **DynEva**, **Dental** and confirm the dialog box that is displayed with **Yes**.

The **Volume** task card is closed. The other task card is displayed in its place.

CHAPTER
O.2

Loading and Displaying Images

On the **Volume** task card you can measure the volume of a VOI and the associated parameters. The VOI is defined by defining a ROI in one or more images, or by setting a seed point in one of the images.

For volume evaluation you require a series of tomograms, ideally a data set with contiguous or overlapping slices.

Requirements

The image material must fulfill the following conditions:

- ❏ Only images of one patient must be loaded for evaluation with Volume.
- ❏ The scans must have been acquired with the same gantry tilt and table height.
- ❏ Only image data sets with the same slice orientation must be used.
- ❏ The loaded images must have the same zoom factor and the same reconstruction center.
- ❏ At least four images must be loaded before volume evaluation can be performed.
- ❏ The time range between the first and the last image must not exceed one hour.
- ❏ The data capacity of the volume must not exceed 1024 images with matrix dimensions of 512 x 512 pixels.

Checks by your system

After all images are loaded, your system checks whether the sorted images have an equally spaced ascending or descending timestamp. If that is not the case, a warning box is displayed but loading is continued.

If the distance between slices and the slice thickness of the loaded images are not identical, a warning box is also displayed.

Loading original images

If the **Volume** card has not been displayed yet, you can start the volume application and load the images into the task card in a single action. After that, you can load new series for evaluation into the open **Volume** card, for example, by drag-and-drop.

Loading / starting Volume

✧ Open the **Patient Browser** (**Patient** > **Patient Browser**).

✧ Select the required series.

✧ Call up **Patient** > **Volume** on the menu bar of the **Patient Browser**.

Or

✧ Click on the **Volume** button on the toolbar of the **Patient Browser**.

Loading the next series

If the **Volume** task card is open, e.g. because you have already performed evaluation, you can load the next series for evaluation with a double-click or by drag-and-drop.

✧ Call up **Patient** > **Patient Browser** from the main menu to open the **Patient Browser**.

✧ Select a series that you want to evaluate.

✧ Drag your image selection onto the **Volume** task card holding the left mouse key down (drag-and-drop).

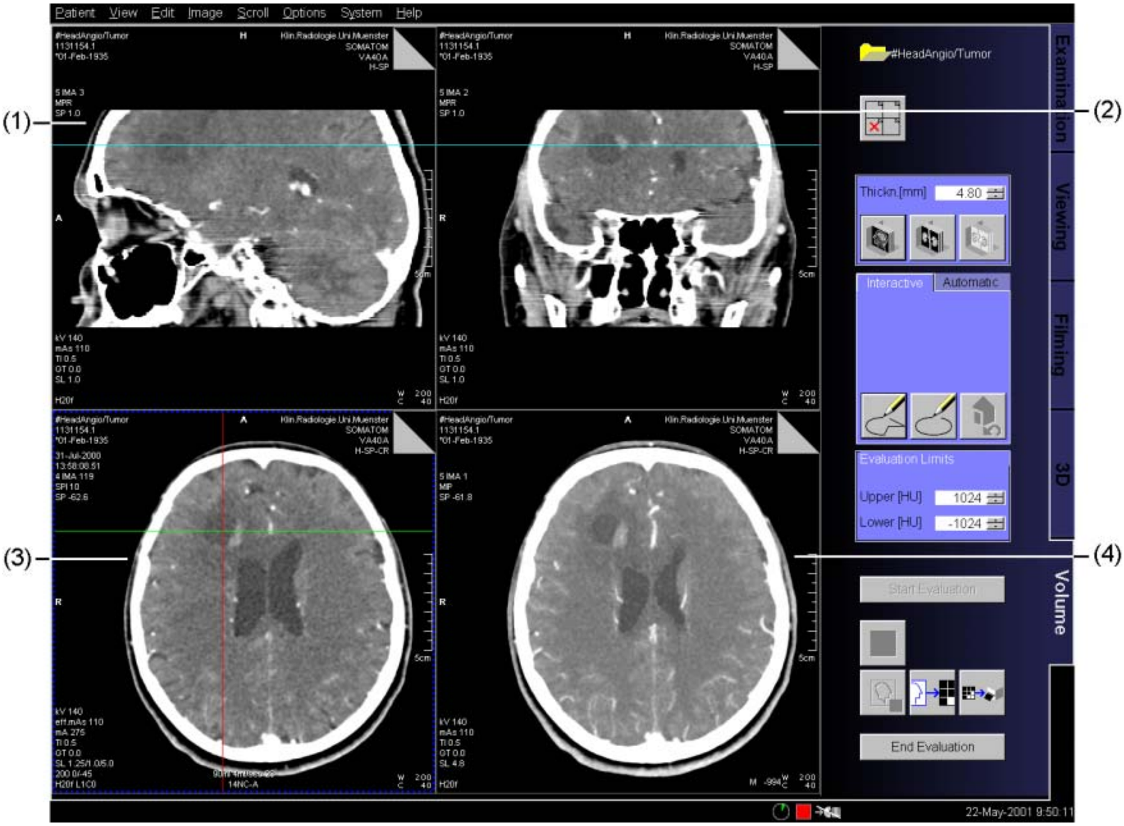
Or

✧ Double-click on your selection to load the images into **Volume**. The **Volume** task card must be in the foreground.

Changing the image display

In the image area of the Volume task card you can see the sagittal, coronal, and axial views of the loaded tomograms in the first three segments. The image stack with the axial view is sorted in the cranio-caudal direction. The tomogram on top is nearer the head than the bottommost tomogram.

From the loaded data set, MIP or MPR images are reconstructed and displayed in the lower right segment.



Thickn.[mm] 4.80
Upper [HU] 1024
Lower [HU] -1024

(1) Original image in sagittal view

(2) Original image in coronal view

(3) Original image in axial view

(4) MaxIP/MinIP/MPR/result table thick-slice

Scrolling through the image stack

In each segment you can scroll through the image stack using either mouse or the keyboard.

✧ Click on the dog ears in the image stack to scroll image by image.

Or

✧ Call up **Scroll** > **Next image** or **Previous image** from the main menu or press the **Image +** or **Image -** key to scroll one image forward or back within a series.

Or

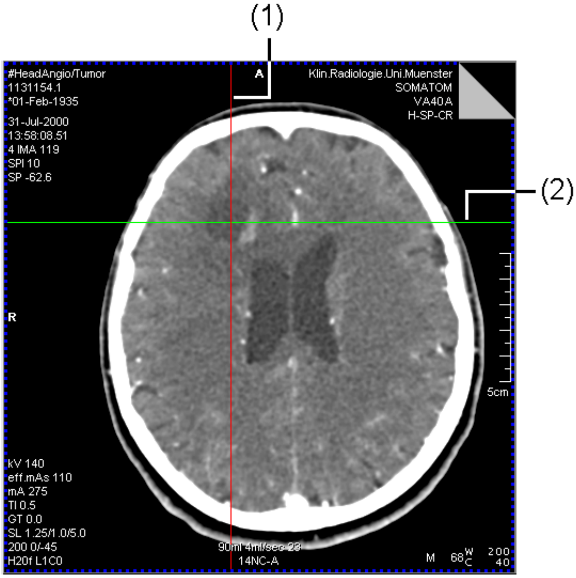
✧ Call up **Scroll** > **First page** or **Last page** to scroll to the first or last image in the image stack.

Scrolling using the navigation lines

In addition to scrolling using the mouse, you can use the navigation lines to have the required sections displayed in the individual segments. The navigation lines are displayed after you have loaded the original images (except for the MIP/result segment).

Axial projection

The two navigation lines in the axial projection show the current position of the sagittal and coronal intersection plane.



(1) Sagittal navigation line

(2) Coronal navigation line

Sagittal/coronal projection In the sagittal and coronal segment, one horizontal navigation line is displayed. It shows the position of the currently displayed axial image.

(1) Axial navigation line

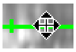
Moving navigation lines

By moving the navigation lines in the segments you can scroll through the image stacks to the required axial, sagittal or coronal image.

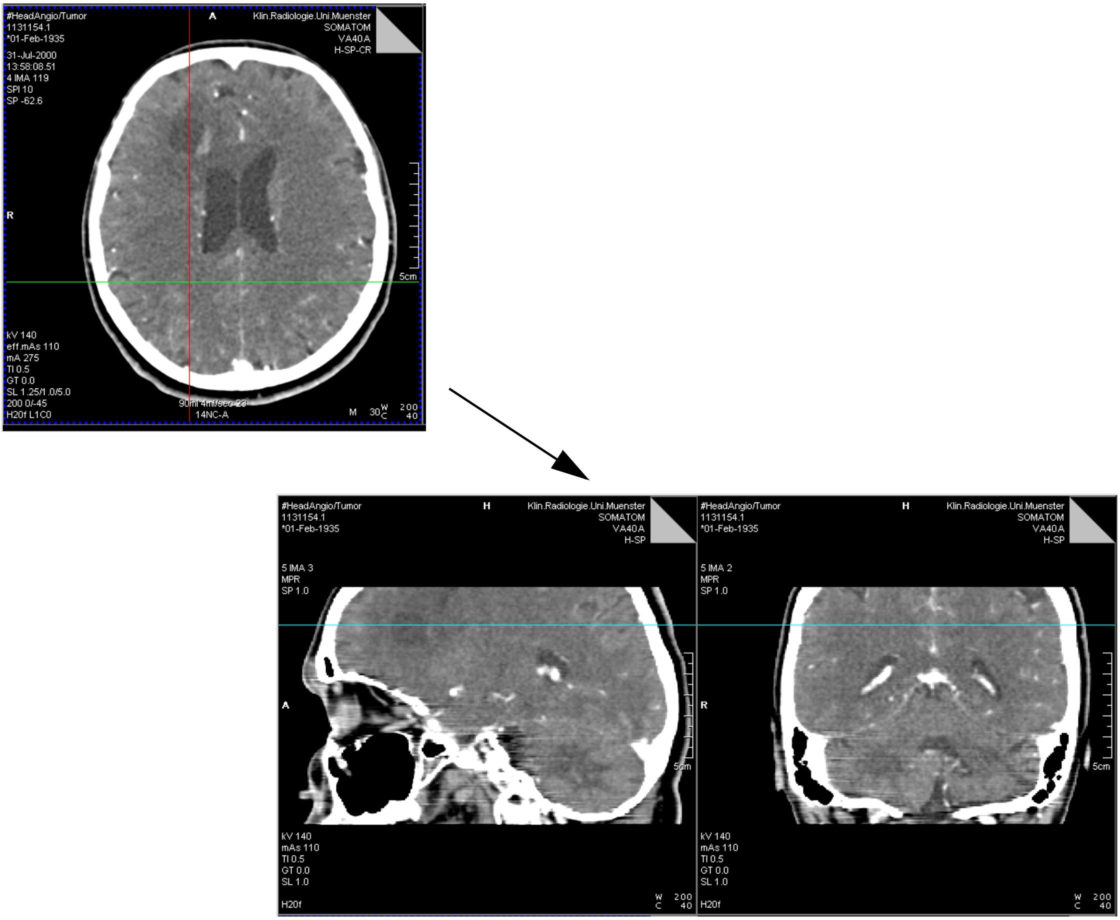
❏ In the sagittal segment you can scroll by moving the sagittal navigation line in the axial segment.

❏ In the coronal segment you can scroll by moving the coronal navigation line in the axial segment.

❏ In the axial segment you can scroll by moving the axial navigation line in the sagittal or coronal segment.



✧ You can move the navigation line to the required position holding the left mouse key down.



After each navigation, the view is updated in the segments.

Zooming and handling images

To obtain a clearer view of details, you can zoom the images and position image sections in the center of the segment.

✧ Call up **Image** > **Zoom & Pan On** to activate the zoom/pan function.

Zooming an image

✧ Place the mouse cursor on the edge of the image.

✧ Move the mouse up or down to enlarge or reduce the image.

Panning an image

✧ Place the mouse cursor in the center of the image.

✧ Move the image to the desired position holding the left mouse key down.

➪ If you later want to deselect the zoom/pan function, just call up **Image > Zoom & Pan On** again.

Showing/hiding image text display

The following image information is displayed in the original images:

❏ Patient and examination data
❏ System on which the images were acquired
❏ Scan parameters
❏ Window values

→ Page A.1–39, *Text information in medical images*

You can switch off the image information if it covers structures of interest.

✧ Selecting **View** > **No Text** from the main menu to switch image text display off.

✧ If you want to have the image text information display, select **View** > **All Text**.

CHAPTER
O.3 *Volume Evaluation*

After you have loaded the images on to the **Volume** card for volume evaluation, you can start with the volume definition and complete with the volume evaluation.

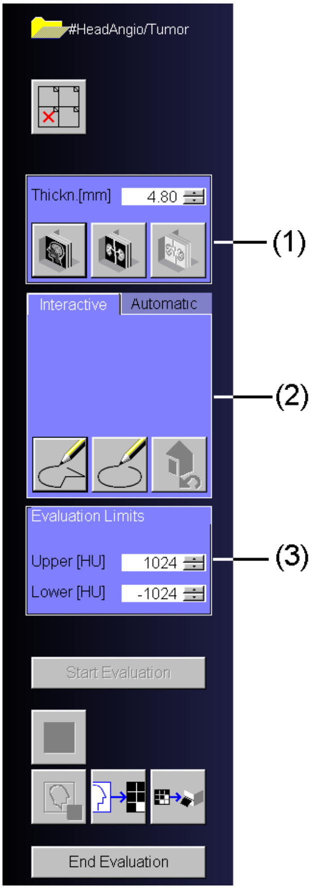
How to proceed

Volume definition and evaluation is performed in the following steps:

- ❑ Setting the sliding MIP (MaxIP, MinIP) or MPR display and removing unnecessary images
- ❑ Interactive and/or automatic volume definition
- ❑ Starting evaluation using the **Start Evaluation** button
- ❑ Automatic calculation of the volume and statistical parameters
- ❑ Storage of the results and documentation on film.
- ❑ Termination of evaluation using the **End Evaluation** button

Control area

You will perform volume definition and evaluation using the buttons and input fields in the control area. It contains the following input areas:



(1) Setting the sliding MIP/MPR images

(2) Interactive/automatic volume definition

(3) Evaluation limits

Preparing volume calculation

Before you start the volume definition, you will first optimize the display of the images. This makes interactive volume definition easier. You can delete images that you do not require for volume calculation from the original data set.

Defining the sliding MIP/MPR display

You can change the display of the images in the MIP/results segment using the display mode and the slice thickness.

Slice thickness

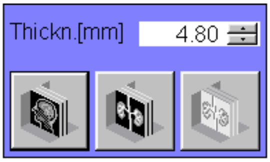
The sliding MIP/MPR images are calculated from volume slabs from the original images of the axial segment. You can define the thickness of the volume slabs freely, but thickness may not be less than slice thickness of the axial images.


Thickn.[mm] 4.80

✧ Enter the new value for the slice thickness and confirm it with the **Enter** key.

As soon as you have entered another value for the slice thickness, the images are reconstructed again.

Display mode



Thickn.[mm] 4.80

✧ Click on the **MaxIP** option to have the MIP images displayed with maximum intensity projection according to the selected thickness in mm (maximum grayscale values).

Or

✧ Click on the **MinIP** option to have the MIP images displayed with minimum intensity projection according to the selected thickness in mm (minimum grayscale values).

Or

✧ Click on the **MPR** option to have images displayed with average grayscale values according to the selected thickness in mm.

Deleting images

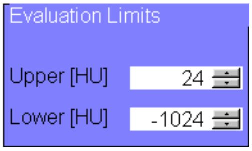
You can delete images that you do not require for evaluation from the image stack in the axial segment.

✧ Click on the **Delete Image** button to delete the image displayed in the axial segment.

As soon as you have deleted one image from the image stack, the images in the remaining segments are reconstructed again.

> **NOTE**
>
> Reconstruction may take some time after deletion of a great number of images

Setting evaluation limits


Evaluation Limits

Upper [HU] 24

Lower [HU] -1024

Using the evaluation limits you can perform volume calculation within a defined HU value range.

✧ Enter the new evaluation limits and confirm them with the **Enter** key.

➩ The default is -1024 for the lower evaluation limit and 3071 for the upper evaluation limit.

> **NOTE**
>
> The **Evaluation Limits** can also be modified after volume definition has been completed.

Interactive volume definition

In interactive volume definition, you can draw elliptical or freehand ROIs in individual images. You can use these ROIs to define a combined VOI. You can then edit the ROIs you have drawn in axial and MIP/MPR views.

Drawing ROIs

You can draw the ROIs in the axial segment or in the MIP/result segment. The ROIs drawn in the MIP/result segment are also shown in the axial segment, within the center slice image of the volume slab that was used to calculate the MIP/MPR image.
→ Page O.3–3, *Slice thickness*

In the sagittal and coronal segment you can see the ROIs in the view in question.

NOTE

To define a VOI you do not need to draw a ROI in every axial or MIP image. It is sufficient to define the ROIs in a few representative images. You system then interpolates the volume between these slice planes.
→ Page O.3–13, *Interpolated ROIs*

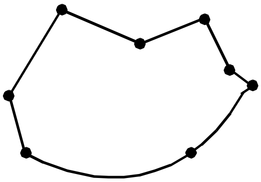
Freehand ROI

✧ Click on the **Freehand ROI** button on the **Interactive** subtask card.

✧ Click into the image to define a starting point.

✧ Hold the mouse key pressed and draw a border round the region of interest to you.

Or



✧ Draw the ROIs using vertices by clicking with the mouse each time you change direction (polygon definition).

✧ Double-click on the end point to close the ROI.

The program connects the starting point to the end point to form a closed ROI.

➩ You can also draw a freehand ROI combining the two methods (dragging holding the mouse key pressed, setting vertices).

Elliptical ROI

✧ Click on the **Elliptical ROI** button on the **Interactive** subtask card.

✧ Click into the image and drag open an ellipse holding the left mouse key pressed.

Undo

If you are not happy with the ROI you have drawn, you can undo the last step at any time.

✧ Simply click on the **Undo** button.

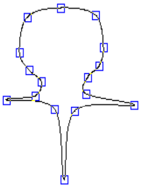
Editing ROIs

You can edit manually drawn and interpolated ROIs in the axial or MIP/result segment before volume calculation, and therefore adapt them to the relevant volume range.

Base points/selection

Depending the changes you want to make to a ROI, show the associated base points or select the ROI.

✧ Click on the border of the ROI.

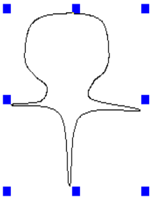


The mouse cursor changes shape.

Base points are displayed via which you can change the contour of the ROI.

Or

✧ Click inside the ROI to select it.



A surrounding rectangle is displayed which you can use to move, resize, and delete the ROI.

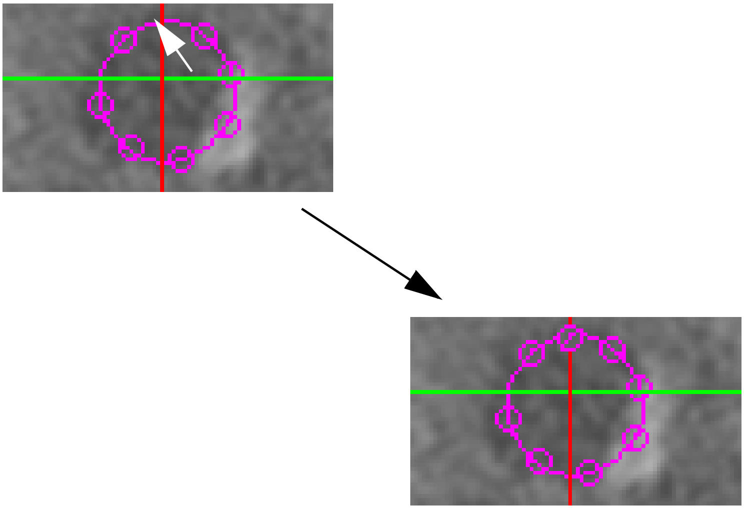
After selecting the ROI or displaying the base points, edit the ROIs using the mouse or call up the required functions from the popup menu (right mouse key).

Adding base points

To enlarge a ROI or to define shapes more accurately, you can insert base points.

✧ Click on the line with the left mouse key between two base points.

A new base point is added.



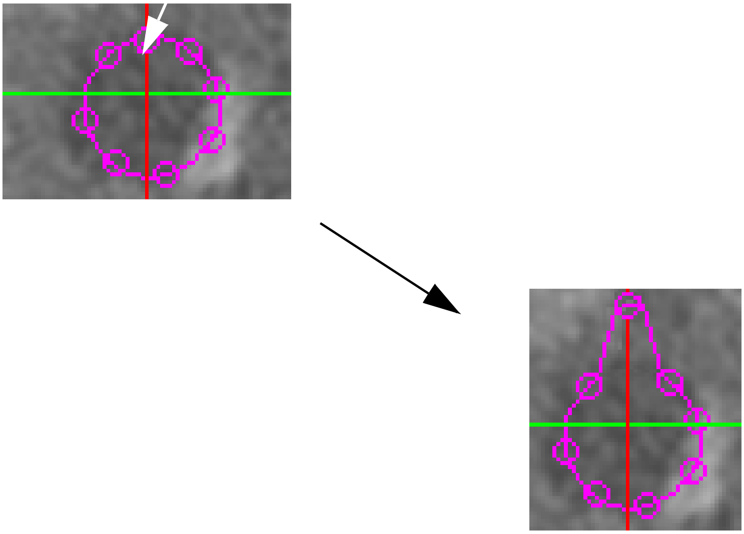
Moving base points

You can change the shape of the region by moving individual base points.

✧ Click on one base point with the left mouse key.

✧ Drag the base point to a new position holding the mouse key pressed.

The base point is moved.



Deleting ROIs

✧ Click on the ROI that you want to delete.

✧ Call up the popup menu (right mouse key) and select **Delete ROI**.

Or

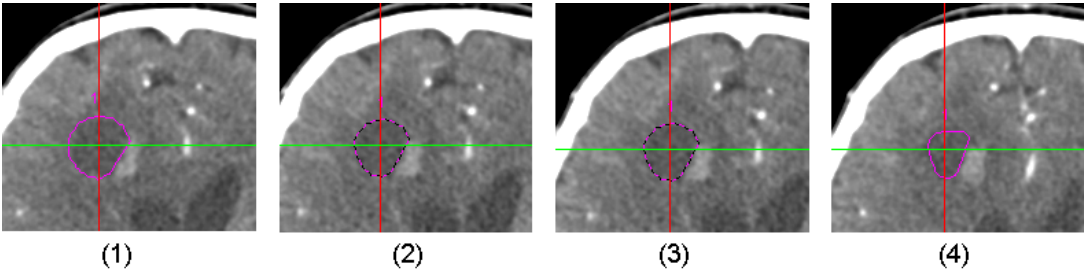
✧ Select **Delete All ROIs** from the popup menu to delete all ROIs.

Interpolated ROIs

If tomograms without ROIs are between two slice images with ROIs, you system interpolates the missing ROIs from the existing ROIs if they overlap in vertical direction.

Example

You draw a ROI in the 1st image and in the 4th image. Your system creates the suitable ROIs for the 2nd and 3rd image from it by interpolation. The interpolated ROIs are displayed with dashed contour lines.



✧ If necessary, edit the interpolated ROIs by selecting and modifying the interpolated ROIs just as if they were drawn ROIs.
→ Page O.3–10, *Editing ROIs*

As soon as you have edited an interpolated ROI, it is classified as a ROI defined by you (confirmed ROI) and marked with a continuous contour line.

➩ If you confirm an interpolated ROI or delete a drawn ROI, the interpolated ROIs affected are recalculated.

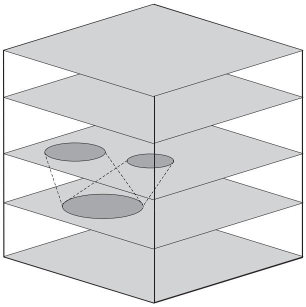
After starting evaluation, all interpolated ROIs are displayed as confirmed.

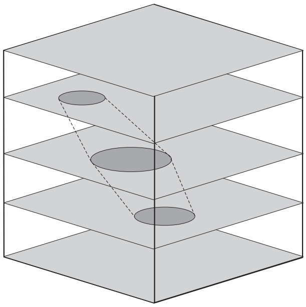
Linking and unlinking ROIs

You can define complex volumes using the automatic (overlap) and manual (mark&link) method.

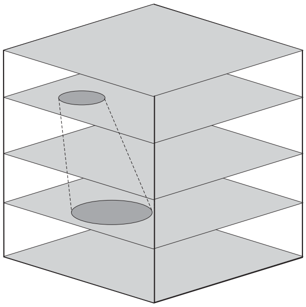
Overlapping method

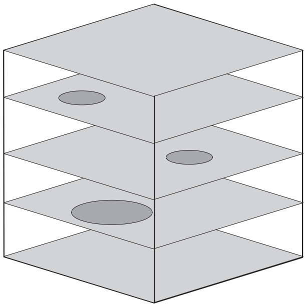
ROIs without a common point of projection are automatically linked to form one volume as soon as you draw another ROI that overlaps the existing ROIs. In that case, the position of the overlapping ROI in the image stack is irrelevant.





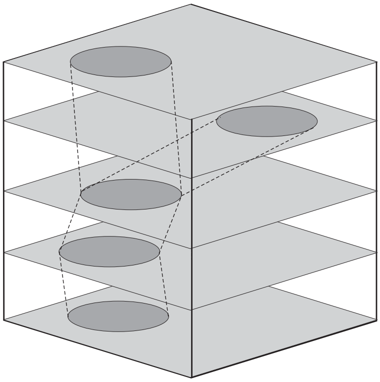
ROIs linked by interpolation are unlinked again if you draw an ROI (on an intermediate slice) which does not overlap previously defined ROIs.





Mark & link method

If two ROIs do not have a common projection point, you can link them manually for interpolation.



✧ Click on the first ROI with the left mouse key.

✧ Call up **Mark** from the popup menu (right mouse key) to mark the ROI for linking.

✧ Click on the second ROI and select **Link** from the popup menu.

The two ROIs are interlinked.

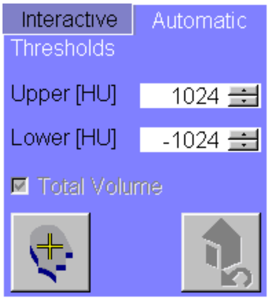
➩ If you have linked the wrong ROIs, select **Unlink** in the popup menu (right mouse key) and to remove the link again. Interpolation is no longer performed between these ROIs.

Automatic volume definition

With automatic volume definition, set a starting point in an axial tomographic image. With defined search limits or optionally delimiting ROIs you can restrict your expansion range for region growing. You can also set more than one starting point to combine several volumes to form one overall volume. As soon as you are happy with the VOI you have defined, start evaluation.

Setting a starting point

For automatic volume definition, you can set a seed point in a tomographic image in the axial segment in the region that you want to define as a volume. Starting from this seed point, your system detects all voxels that are within the defined grayscale range and which are neighbouring each other. As soon as there is a break in neighbouring voxels the region growing stops.
→ Page O.3–6, *Setting evaluation limits*



Upper [HU] 1024

Lower [HU] -1024

☑ Total Volume

✧ Click the **Automatic** subtask card into the foreground to switch on the automatic volume definition mode.

✧ Set the threshold for region growing in the **Upper [HU]** and **Lower [HU]** spin boxes and confirm with the **Enter** key.

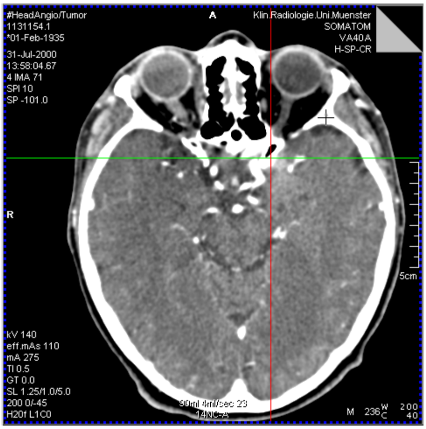
Seed Point

✧ Scroll in the axial segment to the image in which you can recognize the region of interest clearly.

✧ Click on the **Set Seed Point** button.

The mouse cursor becomes a graphics cursor.

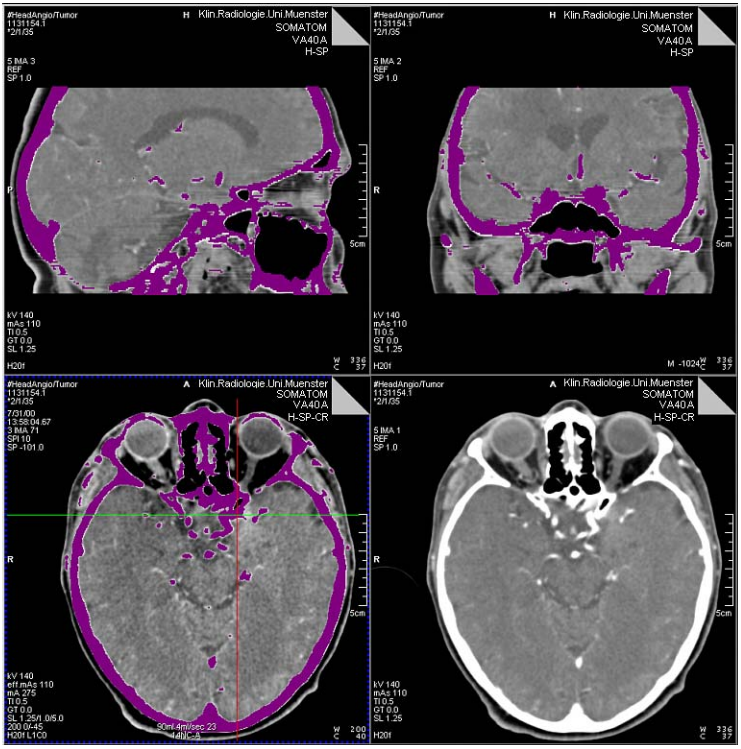
✧ Click into the required region with the left mouse key to set the **Seed Point** there.



Automatic volume recognition

After you have set the starting point, automatic volume recognition begins.

The pixels that belong to the volume recognized are highlighted in color in all segments.



More than one volume

You have the possibility of setting several starting points one after the other. That gives you several volumes that you can combine to form an overall volume later.

✧ Click on **Set Seed Point** for each new volume definition and set successive further starting points in the axial segment until you have defined all partial volumes.

Undo

If you are not happy with the definition of the **Seed Points**, you can undo the last step.

✧ Click on the **Undo** button to clear the last **Seed Point** you have set.

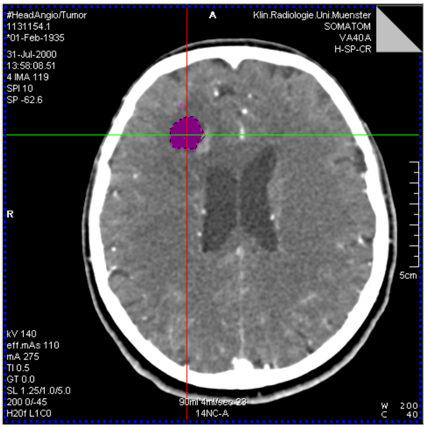
Combining interactive and automatic volume definition

By combining interactive with automatic volume definition, you can restrict the search range spatially starting from a seed point.

✧ First define a bounding VOI for which you draw one or more ROIs in the axial images.
→ Page O.3–7, *Drawing ROIs*

✧ Then set the **Seed Point** in the interactively defined VOI.
→ Page O.3–16, *Setting a starting point*

Automatic volume definition is limited to the bounding VOI and is performed taking the defined threshold values into account.



Performing evaluation

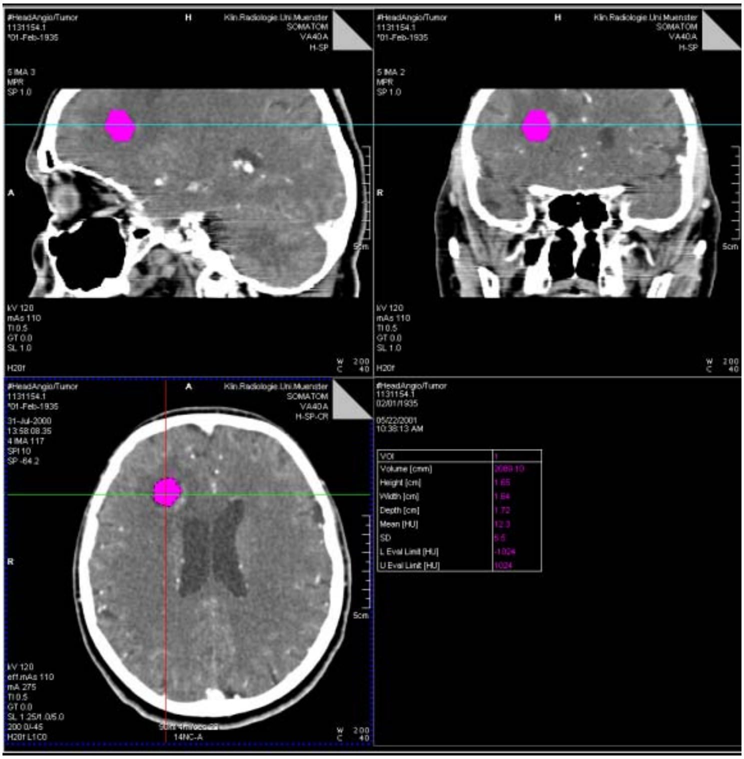
After you have defined the required VOI, start volume calculation.

✧ Click on the **Start Evaluation** button.

The volume calculated and further statistical parameters will be listed in the result window (bottom right).

The result table is marked in the same color as the associated volume.

➪ You can configure result output of volume evaluation.
→ Page O.4–1, *Configuring Volume Evaluation*



VOI	1
Volume [cmm]	2089.10
Height [cm]	1.65
Width [cm]	1.64
Depth [cm]	1.72
Mean [HU]	12.3
SD	5.5
L Eval Limit [HU]	-1024
U Eval Limit [HU]	1024

Toggling the MIP/result segment

Using the **MIP/Result Image** button you can toggle between display of the MIP/MPR images and the results images.

✧ Click on the **MIP/Result Image** button to display the result table or the MIP images.

Or

✧ Call up **MIP/Result Image** from the popup menu (right mouse key).

Filming and storing results

You can quickly and easily film and store the results of a volume evaluation in a database directly from the task card. To film, first select the required images.

Selecting images

✧ Select one or more images with the mouse by clicking on them (multiple selection holding the **Ctrl** or Shift key down).

Or

✧ Call up **Edit** > **Select All** from the main menu to select all images.

Or

✧ Call up **Edit** > **Select On Succeeding** to select the displayed image and all successive images in the series.

➪ With **Edit** > **Deselect All** you can cancel your image selection

Filming

✧ Click on the **Copy to Film Sheet** button to transfer the selected images to the virtual filmsheet.

➪ On the **Filming** task card, you can then change the view of the images.

✧ Click on the **Expose Film Task** button to expose the images transferred to the filmsheet on film immediately.

Storing

✧ Click on **Copy to Disk** to store your results

The results of volume evaluation are stored as new series in the local database. The first series contains all input images with the confirmed ROIs. The results window, the sagittal, coronal, axial, and MIP/MPR images are stored in a second series.

➩ If you have deleted some images before volume evaluation, they are not stored.

NOTE

When exporting/importing images or sending them in the network, color overlays are reduced to one color due to technical reasons.

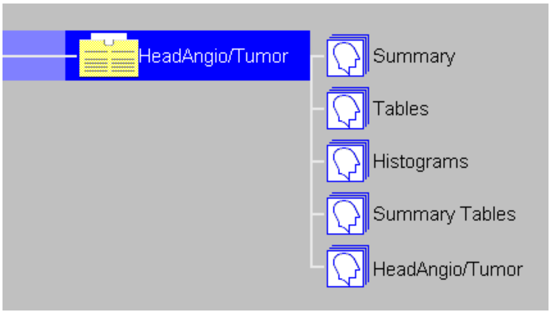
Closing evaluation

After you have completed volume calculation and output the results, you can define a new volume and evaluate it. If you do not want to perform further calculations, close your evaluation.

✧ Click on the **End Evaluation** button.

➩ If you have not yet stored your results, a message window appears.

You can call up the results you have stored and display them in the 2D **Viewing** from the **Patient Browser** at any time.



CHAPTER

O.4

Configuring Volume Evaluation

In **Volume Configuration** you can adapt the evaluation functions of the **Volume** task card to your requirements.

You can change the following settings:

❑ Unit for volume calculation

❑ Output of statistical parameters

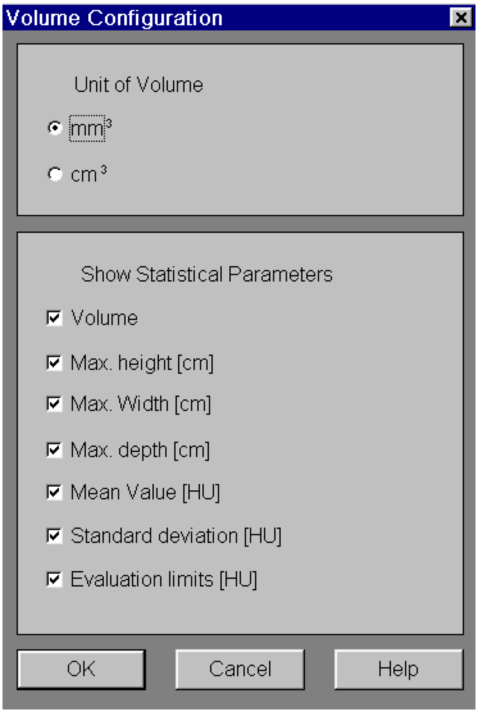
✧ Call up the **Configuration platform** (**Options > Configuration** in the main menu).

✧ Select the configuration window of the **CT Volume** task card.

CT Volume

➩ The changes are taken into account in the configuration in the next calculation.

The **Volume Configuration** window is displayed.



Volume Configuration

Unit of Volume

● mm³

○ cm³

Show Statistical Parameters

☑ Volume

☑ Max. height [cm]

☑ Max. Width [cm]

☑ Max. depth [cm]

☑ Mean Value [HU]

☑ Standard deviation [HU]

☑ Evaluation limits [HU]

OK

✧ Click on **OK** to save the new settings after the changes you have made.

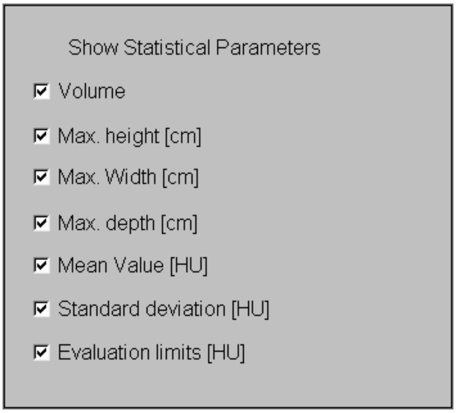
Or

Cancel

✧ Click on **Cancel** to close the **Volume Configuration** window. All settings remain unchanged.

Output of statistical parameters

In the **Show Statistical Parameters** area, you can define which statistical parameters are to be shown in the result window.



Show Statistical Parameters

☑ Volume

☑ Max. height [cm]

☑ Max. Width [cm]

☑ Max. depth [cm]

☑ Mean Value [HU]

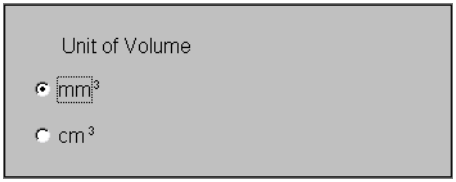
☑ Standard deviation [HU]

☑ Evaluation limits [HU]

✧ Select the statistical parameters you require with the checkboxes.

Unit for volume calculation

The calculated volume can be displayed either in mm³ or in cm³.


Unit of Volume

● mm³

○ cm³

✧ Select the required unit using the radio buttons in the **Unit of Volume** area.

PART
P

Perfusion CT (Option)

P.1 Introduction

P.2 Performing Perfusion Calculation

P.3 Evaluating and Documenting Results

P.4 *Changing Default Settings*

P.5 *Configuring Perfusion CT*

P.6 *Reference Information*

CHAPTER

P.1 Introduction

Perfusion CT is an easy to use software application permitting cerebral perfusion imaging. It is based on dynamic CT images acquired directly after the injection of contrast media. A potential application of this program is the early diagnosis of acute stroke.

By providing images of blood flow, blood volume and time to peak from one set of dynamic CT images Perfusion CT allows a quick and reliable assessment of the type and extent of perfusion disturbances.

Concepts

Perfusion imaging is based on the following concept:

❑ Peripheral intravenous injection of a compact bolus of iodine contrast (e.g. 40 ml with 8 ml/s).

❑ Fast dynamic data acquisition in one or two slices through the basal ganglia for typically 30 to 40 seconds with a sampling frequency of at least 1 image per second. Scanning must be performed using dynamic Multiscan (for the Volume Class fast dynamic sequence is also possible).

❑ Soft tissue extraction and preprocessing in order to improve noise performance.

❑ Application of a tracer kinetic model to the pixel time density curves (maximum slope model)

Perfusion performs a mapping of calculated model parameters to images that display:

- Cerebral blood flow (CBF)
- Cerebral blood volume (CBV)
- Time to bolus peak
- Time to bolus start

Calling up Perfusion CT

You can call up the **Perfusion** task card without loading images so that it is initially empty.

✧ Call up **Patient > Perfusion** in the main menu.

The **Perfusion** task card is displayed. All buttons and most menu entries are still dimmed.

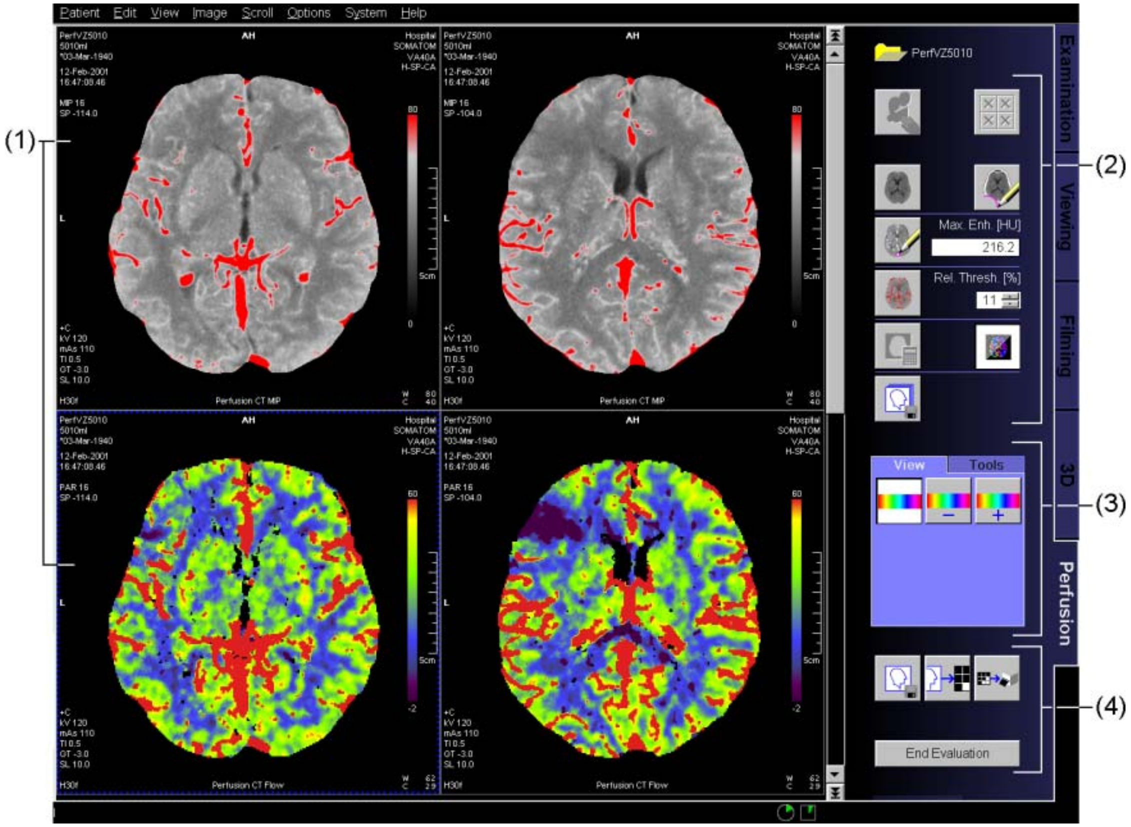
Or

✧ Click on the **Perfusion** tab if you have switched to another task card in the meantime.

The **Perfusion** task card is subdivided into two areas.

The **control area** contains subtask cards and buttons for performing calculations and for image processing.

The **image area** is used to display the original and results images. It is subdivided into four segments. For multi slice reconstructions, the image area simultaneously displays the images of the same acquisition time.



Max. Enh. [HU] 216.2

Rel. Thresh. [%] 11

(1) Segments of the image area
(2) Buttons for image editing and perfusion calculation (arranged from top to bottom acc. to workflow)
(3) Subtask cards for displaying and evaluating result images
(4) Buttons for documenting and terminating perfusion evaluation

Closing Perfusion CT

As soon as you no longer want to perform the perfusion evaluation, you can close the **Perfusion** task card again.

✧ Call up **Patient > Close Perfusion**.

The task card is closed, the **Perfusion** tab disappears again.

Or

✧ Call up another task card, e.g. **Pulmo** or **Dental** and confirm the displayed dialog box with **Yes**.

The **Perfusion** task card is closed and another task card is displayed instead.

Or

✧ Click on the button **End Evaluation** to close the evaluation of the loaded data set.

✧ Click on **Yes** in the dialog box displayed to close the images and results of the current patient.

Or

✧ Click on **No** to return to the current evaluation.

CHAPTER

P.2

Performing Perfusion Calculation

Perfusion CT is an application program for the assessment of cerebral ischemia. With this program you can process dynamic CT images of the brain and map cerebral perfusion parameters.

The individual steps of perfusion calculation are ordered from top to bottom on the **Perfusion** task card. At the start, only the first button is active, indicating that you must perform that step first. Once you have done so, the next button becomes active, indicating that you should now move on to the next step, and so on.

Sequence of perfusion calculation

A perfusion calculation comprises the following steps:

- ❏ Loading original images, inspecting them, and removing unsuitable images from the **Perfusion** task card
- ❏ Performing soft-tissue segmentation and automatic contour finding
- ❏ Defining vessels via enhancement comparison with a reference vessel
- ❏ Performing perfusion result calculation

NOTE

You can stop at any point in the sequence of perfusion calculation and repeat one of the previous steps. You will then have to repeat all the subsequent steps.

Loading images

You can load original dynamic CT-images for perfusion calculation into the **Perfusion** task card. You can also load previously calculated result images and display and evaluate them.

Loading images with the Patient Browser

In the **Patient Browser**, you select the images from one study or series of a study and load them into the **Perfusion** task card.

✧ Call up the **Patient Browser** (**Patient > Patient Browser**).

✧ Select the examination data in question in the navigation or content area.
→ Page D.2–6, *Scrolling through and selecting patient data*

✧ Call up **Patient > Perfusion** in the main menu or click on the **Perfusion** button on the toolbar of the **Patient Browser**.

Or

✧ Place the **Perfusion** task card on top of the card stack.

✧ Double-click on the required data in the **Patient Browser** or drag&drop them into the task card.

Image prerequisites

A consistency check of the loaded image stack is performed automatically. It ensures that all images loaded for processing belong to the same series of the same patient, have been acquired at the same table position and at consistent time intervals, and so on.

If inconsistencies are found, the system issues a warning or an error message. A warning message means you should examine the image stack, and if necessary, reload it. An error message means you cannot use the stack for further processing.

General Prerequisites

☐ The Perfusion program accepts only tomogram images

☐ Only dynamic CT images can be used (same table position at different points of time)

☐ You can load a maximum of 4 slices. A typical dynamic series consists of 1 or 2 slices of 40 images of 10mm slice thickness.

Scanning prerequisites

Perfusion CT was designed and tested for the processing of dynamic image sequences of the brain on SOMATOM CT scanners.

❑ Data must always have been acquired or reconstructed with a sampling rate of at least 1 image per second.

❑ The primary anatomy that the software expects for its semi-automatic analysis are standard slices through the basal ganglia.

❑ Other levels of the brain can be processed, but the slice should contain the occipital segment of the superior sagittal sinus above the confluence of sinuses.

Any deviation from these requirements may cause deviating and even incorrect results. If the influence of such factors is not fully understood by the physician, the interpretation of the resulting parameter images can be misleading!

CAUTION

Source of danger: Inappropiate input data

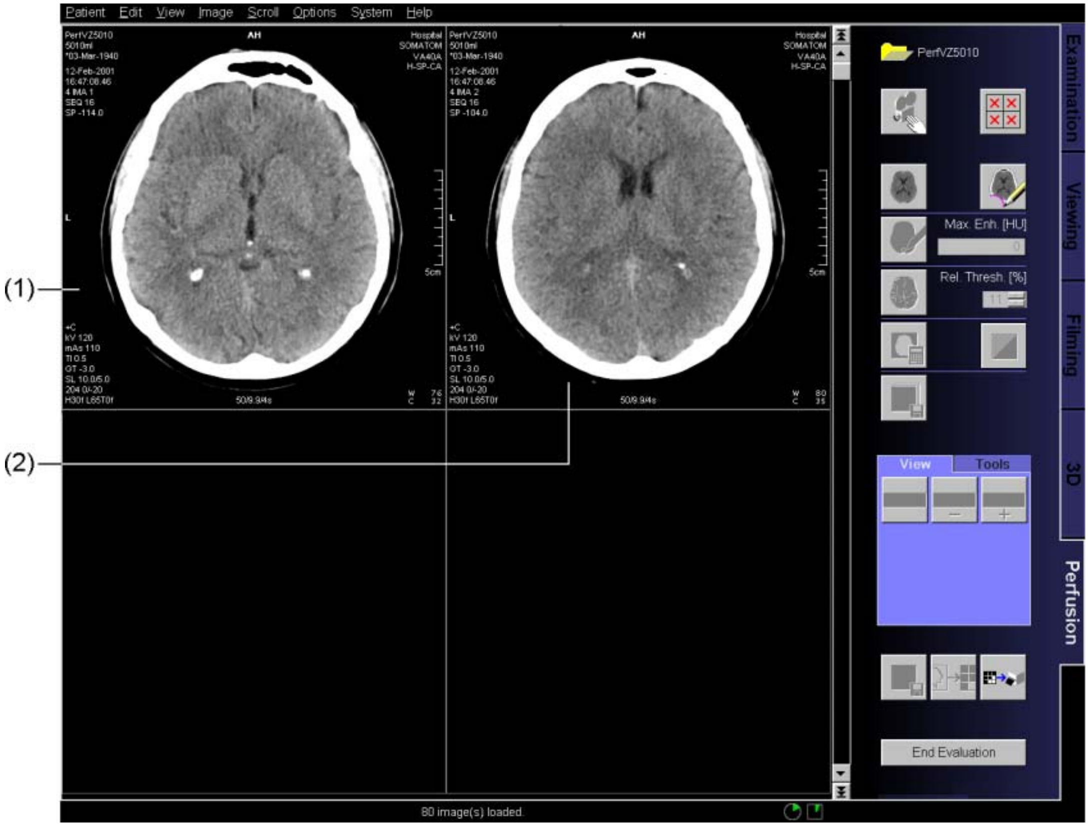
Consequence: Misleading or incorrct interpretation of results

Remedy: Only use fast dynamic scan data of the brain acquired on SOMATOM CT scanners for perfusion evaluation

Display of the input images

The loaded images are sorted in stacks according to the acquisition time.

For multi slice reconstructions, the image area simultaneously displays the images of the same acquisition time, e.g.:



(1) Tomogram at first reconstructed slice position

(2) Tomogram at second reconstructed slice position (acquired at the same time)

Inspecting the input images

Before starting the Perfusion CT evaluation, you may want to scroll through the image stack, check the images and optimize their display.

You may also want to remove some images (for example, with severe motion artefacts) from the stack before you start the perfusion calculation.

Scrolling in the image stack

In the image area you can scroll page by page through the original data set.

✧ Move the arrow buttons up and down along the scroll bar next to the segment.

Or

✧ Scroll with the **Image+** and **Image-** buttons on your symbol keypad through the series.

➩ To page you can also use the **Scroll** menu and the **Page up**, **Page down**, **Home** or **End** symbol keys.
→ Page E.3–7, *Scrolling page by page*

Movie display

Movie display allows you to display the loaded images against time making it easier to detect motion artifacts.

✧ Call up **Scroll > Interactive Movie On** or click on the button to activate the movie function.

✧ Keep the left mouse key pressed and move the mouse upward/downward to run the film forward/backward.

➩ The faster you move the mouse, the faster the sequence of images in the movie display.

✧ Uncheck **Interactive Movie On** in the **Scroll** menu or click on the button again to terminate the movie function.

Changing the image display

While browsing through the image set you may want to adjust the window values and hide the image text for better image display.

Windowing

✧ Move the mouse down/up or left/right in one of the image segments keeping the center mouse key pressed.
→ Page E.4–11, *Windowing with the mouse*

Or

✧ Window the images with the tuning knobs on the control box (only Navigator).
→ Page E.4–10, *Windowing with the control box*

➩ With **Image > Home Window** in the main menu or **Home Window** in the popup menu (right mouse key) the old window settings are restored with which you loaded the images from the local database.

NOTE

To window just a single image, uncheck **Windowing All On** in the **Image** menu.

After calculation and for a reloaded **Perfusion CT Set**, images of the same type are windowed together. To switch this function off, uncheck **Windowing on Image Type On** in the **Image** menu.

Image text and scale bar

You can hide image information if it covers interesting structures.

✧ Select **View > No text** to switch off the display of the image text and the scalebar.

Removing input images

Some images may be detrimental to the calculation, for example, images with severe motion artifacts.

NOTE

Deleting an image will remove it from the **Perfusion** task card and exclude it from perfusion calculation but will not remove the image from the local database.

✧ Scroll to the images that you want to remove.

➩ You always remove the images of all slice positions scanned at the same point in time.

✧ Click on the button **Remove Input Image** to delete all images currently visible in the image area.

Segmentation

Segmentation identifies the area of the brain whose perfusion characteristics are to be analyzed. This preparatory step before perfusion calculation combines both contour finding (skull) and the identification of the relevant HU range that defines soft tissue.

Starting segmentation

During segmentation a segmentation mask (pixel area of brain tissue and vessels) is determined for each slice. The calculation of the segmentation mask is always performed with the first image of each image stack.

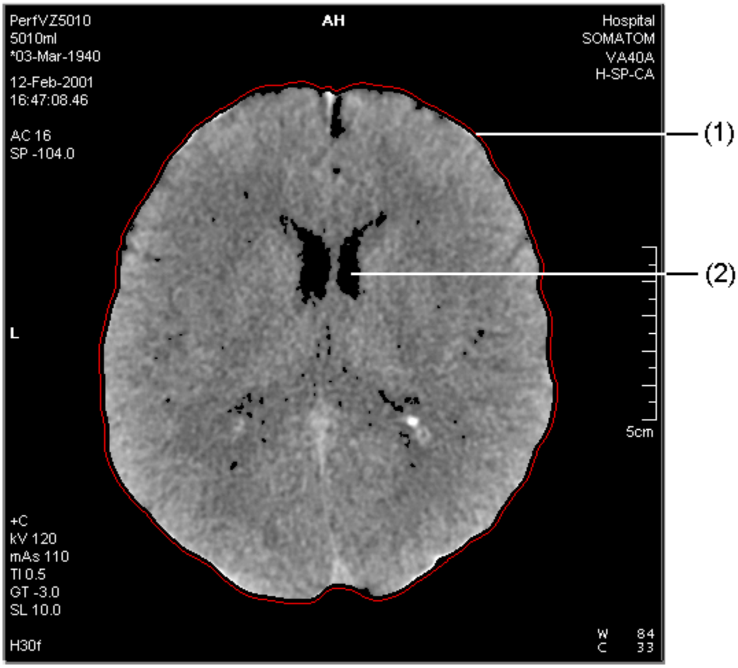
Automatic contour finding identifies the inner skull contour.

➪ In the **Properties** dialog box you can modify the default parameters used for the segmentation calculation.
→ Page P.4–2, *Properties for segmentation*

✧ Click on the button **Segmentation** to start soft-tissue segmentation and automatic contour finding.

The first scan of the series is used for segmentation.

The segmentation results of each slice position are displayed in the corresponding image segments.



(1) Found contour
The area outside found contour and the area within the shrink range are displayed in black (i.e. they will be excluded from further calculation).

(2) All pixels inside the found contour that do not fall within the specified HU range will also be excluded from further calculations (displayed in black).

Bridging defects

If the skull bone does not define a closed area (e.g. an intervening “hole” in the skull bone) you will have to bridge the defect and repeat automatic contour finding.

✧ Click on the **Bridge** button in the control area.

The images that correspond to the first acquisition time are displayed again.

✧ Move the cursor into an image and draw a line to bridge the defect keeping the left mouse key pressed.

✧ Finish the line with a double-click.

➩ If you are not satisfied with the entered line, click on **Bridge** again and repeat the above steps to redraw the line.

✧ Click on the button **Segmentation** to restart soft-tissue segmentation and automatic contour finding.

Vessel definition

Perfusion calculation requires the identification of a vessel (the reference vessel) showing the maximum contrast enhancement. In the next step, the system identifies vessels by comparing enhancement values with the maximum contrast enhancement found in the reference vessel.

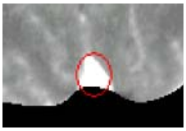
Defining the reference vessel

The reference vessel must be a vessel large enough and sufficiently orthogonal to the scan section, so that it does not exhibit partial volume effects. For a typical slice through the basal ganglia this is the superior sagittal sinus.

Reference Vessel

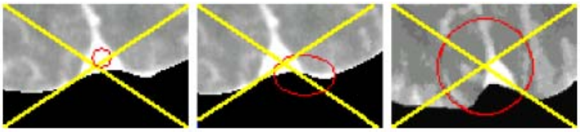
✧ Click on the **Reference Vessel** button.

The system calculates the maximum intensities over all images of each slice position and maps them in MIP images.



✧ Draw an ellipse around the superior sagittal sinus in a suitable MIP image.

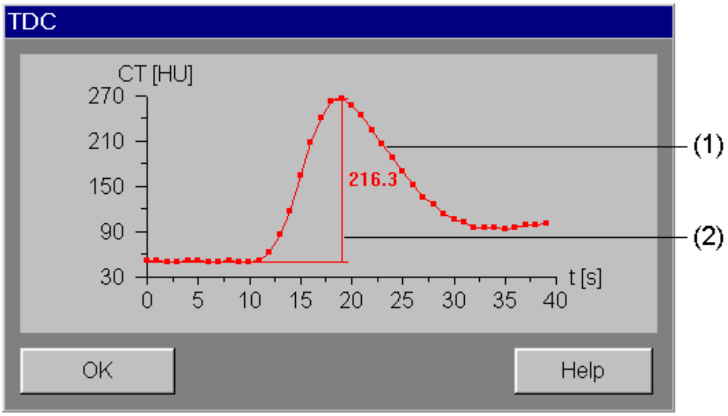
➩ The ellipse can be a little larger than the reference vessel but must not be significantly smaller or cut across it, e.g.:



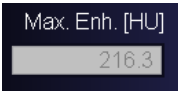
➩ If the ROI is drawn incorrectly or severe motion occurred, the system issues an error message. In that case draw a new (smaller) ROI.

TDC dialog box

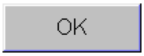
As soon as you release the mouse button, the enhancement curve of the reference vessel is calculated and displayed in the **TDC** dialog box.



(1) Time density curve (TDC)
(2) Point in time and numerical value of maximum enhancement


Max. Enh. [HU] 216.3

The maximum enhancement value is also entered into the **max. Enh.[HU]** field in the control area of the task card



✧ Confirm the reference vessel definition with the **OK** button.

➪ If the TDC curve is not as expected redraw the ellipse around the superior sagittal sinus.

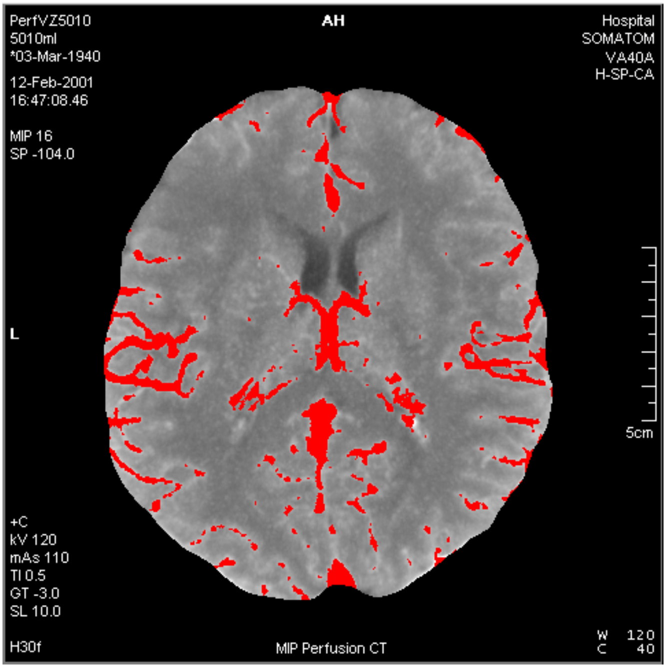
Performing vessel definition

In this step, any area of the brain showing at least a certain percentage of the maximum contrast enhancement found in the reference vessel will be identified as a vessel in the MIP image.

Starting vessel definition

✧ Click on the **Define Vessel** button to start detection of the blood vessels.

The vessels identified will be marked with color in the MIP images.



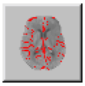
Changing the threshold

10% is a typical **Relative Threshold** for vessel definition. You may want to choose a slightly higher or lower value depending on the bolus quality found in your study.


Rel. Thresh. [%]
12

✧ Click on the up/down arrows of the **Rel. Threshold** spin box until the main vessels are clearly visible.

Or



✧ Enter a numerical value in the spin box and click on the **Define Vessel** button to apply the new threshold.

➪ 8 to 12% are percentages commonly used.

NOTE

Enter a threshold such that most of the vessels are identified and colored as vessels but avoid creating too many single colored pixels.

For low flow rates, a threshold of up to 20% may be necessary.

Perfusion result calculation

Perfusion calculation performs pixel-by-pixel analysis of the contrast enhancement curve within the area identified during segmentation. The results of this calculation are mapped in a set of parameter images that display various aspects of cerebral perfusion.

Perfusion calculation with optimization

The main purpose of the optimization mode of Perfusion CT is to reduce the noise caused by the relatively small enhancement in areas with low perfusion. In general, the quality of the result images is significantly better if the optimization option is used.

➪ In the **Optimization Limits** dialog box expert users can modify the parameters applied in the optimization algorithm.
→ Page P.4–5, *Modifying the optimization limits*

Starting calculation

✧ Ensure that **Optimize On/Off** is activated (default setting).

➪ With the **Optimize On/Off** button deactivated, the system performs the perfusion calculation without optimization and displays the parameter images on completion.

✧ Click on the **Calculate** button to initiate perfusion calculation.

The program now identifies the earliest onset of contrast enhancement and the minimum rise time.

Optimization results

The results of the optimization are displayed in the **Optimization** window (TDC and numerical values of the optimization parameters). In addition, the areas with the earliest start and shortest rise times are mapped in the MIP images.

Lower Limits

Start [s] 6.9

Rise [s] 5.0

Upper Limits

Start [s] 15.9

Peak [s] 27.9

☐ Continue without optimization

Max. Enh. [HU] 216.5

Rel. Thresh. [%] 11

✧ Check whether the detected areas are early arteries and whether the **TDC** curve is as expected.

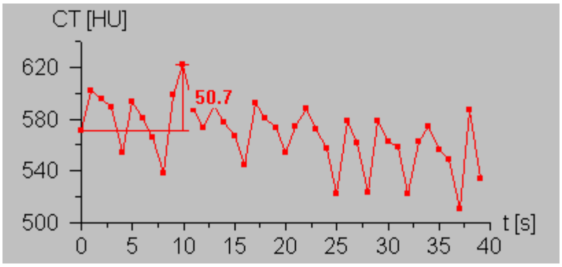
OK

✧ Click on **OK** to perform the perfusion calculation with optimization.

Perfusion calculation without optimization

If the detected areas are no early arteries or if the TDC curve is unreasonable you can perform the perfusion calculation without optimization or adjust the optimization limits manually.

Example (aberrant TDC curve)



Switching off optimization

☑ Continue without optimization

✧ Check **Continue without optimization** in the **Optimization** dialog box and confirm with **OK**.

The perfusion calculation is then performed without optimization.

Manual adjustment

OK

✧ Click on **OK** to conclude the perfusion calculation with optimization (this will produce incorrect results).

✧ Adjust the optimization limits.
→ Page P.4–5, *Modifying the optimization limits*

✧ Click on the **Calculate** button to repeat perfusion calculation with the new optimization parameters.

Displaying result images

After you have started the perfusion calculation, the system produces a set of up to seven parameter images showing various aspects of perfusion.

Sets of result images

The system generates a standard set of parameter images and additional parameter images depending on the configuration.
→ Page P.5–2, *Calculation settings*

Standard set

- **MIP**
  Temporal Maximum Intensity Projection (over the full time span)
- **Flow**
  Cerebral blood flow image (ml/min/100ml)
- **Blood Volume**
  Blood volume image (relative volume ratio of blood). The image is scaled in 1000:1, therefore e.g. a value of 30 in the image means 3% blood volume.
- **Time to Peak**
  Time of local peak enhancement. The image is scaled in 0.1 s, therefore e.g. a value of 182 in the image means 18.2 seconds. If optimization is turned on, the zero time point is set to the lower limit for the time to start.

Optional set

The following parameter images are optionally calculated:

❏ **Average**
Averaged image

❏ **Peak Enhancement**
Maximum contrast enhancement

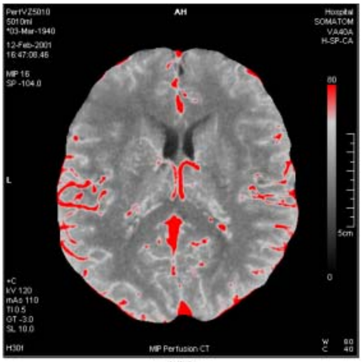
❏ **Time to Start**
Time of local perfusion onset (the image is scaled in 0.1 s as above). If optimization is turned on, the zero time point is set to the lower limit for the time to start.

Arrangement of result images

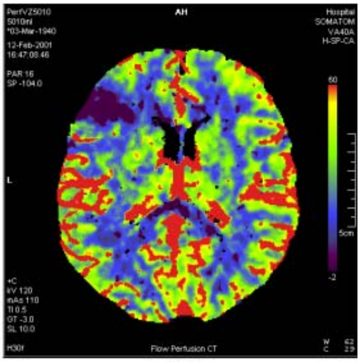
The result images are displayed according to image type and slice position.

Examples

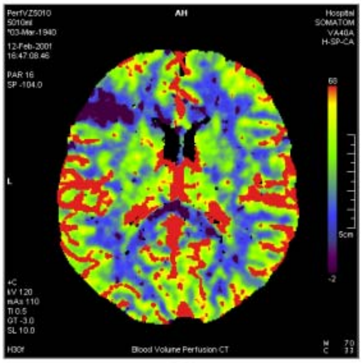
Perfusion calculation at e.g. two slice positions (multi row) and at one slice position (single row*, in square brackets):



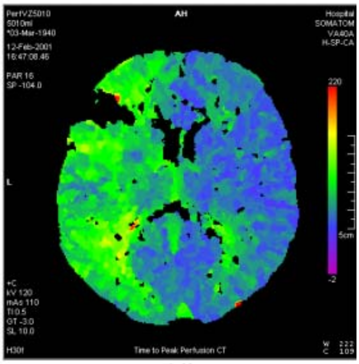
(1)



(2)



(3)



(4)

(1) **MIP** image in segment 1/2 [segment 1*]
(2) **Flow** image in segment 3/4 [segment 2*]
(3) **Blood Volume** image in segment 1/2 on the second page [segment 3*]
(4) **Time to Peak** image in segment 3/4 on the second page [segment 4*]

Color and gray scale representation

Perfusion CT allows the display of parameter images in color similar to nuclear medicine. If used appropriately, color can be a powerful tool for the optimal presentation of findings.

If used inappropriately, however, display in color can easily suppress or overemphasize certain pathological findings. The continuous gray scale display of the result images is much less sensitive to such effects.

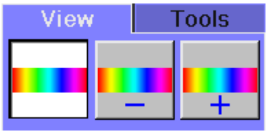
CAUTION

Source of danger: Inappropriate use of color display

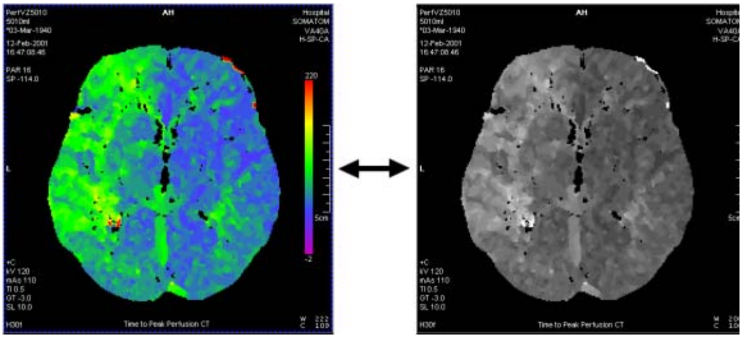
Consequence: Certain pathological findings are suppressed or overemphasized

Remedy: Use continuous gray scale display as reference for diagnosis and use color with care

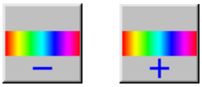
Color and gray scale



- Click on the **Color** button on the **View** subtask card to toggle between color and gray scale presentation of the images.



Windowing color images



- Move the mouse left or right in an image keeping the center mouse key pressed (fast windowing).
- Click on the **Color-** or the **Color+** button to fine-adjust the coloring of the result images.

The color palette in all color images of the same type as the one currently active will be updated accordingly.

CHAPTER
P.3

Evaluating and Documenting Results

In addition to perfusion calculation this program also allows you to calculate and display parameter values for regions of particular interest.

❏ You can evaluate individual ROIs or compare parameter values of the same section of the right and left half of the brain.

❏ With the TDC function you can perform TDC analysis at any position in an image.

At the end of your evaluation save your result images (grey scale or color) and expose selected images on film for documentation.

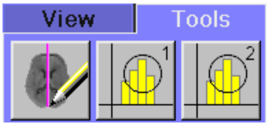
Evaluating result images

You can evaluate individual regions of interest in an image or you can mirror ROIs along a midline to compare parameter values of the same section of the right and left half of the brain. ROI only works in gray-scale presentation.

Evaluating ROIs

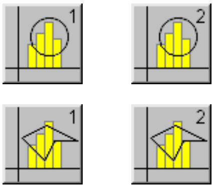
You can draw up to two individual ROIs in an image.

✧ Switch to gray scale presentation of the images.
→ Page P.2–24, *Color and gray scale*



✧ Click the **Tools** subtask card into the foreground.

Drawing ROIs



✧ Click on the button **Circular ROI 1** / **Circular ROI 2**.

Or

✧ Click on the button **Freehand ROI 1 / Freehand ROI 2** to draw a a polygon or freehand region.

✧ Draw the corresponding region of interest in one of the parameter images.

As soon as you release the mouse button (circular ROI) or perform a double-click (freehand ROI), the ROI evaluation results are calculated and displayed for all images.
→ Page P.3–4, *Evaluation Results for ROI 1 and ROI 2*

➩ If you have misplaced a ROI you can correct it by simply repeating the drawing.

Removing ROIs

✧ In order to delete a specific ROI click on the respective **ROI** icon of the same number twice.

Or

✧ Call up **Edit > Delete Graphics** to clear the images of all previously drawn ROI graphics and labels.

This also resets all selections and settings so far made so that you can start ROI evaluation anew.

Mirroring ROIs

You can mirror ROIs along a midline to compare parameter values of the same section of the right and left hemisphere of the brain.

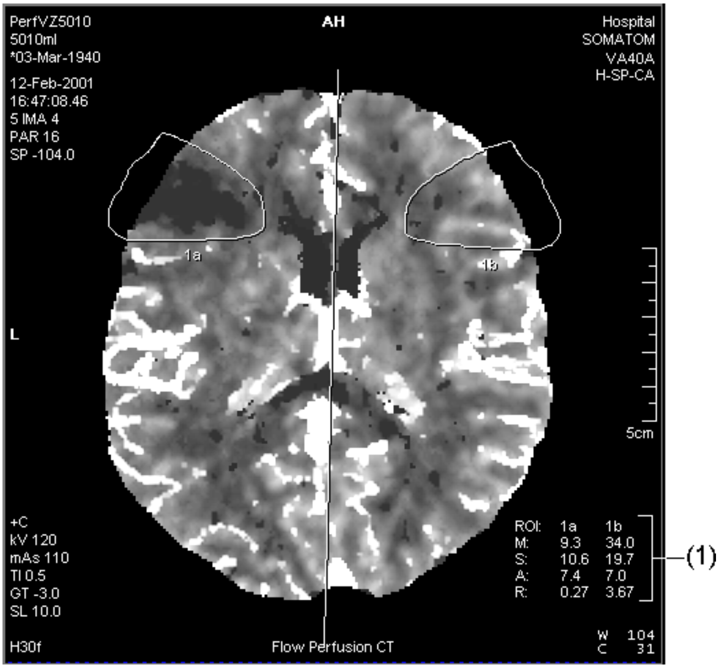
✧ To mirror evaluation ROIs, click on the **Midline** button.

✧ Draw a symmetry axis into one of the displayed images keeping the left mouse key pressed.

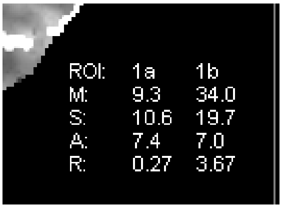
All existing ROIs will be mirrored. As soon as you draw a new ROI, it is mirrored around this axis, too.

Evaluation Results for ROI 1 and ROI 2

The evaluation results appear as a text overlay on the images. You can select and reposition the results with the mouse.



ROI:	1a	1b
M:	9.3	34.0
S:	10.6	19.7
A:	7.4	7.0
R:	0.27	3.67



ROI:	1a	1b
M:	9.3	34.0
S:	10.6	19.7
A:	7.4	7.0
R:	0.27	3.67

(1) **M:** Mean value (excluding background and CSF space. Vessels are only suppressed when configured)
S: Standard deviation
A: Area of all pixels (in cm^2) for which the mean value is calculated
R: Ratio of mean of ROIs. Means are compared according to the following rules:
- ❑ Without mirroring ROIs at the midline:
  Mean of ROI 1a to mean of ROI 2a and vice versa
  (Ratio of mean of ROI 2a to mean of ROI 1a)
- ❑ When ROIs are mirrored at midline:
  Mean of ROI 1a to mean of ROI 1b (and vice versa)
  Mean of ROI 2a to mean of ROI 2b (and vice versa)

Displaying Time Density Curves

The TDC function calculates and displays time density curves for any area or small circle of fixed size you select in the image currently displayed.

➪ The time density curve evaluation is only possible directly after the perfusion calculation but not for reloaded parameter images. Note that you cannot evaluate images when displayed in color mode.

TDC ROI and TDC Lens

✧ Click on the button **TDC ROI** to calculate the time density curve for an area in the result image.

✧ Draw the ROI in the image.

Or

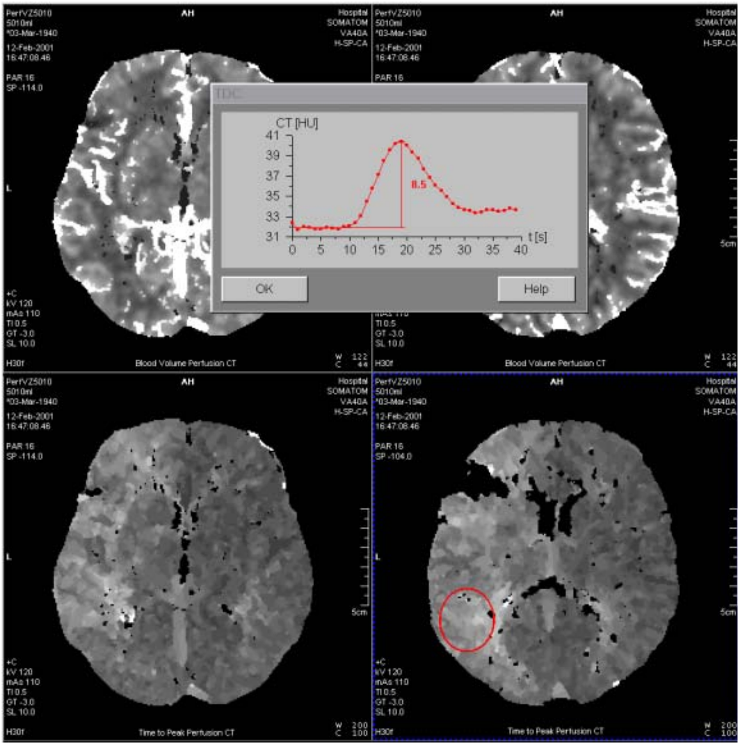
✧ Click on **TDC Lens** to calculate the TDC for a small circle of fixed size in the image.

✧ Click at the position where you want to have the TDC calculated.

➪ In **Perfusion Configuration** you can change the size of the circular **TDC Lens** area.
→ Page P.5–5, *TDC Lens*

TDC dialog box

The time density curve is displayed in the **TDC** dialog box.



➪ You can draw a new ROI or evaluate a different position in the image using the **TDC Lens** without closing the **TDC** dialog box.

OK

✧ Click on **OK** to close the **TDC** dialog box again.
The TDC Lens/ROI is no longer displayed.

Storing and filming result images

Before you finish evaluation store the result images in the local database. From the **Perfusion** task card, you can film your result images quickly and easily for documentation purposes.

Storing result images

You have two possibilities for saving resultant images of a Perfusion CT calculation to the local database:

❑ **Save Set**
Save a complete set of parameter images (all images in a series). This set is always saved as grayscale images without graphics and can be reloaded to **Perfusion** for further evaluation and color display.

❑ **Save single images**
These are saved depending on the current display option as grayscale images or as color images (DICOM RGB format).

Save Set

✧ Click on the button **Save Set**.

The complete set of parameter images is saved to the local database as a grayscale series (without graphics) per patient. The set is named **Perfusion CT Set**.

Save single images

✧ Select the image(s) you want to save.

Or

✧ Call up **Edit > Select Series** in the main menu or **Select Series** in the popup menu (right mouse key) to select the complete series.

Depending on the current display option, the images will be saved as grayscale or color images.

✧ Click on **Save** to store your selection.

The images are saved per patient in the local database. The series created are named **Perfusion CT Gray** or **Perfusion CT Color**. All subsequent images are collected there.

NOTE

Your can only load grayscale images back to Perfusion for further evaluation.

Color images can be viewed using the **Viewing** task card and printed by copying them to the **Filming** task card.

Filming result images

You can film the results of a Perfusion evaluation directly from the task card quickly and easily.

✧ Select the images that you want to film.

Or

✧ Call up **Edit > Select Series** in the main menu to film the complete series.

✧ Click on **Copy to Film Sheet** to transfer the selected images to the Filming card.

✧ Click on **Expose Film Task** to expose all images on the **Filming** task card to film.

Terminating evaluation

There are two ways to end a Perfusion CT evaluation:

- ❏ Close the current evaluation but keep the **Perfusion** task card open for the next patient.
- ❏ Close the evaluation and the **Perfusion** task card.

Closing evaluation

✧ Click on the button **End Evaluation** in the control area to close the evaluation.

Closing the task card

✧ Call up **Patient > Close Perfusion** in the main menu.

The task card will be closed and the tab disappears.

CHAPTER

P.4

Changing Default Settings

All default settings necessary to successfully perform perfusion calculation are made when Perfusion CT is installed. In general, these settings need not to be modified.

Experienced users, however, can adapt a number of calculation parameters to their personal preferences:

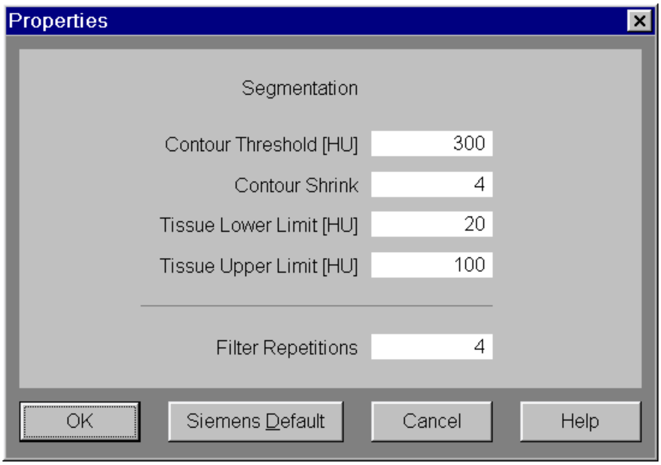
❏ In the **Properties** dialog box, you can adapt the default property values for segmentation to your needs.

❏ In the **Optimization Limit** dialog box, you can enter values for areas with suspected late enhancement onset.

Properties for segmentation

In the **Properties** dialog box, information about the segmentation parameters currently used are displayed. You can change these default settings and apply your changes to the actual calculation.

✧ Call up **Edit > Properties** in the main menu to display the **Properties** dialog box.



Properties

Segmentation

Contour Threshold [HU] 300

Contour Shrink 4

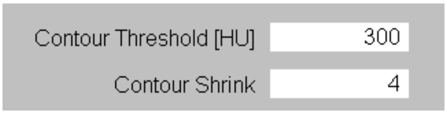
Tissue Lower Limit [HU] 20

Tissue Upper Limit [HU] 100

Filter Repetitions 4

Contour finding

Automatic contour finding identifies the inner skull contour. This calculation is based on a contour threshold value which you can set in the **Properties** dialog. The found contour can be shrunk by a few pixels to prevent borderline artifacts.



Contour Threshold [HU] 300

Contour Shrink 4

✧ Change the **Contour Threshold [HU]** value, if necessary.

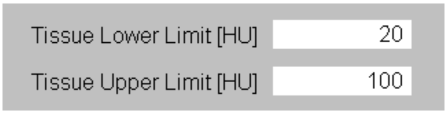
➩ A threshold HU value of 300 is recommended for the skull bone.

✧ Change the **Contour Shrink** value, if necessary.

➩ A value of 4 pixels is recommended, but you may want to enter a higher value to compensate motion artifacts.

Tissue limits

The range between the **Tissue Lower Limit** and **Tissue Upper Limit** (in HU) defines the soft-tissue window of the brain. All pixels within this range are included in the perfusion calculation.



Tissue Lower Limit [HU] 20

Tissue Upper Limit [HU] 100

✧ Set the **Tissue Lower Limit [HU]** to HU 10 - 20 (depending on the patient) to exclude cerebrospinal fluid.

✧ Set the **Tissue Upper Limit [HU]** to HU 100 or lower (depending on the patient) to exclude potential vascular calcification.

Filtering

The **Filter Repetitions** value determines the intensity of smoothing. Smoothing is a process that improves the quality of the calculated parameter images by decreasing the noise level of the original dynamic CT images.

Four repetitions are usually sufficient, but you may want to enter a higher value depending on the image quality of the original images.

Filter Repetitions 4

✧ Enter the number of repetitions in the input field.

Modifying the optimization limits

You can edit the optimization limits only after an initial calculation of Perfusion CT.

Purpose of optimization

Optimization improves analysis in the low-flow regions. The quality of parameter images is thus significantly better if optimization is enabled.

- ❏ With optimization on, the system analyzes the dynamic image series in order to identify the earliest onset of contrast enhancement and the minimum rise time. These times are the **Lower Limits**.
- ❏ In order to adjust the **Upper Limits** for the time of contrast enhancement, start and peak values are used. The upper limits have been calculated during the reference vessel definition and are adequate in most cases.

Optimization restricts the range of parameter variations during the fit of the tracer kinetic model by setting limits to several easily definable time points. If these time limits are set incorrectly so as to overrestrict the model's capability to fit the data, incorrect results may be obtained.

Please bear in mind that the behavior of the optimization algorithm depends significantly on the prior data. This data is valid only for the recommended standard slice through the basal ganglia, and only if the superior sagittal sinus is used as the reference vessel.

CAUTION

Source of danger: Setting of inapproriate limits for the optimizaion algorithm

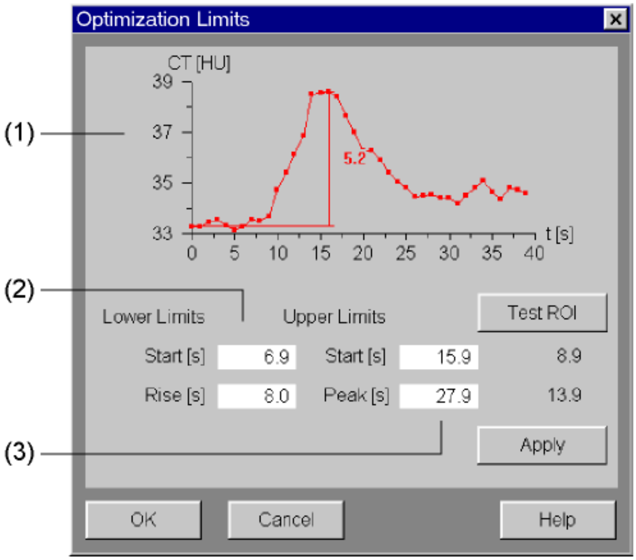
Consequence: Incorrect values may result

Remedy: Only modify the limits manually if you have an adequat understanding of what the modification of these time points entails. Use the images calculated without optimization as a control reference. Do not use optimization in case of any doubt.

Setting new optimization limits

Use the **Optimization Limits** dialog box to adjust the values of the optimization limits.

✧ Call up **Edit > Optimization** in the main menu to display the **Optimization Limits** dialog box.



Lower Limits		Upper Limits		
Start [s]	6.9	Start [s]	15.9	8.9
Rise [s]	8.0	Peak [s]	27.9	13.9

(1) TDC for testing ROI (initially empty)

(2) Earliest onset of contrast enhancement and minimum rise time identified in the images (**Lower Limits**).

(3) Upper limits calculated during reference vessel definition

Drawing a test ROI

- Select a parameter image where late enhancement onset areas are visible.

- Click on the **Test ROI** button in the **Optimization Limits** dialog box.
- Draw an elliptical ROI over the area of suspected late enhancement onset.

When you release the mouse button, the system displays the enhancement curve for the selected ROI. You can repeat drawing the ROIs as many times as you need to.

Applying new limits

If you find higher limit values than the ones calculated for the reference vessel definition, you can transfer the new values into the upper limit boxes.

- Click on the **Apply** button for the new values to take effect.

> **NOTE**
>
> The new values will only be accepted by the system if they are higher than those calculated during the definition of the reference vessel.
>
> Alternatively you can also enter the values into the **Start [s]** and **Peak [s]** limit fields.

Modifying Lower Limits

Start [s] 6.9

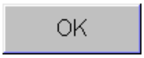
Rise [s] 8.0

✧ Enter the value for the earliest onset of contrast enhancement into the **Start [s]** field.

✧ Enter the value for the minimum rise into the **Rise [s]** field.

➩ When you apply the results of the **Test ROI** function later on, these values will be overwritten.

Restarting calculation



✧ Click on **OK** to close the **Optimization Limits** dialog box.

Or

✧ Click on **Cancel** to exit without changing the limit values.

✧ Click on the **Calculate** button to repeat the perfusion calculation with the new limit values.

CHAPTER
P.5

Configuring Perfusion CT

All program settings necessary to successfully perform perfusion calculation are made when Perfusion CT is installed.

You can change the user-specific parameter settings for Perfusion CT evaluation in the **Perfusion Configuration** window. The changes will be applied at the next evaluation session.

You can configure the following settings in the **Perfusion Configuration**:

❑ Enable/disable the calculation and output of additional parameter images

❑ Special parameter settings for perfusion calculation and evaluation

✧ Call up **Options > Configuration** in the main menu.

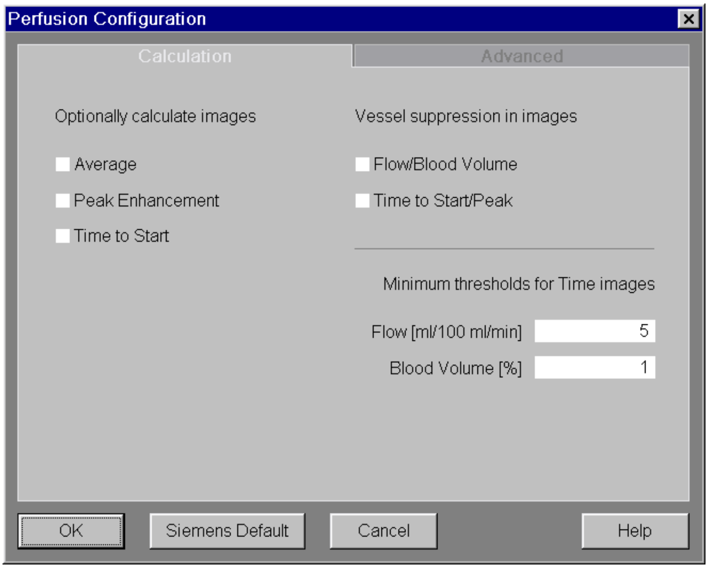
✧ Double-click on the button **Perfusion CT** to display the **Perfusion Configuration** window.

In the **Basics** part of this manual you can read how to call up and exit configuration windows, save changes, or reset settings back to the as-delivered state.
→ Chapter A.2, *Configuring the User Interface*

Calculation settings

On the **Calculation** subtask card, you can enable the calculation of additional result images, configure the suppression of vessels, and set minimum thresholds for time images.

✧ Click the **Calculation** subtask card into the foreground.



Optionally calculate images

☐ Average

☐ Peak Enhancement

☐ Time to Start

Vessel suppression in images

☐ Flow/Blood Volume

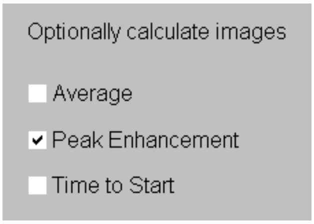
☐ Time to Start/Peak

Minimum thresholds for Time images

Flow [ml/100 ml/min] 5

Blood Volume [%] 1

Optionally calculated images



Optionally calculate images

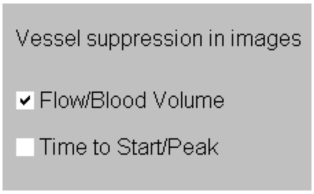
☐ Average

☑ Peak Enhancement

☐ Time to Start

✧ Check the check boxes of the result images which you want to have calculated in addition to the standard set.
→ Page P.2–20, *Sets of result images*

Vessel suppression



Vessel suppression in images

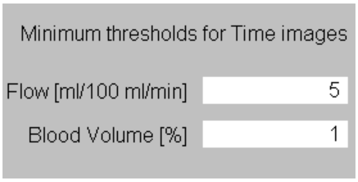
☑ Flow/Blood Volume

☐ Time to Start/Peak

✧ Check the check boxes of the result images in which you want to have the display of vessels suppressed.

Threshold for Time Images

Only pixels that have a flow value (in ml/100ml/min) and blood volume value (in %) higher than the value entered here, will be displayed in the time images.



Minimum thresholds for Time images

Flow [ml/100 ml/min] 5

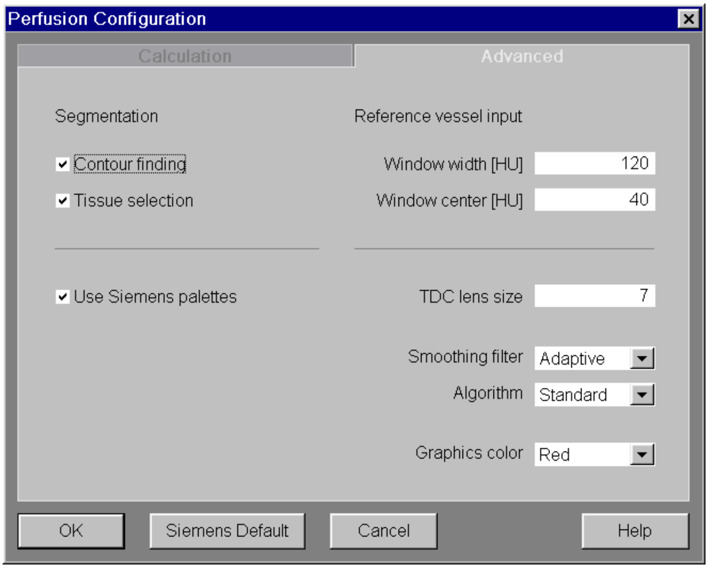
Blood Volume [%] 1

✧ Enter the new threshold values in the input fields.

Advanced settings

On the **Advanced** subtask card, you can configure non-standard segmentation.

✧ Click the **Advanced** subtask card into the foreground.



Segmentation

☑ Contour finding

☑ Tissue selection

☑ Use Siemens palettes

Reference vessel input

Window width [HU] 120

Window center [HU] 40

TDC lens size 7

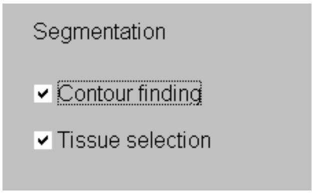
Smoothing filter Adaptive

Algorithm Standard

Graphics color Red

Segmentation

The check boxes enable preparation steps for the segmentation. Both check boxes are usually checked.



☑ Contour finding

☑ Tissue selection

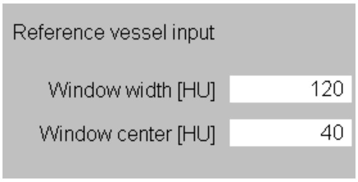
✧ Disable one or both check boxes if you want to perform a non-standard calculation.

❑ **Contour finding**
Automatic contour finding identifies the inner skull contour, if enabled. The contour defines the area of the CT image within which perfusion will be calculated.

❑ **Tissue selection**
The program defines the soft-tissue window of the brain, if enabled. All pixels within a given HU range are included in the perfusion calculation.
→ Page P.4–2, *Properties for segmentation*

Reference vessel input

Initial window setting for the MIP image display during reference vessel input.
→ Page P.2–13, *Defining the reference vessel*



Window width [HU] 120

Window center [HU] 40

✧ Change the window values in the input fields, if necessary.

TDC Lens

Predefined size of the **TDC Lens** on the **Tools** subtask card.

TDC lens size 7

✧ Overwrite the numerical value if you want to change the size of the **TDC Lens**.

Smoothing filter

Prefiltering reduces the set of loaded CT images to a 256 matrix, the matrix size used for perfusion calculation. The purpose of this step is to improve image quality of calculated parameter images by decreasing the noise of the input images.

Two filter options are available:

- Adaptive - a vessel adaptive filter (running mean filter) which smooths vessels and tissue separately.
- Gauss - a Gauss filter that does not differentiate between tissue types.


Smoothing filter Adaptive

✧ Select the smoothing filter in the selection list.

NOTE

It is strongly recommended to only use the **Adaptive** option.

Algorithm

In the **Algorithm** selection list you can chose between two calculation algorithm, **Standard** and **No Smooth**.


Algorithm Standard

✧ Select the **Standard** algorithm (default setting).

Or

✧ Select No Smooth, if you want to deactivate smoothing over time.

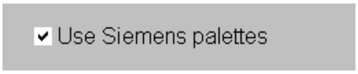
Graphics color


Graphics color Red

Here you can set the color for the representation of all graphic objects (skull contour, ROIs, and curves).

✧ Select a **Graphics color** in the selection list

Color palette


☑ Use Siemens palettes

If enabled (default setting), Perfusion CT automatically assigns a suitable color palette for each image type, whenever you switch to color representation.

If disabled, you can assign a customized color palette (in preparation). Please contact your application specialist.

CHAPTER

P.6 Reference Information

In this chapter you will find additional information as well as recommendations to be considered for Perfusion CT evaluation:

- ❏ Application hints for the examination of acute stroke
- ❏ Interpretation of Perfusion CT results
- ❏ Background information

At the end of this chapter, a list of references is appended for further information.

Application hints for the examination of acute stroke

Perfusion CT is a software application processing standard dynamic CT data of the brain. Therefore, the preparatory steps and guidelines for the application of contrast, the scan settings and the timing of the examination are similar to any dynamic CT examination after injection of a compact bolus of contrast.

The following facts and recommendations are included as a guide to physicians. They are intended as help during the examination of patients with the clinical suspicion of acute ischemic stroke, after standard CT has excluded cerebal hemorrhage.

The settings and parameters mentioned below are not necessarily mandatory. They were used in clinical studies [4, 5, 6, 8] but they might have to be adapted to the individual patient if required by the specific situation.

Slice selection

The examination slice is best positioned at the level of the basal ganglia in order to include those vascular territories of the brain that are frequently affected by perfusion impairment associated with acute stroke in the carotid territory.

The slice angulation should be adjusted perpendicular to the posterior segment of the superior sagittal sinus. The example images also illustrate this slice selection.

To minimize the influence of noise, the largest possible slice width should be used (typically 10 mm). For Multi-Slice systems two adjacent 10 mm slices are usually the best choice.

Contrast injection

Perfusion CT of the brain is based on the evaluation of the first passage of a bolus through an organ that has:

❏ a very short transit time (approx. 3 to 5 seconds) and

❏ a relatively small fractional blood volume (approx. 2 to 5%).

The former requires a relatively compact bolus for optimal time resolution, the latter a certain minimum amount of contrast media for an optimal signal to noise ratio.

In the controlled clinical studies [4, 5, 6, 8], typically 50 ml of non-ionic contrast (300-mg/ml iodine and more) were used. Because of the short transit time, image quality of perfusion images is best if the bolus is administered in as short a timespan as possible. The studies quoted above used flow rates of 10 ml/s and more for the injection of 50 ml of contrast media into an antecubital vein.

There is rising evidence, however, that by sacrificing some of the spatial resolution, the examination can also be done with smaller amounts of contrast (35 to 40 ml) and correspondingly smaller flow rates of 6 to 8 ml/s, if flow rates of 10 ml/s are considered not recommendable for a specific patient. In these cases it is particularly helpful to consider a saline chaser bolus. In any case, a state-of-the-art power injector is recommended.

Additional measures to facilitate the injection, like using a large gauge cannula (up to 14 gauge were used in the clinical studies, 16 or 18 are usually sufficient) and warming the contrast media to body temperature to reduce its viscosity, should be considered.

As with any contrast medium application, verify that the particular models and brands that you use in the chain injector -> contrast medium -> cannula are approved by their respective manufactures for the use with the parameters you select.

Data acquisition and timing

To reliably resolve the fast hemodynamics of the brain it is essential to use high temporal resolution. A suitable dynamic mode must be used (dynamic Multiscan or fast dynamic sequence)! The timing and the total examination time have to fulfill two requirements:

- To get a stable baseline, the first few seconds (the absolute minimum is 2 seconds) of the data acquisition should fall in the pre-contrast phase before contrast enhancement begins.
- The examination should optimally continue until late bolus peak arrival in areas with collateral supply has been covered.

The studies have shown that a total examination time of 40 seconds is usually sufficient to cover this time interval. An example for an injection protocol could be:

- 40 ml injected in 5 seconds,
- start delay set to the minimum value possible (4s),
- injection and scan started at the same time (this means the actual scan starts 4 seconds after the injection begins)
- data acquisition for 40 seconds.

Such a standard protocol may be slightly modified for specific reasons; for instance, the start delay can be increased by a few seconds for patients with very low cardiac output.

Image reconstruction

Images should be reconstructed with a sampling frequency of at least 1 image per second. Experience has shown, however, that for routine applications one image per second is also sufficient.

For scientific studies on sub-second scanners, a higher temporal resolution can be used (one image every 0.5 or 0.75 seconds).

For continuously acquired data the image sampling frequency should not be less than the rotation frequency.

A „standard” reconstruction kernel should be used, details depend on viewing requirements.

Perfusion CT contains its own smoothing procedure.

Interpretation of Perfusion CT results

For the interpretation of Perfusion CT images of patients with symptoms of acute stroke it has to be kept in mind, that even on multi-slice scanners, Perfusion CT is not a volume technique. This means that very small ischemic lesions completely outside the scan level can potentially be missed.

A controlled clinical study carried out on 74 patients, shows however, that even with this limitation Perfusion CT had 91% sensitivity and 100% specificity to detect early ischemia [4, 5, 6].

- 100% specificity means that everything that showed up as perfusion disturbance in Perfusion CT was really there (no false positives).
- 91% sensitivity means that 9% of ischemic lesions did not show up on the perfusion images because they were completely outside the scan field.

The impact of these findings on patient management depends on the treatment strategy used. In the setting of the study it was concluded that none of these small lesions would have been treated under the implemented treatment regime of the hospital.

This conclusion can, of course, not be generalized. It is nevertheless important to keep this limitation in mind and interpret negative Perfusion CT results appropriately in combination with all the available clinical and diagnostic information. The high sensitivity and specificity of Perfusion CT has been confirmed in a second independent study on 70 patients [8].

It has meanwhile also been shown that Perfusion CT parameter images can additionally be used to successfully discriminate between core infarct areas and tissue at risk with an accuracy of about 80% [9].

Background information

Dynamic scan modes are mostly used to display and evaluate the temporal change of iodine contrast enhancement in organs with the aim to assess potential disturbances of their perfusion. Sets of dynamic images are either evaluated using the standard **Dynamic Evaluation** application or specialized analysis software like the **Perfusion CT** application.

Conventional evaluation techniques have mainly relied on an ROI-based analysis.

Although it has been possible to generate descriptive parameter images with the dynamic evaluation feature for quite a time, the diagnostic value of functional images has only recently become fully apparent during intensive clinical testing of the Perfusion CT software package.

Image quality of parameter images

"Image quality" of perfusion parameter images as a function of the scan parameters of the original dynamic scan sequence is a relatively new issue, which will be addressed briefly in the following text. Additional considerations on patient radiation exposure will also be discussed.

Perfusion CT analyses the increase of CT-numbers caused by iodine enhancement, which is often relatively small and appears on a background of high noise.

- For ROI based approaches, which average over a sufficiently large number of pixels, noise is a minor issue.
- Image generating approaches like Perfusion CT assess changes on a pixel by pixel basis and are therefore more sensitive to noise.

The quality of parameter images depends primarily on the ratio of enhancement and noise. As reducing the noise by increasing the mA settings also increases the patient dose, scan parameters must be optimized to achieve the best signal-to-noise ratio for a given dose.

Slice thickness

Brain perfusion is measured with dynamic CT in a "typical slice" through the basal ganglia. For a low sigma the largest slice width available should always be used.

For most scanners this will be 10 mm, for the Volume Zoom there is a choice of either scanning two adjacent 10 mm slices or one fused 20 mm slice.

Tube voltage

It is a well known fact that materials with high atomic numbers such as iodine have significantly higher CT values for lower kV settings (this is exploited e.g. for Xe CT and Osteo CT). The following data measured on SOMATOM Volume Zoom exemplify this:

kV	80	120	140
Iodine enh. (arb. units)	157	100	85

This effect strongly favors the lowest kV setting, but it is partly counteracted by considerably increased noise levels. To keep image noise constant, for example, 80 kV roughly require a 3-fold increase in mAs over 120 kV.

For constant signal-to-noise-ratio the mAs need to be raised less. Nevertheless, technical generator limitations prohibit on some scanners selecting 80kV with appropriate tube current values.

The standard scan protocols on your scanner for Perfusion CT of the brain take this into account and select the lowest kV setting possible under these restrictions.

Rotation time and mA setting

Dynamic scans of the brain must be done with sufficient temporal resolution to get complete data for the pixel time attenuation curves. These data are best acquired continuously for gap-free coverage. For half second scanners, a fast sequence acquisition can also be used.

It is difficult to determine precise numbers for the minimum temporal resolution and for the minimum mAs settings necessary. These will depend mainly on the required spatial and temporal resolution to answer a specific clinical question. For SOMATOM Plus S systems, on which the bulk of the initial data used in the controlled studies of acute ischemic stroke were acquired, 120 kV, 210 mA, 1.0 second rotation and an image reconstruction increment of 1.0 second provided sufficient image quality to reliably detect in-plane perfusion disturbances in acute stroke.

Because of different geometric setups and kV selection, these settings were adapted to roughly equivalent settings for the newer scanners (refer to the respective standard scan protocols). For acute stroke, the primary indication for which Perfusion CT is released, sub-second rotation times do not appear to significantly improve the clinical diagnosis. Higher temporal sampling rates might be more important for other perfusion disturbances where smaller differences in bolus arrival times than those seen in stroke are clinically relevant. This, however is still an issue under investigation.

The image reconstruction increment should be set at 1.0 sec. On the Volume Class scanners the dynamic sequence mode with a rotation time of 0.5 seconds and a cycle time of 1.0 seconds provide equivalent temporal resolution.

Slice selection

When scanning the brain it is important to keep in mind that the eye lens can be relatively close to the scan region. The eye lens is a radiation sensitive organ that can potentially develop a cataract when exposed to high radiation doses. The eyes should therefore never be in the scan plane! The standard slice through the basal ganglia routinely used for acute stroke assessment is far enough away from the eyes (about 3 cm) to stay far below critical values (see below). For potential scientific studies of the lower brain these issues and resulting limitations must be carefully observed.

Typical dose values

Estimates for the effective dose for typical scan parameter settings of an examination of patients with suspected ischemic stroke range from about 1.5 mSv to about 3 mSv (depending on kV and number of slices selected). This is not significantly larger than the effective dose of a plain cranial CT examination.

The maximum in-slice (surface) dose value can be up to about 500 mGy. The eye lens dose can be estimated from dose profile measurements, which show (data for Plus 4) that for a distance of 1, 2 and 3 cm from the middle of the slice the dose falls off to approximately 13%, 8% and 5% of the maximum value respectively.

Indications for use of Perfusion CT

Perfusion CT is a software application that permits cerebral perfusion imaging based on dynamic CT images continuously acquired after the injection of contrast media.

Parameter Images

The application allows visualization of apparent blood flow in brain tissue and pictorially illustrates perfusion-related parameters (relative cerebral blood flow, relative cerebral blood volume, time to peak) by generating images of cerebral blood flow (CBF), cerebral blood volume (CBV), and local bolus timing (time to peak) from one set of dynamic CT images.

Perfusion CT aids the physician in the assessment of the type and extent of cerebral perfusion disturbances. The software also allows the calculation of mirrored regions of interest and the visual inspection of time density curves.

Scanning level

For examination of patients suspected to suffer from acute ischemic stroke, it is recommended that an appropriate CT scanning level (i.e. level of the basal ganglia) be used in order that those vascular territories of the brain are included, which are frequently affected by perfusion impairment associated with acute stroke in the carotid territories.

With Perfusion CT application, areas of decreased perfusion appear as areas of changed signal intensity (lower for CBF and CBV, higher for the time to peak). Such areas of decreased perfusion have been associated with the presence of ischemic stroke.

Appropriate use

Perfusion CT was designed and tested for the processing of dynamic image sequences of the brain reconstructed with a sampling rate of least 1 image per second. The algorithms used in the software package are primarily optimized for processing standard slices through the basal ganglia. Other levels of the brain can be processed, but the slice should contain the occipital segment of the superior sagittal sinus above the confluence of sinuses.

Clinical trial results support use of the Perfusion CT application on images acquired within the hyperacute phase of ischemic stroke from a single dynamic scan of one slice through the basal ganglia after cerebral hemorrhage has been excluded using standard CT.

With this slice selection, Perfusion CT results showed a sensitivity of 90% and a specificity of 100% to accurately detect and classify the type and extent of the under-lying ischemic process. Sensitivity and specificity of the package when used outside of these recommended guidelines have yet to be established.

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APPENDIX

R

Index, Glossary, and Hints

CHAPTER

R.1 Glossary

Acquisition field center	Center of the *acquisition field plane*.
Acquisition field plane	Plane in which the X-rays penetrate the patient's body.
Algorithm	General computation procedure. *In this case:* image reconstruction from the measured *raw data*.
Anode	Positive electrode in the x-ray tube (source of radiation).
AP	**A**ntero-**P**osterior from front to back
API	**A**utomatic **P**atient **I**nstruction; breathing instructions to the patient.
Archiving	Image data can be transferred to the archive (*CD-R*, *MOD*, magnetic tape) for long-term storage.
Artifact	Structure in a medical image which does not represent any anatomical structure and which impairs the representation of the anatomical structure (e.g. stripes).
Attenuation	The ratio of x-ray beam intensity prior to and after passing through an attenuating object.
Attenuation profile	Local distribution of attenuation values from one direction of projection of the fan beam.
Beam hardening artifact	*Artifact* caused by the change in the x-ray spectrum as radiation passes through the object being scanned.
Bolus	A *CARE* application (optional). With the bolus function you can directly monitor the contrast medium bolus in the ROIs of a reference scan defined by the user. As soon as the preset contrast medium density increase is reached, the examination is triggered.
Calibration	Procedure for adjusting the sensitivity of the individual detector channels; used for correction of measurement data.
CARE	**CARE** (**C**ombined **A**pplications to **R**educe **E**xposure) aims to achieve optimum image quality while at the same time reducing the radiation and contrast medium dose for the patient.
CD-R	**C**ompact **D**isk **R**ecordable

Cluster	A chain of slices acquired rapidly in *Sequence CT* mode within a breath-hold.
Convolution	Mathematical procedure for image reconstruction in computed tomography.
CPU	**C**entral **P**rocessing **U**nit, part of the computer that performs the calculations. The speed of the CPU not only determines factors such as the *RAM* configuration but also the processing speed of the computer.
CT value	Number used to quantify the beam *attenuation* capability of an object. The scale uses water as a reference with a CT value of 0 (air: CT value of –1000).
CT	**C**omputed **T**omography
CTA	**CT A**ngiography Display of the vascular system using *CT*.
CTDI	**CT D**ose **I**ndex, calculated as absorbed dose to lucite PMMA according to 21CFR, § 1020.33. The Integral of the dose profile is calculated along a line perpendicular to the tomographic plane (from **-7T** to **+7T**, *T* is the nominal tomographic slice thickness).
CTDI 100	**CT D**ose **I**ndex, calculated as absorbed dose to air according to IEC 60601-2-44. The Integral of the dose profile is calculated along a line perpendicular to the tomographic plane (from **-50mm** to **+50mm**).
CTDI w	The **w**eighted **CT D**ose **I**ndex (IEC 60601-2-44) is the approximation of the average dose over a single slice in the standard head or body CT dosimetry phantom, expressed in terms of absorbed dose to air (mGy).
Detector	Component of the scanning system which measures the beam intensity after radiation has passed through the object being scanned.
Detector array	System of *detectors* for acquiring radiation intensities.
Density determination	Quantitative evaluation of the *CT values* in a CT image.

DICOM	**D**igital **I**maging and **CO**mmunications in **M**edicine Standard for exchanging medical images.
Digital camera	Camera to which image data is digitally transferred.
Documentation	Transfer of image results to transparent film.
Dose	The total effect of radiation on a defined absorption volume of the body.
Dual Topo	Combination of two *Topograms* with different tube positions (AP and lateral).
Dynamic Multiscan	Scanning technique of continuous data acquisition of multiple *scans* over single slice location.
eff mAs	Effective Milliampere per second. Unit used to calculate a measure for the product of the tube current (mA) and scan time (s) for multi-row detectors. Equivalent to the applied radiation dose. eff mAs = mA * RotTime / [Pitch / number of detector rows]
Fan beam device	CT system in which an arc-shaped detector array and an x-ray tube generating a fan-shaped beam rotate about the patient.
File	Unit of data stored on the storage medium in the computer. A file might be an image, a database or a program.
Flying focal spot	Electromagnetic deflected focal spot for sampling each object detail from two slightly different perspectives. Used to reduce sampling artifacts.
Focal spot	Focal spot of an x-ray tube.
FOV	**F**ield **O**f **V**iew, Reconstruction field with the help of which the tomogram is calculated.
Gantry	Scanning unit of a CT system including the x-ray tube and the *detector array*.
Hard disk	Part of the computer on which data and programs are stored for quick access.
Hardware	Technical physical equipment of a computer system, in contrast to software.
Highlighting	Bright display of a range of CT values during windowing.

HIS	**H**ospital **I**nformation **S**ystem Network for transmitting patient data and images within a hospital
Histogram	Graphic and numerical display of frequency of CT values in a selected region.
Homogeneity	Characteristic of image quality which describes how accurately CT values are measured when a homogeneous object is scanned and displayed by the CT system.
Hounsfield unit	Unit used to measure the *CT value*.
HU	Abbreviation of **H***ounsfield* **U***nit*.
ICT	**I**nterventional **C**omputed **T**omography Acquisition method providing more space between the patient table and gantry, e.g. for use of a C-arm.
Image control system (ICS)	Computer on which the CT scanner is controlled.
Image data compression	Data is compressed when storing images for more efficient use of the storage capacity of the data carrier. The *image matrix* is maintained.
Image evaluation system (IES)	Optional system for image evaluation.
Image matrix	Size of a medical image in *pixels*, e.g.: 512 x 512, 1024 x 1024.
Image mode	In image mode filming, the transfer of the images to the camera takes place image by image. (see also *page mode*)
Image reconstruction	Computation of the CT image from the measured *raw data*.
Image reconstruction system (IRS)	Computer for reconstruction of the CT images from the measured *raw data*.
kV	Kilovolt (1 kV = 1 000 Volt); unit used to measure the tube voltage.
Laser camera	Camera which utilizes a laser beam for exposing images.
LED	**L**ight **E**mitting **D**iode, semi-conductor element that lights up like a bulb.

Low contrast resolution	Resolution of minute image details when there is little differentiation in density. For example, in soft tissue.
mA	Milliampere (1 mA = 1/1000 A); unit used to measure the tube current.
mAs	Milliampere per second product; unit used to measure the product of the tube current (mA) and scan time (s). Equivalent to the applied radiation dose.
MCA	**M**otion Artifact **C**orrection **A**lgorithm: algorithm correcting motion artifacts.
Measurement field	The field from which the *detector array* acquires data in the *gantry*.
MIP	**M**aximum **I**ntensity **P**rojection is a method for 3D display: Along the viewing direction through a volume, the *voxel* with the strongest absorption is displayed in the result image in each case.
MinIP	**Min**imum **I**ntensity **P**rojection, like *MIP* but visualization of the darkest *voxels* (areas of least absorption).
MOD	**M**agneto **O**ptical **D**isk resp. Drive; system for longtime data storage.
Motion artifact	*Artifact* caused by patient movement during the scan.
Mouse	Operating element at the computer to direct the input cursor on the monitor und to adjust window values.
MPR	**M**ulti **P**lane **R**eformatting: a function with the help of which new interfaces of freely selectable orientation from tomograms can be calculated.
MTF	**M**odulation **T**ransfer **F**unction; the frequency-dependent ratio of object contrast to image contrast. The MTF permits qualitative determination of the spatial resolution of an imaging system.
Multiformat camera	Camera with selectable segmented film format; allows for exposures of multiple images on a single film.

Noise	Unwanted interference in the signal caused by random factors and containing no information regarding the object being scanned.
Operating system	Group of computer programs required for general operation of the computer and its periphery.
Osteo CT	Semiautomatic bone mineral density measurement and evaluation method for the quantitive assessment of bone mineral content in the lumbar spine.
PA	**P**osterio **A**nterior
PACS	**P**icture **A**rchiving & **C**ommunication **S**ystem Siemens network for archiving and transmitting medical images.
Page Mode	In page mode filming, the entire film sheet is composed in the computer and then transferred to the camera. (see also *image mode*)
Partial volume artifact	*Artifact* caused by bone structures which are only partially included in the slice being scanned.
Partial scan	*Scan* for which only a section (240°) of the revolution of the X-ray tube is used to measure a body slice.
Phantom	Measuring object whose *weakening* properties is similar to human; Reference body used for functional and quality assurance tests.
Pitch	Term applicable only to *Spiral CT*. It is defined as the ratio of table feed per rotation to slice width of one detector row.
Pixel	Image element of the two dimensional image.
Pulmo CT	Option for evaluation of the *CT values* of the lung tissue.
RAM	Fast, non-permanent memory (**R**andom **A**ccess **M**emory) with which the computer operates. The size of the available RAM determines other factors, including the processing speed. Data are stored long-term on *hard disk*, *MOD* or *CD-R*.
Raw data	Preprocessed measurement data. A raw data file corresponding to each scan is used to reconstruct the CT image.

Real Time Display	Displaying of the measured image synchronous to the scanning and just after the aquisition of a slice (rotation) is finished.
Real Time Recon	Reconstruction synchronous to scanning with an additional delay for displaying the first image.
Rendering	General procedure for constructing images using a computer.
RIS	**R**adiology **I**nformation **S**ystem Network for transmitting patient data and displays to radiology departments, see also *HIS*
ROI	A region of the CT image which can be selected with respect to position, size and shape, and in which quantitative evaluations are performed (**R**egion **O**f **I**nterest).
RTD	**R**eal **T**ime **D**isplay, see there
Scan	CT acquisition of a slice.
Scan time	Period in which radiation is released during a CT scan.
Scatter radiation	Radiation whose direction of dispersion is modified through the interaction with a material.
Secondary slice	Calculation of a selectable slice from a series of adjacent or overlapping slices.
Sequence CT	Scanning technique with single *scans* and optional table feed between the scans.
Slice thickness	Thickness of the slice to be scanned.
Software	Programs of a computer.
Spiral CT	Scanning technique with continuous rotation, continuous data acquisition and continuous table travel.
Spiral scan	Scan technique: the patient table is continually driven into the gantry causing a spiral-shaped movement.
SSD	**S**haded **S**urface **D**isplay: Rendering technique for the 3D surface construction; only *voxels* the *CT values* of which exceed a defined threshold value are considered.
Tomogram	*Scan* of a slice perpendicular to the longitudinal axis of the patient.

Topogram	Frontal or lateral survey *scan*, similar to a conventional x-ray exposure.
Turbo Recon	Option to speed up the reconstruction process.
UFC	**U**ltra-**F**ast **C**eramic *Detectors* from Siemens with short decay time for fast *Scans*.
UPS	**U**ninterrupted **P**ower **S**upply ensures operation even during short power failures.
VAR	**V**olume **A**rtifact **R**eduction Procedure for reducing *partial volume artefacts*.
VRT	**V**olume **R**endering **T**echnique *Rendering* technique for 3D visualization
Voxel	Mapped volume element determined by the pixel size of the image matrix and the slice thickness.
Working memory	see *RAM*
Windowing	Display of a selectable portion of the CT values using optimized contrast range of the monitor.

CHAPTER
R.2

Frequently Asked Questions

General

System Restart

What must I watch out for when restarting the system with two consoles?

✧ First start the Navigator and then the Wizard (optional).

➪ As data are continuously being transferred between the two consoles, you must restart the Wizard whenever you restart the Navigator.
Only then can you be sure that the Wizard is accessing the most up-to-date examination data.

Examination

Comments

What must I watch out for when changing a comment?

✧ Close the patient in all applications.

✧ Select the patient in the **Patient Browser** and call up **Edit > Correct**.

✧ Change the comment text in the **Image Comment** input field. Or select a comment from the selection list.

The comment list is grayed out if the patient is currently being processed in a task card (e.g. **Viewing**).

Parameter inputs

Why have the entries that I made in the spin box with the keyboard not been accepted?

Always remember to confirm the numeric entries you make in a spin box with the return key.

Scan protocols (only Navigator)

How can I create and store a new scan protocol?

✧ Register a fictional patient (e.g. “New Scan Protocol”) with the settings **Head first**, **Supine**.

✧ Set the table height to scan position and the horizontal position to 0.

✧ Load a suitable scan protocol and change it to suit your requirements.

⇨ At least one recon job must be defined.

✧ Call up **System > Run > Save Scan Protocol** and store the protocol under a suitable name.

⇨ You can access the new scan protocol in the **Patient Model Dialog** and (once you have restarted the system) in the **Patient Registration** window.

Scan protocols (only Navigator)

How do I distinguish between examinations for adults and children?

Special scan protocols with a lower radiation dose and other settings for image calculation have been created for examinations of children.

✧ Make sure that you have selected one of these scan protocols and not a protocol for adults if you are examining a child. (e. g. *ChildHead* instead of *HeadSpi*)

Patient Browser

Updating data

Why does the examination that I have just completed not appear in the Patient Browser?

Call up **View** > **Refresh** in the **Patient Browser** menu to update the display.

Patient data

How can I subsequently change the name of a patient?

✧ Select the patient in the **Patient Browser** and call up **Edit > Correct**.

➩ You can only make these changes on the Navigator.

Comments

How can I subsequently add comment texts to a patient?

✧ Call up **Edit > Correct**.

In the dialog box **Correct**, enter your comment text in the **Image Comment** input field.

Data on MOD

How do I export / import raw data to or from MOD?

You can export raw data to MOD and import them in the same way as patient and examination data stored in the local data base.

Data on MOD

How do I save compressed data to MOD?

✧ Call up **Options > Configuration** and double-click on the **Transfer** button.

✧ In the dialog box **Transfer Configuration**, click the **Export** subtask card into the foreground.

✧ Select the MOD drive for data compression.

✧ Select how you want to compress the data in the selection list **Compression Type**.

✧ In the input field **Quality Factor,** select which image quality the compressed data are to be stored in.

Memory capacity (only Navigator)

How do I avoid memory problems in the raw data memory?

✧ Catch up on outstanding reconstructions of your scans quickly. In this way, you avoid that old raw data are occupying storage space.

✧ If you have protected raw data from deletion, remember to remove it again in the **Patient Browser** after you have processed the data.

Viewing

Window values

What should I watch out for when changing window values?

✧ If you want to change/add to default window values, call up **Options > Configuration** in the main menu.

✧ Double-click on the **Viewing** button in the configuration panel.

✧ Call up the **Evaluation General** card.

✧ Overwrite the entry in the field **Default Window** with a new name and confirm with **Apply**.

Restart the console to apply the altered window values.

Window values

How can I apply altered window values without restarting the system?

✧ Change the window value settings in **Viewing Configuration** on the **Evaluation General** card.

✧ Load the series into the **Viewing** task card and assign the new window values via the window **Image > Windowing**.

The next time you restart the system the changes you have made to the window settings are applied.

Image display

How do I display images in the Viewing card in 4:1 layout when only one image is visible in the top left segment?

In the subtask card **View,** change the image display from large format layout to 4:1 layout with the icon buttons.

Image display

How do I display the loaded images in reverse order?

Call up **Sort** > **Reverse order** in the main menu.

APPENDIX

R.3 Subject Index

APPENDIX

R.4 User Interface Index