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ECG Data-Acquisition and Classification System by Using Wavelet-Domain Hidden Markov Models

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***Abstract*— This article is concerned with the classification of ECG pulses by using state of the art Continuous Density Hidden Markov Models (CDHMM's). The ECG signal is simultaneously observed at three different level of focus by means of the Wavelet Transform (WT). The types of beat being selected are normal (N), premature ventricular contraction (V) which is often precursor of ventricular arrhythmia, two of the most common class of supra-ventricular arrhythmia (S), named atrial fibrillation (AF), atrial flutter (AFL), and normal rhythm (N). Both MLII and V1 derivations are used. Run time classification errors can be detected at the decoding stage if the classification of each derivation is different. These pulses are selected for a posterior physician analysis. Experimental results were obtained in real data from MIT-BIH Arrhythmia Database and also in data acquired from a developed low-cost Data-Acquisition System.**

I. INTRODUCTION

The analysis of the electrocardiogram as a diagnostic tool is a relatively old field and it is therefore often assumed that the ECG is a simple signal that has been fully explored. However, there remain difficult problems in this field that are being incrementally solved with advances in techniques from the fields of filtering, pattern recognition, and classification, together with the leaps in computational power and memory capacity that have occurred over the last couple of decades [1].

Electrical instability of the heart, which can be identifiable in the ECG, leads to an abnormal synchronized contraction sequence reducing pumping efficiency. This phenomenon named arrhythmia can be classified as frequent or infrequent (sporadic). Infrequent arrhythmias can be evaluated by long-term ambulatory ECG monitoring (Holter), which produces a quantity of beats greater than 10^5. This huge quantity of data requires automatic diagnosis equipment which allows reducing the time required for diagnosis, increasing the quality of life.

Atrial fibrillation (AF) is perhaps the most common arrhythmia encountered in clinical practice, affecting about 0.5-1% of the general population. AF is not only related to frequent symptoms and reduced quality of life but also constitutes a major risk factor for stroke and mortality from cardiovascular and all other causes [2]. AF pathology is usually diagnosed based on ECG analysis.

Normally continuous monitoring over an extended period of time is required in order to increase the understanding of patient's cardiac abnormalities. Such situations require continuous monitoring by the physicians or alternatively the aid of automated arrhythmia detection equipment, which can be able to identify different types of arrhythmias.

This problem of cardiac arrhythmia detection can be viewed as a pattern recognition problem, since it is possible to identify a finite number of different patterns (arrhythmias).

HMMs have been successfully applied to pattern recognition problems in applications spanning automatic speech recognition [3], image segmentation [4], ECG modeling [5] and cardiac arrhythmia analysis [6]. The most common approach regarding HMMs training is finding the stochastic distribution that best fits the data. Usually this data is derived from the waveform from some type of signal processing usually known as feature extraction method. Recently advanced signal processing techniques as Fourier Transform, Linear Predictive Analysis, Lyapunov Functions [7] and Multivariate Analysis (MA) have been used in order to feature extraction in the HMMs framework. MA allows observing the signal at various scales emphasizing some hidden particularities not viewed at other scales. Wavelet Analysis (WA) is perhaps the most common form of MA. Recently WA was been successfully combined with HMMs especially regarding ECG segmentation [8].

The Wavelet Transform (WT) has the advantage over conventional techniques that time/frequency representation can be more accurately modeled by decomposing the signal in the corresponding scales. When the composition level decreases in the time domain it increases in the frequency domain providing zooming capabilities and instantaneous characterization of the signal [9, 13].

The baseline system is a Bakis or left-to-right Continuous Density Hidden Markov Models (CDHMMs) with a Gaussian Mixture Model (GMM) associated to each model state transition. The ECG signal is previously sliced in singular pulses by using the Pan-Tompkins [10] algorithm and each pulse class is modeled by a six state model, modeling the Q-S, S-T, T, T-P, P and P-Q events. Experimental results from the MIT-BIH Arrhythmia Database using more than 2000 training pulses and 3400 testing pulses are presented. Additionally more than 600 pulses acquired by our Data-Acquisition System from

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patients of the Braga Hospital were tested under supervision of a Cardiologist.

II. DATA-ACQUISITION SYSTEM

In order to assist our medical staff in the diagnosis of their patients a Data-Acquisition System which layout is show in figure 1 was developed. The hardware consists of a printed circuit board (PCB), including signal conditioning, filtering and amplification.

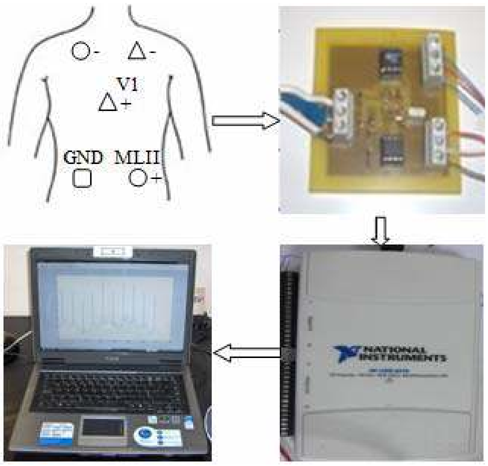


Figure 1 Block diagram of the developed Data-acquisition System

Modified limb lead II (MLII) and modified lead V1 carry sufficient information regarding automatic diagnosis purposes since the electrodes position follows the five leads standard Holter. The electrical activity of the heart is filtered, amplified and converted into a digital signal. A data-acquisition board, NI USB – 6210, set in differential mode was used to control the acquisition hardware and A/D conversion.

Both the software for acquisition and monitoring were developed in MATLAB. A database (DB) for storing the signals for future analysis was also developed. For each acquired signal, a new file is created in the DB with all obligatory parameters filled as described in [11]. Afterwards, MLII and V1 signal named 300 and 301 were converted in to MIT-BIH 212 signal format.

III. WAVELETS ANALYSIS OF ECG

The wavelet transform (WT) is a signal representation in a scale-time space, where each scale represents a focus level of the signal and therefore can be seen as a result of a band-pass filtering.

The most usual way to sample the time-scale plane is on a so-called “dyadic” grid, which means that sampled points in the time-scale plane are separated by a power of two.

As the scale represents the level of focus from the which the signal is viewed, which is related to the frequency range involved, then digital filter banks are appropriated to break the signal in different scales (bands). If the progression in the scale is “dyadic” the signal can be sequentially half-band high-pass and low-pass filtered.

The output of the high-pass filter represents the detail of the signal. The output of the low-pass filter represents the approximation of the signal, for each decomposition level, and will be decomposed in its detail and approximation components at the next decomposition level, and the process proceeds iteratively in a scheme known as wavelet decomposition tree, which is shown in figure 2. After the filtering half of the samples can be eliminated according to the Nyquist’s rule, since the signal now has only half of the frequency.

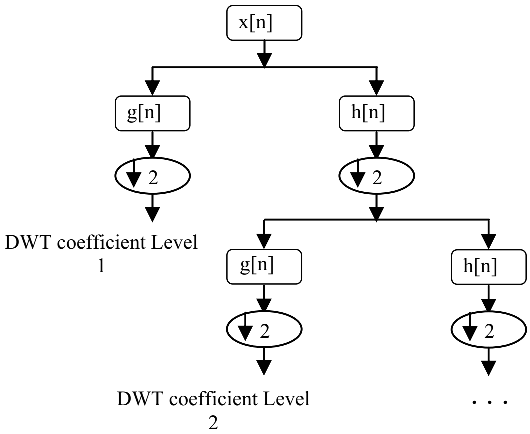


Figure 2 Wavelet decomposition tree

This very practical filtering algorithm yields as Fast Wavelet Transform (FWT) and is known in the signal processing community as two-channel subband coder [12].

One important property of the Discrete Wavelet Transform (DWT) is the relationship between the impulse responses of the high-pass (g[n]) and low-pass (h[n]) filters, which are not independent of each other and they are related by

$$g[L-1-n] = (-1)^n h[n] \tag{1}$$

where L is the filter length in number of points. Since the two filters are odd index alternated reversed versions of each other they are known as Quadrature Mirror Filters (QMF). Perfect reconstruction requires, in principle, ideal half-band filtering. Although it is not possible to realize ideal filters, under certain conditions it is possible to find filters that provide perfect reconstruction. The most famous ones were developed by Ingrid Daubechies and they are known as Daubechies wavelets. In the ambit of this work only the tree least scales of Daubechies wavelets with 2 vanishing moments (db-4) were used.

The multiresolution analysis based on the DWT can enhance small differences when the signal is simultaneously observed at the most appropriate scales. Figure 3 shows the result of the application of the DWT one cycle of a normal ECG.

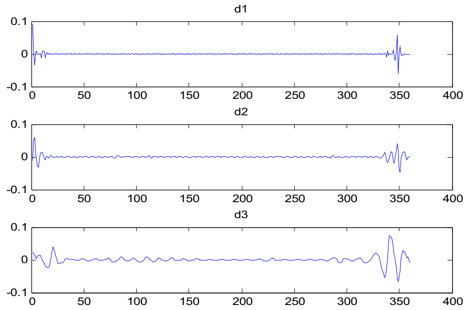


Figure 3 One ECG pulse viewed at scales d1, d2 and d3

From the figure we can observe that d1 level (frequency ranges of 90-180Hz) emphasize the high frequency content of complex QRS when compared with P and T waves. D2 and d3 levels show clearly that other waves of small frequencies not seen at d1 scale are just appearing.

The features used in the scope of this work are simultaneous observations of d1, d2 and d3 scales, therefore the observation sequence generated after the parameter extraction is of the form $\mathbf{O}=(\mathbf{o}_1, \mathbf{o}_2, \ldots \mathbf{o}_T)$ where T is the signal length in number of samples and each observation $\mathbf{o}_t$ is a tri-dimensional vector. Each element of the observation vector is derived from the Inverse Wavelet Transform (IWT) of the selected scale.

IV. HIDDEN MARKOV MODELS

Hidden Markov models are a doubly stochastic process in which the observed data are viewed as the result of having passed the hidden finite process (state sequence) through a function that produces the observed (second) process.

In the pattern recognition paradigm each class of beat is represented by a separate model and after decoding, the class for which the probability (likelihood) of occurrence is greater is selected. Since the ECG is characterized by a time sequence waves occurring almost always in the same order which reflects the sequential activity of the cardiac conduction system an HMM structure where the states are connected in a left-to-right order was adopted. In [5] it is shown that a full connected HMM is eventually more appropriate for HMM modeling since the beat sequence reproduced by this kind of HMM is almost perfect. Figure 4 shows the model structure adopted for the several pathologies considered in the ambit of this paper.

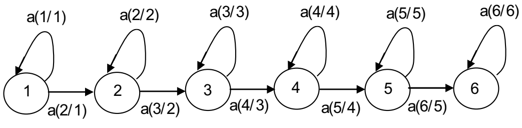


Figure 4 A left-to-right HMM with 6 states

The next issue is the choice of the number of Gaussian mixtures. For continuous models (CDHMMs), it has been found that it is more convenient and sometimes preferable to use diagonal covariance matrices with several mixtures, rather than fewer mixtures with full covariance matrices. The reason is the difficulty in performing reliable re-estimation of the off diagonal components of the covariance matrix from the necessarily limited training data. The HMMs in this work use five Gaussian mixtures per transition.

The output probability density function, which defines the conditional likelihood of observing a set of features when a transition through the model takes place, is usually a multivariate Gaussian mixture for the most engineering applications involving hidden Markov models. These probability density functions are associated with the transitions which configures a Continuous Density Hidden Markov Models (CDHMMs) Mealy machine and are given by

$$f(y/u_t)=\sum_{i=1}^{C} b_{u_t,i}\, G(y_t,\mu_{u_t,i},\Sigma_{u_t,i}) \tag{2}$$

where c is the number of components in the Gaussian mixture, G(…) stands for bi-variate normal distribution with mean vector and covariance matrix for the i^{th} mixture component and transition u_t given respectively by $\mu_{u_t,i}$ and $\Sigma_{u_t,i}$. As the components of observation vector are assumed iid G(…) function in equation (2) is simply the product of five Gaussian functions. The mixture coefficients $b_{u_t,i}$ satisfy, for each transition u_t, to

$$\sum_{i=1}^{C} b_{u_t,i}=1 \tag{3}$$

so that, equation (2) is a probability density function. In our experiments the observations were modeled by five components in the Gaussian mixture (C=5) in order to fit best data with multimodal distributions.

The Estimation of HMM parameters from a set of representative training data can be done by using the Baum-Welch algorithm which is based on the decoding of all the possible state sequence, or alternatively by using the Viterbi algorithm which is based on the most likely state sequence [3]. The adopted training was the MLE procedure in the Viterbi framework, which goal is to maximize iteratively the following probability density function

$$f(Y/\lambda)=f(Y/S,\lambda)P(S/\lambda) \tag{4}$$

where Y is the observation sequence, S the most likely state sequence and λ the set of HMM parameters. The model reestimation formulas can be found in [3].

V. EXPERIMENTAL RESULTS

Experimental results were evaluated by using the MIT-BIH Arrhythmia Database. Normal (N) and premature ventricular contraction (V) beats, in atrial fibrillation (AF), atrial flutter (AFL) and normal (N) rhythms were selected.

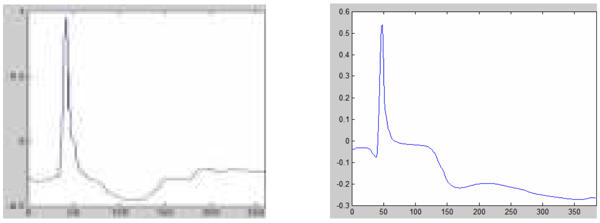
The training set contains the 121, 122, 221 and 222 records and the testing set contains the 105, 112, 121, 122, 210, 221 and 222 records of the MIT-BIH arrhythmia database, 300 and 301 of the Data-Acquisition System. For the training set 1445 normal (N) pulses of 121 (N rhythm) and 122 (N rhythm), 682 normal and premature ventricular contraction (V) pulses of 221 (AF rhythm) and 197 normal pulses of 222 (AFL rhythm) records were used. The testing set contains 3024 pulses of 105, 112, 121, 122, 300 and 301 records, 1011 pulses of 210 and 221 records and 246 pulses of 222 records, which means that data for training and testing purposes was obtained from different patients, which is normally known as patient-independent analysis. Table 1 shows the HMM based pulse classification system using features from wavelets selected from IWT at three different scales, respectably d1, d2 and d3. Both MLII and V1 signals were used each one with their own HMM. A pulse is considered classified if the score from both models agree, otherwise the pulse is considered wrong. Wrong pulses are separated for posterior analysis by the physician while the misclassified pulses shown in Table 1 are derived from classified pulses.

TABLE 1
THE CONFUSION MATRIX ASSOCIATED DWT

	AFN	AFV	AFLN	NN	Total	Pr+
AFN	864	0	0	0	864	1
AFV	0	114	0	0	114	1
AFLN	0	0	237	0	237	1
NN	33	0	9	3024	3066	0.98
Total	897	114	246	3024	4281	
Sensitivity	0.96	1	0.96	1		

The row labeled “Total” means the total number of beats used in experiment for each class listed in the corresponding column.

Figure 5a and figure 5b shows two pulses for which the result of the decoding process was a different class for each derivation. This constitutes a recognition error detected at run time and these pulses are separated for posterior analysis by the physician. The first pulse is clearly an “A” pulse and the second is a “j” pulse so not belonging to the considered arrhythmia classes.



5a 5b

Figure 5a and 5b Selected pulses for posterior analysis by the physician

VI. CONCLUSION

This paper reports a robust ECG classification system, regarding the cardiac arrhythmia detection, capable of working as first trial equipment, requiring however physician intervention for reliable diagnosis requirements. Uncertainty about classification by the automatic recognizer is signaled and the physician is required to make diagnosis based on medical knowledge and/or in complementary exams. This system takes advantage of advanced signal processing techniques as WT and HMM’s. WT allows observing the signal at different scales, each one emphasizing some signal properties and characteristics. By using simultaneously different scales more signal properties can be simultaneously observed hence better characterized will be the ECG pulse. As a matter of fact, different and opposite properties as the low content frequency of the P-wave and the high content frequency of the QRS can be accurately simultaneously observed. HMM’s are statistical models adequate for modeling signals of non-stationary nature. Assuming that WT can emphasize the non-stationary of the ECG by emphasizing their frequency content that varies with time, then HMM’s appear as a natural model with recognized capacities to break the ECG in quasi-stationary segments. Hence both techniques can complement each other in the analysis of signals of non-stationary nature.

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