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Using Hidden Markov Models for ECG Characterisation

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1. Introduction

Recent research on biomedical signal processing especially ECG analysis mostly focused on the use of Hidden Markov Models (HMM). The general aim of any signal segmentation method is to partition a given signal into consecutive regions of interest. In the context of the ECG then, the role of segmentation is to determine as accurately as possible the onset and offset boundaries, as well as the peak locations, of the various waveform features, such that the ECG interval measurements may be computed automatically and the study of waveform patterns will be facilitated (Sayadi & Shamsollahi, 2009). Ad hoc algorithms have been developed in order to help cardiologists to segment large amounts of ECGs. But these algorithms do not provide a precise segmentation, and repetitive corrections have to be made. Wavelet parametrisation is known to highlight discontinuities in the signal, and has proven to give good results for ECG segmentation (Kawaja et al., 2006; Thomas et al., 2006). A statistical model helps to regularize the detection, resulting in a more robust delineation. One of the advantages of probabilistic models over traditional methods is that a confidence measure for each segmented signal is given by the log likelihood of the observed signal given the model (Thomas et al., 2006).

The main focus of this chapter is to introduce some new and robust HMM associated with wavelet transform based methods for ECG analysis. The chapter begins with a review of the literature on the use of HMM to analyse ECG signals. We then consider in detail the suitability of HMM to provide a faithful statistical description of the ECG. In particular, we examine the validity of the various assumptions inherent in the HMM framework in the context of the ECG. Following this, we consider a number of specific issues in developing an HMM for ECG segmentation, including the choice of model architecture, type of observation models. Then a combination of HMM approach with wavelet properties will be explained.

1.1 Previous works

The use of hidden semi-Markov models (HSMM) for ECG segmentation has been considered previously in (Thoraval et al. 1994), the segmentation process is effected by an HSMM, where each state in the model corresponds to a particular aspect of a given ECG waveform feature. Specifically, the model architecture makes use of separate onset, middle and offset states for each waveform feature. This enhanced state space is motivated by the

need to match the stationarity assumption for each HSMM state, with the transitory nature of the observations over the time course of a particular ECG waveform. The observation and duration densities for the HSMM are modelled by Gaussians (with diagonal covariance matrices in the specific case of the observations). The performance of the model is demonstrated qualitatively on a sample ECG waveform (Hughes, 2006).

Wavelets and statistical methods can be used complementarily for ECG delineation, as reported previously in (Clavier et al., 1998, 2002), to associate a local and a global segmentation. Hidden Markov models (HMM), are applied to the coefficients of an ECG wavelet transform. This transform also showed the signal singularities, but it was too sensitive to noise. The association of the two methods made it possible to solve cases where they would fail if they were used alone. The ECG was segmented in three steps: first, a redundant multiresolution analysis was applied to the ECG signal; secondly, the R-wave was detected by a threshold on the wavelet coefficients; thirdly, a segmentation algorithm based on an HMM representing a beat was applied to isolate the P wave. The observations were the wavelet coefficients, whose probability densities were estimated by a non-parametric model.

Lepage et al., 2000, have presented a HMM associated with wavelets to improve an automatic segmentation of the ECG signal. While HMM describes the dynamical mean evolution of cardiac cycle, the use of wavelet analysis in association with the HMM leads to take into account local singularities. The parameters of this HMM model (means, variances and transition probabilities) are estimated using EM algorithm by modifying the parameter estimation by using the stochastic expectation maximisation algorithm (SEM) instead of the EM which avoids staying in local minima. Some good results were obtained at several scales, showing the good localization properties of wavelet, but the results were not as reliable as those obtained with the 10 state HMM method. It is sometimes really difficult to choose the coefficient that represents the beginning, the middle or the end of a wave, when the changes of state are too close or too numerous.

Graja & Boucher, 2005, have proposed a new ECG delineation method which uses a hidden Markov tree (HMT) model. Using wavelet coefficients to characterize the different ECG waves and, then linking these coefficients by a tree structure enabling wave change to be detected. The idea is to develop probability models for the wavelet transform of a signal and to analyze the dependency of wavelet coefficients through scales. In fact, it is well-known that wavelet coefficients have a non-Gaussian distribution. Making the assumption that it can be described by a mixture of Gaussian distributions. To pick up the relationships between states, they use a HMM on a wavelet tree with a hypothesis of clustering and persistence (Crouse et al., 1998).

Thomas et al., 2006, have used machine learning approach to ECG segmentation consists in building a model λ of the signal, and in using the most likely state sequence for a given observation sequence in order to find the wave transitions. To be able to segment unspecified ECGs with high accuracy, they implemented a multi-HMM approach. This method consists in performing a Bayesian clustering of the training base (Li, & Biswas, 2000). The training base is divided in K classes of ECGs which have similarities and K HMM are trained and exploited to provide great generalization capabilities and high accuracy at the same time. This HMM clustering algorithm is simply a variation of the K-Means algorithm, where the clusters are defined by HMM rather than by centers in the data space (Thomas et al., 2007).

Online HMM adaptation for ECG analysis has been successfully carried out by Müller et al., 2006, they have introduced the online HMM adaptation for the patient ECG signal adaptation problem. Two adaptive methods were implemented, namely the incremental version of the expectation maximization (EM) and segmental k-means algorithms. The system is adapted to the ECG of the individual in an unsupervised way. For that, the segmentation output is used to reestimate the HMM parameters of each waveform.

Andraão et al., 2007, have presented an original HMM approach for online beat segmentation. The HMM framework is highly suitable for the ECG problem. This approach addresses a large panel of topics like : waveforms modelling, multichannel beat segmentation and classification, and unsupervised adaptation to the patient's ECG. The segmentation task is carried out by generic HMM of each beat waveform. One important feature of this approach is the generic model adaptation strategy to each individual, which is non supervised (there is no need of manual labels). The HMM are used to carry out beat detection and segmentation. The main contributions are based on the following (Andraão et al. 2003, 2004, 2006). Firstly, waveform modelling (and not beat modelling) using generic HMM (trained through examples from several individuals). In this way, HMM are trained taking into account the morphology diversity of each waveform. Secondly, better waveform segmentation precision by adapting a generic model to each individual. The model adaptation is done in an unsupervised way, eliminating waveform manual labelling (Laguna et al., 1997).

1.2 Contributions and chapter organization

In our works, we have developed three original hybrid segmentation algorithms based on : Firstly, Modulus Maxima Wavelet Transform (MMWT) that has been successfully combined with Hidden Markov Models (HMM) providing reliable beat segmentation results (Krimi et al. 2008). In the MMWT, the wavelet transform local extrema is used to characterize singularities in the signal. One very successful method described in (Cuiwei et al., 1995), uses the ECG wavelet transform modulus maxima properties to characterize the different ECG complexes. A rule based system is used to detect QRS waves and differentiate them from T waves and noise artifacts. This method has also been extended for T and P wave's detection (Jouck, 2004).

Secondly, Pitch Synchronous Wavelet Transform (PSWT) and Hidden Semi-Markov Models (HSMM) (Krimi et al., 2007). The combination of these two methods has shown to be very efficient tool for ECG delineation. As noted in other studies on the HMM, the self transitions of the HMM cause an incorrect modelling of segment durations. An extension of the HMM, the Hidden Semi Markov model HSMM, largely solves this problem. PSWT, has been effectively used in speech, music signals (Evangelista, 1993) and waveform interpolation coding scheme (Chong et al., 2000). The (PSWT) is based on a modelling concept, which is able to capture period to period signal fluctuation by basis elements means that are comb-like in the frequency domain. This technique relies primarily on the high peaks positions corresponding to the ECG R wave. The principle consists in estimating the periodicity (pitch period) with the autocorrelation function and dividing the original signal into pseudo-periodic segments using the time points obtained from the considered pitch detector algorithm; this segmentation leads to the pitch synchronous representation. By applying the wavelet transform to this representation and synthesis only the approximation component we can obtain the dominating pitched signal's behaviour, so the ECG estimation.

Thirdly (in progress), Multiscale Product Wavelet Transform (MPWT) in association with Hidden Markov Tree (HMT). The idea of this study is to detect singularity not via local maxima of the wavelet coefficients signals but via the product of the wavelet coefficients. Rosenfeld and co-workers (Rosenfeld, 1970) suggested forming multiscale point-wise products. This is intended to enhance multiscale peaks due to edges, while suppressing noise, by exploiting the multiscale correlation due to the presence of the desired signal (Besrouf & al., 2009). MPWT is based on Mallat's and Hwang's approach (Mallat & Hwang, 1992) for singularity detection via local maxima of the wavelet coefficients signals. It acted as the parameter extraction stage necessary to build the observation sequence of our original HMT based segmentation approach.

2. Background information

This section provides a brief review of Hidden Markov Models (HMM), Hidden Markov Tree (HMT) and Hidden Semi-Markov Models (HSMM).

2.1 Hidden Markov Models (HMM)

To model a sequence $W = w^1, w^2, \dots, w^T$; with $w^t \in \mathbb{R}^N$, a continuous HMM is defined with the structure $\mathcal{G} = \langle Q, A, \pi, B \rangle$ where (Milone et al., 2010) :

- i. $Q = \{Q\}$ is the set of states, where Q is a discrete random state variable taking values $q \in \{1, 2, \dots, N_Q\}$
- ii. $A = [a_{ij}]$ is the matrix of transition probabilities with $a_{ij} = \Pr(Q^t = j | Q^{t-1} = i) \forall i, j \in Q$, where $Q^t \in Q$ is the model state at time $t \in \{1, 2, \dots, T\}$, $a_{ij} \geq 0 \forall i, j$ and $\sum_j a_{ij} = 1 \forall i$
- iii. $\pi = [\pi_j = \Pr(Q^1 = j)]$ is the initial state probability vector. In the case of left to right HMM this vector is $\pi = \delta_1$
- iv. $B = \{b_k(w^t)\}$ is the set of observation (or emission) probability distributions $b_k(w^t) = \Pr(W^t = w^t | Q^t = k) \forall k \in Q$

Assuming a first order Markov process and the statistical independence of the observations, the HMM likelihood can be defined using the probability of the observed data given the model:

$$L_{\mathcal{G}}(W) = \sum_{\forall q} L_{\mathcal{G}}(W, q) \triangleq \sum_{\forall q} \prod_t a_{q^{t-1}q^t} b_{q^t}(w^t) \quad (1)$$

where $\forall q$ stands for over all possible state sequences $q = q^1, q^2, \dots, q^T \in Q$ and $a_{01} = \pi_1 = 1$.

To simplify the notation, we will indicate $\Pr(w^t | q^t)$ as equivalent to $\Pr(W^t = w^t | Q^t = q^t)$ or in a similar way $\Pr(q^t | q^{t-1}) \equiv \Pr(Q^t = q^t | Q^{t-1} = q^{t-1})$

The EM algorithm is the most widely used way to maximize this likelihood (Duda et al., 2001). The forward-backward algorithm provides an efficient method for the expectation step (Baum et al., 1970). The expected values for the state probabilities in \mathcal{G} can be calculated with the recursions

$$\alpha^t(j) \triangleq \Pr(w^1, \dots, w^t, q^t = j | \mathcal{G}) = b_j(w^t) \sum_i \alpha^{t-1}(i) a_{ij} \quad (2)$$

$$\beta^t(j) \triangleq \Pr(w^{t+1}, \dots, w^T, q^t = j | \mathcal{G}) = \sum_k a_{jk} b_k(w^{t+1}) \beta^{t+1}(k) \quad (3)$$

Initialized with $\alpha^1(i) = \pi_i b_i(w^1) \forall i$ and $\beta^T(k) = 1 \forall k$. Then, the probability of being in state i at time t is

$$\gamma^t(i) \triangleq \Pr(q^t = i | W, \mathcal{G}) = \frac{\alpha^t(i) \beta^t(i)}{\sum_i \alpha^t(i) \beta^t(i)} \quad (4)$$

And the probability of being in state i at time $t-1$, and in state j at time t is

$$\xi^t(i, j) \triangleq \Pr(q^{t-1} = i, q^t = j | W, \mathcal{G}) = \frac{\alpha^{t-1}(i) a_{ij} b_j(w^t) \beta^t(j)}{\sum_i \alpha^t(i) \beta^t(i)} \quad (5)$$

The learning rules can be obtained by maximizing the likelihood of the data as a function of the model parameters (Huang et al., 1990). Thus, the transition probabilities can be estimated with

$$a_{ij} = \frac{\sum_t \xi^t(i, j)}{\sum_t \gamma^t(i)} \quad (6)$$

These equations can be easily extended for training from multiple observation sequences (Liporace, 1982).

The corresponding learning rules for the parameters of the observation distributions are dependent on the chosen model for $b_k(w^t)$.

2.2 Hidden Markov Tree (HMT)

Let $W = [w_1, w_2, \dots, w_N]$ be the concatenation of the wavelet coefficients obtained after performing a DWT with J scales, without including w_0 , the approximation coefficient at the coarsest scale. Therefore, $N = 2^J - 1$. The HMT can be defined with the structure $\theta = \langle U, \mathfrak{R}, \pi, \varepsilon, F \rangle$, where (Milone et al., 2010):

- i. $U = \{u\}$ with $u \in \{1, 2, \dots, N\}$, is the set of nodes in the tree.
- ii. $\mathfrak{R} = \bigcup_u \mathfrak{R}_u$ is the set of states in all the nodes of the tree, denoting with $\mathfrak{R}_u = \{R_u\}$ the set of discrete random state variables in the node u , and R_u taking values $r_u \in \{1, 2, \dots, M\}$
- iii. $\varepsilon = [\varepsilon_{u, mn}]$ with $\varepsilon_{u, mn} = \Pr(R_u = m | R_{\rho(u)} = n) \forall m \in \mathfrak{R}_u, \forall n \in \mathfrak{R}_{\rho(u)}$ is the array whose elements hold the conditional probability of node u , being in state m , given that the state in its parent node $\rho(u)$ is n and satisfy $\sum_m \varepsilon_{u, mn} = 1$

- iv. $\pi = [\pi_\rho]$ with $\pi_\rho = \Pr(R_1 = \rho) \forall \rho \in \mathfrak{R}_1$ the probabilities for the root node being on state ρ .
- v. $F = \{f_{u,m}(w_u)\}$ are the observation probability distributions, with $f_{u,m}(w_u) = \Pr(W_u = w_u | R_u = m)$ the probability of observing the wavelet coefficient w_u with the state m (in the node u).

Additionally, the following notation will be used :

- $C(u) = \{c_1(u), \dots, c_{N_u}(u)\}$ is the set of children of the node u .
- T_u is the subtree observed from the node u (including all its descendants).
- $T_{u \setminus v}$ is the subtree from node u but excluding node v and all its descendants.

As in the sequence q for HMM, we will use the notation $r = [r_1, r_2, \dots, r_N]$ to refer a particular combination of hidden states in the HMT nodes.

Assuming that the following three basic properties in the HMT are true :

$$1. \quad \Pr(r_u = m | \{r_v / v \neq u\}) = \Pr(r_u = m | \{r_{\rho(u)}, r_{c_1(u)}, r_{c_2(u)}, \dots, r_{c_{N_u}(u)}\})$$

the Markovian dependencies for trees

$$2. \quad \Pr(W | r) = \prod_u \Pr(w_u | r_u) \text{ the statistical independence of the observed data given the hidden states}$$

$$3. \quad \Pr(w_u | r) = \prod_u \Pr(w_u | r_u) \text{ the statistical independence of the observed coefficient in node } u \text{ to the states in the other nodes of the tree and using the standard definition } L_\theta(w, r) \triangleq \Pr(w, r | \theta) \text{ the HMT likelihood is}$$

$$L_\theta(w) = \sum_{\forall r} L_\theta(w, r) \triangleq \sum_{\forall r} \prod_u \varepsilon_u r_u r_{\rho(u)} f_{u,r_u}(w_u) \quad (7)$$

where $\forall r$ means that we include all the possible combinations of hidden states in the tree nodes and $\varepsilon_1 r_1 r_{\rho(1)} = \pi_{r_1}$

For the computation of the expected values in the EM algorithm, the upward-downward recursions are used, in a similar way than the forward-backward ones in HMM. For this algorithm the following quantities are defined (Ronen et al., 1995) :

$$\alpha_u(n) \triangleq \Pr(T_{1 \setminus u}, r_u = n | \theta) \quad (8)$$

$$\beta_u(n) \triangleq \Pr(T_u | r_u = n, \theta) \quad (9)$$

$$\beta_{\rho(u),u}(n) \triangleq \Pr(T_u | r_{\rho(u)} = n, \theta) \quad (10)$$

In the upward step the β quantities are computed as

$$\beta_u(n) = f_{u,n}(w_u) \prod_{v \in C(u)} \beta_v(m) \varepsilon_{u,mn} \quad (11)$$

Initialized with $\beta_u(n) = f_{u,n}(w_u) \forall u$ in the finest scale. Then, $\beta_{\rho(u),u}(n)$ is computed and the iterative process follows in the previous level, in an upward inductive tree traversal.

When the upward step reaches the root node, the downward step computes

$$\alpha_u(n) = \sum_m \frac{\varepsilon_{u,mm} \beta_{\rho(u)}(m) \alpha_{\rho(u)}(m)}{\beta_{\rho(u),u}(m)} \quad (12)$$

Starting from $\alpha_1(m) = \Pr(r_1 = m | \theta) = \pi_m$. The other two useful quantities are the probability of being in state m of node u

$$\gamma_u(m) \triangleq \Pr(r_u = m | w, \theta) = \frac{\alpha_u(m) \beta_u(m)}{\sum_n \alpha_u(n) \beta_u(n)} \quad (13)$$

And the probability of being in state m at node u , and the state n at its parent node $\rho(u)$

$$\xi_u(m, n) \triangleq \Pr(r_u = m, r_{\rho(u)} = n | w, \theta) = \frac{\beta_u(m) \varepsilon_{u,mn} \alpha_{\rho(u)}(n) \beta_{\rho(u)}(n) / \beta_{\rho(u),u}(n)}{\sum_n \alpha_u(n) \beta_u(n)} \quad (14)$$

If we consider the maximization for multiple observations $W = \{w^1, w^2, \dots, w^L\}$, with $w \in \mathbb{R}^N$, the conditional probabilities $\varepsilon_{u,mm}$ can be estimated from $\varepsilon_{u,mm} = \frac{\sum_l \xi_u^l(m, n)}{\sum_l \gamma_{\rho(u)}^l(n)}$ and using a normal distribution for the observation probability distributions

$$f_{u,r_u}(w_u) = \frac{1}{\sqrt{2\pi\sigma}} \exp\left(-\frac{1}{2} \frac{(w_u - \mu_{u,r_u})^2}{\sigma_{u,r_u}^2}\right) \quad (15)$$

We have (Crouse, et al., 1998)

$$\mu_{u,m}(w_u) = \frac{\sum_l w_u^l \gamma_u^l(m)}{\sum_l \gamma_u^l(m)} \quad (16)$$

$$\sigma_{u,m}^2 = \frac{\sum_l (w_u^l - \mu_{u,m})^2 \gamma_u^l(m)}{\sum_l \gamma_u^l(m)} \quad (17)$$

2.3 Hidden Semi-Markov Models (HSMM)

A HSMM consists of a pair of discrete-time stochastic processes $\{s_t\}$ and $\{X_t\}$. Similar to HMM, the observed process $\{X_t\}$ is related to the unobserved semi-Markovian state process $\{s_t\}$ by the so-called conditional distributions (Bulla et al., 2010).

Let $X_T^1 := (X_1, \dots, X_T)$ denote the observed sequence of length T . The same convention is used for the state sequence s_t , and θ denotes the set of model parameters. The state process is a finite-state semi-Markov chain, which is constructed as follows. A homogeneous Markov chain with J states, labelled $1, \dots, J$ models the transitions between different states.

The stochastic process $\{s_t\}$ is specified by the initial probabilities $\pi_j := P(s_1 = j)$ with :

$\sum_j \pi_j = 1$ and the transition probabilities p_{ij} . For states $i, j \in \{1, \dots, J\}$ with $j \neq i$, these are given by

$$p_{ij} := P(S_{t+1} = j | S_{t+1} \neq i, S_t = i) \quad (18)$$

Satisfying $\sum_j p_{ij} = 1$ and $p_{ii} = 0$. The diagonal elements of the transition probability matrix (TPM) of a HSMM are required to be zero, since we separately model the run length distribution and do not consider the case of absorbing states. This distribution, also referred to as sojourn time distribution, is associated with each state. It models the duration the process $\{s_t\}$ remains in the state j and is defined by

$$d_j(u) := P(S_{t+u+1} \neq j | S_{t+u} = j, \dots, S_{t+2} = j | S_{t+1} = j, S_t \neq j) \quad (19)$$

The combination of a Markov chain, modelling state changes, and runlength distributions, determining the sojourn times in the states, define $\{s_t\}$ and illustrate the main difference between the HMM and the HSMM. The semi-Markovian state process $\{s_t\}$ of a HSMM does not have the Markov property at each time t , but is Markovian at the times of state changes only.

The observed process $\{X_t\}$ at time t is related to the state process $\{s_t\}$ by the conditional distributions $b_j(x_t)$, which are either probability functions in the case of discrete conditional distributions or probability densities in the case of continuous conditional distributions :

$$b_j(x_t) = \begin{cases} P(X_t = x_t | S_t = j) & \text{for discrete } X_t \\ f(X_t = x_t | S_t = j) & \text{for continuous } X_t \end{cases} \quad (20)$$

For the observation component, the so-called conditional independence property is fulfilled:

$$P(X_t = x_t | X_T^1 = x_T^1, \dots, S_1^{t-1} = s_1^{t-1}, S_t = j, S_{t+1}^T = s_{t+1}^T) = P(X_t = x_t | S_t = j) \quad (21)$$

That is, the output process at time t depends only on the value of S_t .

3. Proposed ECG segmentation techniques

3.1 Modulus maxima wavelet transforms and hidden Markov models based method

This technique is based on the combination of two mathematical techniques namely the Wavelet Transform (WT) and Hidden Markov Models (HMM). In this method, we first localize edges in the ECG by wavelet coefficients, then, features extracted from the edges serve as input for the HMM. This new approach was tested and evaluated on the manually annotated database QT database (Laguna & al., 1997), which is regarded as a very important benchmark for ECG analysis. We obtained a sensitivity $Se = 99,40\%$ for QRS detection and a sensitivity $Se = 94,65\%$ for T wave detection.

3.1.1 Modulus maxima wavelet transforms

The modulus maximum describe any point u_0, s_0 such that the $|W_{s_0} f(u)|$ is locally maximum at $u = u_0$. This implies that (Chen, 2006)

$$\left. \frac{\partial W_{s_0} f(u)}{\partial u} \right|_{u=u_0} = 0 \quad (22)$$

When the WT is at fine scale, singularities are detected by finding the abscissa where the wavelet modulus maxima converge (Mallat & Hwang, 1992). The zero-crossings of the WT, which is also at fine scale, correspond to the maxima or minima of the smoothed uniphase signal (Mallat, 1991).

$$W_s f(u) = \int_{-\infty}^{+\infty} f(t) \frac{1}{\sqrt{s}} \Psi^* \left(\frac{t-u}{s} \right) dt \quad (23)$$

The singularities in the arrhythmia waveform can be conveniently detected by employing wavelet transform (WT). WT of a function f is a convolution product of the time series with the scaled and translated kernel Ψ , and is given by (Strang & Nguyen, 1996):

$$W_{s,u_0}(f) = \int_{-\infty}^{+\infty} \frac{1}{s} \Psi \left(\frac{u-u_0}{s} \right) f(x) dx \quad (24)$$

$$W_{s,u_0}(f) \alpha |s|^{h(u_0)} \quad s \rightarrow 0^+ \quad (25)$$

Where s is the scale parameter and u_0 is the translation parameter. The ability of WT to reveal even the weaker singularities within the time series by adjusting s makes it an indispensable tool for singularity analysis.

The continuous WT described in Equation (24) is an extremely redundant and a computationally expensive representation. The wavelet transform modulus maxima (WTMM) method (Hwang, 1994) changes the continuous sum over space into a discrete sum by taking the local maxima of $|W_{s,u_0}(f)|$ considered as a function of u . An important feature of these maxima lines is that, each time the analyzed signal has a local Hölder exponent $h(u_0)$ less than the analyzing wavelet, there is at least one maxima line pointing toward u_0 along which Equation (25) holds (Arneodo, 1995, Joshi, 2006).

3.1.2 Selecting edge localization

First, In the WTMM (Mallat, 1999), the WT local extrema is used to characterize singularities in the signal. One very successful method described in (Cuiwei et al., 1995), uses the ECG wavelet transform modulus maxima properties to characterize the different ECG complexes. A rule based system is used to detect QRS waves and differentiate them from T waves and noise artifacts. This method has also been extended for T and P wave's detection (Jouck, 2004). In the ECG substantial information is carried in the peaks, so if we want to use a segment model, it would be preferable to model a segment around the ECG peaks. The rising and falling edges in a signal can be easily identified by the WT coefficients.

A positive modulus maximum corresponds to a rising edge and a modulus maxima corresponds to a falling edge. The modulus maximum alone do not provide sufficient information to determine the edge onset and offset. When the analyzing wavelet is the derivative of a smoothing function $\theta(u)$, the wavelet transform can be interpreted as the derivative of the original signal $f(u)$ smoothed by $\theta(u)$.

As the zero crossings of $Wf(u,s)$ correspond to zero crossings of $df(u)/du$ - the derivative of $f(u)$ - a rising or falling edge onset and offset can be derived from the zero crossings in $Wf(u,s)$. So, by determining the modulus maxima locations and the zero crossing near the modulus maxima, the onset and offset as well as the point of inflection of an edge can be determined. The area between the ECG onset and offset is characterized by constant sign wavelet coefficients - either all positive or all negative. The scale selection u , determines the resolution details of $f(u)$ that are visible in the $Wf(u,s)$, and thus also the edges resolutions that can be detected. When only coarse scales are selected, only coarse details of $f(u)$ are detectable. When only fine scales are selected, the fast varying details of $f(u)$ are visible. As fine scales give a better time-resolution, it would be preferable to use fine scales to more precisely determine the edge onset and offset.

However, ECG signals are often subject to high frequency noise, and at small scales this noise distorts the wavelet transform. So, we want to select scales such that the ECG peaks oscillations are visible in the wavelet transform, but not so small that the noise in the signal becomes too dominant in the wavelet transform. From empirical tests, it became apparent that selecting only one scale to detect edges did not suffice. The edges resolutions make up the ECG peaks are too broad to be captured by one scale WT. Therefore it is necessary to use multiple scales to detect edges. Unfortunately, it is not guaranteed, that if the wavelet coefficients at one scale have constant sign in one area, that the wavelet coefficients in that area on another scale also have constant sign. In order to deal with this, the area in which an edge of $f(u)$ is localized is determined as follows :

We selected two scales that respond well to the edges time-frequency resolution that make up the ECG peaks. The finest of the two scales has the best time resolution to determine the edges onset and offset, but the high frequency noise in the ECG is also visible at this scale. In the wavelet coefficients on the more coarse scale, noise is less dominant, but some time resolution is lost. Therefore the wavelet transform at both scales is combined to detect edges. An edge is only detected, when in a certain signal $f(u_t, \dots, u_{t+d})$ area, wavelet coefficients on both scales $Wf(u_t, \dots, u_{t+d}, s)$ have the same sign.

3.1.3 ECG edges localisation as HMM front end

The edges in the ECG are localized and features extracted from the edges serve as input for the HMM. The Viterbi algorithm for the HMM (Koski, 1996) can be interpreted as a search in the model state-time space. In the optimal solution search, states are assigned to observations to maximize the likelihood function. In other words, segments are modelled around observations that have a high probability to belong to a certain state when a Gaussian mixture model is used to model the observation probabilities (the wavelet coefficients). It is known that important information about the signal is carried in the wavelet transform modulus maxima. This information can improve discrimination between the ECG characteristics. The problem is that in the Viterbi algorithm the whole signal is searched, and that in some search areas no modulus maxima are present. For this reason it is hard to model the modulus maxima information into the probability calculations for the HMM observations.

This problem can be solved if only parts of the signal where modulus maxima are present are processed. In the edge wavelet transform at least one modulus maxima must be present. The segment is modelled from one zero crossing in the one scale wavelet coefficients the next zero crossing. Somewhere between the zero crossings we must have an inflection point,

where the wavelet coefficients change direction (from rising to falling or vice versa), otherwise all wavelet coefficients in the segment would have to be zero. So, when a segment has been localized, further information from the wavelet coefficients in the segment can be extracted. This information is then used as an observation for the HMM. In contrast to the previous Markov models implementation, the observations no longer correspond to an ECG time sample, but an ECG segment time.

3.1.4 Experiments and results

In order to evaluate our performance method for ECG delineation, we use a standard QT database (Laguna & al., 1997). This is a manually annotated database, consisting of 105 records, two leads each. The records contain both automatic and manual annotations. The automatic annotations are available for the whole signal; the manual annotations are made for 30 to 100 beats for each record. In the tests performed, only the manual annotations are used as a reference. Not all records are used in the evaluation, some records have no T peak annotation or normal beat annotations, these records have been excluded. To assess the detection performance of the different waves we calculated the sensitivity Se and the positive predictivity P_+ of several events. In the QT database, when a QRS_{peak} is annotated, the rest of the beat is also annotated (at least the QRS_{on} and QRS_{off} and the T_{peak} and T_{end}). Therefore, the P_+ can only be calculated for other events than the QRS_{peak} . In an annotated beat, each absent manual annotation in the automatic detection neighbourhood can be considered as a false positive. Therefore, the wave detection rates are calculated as follows : a true positive is calculated for the QRS complex and the T wave, when at the annotated QRS_{peak} or T_{peak} the HMM of our method is in the QRS or T state respectively. When this is not the case, a false negative is recorded. For our method there are several states that relate to the QRS complex and T wave. The states related to the QRS complex are the states $\{Q, R, S, RST\}$, those related to the T wave are the states $\{T_1, T_2, RST\}$. The $\{RST\}$ state models a weak transition from the QRS complex to the T wave, therefore both the QRS complex and the T wave are associated with this state. As argued above, the P_+ can not be computed for QRS detection, but this can be computed for the QRS complex onset QRS_{on} , and the T wave offset T_{off} . For these events the Se and P_+ are calculated, as well as the mean (m) and the standard deviation (s) of the time differences between the cardiologist and automatic annotations. Furthermore, for the beats annotated by the cardiologist in the QT database, the QT time mean and standard deviation of these beats is measured $manQTt$. The mean and standard deviation of the time difference between the manual and automatic QT times is measured as ϵQTt . These differ from the errors of QRS_{on} and T_{off} , as they are calculated over all manual annotations and all automatic annotations. The proposed method is only trained on the whole concatenated test set and not on individual records. The results are shown in Table 1.

In this method only parts of the ECG signal that are detected by the edge localization method can be classified. As a consequence, when an edge is not detected when it should be, this part of the signal is always misclassified. Furthermore, the edge detection algorithm determines the edges onset and offset. The results of the T_{off} error mean show a positive bias (45ms). This means that most edges related to the T-wave are truncated too late in comparison to the cardiologist's annotations. Edges are truncated, when at the finest scale, the wavelet coefficients change sign. This is a very simple and straight forward approach,

Parameter	QRS	QRS _{on}	T	T _{off}	manQTt	εQTt
Se (%)	99,40	95,34	94,65	86,16	-	-
P+ (%)	-	90,75	-	83,56	-	-
m(ms)	-	-5,80	-	45	422,10	38
s (ms)	-	31,10	-	77,30	72,20	74,3
# annotations	3473	3473	3512	3512	-	-

Table 1. WTMM and HMM based method detection results

but unfortunately, often this does not concur with the cardiologists annotations. A possible solution to this is to truncate an edge sooner. For instance by using an even finer wavelet scale, or by truncating an edge when the wavelet coefficients cross at a certain threshold value, instead of zero. It should be noted, that these measures might increase T_{off} delineation precision (*m* and *s*) and the T_{off} sensitivity *Se*, but they would have little impact on detection rates (T sensitivity). Our HMM topology is able to model a great variety of ECG morphologies. Still, there are many different topologies possible, which may improve performance. This is an elementary problem in hidden Markov modelling; the topology and some of the model parameters are determined by experimentation and thus most likely to be suboptimal. The HMM model used has more states than annotated events present in the database. This is because some ECG waveforms are segmented more precise than in the manual annotations. As a result, it is hard to calculate the right parameters for the states related to the segments that are not annotated explicitly in the database. The obvious solution is to annotate the database more precisely, but this is a time consuming and expensive job. The resulting parameters can still not be proved to be optimal, and another HMM topology might be required, which would issue another database annotation. For this reason some of the states share parameters, these are the parameters that can be easily extracted from the database. The segment features that have been chosen as observations for the proposed HMM have shown to be discriminative between states.

3.2 Pitch synchronous wavelet transform and hidden semi-Markov models based method

In this technique we develop a new approach to ECG analysis, combining Pitch Synchronous Wavelet Transform (PSWT) and Hidden Semi-Markov Model (HSMM) for tracking the typical ECG cycle. The combination of these two techniques was examined in a way that the PSWT of an ECG signal was an input for the HSMM. This approach was tested and evaluated on the manually annotated QT database. Experimental results show the accuracy of the proposed technique for all corrupted ECG tested reaching a sensitivity *Se*=99,95% for QRS detection and *Se*=97,79% for T detection.

3.2.1 Pitch synchronous wavelet transform

The Pitch Synchronous Wavelet Transform (PSWT) is developed as an extension of the wavelet transform that is suitable for pseudo periodic signals like speech signals; electroencephalogram (EEG) signals; seismic signals and so more. Electrocardiogram (ECG) signals, i.e. heartbeat signals, exhibit pseudo-periodic behaviour. Nearby pulses are very similar in shape, but of course various evolutionary changes in the behaviour are medically significant (Goodwin, 1997).

PSWT is a periodic and pseudo periodic signals decomposition approach. It is based on a pitch synchronous technique which leads to convert the signal into a whole of vectors

having variable length and to apply thereafter to the sequence obtained a traditional wavelet transform. This shows its capacity on one hand to analyze according to a periodic approach and on several scales the signals with periodic behaviour and on the other hand to take account of signal variabilities period per period (Evangelista, 1995)

A pseudo-periodic signal $x[n]$ is first converted into a sequence $v[k] = \{v_q[k]\}$ of variable length vector $v_q[k]$, each containing the sample of one period signal. The indexes $q = 0, \dots, p[k]-1$ and k are respectively the inter-period and the period count index and $p[k]$ is a sequence of integer local pitch periods extracted from $x[n]$. Based on this representation the sequences of components are, then, analysed by means of an array of wavelet transform. Given a set of decomposition levels $l = 1, 2, \dots, L$, the pitch synchronous wavelet expansion of the signal $x[n]$ is defined by the following sum :

$$x[n] = \sum_{l=1}^L w_l[n] + r_L[n] \quad (26)$$

Where the scaling residue (estimation) $r_L[n]$ represents the average behaviour of $x[n]$ while the partial (details) $w_L[n]$ represents the fluctuations at scale 2^L local periods. In the transform domain the scaling residue and the partial are represented by the expressions :

$$x[n] = \sum_{l=1}^L w_l[n] + r_L[n] \quad (27)$$

$$w_l[n] = \sum_{m,q} S_{l,m,q} \xi_{l,m,q}[n] \quad (28)$$

Where $\xi_{l,m,q}[n]$, $S_{l,m,q}[n]$ (m, q integers adapted to the periodicity of the signal $x[n]$), $\sigma_{l,m,q}$ and $S_{l,m,q}$ represent a finite scale pitch synchronous wavelet, L level scaling sequences and the expansion coefficients, respectively (Elloumi et al., 2004).

3.2.2 Pitch synchronous wavelet transform as HSMM front end

The PSWT coefficients can be employed as a front end to a Markov Model as individual samples (the normal HMM) or as a segment of samples (the HSMM or Segmental Markov Model). In the sample based model, a state transition is made at each time step, and the occurrence probability of a given state is calculated from one observation O_t - that represents the wavelet coefficients from one time-sample $W_u(t,s)$ - In the segment based model, a state transition is made only after a certain number of time steps, d , and the probability for a state is calculated from multiple observations $O_t \dots O_{t+d}$ - that represent multiple pitch synchronous wavelet coefficients, $W_u(t \dots t+d, a)$ - In the HSMM, the probability of the segment observations $P(O_t, \dots, O_{t+d})$, is calculated as the product of the individual observations that make up the segment, as if they were independent identically distributed observations.

3.2.3 Experiments and results

The results of our method trained on individual records of the test database are considerably high. There are only a small number of records who fail good detection.

Record *sel36*, has the worst detection rate. This record has a rhythm of one or two normal beats followed by PVC (Premature Ventricular Contraction). As a result, the durations of the QRS complexes that are recorded are divided into two clusters : One for the normal QRS complexes that have a relatively short duration, and one for the PVC's that have a long duration. From the sensibility Se and the positive predictivity P_+ values, we can gather that there are slightly more false positives than false negatives. This may be a disadvantage for applications in which we need to be sure that only QRS complexes are detected. It may be possible to change this relation by changing parameters in our future work analysis. This extensive model which models the ECG waveforms more accurate might improve detection rates. The results shown in Table 2 are considerably high. There are only a small number of records who fail good detection, $Se=99,95\%$ and $P_+=97,39\%$ for QRS_{on} and $Se=95,68\%$ and $P_+=96,57\%$ for T_{off} .

Parameter	QRS	QRSon	T	Toff	manQTt	ϵQTt
Se (%)	99,95	99,95	97,79	95,68	-	-
P+ (%)	-	97,39	-	96,57	-	-
m(ms)	-	9,95	-	0,76	408,8	-9,7
s (ms)	-	7,2	-	22,7	52,1	14,1
# annotations	2093	2093	2131	2131	-	-

Table 2. PSWT and HSMM based method detection results

3.3 Multiscale product wavelet transform and hidden Markov tree based method

3.3.1 Multiscale product wavelet transform

The WT is a multi-scale analysis which has been shown to be very well suited for speech processing as Glottal Closure Instant (GCI) detection, pitch estimation, speech enhancement and recognition and so on. Moreover, a speech signal can be analysed at specific scales corresponding to the range of human speech (Berman & Baras 1993, Kadambe, 1992). (Witkin, 1981) provided the foundation for scale space theory by generalizing Rosenfeld's work (Rosenfeld, 1970), in which smoothing filters at dyadic scales were used. Based essentially on forming multiscale products of smoothed gradient estimates, this approach attempts to enhance the peaks of the gradients caused by true edges, while suppressing false peaks due to noise. The wavelet transform acts as an edge detector, and the detail coefficients should be equivalent to the estimated gradients. This method was first used in image processing (Xu et al., 1994) rely on the variations in the WT decomposition level. They use multiplication of WT of the image at adjacent scales to distinguish important edges from noise. Continuous WT produces modulus maxima at signal singularities allowing their localisation. However, one-scale analysis is not accurate. So, decision algorithm using multiple scales is proposed by different works to circumvent this problem (Bouazid & Ellouze, 2007, 2009).

So if the wavelet is chosen to have one vanishing moment, modulus maxima appear at discontinuities of the signal and represent the maxima of the first derivative of the smoothed signal. The MP (Sadler & Swami, 1999) consists of making the product of wavelet transform coefficients of the function $f(n)$ at some successive dyadic scales as follows

$$p(n) = \prod_j w_{2^j} f(n) \quad (29)$$

Where $w_{2^j} f(n)$ is the wavelet transform of the function $f(n)$ at scale 2^j .

This expression is distinctly a non linear function. The product $p(n)$ reveals peaks at signal edges, and has relatively small values elsewhere. Singularities produce cross-scale peaks in wavelet transform coefficients, these peaks are reinforced by the product $p(n)$. Although particular smoothing levels may not be optimal, the non linear combination tends to reinforce the peaks while suppressing spurious peaks. The signal peaks will align across scales for the first few scales, but not for all scales because increasing the amount of smoothing will spread the response and cause singularities separated in time to interact. Thus, choosing too large scales will result in misaligned peaks in $p(n)$. An odd number of terms in $p(n)$ preserves the sign of the edge (Bouزيد et al., 2006).

Motivated by the efficiency of the multiscale product in improving the edge detection, this method is applied on ECG signal and then can outperform the wavelet transform precision in weak singularity detection (Besrouer et al., 2009).

4. Conclusion and future work

In this chapter, we have proposed some new techniques for ECG characterisation based on modulus maxima wavelet transform, pitch synchronous wavelet transform and in the future work multiscale product wavelet transform as respectively front ends of hidden Markov models, hidden semi-Markov models and hidden Markov tree. These innovative methods were then applied to the conventional QT database, according to the first method we have a $Se=99,40\%$ for QRS detection and a $Se=94,65\%$ for T wave detection. The second method have reached a $Se=99,95\%$ for QRS detection and a $Se=97,79\%$ for T detection.

The combination of these techniques has shown to be very efficient tool for ECG delineation; the good time-frequency resolution of the wavelet transform can successfully overcome some of the inherent problems of the ECG signal, such as noise and baseline drift. The HMM Markov chain can successfully capture the structural ECG properties, such as the cyclic ECG characteristics occurrences. These methods have a more intuitive approach to ECG delineation : focusing on relevant ECG parts, that are easily distinguishable, instead of ECG individual samples. It can be concluded, that the results of our methods can compete with other published work, and is a good candidate for further development.

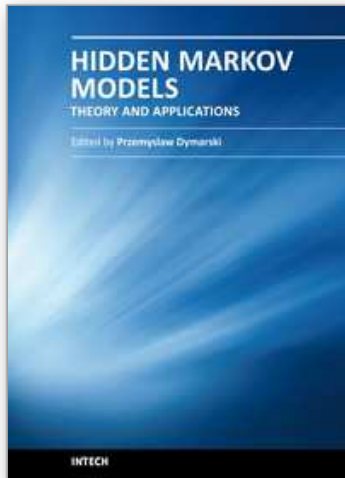
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Hidden Markov Models (HMMs), although known for decades, have made a big career nowadays and are still in state of development. This book presents theoretical issues and a variety of HMMs applications in speech recognition and synthesis, medicine, neurosciences, computational biology, bioinformatics, seismology, environment protection and engineering. I hope that the reader will find this book useful and helpful for their own research.

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