PITCH SYNCHRONOUS WAVELET AND HIDDEN SEMI-MARKOV MODELS BASED METHOD FOR ECG ANALYSIS

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ABSTRACT

In this paper 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.

1. INTRODUCTION

The ElectroCardioGram (ECG) is an electrical activity recording of the hearth. The ECG is widely used for diagnosing many cardiac diseases. Most of the clinically useful information from the ECG is found in the amplitude and intervals defined by its characteristic points. These characteristic points are the P, QRS and T waves.

Much research has been done in the past on automatic ECG analysis. Two main approaches to ECG analysis can be distinguished: QRS detection algorithms and ECG delineation algorithms. QRS detection focuses on the detection of the peak of the QRS wave. A wide diversity of algorithms has been proposed in literature [1]. The QRS complex detection is necessary to determine the heart rate, which is essential for modern pacemakers.

In this paper, we focus on a new technique for ECG delineation, namely the Pitch Synchronous Wavelet Transform (PSWT) with Hidden Semi Markov Models (HSMM).

The Pitch Synchronous Wavelet Transform (PSWT) is based on a modelling concept, which is able to capture period to period fluctuation of the signal by means of basis elements that are comb-like in the frequency domain. This technique relies primarily on the positions of high peaks corresponding to the R wave of the ECG. 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 [2].

Hidden Markov Models (HMM) allow us to characterize the occurrences of ECG patterns (P, QRS,T) waves with a probability density function, and still preserve the cyclic structural properties of the ECG by its underlying Markov chain. In [3] a thorough overview of Hidden Markov Models is given and in [4] the theory of Hidden Markov Models is applied to ECG analysis.

The paper is organized as follows: in section 2, Pitch Synchronous Wavelet Transform (PSWT) is presented, in section 3 we describe the Hidden Semi Markov Model (HSMM) with the combination of the PSWT. Results and discussion were given in section 4. Finally, section 5 concludes this work.

2. PITCH SYNCHRONOUS WAVELET TRANSFORM

This section considers applying the wavelet transform in a pitch-synchronous fashion as originally proposed in [2],[5]. 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 [6].

Pitch synchronous schemes have often been used to describe speech and musical sounds. These differ from standard block-based approaches in that they do not analyse a fixed amount of samples but a varying number that depends on the pitch of the signal. This idea was combined with the theory of wavelets by G. Evangelista in [2].

Pitch synchronous wavelet transform 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 [5],[6].

Wavelet analysis achieves a good balance between time and frequency resolution across a number of bands by decomposing the ECG signal into elementary functions at different scales, well localized in both domains. This approach characterizes the local regularities of signals, pivotal to distinguishing ECG waves from serious noise; artifacts and baseline drift [7]. QRS complex is the most prominent wave in an ECG signal; this is why detection of QRS complex is the very first job to be done. Throughout the whole data if we can locate the positions of the QRS complexes, then detection of other waves such as P-wave can be done [9].

The wavelet transform represents the signal in a scale-time space, where each scale can be seen as the result of a pass band filtering. The frequency bands depend on the scale and also on the type of the chosen wavelet function. From the mother wavelet $\psi \in L^2(\mathbb{R})$ with zero mean, the class of wavelets is then [8]:

$$\overline{\psi}_a(t) = \frac{1}{\sqrt{a}}\psi^*\left(\frac{-t}{a}\right) \quad (1)$$

Where $\psi_a(t)$ is a wavelet in the scale a and ψ^* represents the wavelet complex conjugate. Thus, the wavelet transform is given by:

$$Wx(t,a) = x * \overline{\psi}_a(t) = \frac{1}{\sqrt{a}}\int_{-\infty}^{+\infty} x(t)\psi^*\left(\frac{\tau - t}{a}\right)d\tau \quad (2)$$

This equation shows that the wavelet transform is the convolution between the signal and the wavelet function at scale a. Moreover, it can also be viewed as the correlation computation between the wavelet function and the ECG signal.

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* $q = 0, ..., p[k]-1$ 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 $l = 1, 2, ..., L$, the pitch synchronous wavelet expansion of the signal $x[n]$ is defined by the following sum:

$$x[n] = \sum_{l=1}^{L} w_l[n] + r_L[n] \quad (3)$$

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:

$$r_L[n] = \sum_{m,q} \sigma_{L,m,q}\vartheta_{L,m,q}[n] \quad (4)$$

$$w_l[n] = \sum_{m,q} S_{l,m,q}\xi_{l,m,q}[n] \quad (5)$$

Where $\xi_{l,m,q}[n], \vartheta_{L,m,q}[n]$ (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 [10].

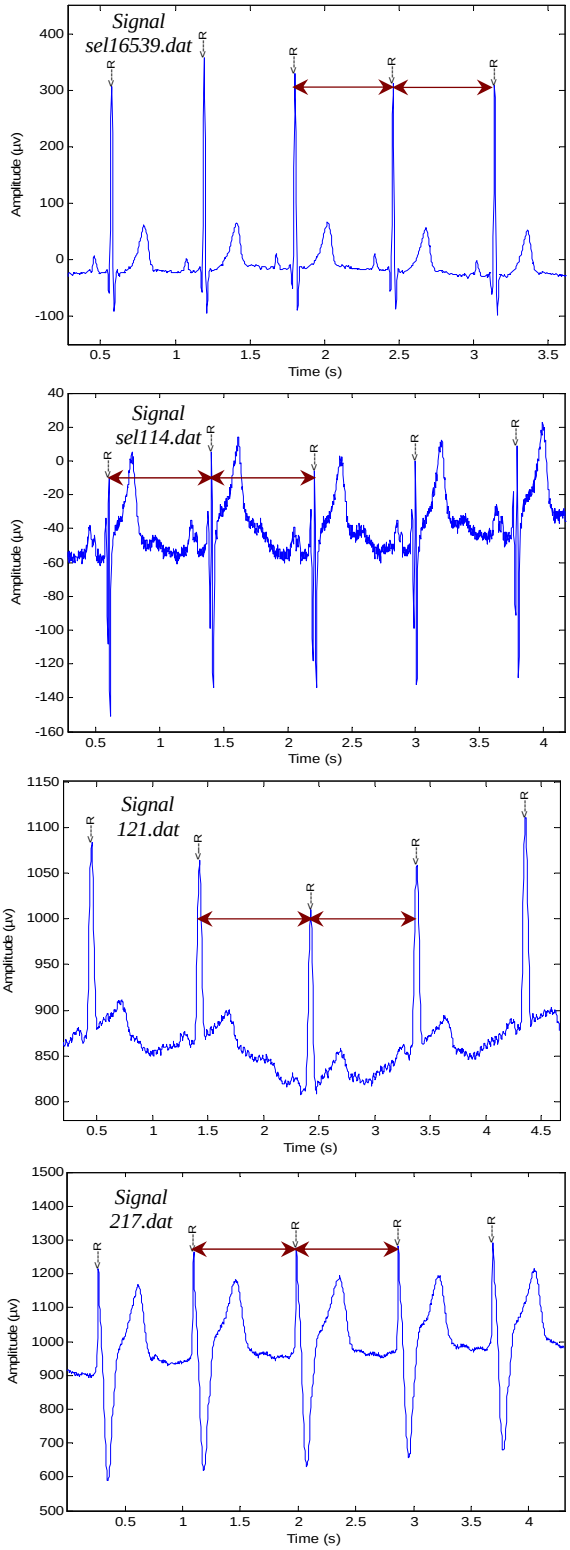

Figure 1 – One period (cycle) estimation by PSWT for different signals taken from *QT database*

We have chosen those signals from *QT* database because they show many kinds of pathological ECG signals (noise, baseline drift, ambiguous waves, Artefacts, etc).
We show in figure 1 the one period (cycle) estimation by PSWT for different types of ECG signals taken from *QT* database: the first one from healthy patient (*Signal sel16539.dat*), the second (*Signal sel114.dat*) from a patient how have high T waves, larger than the R peaks and corrupted by noise, the third (*Signal 121*.dat) from a patient having baseline drift and the fourth (*Signal 217*.dat) from a patient showing ambiguous waves.

3. HSMM FOR ECG ANALYSIS

We developed a HSMM to analyse ECG signals. The developed HSMM has the same topology as the normal HMM without the self transitions and is similar to the HSMM presented in [11]. It consists of five states, the P, QRS and T states. The b_1 and b_2 states model the baseline of the ECG between these peaks, as shown in figure 2. No baseline segment is modelled between the QRS complex and the T wave. This is because in the manually annotated databases used for evaluation, the onset of the T wave is not annotated. This makes extracting specific information from this part of the ECG complicated.

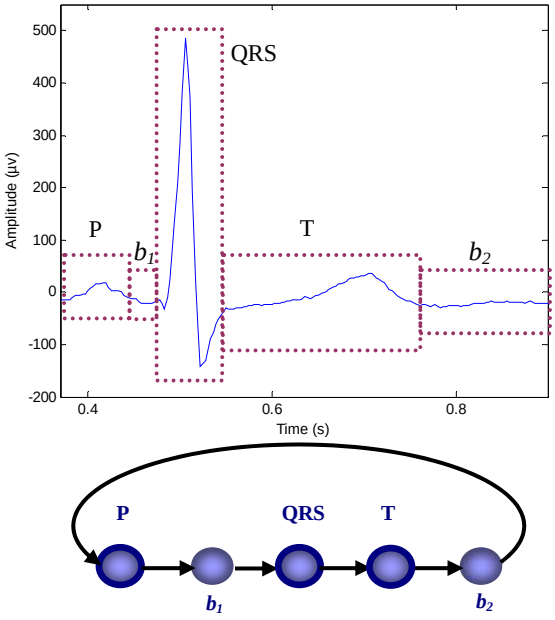

Figure 2 – HSMM topology model designed to ECG delineation

3.1. HSMM Theory

A Hidden Markov model is a system defined to be in one of N states, $S_1, S_2, ..., S_N$, at any discrete time step, $t = 1, 2, ..., T$. At each discrete time step the model switches from its current state to a different (or possibly the same) state, according to a certain state transition probability.
In a first order Markov model the probability of being in state j at time $t+1$ is only dependent on the state at time t. We denote the actual state the system is in at time t as q_t. The state transition probabilities are then:

$$a_{ij} = P(q_t = S_j \mid q_{t-1} = S_i) \quad (6)$$

In a conventional HMM the probability to stay in state i, regardless of the observations made, for t time steps and then leaving it's:

$$P(q_1, ..., t_{t-1} = i, q_t \neq i) = (a_{ii})^{t-1}(1 - a_{ij}) \quad (7)$$

This probability is the geometric probability density function (*pdf*) with respect to t.
In most applications this *pdf* is not adequate for the events durations in the signal at hand, therefore it is desirable to model the time spent in a state more accurately.
In the human ECG, the T-peak normally has the longest duration. Therefore, it is harder to model it properly with a standard HMM; the probabilities of staying in the same state (the T-state) during the whole span of the T-wave become very low. The Hidden Semi-Markov Model (HSMM) is better equipped to model this.
In the HSMM the self-transitions of the states are set to zero, a probability density function $p_i(d)$ is modelled for each state i to govern the time probability d spent in each state. This differentiation is best understood if we look at the generative aspect of the HMM and the HSMM [11].

In the HSMM there is an extra step to take before the state transition step, in order to model the time spent in a state before going to the next state:

- An initial state $q_1 = S_i$ is chosen according to the initial state distribution π_i.
- A state duration, d, is chosen according to $p_i(d)$.
- Observations $O_t,\ldots, O_{t+d}$ are generated according to the observation probability $b_i(O_t)$.
- The next state $q_{t+d+1} = S_j$ is chosen according to the state-transition matrix $A = \{a_{ij}\}\ 1 \le i, j \le N$.*
- Steps 2-4 are repeated until $t = T$.

3.2. Segment Modelling

In the HSMM a segment is the sequence of observations $O_t,\ldots, O_{t+d}$, observed while remaining in a single state i. The probability of such a sequence is calculated as:

$$P(O_t, ..., O_{t+d}) = \prod_{s=t}^{t+d} b_i(O_s) \quad (8)$$

Like in the standard HMM, each state has a *pdf* and the probability of an observations sequence is calculated as if the observations are independent and identically distributed. In ECG analysis, when we would like to model, for instance, a T wave, the samples taken from the T wave are not independent of each other and are not all distributed according to the same *pdf*. In order to overcome this shortcoming of the HMM and HSMM, it has been proposed to model a segment as a whole and not as individual samples. The probability $P(O_t, \ldots, O_{t+d} | q_t = S_i)$ is calculated by a specific segment model. In [12] a number of different segment models are presented. These segment models give a different approach to model the probability $P(O_t,\ldots,O_{t+d})$, but the segment model is not essentially different from the HSMM.

3.3. PSWT as input for the HSMM

The ECG PSWT coefficients can be employed as an input 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, $Wx(t,a)$].

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 $O_t \ldots O_{t+d}$ [that represent multiple pitch synchronous wavelet coefficients, $Wx(t \ldots t+d, a)$].

In the HSMM, the probability of the segment observations $P(O_t,\ldots,O_{t+d})$, is calculated as the product of the individual observations that make up the segment, as if they where independent identically distributed observations.

4. RESULTS AND DISCUSSION

In order to evaluate our performance method for ECG delineation by PSWT as input to HSMM, we use a standard database: *QT* database (QTDB) [13], which is freely available from the Physionet website. 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. The record names excluded from the test set are: *sel232*, *sel35* and *sel37*.

To asses the detection performance of the different waves we calculated the sensitivity *Se* and the positive predictivity P_+ of several events.

$$Se = \frac{TP}{TP + FN} \quad \& \quad P_+ = \frac{TP}{TP + FP} \tag{9}$$

Where,

- TP is the number of True Positive detections, a true positive is recorded when at a certain point the cardiologist annotates a wave and the method also detects a wave in a certain annotation neighbourhood.
- FN is the number of False Negative detections, a false negative is recorded when the cardiologist annotates a wave, but that wave is not detected by the detection method.
- FP is the number of False Positive detections, a false positive is recorded when the method detects a wave at a certain point, but the cardiologist did not annotate a wave there. The false positive calculation is a problem for the QTDB, as noted in [14]. When there is no annotation, we do not know for certain whether the cardiologist considered that no wave was present or that the wave could not be annotated confidently because of noise or other causes.

In the QTDB, 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 then the QRS-peak. In an annotated beat, each absent manual annotation in the neighbourhood of an automatic detection can be considered as a false positive.

Therefore, the wave detection rates are calculated as follows:

A TP is calculated for the QRS complex and the T-wave, when at the annotated QRS-peak or T-peak the HSMM of the PSWT method is in the QRS or T state respectively. When this is not the case, a FN is recorded.

As argued above, the P_+ can not be computed for QRS detection, but this can be computed for the onset of the QRS complex QRS_{on}, and the offset of the T-wave 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 QTDB, the mean and standard deviation of the QT time of these beats is measured *manQTt*. The mean and standard deviation of the time difference between the manual and automatic QT times is measures 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.

4.1. Single set

The *single set* is performed with HSMM as described in section 3. We use the PSWT of the ECG signal as input for the HSMM. The observation probabilities are modelled with Gaussian Mixture Models with 2 mixtures.

In this test, for each record, one lead is chosen and the HSMM is trained in a supervised manner on that lead. The results are shown in Table 1.

Table 1: Characteristic of the validation database

Parameter	QRS	QRS_{on}	T	T_{off}	*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		

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 Sensitivity and positive predictive value 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.

5. CONCLUSION

In this study, the emphasis is on the combination of the PSWT and HSMM for ECG analysis. 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. The HSMM has been researched and implemented.
This extensive model which models the ECG waveforms more accurate might improve detection rates. The results of this method trained on individual records of the test database 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}.

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