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# ECG Signal Analysis Through Hidden Markov Models

Rodrigo V. Andreão\*, Bernadette Dorizzi, and Jérôme Boudy

**Abstract**—This paper presents an original hidden Markov model (HMM) approach for online beat segmentation and classification of electrocardiograms. The HMM framework has been visited because of its ability of beat detection, segmentation and classification, highly suitable to the electrocardiogram (ECG) problem. Our approach addresses a large panel of topics some of them never studied before in other HMM related works: waveforms modeling, multichannel beat segmentation and classification, and unsupervised adaptation to the patient's ECG. The performance was evaluated on the two-channel QT database in terms of waveform segmentation precision, beat detection and classification. Our waveform segmentation results compare favorably to other systems in the literature. We also obtained high beat detection performance with sensitivity of 99.79% and a positive predictivity of 99.96%, using a test set of 59 recordings. Moreover, premature ventricular contraction beats were detected using an original classification strategy. The results obtained validate our approach for real world application.

**Index Terms**—Ambulatory electrocardiography, hidden Markov models, on-line adaptation, PVC detection, signal segmentation.

## I. INTRODUCTION

THE automatic analysis of the electrocardiogram (ECG) has been the subject of intense research during the last three decades and is well-known in the biomedical engineering field. The particular interest for ECG analysis comes from its role as an efficient noninvasive investigative method which provides useful information for the detection, diagnosis and treatment of cardiac diseases [1].

Presently, the ambulatory electrocardiography (AECG) is particularly studied since it provides precise and rich information from the clinical point of view for the diagnostic of cardiac diseases. The automatic analysis of the AECG can considerably help the physician, reducing the time spent to analyse recordings of 24 and 48 h of duration [2].

The ECG signal has a time periodicity allowing to define an elementary beat composed by specific waveforms, appearing periodically in time. Fig. 1 shows a heartbeat and its respective waveform labels. The study of the waveform amplitudes and patterns constitutes the basis of the ECG signal analysis. For instance, one can easily show that the heart rate is esti-

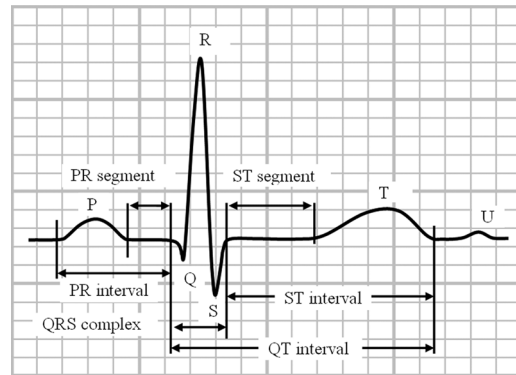


Fig. 1. Heartbeat observed on an ECG with its elementary waveforms and intervals identified.

mated after detecting the QRS-complex from a beat sequence. In the same way, the time-distance between two consecutive QRS-complexes, known as RR-interval, is used to detect premature beats. We can extend this analysis to other conditions like the ST-segment deviation from a long period, necessary to early diagnosis of ischemia. As a result, reliable ECG analysis depends directly on the ECG beat segmentation results [1], [3].

Most works in this field employ heuristic rules to segment heartbeat automatically from the ECG signal after performing a suitable preprocessing technique [4]–[9], and many authors underline the advantages of the wavelet transform. The multiscale decomposition improves robustness, when the signal is corrupted by noise [6], [10], [11]. On the other hand, regarding the beat classification task, a large number of methods have already been proposed. In general, the classification approaches are heuristic [12]–[14], namely decision trees and fuzzy logic [15], and statistics, namely discriminant analysis [15], hidden Markov models (HMMs) [16], neural networks [17]–[21], and statistical ruled based systems [22]. Among the statistical approaches, the HMMs have drawn attention since Coast's pioneer work [23], [16].

In the approach of Coast *et al.*, the HMM topology keeps the beat structural characteristics while the model parameters take into account the statistical nature of the observations [16]. The HMMs can model a waveform sequence namely, the duration of each waveform and interval within a beat [16]. Moreover, the intra-individual variability of the beat length, particularly due to the heart rate variations, can be incorporated into the model state transitions. Another advantage of the HMMs is their ability to carry out at the same time three different tasks: beat detection, segmentation and classification. Furthermore, the HMMs replace the heuristic rules commonly used for waveform detection, which generally requires thresholds. Following Coast *et*

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*al.*, other works using HMMs were implemented specially to the isolated beat segmentation problem aiming at detecting the P wave [24], [25].

In this paper, the HMMs are used to carry out beat detection and segmentation. Our main contributions are based on the following [26], [27].

- 1) Waveform modeling (and not beat modeling) using generic HMM (trained through examples from several individuals). In this way, HMMs are trained taking into account the morphology diversity of each waveform.
- 2) Better waveform segmentation precision by adapting a generic model to each individual. The model adaptation is done in an unsupervised way, eliminating waveform manual labeling [16].

With regard to the classification problem, our system takes advantage of two complementary approaches: statistical and heuristic. As a result, it was not necessary to model beforehand different beat abnormalities using specific HMM. Each abnormal beat class (e.g., premature ventricular beats) can be taken into account by only adding new rules associated to it.

Finally, a fusion strategy which explores information obtained from multiple channels is proposed to be a postprocessing phase aiming at making the beat segmentation and classification tasks more reliable and efficient.

This paper is organized as follows. In Section II, we describe our beat segmentation approach based on HMMs. Section III presents our ECG analysis system which performs both beat segmentation and classification. Section IV validates the system through experiments on the QT database. The paper ends with conclusion and future works.

## II. MARKOVIAN APPROACH TOWARDS AUTOMATIC ECG SEGMENTATION

### A. HMM Overview

A HMM is a stochastic state machine, characterized by the following parameter set:

$$\lambda = (\mathbf{A}, \mathbf{B}, \boldsymbol{\pi}) \quad (1)$$

where  $\mathbf{A}$  is the matrix of state-transition probabilities,  $\mathbf{B}$  is the observation probability, and  $\boldsymbol{\pi}$  is the initial state probability.

One way to characterize HMMs is by the structure of the transition matrix  $\mathbf{A}$ , which can be fully connected (ergodic). However, the left-right structure is more appropriated to model the ECG signal (see Section II-C).

The observations of a HMM  $\mathbf{O} = (\mathbf{o}_1 \mathbf{o}_2 \dots \mathbf{o}_T)$  are continuous signal representations (signal features), modeled by a Gaussian probability density function of the form

$$b_j(\mathbf{o}_t) = \frac{1}{\sqrt{2\pi|\mathbf{U}_j|}} \exp \left\{ -\frac{1}{2}(\mathbf{o}_t - \boldsymbol{\mu}_j)^T \mathbf{U}_j^{-1}(\mathbf{o}_t - \boldsymbol{\mu}_j) \right\} \quad (2)$$

where  $\mathbf{o}_t$  is the observation vector at time  $t$ ,  $\boldsymbol{\mu}_j$  is the mean vector, and  $\mathbf{U}_j$  is the covariance matrix at state  $j$ . The size of

the observation vector  $\mathbf{o}_t$  is related to the number of distinct observation symbols (continuous or discrete) used to represent the signal.

The parameters estimation can be seen as an optimization problem. The solution of this problem can be obtained by maximizing locally the likelihood  $P(\mathbf{O}|\lambda)$  of the model  $\lambda$  using an iterative procedure such as the Baum-Welch method (which is a particular case of the expectation-maximization method) or using gradient techniques [28]. In the speech recognition field, where the HMMs became so popular, the Baum-Welch method, also called as forward-backward algorithm, is considered a standard for HMM training. Furthermore, in biomedical applications using HMMs, this method is also widely employed [29].

### B. Parameter Extraction

This phase allows the representation of the ECG signal by an observation sequence. We have chosen to use a continuous wavelet transform to perform this task, corresponding to different frequency bands [30].

The mother wavelet must match as much as possible the shape presented in the signal. According to the work of Torrence and Combo [31], the Mexican Hat is more suitable to peak detection because of its shape and good time resolution. However, few works have explored so far this wavelet function to ECG analysis (particularly in the QRS detection problem) [21], [32], remaining more predominantly the choice of other functions like the quadratic spline [6], [11] and the first derivative of the Gaussian function [10].

The Mexican Hat function is defined as

$$Wf(n, j) = \sum_{m=0}^{M-1} f[m] \times \bar{\psi}_j[m-n] \quad (3)$$

$$\bar{\psi}_j[n] = \frac{1}{\sqrt{2^j}} \frac{2}{\sqrt{3\pi^{1/4}}} \left[ 1 - \left( \frac{n}{2^j} \right)^2 \right] \exp \left[ \frac{1}{2} \times \left( \frac{n}{2^j} \right)^2 \right] \quad (4)$$

where  $f$  is the sampled signal composed of  $M$  samples,  $\bar{\psi}_j$  is the Mexican Hat wavelet function at the dyadic scale  $j$  for  $j \in \mathbb{N}$ , and  $-5 \leq n \leq 5$  for  $n \in \mathbb{Z}$ . Besides the wavelet type, it is necessary to specify the scales to be employed. We have noted that the first 4 dyadic scales (scale  $s = 2^j$ , where  $j = 1, 2, 3$  and 4) contain most of the signal information, and that the scales higher than  $s = 2^4$  can be excluded. Moreover, we have also observed after performing some experiments that the scale  $j=1$  is very affected by noise and that its elimination does not imply a loss of performance. For more details on wavelet transforms, the reader may refer to [33].

### C. Heartbeat Modeling

As shown previously (Fig. 1), a heartbeat can be seen as a waveform sequence, separated by isoelectric segments (PQ and ST segments). Moreover, these waveforms are produced cyclically. Therefore, it is reasonable to consider each waveform or segment as a state of a left-right Markov model. From this analysis, Coast *et al.* proposed the use of a HMM to segment the ECG signal [16] (see Fig. 2).

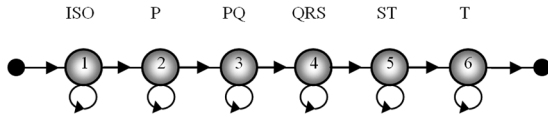


Fig. 2. Left-right HMM model of a normal beat [16].

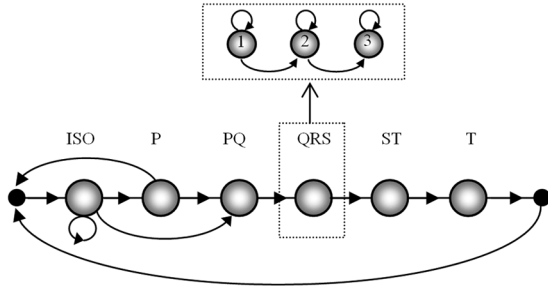


Fig. 3. Beat model composed of connected HMM of each beat waveform and segment. The transition from P to ISO models ECG signals with P waves not conducted by a ventricular activity. The transition from ISO to PQ models ECG signals with supraventricular arrhythmias without visible P wave.

The HMM topology of Fig. 2 is suitable to model a normal beat. By removing some states from this topology, other beat types can be modelled. Coast *et al.* underlined, however, one drawback of their model, where for example an atrial activity not conducted (i.e., a heartbeat where the P wave is not followed by a QRS complex) cannot be modeled [16]. Another drawback is related to the way the model is trained. It means that, if one wants to model a new P wave morphology (or a QRS complex), a complete new beat model must be built. Thus, when several morphological classes of one beat waveform are present, several beat models have to be built, increasing the complexity substantially.

These remarks drove us to conceive one beat model based on connected elementary HMMs of each waveform and segment, called elementary waveform models (see Fig. 3). Consequently, we will be able to model a great variety of beats simply by combining the elementary waveform models.

The beat model of Fig. 3 can take into account other beat types through the arcs or transitions among the waveform models, as follows.

- 1) *Transition from P wave model to ISO model:* This transition represents P waves not conducted by a ventricular activity (typical symptom of bundle block [34]).
- 2) *Transition from ISO to QRS model, skipping P wave model:* In this case, ventricular and supraventricular arrhythmias without visible P wave can be modeled [34].

The transitions are equiprobable and considered to be equal to one. It is important to point out that this model is consistent with the constraints of the heart electrical activity.

#### D. Generic Model

Our first goal is to build a generic system which is adapted to a population. Certainly, considering the ECG signal diversity among different individuals, we cannot expect from such a system an optimal result for each individual. Therefore, this generic system will be the starting point before building, for each individual, a more adaptive model.

1) *Training:* The HMM training consists of estimating the model parameter set  $\lambda = (\mathbf{A}, \mathbf{B}, \pi)$  from the observation sequence  $\mathbf{O}$ . The HMM parameter estimation is carried out by the Baum-Welch method (expectation-maximization method) [28], [36]. Each HMM is adapted to its respective waveform patterns. The number of states of each model was specified empirically after some simulations. Starting with one state per model, we increased the number of states until we achieve a good compromise on complexity versus performance: 3 states for the ISO, P wave, and QRS-complex models; 2 states for the PQ and ST segment models; 6 states for the T wave model. It must be pointed out that the number of states must be proportional to the duration of each beat waveform [34]. Additionally, histograms of the observations values for every state of every HMM were constructed. It was observed that most of the histograms appeared to be well fitted by a single Gaussian. For this reason, we considered only one Gaussian density function per state.

After training one HMM for each waveform, the multiple model training procedure starts. The number of models for each waveform depends on the variety of morphologies present in the training set. The number of models used to represent the QRS-complex is greater than the number of models of the other waveforms due to its variability. The training algorithm is called HMM likelihood clustering, and it was firstly applied by Rabiner to the speech recognition problem [35]. We have used 4 HMMs for the QRS complex waveforms, 2 HMMs for each of the other waveforms, and 1 HMM for the ISO model.

2) *Automatic ECG Segmentation:* The ECG segmentation can be seen as the decoding procedure of an observation sequence in terms of beat waveforms. The main point of our decoding procedure is the use of the one-pass algorithm [28], which was originally conceived to perform online decoding when working with connected HMMs. This method has been widely employed in the speech recognition field [28] to reduce significantly the complexity of the decoding problem. It works on two dimensions: time and level. In our case, we have associated the level to the waveform position in the beat model. Hence, level 1 represents the isoelectric line or ISO model, level 2 the P wave model, and so on until level 6 which represents the T wave model.

The main idea of the method is to do a time warping between the observation sequence and the connected HMMs through a Viterbi decoding procedure. However, to pass from one level  $l$  to another level  $l+1$ , we only consider the most likely model from level  $l$ .

#### E. Individualizing the Generic Model

Generic model is able to provide waveform segmentation of a beat sequence no matter the individual, even if the individual is not present in the training set. However, the performance of the system in terms of segmentation precision (particularly of the P wave) decreases when working on signals very different from those present in the training set. For this reason, we expect a significant performance improvement after adapting the generic model to the individual's specific waveforms.

The individualization of the generic model corresponds to the re-estimation of each generic HMM on a new training set (specific to the individual) via Baum-Welch method. The training set

is built from the segmentation and labeling of the ECG signal in an unsupervised way by the one-pass algorithm (see Section II-D). We propose a HMM adaptation strategy divided into the following two stages.

- 1) *Stage 1*: The generic models are adapted one time to the ECG signal morphologies of the individual using the first frame (20 s.) of the ECG signal. At this stage, we match the segmentation results generated by the generic model with those generated by a heuristic approach in order to fit more precisely the different parts of the heartbeat to the individual's specific waveforms. It will be described in more detail later.
- 2) *Stage 2*: This stage aims at adapting the Markov model to the individual's signal fluctuations which can happen during long-term recordings. The Markovian approach is already able to precisely segment new individual's heartbeats. The covariance matrices of the Gaussian density functions are updated only when the matrix coefficients are larger than the previous one.

Stage 1 adaptation is performed on the observation sequence extracted from the ECG and more precisely on the scale  $j=2$ , on which the QRS-complexes are in general better detected. One simple threshold corresponding to 25% of the maximum amplitude is then employed to detect the QRS peaks. It is enough to detect true QRS complex and to reject low amplitude peaks due to artifacts. Afterwards, the RR interval between consecutive peaks is checked. For RR intervals below 200 ms, only the highest peak is considered [13], [14]. The second goal of the heuristic approach is to adjust the waveform onset and offset labeled by the generic model according to the waveform amplitudes specific to the individual. The following two algorithms were implemented.

- 1) *QRS-complex onset and offset correction*: This procedure consists of following the ECG signal slope around the QRS-complex onset and offset (labeled by the generic model) until the slope value is small enough and the signal amplitude decreases below 0.02 mV [37]. Then a new value of onset or offset is calculated. The ECG signal is processed beforehand by a low-pass filter in order to reduce the high frequency noise [37].
- 2) *P wave onset and offset correction*: P wave correction is carried out at scale  $j=2$  of the Mexican Hat wavelet transform. We have considered the P wave peak as the local maxima before the QRS-complex onset and the P wave onset and offset as two negative local minima located, respectively, before and after the local maxima.

Since the magnitude of one ECG recording is not necessarily the same as the one of the training set of the models, we compute a gain factor  $G$  during the first ECG signal frame. The gain factor  $G$  is obtained by dividing the peak-to-peak mean amplitude of the QRS-complexes of the training set by the peak-to-peak mean amplitude of the QRS-complexes detected at the first recording frame.

### III. AUTOMATIC BEAT SEGMENTATION AND CLASSIFICATION

Our HMM approach described in Section II becomes *layer 0* of a two-layer architecture as follows (see Fig. 4): In *layer 1*, the waveforms are gathered to build a beat sequence. Each beat

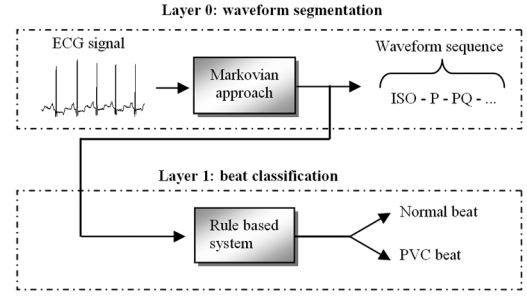


Fig. 4. General block diagram of our beat segmentation and classification system.

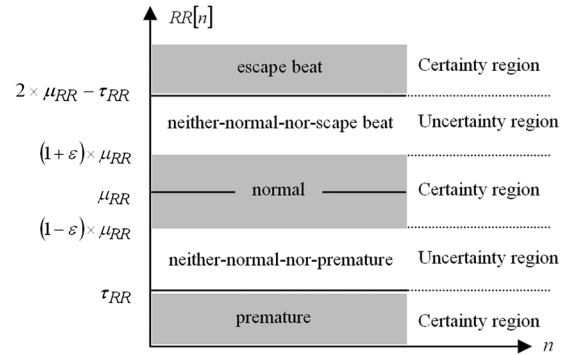


Fig. 5. Graphical illustration of the certainty and uncertainty regions of three beat classes employed to classify the RR intervals: (a) certainty regions: premature, normal, and escape beat; (b) uncertainty regions: neither-normal-nor-premature and neither-normal-nor-escape beat.

is then classified as normal or abnormal. Only two classes were considered: normal beats and premature ventricular contraction (PVC) beats.

#### A. Premature Ventricular Beat Detection

PVC beats have two well defined features which are sufficient to distinguish this abnormality from the other ones: beat prematurity and enlarged QRS morphology.

1) *Premature Beats*: One beat is premature (earlier than expected) when the length of its interval  $RR$  is below a threshold  $\tau_{RR}$ . On the other hand, when the interval  $RR$  length is above a threshold  $\tau_{RR}$ , the beat is classified as normal or escape beat (later than expected). We compute the threshold  $\tau_{RR}$  adaptively taking the mean value  $\mu_{RR}$  of the last  $N_{RR}$  normal RR intervals.

Beat classification in terms of the RR interval is very sensitive to the threshold. The most suitable way to overcome this problem relies on the definition of an uncertainty region at the class boundary (see Fig. 5). Thus, the system becomes more robust to interval  $RR$  variations closer to the threshold. The new boundaries are placed in positions  $(1 \pm \epsilon) \times \mu_{RR}$  around the mean value  $\mu_{RR}$ . The value  $\epsilon$  is empirically estimated after simulations on a training set composed of 19 recordings (see Section IV-A).

In addition, we added a decision logic to manage the cases where the RR interval falls in the uncertainty region: a) when two consecutive intervals  $RR[n-1]$  and  $RR[n]$  are in the same uncertainty region, the beat  $n-1$  becomes normal; b) when beat  $n-1$  is neither-normal-nor-premature and the beat  $n$  is neither-normal-nor-escape beat, beat  $n-1$  becomes premature.

The decision logic b) classifies a doubtful beat as premature, since this beat is followed by a compensatory pause at time  $n$ .

2) *Ventricular Beats*: A ventricular beat is characterized by a QRS-complex wider than the normal size due the existence of a depolarization wave originating in an ectopic pacemaker in the ventricles, instead of taking the fast and normal pathway of the conduction system [34], [40]. To classify a ventricular beat, it is necessary to estimate the individual's normal shape of its QRS-complex.

In this paper, the QRS-complexes are labeled normal or abnormal by the likelihood of each QRS-complex given by the HMM. The normal QRS is defined as the individual's dominant model  $\lambda_d$  among several slightly different generic QRS-complex HMMS in the first 20 s. of the ECG recording. The HMM which has segmented most of the QRS-complexes is defined as the individual's dominant HMM  $\lambda_d$ . Then, the likelihood  $P(\mathbf{O}|\lambda_d)$  of every QRS-complex observation  $\mathbf{O}$  given the dominant model  $\lambda_d$  is computed. An abnormal QRS is defined in the remaining of the ECG recording when the likelihood values of the observation sequence  $\mathbf{O}$  of each QRS-complex segmented given the dominant model  $\lambda_d$  is smaller than  $\tau_{QRS}$ . If the QRS complex is normal the decision threshold  $\tau_{QRS}$  is readapted.

### B. Multichannel Fusion

Our system was conceived for a single-channel context. However, when multichannel information is available, it is possible to explore the complementarity of the information among channels in order to improve performance. For instance, a beat detection error can occur in only one lead, since the QRS shape and the signal to noise ratio may differ among channels. In this situation, the only way to certify that a beat has been well detected is by comparing the information from different leads.

Even though we guarantee that all beats were correctly detected, the classification task is still prone to errors when only one channel is available. Indeed, the QRS shape of some abnormal beats may not be identified in some leads (e.g., premature ventricular beats may be misclassified whenever the QRS shape is not clearly wider than the normal one).

The discussion above leads us to take advantage of multiple leads. For this reason, we performed two types of fusion, namely one at *layer 0* and another at *layer 1* of our system. The fusion strategy at *layer 0* aims at confirming beat detection, whenever it is detected in all channels available. We have considered that a beat detected in one channel corresponds to the one detected in another channel when the distance between the labels is shorter than 200 ms (the label is placed on the QRS-complex peak of highest amplitude). In that case, a simple logic AND operation is used. On the other hand, the goal of the fusion strategy at *layer 1* is to use the complementarity of each channel. In fact, some abnormal beats are not detected in all leads. Thus, by using a simple logic OR, a beat is classified as abnormal only if there exist at least one lead where such a phenomena occurs.

## IV. EXPERIMENTS

### A. QT Database

The QT database fills a gap in the available ECG databases, since it provides manual labels of the beat waveforms: P wave,

TABLE I  
NUMBER OF EXAMPLES OF EACH BEAT WAVEFORM IN THE TRAINING SET

QTDB – HMM training	
Waveform	Number of examples
P wave	660
PQ segment	719
QRS-complex	770
ST segment	339
T wave	760
ISO (isoelectric line)	697

TABLE II  
NUMBER OF NORMAL (N) AND PVC BEATS IN BOTH TRAINING AND TEST SETS

Corpus	Normal beats	PVC beats
Training	20809	321
Test	60168	1375
Total	80977	1696

QRS-complex, T and U waves [39]. It also gathers several recordings from different databases belonging to the Physionet Bank [40], including the MIT-BIH Arrhythmia Database, the European Society of Cardiology ST-T Database, and several other ECG databases collected at Boston's Beth Israel Deaconess Medical Centre. Additional recordings were also chosen from patients who experienced sudden cardiac death, and age-and-gender matched patients without diagnosed cardiac disease.

This database contains 105 two-channel recordings of 15 min, sampled at 250 Hz. All recordings include labels of waveform peaks and boundaries of at least 30 beats, given a total of 3623 beats. Two independent set of annotations were made by two cardiologists. The first expert annotated all recordings while the second one annotated only 11 recordings. The second set of annotations was not used in this paper because it was less representative [11]. Finally, 82 files have all their QRS complexes manually labeled and the beat class specified among more than 13 different beat families. These labels correspond to the original annotations provided by the source database. It is important to note that the type of the ECG leads associated to each channel is different for each recording, according to the physician's choice. Additional labels generated by the Laguna's approach are supplied with the database [5], [39].

We divided the QT database in different training and test sets as described below.

1) *Layer 0—HMM Training and Test Sets*: The QT database offers a great variety of beat morphologies and noise background. The training set is composed of 77 recordings, where 10 labeled beats were randomly selected from channel 1 of each recording. Then, the selected beats were segmented in both channels 1 and 2 by means of the waveform labels. P waves masked by noise were removed from the corpus. Table I summarizes the training set, used to train the generic models. Furthermore, a second random selection of 10 labeled beats from each recording was necessary to carry out supervised training of the individual's HMM. Finally, a test set including all 105 recordings of the QT database was used to evaluate the system performance.

TABLE III

WAVEFORM SEGMENTATION PRECISION IN MILLISECONDS (MEAN  $\mu$  AND STANDARD DEVIATION  $\sigma$ ) BETWEEN THE AUTOMATIC APPROACHES AND THE MANUAL LABELS OF THE QT DATABASE, USING ALL 105 RECORDINGS

Approach	Precision in ms											
	P wave				QRS-complex				T wave			
	Onset		Offset		Onset		Offset		Onset		Offset	
	$\mu$	$\sigma$	$\mu$	$\sigma$	$\mu$	$\sigma$	$\mu$	$\sigma$	$\mu$	$\sigma$	$\mu$	$\sigma$
(i) generic HMM training	16.0	18.2	-2.3	15.2	11.7	8.4	2.9	10.5	-15.1	24.0	3.1	29.9
(ii) individual's HMM training	1.2	14.4	-5.4	11.0	4.7	7.8	-4.2	8.9	-13.9	18.0	14.9	24.0
(iii) generic HMM adapted to each individual	12.5	13.8	-6.1	11.7	9.1	7.6	2.6	10.2	-9.8	9.3	12.1	21.5
Laguna	14.0	13.3	-0.1	12.3	-3.6	8.6	-1.1	8.3	-	-	13.5	27.0
Martinez	2.0	14.8	1.9	12.8	4.6	7.7	0.8	8.7	-	-	-1.6	18.1

2) *Layer 1—Training and Test sets*: The QT database aims particularly at evaluating segmentation approaches. However, the number of beats labeled as PVC in this database (1696 beats) is sufficient to test a PVC classification approach.

We took 19 out of the 82 recordings containing beat labels with the purpose of estimating the parameters employed in our PVC detection approach. The other 59 recordings compose our test set. The total number of normal and PVC beats is shown in Table II. We point out that the beats which are neither normal nor PVC were considered as normal in our experiments, which introduces a bias in the results. In fact, these beats correspond to 3% of the number of normal ones, which validates the protocol.

Three HMM training methods have been implemented: 1) Generic model training (Section II-D); 2) Individual's model training; 3) Generic models adapted to each individual (Section II-E). The individual's model training method is similar to the generic model training, except that the training set is taken from a single individual. Given the fact that the individual's training method works with a restricted number of examples for each individual, only one HMM per waveform was employed.

#### B. Layer 0 Results

The experiments at *layer 0* evaluate the segmentation performance of our HMM approach in terms of the following two parameters.

- 1) *Precision*: The onset and offset points of every detected waveform are compared to the manual labeled ones. As a result, we obtain a mean  $\mu$  and a standard deviation  $\sigma$  of the errors between our approach and the physician. The standard deviation for all recordings is computed as the average of the standard deviation of each recording [11].
- 2) *Waveform detection*: It gives the percentage of waveforms correctly detected, according to the labels produced by a physician.

In the first experiment, we compare our Markovian approach with the Laguna's and Martinez's heuristic approaches [5], [11], [41], on all the 105 recordings of the QT database, as shown in Tables III and IV. The generic model training method presents good segmentation results, but they are clearly inferior to those of the individual's model training method. In fact, the difference in performance is more visible on some beat waveforms (P-wave and the T-wave offset) having low amplitude, since these cases demand a more precise identification of the waveform onset and

TABLE IV

PERCENTAGE OF WAVEFORMS CORRECTLY DETECTED ACCORDING TO THE MANUAL LABELS OF THE QT DATABASE

Approach	Detection (%)		
	P wave	QRS	T wave
(ii) individual's HMM training	98,65	99,92	99,94
(i) generic HMM training	93,80	99,94	99,97
(iii) generic HMM adapted to each individual	96,43	99,92	99,94
Laguna	97,70	99,92	99,77
Martinez	98,87	99,97	99,00
Number of manual labels of the QT database	3194	3623	3543

offset. On the other hand, the adaptation of the generic models to each individual improved the generic model segmentation precision as expected.

Results from Table III point out that our approach reaches similar performances to those considered as the best one in the literature on the QT database [11] (4 ms can be seen as a segmentation error of only one sample between the automatic and the manual labeling, since the sampling frequency is 250 Hz). It is important to remark, nevertheless, that Laguna and Martinez computed the segmentation precision considering for each detected point (onset and offset) the channel which produced the less error [11]. Our strategy is different; we have used only one channel per recording in order to be coherent with the fact that the physician chooses the lead with the best signal quality before segmenting it.

Regarding the wave detection results from Table IV, we note that the P wave detection accuracy of the generic model is 5% less than the one of the individual's model, while the generic models after adaptation to each individual is only 2% less. This accuracy reduction compared to the individual's model did not occur to the QRS-complex detection. Concerning the generic model adapted to the individual, its reduced accuracy in terms of P wave detection can be explained by the influence of three particular recordings (sele0116, sel38, and sel40) with low amplitude P wave. Moreover, our amplitude control can affect in certain cases the P wave detection accuracy, since it changes the signal magnitude according to the average of the first QRS-complex peaks.

TABLE V  
QRS-COMPLEX DETECTION PERFORMANCE (IN TERMS OF SENSIBILITY SE AND PP) ON A TEST SET OF 59 RECORDINGS

QRS-complex detection					
Channel	TP	FP	FN	Se (%)	PP (%)
1	61468	258	75	99,88	99,58
2	61444	1248	99	99,84	98,01
Fusion	61414	24	129	99,79	99,96

In some particular cases where the P wave is hardly detected, it is convenient to perform manual labeling of these waves yielding to a suitable P-wave model re-estimation. Indeed, the individual's model results showed that a small number of examples is enough to train appropriately the HMM. All these considerations are not valuable for the heuristic approaches.

Finally, the experiments underlined the segmentation precision of our Markovian approach. It is still possible to improve the system by modeling explicitly the waveform duration [35]. As a result, we could avoid to segment the waveforms whose duration deviates too much from the estimated one.

### C. Layer 1 Results

We evaluated at *layer 1* our system ability in detecting PVC beats using a test set of 59 recordings from the QT database (see Section IV-A). Only the segmentation results provided by the adaptation of the generic models to each individual were taken into account. Two criteria were employed in accordance to the recommendations to assess performance of beat detection approaches [42]: sensibility and positive predictivity (PP). Sensitivity (Se) is related to the fraction of events correctly detected

$$Se = \frac{TP}{TP + FN} \quad (5)$$

where TP (true positive) is the number of matched events and FN (false negative) is the number of events that were not detected by our approach. The denominator of (5) gives the total number of annotated events in the test set. On the other hand, PP gives the ability of detecting true events

$$PP = \frac{TP}{TP + FP} \quad (6)$$

where FP (False Positive) is the number of events detected by our approach and nonmatched to the manual labels. A detected beat matches the manual label when the interval between both labels is shorter than 150 ms [42].

We assessed both QRS-complex and PVC beat detection performances, as shown in Tables V and VI, respectively. It can be observed that the QRS-complex detection results after fusion attains  $Se = 99.79\%$  and  $PP = 99.96\%$  (see Table V). Concerning the PVC detection accuracy (see Table VI), the effect of the fusion strategy improving both sensibility and PP is very clear.

It can be concluded from Table V that our Markovian approach achieves high beat detection performances, confirming

TABLE VI  
PVC BEAT DETECTION PERFORMANCE (IN TERMS OF SE AND PP) ON A TEST SET OF 59 RECORDINGS

PVC detection					
Channel	TP	FP	FN	Se (%)	PP (%)
1	885	453	490	64,36	66,14
2	809	144	566	58,84	84,89
Fusion	1199	201	176	87,20	85,64

the results of *layer 0* (Section IV-C). Our system was evaluated in terms of PVC beat detection through a nonsupervised classification approach. We achieved, respectively, 87.2% and 85.6% of PVC detection sensibility and PP. The previous work of Coast [16], acting on a small test set of 6 recordings and carrying out supervised training of the HMM, achieved 97.3% of sensibility and 85.7% of PP. Despite the difference in terms of sensibility between both approaches, the good results obtained by our approach, which uses a simple set of rules and works in a nonsupervised way, validates it in a realistic application.

False beat detection is almost insignificant since PP attains nearly 100%, thanks to the fusion strategy (see Table V). Reliable beat detection is a main issue for the automatic systems. Likewise the fusion strategy exploring the complementary information of two ECG channels improved significantly the PVC beat detection performance (see Table VI).

These results show that knowing only the dominant QRS shape of each patient, and thanks to some additional rules, our system is able to classify morphologies only from the modeling of elementary waveforms. This is a real improvement on other HMM approaches which perform the same classification task using supervised statistical learning [16].

## V. CONCLUSION

In this paper, we have proposed an automatic beat segmentation and classification system based on a Markovian approach. The system carries out ECG signal analysis in two layers. At *layer 0*, the ECG signal is segmented in terms of the beat waveforms: P wave, PQ segment, QRS-complex, ST segment and T wave. This is performed thanks to a robust and precise waveform modeling through independent HMMs. Then, at *layer 1*, the system identifies premature ventricular contraction beats, thanks to the use of some simple rule based system.

Our segmentation approach is original in the sense that the segmentation task is carried out by generic HMM of each beat waveform. The HMMs were trained on large set of waveform examples from different individuals. This modeling gives us a good representation of the morphologies that can be found in an ECG. One important feature of our approach is the generic model adaptation strategy to each individual, which is nonsupervised (there is no need of manual labels).

The use of rules plays an important role for beat classification. Indeed, our system does not require a HMM to model every specific abnormal beat class. Instead, a set of rules is used to characterize each class from the characteristics of the elementary waves.



Finally, we combined multichannel<sup>1</sup> complementary informations, using a fusion strategy adapted to the needs of our system.

The observations modeled by the Markovian approach were obtained after a wavelet transform of the ECG signal. The Mexican Hat mother wavelet was chosen considering, among other things, its ability to peak detection. It is important to remark, however, that a quantitative study of the influence of different wavelets in system performance is worth to be conducted. This study will probably lead to the use of different combination of wavelet transforms combined together, in order to take benefit of their respective qualities.

Our system was conceived with the objective to perform automatic online ambulatory ECG analysis. This is a main challenge due in particular to the diversity of morphologies which are most corrupted by noise and to the intra-individual waveform variability. So a plausible test would be to offer some tools in this direction without supplying a global treatment by a physician. We assessed the system performances using the QT database as it corresponds to the ambulatory conditions. In the first experiment, we have studied the beat segmentation precision, showing that our results compare favorably to other works on the same database. Moreover, our system was evaluated in terms of PVC beat classification, presenting once more good performance. The performances obtained allow us to point out the advantages of our approach according to the state of the art.

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<sup>1</sup>We have called multichannel fusion every time two different leads are combined together. The number of channels or leads depends on the ECG database.

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