Automatic P-wave analysis of patients prone to atrial fibrillation

L. Clavier[1] **J.-M. Boucher**[2] **R. Lepage**[2] **J.-J. Blanc**[3] **J.-C. Cornily**[3]

[1]École Nouvelle d'Ingénieurs en Communications, Villeneuve d'Ascq, France
[2]École Nationale Supérieure des Télécommunications de Bretagne, Brest, France
[3]CHU de la Cavale Blanche, Brest, France

Abstract—*A method is presented for automatic analysis of the P-wave, based on lead II of a 12-lead standard ECG, in resting conditions during a routine examination for the detection of patients prone to atrial fibrillation (AF), one of the most prevalent arrhythmias. First, the P-wave was delineated, and this was achieved in two steps: the detection of the QRS complexes for ECG segmentation, using a wavelet analysis method, and a hidden Markov model to represent one beat of the signal for P-wave isolation. Then, a set of parameters to detect patients prone to AF was calculated from the P-wave. The detection efficiency was validated on an ECG database of 145 patients, including a control group of 63 people and a study group of 82 patients with documented AF. A discriminant analysis was applied, and the results obtained showed a specificity and a sensitivity between 65% and 70%.*

Keywords—*Atrial fibrillation, ECG segmentation, P-wave, Hidden Markov model, Wavelets, ECG database*

Med. Biol. Eng. Comput., 2002, **40**, 63–71

1 Introduction

ATRIAL FIBRILLATION (AF) is an arrhythmia that is prevalent among elderly people: it affects 2–5% of people over 60 years old and 10% of people over 70 years old. It results in partial disorganisation of the atrial electric activity owing to two electrophysiological conditions: slowed conduction velocity in various atrial areas and heterogeneity of the cell refractory period. Although it is not a lethal disease, it can have very disabling complications, such as cardiac failure and atrial thrombosis, with the subsequent risk of a stroke, as reported in KANEL *et al.* (1982).

The aim of this study was to try to detect automatically patients prone to AF using a routine electrocardiogram (ECG) with standard equipment in a cardiology department. The detection of an abnormal P-wave can lead to three major consequences: first, for patients with previous palpitations, it can lead support to the hypothesis that they were caused by AF; secondly, attention can be paid to patients with embolic events; and thirdly, in the future, it can also lead to the prescription of preventive anti-arrhythmic or anticoagulant drugs. The important question of the time interval between the detection of the abnormal P-wave and the initiation of AF is under study and will not be discussed here.

To obtain an automatic measurement of the P-wave parameters used in the detection procedure, we need to perform an ECG segmentation to isolate the P-wave accurately. The advantages of automatic P-wave delineation over a manual one are related to measurement reproducibility and quality. The results do not depend on the ability of the observers, and general rules are easier to define. The study is not limited to a few P-waves, and so better statistical results are established.

However, P-wave delineation is more difficult to implement than QRS-complex detection, for which many efficient algorithms exist. This is mainly owing to the low P-wave signal-to-noise ratio and to the P-wave shape, which varies from one patient to another and sometimes even for a single patient. Many approaches have been tested to perform P-wave detection. Each has its own advantages and drawbacks. Adaptive filters, which suppress the QRS complex and T-wave for better detection of the P-wave, as reported in THAKOR and ZHU (1991), need the estimation of the filter order and a reference signal. Methods based on a discrete cosine transform and auto-regressive modelling, as shown in NIRANJAN and MURTHY (1993), sometimes miss low-amplitude P-waves. Methods based on time-frequency transforms, such as those in ABEYSEKERA (1994), or wavelets, in LI *et al.* (1995), detect time changes or local singularities in the signal, but, as they are very sensitive to noise, a good delineation sometimes fails. Moreover, they are tested on certain configurations of the learning database and cannot necessarily be adapted to new records.

Hidden Markov models are statistical methods based on the probability density of certain parameters, such as the signal slope. They describe the mean evolution of the cardiac cycle and they give robust ECG segmentations, as reported in COAST *et al* (1990). However, they are sensitive to the learning base building. Wavelets and statistical methods can be used complementarily for P-wave delineation, as reported previously in CLAVIER *et al.* (1998), to associate a local and a global segmentation.

Correspondence should be addressed to Dr J.-M. Boucher; email: JM.Boucher@enst-bretagne.fr

Paper received 20 February 2001 and in final form 12 October 2001
MBEC online number: 20023633

After the P-wave delineation, parameters are extracted from the P-wave to build a vector used in classical discriminant analysis. Two hypotheses are formed about the consequences of atrial arrhythmia on an ECG: a change in the P-wave pattern with longer P-wave, and an increase in the high-frequency part of the P-wave third quarter, as reported previously in STAFFORD *et al.* (1991).

The lengthening of the P-wave duration in patients who have suffered from atrial fibrillation has been reported by many investigators and is used by physicians as a detection test. In the case of a triggered signal-averaged ECG, paroxysmal atrial fibrillation is detected, with a specificity of 48% and a sensitivity of 91%, when the average duration of the P-wave exceeds 120 ms, as reported in FUKUNAMI *et al.* (1991). Another experiment using a high-gain signal-averaged oesophageal lead obtained a specificity of 100% and a sensitivity of 85% when the same average duration exceeded 110 ms, as reported in VILLANI *et al.* (1994).

The RMS voltage of the last 20ms of filtered P-wave has also been reported as being a good criterion, giving a specificity of 54% and a sensitivity of 95% if the value is less than 3.5 μV, as reported in FUKUNAMI *et al.* (1991). The ratio of spectral power contained in the 20–50 Hz band and in the 0–20 Hz band is known to be greater for patients with AF, as reported in CZYS *et al.* (1993), and the ratio of the power contained in the 20–30 Hz band and in the 0–30 Hz band is known to be smaller, as reported in RAITT *et al.* (1997). Except for the P-wave duration, these parameters remain controversial and are not used by physicians.

2 Method

2.1 *Database*

We recorded a 12-lead ECG in resting conditions, but we only worked on lead II, where the P-wave was most visible. International ECG databases are available (CSE database, MIT-BIH database), but they are not devoted to AF, with few records on this subject and very little information on the patients. Therefore we created our own database, in collaboration with Brest University Hospital. The signal was sampled at 1 kHz and, only for P-wave delineation, was bandpass filtered between 0.01 Hz and 40 Hz. The records lasted 1 min (about 60 beats).

To detect patients prone to AF, we considered 145 patients divided into two groups. For each patient, an echocardiogram was recorded, so that the cardiac chamber dimension could be analysed.

The control group included 63 people (38.4 years old ± 14.0; 48 men and 15 women) without any history of atrial tachycardia and with echocardiographically normal atria. The study group included 82 patients (61.4 years old ± 13.8; 48 men and 34 women) with documented AF treatment who had sinus rhythm restored a few hours or days before analysis: 10 paroxysmal AF, 30 counter shock, 42 medical.

2.2 *ECG segmentation and P-wave delineation*

As already mentioned, hidden Markov models (HMMs), using the ECG slope as observations, can allow ECG segmentation, as shown by COAST *et al.* (1990). We tested the method and found that it was efficient, but that it suffered from a lack of reliability, as it failed in some cases. To improve this method, it was not directly applied to the ECG slope, but 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.

2.2.1 *Multiresolution analysis:* A schematic diagram of a multiresolution analysis is presented in Fig. 1. It consists of a subband analysis with four levels of resolution. The low-pass and high-pass filter coefficients are obtained from the Haar scale and wavelet functions. It is a redundant analysis, which means that no sub-sampling occurs between the different levels of resolution. Many wavelets were tried, and it appeared that the Haar wavelet gave the best results; this could be explained by its ability to approximate the first derivative of the ECG signal.

2.2.2 *Beat separation:* To have an HMM for the P-wave delineation with only a few states and with a simple model, it was preferable to separate beats before applying the HMM. The beat isolation was achieved by QRS-complex detection, using a modified version of an algorithm proposed by PAN and TOMPKINS (1985). Instead of the slope, we used the wavelet coefficients. The signal was then divided into beats, starting 350 ms before an R peak: in most cases, this instant corresponds to the iso-electric line. This algorithm was efficient enough for resting ECGs, and very few errors resulted from this detection.

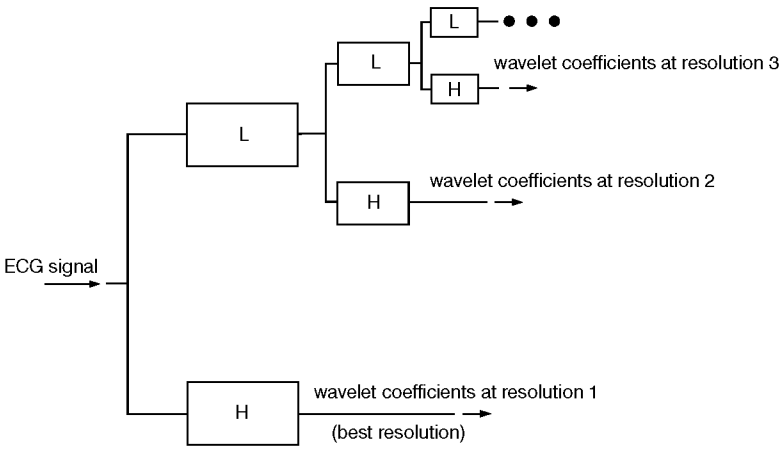

Fig. 1 *Redundant multiresolution analysis. L = low-pass filter; H = high-pass filter*

2.2.3 *P-wave delineation:* The ECG represents the electric activation of the heart with a regular cardiac cycle in sinus rhythm: first, the atria are depolarised (P-wave), then the ventricles (QRS complex), and, finally, the ventricles are polarised (T-wave). A state can be associated with each heart activation time. The dynamics of the state transitions can be described by an HMM, as reported in COAST *et al.* (1990), based on the hypothesis that, at a given instant, the state of the system only depends on the previous state. In addition, the states (the electrophysiological process) are not observed directly but through a set of stochastic processes producing the observed ECG signal. The aim of the segmentation procedure is to estimate the states automatically from the ECG record. In our case, the observed data were the wavelet coefficients.

A Markov chain is mathematically represented by the set of the N states $Q=(S_i|i=1,\ldots,N)$. The state transition probability matrix $A=(a_{ij}|i=1,\ldots,N;\ j=1,\ldots,N)$, where a_{ij} is the probability of going from state S_i at time t-1 to state S_j at time t, and the initial state probability vector $P=(p_i|i=1,\ldots,N)$, where p_i is the probability of the model being *a priori* in state S_i, are the parameters of the Markov model. The conditional probability distributions $F=(f_j(x)j=1,\ldots,N)$, associated with the states where x is the observation vector, describe the statistical link between the measurements and the states.

Three basic problems must be solved for this hidden Markov model: the choice of the state model that best matches the observations, the finding of the 'correct' state sequence from the observations and the estimation of the parameter set of the model from these observations.

An experimental analysis of the database with various ECG shapes led us to answer the first problem by modelling a beat using ten states: four iso-electric segments and two states per wave, as follows:

A: state iso_1 = iso-electric line
B: state P_1 = positive slope of atrial activation
C: state P_2 = negative slope of atrial activation
D: state iso_2 = iso-electric line
E: state Q_1 = positive slope of ventricular activation
F: state Q_2 = negative slope of ventricular activation
G: state iso_3 = iso-electric line
H: state T_1 = positive slope of ventricular polarisation
I: state T_2 = negative slope of ventricular polarisation
J: state iso_4 = iso-electric line.

This model can be used for any lead, but the states would then not necessarily correspond to the same activation times. Pathologies can modify the ECG's evolution and have to be included in the learning base to be recognised. To represent this evolution, our model was based on a left–right (or Bakis) model: the state index increases with time. However, such a model is not sufficient. We added more possible transitions to allow the model to go back and to skip some states (see Fig. 2).

Fig. 2 shows that the QRS complex can be described by various state transitions between the PQ and ST segments. The first has two states Q_1–Q_2, the second has three states Q_1–Q_2–Q_1, and the third has Q_2–Q_1–Q_2. In the Markov model, the probabilities of these events are estimated from the segmentation learning base.

We therefore defined a left–right model (Fig. 3) with, at most, the possibility of skipping one state except after P_2, Q_2 and T_2 (if the model does not go back, it necessarily goes to the following state) and with three other allowed transitions (P_2–P_1, Q_2–Q_1 and T_2–T_1) from these states.

Fig. 3 shows the state transitions that were obtained from a detailed examination of the segmentation learning base. The numbers at the nodes of the graph (inside the ellipses) are the *a priori* state probabilities, and the numbers on the oriented edges are the state transition probabilities.

To estimate the parameter set (A, B, F) that corresponded to the third problem of the HMM, a learning database of 240 beats, which included all the configurations encountered in the database, was extracted from the control group database. These beats were manually segmented into states. The transition probabilities and the *a priori* probabilities were directly estimated by counting the event percentage.

The conditional probability densities of the wavelet coefficients in each state could be estimated from a histogram obtained from the learning database. However, as it was a continuous density, it was preferable to smooth such an estimate using the non-parametric kernel method of SAOUDI *et al.* (1997) with a Gaussian kernel. The set of observed wavelet coefficients $X=\{X_i|i=1,\ldots,M\}$ of each state belonging to a bounded support $[a,b]$; a diffeomorphism $\phi(x)=\ln((x-a)/(b-x))$

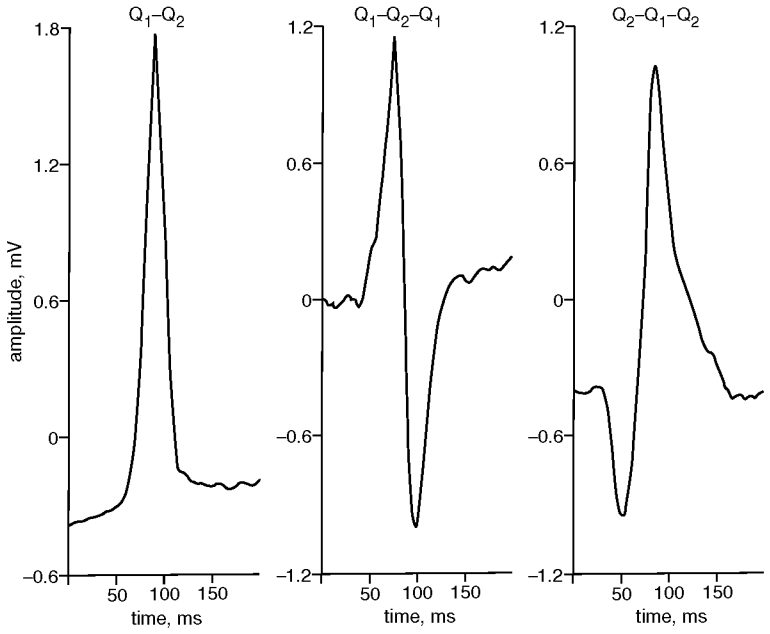

Fig. 2 *QRS complex shapes: three different state sequences*

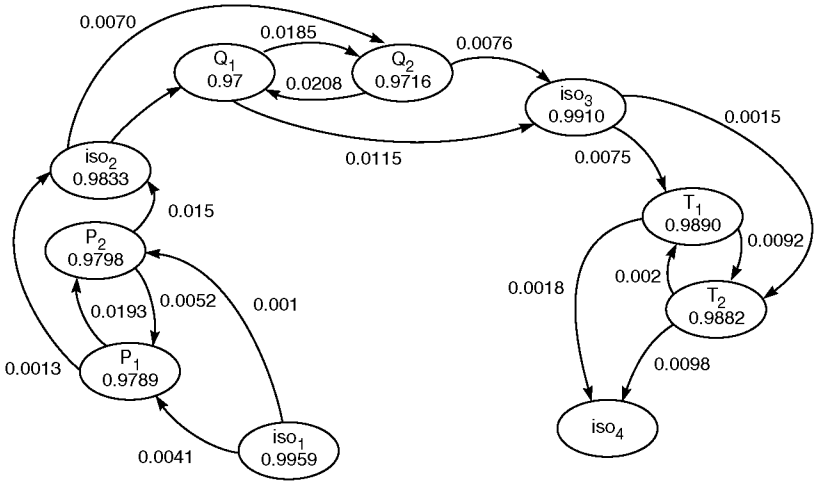

Fig. 3 *Possible transitions of hidden Markov model for ECG*

transforms the infinite support of the Gaussian density into a bounded support $[a,b]$, matched to the data histogram. The kernel estimator is of the form $\hat{f}_M(x) = |\phi'(x)|/(Mh_M)\sum_{i=1}^{M} K[(\phi(x) - \phi(X_i))/h_M]$, where the kernel is defined by

$$K(x) = 1/\sqrt{2\pi h_M^2}\exp(-x^2/2h_M^2)$$

and where $h_M = 1/M^{\alpha}$ is a sequence of positive real numbers called bandwidth with $o \leq \alpha \leq 1$ (Fig. 4).

Having defined the states and having estimated the model parameters, the second problem to analyse was how to find the most likely state sequence from an ECG record; this was solved by the Viterbi algorithm. A good state-of-the-art assessment of HMM is given by RABINER (1989).

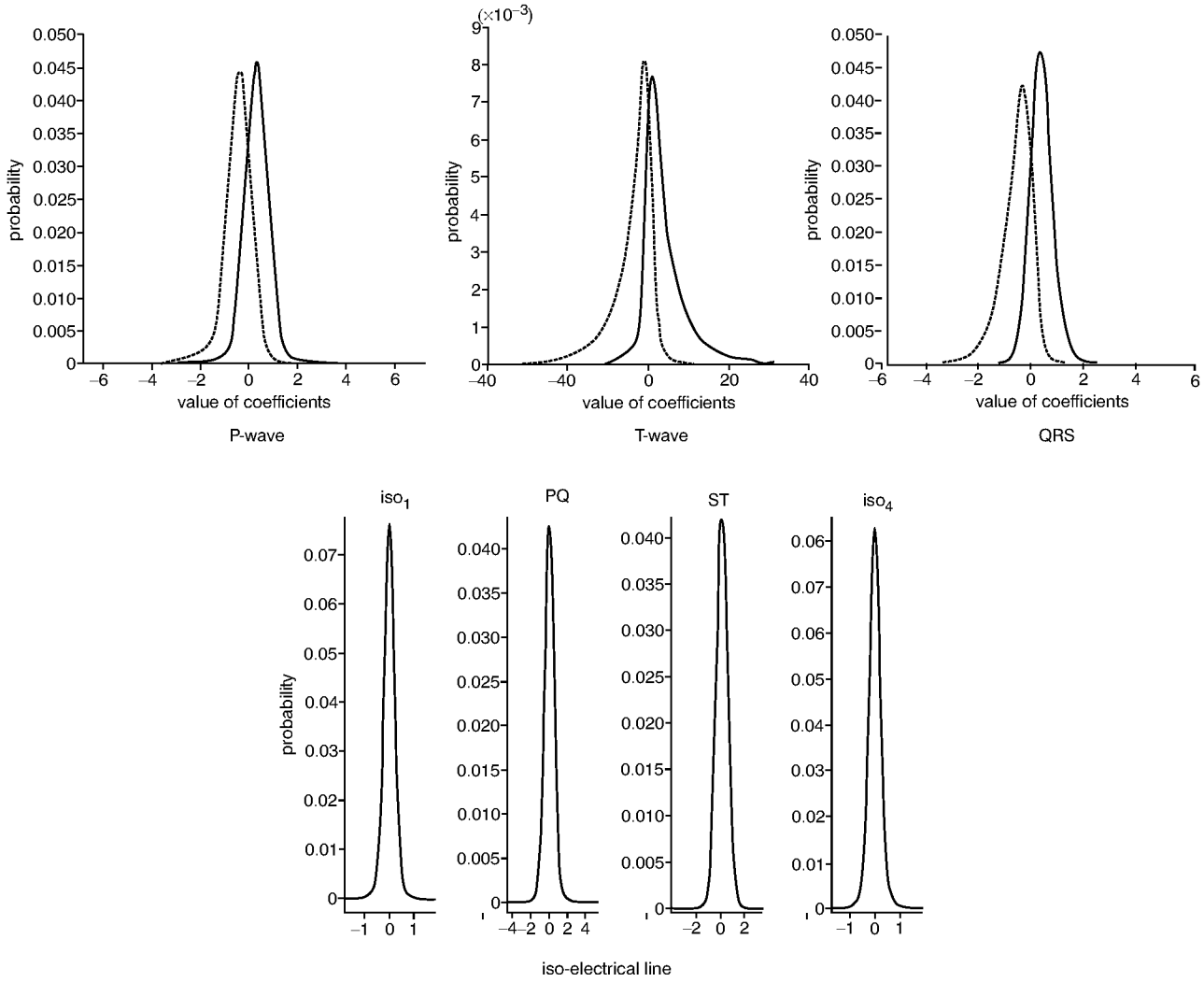

Fig. 4 *Probability density function of wavelet coefficients in each state. P- and T-waves and QRS complex are mainly modelled by two states. Iso-electric line parts are modelled by one state. Probability distribution of wavelet coefficients of each state is estimated by kernel method from segmentation learning base*

This method was applied to each resolution level and produced four segmentations for one ECG signal. The problem was how to select the resolutions giving the best results. Some of them were excluded on medical grounds: for instance, it was known that a P-wave has a duration between 60 and 190 ms, and we were able to suppress those that were outside these limits. For the others, the values were averaged, which could be seen as a special case of fuzzy decision.

2.3 *P-wave classification*

After the isolation of a P-wave by segmentation, parameters were measured so that we could proceed to a classification by discriminant analysis.

Four types of parameter were defined as follows:

2.3.1 *Time parameters:* The P-wave duration was easily computed from the delineation.

2.3.2 *Shape parameters:* One of them was computed by the repartition function method of RIX and MALENGE (1980). If $f(t)$ is the function describing a shape, the repartition function is defined by

$$F(X) = \int_{-\infty}^{X} f(t)dt \Big/ \int_{-\infty}^{\infty} f(t)dt$$

To compare two shapes $f(t)$ and $f'(t)$, the area of the difference between $F(X)$ and $F'(X)$ is computed and is compared with a threshold that is estimated from the learning base. In our database, the P-waves were gathered in five classes: symmetrically shaped P-waves, P-waves with slowly descending values, P-waves with slowly ascending values, bimodal P-waves and diphasic P-waves (Fig. 5). After many trials, it was found that a fourth-order polynomial was a good trade-off for the approximation of these shapes, and these parameters were used in the discrimination.

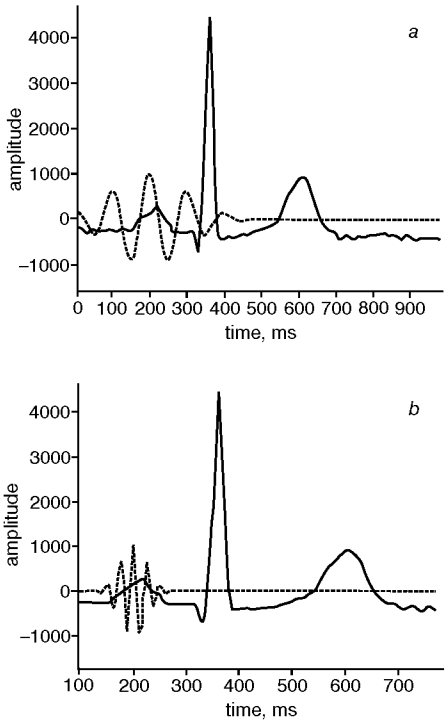

Fig. 6 *Influence of QRS on P-wave wavelet parameters. (a) Morlet wavelet for P-wave analysis between 3.9 and 7.8 Hz includes parts of QRS complex, which is not the case in (b) for P-wave analysis between 7.8 and 15.6 Hz*

2.3.3 *Spectral parameters:* These were extracted from a Morlet continuous wavelet analysis, as proposed in CLAVIER *et al.* (1997), obtained on the isolated P-wave. Two experiments were carried out. In one case, the whole P-wave was used. In the other case, the QRS complex was suppressed; this avoided having to take it into account (Fig. 6) (for low frequencies, the wavelet extends to the QRS complex, which has higher amplitude and

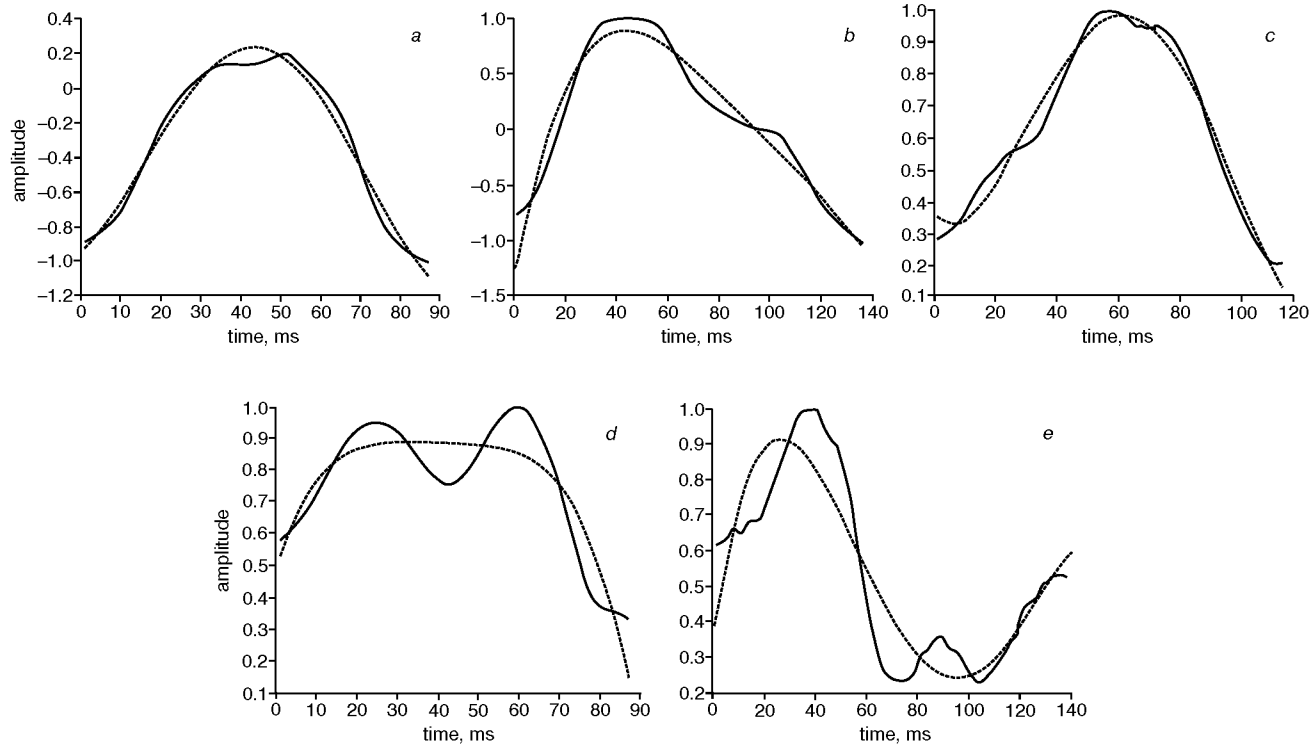

Fig. 5 *P-wave approximation. (——) Five examples of P-waves belonging to different classes. (· · · · ·) Approximation by fourth-order polynomial. (a) class 1; (b) class 2; (c) class 3; (d) class 4; (e) class 5*

disturbs the P-wave analysis). As we knew the position of the P-wave, we replaced the rest of the ECG with an iso-electric line.

The following parameters were chosen in each case: if D is the P-wave beginning and F is its end (in ms), the parameters are the energy mean and variance computed in the temporal windows D–F, D–$D+60$, F–60–F and in the following spectral bands: 0.9–1.9 Hz, 1.9–3.9 Hz, 3.9–7.8 Hz, 7.8–15.6 Hz, 15.6–31.2 Hz, 31.2–62.4 Hz.

2.3.4 *Wavelet entropy parameters of* LEMIRE *et al. (2000)*

$$WTE_s = \sum_k |w_{s,k}| / \sum_i |w_{s,i}| x \ln\left(|w_{s,k}| \sum_i |w_{s,i}| \right)$$

where $w_{s,k}$ are the wavelet coefficients at scale s and position k computed by a wavelet bi-orthogonal filter bank.

The use of all these parameters gave a vector of 117 components: the P-wave duration; the repartition function; four polynomial parameters; 39 values of entropy; 18 values of energy for the P-wave; 18 values of variance for the whole P-wave; 18 values of energy for the P-wave with suppression of the QRS; and 18 values of variance for the P-wave with suppression of the QRS.

As many parameters were correlated or without significance for this classification, a feature selection was necessary. It was made by a Fisher discriminant analysis that led to a hierarchical choice of the parameters. For the evaluation of the classification, we only considered two cases:

l=3, with three main features for the wavelet analysis without a suppressed QRS:

the repartition function value

the energies in the band 3.9–7.8 Hz for D–F

31.2–62.4 Hz for D–F

l=10, with ten features for the wavelet analysis without a suppressed QRS:

two polynomial coefficients

the repartition function value

the energies in the band 31.2–62.4 Hz for D–$D+60$,

0.9–1.9 Hz for $F-60$–F

15.6–31.2 Hz for $F-60$–F

31.2–62.4 Hz for $F-60$–F

0.9–1.9 Hz for D–F

3.9–7.8 Hz for D–F

31.2–62.4 Hz for D–F

3 Results

3.1 *Automatic P-wave delineation results*

Two examples are given in Fig. 7. In the first example, related to a diphasic P-wave, the P-wave duration is 107 ms, with an error of 5 ms compared with a manual segmentation. In the second example, with a diphasic P-wave, the duration is 115 ms, and the error is 2 ms. One difficulty was to find a compromise between sensitivity to noise and the detection of small artefacts, as shown on the first P-wave in Fig. 7. This was done during the learning process and had to be decided according to the quality of the ECG recordings.

Although the signal could generally be well segmented, errors could occur on some particular beats. Continuing the analysis including wrongly segmented beats could lead to severe mistakes. We therefore implemented a procedure to detect as many wrongly segmented beats as possible. We used two criteria:

(i) The first involved considering each P-wave individually: a duration of less than 60 ms or of more than 190 ms was not realistic and so we excluded P-waves not included in those limits.

(ii) The second took into account the set of P-wave duration estimates: large differences between consecutive beats were highly unlikely. In fact, the size of the heart and the conduction speed do not usually change during such a short time. Therefore we omitted P-waves with a duration too different from the mean duration of all the segmented P-waves.

In a statistical analysis, the choice of learning base is critical. All the cases that could be encountered have to be included. However, the learning phase can be repeated when a new configuration appears, so that the model can be adapted. We tried to include most of the configurations we encountered, especially the different P-wave shapes (Fig. 4) described by CLAVIER *et al.* (1996). We selected 24 patients and ten beats for each of them in the segmentation learning procedure. We obtained 119 segmentations with an error under 10 ms, 42 segmentations with an error between 10 ms and 20 ms and 18 segmentations with an error over 20 ms.

3.2 *Automatic P-wave delineation compared with manual delineation*

One difficulty was to know whether the segmentation was good or not. We compared the mean values of the P-wave duration resulting from automatic segmentation with those resulting from manual segmentation performed by specialists for each patient. Although the beats were amplified, specialists could make errors, as follows:

(i) the onset and end of the P-waves are difficult to define; if those instants have a well-defined electrophysiological meaning, they are not easily seen on the recording

(ii) the number of beats and the eye of the operator are also sources of inaccuracy.

We compared the results of manual and automatic segmentations by taking the duration of the P-wave as a parameter. Two different cardiologists (cardiologists 1 and 2) performed two manual segmentations. First, we compared their segmentations on the same plot (see Fig. 8).

The line in Fig. 8 corresponds to the linear regression of the data, and its slope gives the correlation coefficient. The coefficient of correlation between these two manual segmentations was 79%, and the associated standard deviation was 11 ms. It means that an automatic segmentation that would give results with the same degree of accuracy would be valid for the P-wave delineation.

To compare these manual segmentations with an automatic one, we plotted the mean (cardiologist 1, cardiologist 2) against automatic segmentation (Fig. 9). We found a correlation coefficient of 77% and a standard deviation of 13 ms.

Even if there was a slight difference between the manual and automatic segmentations, in terms of dispersion, we concluded that the automatic method was sufficiently efficient. A segmentation with an error between 10 ms and 20 ms can be considered as acceptable for the classification.

3.3 *Results of classification*

The system evaluation had to take the small size of the database into account, as in RAUDYS and JAIN (1991). On one

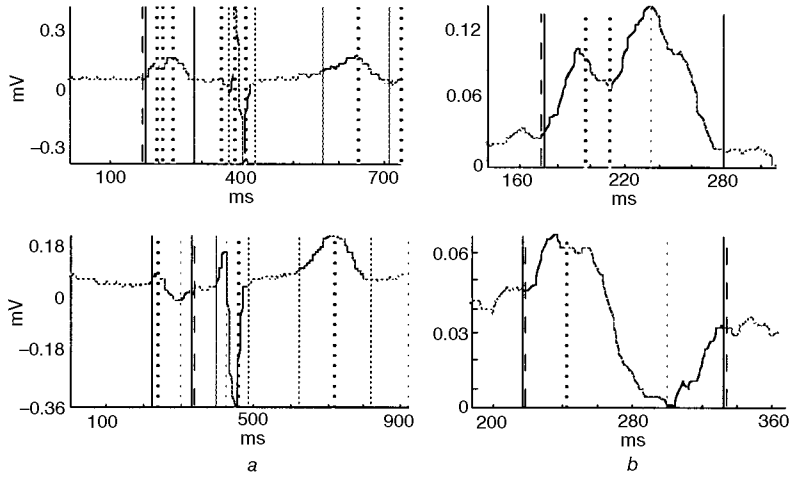

Fig. 7 *Segmentation of two different beats. (a) Automatic beat segmentation: (——) wave or iso-electric line; (· · · · ·) different recognised states in each wave. (b) P-wave part of each beat: upper figure is bimodal: automatic delineation measures 107 ms when manual delineation gives 112 ms; bottom figure is diphasic: automatic delineation measures 115 ms when manual delineation gives 117 ms*

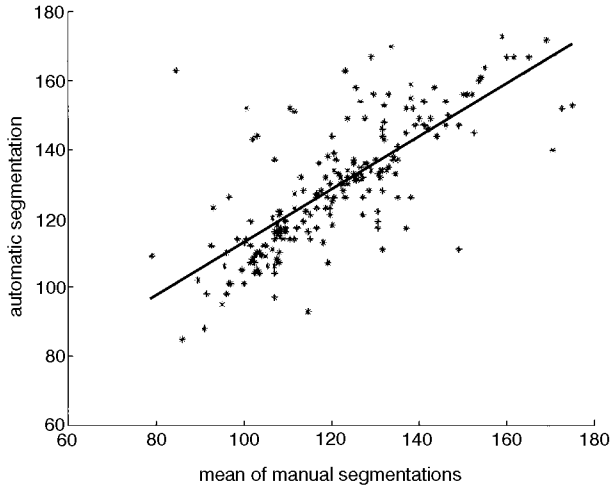

Fig. 8 Comparison between manual segmentations on P-wave duration. Each point represents measurement vector of P-wave duration estimated by two cardiologists. (——) Linear regression of these data. Estimated correlation coefficient is 0.79

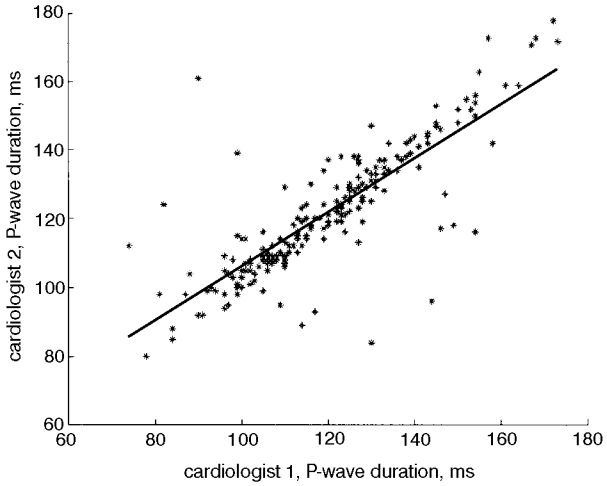

Fig. 9 *Comparison between manual and automatic segmentation on P-wave duration mean. Each point represents measurement vector of P-wave mean duration, estimated by two cardiologists on horizontal axis and by HMM method on vertical axis. (——) Linear regression of these data. Estimated correlation coefficient is 0.77*

hand, the resubstitution method R, which uses the same set for training and testing, is known to be a biased estimate of the error probability and to give an optimistic value. On the other hand, the holdout method H, which consists in splitting the whole database in two, one part for training, the other part for testing, gives an unbiased estimate of the error probability, but overestimates it. A good compromise was to compute the mean M of these estimators to have a more realistic value of the true error probability. The learning and test bases contained N samples, divided into two sets of N_1 samples of AF patients and N_2 healthy subjects. The number l of selected parameters had to stay low, because the ratio N/l had to be large enough to preserve the generalisation properties of the classification system. A classic linear discriminant analysis was used for the detection. A ten-fold trial was made, where we randomly chose the two bases among the 145 patients and we estimated the specificity and sensitivity of the test as a function of the number of selected parameters.

Table 1 shows these values for $N=64$, $N_1=N_2=32$, $l=3$ or 10.

4 Discussion

4.1 *Database*

In spite of the young age of the patients, the control group could have included some patients prone to AF. However, the mean age of the group, lower than that of the study group, justified the fact that this group was reliable. An age-matched group had to be built to confirm the results, but we needed to be sure that the people included would not have an AF accident in the years following the recording.

Table 1 Specificity S_p and sensitivity S_e of discriminant analysis with $l=3$ or 10 for resubstitution method, holdout method and mean (associated standard deviation in brackets)

l	3	10
R	$S_p=0.69$ (0.12) $S_e=0.70$ (0.08)	$S_p=0.76$ (0.08) $S_e=0.7$ (0.07)
H	$S_p=0.69$ (0.14) $S_e=0.63$ (0.14)	$S_p=0.55$ (0.13) $S_e=0.67$ (0.09)
M	$S_p=0.69$ $S_e=0.67$	$S_p=0.66$ $S_e=0.69$

4.2 *Segmentation*

This segmentation method, based on HMM, is evolutional, because the state model can be easily modified if new cases are introduced into the learning base, and robust, because it is based on a statistical model. In particular, the state number was experimentally defined and fitted with the database, as proved by the segmentation results. The description of the different waves by two states could seem rough, but it gave a relatively simple state model that worked. An explanation is that the Haar wavelet gives access to the slope of the waves at a different resolution, and a discrimination with a positive or negative value is sufficient. The main errors were due to configurations that were too rare in our database and consequently not present in the learning base.

Although the above-defined states are sufficient for any encountered situation, the allowed transitions are not. For example, a premature ventricular beat (a QRS complex appearing without a P-wave before it) cannot be modelled. Such a situation would be possible if a transition from state A (Iso_1) to state E or F (Q_1 or Q_2) existed. We did not consider such situations, because they were not frequent enough in our database. However, the results are good, and the advantages of the model are that it is quite simple and can evolve: it can be modified for new configurations if the learning base is adapted, as follows:

- we can change the compromise between robustness to noise and detection of small artifacts
- we can increase the learning base to be able to recognise as many configurations as possible
- we can add new parameters to describe each state better, for example using more than one lead.

Another method would be to build an observation vector from the redundant wavelet analysis and to use it in a single HMM segmentation: this has not been tried, because we thought that the proposed method of segmentation was sufficient for our purpose of classification. However, to be rigorous, it ought to be tested and compared.

4.3 *Classification*

Compared with the previously reported results of FUKUNAMI *et al.* (1991) and of VILLANI *et al.* (1994), it seems that the sensitivity and the specificity are very poor. However, in the previous cases, the experiments were made with a smaller database, as in FUKUNAMI *et al.* (1991), or with an invasive method, as in VILLANI *et al.* (1994). Results here correspond to a more classic situation for large-scale disease prevention, and the values obtained are already sufficient to indicate that such a method could be efficient to detect a large percentage of people prone to AF. However, a long-term study must be carried out to discover whether the parameters are adapted to this purpose. Patients detected as at risk of AF must periodically be tested; we also need to build reference groups including the different shapes of the P-waves. The results of the classification will have to be confirmed by such a long-term study.

It must be stressed that P-wave duration, which is the parameter generally used by physicians, seems to have a less discriminating power than shape and spectral parameters. In fact, the repartition function also includes a dependency on the P-wave duration through the integration, which can explain that this parameter can be substituted for the P-wave duration for the classification.

5 Conclusions

This paper presents a P-wave segmentation method applied to automatic classification of people prone to atrial fibrillation, one of the most prevalent cardiac arrhythmias. The study was performed on lead II of a standard 12-lead electrocardiogram. The P-wave delineation procedure, based on hidden Markov models, took into account some statistical properties of the signal, but also some electrophysiological properties. The automatic P-wave delineation was in accordance with the manual one, made by cardiologists. In the context of a P-wave analysis by a classic ECG examination, the classification results are promising and lead us to think that this method would be useful for medical diagnosis.

References

ABEYSEKERA, R. M. (1994): 'Detection and classification of ECG signals in the time frequency domain', *Appl. Signal Process.*, **1**, pp. 35–51

CLAVIER, L., BOUCHER, J. M., and BLANC, J. J. (1996): 'P-wave parameters for atrial fibrillation risk detection'. 18th Annual International Conference of IEEE Engineering in Medicine Biology Society (IV), pp. 1367–1368

CLAVIER, L., MAHEU, B., PROVOST, K., MANSOURATI, J., BOUCHER, J. M., and BLANC, J. J. (1997): 'Shape and time and frequency domain analysis in addition to P-wave duration markedly improves detection of patients prone to atrial fibrillation', *PACE, NASPE Abstr.*, **20**, p. 1116

CLAVIER, L., BOUCHER, J. M., and POLLARD, E. (1998): 'Hidden Markov models compared to the wavelet transform for P-wave segmentation in ECG signals' IX European Signal Processing Conference, Rhodes, (IV), pp. 2453–2456

COAST, D. A., STERN, R. M., CANO, G. G., and BRILLER, S. A. (1990): 'An approach to cardiac arrhythmia analysis using hidden Markov models', *IEEE Trans. Biomed. Eng.*, **37**, pp. 826–836

CZYS, Z., PETELENZ, T., FLAK, Z., SOSNOWSKI, M., and LESKI, J. (1993): 'A time frequency domain analysis of atrial late potentials for paroxysmal atrial fibrillation and assessment', *Comput. Cardiol.*, pp. 45–48

FUKUNAMI, M., YAMADA, T., OHMORI, M., KUMAGAI, K., and UMEMOTO, K. (1991): 'Detection of patients at risk of paroxysmal atrial fibrillation during sinus rhythm by P wave-triggered signal-averaged electrocardiogram', *Circulation*, **83**, pp. 162–169

KANEL, W. B., ABBOTT, R. D., SAVAGE, D. D., and MCNAMARA, P. M. (1982): 'Epidemiologic features of chronic atrial fibrillation: the Framingham Study', *N. Engl. J. Med.*, **306**, pp. 1018–1022

LEMIRE, D., PHARAND, C., RAJAONAH, J. C., DUBE, B., and LEBLANC, A. R. (2000): 'Wavelet time entropy, T-wave morphology and myocardial ischemia,' *IEEE Trans. Biomed. Eng.*, **47**, pp. 967–970

LI, C., ZHENG, C., and TAI, C. (1995): 'Detection of ECG characteristic points using wavelet transform', *IEEE Trans. Biomed. Eng.*, **42**(1), pp. 21–28

NIRANJAN, U. C., and MURTHY, I. S. N. (1993): 'ECG component delineation by Prony's method', *Signal Process.*, **31**, pp. 191–202

PAN, J., and TOMPKINS, W. J. (1985): 'A real-time QRS detector', *IEEE Trans. Biomed. Eng.*, **32**, pp. 230–236

RABINER, L. R. (1989): 'A tutorial on hidden Markov models and selected applications in speech recognition', *Proc. IEEE*, **77**, pp. 257–286

RAITT, M. H., INGRAM, K. D., and SHINNAMON, A. F. (1997): 'Frequency analysis of the signal averaged P-wave differentiates patients with history of atrial fibrillation from controls independent to P-wave duration', *PACE, NASPE abstracts*, **20**, p. 1220

RAUDYS, S. J., and JAIN, A. N. (1991): 'Small sample size effects in statistical pattern recognition: recommendations for practitioners', *IEEE Trans. Pattern Anal. Mach. Intell.*, **13**, pp. 252–264

RIX, H., and MALENGE, J. P. (1980): 'Detecting small variations in shape', *IEEE Trans. Syst Man Cybern.*, **10**, pp. 90–96

SAOUDI, S., GHORBEL, F., and HILLION, A. (1997): 'Some statistical properties of the Kernel diffeomorphism estimator', *Appl. Stochast. model Data Anal.*, **13**, pp. 39–58

STAFFORD, P. J., TURNER, I., PHIL, D., and VINCENT, R. (1991): 'Quantitative analysis of signal-averaged P-wave in idiopathic paroxysmal atrial fibrillation', *Am. J. Cardiol.*, **68**, pp. 751–755

THAKOR, N. V., and ZHU, Y. S. (1991): 'Applications of adaptive filtering to ECG analysis : noise cancellation and arrhythmia detection', *IEEE Trans. Biomed Eng.*, **38**, pp. 785–794

VILLANI, G. Q., PIEPOLI, M., CRIPPS, T., ROSI, A., and GAZZOLA, U. (1994): 'Atrial late potentials in patient with paroxysmal atrial fibrillation detected using a high gain, signal averaged oesophageal lead', *Pacing Clin. Electrophysiol.*, **17**, pp. 1118–1123

Authors' biographies

LAURENT CLAVIER received his engineering degree in electronics from ENSHEEIT, Toulouse, France, in 1993, and PhD, in 1997, from Rennes University, France. He is currently Assistant Professor at ENIC, Lille, France. His research interests include electrocardiographic signal processing and digital communications.

RONAN LE PAGE received his DEA in Electronics & Optronics from Brest University, France. He is currently working on his PhD in the Signal & Communication Department of ENST Bretagne, France.

JEAN-MARC BOUCHER received his engineering degree in telecommunications from ENST, Paris, France, in 1975 and HDR in 1995, from Rennes University, France. He is currently Professor at ENST Bretagne, France. His current research interests include estimation theory and wavelets with applications to radar and sonar and seismic and electrocardiographic signals.

JEAN-CHRISTOPHE CORNILY received his MD from Brest University. He works in the Cardiology Department of Brest University Hospital.

JEAN-JACQUES BLANC is Professor of Medicine and Head of the Cardiology Department of Brest University Hospital. His research interests include atrial fibrillation and heart rate variability.