Fast parallelized algorithm for ECG analysis

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Abstract: - A new approach based on the adoption of wavelet transforms is presented for the R point localization in ECG signals. The conceived real time signal processing technique, which uses a fast parallelized algorithm, has been evaluated adopting the standard MIT-BIH Arrhythmia database which includes specially selected holter recordings with anomalous but clinically important phenomena. In the procedure a soft thresholding technique is applied to dyadic scales in which the ECG signal is decomposed. Therefore, noise contribution is reduced and then signal is easily reconstructed in the time domain for further processing. Moreover, the tool analyzes the signal on different level wavelet representation at the same time showing a great parallelism degree and an enhancement in processing time. To evaluate the algorithm noise immunity, the MIT-BIH Noise Stress Test Database has been adopted containing baseline wander, muscle artifacts and electrode motion artifacts as noise sources. The obtained performance shows the method validity in terms of algorithm speed up and characteristic parameter values. In fact, sensitivity and positive predictivity values of about 99.8% are obtained with a detection error rate of about 0.4%. Moreover, the conceived procedure gives satisfactory results also for ECG signals heavily corrupted by noise

Key-Words: - ECG, QRS, wavelet transform, parallel filter bank, signal processing, parallel computing

1 Introduction

Electrocardiography is an important tool in diagnosing the heart condition and consequently in discovering many cardiac diseases The Electrocardiogram (ECG) is a non invasive graphic record representing direction and magnitude of the heart electrical activity that is generated by depolarization and repolarization of the atria and the ventricles. Therefore it provides valuable information about the functional aspects of the heart and of the cardiovascular system and consequently is widely used for cardiac disease diagnostic and for urgent treatments of ill patients [1] In fact, an early detection of heart abnormalities can prolong life and enhance its quality adopting suitable cures. Most of the clinically useful informations for cardiac state health are indicated by the ECG shape such as intervals and amplitudes of the signal.

The QRS detection is the most important task in ECG signal analysis systems. In fact, after the QRS identification, the heart rate may be calculated and other parameters can be examined to avoid serious pathologies such as ischemia. For example, accuracy of RR intervals is crucial for reliable heart rate variability (HRV) analysis, which is widely considered to provide a simple non-invasive and quantitative assessment of cardiac-autonomic function in health and in disease states [2]. HRV analysis has been increasingly recognized as a useful tool for understanding autonomic regulation during sleep as well as patient screening in obstructive sleep apnea syndrome, congestive heart failure and other disorders [3], [4], [5].

Due to the non-stationary behaviour of biological signals, disease symptoms may not show up all the time but would manifest at certain irregular intervals during the day. Therefore, the study of ECG pattern by analysts may have to be carried out over several hours (such as nigh-time data or 24 hours holter monitoring) with an high probability of missing vital informations. Therefore, computers based analysis is advisable. The implementation of a procedure for detection of P wave, QRS complex and T wave is a difficult task due to the time varying behaviour of the human body and consequently all processing methods should change their state during measurement. Moreover, noise contamination, due to baseline drifts changes, motion artifacts and muscular noise, is frequently encountered.

Classical QRS detectors are composed of a preprocessor stage for QRS complex emphasizing and a decisional stage for QRS enhanced signal thresholding. The ECG signal is first band-pass filtered for noise reduction and then differentiated for R wave large slope emphasizing. After passing through the filter, the signal may be squared for QRS high frequency content exploiting. A short time energy estimate is obtained by smoothing the resulting signal by a moving window integration. The window duration and the choice of the filter bandwidth is a difficult task. In fact, the choice of a suitable bandwidth is a trade off between noise reduction and high frequency details: adopting a too large band, noise reduction suffers while with a too narrow band, high frequency QRS details are lost. The duration of the sliding window is a trade off between false and missed detections. Fixed band-pass filter/short time energy techniques do not accurately merge with morphological differences in ECG waveform which increase the complexity of QRS detection. Therefore, the problem solution is very complex because [6], [7], [8]:

- signal frequency band of the QRS wave is different for different subjects and even for different heart cycles of the same subject;
- noise and QRS complex pass-bands overlap.

Many different approaches have been used to improve the accuracy of QRS detection, including the use of the Hilbert transform, genetic algorithms, procedures adopting artificial neural networks, filter banks, heuristic methods based on nonlinear transforms and wavelet transforms [8], [9], [10], [11], [12], [13], [14], 15].
In this paper an improved signal processing technique, able to provide an easy implementation in design tools, is presented. Since heart rate has to be evaluated, the procedure is oriented towards R characteristic point detection; in fact the algorithm estimates the heart rate as inverse of the time interval between two consecutive R peaks. For R point localization, the wavelet transform is used. Moreover, for parallel computing and for implementation in design tool, parallel filter banks have used in the adopted technique. Experimental results show the method validity and its high sensitivity and predictivity parameters. In fact, results with minimum interferences from noise and artifacts have been obtained. Compared with other numerical procedures present in literature, the new method improves the speed up, shows an high noise immunity and is quite independent to time-varying morphologies in QRS complex.

2 ECG technique

A single normal cycle of the ECG represents successive atrial depolarization/repolarization and ventricular depolarization/repolarization which occur in every heartbeat.
Each hearth beat produces a series of deflections away from the baseline on the ECG signal. These deflections represent the time evolution of the heart electrical activity. One heartbeat produces a single normal cycle of the ECG that is indicated with the letters P, Q, R, S and T (figure 1) [16].

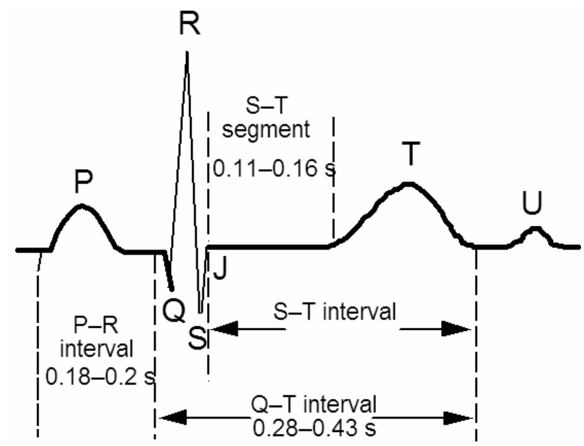

Figure 1 ECG characteristic shape

Typical standard ECG signal can be decomposed into three groups of basic elements:

1. waves which are deviations from the isoelectric line (baseline voltage) such as P; Q; R; S; T; U;
2. segments that are isoelectric line between waves;
3. intervals that represent periods including segments and waves.

The ECG signal can be divided into the following sections:

- The P wave represents the atria activation (depolarization). The first half of the P wave is the activation of the right atrium, whereas the second half is the activation of the atria septum and the left atrium. The normal shape of the P wave does not include any notches or peaks and its duration can vary between 0.08 and 0.11sec. in normal adults
- The PQ interval represents the time between the beginning of atrial depolarization and the beginning of ventricular depolarization
- The QRS complex is a general term representing activation in the ventricles and is a result of the depolarization of the ventricles. The Q and S waves represent negative

(downward) deflections on the plot of the lead, and the R wave represents positive (upward) deflection. The duration is normally less than 100ms a higher value can reflect an abnormality due to intraventricular conduction

- The T wave results from ventricular repolarization, whereby the cardiac muscle is prepared for the next cycle of the ECG. The normal morphology of the T wave is rounded and asymmetrical
- The S–T segment is measured from the end of QRS complex to the onset of the T wave. This segment represents the early stage of ventricular repolarization and under normal conditions is isoelectric (constant potential). A marked displacement of the S–T segment signifies coronary artery disease
- The P–R interval represents the atrioventricular (AV) conduction time, i.e. the time required for the electrical impulse to propagate from the sinus node through the atrium and the AV node to the ventricles (which results in ventricular depolarization). The normal range of the P–R interval is 120ms to 200ms. This interval can vary with heart rate.
- The Q–T interval reflects the total duration of ventricular systole, and is measured from the onset of the QRS complex to the end of the T wave. Normally the Q–T interval is less than half the previous R–R interval. A long QT interval can be associated with heart failure, ischaemic heart disease, bradycardia, some electrolyte disorders (e.g. hypocalcaemia) and can be consequence of different drugs taking.

Frequently the ECG signal is corrupted by noise. Baseline wander and 50Hz power line are predominant interference sources. Baseline wander is mainly caused by patient breathing, movement, bad electrodes, improper electrode site preparation, etc. The frequency range of baseline wander is usually below 0.5Hz, which is close to the frequency range of ST segments. For this reason, this type of noise could easily lead to false diagnosis. Eliminating the baseline wander and the power line interference in ECG signals is usually the necessary pre-processing step to enhance the signal characteristics for diagnosis [17].

3 Wavelet Transform Principles

Wavelet transform provides temporal and spectral information simultaneously, so it is suited for determining characteristic points of non stationary and fast transient signals, such as ECG signals. This feature is suitable to distinguish the ECG signal from noise and interferences.

The wavelet method decomposes a time variant signal into several components having various scales or resolutions. A suitable time and frequency limited wavelet is chosen as “mother”. Scaling and shifting the mother wavelet, a family of functions called “daughter” wavelets is generated. For small scale factor values, wavelet is constructed in the time domain and gives information about fine details of signals. Therefore, a global view of the signal is obtained by scale factor large values. The wavelet transform of a time signal at any scale is the convolution of the signal and a time-scaled daughter wavelet.

There are essentially two types of wavelet decompositions: the redundant ones (generally continuous wavelet transform), and the nonredundant ones (orthogonal, semi-orthogonal, or biorthogonal wavelet bases) [18]. The first type is preferable for feature extraction because it provides for a description that is truly shift-invariant. The second type is preferable for data reduction, or when the representation orthogonality is an important factor. However, the choice between these types of decompositions has to take into account computational considerations, too. A decomposition in terms of wavelet bases using Mallat fast algorithm is typically orders of magnitude faster than a redundant analysis, even if the fastest available algorithms are used [19], [20].

As the aim of this paper is the implementation of a fast parallelized algorithm, a non-redundant wavelet decomposition has been chosen. To determine the best wavelet function to be used, the ECG signal properties have been studied, such as the shape and the time localization of events. Temporal signal shape is an important parameter, so orthogonal wavelets are unsuitable to be used. In fact they are unable to provide symmetry in the time domain and they introduce non-linear phase shift. The signal shape is maintained if the phase shift is linear. Thus the wavelet to be adopted should be a symmetrical function [21], [22]. Spline wavelets have properties satisfying the previous requirements and are well-known in literature for their properties and advantages [23], [24], [25], [26], [27], [28].

The QRS detection is composed of slopes and local maxima/minima occurring at different time instants inside the cardiac cycle, the adoption of a spline function as mother wavelet is a suitable choice.

The higher order of the spline wavelet results in the sharper frequency response of the equivalent FIR filter, that is always desirable, but this FIR filter has longer coefficient series, leading to greater

computational time consumption. Therefore, the cubic spline wavelet is assumed to have an order high enough for this application [8], [21].
Traditional wavelet theory considers a decomposition algorithm with an iterative structure [29] (in particular an asymmetrical tree structure) that does not efficiently merge with the novel computational techniques, such as parallel processing, concurrent programming and design tools. In this study the a' trous and the Mallat algorithms for parallelized filter bank design have been used [30]. The algorithm generates a set of parallelized perfect-reconstruction filter banks for an arbitrary number of end-nodes of a traditional tree structure [31].

4 Procedure Description

The implemented procedure, called R_POINT_DETECTOR, processes ECG data in real time without any pre-filtering procedure, showing an high noise immunity degree.
For the method implementation, no external trigger source is necessary; therefore the ECG signal is the only input (figure 2).

Figure 3 shows the adopted algorithm model in which the obtained results are indicated as:

- '*R_Number*' that evaluates the number of R points present in the frame under test;
- '*R_Indices*' that indicates the time position of located singularities

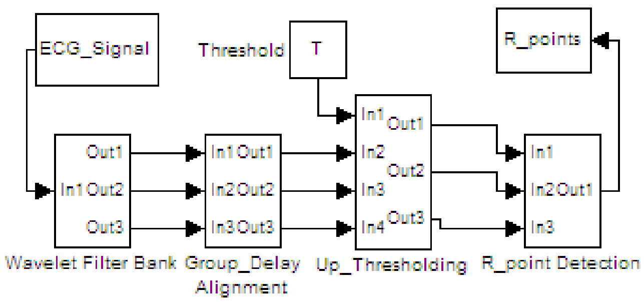

Figure 2 'R_POINT_DETECTOR' System model.

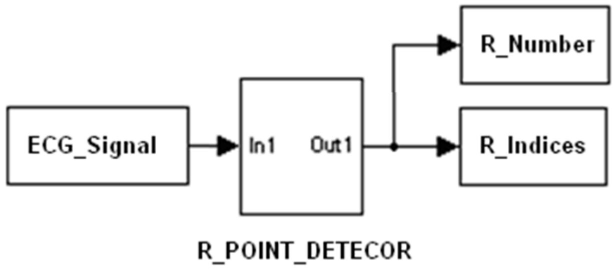

Figure 3 Algorithm model realized with the software tool MATLAB Simulink®

The choice of a suitable mother wavelet is basic to rich high performance for the proposed QRS detection technique. Since QRS complex general shape is similar to bi-orthogonal wavelet functions, choosing these functions as mother wavelet, QRS complexes could be reproduced by few wavelet coefficients reducing computation time and memory requirements [22]. A wide variety of functions can be chosen as mother wavelets but, after validation procedure tests, wavelet bior 3.3 has been adopted because it allows the perfect signal reconstruction keeping phase shift linear. Wavelet bior 3.3 is a cubic spline (figure 4)
To locate R points and consequently QRS complexes, the method decomposes the ECG signal into six dyadic scales so to reduce noise sensitivity significantly (figure 5). Signal lower frequency components are in high degree scales while higher frequency components are in low degree scales.
According to the power spectra of ECG signal and of noise and artifacts, it is evident that the larger contribute of the true signal is located in scales 4, 5 and 6, while scales 1, 2 and 3 are mostly affected by noise [32].
As QRS complexes are transient in ECG signal, they are detected exploiting the property that the absolute value of the dyadic wavelet localizes maximum points across several consecutive scales at the instant of transient occurrence. For noise reduction, soft thresholding technique is applied to levels 1, 2, 3. It is a point processing operator able to attenuate noise energy. In fact, wavelet transform compacts signal energy into a small number of coefficients having large amplitudes and spreads noise energy over a large number of wavelet coefficients with small amplitudes. Threshold operation reduces noise energy by removing those small coefficients while maintaining signal energy. For a given function p(y), the soft thresholding operator (Γ_λ) is defined as:

$$(\Gamma_{\lambda} p)(y) = \begin{cases} p(y) - \lambda & \text{if } p(y) > \lambda \\ p(y) + \lambda & \text{if } p(y) < -\lambda \\ 0 & \text{otherwise} \end{cases} \quad (1)$$

Several approaches have been proposed for threshold (λ) selection [33]. The choice is a trade off between two parameters; in fact a large λ value removes a significant amount of signal energy while a small λ value does not suppress a large amount of noise. The adopted value derives from a statistical study. In this way noise is reduced and then signal is reconstructed in time domain for further processing.

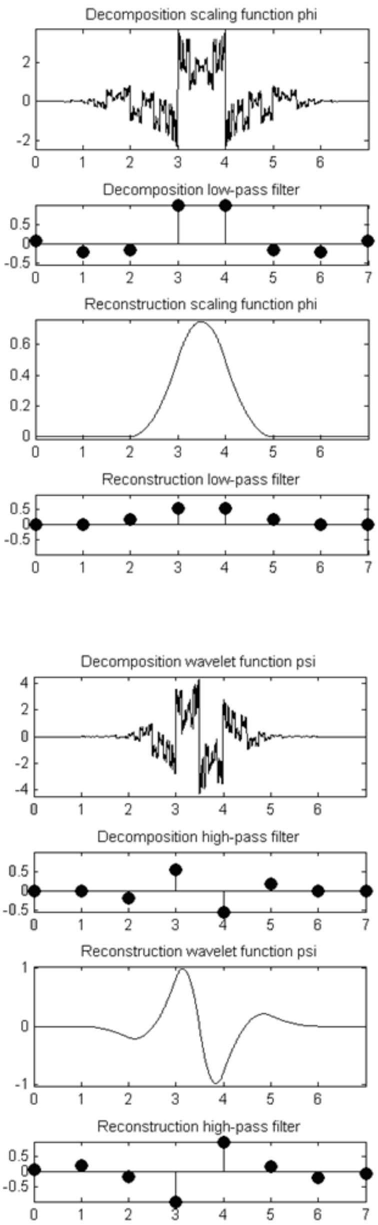

Figure 4 Wavelet ‘bior3.3’.

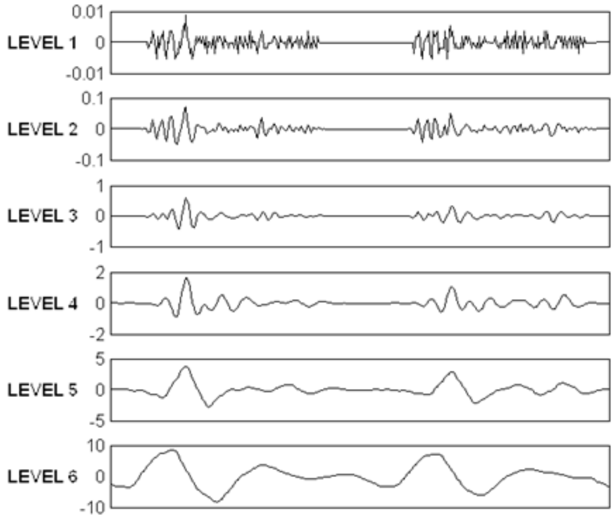

Figure 5 Decomposition of ICG signal over six diadic scales using a’ trous algorithm.

ECG signal representation in wavelet domain is particularly indicated for noisy signals. In fact for searching characteristic points, processing of noise free scales only, such as scales 4-5-6, is sufficient. The procedure greater advantage is evident in comparison with frequency analysis which needs informations of the overall bandwidths for R point localizations.

The method uses an evolution of the classical Mallat decomposition, called a’ trous algorithm. The a’ trous algorithm for non-ortogonal wavelets uses the same filter bank structure as the Mallat algorithm [34], but differs for high pass and low pass FIR filters. It has been demonstrated that after the application of wavelet filters for j-times, the precision of a’ trous algorithm is 2j time higher then Mallat algorithm [35] (table 1).

Resolution	**1**	**2**	**……**	**j**
Algorithm	***Precision***	***Precision***	**……**	***Precision***
Mallat	1/512	1/256	……	2^j/1024
a’ trous	1/1024	1/1024	……	1/1024

Table 1 Precision of the Mallat and the a’ trous algorithms varying decomposition levels

Usually, wavelet decomposition algorithms make use of filters in a tree structure. This is unsuitable for both the parallel computing and the implementation by design tools. To overcome these limits, equivalent parallel filter banks are used. However, the output signal realignment is necessary to equalize the delay introduced by each filter. This structure makes the algorithm attractive for a hardware implementation.

At this step the method first spots the positions of all QRS complex peaks, then the R point localizations. A point of maximum value is present in component signals (scales 4-5-6) in the same locations of each singularity in ECG signal.

The parallel behaviour of the procedure makes the contemporary search of singularity points in each scale, possible. Therefore, the time necessary for the execution of this step is independent of the number of scales used for the signal decomposition. Making use of a parallel procedure, the proposed method looks inside scale 4, scale 5 and scale 6 for zero crossing points and for local maximum points. Singularities are selected adopting a threshold technique: in fact only points higher than the adopted threshold value are considered. Finally, a local maximum point (peak) is taken into account only if it is immediately followed by a zero crossing point. If a local maximum point is followed by another local maximum point, it is discharged. Occurrence of too closed peaks inside a decomposition scale is solved replacing them with one new virtual peak located in a middle position between them. In figure 6 the spatial representation of local maximum points after the replacement of too close maximums, is shown. For instance, peaks P and Q of scale 4 selected by the method as to close points, are replaced by the point R in a new spatial representation named scale 4a.

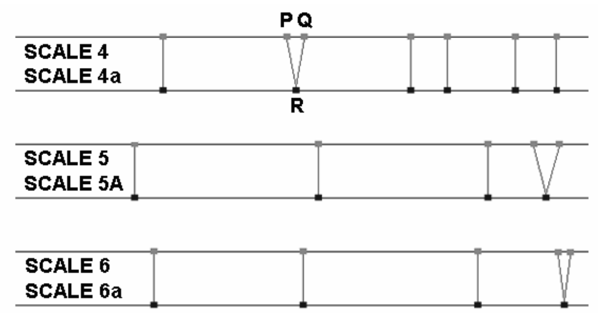

Fig.6 Procedure for too close peaks management

Each processed scale gives information about the same signal, so points located inside each scale are related to each others. For this reason, the method executes a tracing across scales to locate overlapping singular points. However, as the perfect coincidence of two or more points is almost impossible, a confidence interval of occurrence is associated to each point.

For software implementation, a window having a suitable size is constructed around each singular point considering one scale at a time. The generic window in a generic scale is analyzed to determine if peaks of other scales are located inside it. The research is iterated both for all windows of a scale and for all scales. The method defines as valid peaks those that are present inside the window in two out of three scales at least. The best estimate of the valid peak position (the true R point position) is obtained averaging peak positions inside the different scales.

Figure 7a shows the characterization of a new spatial representation named scale 4b for peaks of scale 4a consequently to the definition of a confidence interval for each point. For instance, the method defines a window for peak S and verifies if peaks of the other scales are located inside this window. In this example, point T of scale 6a is inside the window. Therefore point U is defined as “valid” value in the new representation named scale 4b. U point localization is in the middle between S and T positions. Figure 7b and figure 7c show the same analysis for points belonging to scales 5a and 6a, respectively.

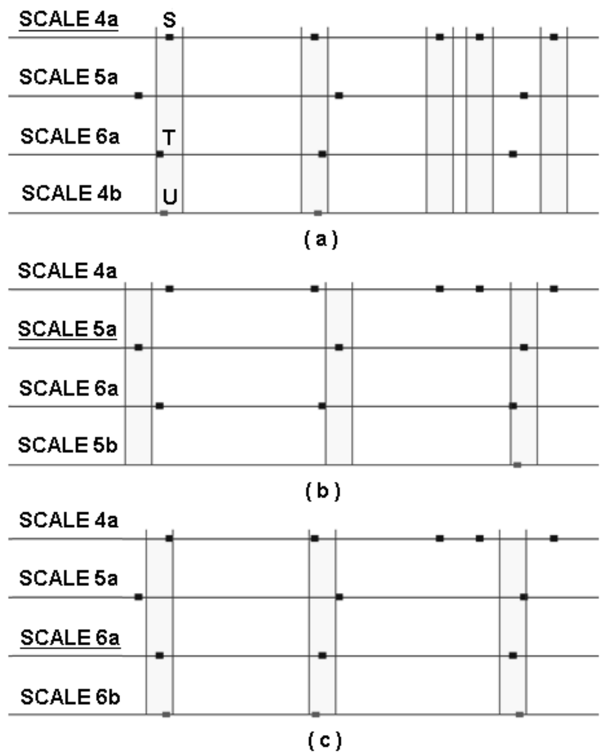

Figure 7 Parallel procedure for peak validation

Points of scales 4b, 5b and 6b are grouped in one spatial representation indicated in figure 8 with TEMP. Points that are too closed in TEMP are replaced with one peak having the middle location as shown in representation named OUTPUT.

In conclusion, the following steps characterize the new method:

1. signal processing in PARALLEL filter banks for wavelet decomposition;
2. PARALLEL searching for local maximum points inside scales which contain the widest noise free signal contribute;
3. replacement of too close peaks in each scale;
4. validation of peak points for each scale with respect to peak position in other scales;
5. R-point localizations adopting a simple decisional algorithm.

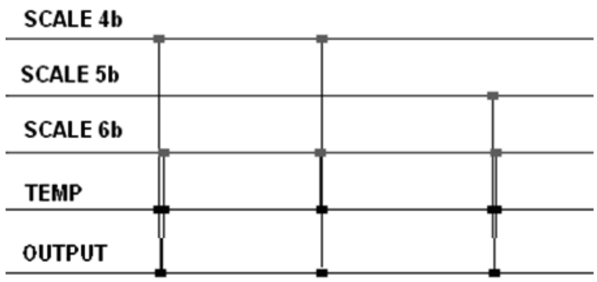

Figure 8 Procedure last step for R point location.

5 Results and Discussion

Software detection algorithms for medical applications require detection performance evaluation according to the ANSI/AAMI standard. The parameters used to evaluate algorithms are:

Sensitivity: $$Se = \frac{TP}{TP + FN} \quad (2)$$

Positive Prediction: $$P = \frac{TP}{TP + FP} \quad (3)$$

Detection error rate: $$DER = \frac{FP + FN}{TP + FN} \quad (4)$$

where:

- TP (the number of true positives) is the number of correct identifications of R points present in the signal under test;
- FN (the number of false negatives) is the number of R points present in the signal that the algorithm is not able to detect;
- FP (the number of false positive) is the number of R points detected by the algorithm but really not present in the signal.

The evaluation of the proposed detection methodology is carried out using recorded data from the standard MIT-BIH Arrhythmia database which includes specially selected holter recordings with anomalous but clinically important phenomena [36]. The signals contained in the reference database are sampled at 360 Hz and are characterized by 12-bit /sample resolution.

Denoting with R* the R point average value, simulations show that optimal threshold value is 0.55R*. In this situation Se and P values of about 99.8% are obtained, respectively (figure 9). For different threshold values, the above mentioned parameters decrease in dependence on the chosen threshold value. In fact, values lower than 0.55R* make performance worse because determine the increase of the FP parameter while values higher produce the growth of FN.

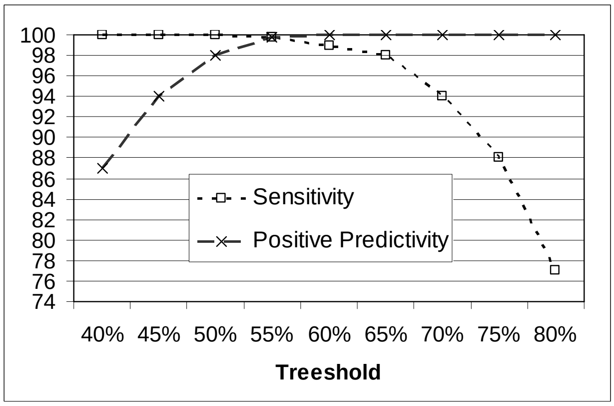

Figure 9 Se and P vs. threshold values.

Adopting the proposed procedure, the shape of the DER curve as a function of threshold values is indicated in figure 10, which confirms 0.55R* value as optimal choice for the detection error rate parameter minimization.

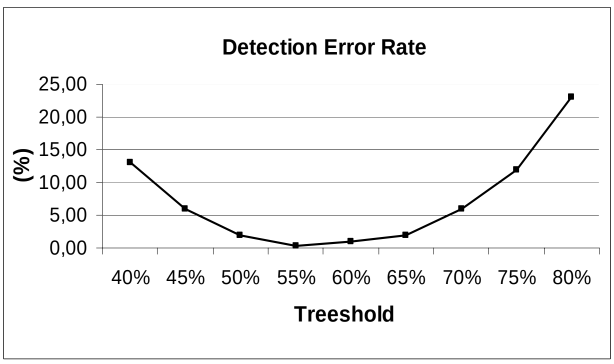

Figure 10 DER parameter vs. threshold values.

Comparing the procedure to other approaches, it is noted that the method exhibits good results and, at the same time, minimizes computational efforts. The absence of the signal pre-filtering stage avoids additional computations other than the wavelet calculation and the subsequent feature extraction procedure. Moreover, the realized algorithm is suitable for real time signal processing and ambulatory applications (low computational load), contrary to some other implementations [28], [23], [8]. In fact in [8], the use of fast decomposition algorithms is precluded for the choice of a custom non-orthogonal mother wavelet, in [28] 600 samples of ECG signal are analyzed each time, so the procedure does not work on every incoming sample, while in [23] the scale thresholds are updated considering excerpts of 216 samples for each scale with an higher amount of data to store, which does not meet requirements of ambulatory applications.

To evaluate the algorithm noise immunity, records from the MIT-BIH Noise Stress Test Database containing predominantly baseline wander (due to heavy respiratory activity), muscle artifacts (due to electrical activity of muscles) and electrode motion artifacts (due to the physical electrode motion that causes changes in the skin-electrode potential), have been also considered. Electrode motion artifact is generally considered the most troublesome, since it can mimic the appearance of ectopic beats and cannot be removed easily by simple filters, as noise of other types [37].
The obtained performance confirm that the algorithm is immune from noise up to S/N ratio values equal to 24dB. Increasing the noise contribute, FN keeps almost constant while a growth of FP is observed, which makes the performance worse. In figure 11 the ECG is compared with the same signal having 24dB and 18dB S/N ratio, respectively [37]. It is evident the heavy effect of noise in corrupting the original signal even with a 24dB S/N ratio. Moreover, the algorithm performance slightly reduces for S/N ratio equal to 18dB reaching the following values as regards the characteristic parameters: Se= 95%, P= 96.5%
In figure 12 the algorithm behaviour as a function of different S/N values is shown. It is evident that Se parameter is almost constant depending on FN parameter, therefore it is rather unaffected by noise corrupting ECG signal. For S/N values lower than 24dB, P is dependent on noise signal amount, decreasing as FP grows while the DER curve shape is almost linear as it was expected.
Therefore, results with minimum interferences from noise and artifacts have been obtained, confirming the algorithm high noise immunity degree

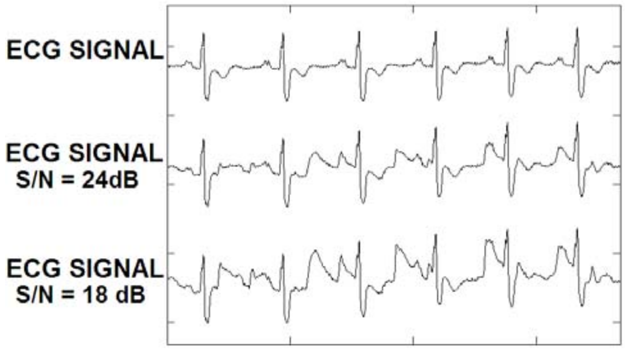

Figure 11 ECG signal compared with noisy ECG signals

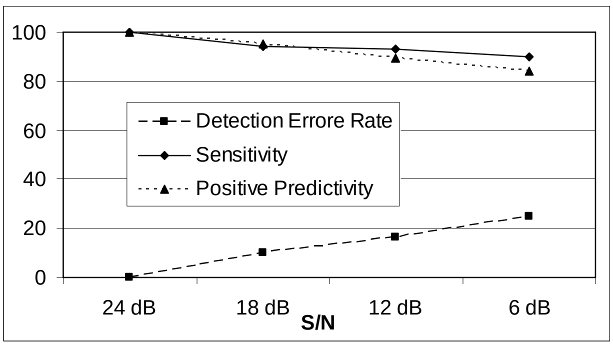

Figure 12 Characteristic parameter shapes vs. S/N ratio

6 Conclusion

In this paper, a real-time procedure for the ECG analysis is presented and validated. For the R point detection it combines the threshold technique and the wavelet transform. The adopted algorithm optimizes the computational time as it processes the ECG signal with a parallel procedure.
The algorithm has been validated using the MIT-BIH Arrhythmia standard database which contains a wide variety of ECG signal morphologies. The technique presents high sensitivity and predictivity parameters: in fact values of about 99.8% are obtained with a suitable threshold value. Moreover, the algorithm noise immunity also has been tested considering noise records from the MIT-BIH Noise Stress Test Database.
Furthermore, the efficiency of the proposed procedure is demonstrated by its adaptation

capability both for different QRS morphologies and various cardiac rhythms. The adopted procedure is independent of the signal shape and consequently can be used for all those biological signals requiring a precise peak localization in presence of noise and artifacts. In fact, authors are now testing the algorithm adopting other biological signals. The preliminary procedure results are confirming the algorithm general validity and its capability to detect correctly peak values even in presence of noise, purposely added to the original signal.

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