Detection of QRS complexes in ECG signals based on Poisson Transform and Root Moments

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***Abstract*— This paper is concerned with the detection of QRS complexes in an electrocardiogram (ECG) waveform. The precision in the identification of QRS complexes is of great importance for the reliability of an automated ECG analyzing system and thus, for the diagnosis of cardiac diseases. Many algorithms have been developed during the last thirty years, each of which has different strengths and weaknesses. In the proposed algorithm a threshold is set and the crossing points between it and the QRS complexes are determined. This has the advantage of ensuring that the R-peaks are contained between the crossing points provided that these are determined accurately. The use of Poisson techniques coupled with Root Moments theory enables us to map this part of the problem into a problem of estimating the zeros of a polynomial that lie on the circumference of the unit circle. This locator polynomial has an order equal to twice the total number of peaks within a data block. The roots of the locator polynomial produce the bounds on the R-peaks mentioned above. The effectiveness of the proposed algorithm is tested by using recordings obtained from the MIT-BIH arrythmia database.**

I. INTRODUCTION

The detection of the R-peaks and consequently of the QRS complexes in an ECG signal provides information on the heart rate, the conduction velocity, the condition of tissues within the heart as well as various other abnormalities and, thus, it supplies evidence to support the diagnoses of cardiac diseases. For this reason, it has attracted considerable attention over the last three decades.

The algorithms in the relevant bibliography adapt a range of different approaches to yield a procedure leading to the identification of the waves under consideration. These approaches are mainly based on derivative-based techniques [1]–[3], *classical* digital filtering [4]–[9], adaptive filtering [10], [11], wavelets [12]–[15], neural networks [16], [17], hidden Markov models [18], mathematical morphology [19], genetic algorithms [20], Hilbert Transform [21], [22], syntactic methods [23], maximum a posteriory estimation [24] and zero-crossing-based identification techniques [25].

In the non-syntactic algorithm presented here, the high accuracy achieved in detecting QRS complexes is accompanied with robustness and low computational complexity.

At the beginning of the proposed algorithm, the enhancement of the QRS part of the ECG is achieved by the reduction of the level of the P and T waves, followed by suppression of some noticeable disturbances in the signal. These disturbances result mainly due to baseline drift, power line interference and interferences from other physiological sources [25]. Bandpass filtering is typically used to attenuate the frequencies related to the above noise sources which lie outside the frequency band occupied by the QRS complex. In our approach, the resulted filtered QRS complex is smoothed by considering its Poisson transform. Afterwards a threshold is set and from each couple of the points produced by the intersection of the threshold line with the ECG signal, the corresponding R-peak is estimated as the midpoint. The main idea, behind the novel steps introduced at this point, is that the unit circle can be seen as the z-transform of the threshold line which has been shifted to meet the x-axis. Thus, the zero-crossings can be identified from the location of the zeros in the unit circle. The identification of the zero-crossings leads to the estimation of the R-peaks. This idea is implemented through the use of relationships taken from the Poisson Transform and Root Moments theory.

The strength of the proposed algorithm lies on the fact that the location of the R-peaks is bounded from above and below by the location of the cross-over points, hence none of the peaks can be ignored.

A set of recordings from the MIT-BIH arrythmia database [26] is used to measure the accuracy of the algorithm and its reliability is evident by the results obtained.

This paper is structured as follows:

In Section II, the Poisson Integral Transform is presented for the case of a real, causal and stable sequence. Then, the concept of the Poisson P kernel is introduced so as the Poisson P Transform to be seen as the result of a convolution. This section also presents in a very compact way important aspects related to the Root moments theory. A set of important relationships which will be used in the implementation of the proposed algorithm is given.

Section III, deals with the main core of the paper and is focused on describing the steps consisting of the preprocessing stage dealing with feature extraction and the decision making stage involved in the R-peak detection. The evaluation of the performance of the proposed algorithm is dealt in Section IV.

II. FUNDAMENTAL RELATIONSHIPS

A. Poisson Transform Relationships

Let us assume a causal sequence $f[n]$, that is, $f[n] = 0$ $\forall n < 0$, where $n \in \mathbb{Z}$. As known, the z-transform of the above sequence is defined as the power series

$$F(z) = \sum_{n=0}^{\infty} f[n] z^{-n}, \tag{1}$$

where z is a complex variable. The Poisson P integral transform for any real, causal and stable sequence $f[n]$ is

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given by

$$F(re^{j\omega}) = \frac{1}{2\pi}\int_{-\pi}^{\pi} F(Re^{j\mu})P_{R,r}(\omega-\mu)d\mu, \quad (2)$$

where $re^{j\omega}$, $Re^{j\mu}$ are the polar forms of two points on the z-plane, lying on concentric positively oriented circles centered at the origin with radii r, R correspondingly ($r > R \geq 1$) and $P_{R,r}(\omega)$ symbolizes the Poisson P Kernel given by

$$P_{R,r}(\omega) = \frac{r^2 - R^2}{R^2 + r^2 - 2Rr\cos\omega}. \quad (3)$$

By assuming the unit circle ($R = 1$) and using (2), the following log-magnitude relationship is obtained

$$\ln|F(re^{j\omega})| = \frac{1}{2\pi}\int_{-\pi}^{\pi} \ln|F(e^{j\mu})|P_{1,r}(\omega-\mu)d\mu, \quad (4)$$

which can be written as

$$\ln|F(re^{j\omega})| = \frac{1}{2\pi}\ln|F(e^{j\mu})| * P_{1,r}(\omega). \quad (5)$$

The *smoothing* property of the Poisson P kernel, highlighted in [27], justifies the use of the above equation in the algorithm under consideration.

B. Root Moments Relationships

Consider an nth degree polynomial

$$F(z) = z^n + p_1 z^{n-1} + p_2 z^{n-2} + ... + p_n, \quad (6)$$

with roots $\{r_i\}$, for $i = 1, \cdots, n$, where $\{p_i\}$ is a set of coefficients characterizing the above polynomial. Then, the (first order) root moments of $F(z)$, denoted here by S_m^F, is given by

$$S_m^F = r_1^m + r_2^m + ... + r_n^m = \sum_{i=1}^{n} r_i^m, \quad (7)$$

where m is an integer. At this stage we present some relationships involving the root moments which are to be used later in the development of the proposed algorithm. $F(z)$ can be represented as a product of

$$\begin{aligned} F(z) &= K\prod_{i=1}^{n_1}(1-\alpha_i z^{-1})\prod_{i=1}^{n_2}(1-\beta_i z^{-1}), \quad (8)\\ &= K\cdot F_{in}(z)\cdot F_{out}(z). \end{aligned}$$

where K is a real constant, $\alpha_i < |z|$ ($\forall i = 1, \cdots, n_1$) and $\beta_i > |z|$ ($\forall i = 1, \cdots, n_2$) are respectively the roots of $F(z)$ inside and outside a circle having a radius of $|z|$ and n_1 and n_2 are correspondingly the number of zeros inside and outside the above circle ($n = n_1 + n_2$).
Taking the logarithm of (8) and expanding the term through the use of Laurent Series, it is possible to show that,

$$\ln[F(z)] = \ln K_1 - n_2 \ln z - \sum_{m=1}^{\infty}\left(\frac{S_m^{F_{in}}}{m}z^{-m} + \frac{S_{-m}^{F_{out}}}{m}z^{m}\right), \quad (9)$$

where the root moments S_m of the minimum phase factor denoted by $S_m^{F_{in}}$ and the root moments S_{-m} of the maximum phase factor represented by $S_{-m}^{F_{out}}$ can be calculated through the use of (7) and K_1 is a constant. Evaluating $\ln[F(z)]|_{z=e^{j\omega}}$ yields

$$\begin{aligned} \ln[F(e^{j\omega})] &= \ln K_1 - n_2 j\omega \\ &\quad - \sum_{m=1}^{\infty}\left(\frac{S_m^{F_{in}}}{m}e^{-jm\omega} + \frac{S_{-m}^{F_{out}}}{m}e^{jm\omega}\right). \quad (10) \end{aligned}$$

The logarithm of the magnitude as well as the phase of $F(e^{j\omega})$ are given respectively from the following equations

$$\ln|F(e^{j\omega})| = \ln K_1 - \sum_{m=1}^{\infty}\left(\frac{S_m^{F_{in}}}{m} + \frac{S_{-m}^{F_{out}}}{m}\right)\cos(m\omega), \quad (11)$$

$$\angle F(e^{j\omega}) = -n_2\omega + \sum_{m=1}^{\infty}\left(\frac{S_m^{F_{in}}}{m} - \frac{S_{-m}^{F_{out}}}{m}\right)\sin(m\omega). \quad (12)$$

From (11) and (12) the following equations are obtained,

$$S_m^{F_{in}} + S_{-m}^{F_{out}} = -\frac{m}{\pi}\int_{-\pi}^{\pi}\ln\left[\frac{|F(e^{j\omega})|}{K_1}\right]\cos(m\omega)d\omega, \quad (13)$$

$$S_m^{F_{in}} - S_{-m}^{F_{out}} = \frac{m}{\pi}\int_{-\pi}^{\pi}[n_2\omega + \angle F(e^{j\omega})]\sin(m\omega)d\omega \quad (14)$$

[28], [29]. The above relationships provide the tools for estimating the roots of a polynomial which lie on the circumference of a unit circle and are going to be implemented in the developed algorithm.

III. Algorithm for Detecting the R-Peaks

The focus of the proposed algorithm is to identify the crossing points after the appropriate threshold cutting the QRS complexes, is chosen. The implementation of this target is achieved through the following steps indicated in the block diagram of the proposed detector presented in Fig. 1.
At the beginning, the intention is focused on the isolation of the QRS complexes. As known, the frequency content of P and T waves is in the range of 0.5 Hz to 10 Hz, the base line and motion artifacts have a power spectra of 0.5 Hz to 7 Hz [30] and the power line interference occupies 50 Hz to 60 Hz [31]. The QRS complex spectra may have frequency components of up to 40 Hz [1]. In order to attenuate the frequencies characterizing the different types of noise as well as the frequencies occupied by the P and T waves, a bandpass filter is used and the cutoff frequencies are set at 18 and 35 Hz. For illustration, a portion of the resulted normalized bandpass filtered ECG signal is presented in Fig. 2(b). The next step is to assume the conversion of the above filtered ECG signal to a representation which can be considered as a time signal that imitates a frequency magnitude response. This conversion is necessary since the magnitude response is an even and continuous function with the first order derivatives at 0 and π equal to zero [28]. In order to ensure that the above conditions are satisfied, the signal is buffered at both ends, time-reversed and its absolute value is taken. Evidently, the obtained *modified* ECG signal (Fig. 3(a)), will have double the number of R-peaks contained in the raw signal. Moreover the R-peaks will be located symmetrically with respect to the axis defined by the end of the buffering. The *modified* ECG signal is then convolved with the Poisson P kernel. By setting $r \to 1$, the resulted signal becomes smoother and thus the QRS complexes become broader although the location of their peaks is not affected.
Once the above *smoothed modified* ECG signal is obtained (Fig. 3(b)), a threshold is then set and the crossing points between it and the QRS complexes under consideration are

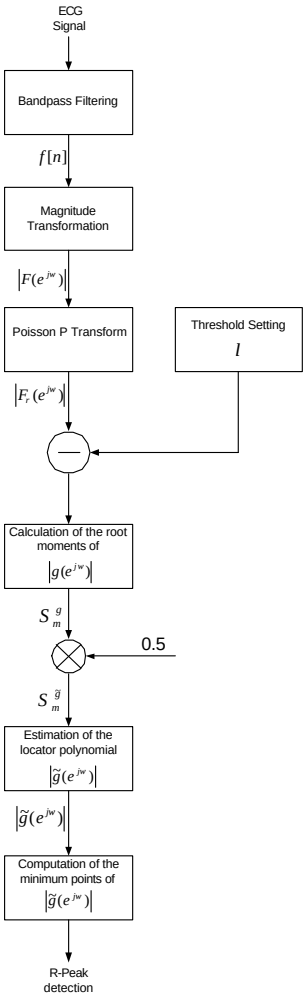

Fig. 1. Block diagram of the Detector

determined. This has the advantage of ensuring that the R-peaks are contained between the crossing points provided that these are defined accurately. From each couple of the points produced by the intersection of the threshold line with the QRS complex, the middle point corresponding to the relevant R-peak should be estimated.

Through shifting the *smoothed modified* ECG signal on the y-axis, by the height of the threshold (Fig. 4(a)), the cutting points obtained from the intersection of the threshold with the signal can be seen as zero-crossings. The magnitude of the *shifted smoothed modified* signal, denoted by $|F(re^{j\omega})|$ and considered as the *final preprocessed* signal is presented in Fig. 4(b).

The final aim is the estimation of the middle point for each pair of zero crossings. The identification of the zero crossings can be achieved by mapping this problem into the problem of estimating the zeros on the unit circle of the polynomial $|F(e^{j\omega})|$, i.e. by defining a polynomial $|g(e^{j\omega})|$ given by

$$|g(e^{j\omega})| = \prod_{i=1}^{k} |(1 - e^{j\phi_i} e^{-j\omega})|, \tag{15}$$

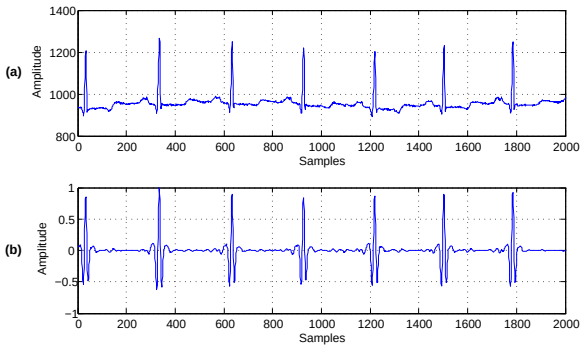

Fig. 2. Record 100: (a) Raw ECG (b) Bandpass filtered ECG

where $e^{j\phi_i}$ symbolizes the i-th zero on the unit circle and k is an even number, representing the total number of zeros. Since $r \to 1$, $|F(re^{j\omega})|$ can approximate faithfully the magnitude response $|F(e^{j\omega})|$. The transition from $|F(e^{j\omega})|$ to the locator polynomial $|g(e^{j\omega})|$ which defines the location of the zero crossings can be realized by using aspects adopted from the Root Moments theory, through a technique described in details in [32].

The procedure leading to the estimation of the mid point from each pair of zero crossings is based on the following observations.

If ϕ_i,ϕ_{i+1} denote the location on the unit circle of two zeros belonging to the same neighborhood and ϕ_l denotes the location on the unit circle of their midpoint,

$$\phi_l = \frac{\phi_i + \phi_{i+1}}{2}, \tag{16}$$

we have approximately,

$$(1 - e^{j\phi_i} e^{-j\omega})(1 - e^{j\phi_{i+1}} e^{-j\omega}) \simeq (1 - e^{j\phi_l} e^{-j\omega})^2. \tag{17}$$

Let $|\tilde{g}(e^{j\omega})|$ be the locator polynomial which locates the position of the mid points. Evidently,

$$|g(e^{j\omega})| = \prod_{l=1}^{\frac{k}{2}} |(1 - e^{j\phi_l} e^{-j\omega})|^2 = |\tilde{g}(e^{j\omega})|^2 \tag{18}$$

and using (13) the following equation is obtained,

$$S_m^g = 2S_m^{\tilde{g}} \Rightarrow S_m^{\tilde{g}} = \frac{S_m^g}{2}. \tag{19}$$

Thus, by calculating the root moments of $|g(e^{j\omega})|$, the estimation of the root moments of the locator polynomial $|\tilde{g}(e^{j\omega})|$ can be achieved.

By computing the root moments of $|\tilde{g}(e^{j\omega})|$ and using the results obtained from (10), the corresponding coefficients can be estimated. The magnitude response of $\tilde{g}(e^{j\omega})$ (refer to Fig. 5(a)) can be obtained from the above coefficients. The minimum points of the resulted magnitude response correspond to the detection of the R-peaks (Fig. 5(b)).

IV. Results and Discussion

The accuracy of the algorithm was tested by applying it to all the records obtained from the MIT-BIH arrythmia database [26]. The above database contains 48 records and

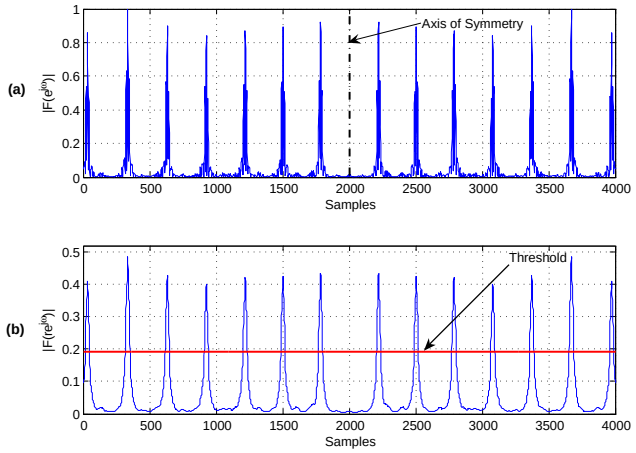

Fig. 3. Record 100: (a) Modified ECG (b) Smoothed modified ECG

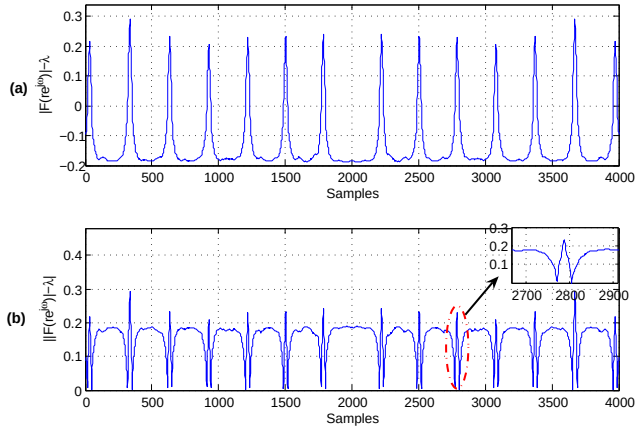

Fig. 4. Record 100: (a) Shifted smoothed modified signal (b) Magnitude of the shifted smoothed modified signal

each of them is about 30 minutes long. The ECG signals are sampled at 360 Hz. The algorithm was implemented through the use of MATLAB.

To assess the performance two statistical measurements were used [33]. These are the Sensitivity (Se), which gives the fraction of real events that are correctly detected and it is defined by,

$$Se = \frac{TP}{TP+FN}, \tag{20}$$

and the Positive Predictivity (+P) which is the fraction of detections that are real events and it is defined by,

$$+P = \frac{TP}{TP+FP}, \tag{21}$$

where FN (False Negatives) denotes the number of missed detections, FP (False Positives) represents the number of extra detections and TP (True Positives) is the number of the correctly detected QRS complexes.

The r parameter of the Poisson P transform was adjusted to be close to 1 for the testing of these records.

Table I shows the results of the algorithm for all the records of the MIT-BIH arrythmia database. The average Sensitivity

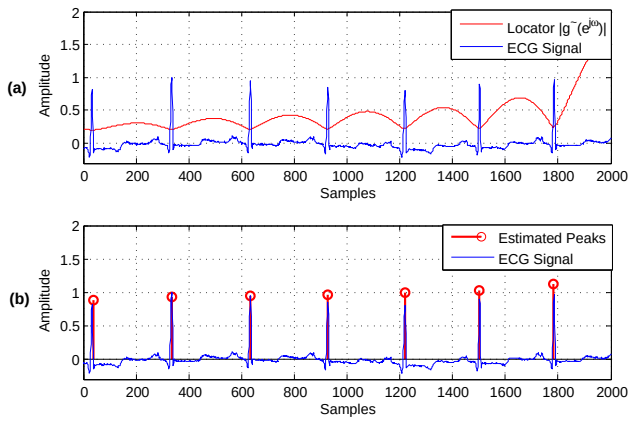

Fig. 5. Record 100 : (a) Locator polynomial $|\tilde{g}(e^{j\omega})|$ (b) Location of estimated peaks

of the algorithm is 99.64 % and its Positive Predictivity is 99.73 %. Most of the FN and FP QRS complexes were found in records 104, 203 and 207. The ECG waveforms in the above records are characterized by high complexity which leads to intrinsic difficulties in detecting the QRS complexes. There are also some other records like 108, 200, 201, where because of they inherent too much noise the application of the present algorithm gave fairly good but not perfect results. Fig. 6 and Fig. 7 present part of the records 203 and 108 respectively. In spite of the baseline drift and the complex form of the ECG which is evident in the relevant figures, the proposed algorithm performed quite well.

For the case of the very noisy records 105 and 108, comparisons between the performance of the proposed algorithm and that of a selection of very well known algorithms can be made by looking at Table II. More specifically,

- For the record 105, both the +P and the Se achieved with the use of our algorithm reach very high levels. This record was classified as one of the most noisy of the files considered.
- For the record 108, the +P as well as the Se corresponding to the algorithm presented in this paper also obtain very high values. Record 108 is characterized by high noise which makes the detection of QRS complexes very difficult.

The effort for possible improvements in the algorithm should be directed towards more effective filtering in the preprocessing stage as well as better threshold adjustment. In this way, there is a good chance of achieving even higher detection rates.

Both the robustness of the algorithm (is not too sensitive in the parameters) and the speed of the detection (low complexity of the algorithm and hence low computational load) can be characterized as very satisfactory.

V. Conclusion

A new algorithm is presented for the detection of the QRS complexes in an ECG signal. This algorithm is based on the determination of the crossing points between the ECG waveform and the threshold, by using the Poisson P transform and

TABLE I

PERFORMANCE OF THE ALGORITHM

Record No.	TP	FN	FP	Se(%)	P(%)
100	2273	0	0	100.00	100.00
101	1863	2	7	99.89	99.63
102	2187	0	0	100.00	100.00
103	2084	0	0	100.00	100.00
104	2195	34	41	98.47	98.17
105	2556	16	4	99.38	99.84
106	2014	13	4	99.36	99.80
107	2137	0	0	100.00	100.00
108	1751	23	16	98.70	99.09
109	2529	3	4	99.88	99.84
111	2124	0	0	100.00	100.00
112	2539	0	0	100.00	100.00
113	1795	0	0	100.00	100.00
114	1876	3	0	99.84	100.00
115	1951	2	0	99.90	100.00
116	2395	17	0	99.30	100.00
117	1535	0	0	100.00	100.00
118	2286	2	0	99.91	100.00
119	1987	0	0	100.00	100.00
121	1859	4	0	99.79	100.00
122	2476	0	0	100.00	100.00
123	1518	0	0	100.00	100.00
124	1618	1	0	99.94	100.00
200	2597	4	4	99.85	99.85
201	1985	15	4	99.25	99.80
202	2131	5	0	99.77	100.00
203	2908	72	61	97.58	97.95
205	2647	9	16	99.66	99.40
207	2249	83	112	96.44	95.26
208	2926	29	5	99.02	99.83
209	3003	2	0	99.93	100.00
210	2631	19	5	99.28	99.81
212	2747	1	0	99.96	100.00
213	3246	5	1	99.85	99.97
214	2247	15	0	99.34	100.00
215	3361	2	0	99.94	100.00
217	2206	2	0	99.91	100.00
219	2284	3	0	99.87	100.00
220	2048	0	0	100.00	100.00
221	2424	3	0	99.88	100.00
222	2477	6	3	99.76	99.88
223	2602	3	0	99.88	100.00
228	2048	5	22	99.76	98.94
230	2256	0	2	100.00	99.91
231	1571	2	0	99.87	100.00
232	1775	5	6	99.72	99.66
233	3060	19	0	99.38	100.00
234	2749	4	0	99.85	100.00
Total	109321	420	312	99.64	99.73

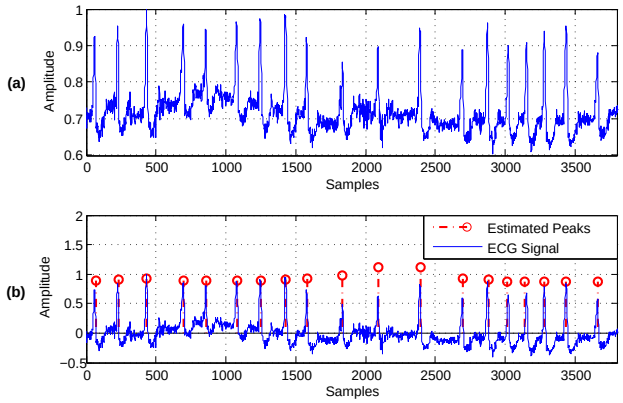

Fig. 6. Record 203: (a) Raw ECG (b) Estimated R-peak locations

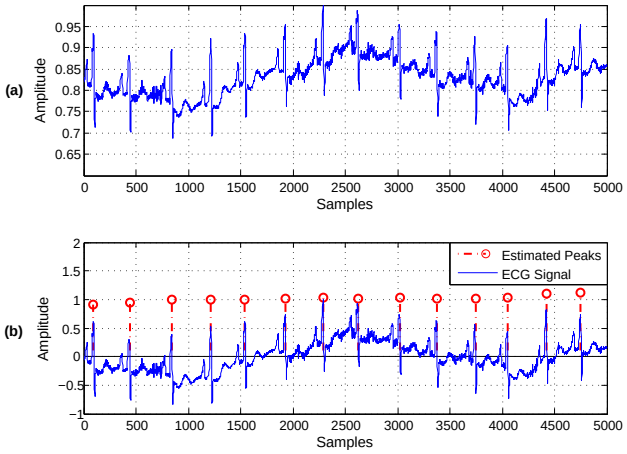

Fig. 7. Record 108: (a) Raw ECG Signal (b) Estimated R-peak locations

the root moments theory. This approach has the advantage of ensuring that the R-peaks are contained between the crossing points when these are determined accurately. The algorithm is evaluated for a number of records obtained from the MIT-BIH Arrythmia database. The accuracy of the new algorithm in detecting the QRS complexes is very high due to the criteria used (average Sensitivity of 99.64 % and average Positive Predictivity of 99.73 %).

TABLE II

COMPARISON OF THE PERFORMANCE

Algorithms	Recordings			
	105		108	
	Se(%)	P(%)	Se(%)	P(%)
Proposed Algorithm	99.38	99.84	98.70	99.09
Zero Crossing Counts [34]	99.49	98.71	98.24	97.85
Pan-Tompkins [35]	99.15	97.46	98.77	89.86
Hamilton-Tompkins [36]	99.15	97.97	97.39	97.23
Fuzzy reasoning [37]	99.33	97.97	99.01	98.61
Filter Bank [1]	99.26	97.58	96.28	92.17
Genetic Algorithm [20]	99.81	96.76	98.58	92.40

VI. ACKNOWLEDGMENTS

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