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# An efficient selection, scoring, and variation ratio test algorithm for ECG R-wave peak detection

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Jian-Jiun Ding <sup>1\*</sup>, Chen-Wei Huang <sup>1</sup>, Yi-Lwun Ho <sup>2</sup>, Chi-Sheng Hung <sup>3</sup>, Yen-Hung Lin <sup>2</sup>, and Ying-Hsien Chen <sup>3</sup>

<sup>1</sup> Graduate Institute of Communication Engineering, National Taiwan University, Taipei, Taiwan

<sup>2</sup> School of Medicine, National Taiwan University, Taipei, Taiwan

<sup>3</sup> National Taiwan University Hospital, Taipei

**Abstract** A new R-wave peak detection algorithm for electrocardiogram (ECG) signal with very high accuracy and efficiency is developed in this paper. With the proposed techniques of R-wave peak candidate sifting and a Haar-like matched filter, we can accurately determine which point is likely to be an R-wave peak. The point that is impossible to be an R-wave peak will not be further processed. After this process, only about 3-5 points per second are needed to be further checked, which is very helpful for reducing the computation time. Moreover, instead of a conventional filter, the proposed technique of the variation ratio test is used to exclude the peak caused by noise. Furthermore, several posterior processing techniques, such as adaptive thresholds and a regularity test, are proposed to further improve the accuracy. To make the proposed algorithm even more efficient, any transform, including the Fourier and the wavelet transforms, is avoided in our algorithm. The simulations for the MIT/BIH arrhythmia database show that our proposed algorithm achieves an error rate of 0.189%, which is much lower than that of existing methods.

**Keywords** Electrocardiogram, R-wave peak detection, fast algorithm, R-wave peak candidate selection, variation ratio test

## 1. Introduction

Electrocardiogram (ECG) signals provide important information about human heart status. An automatic ECG waveform analysis algorithm with high accuracy and efficiency is helpful for cardiac disease diagnosis and health monitoring.

A typical ECG waveform consists of the feature points P, Q, R, S, and T. The most important one is the R-wave peak. When the position of the R-wave peak is found, P, Q, S, and T points can be determined by their relative positions to the R-wave peak. Therefore, the accuracy of the R-wave peak detection significantly affects the performance of ECG signal analysis.

Many R-wave peak detection algorithms were proposed recently. These detection algorithms can be classified into two classes: time-domain-based algorithms and frequency-domain-based algorithms. Time-domain-based algorithms [1-8] are simpler to implement, while

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transform-domain-based algorithms [9-15] are more robust to interference and have higher accuracies.

In this paper, we develop a new algorithm for R-wave peak detection to simultaneously achieve the goals of "high accuracy" and "high efficiency".

With respect to the goal of efficiency, the proposed algorithm is time-domain-based and the adopted operations are as simple as possible. To reduce the interference from noise and small vibrations, which is usually a problem of time-domain-based algorithms, the variation ratio test technique is applied in our algorithm.

Moreover, to further improve the efficiency, we apply the R-wave peak candidate sifting technique to reduce the number of points for further checking to no more than 5 points per second. To further improve the accuracy, we use the regularity test and adaptive thresholds to refine the results of R-wave peak detection. Simulations show that the computation time needed for our algorithm to analyze a 30-minute ECG signal is less than 0.65 seconds (by a MATLAB program running on a PC). For the MIT/BIH arrhythmia database [16, 17], the proposed algorithm achieves an error rate of 0.189%, which is much lower than that of existing methods.

## 2. Related Work

In recent years, there have been many studies about ECG R-wave peak detection. This section describes several published algorithms. The techniques adopted by these algorithms are summarized in Table I.

The methods in [1-8] are *time-domain -based* and the methods in [9-15] are *transform-domain-based*. The methods in [18-20], which requires filters, can be viewed as an intermediate of the time-domain-based method and the frequency-domain-based methods.

In [1, 2], two derivative-based methods were developed. In [1], the differentiated waveform was utilized to locate the QRS complex. Then, the criteria that consider the steepness, shape, and height of ECG signals were applied to enhance the detection performance. In [2], in addition to derivatives, the time average window and the searching back method are also applied to find the R-wave peak. These derivative-based algorithms have very low computational complexity.

The methods in [3-6] are based on shape analysis. In [3], a topological mapping algorithm is applied to map a one-dimensional ECG signal into a two-dimensional vector. In [4], a very novel algorithm using morphology to remove background noise and the baseline wander of the ECG signal. The method in [5] is also based on morphology, but the multi-frame differential modulus accumulation is applied as well. The algorithms in [4, 5] have very high accuracy for R-wave peak detection.

**Table 1.** Summary of R-wave peak detection algorithms

Methods	Adopted Techniques
[1] Derivation	Differentiation; Slope estimation; Two fixed thresholds
[2] Derivation	Median estimator; Search back; Peak level estimation
[3] Topology	Spatial velocity with 2D vectors; LPF; Single fixed threshold
[4] Morphology	Dilation and erosion; Opening and closing; LPF; Single adaptive threshold
[5] Multiscale	Morphology; Differentiation; Multi-frame accumulation
[6] Geometric	Polynomial model estimation; Single fixed threshold
[7] Three phases	Squaring and moving-average estimation
[8] Zero crossing	Feature extraction; Zero crossing count; BPF; Single adaptive threshold
[9] Hilbert	FFT; RR interval estimation; Hilbert transform; BPF; Single adaptive threshold
[10] Hilbert	Hamilton-Tompkins, Time-average estimation; BPF; Two adaptive thresholds
[11] Wavelet	Discrete wavelet transform (DWT); HPF; Nonlinear LPF
[12] Wavelet	DWT; Cubic spline interpolation; Single adaptive threshold
[13] Wavelet	Four-scale discrete wavelet transform; BPF; Single adaptive threshold
[14] Wavelet	Biorthogonal spline wavelet transform; BPF; Single adaptive threshold
[15] Wavelet	Complex wavelet transform; BPF; Continuous wavelet transform
[18] Filter bank	Magnitude and phase reconstruction; BPF; Subband handling; Two adaptive thresholds
[19] Polynomial	Polynomial filter; Genetic maxima detection
[20] Curve length	Curve length; Adaptive thresholds; BPF
<b>[Proposed algorithm]</b>	Haar-like matched filter; R-wave peak candidate sifting; Noise removal by the variation ratio test; Adaptive thresholds; Location prediction based on regularity

The approach in [6] is based on geometrical matching and genetic algorithms. Moreover, a level-detection algorithm is used to evaluate the similarity between the reference pattern and the input ECG signal.

Another time-domain-based algorithm was developed in [7]. It has three phases: two are for learning and one is for detection. The learning phases are used for distinguishing signals. In [8], an algorithm based on the feature obtained by counting the number of zero

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crossings per segment was proposed. This algorithm is simple but very effective.

The algorithms in [9-15] are *transform-domain-based*. In [9], an algorithm based on the Hilbert transform was proposed. It also applies a band pass filter and peak detection for integrated and differentiated waveforms. The method is easy to implement and has a high detection rate. The work in [10] also adopted the Hilbert transform and used a first-derivative squaring function (Hamilton-Tompkins)

The algorithms in [11-15] use the wavelet transform. In [11], first, the discrete wavelet transform (DWT) was used for denoising the signal. A linear highpass filter (HPF) is then accentuated the QRS complex and a nonlinear lowpass filter (LPF) is used to smooth the signal without destroying R-wave peaks. The algorithm in [12] used a DWT to enhance detection robustness. It used the fact that symmetric wavelet decomposition can precisely retrieve the delta-function peak location. Another DWT-based algorithm was proposed in [13]. It uses the DWT together with a sigma-delta modulator also suppresses the out-of-band noise. Moreover, a pre-processing filter and a post-processing decision process for threshold-based noise suppression are adopted. In [14], an algorithm using the biorthogonal spline wavelet was developed to detect ECG characteristic points using the Mallat algorithm. In [15], another novel algorithm based on the complex Morlet wavelet transform, the bandpass filter (BPF), and the continuous wavelet transform was proposed.

All of the above wavelet-based algorithms can reduce the effect of noise. However, the variation ratio rest proposed in this paper, which is much simpler to implement, also has a good performance for noise reduction.

The methods in [18-20] are all *filter-based methods*. Since the implementation of the filter with a non-constant response may require transforms, they can be viewed as an intermediate of the time-domain based and the frequency-domain based methods. In [18], a multi-rate digital signal processing technique was used for R-wave peak detection. It incorporates a filter bank, decomposes the ECG into sub-bands with uniform bandwidths, and performs independent time and frequency analyses. In [19], an approach used a linear or nonlinear polynomial filter and a genetic optimization algorithm was proposed. In [20], a novel idea of curve length calculation is used to determine R-wave peaks. The algorithm is easy to implement but has a very good performance.

After the locations R-wave peaks and other feature points are precisely determined, one can use the neural network or the machine learning techniques to determine the arrhythmia problem from the ECG signal [21, 22].

We summarize R-wave peak detection algorithms in

Table I. Compared to these algorithms, the proposed algorithm uses R-wave peak candidate sifting and avoids using any operation with large computational load. It also uses the Haar-like matched filter (It can be implemented without using the Fourier transform), the variation ratio test, adaptive thresholds, and location prediction to achieve the goal of high accuracy. These will be described in detail in next section.

### 3. Proposed Algorithm

The flowchart of the proposed algorithm is shown in Fig. 1. Our aim is to simultaneously achieve the goals of (1) high accuracy and (2) less computational loading. To achieve the second goal, all transforms (including the Fourier, wavelet, and Hilbert transforms) are avoided in our algorithm. To achieve the goal of accuracy, many new techniques are adopted in the proposed algorithm.

Compared to the existing methods, the proposed algorithm adopts the *following four new techniques*:

#### (1) R-wave peak candidate sifting:

Instead of processing the ECG signal at all sampling points, we first exclude the sampling points that are impossible to be an R-wave peak. Only R-wave peak candidates, i.e., the points that could possibly be R-wave peaks, are further processed. The number of R-wave peak candidates is *only 3-5 points per second*, which is much less than the number of sampling points of an ECG signal. Therefore, this process is very helpful for improving the efficiency of R-wave peak detection.

#### (2) The Haar-like matched filter:

This technique is used to calculate the score function for R-wave peak candidate sifting.

Although the Haar-like matched filter is a filter, since its coefficients are constants, it can be implemented in a very efficient way without using the Fourier transform.

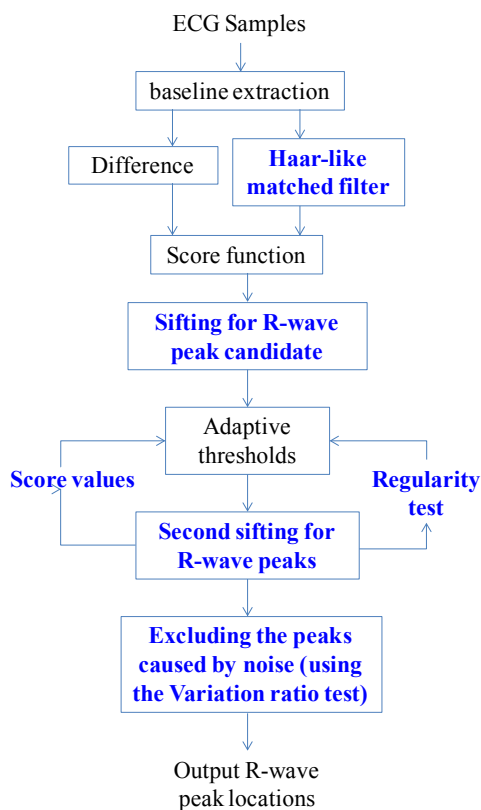
#### (3) The regularity test for adaptive thresholding:

If the distance between a location and its previous R-wave peak is near to a multiple of the predicted RR interval, then the threshold for sifting R-wave peak candidates is lowered. Otherwise, the threshold is increased.

#### (4) The variation ratio test:

Instead of conventional filters, the ratio of the peak-to-peak variation to the total variation is used to exclude peaks caused by noise. This method is much easier to implement than conventional filters.

#### 2.1 Haar-like Matched Filter



**Figure 1.** Flowchart of the proposed R-wave peak detection algorithm. The processes of “Haar-like matched filter”, “sifting for R-wave peak candidate”, “second sifting for R-wave peak candidate”, “regularity test”, and “variation ratio test” are the new techniques proposed in this paper.

A matched filter is usually used for template matching. In ECG signal analysis, one can use a Laplacian of Gaussian (LoG) function or a Haar-like function to approximate the shape of a QRS complex and treat it as the matched filter to detect which point is more probable to be an R-wave peak. Although the LoG function better approximates a QRS complex, for the consideration of efficiency, we suggest that it is better to use a Haar-like matched filter, which is defined as

$$h(n) = c \text{ for } -B_1 \leq n \leq B_1, \quad h(n) = -1 \text{ for } B_1 < |n| \leq B_2, \\ h(n) = 0 \text{ otherwise} \quad (1)$$

where  $c$  is set as  $2(B_2 - B_1)/(2B_1 + 1)$  such that the sum of  $h(n)$  is equal to 0,  $B_1 \cong 0.025f_s$ ,  $B_2 \cong 0.06f_s$ , and  $f_s$  is the sampling frequency of the ECG signal. For the MIT/BIH arrhythmia database, the number of samples is 360 points per second (i.e.,  $f_s = 360$ ),  $B_1$  and  $B_2$  are chosen to be 9 and 21, respectively. Although the Haar-like matched filter is also a filter, it is much easier to implement than other filters.  $h(n)$  can be expressed by rectangular functions

$$h(n) = -\Pi\left(\frac{n}{42}\right) + (c+1)\Pi\left(\frac{n}{18}\right) \quad (2)$$

where  $\Pi(n/2B) = 1$  if  $|n| \leq B$  and  $\Pi(n/2B) = 0$  otherwise. The convolution of  $x[n]$  and  $\Pi(n/2B)$  can be implemented very

efficiently. That is, if

$$y_1(n) = x(n) * \Pi\left(\frac{n}{2B}\right) = \sum_{n=-B}^B x(n)$$

where  $*$  means convolution, then

$$y_1(n) = y_1(n-1) + x(n+B) - x(n-B). \quad (3)$$

Note that, from (3), no Fourier transform and even no multiplication operation are required to implement the convolution of  $x(n)$  and the Haar-like matched filter  $h(n)$  in (2) requires only  $N$  multiplications and  $5N$  additions where  $N$  is number of sampling points.

At the R-wave peak, the output of the Haar-like matched filter is usually large. Therefore, it can reveal which points are more likely to be R-wave peaks.

## 2.2 R-Wave Peak Candidate Sifting

The sampling rate for an ECG signal is usually very high. For example, in the MIT/BIH arrhythmia database, there are 360 points per second for an ECG signal. Therefore, it is inefficient to determine if a sample is an R-wave peak point by point. In this paper, we perform R-peak candidate sifting to exclude the points that cannot be R-wave peaks.

After sifting, only about 3-5 R-wave peak candidates per second are needed to be further processed. Therefore, although many techniques are adopted in the post-processing process, the overall computational load of the proposed algorithm is still greatly reduced. In addition to improving the efficiency, the candidate sifting process can also avoid the misjudgment of R-wave peaks caused by noise and tiny variations.

We use the following rules to determine whether a point is an R-wave peak candidate:

- (i) An R-wave peak candidate should have a large value after convolution with the Haar-like matched filter.
- (ii) The second order difference at the location of an R-wave peak candidate should also be large.
- (iii) Since it very rarely happens that the beat rate of a person is more than 300 beats per second, the interval between two R-wave peak candidates should be larger than  $60/300 = 0.2$  seconds.

According to these three rules, the R-wave peak candidate sifting process is as follows. First, calculate the following score function:

$$s(n) = y(n)[x(n) + c_1 x_2(n)] \quad (4)$$

where  $x[n]$  is the ECG signal after the baseline has been extracted,  $y[n] = x[n] * h[n]$  is the output of the Haar-like matched filter (to satisfy (i)), and  $x_2[n]$  is the second order difference of  $x[n]$  (to satisfy (ii)):

$$x_2(n) = 2x(n) - x(n+1) - x(n-1). \quad (5)$$

The constant  $c_1$  is set at 0.55 for the simulation on the MIT/BIH arrhythmia database [16, 17]. Then, if

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$$|s(k)| > |s(n)| \text{ for } k - 0.2f_s \leq n \leq k + 0.2f_s \quad (6)$$

where  $f_s$  is the number of sampling points per second, then the point  $k$  is an R-wave peak candidate. (This constraint is to satisfy (iii)). In (6), absolute values are compared since R-wave peaks are possible to be negative (This may happen in the premature ventricular contraction (PVC) case).

From (6), the number of R-wave peak candidates is less than five points per second, which is much lower than the original sampling frequency. This is of a great help for improving the algorithmic efficiency.

### 2.3 Adaptive Threshold Using Score Values and Regularity

After R-wave peak candidates are obtained, we use adaptive thresholds and the variation ratio test to further determine whether these candidates are indeed R-wave peaks. We use (a) the absolute values of the score function  $s[n]$  at R-wave peaks and (b) the regularity of RR intervals to adjust the adaptive threshold. The adaptive threshold is calculated from

$$\text{adaptive threshold} = W_1 W_2 \quad (7)$$

$$\text{where } W_1 = T + S_5, \quad (8)$$

$S_5$  is the fifth largest absolute value of  $s[n]$  (defined in (4)) for the R-wave peaks of the most recent 10 second, and  $T$  is a constant. The adaptive threshold is adjusted by  $S_5$  because we think that the magnitude of the score function at the next R-wave peak highly correlates with that of the score function in the previous 10 seconds. We use the 5<sup>th</sup> largest value of  $|s[n]|$  instead of  $\max(|s[n]|)$  to avoid misjudgment in the PVC case (in this case, the R-wave peak is either negative or very large).

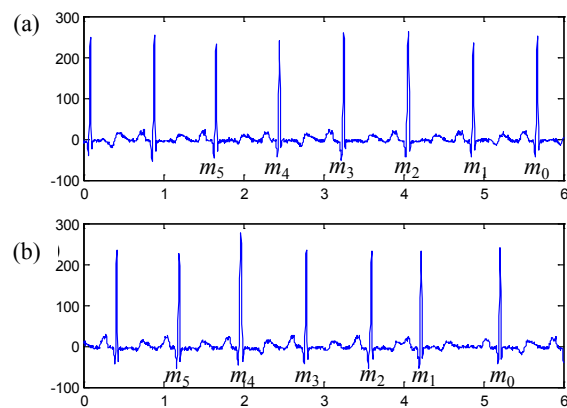
The value of  $W_2$  in (7) is related to the regularity of RR intervals (i.e., the distances between two adjacent R-wave peaks). Suppose that there is an R-wave peak candidate at location  $n$  and we want to determine whether it is indeed an R-wave peak. Also suppose that  $m_1, m_2, m_3, m_4$ , and  $m_5$  are the locations of the five most recently detected R-wave peaks and  $n > m_1 > m_2 > m_3 > m_4 > m_5$ . Then

$$W_2 = \beta_1 + \beta_2 \left| \frac{n - m_1}{I_e} - \text{round} \left( \frac{n - m_1}{I_e} \right) \right| \quad (9)$$

where  $\beta_1$  and  $\beta_2$  are positive constants,  $I_e$  is the RR interval estimated from the following autoregressive model:

$$I_e = \sum_{h=1}^5 \tau_h (m_h - m_{h+1}), \quad \sum_{h=1}^5 \tau_h = 1, \quad (10)$$

and  $\tau_h$  are fixed constants that satisfy  $\tau_1 \geq \tau_2 \geq \tau_3 \geq \tau_4 \geq \tau_5$ . From (9), one can see that if  $n - m_1$  is near to a multiple of the estimated RR interval, then  $W_2$  and hence the adaptive threshold in (7) is smaller. Otherwise, the adaptive threshold is larger.



**Figure 2.** Two segments of an ECG signal in the MIT/BIH arrhythmia database. (a) One can use the locations of the previous five R-wave peaks ( $m_1$  to  $m_5$ ) to estimate the next RR interval. (b) When  $m_1 - m_2$  is much less than the average of the previous four RR intervals, such as the atrial premature contraction (APC) case, it is proper to skip  $m_1$  and use  $m_2$  to  $m_6$  to estimate  $(m_0 - m_2)/2$  where  $m_0$  is the location of the next R-wave peak.

However, in the case where  $m_1 - m_2$  is unusually small (for example,  $m_1 - m_2 < 0.7 \text{mean}(m_k - m_{k+1})$  where  $k = 2, 3, 4$ , and 5), such as the APC case, we can replace  $n - m_1$  by  $(n - m_2)/2$  in (9) and use  $m_2, m_3, m_4, m_5$ , and  $m_6$  instead of  $m_1, m_2, m_3, m_4$ , and  $m_5$  in (10) to estimate the RR interval  $I_e$ , as in Fig. 2.

When we cannot consecutively predict the RR interval correctly (it may happen if atrial fibrillation (AF) occurs), the value of  $\beta_2$  is reduced, since in this case, RR intervals are very irregular and using the predicted RR interval to adjust the adaptive threshold does not make much sense. In addition to control the threshold, detecting the irregularity is also useful for finding the arrhythmia problem in real time [21].

In summary, we use the score values in (4) at R-wave peak candidates and the predicted RR interval to adjust the adaptive threshold. If

$$|s(n)| > \text{adaptive threshold at } n, \quad (11)$$

then we conclude that  $n$  may be a location of the R-wave peak. Then, we use the variation ratio test introduced in the following subsection to further check whether there is indeed an R-wave peak at  $n$  or if the peak is caused by noise. This adaptive thresholding procedure can also be viewed as the second sifting process for R-wave peak candidates.

### 2.4 Noise Removing by the Variation Ratio Test

To improve the accuracy of R-wave peak detection, it is important to reduce the effect of noise. Unlike existing work, we avoid using lowpass and bandpass filters, since we think that they may not preserve the high frequency components of R-wave peaks and increase the

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computational load. Instead, we apply much simpler methods for noise removal. Most local extremes caused by noise are effectively removed by the Haar-like matched filter and R-wave peak candidate sifting process (see Sections 2-1 and 2-2). Although some extremes caused by noise cannot be removed by these processes, they can be removed by the *variation ratio test* introduced in this subsection.

The *variation ratio test* is to calculate

$$\Omega = u_1 / u_2 \quad (12)$$

where  $u_1$  is the peak-to-peak variation and  $u_2$  is the total variation in the region of  $m - 0.1f_s \leq n \leq m + 0.1f_s$  ( $f_s$  is the sampling frequency of the ECG signal):

$$u_1 = \max \{x[n] \mid m - 0.1f_s \leq n \leq m + 0.1f_s\} - \min \{x[n] \mid m - 0.1f_s \leq n \leq m + 0.1f_s\}, \quad (13)$$

$$u_2 = \sum_{n=m-B+1}^{m+B} |x[n] - x[n-1]|, \quad (14)$$

and  $x[n]$  is the ECG signal extracted from the baseline. If  $m$  is indeed a location of R-wave peaks, then  $u_2$  should be only a little larger than  $u_1$  and  $\Omega$  should be close to 1/2. By contrast, if  $m$  is a local extreme caused by noise,  $u_2$  will be much larger than  $u_1$  and  $\Omega$  will be very small.

Note that, the variation ratio test requires no transform, no convolution, and is very easy to implement, but it can very effectively distinguish between peaks caused by noise and true R-wave peaks.

#### 4 Simulation Results

The proposed algorithm was evaluated by using the MIT/BIH arrhythmia database [16, 17] that consists of 48 half-hour two-channel ambulatory ECG recordings. These recordings have 11-bit resolution over 10mV and are sampled at 360Hz.

As the work in [13, 20], we used the standard ground truth from the MIT/BIH database website [16] to test the accuracy of the R-wave peak detection algorithm. As most of the existing works, the ambiguous cases of +, ~, |, x, and ! are excluded, where +, ~, and | belong to isolated QRS-like artifacts, and ! and x are the ventricular flutter wave and the non-conducted P-wave. In total, there are 109494 beats in the ground truth.

True positive (TP), false negative (FN) and false positive (FP) were used to evaluate the detection performance where TP is the number of R-wave peaks in the ground truth successfully detected by our algorithm, FN is the number of undetected R-wave peaks, and FP is the number of detected R-wave peaks that are not R-wave peaks in the ground truth. From these, the sensitivity (SE), positive prediction (+P), and detection error rate (DER) are calculated by

**Table 2.** Performance of the proposed algorithm on the MIT/BIH arrhythmia database [16, 17]. All of the 48 data were tested. The standard ground truth in [16] was used for evaluating the performance.

Tape (No)	Total (Beats)	FN (Beats)	FP (Beats)	SE(%)	+P(%)	DER(%)
100	2273	0	0	100.00%	100.00%	0.00%
101	1865	1	4	99.95%	99.79%	0.27%
102	2187	0	0	100.00%	100.00%	0.00%
103	2084	0	0	100.00%	100.00%	0.00%
104	2229	0	18	100.00%	99.20%	0.81%
105	2572	0	35	100.00%	98.66%	1.36%
106	2027	1	1	99.95%	99.95%	0.10%
107	2137	0	0	100.00%	100.00%	0.00%
108	1763	0	2	100.00%	99.89%	0.11%
109	2532	1	0	99.96%	100.00%	0.04%
111	2124	1	0	99.95%	100.00%	0.05%
112	2539	0	0	100.00%	100.00%	0.00%
113	1795	0	0	100.00%	100.00%	0.00%
114	1879	0	1	100.00%	99.95%	0.05%
115	1953	0	0	100.00%	100.00%	0.00%
116	2412	14	0	99.42%	100.00%	0.58%
117	1535	0	0	100.00%	100.00%	0.00%
118	2278	0	0	100.00%	100.00%	0.00%
119	1987	0	1	100.00%	99.95%	0.05%
121	1863	1	0	99.95%	100.00%	0.05%
122	2476	0	0	100.00%	100.00%	0.00%
123	1518	0	0	100.00%	100.00%	0.00%
124	1619	0	0	100.00%	100.00%	0.00%
200	2601	2	4	99.92%	99.85%	0.23%
201	1963	0	8	100.00%	99.59%	0.41%
202	2136	0	10	100.00%	99.53%	0.47%
203	2980	0	8	100.00%	99.73%	0.27%
205	2656	4	0	99.85%	100.00%	0.15%
207	1860	21	11	98.87%	99.41%	1.72%
208	2955	10	0	99.66%	100.00%	0.34%
209	3005	0	0	100.00%	100.00%	0.00%
210	2650	9	2	99.66%	99.92%	0.42%
212	2748	0	0	100.00%	100.00%	0.00%
213	3251	1	0	99.97%	100.00%	0.03%
214	2262	1	0	99.96%	100.00%	0.04%
215	3363	0	0	100.00%	100.00%	0.00%
217	2208	1	2	99.95%	99.91%	0.14%
219	2154	0	0	100.00%	100.00%	0.00%
220	2048	0	0	100.00%	100.00%	0.00%
221	2427	0	0	100.00%	100.00%	0.00%
222	2483	2	1	99.92%	99.96%	0.12%
223	2605	1	1	99.96%	99.96%	0.08%
228	2053	1	21	99.95%	98.99%	1.07%
230	2256	0	0	100.00%	100.00%	0.00%
231	1571	0	0	100.00%	100.00%	0.00%
232	1780	0	4	100.00%	99.78%	0.22%
233	3079	1	0	99.97%	100.00%	0.03%
234	2753	0	0	100.00%	100.00%	0.00%
<b>Total</b>	<b>109494</b>	<b>73</b>	<b>134</b>	<b>99.933%</b>	<b>99.878%</b>	<b>0.189%</b>

**Table 3.** Performance comparison for the existing algorithms and the proposed algorithm in this paper on the MIT/BIH arrhythmia database [16, 17].

Algorithm	TP	FN	FP	SE	+P	DER
[1]	109309	199	405	99.82%	99.63%	0.55%
[2]	108927	340	248	99.69%	99.77%	0.54%
[3]	109146	335	137	99.69%	99.87%	0.43%
[4]	109231	279	199	99.75%	99.82%	0.44%
[5]	109207	213	204	99.81%	99.80%	0.39%
[6]	59185	1246	521	97.94%	99.13%	2.92%
[7]	115860	277	507	99.76%	99.56%	0.68%
[8]	91006	277	390	99.70%	99.57%	0.73%
[9]	97599	195	411	99.80%	99.58%	0.62%
[10]	105232	2112	884	98.03%	99.17%	2.79%
[11]	102125	529	459	99.55%	00.49%	0.96%
[12]	90693	296	375	99.67%	99.59%	0.74%
[13]	109268	224	154	99.80%	99.86%	0.35%
[14]	102833	101	191	99.90%	99.81%	0.28%
[18]	90535	374	406	99.59%	99.55%	0.86%
[19]	109522	441	545	99.60%	99.50%	0.90%
[20]	109319	177	154	99.86%	99.84%	0.30%
<b>[Proposed algorithm]</b>	<b>109421</b>	<b>73</b>	<b>134</b>	<b>99.93%</b>	<b>99.88%</b>	<b>0.189%</b>

• sensitivity:  $SE(\%) = \frac{TP}{TP + FN} \%$ , (15)

• positive prediction:  $+P(\%) = \frac{TP}{TP + FP} \%$ , (16)

• detection error rate:  $DER(\%) = \frac{FP + FN}{TP + FN} \%$ . (17)

An accurate algorithm will have a higher SE and +P and a smaller DER.

Table II shows the summary of the R-wave peak detection performance of the proposed algorithm on all recordings of the MIT/BIH arrhythmia database.

The results in Table II show that the proposed algorithm is very accurate for R-wave detection. There are 48 half-hour ECG signal in the database, but the numbers of FNs and FPs are only 73 and 134, respectively. The sensitivity (SE) is 99.933% and the positive prediction (+P) rate is 99.878%. The detection error rate (DER) is only **0.189%**. Especially, for healthy and semi-healthy cases (100, 101, 103, 111, 112, 113, 115, 116, 117, 121, 122, 123, 208, 210, 212, 215, 223, 230, 231, and 234), the average DER of the proposed algorithm is only **0.097%**.

The average detection time for each 30-minute ECG data in the MIT/BIH database is less than **0.65 seconds** by a MATLAB program running on a PC, which is very efficient.

Table III compares the detection performance for the standard MIT/BIH arrhythmia database of the proposed algorithm with those of other existing algorithms. As the work in [13, 20], all 48 data were tested, ambiguity cases were excluded, and the standard ground truth given in [16] was used for evaluating the performance of the proposed algorithm. The performance is shown in terms of SE, +P, and DER factors defined in (15)-(17). From Table 3, it can be observed that the performance of the proposed algorithm is the best. The DER of the proposed algorithm is only 0.189%, which is lower than that of all the existing methods. Both the sensitivity (SE) the positive detection (+P) rate of the proposed algorithm are higher than those of the existing algorithms. The results prove that the proposed algorithm is very accurate for R-wave peak detection.

## 5 Conclusion

In this paper, a real-time ECG R-wave peak detection algorithm was proposed. Based on the techniques of Haar-like matched filter, the variation ratio test, adaptive thresholding, and location prediction, the proposed algorithm could detect R-wave peaks very accurately. Simulation results showed that the proposed method achieves a sensitivity of 99.933%, a positive prediction rate of 99.878%, and a detection error rate of 0.189% on the MIT/BIH arrhythmia database. The detection error rate of the proposed method is less than that of the existing methods, proving that the proposed algorithm achieves its goal of high accuracy.

Moreover, since R-wave peak candidate sifting is applied, our algorithm can be implemented in a very efficient way. The proposed Haar-like matched filter and the variation ratio test, which can implemented in the time domain without using any transform, are also helpful for further improving the efficiency.

The average running time for analyzing each of the 30-minute data in the MIT/BIH arrhythmia database was less than 0.65 seconds (by MATLAB and a PC), which proves that the proposed algorithm also achieves the goal of low computational cost.

The proposed R-wave peak detection algorithm will be helpful for diagnosis and health monitoring, because the accurate analysis of cardiac dysrhythmia problems, such as ventricular premature contraction, atrial premature contraction, ventricular fibrillation, and atrial fibrillation, is highly dependent on whether the locations of R-wave peaks can be determined precisely.



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