

Detection of QRS complexes in electrocardiogram using support vector machine

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This paper presents the application of a support vector machine (SVM) for the detection of QRS complexes in the electrocardiogram (ECG). The ECG signal is filtered using digital filtering techniques to remove noise and baseline wander. The support vector machine is used as a classifier to delineate QRS and non-QRS regions. Two different algorithms are presented for the detection of QRS complexes. The first uses a single-lead ECG at a time for the detection of QRS complexes, while the second uses 12-lead simultaneously recorded ECG. Both algorithms have been tested on the standard CSE ECG database. A detection rate of 99.3% is achieved when tested using a single-lead ECG. This improves to 99.75% for the simultaneously recorded 12-lead ECG signal. The percentage of false negative detection is 0.7% and the percentage of false positive detection is 12.4% in the single-lead QRS detection and it reduces to 0.26% and 1.61% respectively for QRS detection in simultaneously recorded 12-lead ECG signals. The performance of the algorithms depends strongly on the selection and the variety of the ECGs included in the training set, data representation and the mathematical basis of the classifier.

Keywords: ECG; QRS complex; SVM

1. Introduction

Electrocardiography is a technique of recording the bio-electric currents generated by the heart. The graphical display of this recording is called an electrocardiogram (ECG), and it provides useful information about the functional status of the heart. Analysis of ECG is of great importance in the detection of cardiac anomalies. In a clinical setting, such as in intensive care units, it is essential for automated systems accurately to detect and classify electrocardiographic signals. The correct performance of these systems depends on several important factors, including the quality of the ECG signal, the applied classification rule, and the learning and testing datasets used. The ECG is characterized by a recurrent wave sequence of P, QRS and T waves associated with each beat. The QRS complex is the most striking waveform, caused by ventricular depolarization of the human heart. Once the

positions of the QRS complexes are found, the locations of other components of ECG, such as P and T waves and ST segments, are found relative to the position of QRS, in order to analyse the complete cardiac period. In this sense, QRS detection is fundamental for almost all automated ECG analysis algorithms.

Numerous QRS detection algorithms are reported in the literature, for example derivative-based algorithms, algorithms based on digital filters, wavelet transform, artificial neural networks, genetic algorithms, syntactic methods and Hilbert transform. Kohler *et al.* [1] described and compared the performance of all these QRS detectors. Recently a few other methods based on Hilbert transform [2], wavelet transform [3], neuro-fuzzy approach [4], filtering technique [5], first derivative [6], curve length concept [7], and moving-averaging incorporating with wavelet denoising [8] have been proposed for the detection of QRS complexes. Christov *et al.* [9] gave a comparative study of

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morphological and time-frequency ECG descriptors for heartbeat classification. Most of these QRS detectors are one channel detectors. A common technique used in the QRS detector algorithm is to employ a scheme that consists of a preprocessor and a decision rule [10]. The purpose of the preprocessor is to enhance the QRS, while suppressing the other complexes as well as the noise and the artifacts. The preprocessor consists of a linear filter and a transformation. The purpose of the decision rule is to determine whether or not QRS complexes are present at a given instant in the signal.

The support vector machine (SVM)-based classification method represents a major development in pattern recognition research. Two innovations of SVMs are responsible for the success of this method, namely the ability to find a hyperplane that divides samples into two classes with the widest margin between them, and the extension of this concept to a higher dimensional setting using the kernel function to represent a similarity measure on that setting. Both innovations can be formulated in a quadratic programming framework, whose optimum solution is obtained in a computation time of a polynomial order. This makes SVMs a practical and effective solution for many pattern recognition and classification problems in bioinformatics. Brown *et al.* [11] describe a successful use of SVM applied to gene expression data for the task of classifying unseen genes. Dehmeshki *et al.* [12] used SVM for the classification of lung data. Chu *et al.* [13] applied SVMs for cancer diagnosis based on micro-array gene expression data and protein secondary structure prediction. SVMs are also applied in ECG signal analysis and arrhythmia classification [14–20], wherein QRS detection is accomplished by using some other technique. An SVM is applied in the present work to detect the QRS complexes in the single-lead ECG and simultaneously recorded original 12-lead ECG signal. The results of both the algorithms are compared.

This paper is structured as follows. §2 presents a brief description of the SVM as classifier for two-class problem. §3 describes preprocessing of the ECG signal. A review of the core algorithm is provided in §4. §5 describes the implementation of SVM using LIBSVM. The performance of the proposed algorithm is demonstrated in §6.

2. Support vector machine

SVM is a new paradigm of learning systems. The SVM technique, developed by Vapnik [21], was proposed initially for solving classification problems of two classes. SVMs use geometrical properties to exactly calculate the optimal separating hyperplane directly from the training data. They also introduce methods to deal with nonlinearly separable cases, i.e. where no separating straight line can be found, as well as with cases in which there is noise and/or outliers in the training data, i.e. some of the training samples may be wrong.

Basically, the SVM is a linear machine working in the highly dimensional feature space formed by the nonlinear mapping of the n -dimensional input vector \mathbf{x} into a K -dimensional feature space ($K > n$) through the use of a mapping $\phi(\mathbf{x})$. The following relation gives the equation of hyperplane separating two different classes:

$$y(\mathbf{x}) = \mathbf{w}^T \phi(\mathbf{x}) = \sum_{j=1}^K w_j \phi_j(x) + w_0 = 0, \quad (1)$$

where $\phi(\mathbf{x}) = [\phi_0(x), \phi_1(x), \dots, \phi_k(x)]^T$ with $\phi_0(x) = 1$ and $\mathbf{w} = [w_0, w_1, \dots, w_k]^T$ is the weight vector of the network. Fulfilment of condition $y(\mathbf{x}) > 0$ means one class and $y(\mathbf{x}) < 0$ means the opposite one.

The most distinctive fact about SVM is that the learning task is reduced to quadratic programming by introducing Lagrange multipliers. All operations in learning and testing modes are done in SVM using kernel functions. The kernel is defined as $K(\mathbf{x}, \mathbf{x}_i) = \phi^T(\mathbf{x}_i)\phi(\mathbf{x})$.

The problem of learning SVM, formulated as the task of separating learning vectors \mathbf{x} into two classes of the destination values either $d_i = 1$ or $d_i = -1$ with maximal separation margin, is reduced to the dual maximization problem of the objective function, defined as follows:

$$Q(\alpha) = \sum_{i=1}^p \alpha_i - \frac{1}{2} \sum_{i=1}^p \sum_{j=1}^p \alpha_i \alpha_j d_i d_j K(\mathbf{x}_i \mathbf{x}_j), \quad (2)$$

with constraints:

$$\sum_{i=1}^p \alpha_i d_i = 0 \quad 0 \leq \alpha_i \leq C, \quad (3)$$

where C is a user defined constant and p is the number of learning data pairs (\mathbf{x}_i, d_i) . C is the regularizing parameter and determines the balance between the maximization of the margin and minimization of the classification error.

The solution with respect to Lagrange multipliers gives the optimal weight vector \mathbf{w}_{opt} as:

$$\mathbf{w}_{opt} = \sum_{i=1}^{N_s} \alpha_{si} d_{si} \phi(\mathbf{x}_{si}) \quad (4)$$

In equation (4) index s points to the set of N_s support vectors, i.e. the learning vectors \mathbf{x}_i , for which the relation

$$d_i \left(\sum_{j=1}^K w_j \phi_j(\mathbf{x}_i) + w_0 \right) \geq 1 - \xi_i \quad (5)$$

is fulfilled with the equality sign. The variables ξ_i are non-negative scalar variables called slack variables. They measure deviation of a data point from the ideal condition of pattern separability, i.e. totally separable patterns.

The output signal $y(\mathbf{x})$ of the SVM in the retrieval mode after learning is determined as the function of kernels

$$y(\mathbf{x}) = \sum_{i=1}^{N_s} \alpha_{si} d_i K(\mathbf{x}_{si}, \mathbf{x}) + w_0 \quad (6)$$

and the explicit form of the nonlinear function $\varphi(\mathbf{x})$ need not be known. The value of $y(\mathbf{x})$ greater than 0 is associated with 1 (membership of the particular class) and the negative one with -1 (membership of the opposite class). Although SVM separates the data into two classes, classification into additional class is possible by applying either the one against one or one against all method in multi-class problems.

3. Preprocessing of ECG signal

A raw sampled ECG signal of a patient is acquired. ECG signals are often contaminated by disturbances such as power line interference and baseline wander. The finite impulse response (FIR) notch filter proposed by Van Alste and Schilder [22] is used to remove baseline wander. The adaptive filter to remove baseline wander is a special case of notch filter, with notch at zero frequency (or DC). This filter has a 'zero' at DC and consequently creates a notch with a bandwidth of $(\mu/\pi) \times f_s$, where f_s is the sampling frequency of the signal and μ is the convergence parameter. Frequencies in the range 0–0.5 Hz are removed to reduce the baseline drift. The filter proposed by Furno and Tompkins [23] is used to remove 50 Hz power line interference.

Slope is used as an important discriminating feature because the slope of the ECG signal is much more in the QRS region than in the non-QRS region. This reduces the burden of the classifier to form complicated decision boundaries. The absolute value of slope at every sampling instant of the filtered ECG signal was calculated to enhance the QRS complexes. These slope values were then normalized. This way a set of 12 normalized slope curves is obtained, one for each lead.

4. QRS detection

4.1. Single-lead QRS detection algorithm

For single-lead QRS detection, input to the support vector classifier is a set of vectors \mathbf{x}_i containing 10 normalized slope values. During the training of SVM, a sliding window of 10 sampling instants is moved over the normalized slope curve taking single-lead at a time. The first pattern vector is formed by taking the first 10 normalized slopes from the first to the 10th sampling instant. The window is moved by one sampling instant and the second pattern vector is formed by taking another set of 10 normalized slopes but now from second to 11th sampling instant. This way, a

sliding window of 10 sampling instants and a jump size of one sample is moved over the normalized slope curve. When the window lies completely in the QRS region, the desired output of the SVM is set to 1, and when it lies completely in the non-QRS region, the desired output is set to -1 . The training patterns for the ECG portion, when the window lies partially in QRS as well as non-QRS regions, are not considered during the training of SVM. The SVM is trained on a set of training data covering a wide variety of ECG signals, picked from CSE ECG database.

On testing, a set of 10 calculated normalized slope values of a particular lead is picked up to form the input vector for the SVM. Then the window is moved forward by one sampling instant and again a set of 10 slopes of ECG are taken to form the next input pattern vector. A train of 1s is obtained at the output of the SVM, when the window traverses through the QRS region and -1 for the non-QRS region. The train of 1s is picked, and using their duration, the average pulse duration of 1s is evaluated. Those trains of 1s whose duration turns out to be more than the average pulse duration are detected as QRS regions and the other ones are detected as non-QRS regions.

4.2. Twelve-lead QRS detection algorithm

In the case of 12-lead simultaneously recorded ECG, the input to the support vector classifier is a set of vectors \mathbf{x}_i containing 12 normalized slope values, one from each of the 12 leads of the ECG at a particular sampling instant. During the training of SVM, a sliding window was moved forward by one sampling instant over the normalized slope curves. When the window lies in the QRS region, the desired output of the SVM is set to 1 and when it lies in the non-QRS region, the desired output is set to -1 . In this case also, the SVM was trained on a set of training data covering a wide variety of ECG signals, picked from the CSE ECG database.

On testing, the normalized value of 12 slopes, one from each of the 12 leads of the ECG at a sampling instant, is used to form the input vector for the SVM. Then the window is moved forward by one sampling instant and a set of 12 slopes, again one from each of the 12 leads of ECG, is taken to form next input pattern vector. A train of 1s is obtained at the output of SVM, when the window traverses through the QRS region, and -1 for the non-QRS region. The train of 1s is picked and, using their duration, the average pulse duration of 1s is evaluated. Those trains of 1s whose duration turns out to be more than the average pulse duration are detected as QRS regions and the other ones are detected as non-QRS regions.

In some cases, when the P or T waves are peaky in nature, the SVM gives a train of 1s but of smaller duration than that of the QRS complex. In order to differentiate

between trains of 1s for the QRS complex and that for P or T waves, an average width or duration of all the trains of 1s is calculated. Those trains whose duration is greater than the average pulse width are picked up as QRS complexes by the algorithm, and those whose duration is smaller than the average pulse width are discarded. Thus, false positive detection of QRS complexes is reduced.

5. Implementation of SVM using LIBSVM

Implementation of SVM for QRS detection in the ECG signal is done by using LIBSVM software [24]. LIBSVM is an integrated software package for support vector classification, regression and distribution estimation. It uses a modified sequential minimal optimization (SMO) algorithm to perform training of SVMs. The SMO algorithm breaks the large quadratic programming (QP) problem into a series of smallest possible QP problems. These small QP problems are solved analytically, which avoids using a time-consuming numerical QP optimization problem as an inner loop [25]. The SMO algorithm is derived by taking the idea of the decomposition method to its extreme and optimizing a minimal subset of just two points at the each iteration. The requirement that the condition $\sum_{i=1}^p \alpha_i d_i = 0$ is enforced throughout the iterations implies that the smallest number of multipliers that can be optimized at each step is 2; whenever one multiplier is updated, at least one other multiplier needs to be adjusted in order to keep the condition true [26].

In the present problem of QRS detection, SVM is constructed using a sigmoid kernel $K(\mathbf{x}, \mathbf{x}_i) = \tanh(\gamma(\mathbf{x} \cdot \mathbf{x}_i) + \nu)$, which takes two parameters γ and ν . The parameter γ can be viewed as a scaling parameter of the input data, and ν as a shifting parameter that controls the threshold of mapping. The values of $\gamma > 0$ and $\nu < 0$ are more suitable for sigmoid kernel [27].

The type of kernel function, its parameters and margin-loss trade-off C should be determined to find the optimal solution. It is not known beforehand which values of C , and which type of kernel function and its parameters are the best for solving this problem of QRS detection. The objective is to obtain the best kernel function, its parameters and margin-loss trade-off C so that the classifier can accurately predict unknown data (testing data). In the present study four-fold cross-validation approach is used to select the kernel function, to tune its parameters and margin-loss trade-off C [28]. For this, the training data are divided into four subsets of equal size. Sequentially one subset is tested using the classifier trained on the remaining subsets. Thus, each instance of the whole training set is predicted once so the cross-validation accuracy is the percentage of data which are correctly classified.

The best generalization performance is achieved with the sigmoid kernel function. There are three free parameters, namely γ , ν of the sigmoid kernel function and margin-loss

trade-off C , which should be determined to find the optimal solution. The optimum values of $C = 2$, $\gamma = 2$ and $\nu = -0.1$ are obtained for the training sets, with cross validation accuracies of 99.01% and 99.34% for the single-lead training set and the 12-lead training set, respectively.

6. Performance evaluation

The performance evaluation of the proposed algorithms for QRS detection is done using 1500 single-lead ECG records and simultaneously recorded 125, 12-lead ECG records of dataset 3 of CSE multi-lead measurement library [29]. This library contains original 12-lead simultaneous ECG recordings of 125 patients covering a wide variety of pathological cases. It should be noted here that the CSE library contains a high percentage of pathological ECGs, and there are some QRSs which are hardly recognized even visually. Every record picked from CSE ECG database is of 10 s duration sampled at 500 Hz, thus giving 5000 samples. Detection is said to be false positive if a non-QRS wave is detected as a QRS complex and it is said to be false negative if the algorithm fails to detect the QRS complex.

The algorithm, when tested using the optimum values of the parameters ($C = 2$, $\gamma = 2$ and $\nu = -0.1$) gives an identification rate of 99.3% for single-lead QRS detection and 99.75% for QRS detection in simultaneously recorded 12-lead ECG signals. Various values of γ ranging from 0.5 to 10 have been tried in the present work with the cross validation accuracy of 98.5% to 99.5%. The number of false positive detections increases for $\gamma > 2$ and the number of false negative detections increases for $\gamma < 2$. Table 1 displays the effect of variation of γ on the percentage of false positive and false negative detections. False negative detection is 0.7% and false positive detection is 12.4% in the single-lead QRS detection; these values reduce to 0.26% and 1.61% respectively for QRS detection in simultaneously recorded 12-lead ECG signals.

The number of false positive detections in the single-lead QRS detection algorithm is more, due to the fact that if we have a peaky P or T wave, it is picked as a candidate QRS complex because its slope is comparable with that of QRS

Table 1. Effect of variation of γ on the percentage of false positive and false negative detections.

γ	Single-lead QRS detection		12-lead QRS detection	
	False positives	False negatives	False positives	False negatives
0.5	12.4%	1.5%	1.61%	1.13%
1	12.4%	1.2%	1.61%	0.6%
2	12.4%	0.7%	1.61%	0.26%
3	14.2%	0.7%	2.12%	0.26%
5	14.6%	0.7%	2.54%	0.26%
10	16%	0.7%	3.52%	0.26%

complex and the algorithm is unable to differentiate between QRS and peaky P or T wave. Whereas in the 12-lead QRS detection algorithm, if we have peaky P or T wave in, for example, a couple of leads, and non peaky P or T wave in the remaining lead, the algorithm is able to differentiate the non-peaky P and T waves, by majority, from the QRS complexes and rejects the P and T waves as a candidate QRS complex. Hence drastic reduction in false positive detection is observed in the 12-lead QRS detection algorithm.

For the 12-lead QRS detection algorithm the window size is 12, containing 12 slope values, one from each of the 12 leads of ECG at a given sampling instant. However, in single-lead QRS detection, various window sizes ranging from 4 to 25 have been tried in the present work. A window size of 10 was found to give the best results because too small and too large window sizes lead to under-capturing and over-capturing of the ECG signal respectively. The performance of the proposed algorithm compares very favourably with the earlier published QRS detectors tested

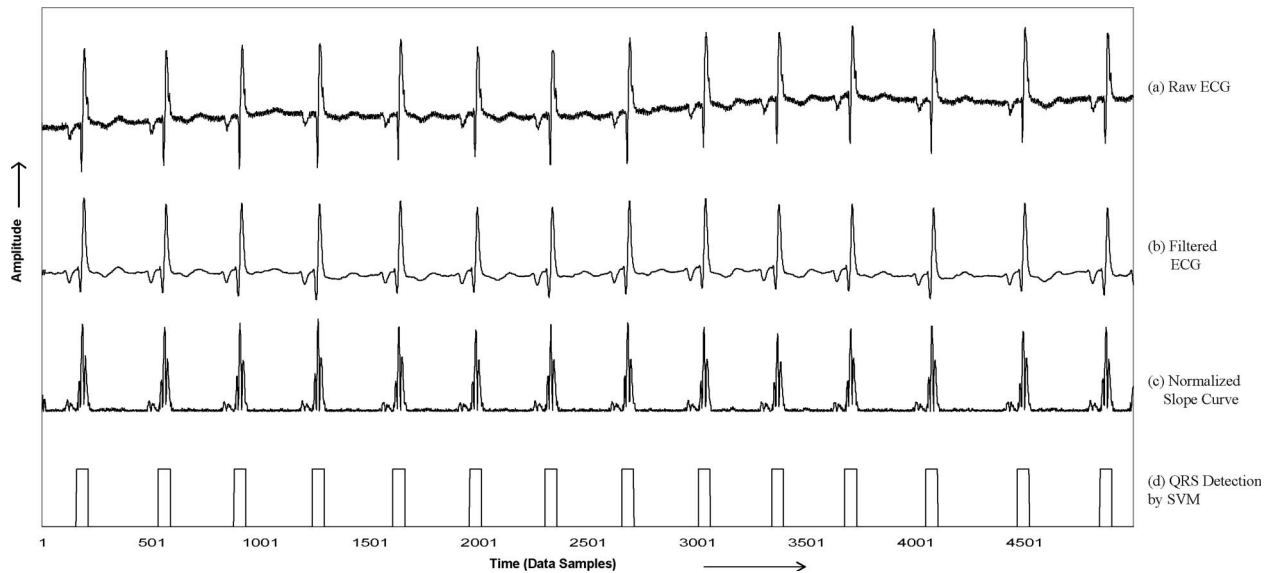


Figure 1. QRS detection for record MO1_027 of CSE ECG database.

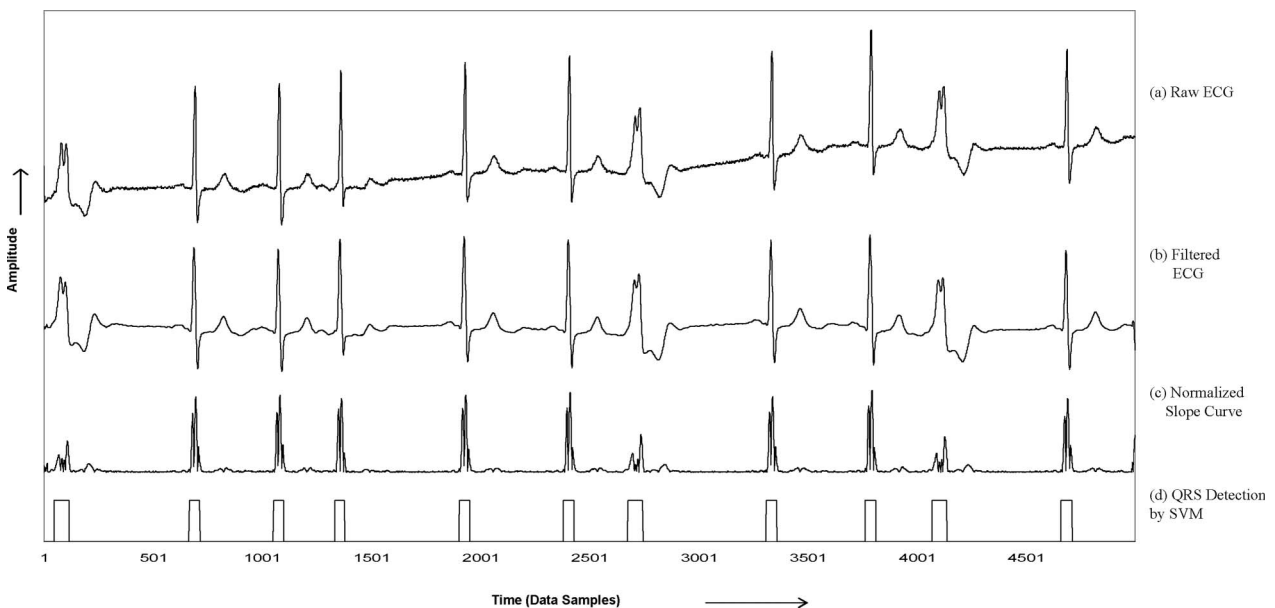


Figure 2. QRS detection for record MO1_103 of CSE ECG database.

on the same database with the QRS detection rate ranging from 98.49% to 99.6% [10,30–34].

Figure 1 shows results obtained at the preprocessing stage and QRS detection of record MO1_027 of lead V1. As depicted in figure 1(b), the preprocessor removes power line interference and baseline wander present in the signal. The P and T waves are not prominent in this case. The slope of the QRS complexes is very high, hence all the 14 QRS complexes are correctly identified by the SVM, as shown in figure 1(d).

Figure 2 shows QRS detection of lead V5 of record MO1_103. Since there is much more ECG signal slope in the QRS region than with the P and T waves, all the QRS complexes present in the ECG signal are correctly identified by the SVM. It may be observed that there is a large variation in the morphology of the QRS complexes. Even

then the algorithm successfully detects all the QRS complexes, demonstrating its effectiveness.

In the lead aVL of record MO1_021, as displayed in figure 3, the T waves are of higher amplitude. These are not detected as QRS complexes due to their lower values of slopes as compare to that of QRS complexes.

Figure 4 shows QRS detection in lead L2 of record MO1_050. As depicted in figure 4, the algorithm fails to detect the first QRS complex of eight, due to lower amplitude and duration than other QRS complexes.

Figure 5 shows QRS detection of record MO1_050. QRS complexes are wider in nature in this case with relatively moderate slope. The R wave amplitude of the first QRS complex in leads L1, L3, L3, aVL, aVL and aVF is smaller than the remaining QRS complexes in the respective leads. SVM successfully detects this QRS complex having lower

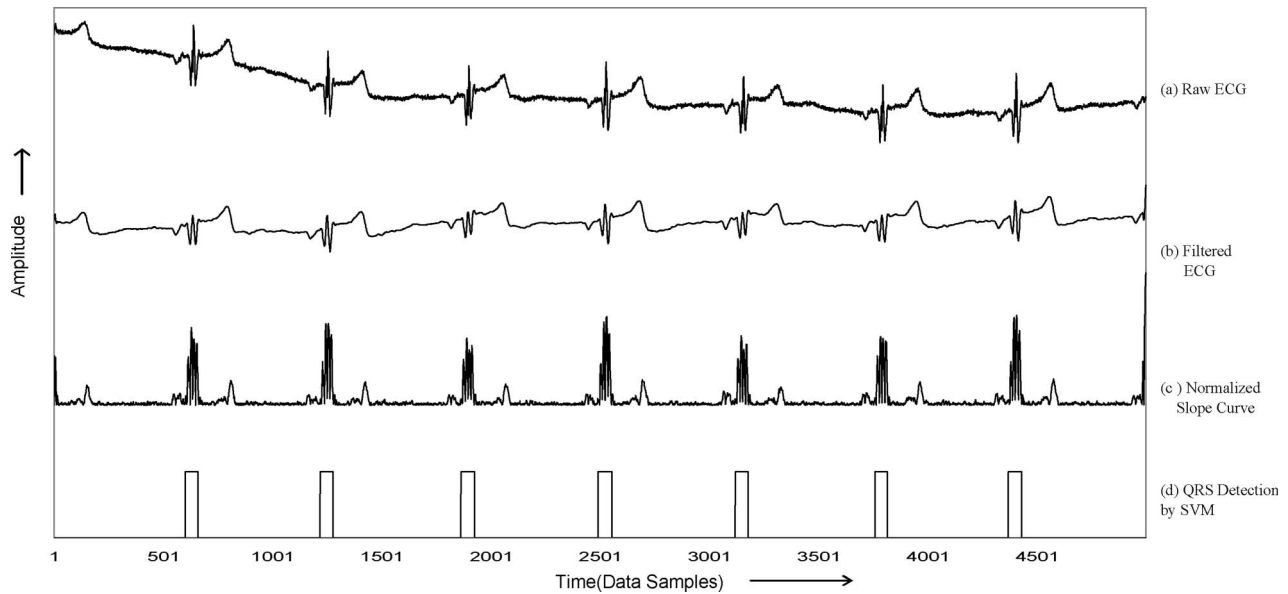


Figure 3. QRS detection for record MO1_021 of CSE ECG database.

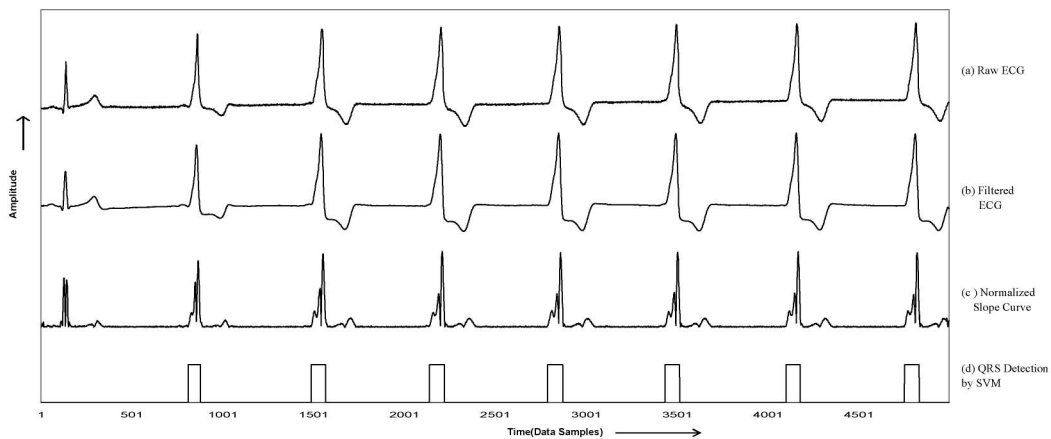


Figure 4. QRS detection for record MO1_050 of CSE ECG database.

amplitude. However, single-lead QRS detection algorithm fails to detect this first QRS complex in these leads as displayed in figure 4. This is an advantage of the 12-lead algorithm over the single-lead algorithm.

Figures 6 and 7 show QRS detections for records MO1_028 and MO1_109, which have a wide variation of QRS morphologies. All the QRS complexes in these cases

are correctly identified by SVM, indicating the effectiveness of the proposed algorithm.

Figure 8 shows QRS detection of record MO1_075, which has extreme variations in the QRS complexes amplitude. As depicted in this figure, of the 13 QRS complexes the algorithm fails to detect three, due to the smaller slope values than other QRS complexes. Any further attempt to

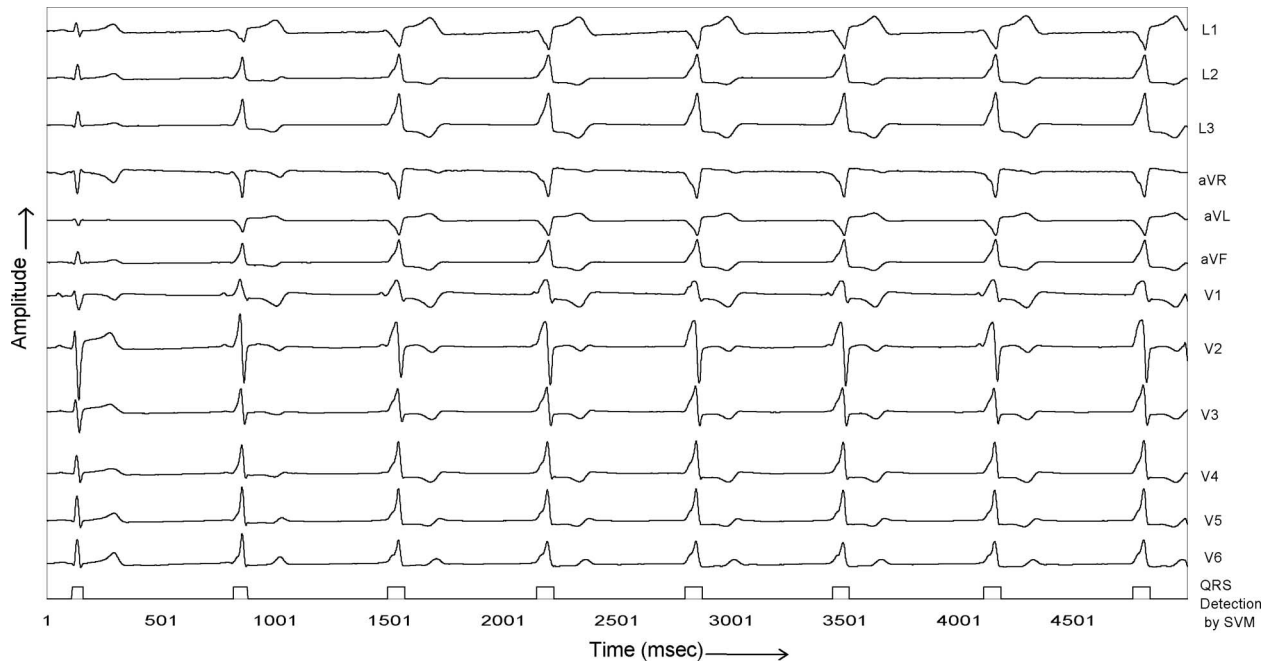


Figure 5. QRS detection for record MO1_050 of CSE ECG database.

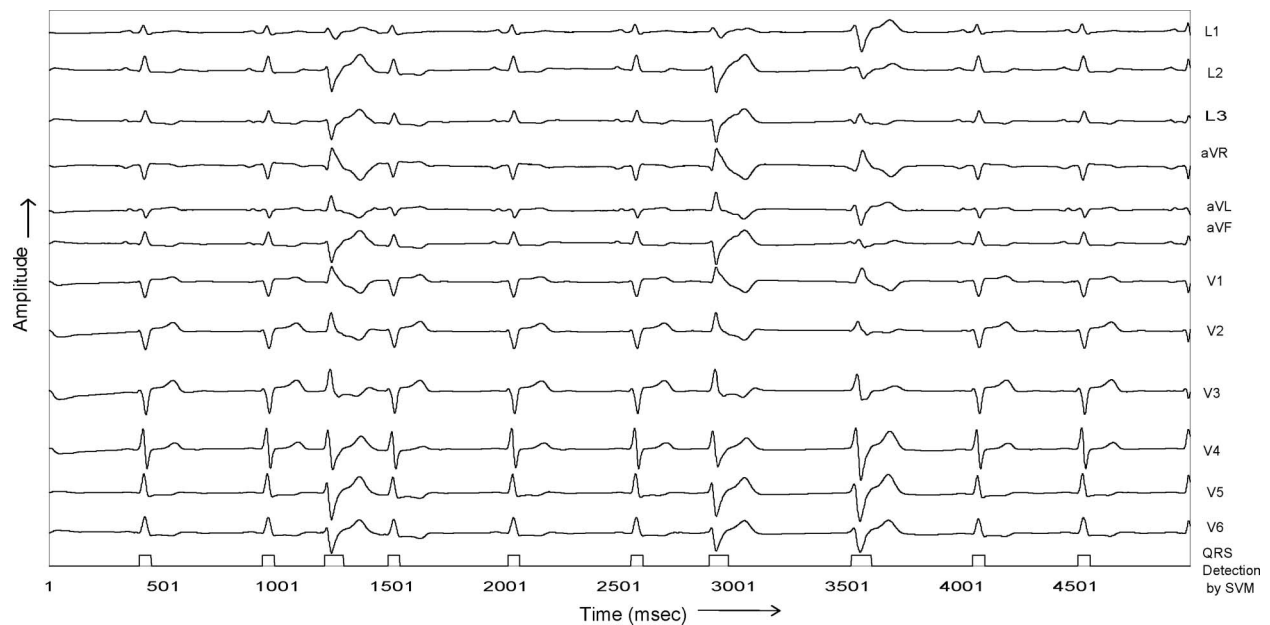


Figure 6. QRS detection for record MO1_028 of CSE ECG database.

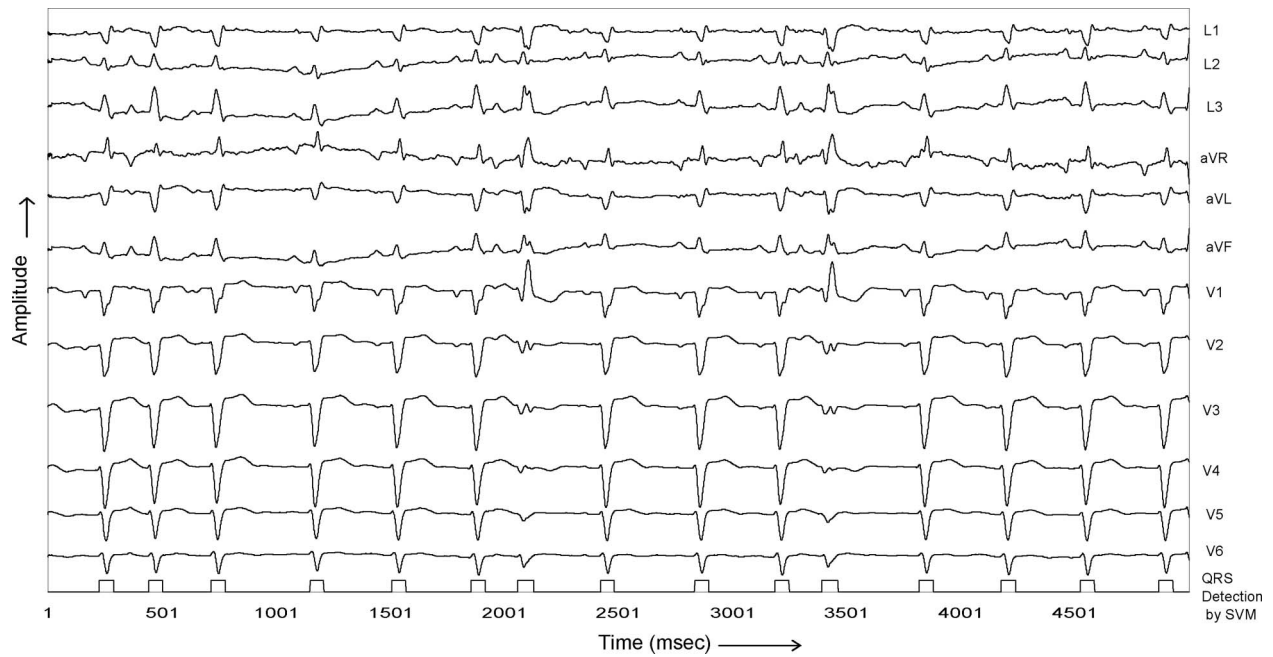


Figure 7. QRS detection for record MOI_109 of CSE ECG database.

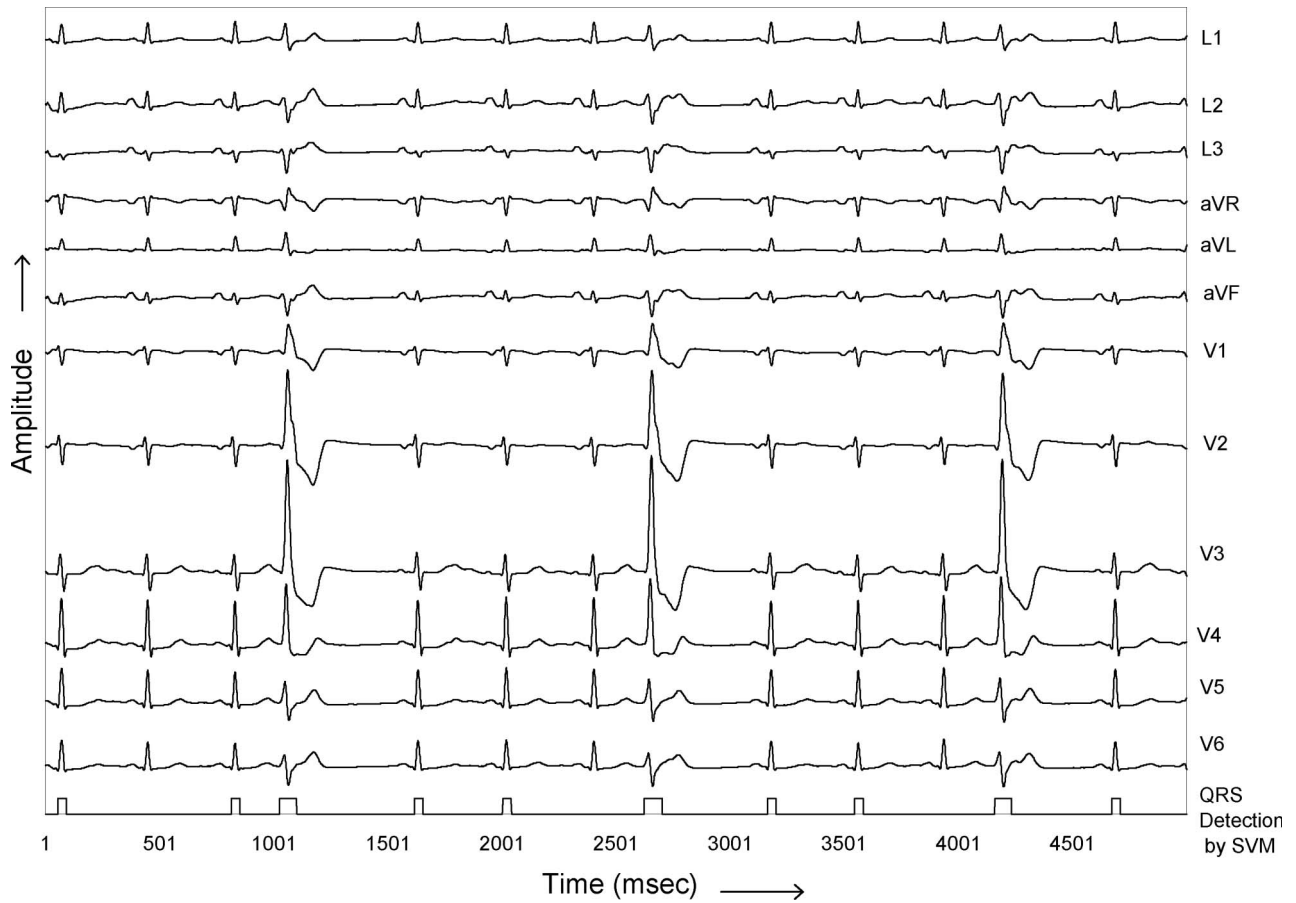


Figure 8. QRS detection for record MOI_075 of CSE ECG database.

remove this false negative by way of adjusting the parameter γ of the SVM detracts the overall detection rate.

7. Conclusion

In this paper, a novel QRS detector using SVM is proposed and evaluated against the standard CSE database. SVM gave very encouraging and consistent results of both algorithms, compared with the methods reported earlier in the literature for the given problem of QRS detection. The percentage of false positive and false negative detections in 12-lead QRS detection algorithm is very low compared to the single-lead QRS detection algorithm. The information about the QRS complexes obtained by this method is very useful for ECG classification and cardiac diagnosis. This information can also serve as an input to a system that allows automatic cardiac diagnosis.

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