COMPARATIVE STUDY OF QRS DETECTION IN SINGLE LEAD AND 12-LEAD ECG BASED ON ENTROPY AND COMBINED ENTROPY CRITERIA USING SUPPORT VECTOR MACHINE

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ABSTRACT

Application of Support Vector Machine (SVM) for QRS detection in single lead and 12-lead Electrocardiogram (ECG) using entropy and combined entropy criterion is presented in this paper. The ECG signal is filtered using digital filtering techniques to remove power line interference and base line wander. SVM is used as a classifier for detection of QRS complexes in ECG. Using the standard CSE ECG database, both the algorithms performed highly effectively. The performance of the algorithm with sensitivity (*Se*) of 99.70% and positive prediction (+*P*) of 97.75% is achieved when tested using single lead ECG with entropy criteria. It improves to 99.79% and 99.15% respectively for combined entropy criteria. Similarly for simultaneously recorded 12-lead ECG signal, sensitivity of 99.93% and positive prediction of 99.13% is achieved when tested using entropy criteria and sensitivity of 99.93% and positive prediction of 99.46% respectively is achieved for combined entropy criteria. The percentage of false positive and false negative are reduced substantially when simultaneously recorded 12-lead ECG signal is used. The proposed algorithms perform better as compared with published results of other QRS detectors tested on the same database.

Index Terms—**ECG, Entropy, Combined Entropy, QRS complex, SVM.**

1. INTRODUCTION

The electrocardiogram (ECG) is an important tool for providing information about functional status of the heart. Analysis of ECG is of great importance in the detection of cardiac anomalies. In a clinical setting, such as intensive care units, it is essential for automated systems to accurately 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, the learning and testing dataset used. The ECG is characterized by a recurrent wave sequence of P, QRS and T- wave 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 like P, T-waves and ST segment etc. are found relative to the position of QRS, in order to analyze the complete cardiac period. In this sense, QRS detection provides the fundamental for almost all automated ECG analysis algorithms.

Numerous QRS detection algorithms such as derivative based algorithms, algorithms based on digital filters, wavelet transform, length and energy transform, artificial neural networks, genetic algorithms, syntactic methods, Hilbert transform etc. are reported in literature. Kohler et al [1] described and compared the performance of all these QRS detectors. Recently few other methods based on pattern recognition [2], Hilbert transform [3], wavelet transform [4], neuro-fuzzy approach [5], filtering technique [6], first derivative [7], curve length concept [8], moving-averaging incorporating with wavelet denoising [9] etc. are proposed for the detection of QRS complexes. Christov et al [10] gave a comparative study of morphological and time-frequency ECG descriptors for heartbeat classification. Most of these QRS detectors are one channel detectors. A common technique utilized in the QRS detector algorithm is to employ a scheme that consists of a noise and the artifacts. The preprocessor consists of a linear filter and a transformation. The purpose of the decision rule is to determine

preprocessor and a decision rule [11]. The purpose of the preprocessor is to enhance the QRS, while suppressing the other complexes as well as the

whether or not QRS complexes are present at a given instant in the signal.

SVMs 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 in to two classes with the widest margin between them, and the extension of this concept to a higher dimensional setting using 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 [12] describes a successful use of SVMs applied to gene expression data for the task of classifying unseen genes. Dehmeshki et al [13] used SVM for the classification of lung data. Chu et al [14] applied SVMs for cancer diagnosis based on micro-array gene expression data and protein secondary structure prediction. SVMs are also applied for ECG signal analysis and arrhythmia classification [15, 16, 17, 18, 19, 20, 21], where in QRS detection is accomplished by using some other technique. SVM is applied in the present work to detect the QRS complexes in the single lead ECG and simultaneously recorded 12-lead ECG signal.

This paper is structured as follows. Section 2 presents a brief description of the SVM for two-class problem. ECG signal preprocessing is described in section 3. A review of the core algorithm is provided in section 4. The performance of the proposed algorithm is demonstrated in section 5.

2. SUPPORT VECTOR MACHINE

SVM is a new paradigm of learning system. The technique of SVM, developed by Vapnik [22], was proposed initially for classification problems of two classes. SVM use geometrical properties to exactly calculate the optimal separating hyperplane directly from the training data. They also introduce methods to deal with non-linearly 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 high 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 $\varphi(\mathbf{x})$. The following relation gives the equation of hyperplane separating two different classes:

$$y(\mathbf{x}) = \mathbf{w}^T \varphi(\mathbf{x}) = \sum_{j=1}^{K} w_j \varphi_j(\mathrm{x}) + w_0 = 0 \quad (1)$$

where, $\varphi(\mathbf{x}) = \left[\varphi_0(\mathrm{x}), \varphi_1(\mathrm{x}), ..., \varphi_k(\mathrm{x})\right]^T$ with $\varphi_0(\mathrm{x}) = 1$ and $\mathbf{w} = [w_0, w_1, \ldots, w_k]^T$ is the weight vector of the network. Fulfillment 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 the so-called Lagrange multipliers. All operations in learning and testing modes are done in SVM using kernel functions. The kernel is defined as $K(\mathbf{x}, \mathbf{x}_i) = \boldsymbol{\varphi}^T(\mathbf{x}_i)\boldsymbol{\varphi}(\mathbf{x})$.

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

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

with constraints

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

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

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

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

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

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(**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 φ(**x**) need not be known. The value of y(**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 ECG signal of a patient is acquired. It is 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 [23] is used to remove baseline wander. The adaptive filter to remove base line 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 $(\mu/\pi)*f_s$, where f_s is the sampling frequency of the signal and μ is the convergence parameter. Frequencies in the range 0-0.5Hz were removed to reduce the base line drift. The filter proposed by Furno and Tompkins [24] is used to remove 50Hz power line interference.

The slope at every sampling instant of the filtered ECG signal is calculated for each lead and these are clustered into two classes, namely QRS and non-QRS classes using K-means of clustering algorithm [25]. Slope is used as an important feature because slope of the ECG signal was much more in the QRS region than in the non-QRS region. The probability, $P_i(x)$ of slope at each sampling instant belonging to each of the two classes is calculated using (7).

$$P_i(x) = \frac{1}{\sqrt{2\pi}\sigma_i} \exp\left[-\frac{1}{2}\left(\frac{x - m_i}{\sigma_i}\right)^2\right] \quad (7)$$

$i = 1, 2$; x = 1,2,…..,5000

where σ_i and m_i are the standard deviation and mean of i^{th} class.

Entropy is a statistical measure of uncertainty. A feature, which reduces the uncertainty of a given situation are considered more informative than those, which have opposite effect. Thus a meaningful feature selection criterion is to choose the features that minimize the entropy of the pattern class under consideration.

The entropy $h_i(x)$ at each sampling instant for QRS and non QRS classes is calculated using (8). These entropies are then normalized.

$$h_i(x) = -P_i(x)\log_e P_i(x) \quad (8)$$

$i = 1, 2$; x = 1,2,….,5000

The combined entropy is then calculated by using (9). Thereafter it is also normalized.

$$h_c(x) = (1 - h_{2n}(x)) * h_{1n}(x) \quad (9)$$

where, $h_{1n}(x)$ and $h_{2n}(x)$ are normalized entropies belonging to the QRS and non-QRS class respectively. The combined entropy is also normalized to obtain normalized combined entropy $h_{cn}(x)$.

The same procedure is applied for remaining leads. In this way, a set of twelve combined entropy curves, one for each lead is obtained.

In order to demonstrate the algorithm used in the present work, consider lead V5 of record MO1_020 of CSE ECG database shown in Fig. 1(a). Fig.1 (b) shows the results of the preprocessing stage of lead V5 of record MO1_020 of CSE ECG database. As depicted in Fig.1 (b), the preprocessor removes power line interference and base line wander present in the raw ECG signal. Fig. 1(c) shows $h_{1n}(x)$, entropy curve for QRS region. It can be seen from this curve that it has lower values in the QRS region and higher values in the non-QRS region. The low value of entropy in the QRS region indicates lower uncertainty or in other words higher certainty of that region belonging to QRS region. Similarly, higher values of entropy in the non-QRS region indicate higher uncertainty or in other words lower certainty of that region belonging to QRS region. Thus the entropy $h_{1n}(x)$ curve

provides critical information about the degree of certainty of a region belonging to QRS region.

Fig. 1(d) shows $h_{2n}(x)$, entropy curve for non-QRS region. It can be seen from this curve that it has lower values in the non-QRS region and higher values in the QRS region. The low value of entropy in the non-QRS region indicates lower uncertainty or in other words higher certainty of that region belonging to non-QRS region. Similarly, higher values of entropy in the QRS region indicate higher uncertainty or in other words lower certainty of that region belonging to non-QRS region. Thus the entropy $h_{2n}(x)$ curve provides critical information about the degree of certainty of a region belonging to non-QRS region.

Now if $[1- h_{2n}(x)]$ curve is seen, it also provides similar information as that of $h_{1n}(x)$ i. e. $[1- h_{2n}(x)]$ gives lower values in the QRS region and higher values in the non-QRS region as shown in Fig.1 (e). Now if the curve, showing the product $h_{cn}(x) = (1-h_{2n}(x))* h_{1n}(x)$, called combined entropy is obtained, it has much lower values in QRS region and much higher values in non-QRS region thus giving even better information compare to $h_{1n}(x)$ and $h_{2n}(x)$, curves shown in Fig.1 (c) and (d). This can be seen in the combined entropy curve shown in Fig.1 (f). Therefore both entropy and combined entropy criteria are used in the present work to obtain the transformed signal for the detection of QRS complexes.

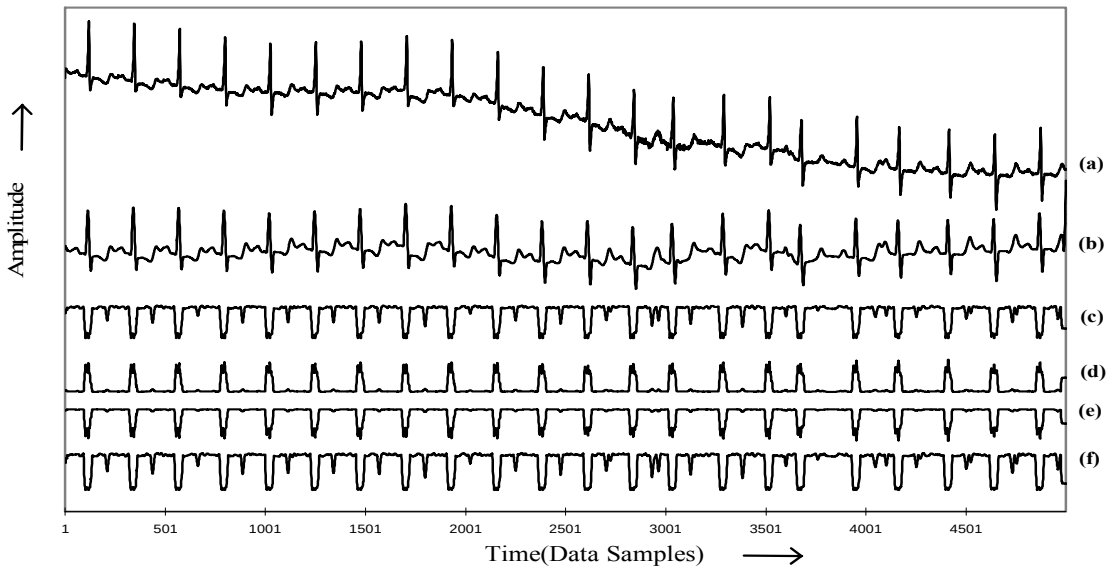

Fig.1 (a) Raw ECG of lead V5 of record MO1_20 of CSE ECG database, (b) Filtered ECG Signal, (c) Entropy QRS, (d) Entropy non-QRS, (e) $[1- h_{2n}(x)]$ curve, (f) Combined Entropy

4. QRS DETECTION ALGORITHM

4.1 Single Lead Algorithm

For single lead QRS detection using entropy criteria, the input vector $\mathbf{x}_i$ to the support vector classifier is a set of normalized entropy values. During the training of SVM, two synchronizing sliding windows of size of ten sampling instants are moved over both the entropy values from the training set. A window size of 10 is selected because too small and too large size of the window leads to under-capturing and over-capturing of the ECG signal respectively. The first pattern vector is formed by taking twenty normalized entropy values (ten belonging to QRS and ten belonging to nonQRS) from first to tenth sampling instant. The windows are then moved forward by one sampling instant and the second pattern vector is formed by taking another set of twenty normalized entropy values but now from second to eleventh sampling instant. This way, sliding windows of size ten sampling instant and a jump size of one sample are moved over the normalized entropy values from the training set. When the window lies in the QRS region, the desired output of the SVM is set to 1 and when it lies in the nonQRS region, the desired output is set to -1.

During testing, a set of twenty calculated normalized entropy values (ten belonging to QRS

and ten belonging to nonQRS) of a particular lead of a subject, from a standard CSE ECG database, are used at an instant to form the input vector for the SVM. The first pattern vector is formed by taking twenty normalized entropy values (ten belonging to QRS and ten belonging to nonQRS) from first to tenth sampling instant. The windows are then moved forward by one sampling instant and again a set of twenty entropies, are taken to form next input pattern vector. In this way, two synchronizing sliding windows of size of ten sampling instants are moved over both the entropy curves. A train of 1's is obtained at the output of SVM, when the windows traverse through the QRS region and -1 for the nonQRS region. Those trains of 1's 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.

The algorithm for single lead QRS detection using combined entropy criteria is same as that of entropy criteria except the size of the input vector. In combined entropy algorithm, we obtain a normalized combined entropy curve. A sliding window of size of ten sampling instances is moved over the normalized combined entropy curve. Thus, input to the support vector classifier is a set of vectors $\mathbf{x}_i$ containing ten normalized combined entropy values.

4.2 Twelve- Lead Algorithm

The input to the support vector classifier is formed by taking a set of vectors $\mathbf{x}_i$, each comprising of twelve QRS and twelve non-QRS normalized entropy values, in all twenty four values at a particular sampling instant, from each of the twelve leads of ECG. During the training of SVM, a sliding window is moved over the normalized entropy curves with a jump size of one sampling instant. When the window lies in the QRS region, the desired output of the SVM was set to 1 and when it lies in the non-QRS region, the desired output was set to -1. The SVM was trained on a set of training data covering a wide variety of ECG signals, picked from CSE ECG database.

On testing, normalized values of QRS and non-QRS entropies, from each of the twelve leads of ECG at a sampling instant was taken to form the input vector for the SVM. Then the window was moved forward by one sampling instant and again a set of QRS and non-QRS normalized entropy, from each of the twelve leads of ECG were taken to form next input pattern vector. A train of 1's is obtained at the output of SVM, when the window traverses through the QRS region and -1 for the non-QRS region. The continuous train of 1's is clubbed to form a pulse of unit amplitude. The trains of 1's are picked and using their duration, average pulse duration of 1's is evaluated. Those trains of 1's 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.

The algorithm for QRS detection in 12-Lead simultaneously recorded ECG using combined entropy criteria is same as that of entropy criteria except the size of input vector. In the case of combined entropycriteria, the input to the support vector classifier is a set of vectors $\mathbf{x}_i$ comprising of twelve normalized combined entropy values, one from each of the twelve leads of ECG at a particular sampling instant.

In some cases, when the P or T waves are peaky in nature, the SVM gives a train of 1's but of smaller duration as compare to that of QRS complex. In order to differentiate between trains of 1's for QRS complex and that for P or T waves, an average duration of all the trains of 1's is calculated. Those trains whose duration is greater than average pulse duration are picked up as QRS complexes by the algorithm and those whose duration is smaller than the average pulse duration are discarded. Thus, false positive detection of QRS complexes can be reduced.

5. 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 [26]. 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 ECG's, and there are some QRS's which are hardly recognized even visually. Every record picked from CSE ECG database is of 10s duration sampled at 500Hz thus giving 5000 samples.

The software used in the present work is LIBSVM [27]. 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. SMO algorithm breaks the large quadratic programming (QP) problem in to 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 [28].

Detection is said to be true positive (TP) if the algorithm correctly identifies the QRS complex and it is said to be false negative if the algorithm fails to detect the QRS complex. False positive (FP) detections are obtained if non-QRS wave is detected as a QRS complex. The two parameters, sensitivity (*Se*) and positive prediction (+*P*) are calculated using the following equations respectively [29]:

$$S_e = \frac{TP}{TP + FN} \tag{9}$$

$$+P = \frac{TP}{TP + FP} \tag{10}$$

The best generalization performance is achieved with the sigmoid kernel function. The kernel parameters γ and *C*, which provided the best classification, are fixed by experiments before learning. The value of *C* =2 make the balance between the maximization of the margin and minimization of the classification error. The error on the training and testing data are identical. An optimal value of γ = 0.2 is obtained which gives *Se* of 99.7% and +*P* of 97.75% for single lead QRS detection using entropy criteria and *Se* of 99.79% +*P* of 99.15% using combined entropy criteria. Improved performance is obtained for QRS detection in simultaneously recorded 12-lead ECG signals with *Se*=99.93% and +*P*=99.13 using entropy criteria and *Se*=99.93% and +*P*=99.46 using combined entropy criteria**.** Various values of γ ranging from 0.05 to 1 have been tried in the present work. The number of false positive detections increases for γ > 0.2 and the number of false negative detections increases for γ <0.2. When entropy criteria is used, the percentage of false negative detection is 0.32 and false positive detection is 2.28 in the single lead QRS detection and it is 0.06 and 0.87 respectively for QRS detection in simultaneously recorded 12-lead ECG signals. Similarly, when combined entropy criteria is used, the percentage of false negative detection is 0.21 and that of false positive detection is 0.86 in the single lead QRS detection and it is 0.06 and 0.54 respectively for QRS detection in simultaneously recorded 12-lead ECG signals. The false positive detections are mainly due to prominent slope of P and T wave in some cases. The window size of twenty four containing twelve normalized QRS entropy values, one from each of the twelve leads of ECG, at a given sampling instant and twelve normalized non-QRS entropy values has been used, for 12-lead QRS detection algorithm using entropy criteria. For 12-lead QRS detection algorithm using combined entropy criteria, window size is twelve containing twelve normalized combined entropy values, one from each of the twelve leads of ECG, at a given sampling instant. However, QRS detection in single lead, various window sizes ranging from 4 to 25 has been tried in the present work. A window size of 10 is found to be optimal to give the best results because too small and too large size of the window leads to under-capturing and over-capturing of the ECG signal respectively. The sensitivity and positive prediction of proposed algorithm for QRS detection is found to be better than the corresponding figures (98.49% to 99.6% for *Se* and 99.43% to 99.6% for +*P*) of the algorithms reported in literature and tested on the same database [11, 30, 31, 32, 33, 34].

Fig.2 shows results obtained at the preprocessing stage and QRS detection of lead L1 of record MO1_075 using combined entropy criteria. As depicted in Fig.2 (b), the preprocessor removes power line interference and base line wander present in the signal. Some of the P and T- waves are prominent in this case. Pulse duration in the prominent T-waves is smaller than average pulse duration and hence rightly not picked up as QRS complex by the algorithm as shown in Fig. 2 (d). Fig.3 shows QRS detection of lead aVF of record MO1_036 using entropy criteria. In this case the P and T- waves are not prominent; hence all the QRS complexes have been correctly detected by SVM.

Fig.4 shows QRS detection of lead V2 of record MO1_106 using combined entropy criteria. T-waves are peaky in this case. Though the entropy in the T-wave region is lower, these T-waves are not detected as QRS complexes by the SVM due to smaller pulse duration.

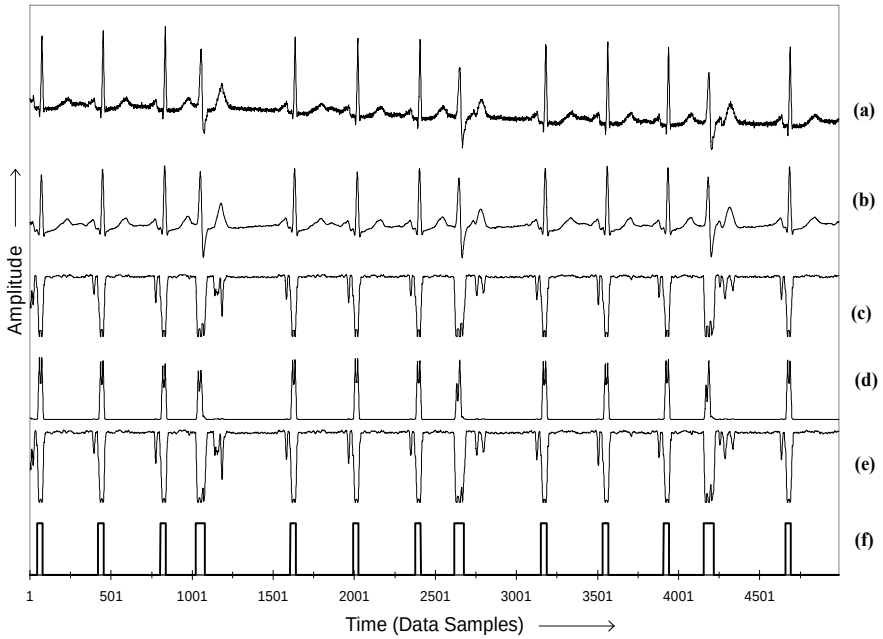

Fig.2 QRS detection of record MO1_075 of CSE database (a) Raw ECG, (b) Filtered ECG, (c) Entropy QRS, (d) Entropy non-QRS, (e) Combined Entropy, (f) QRS Detection by SVM

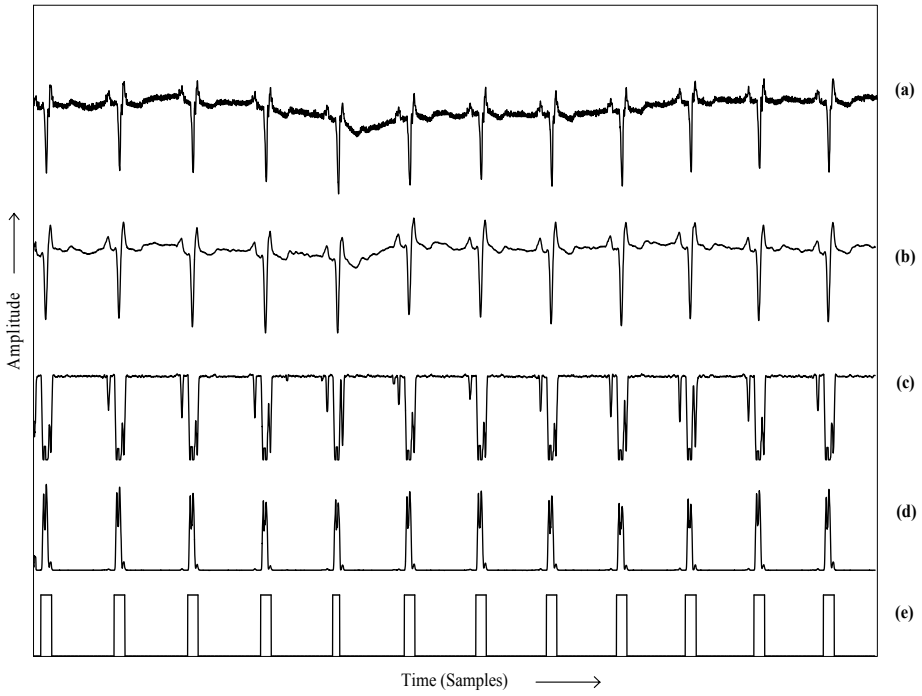

Fig.3 QRS detection of record MO1_036 of CSE database, (a) Raw ECG, (b) Filtered ECG, (c) Entropy QRS,
(d) Entropy non-QRS, (e) QRS Detection by SVM

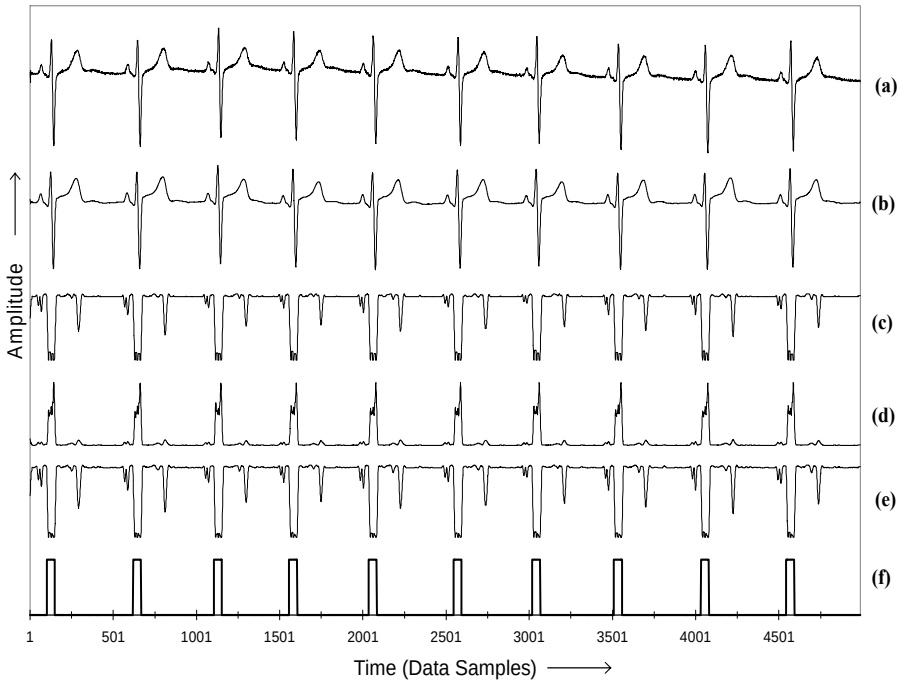

Fig. 4 QRS detection for record MO1_106 of CSE ECG database, (a) Raw ECG, (b) Filtered ECG, (c) Entropy QRS, (d) Entropy non-QRS, (e) Combined Entropy, (f) QRS Detection by SVM

Fig.5 shows 12-lead ECG signal of record MO1_005 of CSE ECG database and beneath it a square wave representing the locations of the QRS complexes as detected by the SVM using combined entropy criteria. It can be seen clearly that the morphology of QRS complexes in the respective leads of ECG signal is consistent; hence all the QRS complexes have been successfully identified by the SVM.

Fig. 6 displays the QRS detection of the record MO1_123 using entropy criteria. In this case, T-waves are of larger amplitude in some leads. These T-waves are not detected as QRS complexes by the algorithm due to their smaller pulse duration. All the QRS complexes in this case are correctly identified by SVM indicating the effectiveness of the proposed algorithm.

In Fig.7, QRS detection of record MO1_045 using combined entropy criteria is displayed. In this case, SVM fails to detect the eighth QRS complex because of the lower amplitude of the R-wave and smaller pulse duration compare to others. There were total 1487 QRS complexes in the database. The proposed algorithm fails to detect only one QRS complex of record MO1_045. Any further attempt to identify/remove this false negative by way of adjusting the parameters of the SVM detracts the over all detection rate of the algorithm.

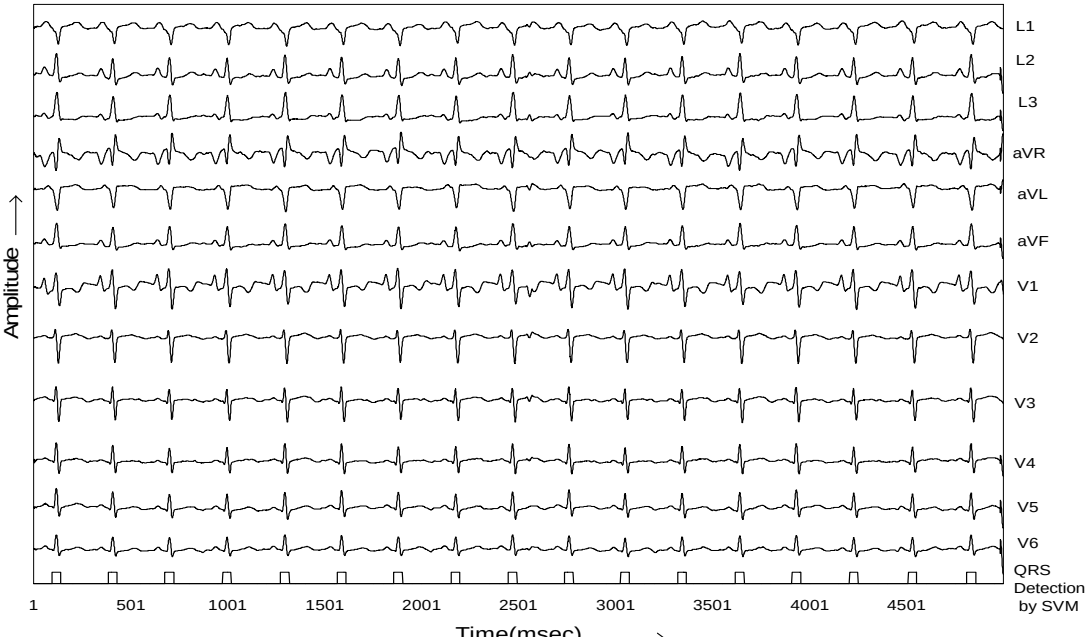

Fig. 5 QRS detection for record MO1_005 of CSE ECG database

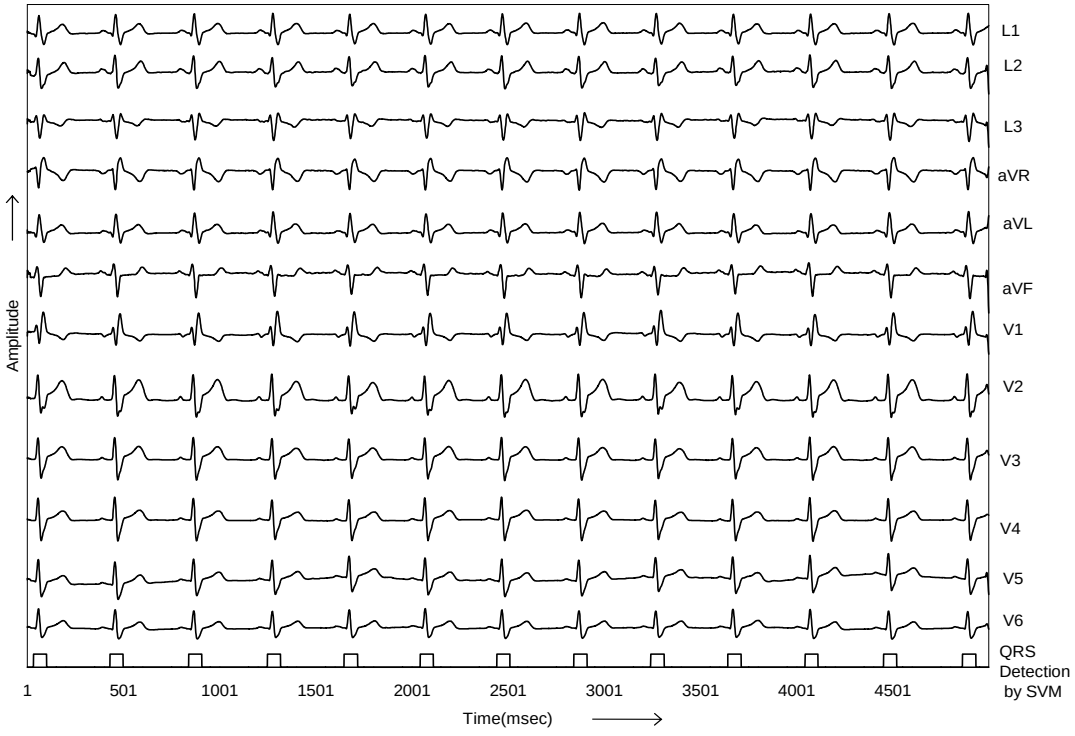

Fig. 6 QRS detection for record MO1_123 of CSE ECG database

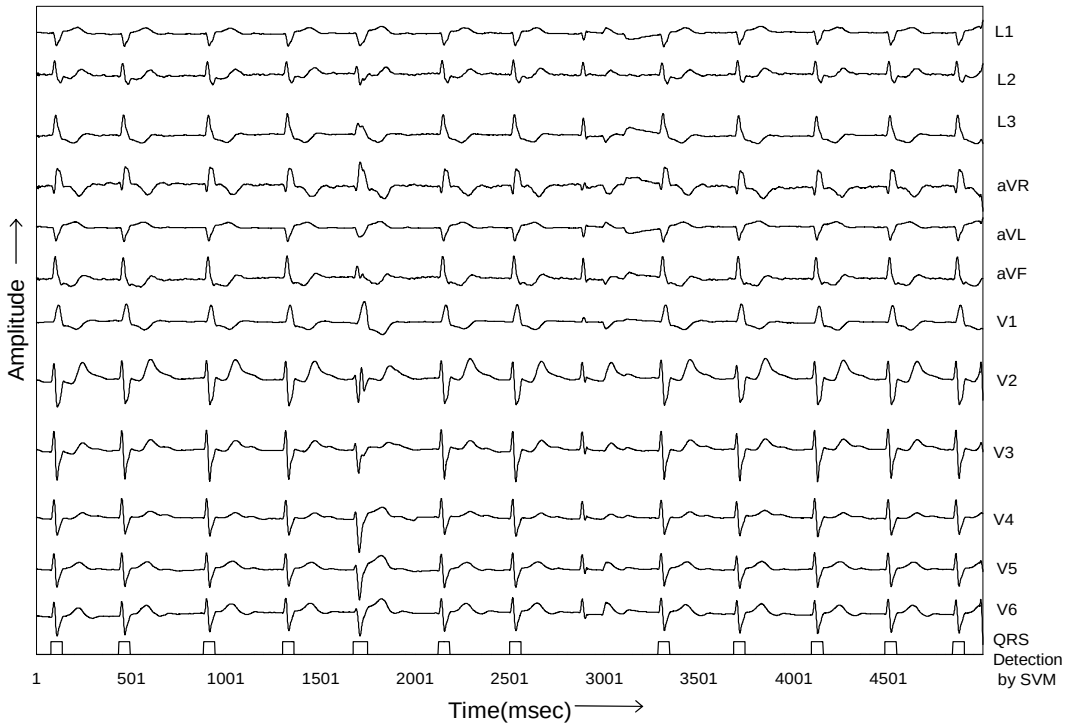

Fig. 7 QRS detection of record MO1_045 of CSE database

6. CONCLUSION

In this paper, a novel QRS detector using SVM is proposed and evaluated on the standard CSE database. SVM gave very encouraging and consistent results for both single lead as well as 12-lead algorithms as compare to the methods reported earlier in the literature for the given problem of QRS detection. Due to high generalization ability of the SVM, the percentage of false positive and false negative detections is very low. 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. 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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