Comparative Study of QRS Detection in Single Lead and 12-Lead Electrocardiogram using Support Vector Machine

S. S. Mehta, and N. S. Lingayat, *Member, IAENG*

***Abstract*— Application of Support Vector Machine (SVM) for QRS detection in single lead and 12-lead Electrocardiogram (ECG) using 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 99.79% and positive prediction (+P) of 99.15% is achieved when tested using single lead ECG. It improves to 99.93% and 99.46% respectively for simultaneously recorded 12-lead ECG signal. The percentage of false positive and false negative is low. 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.**

I. 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. As displayed in Fig. 1, 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.

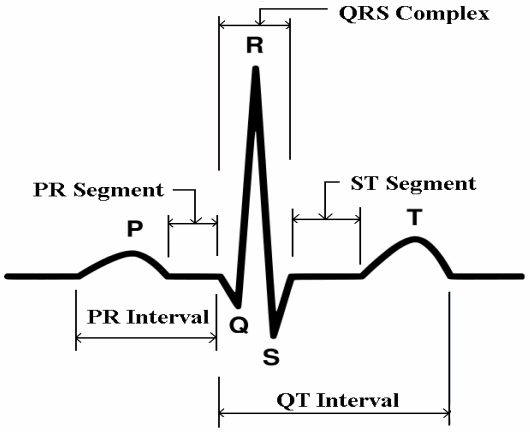

Fig.1 ECG Signal

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 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 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.

Manuscript received April 30, 2007. This work was supported by All India Council for Technical Education (AICTE), N. Delhi, India.

S. S. Mehta is with the Department of Electrical Engineering, MBM Engineering College, J. N. V. University. Jodhpur- 342001, Rajasthan (India). (e-mail: ssmehta_58@rediffmail.com)

N. S. Lingayat is with Department of Electrical Engineering, Institute of Petrochemical Engineering, Dr. B. A. Technological University, Lonere-402103, Maharashtra (India). Presently he is on deputation as a Research Scholar at Department of Electrical Engineering, MBM Engineering College, J. N. V. University. Jodhpur- 342001, Rajasthan (India). (phone: +91 291 2515488, fax: +91 291 2513348, e-mail: nslingayat@yahoo.com).

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: ECG signal preprocessing is described in section 2. Section 3 presents a brief description of the SVM for two-class problem. Implementation of SVM for a given problem of QRS detection is discussed in section 4. The experimental results and discussion of the proposed algorithm are provided in section 5.

II. 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 [22] 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 [23] 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 [24]. Slope is used as an important feature because slope of the ECG signal is much more in the QRS region than in the non-QRS region.

The probability of slope at each sampling instant belonging to each of the two classes is calculated using (1).

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

i = 1, 2; x = 1, 2, ….., s

where σ_i and m_i are the standard deviation and mean of i^{th} class and s represents total number of samples in the ECG signal.

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 [24].

The entropy $h_i(\mathrm{x})$ at each sampling instant for QRS and non QRS classes is calculated using (2). These entropies are then normalized.

$$h_i(\mathrm{x}) = -P_i(\mathrm{x})\log_e P_i(\mathrm{x}), \quad (2)$$

i = 1, 2; x = 1,2,…., s

The combined entropy, $h_c(\mathrm{x})$ is then calculated by using (3).

$$h_c(\mathrm{x}) = (1 - h_{2n}(\mathrm{x}))* h_{1n}(\mathrm{x}) \quad (3)$$

i = 1, 2; x = 1,2,…., s

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

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

Fig. 2 demonstrates the results obtained during preprocessing for lead V5 of record MO1_020 of CSE ECG database. The raw ECG signal is displayed in Fig. 2(a). As depicted in Fig.2 (b), the preprocessor removes power line interference and base line wander present in the raw ECG signal. Fig. 2(c) shows $h_{1n}(\mathrm{x})$, 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 $h_{1n}(\mathrm{x})$ curve provides critical information about the degree of certainty of a region belonging to QRS region.

Fig. 2(d) shows $h_{2n}(\mathrm{x})$, 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

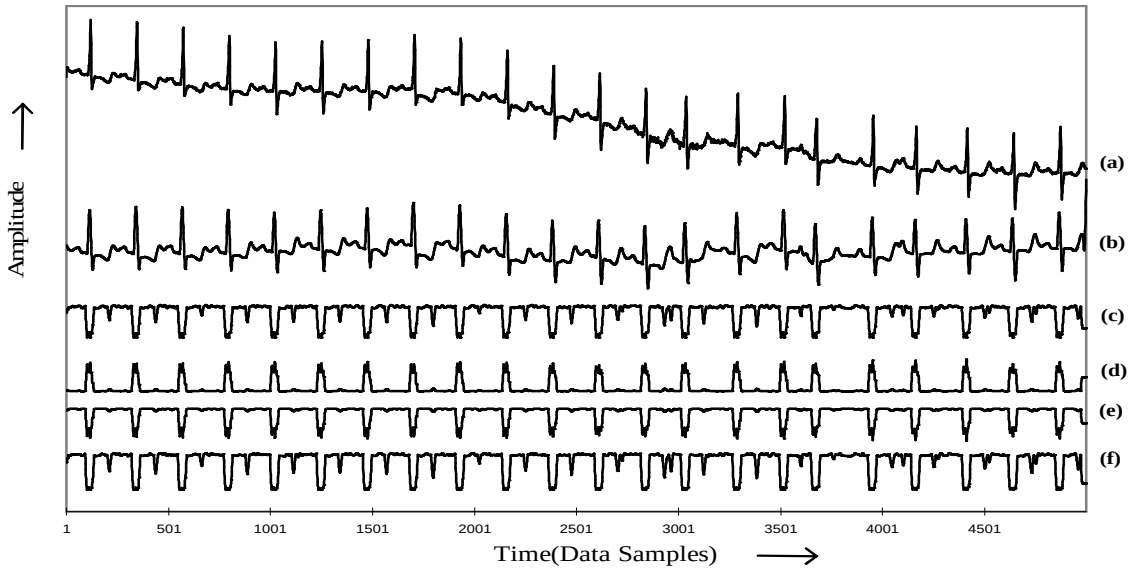

Fig.2 (a) Raw ECG of lead V5 of record MO1_20 of CSE ECG database, (b) Filtered ECG Signal, (c) Entropy QRS, (d) Entropy non-QRS, (e) [1- $h_{2n}(x)$] curve, (f) Combined Entropy

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. 2 (e). Now if the curve, showing the product $h_{cn}(x) = (1\text{-}h_{2n}(x)) * h_{1n}(x)$, 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. 2 (c) and (d). This can be seen in the combined entropy curve shown in Fig.2 (f). Therefore, combined entropy is used in the present work to obtain the transformed signal for the detection of QRS complexes.

III. Support Vector Machine

SVM is a new paradigm of learning system. The technique of SVM, developed by Vapnik [25], is a powerful widely used technique for solving supervised classification problems due to its generalization ability. In essence, SVM classifiers maximize the margin between training data and the decision boundary (optimal separating hyperplane), which can be formulated as a quadratic optimization problem in a feature space. The subset of patterns those are closest to the decision boundary are called as support vectors.

Consider a set of training examples $(\mathbf{x}_1, y_1),.....,(\mathbf{x}_l, y_l)$, where input $\mathbf{x}_i \in R^N$ and class labels $y_i \in \{-1,+1\}$. Decision function of the form $sgn((\mathbf{w}.\mathbf{x}) + b)$ is considered, where $(\mathbf{w}.\mathbf{x})$ represents the inner product of $\mathbf{w}$ and $\mathbf{x}$, $\mathbf{w}$ is weight vector and b is bias. It is necessary to find a decision function $f_{w,b}$ with the properties

$$y_i((\mathbf{w}.\mathbf{x}_i) + b) \geq 1 \qquad (4)$$

$i = 1, ..., l$

In many practical situations, a separating hyperplane does not exist. To allow for possibilities of violating (4), slack variables, ξ_i are introduced like

$$\xi_i \geq 0, \qquad (5)$$

$i = 1, ..., l$

to get

$$y_i((\mathbf{w}.\mathbf{x}_i) + b) \geq 1 - \xi_i \qquad (6)$$

$i = 1, ..., l$

The support vector approach for minimizing the generalization error consists of the following:

$$\text{Minimize:} \qquad \Phi(\mathbf{w}, \xi) = (\mathbf{w}.\mathbf{w}) + C\sum_{i=1}^{l}\xi_i \qquad (7)$$

subject to constraints (5) and (6).

The C is a user defined constant. It is called regularizing parameter and determines the balance between the maximization of the margin and minimization of the classification error.

The above minimization problem can be posed as a constrained quadratic programming (QP) problem. The solution gives rise to a decision function of the form:

$$f(\mathbf{x}) = sgn\left\lfloor\sum_{i=1}^{l} y_i\alpha_i(\mathbf{x}.\mathbf{x}_i) + b\right\rfloor \qquad (8)$$

where α_i are Lagrange multipliers. Only a small fraction of the α_i coefficients are nonzero. The corresponding pairs of $\mathbf{x}_i$ entries are known as support vectors and they fully define the decision function.

By replacing the inner product $(\mathbf{x}.\mathbf{x}_i)$ with kernel function $K(\mathbf{x}, \mathbf{x}_i)$; the input data are mapped to a higher dimensional

space [26]. It is then in this higher dimensional space that a separating hyperplane is constructed to maximize the margin.

IV. Implementation of SVM for QRS Detection

Implementation of SVM for QRS detection in ECG signal is done by using LIBSVM software [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].

In the present problem of QRS detection, SVM is constructed using sigmoid kernel $K(\mathbf{x}, \mathbf{x}_i) = \tanh(\gamma(\mathbf{x}.\mathbf{x}_i) + \nu)$, 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 [29].

A. Single Lead QRS Detection

In single lead QRS detection algorithm, normalized combined entropy values obtained during preprocessing are used for training of SVM. The training set consists of normalized combined entropy values covering a wide variety of QRS morphologies. During the training of SVM, a sliding window of size ten sampling instants is moved over the normalized combined entropy values from the training set. The first pattern vector is formed by taking first ten normalized combined entropy values from first to tenth sampling instant. The window is then moved forward by one sampling instant and the second pattern vector is formed by taking another set of ten normalized combined entropy values but now from second to eleventh sampling instant. This way, a sliding window of size ten sampling instant and a jump size of one sample is moved over the normalized combined entropy 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.

During testing, a set of ten normalized combined entropy values of a particular lead of a subject from a standard CSE ECG database 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 ten combined entropy values of ECG are 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.

B. Twelve- Lead QRS Detection

In twelve lead QRS detection algorithm normalized combined entropy values of all the twelve leads obtained during preprocessing are used for training of SVM. The training set consists of normalized combined entropy values of twelve leads covering a wide variety of QRS morphologies. During the training of SVM, a sliding window of size twelve sampling instants is moved over the normalized combined entropy values from the training set. The first input pattern vector is formed by taking twelve values of normalized combined entropy one each from all the twelve leads at the first sampling instant. The window is then moved forward by one sampling instant and the second pattern vector is formed by taking another set of twelve values of normalized combined entropy, one each from all the twelve leads but now at second sampling instant. 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.

During testing, normalized value of twelve combined entropies, one from each of the twelve leads of 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 twelve combined entropies, again one 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.

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.

V. Experimental Results and Discussion

A. Training Set

In single lead QRS detection training set is formed by taking 9667 samples (normalized combined entropy values) covering a wide variety of QRS morphologies of 12 different subjects. 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.

In twelve lead QRS detection training set consists of 9667, 12-lead samples (normalized combined entropy values) covering a wide variety of QRS morphologies of the same 12 subjects as in single lead QRS detection. The window size of twelve, containing twelve normalized combined entropy values, one from each of the twelve leads of ECG.

B. Parameter Selection

There are three free parameters namely γ, ν of the sigmoid kernel function and margin-loss trade-off C, should be determined to find the optimal solution. It is not known beforehand which C, γ and ν are the best for this problem. The

objective is to obtain best *C*, γ and ν so that the classifier can accurately predict unknown data (testing data). In the present study four- fold cross- validation approach is used to tune these free parameters [30]. In this, the training data is 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 optimum values of *C*=2, γ = 0.2 and ν= -0.1 are obtained for both the training sets with the cross validation accuracy of 98.72% and 99.34% for single lead and twelve lead training set respectively.

C. Performance Evaluation

To evaluate the performance of the QRS detection algorithm, two parameters, sensitivity (*Se*) and positive prediction (*+P*) are used [31] and are defined as:

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

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

where *TP* stands for true positive, *FP* for false positive and *FN* for false negative. Detection is said to be true positive (*TP*) if the algorithm correctly identifies the QRS complex and it is said to be false negative (*FN*) 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 proposed algorithms for QRS detection are tested using 1500, single-lead ECG records and simultaneously recorded 125, 12-lead ECG records of dataset 3 of CSE multi-lead measurement library [32]. 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 ECG library contains a high percentage of pathological ECG's, and there are some QRS's which are hardly recognized even visually.

Every ECG signal from CSE ECG database is of 10s duration sampled at 500Hz thus giving 5000 samples. These 5000 samples are classified into QRS and non-QRS regions after preprocessing. The sensitivity (*Se*) of 99.79% and positive prediction (*+P*) of 99.15% is obtained for single lead QRS detection. Improved performance is obtained for QRS detection in simultaneously recorded 12-lead ECG signals with *Se*=99.93% and *+P*=99.46%**.** 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 reduces to 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 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, 33, 34, 35, 36, 37].

Fig.3 shows results obtained at the preprocessing stage and QRS detection of lead L1 of record MO1_075. As depicted in Fig.3 (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. 3 (d).

Fig.4 shows QRS detection of lead V2 of record MO1_079. In this case the P and T- waves are not prominent; hence all the QRS complexes have been correctly detected by SVM.

Fig.5 shows QRS detection of lead V2 of record MO1_106. 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.

In Fig.6, QRS detection of lead L2 of record MO1_050 is displayed. In this case, SVM fails to detect the first QRS complex because of the lower amplitude of the R-wave and smaller pulse duration compare to others.

Fig.7 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. 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. 8 displays the QRS detection of the record MO1_116. 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.9, QRS detection of record MO1_045 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.

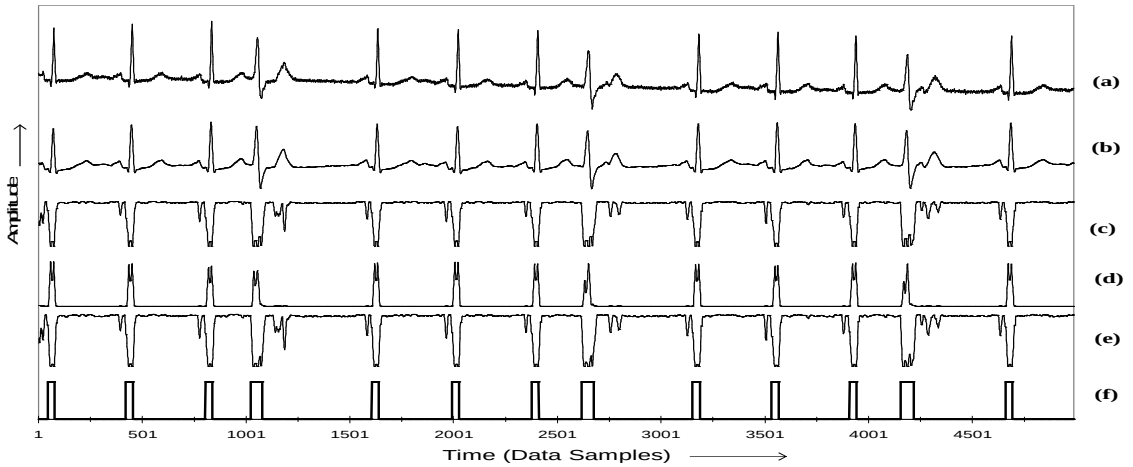

Fig.3 QRS detection of record MO1_075 of CSE database (a) Raw ECG, (b) Filtered ECG, (c) Entropy QRS, (d) Entropy non-QRS, (e) Combined Entropy, (f) QRS Detection by SVM

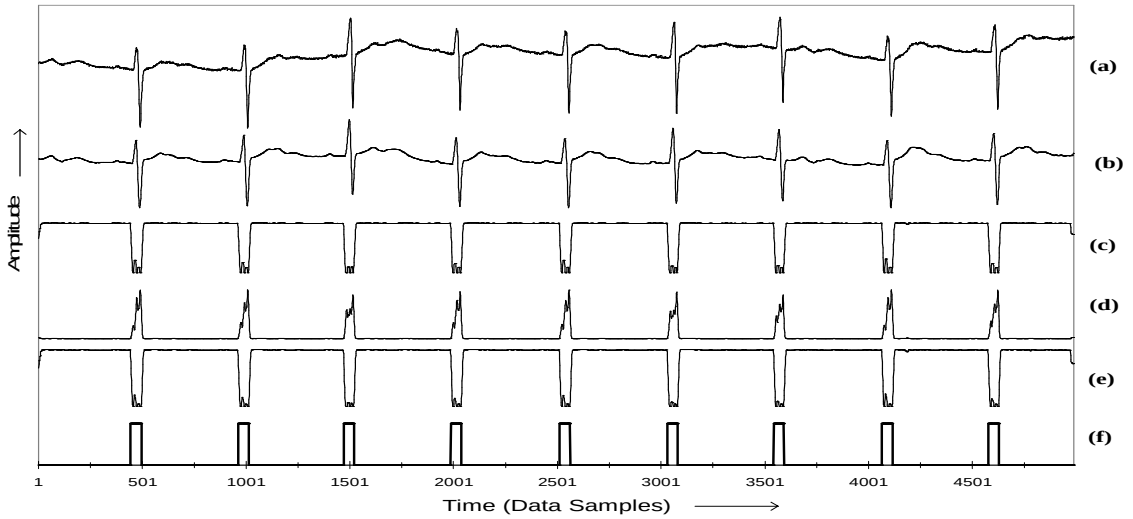

Fig.4 QRS detection of record MO1_079 of CSE database, (a) Raw ECG, (b) Filtered ECG, (c) Entropy QRS, (d) Entropy non-QRS, (e) Combined Entropy, (f) QRS Detection by SVM

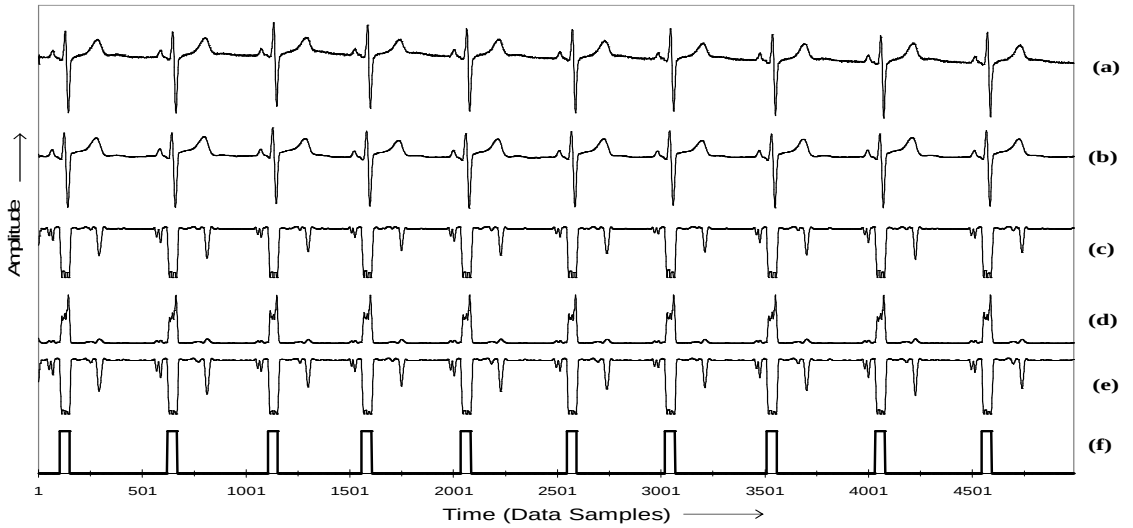

Fig. 5 QRS detection of record MO1_106 of CSE ECG database, (a) Raw ECG, (b) Filtered ECG, (c) Entropy QRS, (d) Entropy non-QRS, (e) Combined Entropy, (f) QRS Detection by SVM

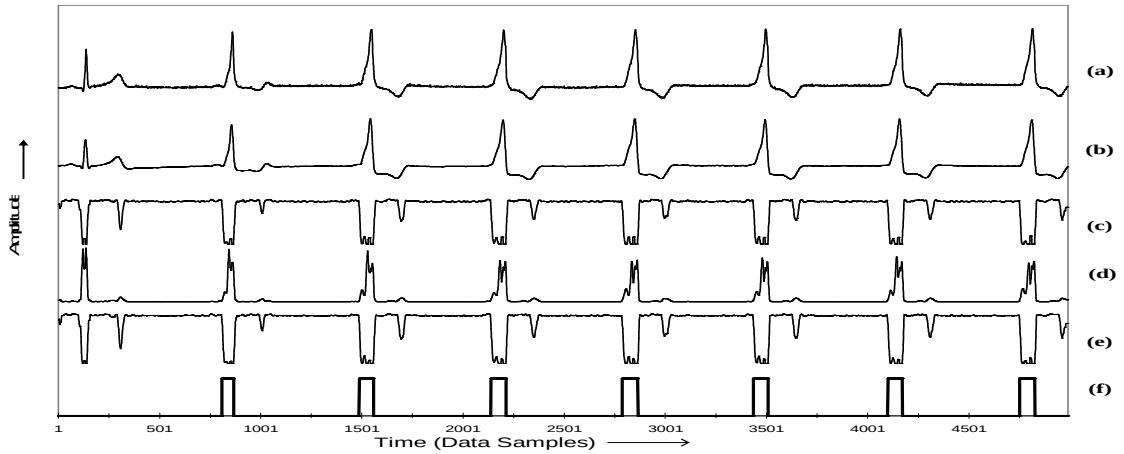

Fig. 6 QRS detection for record MO1_050 of CSE ECG database, (a) Raw ECG, (b) Filtered ECG, (c) Entropy QRS, (d) Entropy non-QRS, (e) Combined Entropy, (f) QRS Detection by SVM

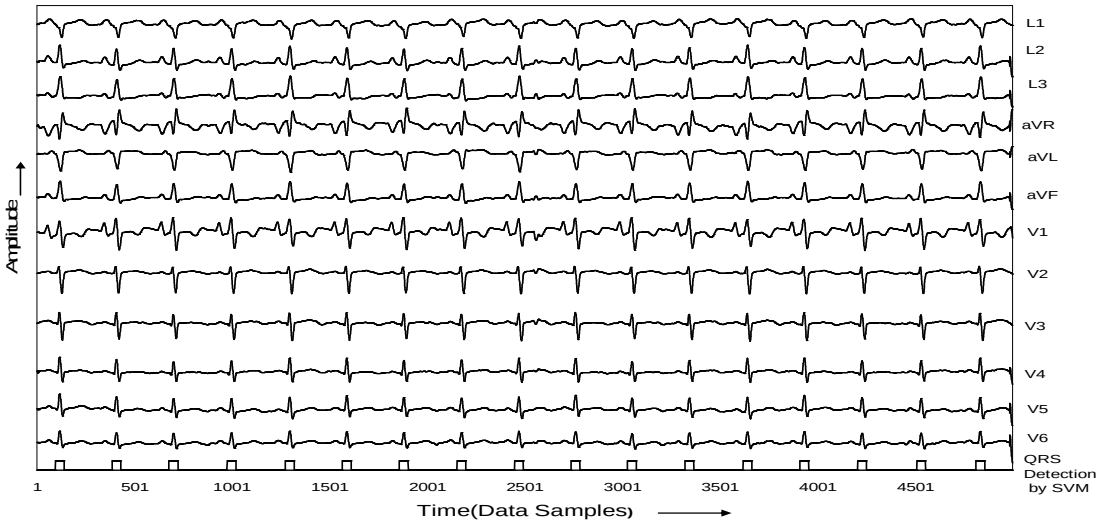

Fig. 7 QRS detection for record MO1_005 of CSE ECG database

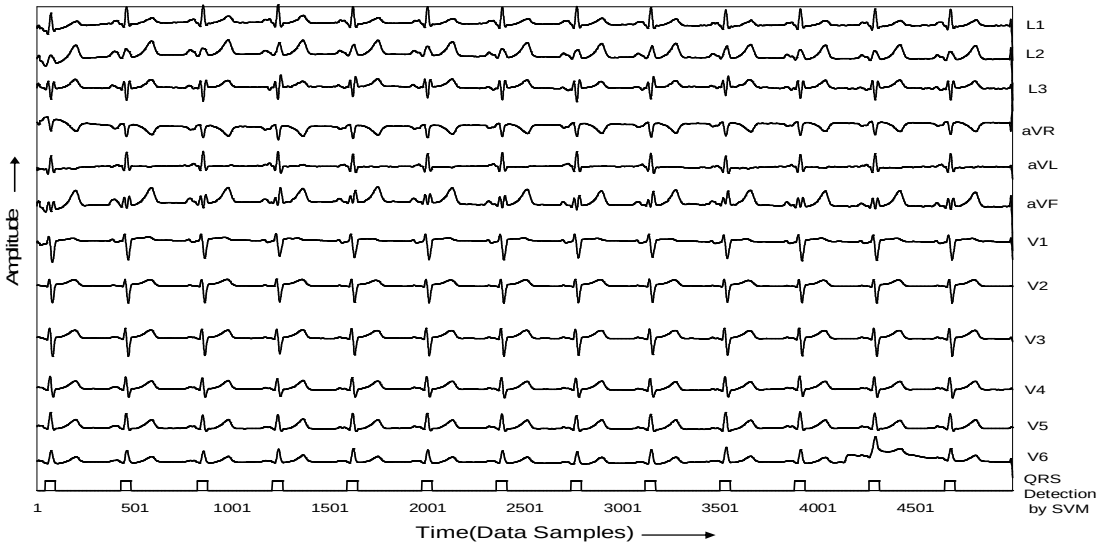

Fig. 8 QRS detection for record MO1_116 of CSE ECG database

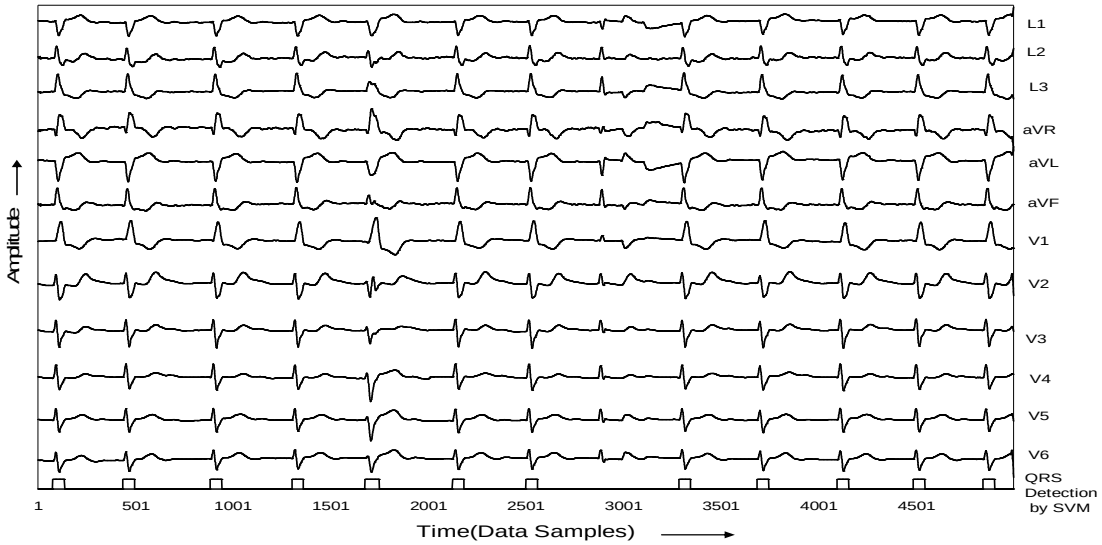

Fig. 9 QRS detection of record MO1_045 of CSE database

VI. 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.

References

[1] B. U. Kohler, C. Henning, R. Orglmeister, The principles of software QRS detection, IEEE Eng. in Med. and Bio., (2002) 42-47.

[2] S. S. Mehta, S.C. Sexana and H.K Verma, Computer-aided interpretation of ECG for diagnostics, Int. Journal of System Science, (1996) 43-58.

[3] D. Benitez, P. A. Gaydecki, A. Zaidi, A. P. Fitzpatrick, The use of Hilbert transform in ECG signal analysis, Comp. in Bio. and Med., 31(2001) 399-406.

[4] S. C. Saxena, V. Kumar, S. T. Hamde, Feature extraction from ECG signals using wavelet transform for disease diagnostics, Int. Journal of System Science, 33 (2002) 1073- 1085.

[5] M. Engin, ECG beat classification using neuro-fuzzy network, Pat. Rec. Letters, 25 (2004), 1715-1722.

[6] S. A. Israel, J. M. Irvine, A. Cheng, M. D. Wiederbold, B. K. Wiederhold, ECG to identify individuals, Pat. Rec., 38 (2005) 133-142.

[7] N. M. Arzeno, C. S. Poon, Z. D. Deng, Quantitative analysis of QRS detection algorithms based on first derivative of the ECG, Proc. of 28th IEEE EMBS annual international conference, New York, USA, (2006) 1788-1791.

[8] M. Paoletti, C. Marchesi, Discovering dangerous patterns in long-term ambulatory ECG recordings using a fast QRS detection algorithm and explorative data analysis, Comp. Methods and Progs. in Biomed., 82 (2006) 20-30.

[9] S. W. Chen, H. C. Chen, H. L. Chan, A real time QRS detection method based on moving-averaging incorporating with wavelet denoising, Comp. Methods and Progs. in Biomed., 82 (2006) 187-195.

[10] I. Christov, G. G. Herrero, V. Krasteva, I. Jekova, A. Gotchev, K. Egiazarian., Comparative study of morphological and time-frequency ECG descriptors for heartbeat classification, Med. Eng. Phy., 28 (2006) 876-887.

[11] F. Gritzali, Towards a generalized scheme for QRS Detection in ECG waveforms, Signal Processing 15 (1988) 183-192.

[12] M. Brown, W. Grundy, D. Lin, N. Cristianini, C. Sugnet, T. Furey, M. Ares, D. Haussler, Knowledge based analysis of micro-array gene expression data using support vector machine, Technical Report, University of California, 1999.

[13] J. Dehmeshki, J. Chen, M. V. Casique, M. Karakoy, Classification of lung data by sampling and support vector machine, Proc. of 26th IEEE EMBS annual international conference, San Francisco, CA, USA, (2004) 3194-3197.

[14] F. Chu, G. Jin, L. Wang, Cancer diagnosis and protein secondary structure prediction using support vector machine, StudFuss, 177 (2005) 343-363.

[15] J. M. Roig, R. V. Galiano, F. J. Chorro-Gasco, A. Cebrian, Support vector machine for arrhythmia discrimination with wavelet transform based feature selection. Computers in Cardiology, 27 (2000) 407-410.

[16] S. Jankowski, A. Oreziak, A. Skorupski, H.Kowalski, Z. Szymanski, E. Piatkowska-Janko, Computer-aided morphological analysis of holter ECG recordings based on support vector learning system, Computers in Cardiology, 30 (2003) 597-600.

[17] S. Jankowski, A. Oreziak, Learning system for Computer-aided ECG analysis based on support vector machines, I.J. of Bioelectromagnetism, 5 (2003), 175-176.

[18] S. Osowski, L. T. Hoai, T. Markiewicz, Support vector machines based expert system for reliable heartbeat recognition, IEEE Trans. Biomed. Eng. 51 (2004) 582-589.

[19] N. Acir, Classification of ECG beats by using a fast least square support vector machines with a dynamic programming feature selection algorithm, Neural Comput. and App., 14 (2005) 299-309.

[20] M. H. Song, J. Lee, S. P. Cho, K. J. Lee, S. K. Yoo, Support vector machines based arrhythmia classification using reduced features, I. J. of Control Auto. and Sys., 3 (2005) 571-579.

[21] N. Acir, A support vector machine classifier algorithm based on a perturbation method and its application to ECG beat recognition systems, Expert Sys. with App., 31 (2006) 150-158.

[22] J. A. Van Alste, T.S. Schilder, Removal of base-line wander and power line interference from the ECG by an efficient FIR filter with a reduced number of taps, IEEE Trans. Biomed. Eng., 32 (1985)1052- 1059.

[23] G. S. Furno, W. J. Tompkins, A learning filter for removing noise interference, IEEE Trans. Biomed. Eng., 30 (1983) 234-235.

[24] J. L. Tou and R. C. Gonzalez, Pattern Recognition Principles, Addison-Wesley Publishing Company MA, 1974.
[25] V. Vapnik, Statistical Learning Theory, Wiley, New York, 1998.
[26] C. J. C. Burges, A tutorial on support vector machines for pattern recognition, Data mining and knowledge discovery, 2(1998) 955-971.
[27] C. C. Chang, C. J. Lin, LIBSVM: A library for support vector machines, Technical report, National Taiwan University, Taiwan, 2004.
[28] J. Platt, Fast training of SVMs using sequential minimal optimization in B. SchPolkopf, C. Burges, A. Smola, (Eds.), Advances in kernel methods: Support vector machines, MIT Press, Cambridge, 1999.
[29] H. T. Lin, C. J. Lin, A study on sigmoid kernels for SVM and the training of non-PSD kernels by SMO-type methods, Technical report, Department of Computer Science and Information Engineering, National Taiwan University, Taiwan, 2003.
[30] C. W. Hsu, C. C. Chang and C. J. Lin, A practical guide to support vector classification, Technical report, Department of Computer Science and Information Engineering, National Taiwan University, Taiwan, 2003.
[31] ANSI/AAMI EC57: Testing and reporting performance results of cardiac rhythm and ST segment measurement algorithms (AAMI Recommended Practice/ American National Standard), 1998.
[32] J. L. Willems, P. Arnaud, J. H. Van Bemmel, R. Degani, P. W. Macfarlane, Chr. Zywietz, CSE working party, Common Standards for Quantitative Electrofcardiography: Goals and main results, Meth Inform. Med., 29 (1990) 263-271.
[33] A. Kyrkos, E. A. Giakoumakis, G. Carayannis, QRS detection through time recursive prediction technique, Signal Processing, 15 (1988) 429-436.
[34] P. Trahanias, E. Skordalalkis, Bottom up approach to the ECG pattern-recognition problem, Med. Bio. Eng. and Compu., 27 (1989) 221-229.
[35] P. Trahanias, E. Skordalalkis, Syntactic pattern recognition of ECG, IEEE Trans. Pattern Anal. Machine Intell., 12 (1990) 648-657.
[36] P. E. Trahanias, An approach to QRS complex detection using mathematical morphology, IEEE Trans. Biomed. Eng., 40 (1993) 201-205.
[37] P. Laguna, R. Jane, P. Caminal, Automatic detection of wave boundaries in multi-lead ECG signals: Validation with CSE database., Comp. and Biomed. Res., 27 (1994), 45-60.

Sarabjeet S. Mehta was born in Kolkata, India in 1958. He received the B.E. degree in Electrical Engineeirng and M.E. degree in Control System from J. N. Vyas University, Jodhpur- Rajasthan (India) in 1980 and 1987 respectively. He received Ph.D. degree in Electrical Engineering from Indian Institute of Technology, Roorke in 1994.

Presently he is Associate Professor and Head, Electrical Engineering Department of MBM Engineering College, J. N. Vyas University, Jodhpur-Rajasthan (India). His research interest includes pattern recognition, artificial neural networks, biomedical engineering, soft computing and electrical machines.

He is a fellow of Institution of Engineers (India) and life member of Indian Society for Technical Education.

Nitin S. Lingayat was born in Shahapur (Thane), India in 1971. He received the B.E. degree in Electrical Engineering from the University of Poona, Pune in 1992 and the M.Tech. degree from Indian Institute of Technology Bombay, Mumbai in 1998. He is Head, Electrical Engineering Department, Institute of Petrochemical Engineering of Dr. B.A. Technological University, Lonere- Maharashtra (India).

He is on deputation as a research scholar in Electrical Engineering Department, MBM Engineering College, J. N. Vyas University, Jodhpur-Rajasthan (India). Presently he is working in the area of biomedical signal processing.