Support Vector Machine for Cardiac Beat Detection in Single Lead Electrocardiogram

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***Abstract*— Among all ECG components, QRS complex is the most significant feature. Entropy based method for the detection of QRS complexes (cardiac beat) in the single lead Electrocardiogram (ECG) is proposed in this paper. Digital filtering techniques are used to remove noise and base line wander in the ECG signal. Entropy criterion is used to enhance the QRS complexes. Support Vector Machine (SVM) is used as a classifier to delineate QRS and nonQRS regions. The performance of the algorithm is evaluated against the standard CSE ECG database. The numerical results indicated that the algorithm achieved 99.68% of the detection rate. The percentage of false positive and false negative is 2.28 and 0.32 respectively. The detection rate depends strongly on the quality of training, data representation and the mathematical basis of the classifier.**

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

I. Introduction

Electrocardiogram (ECG) provides useful 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. As displayed in Fig. 1, ECG is characterized by a recurrent wave sequence P, QRS and T 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 detection 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.

Manuscript received May 3, 2007. This work was supported by All India Council for Technical Education (AICTE), N. Delhi, India.

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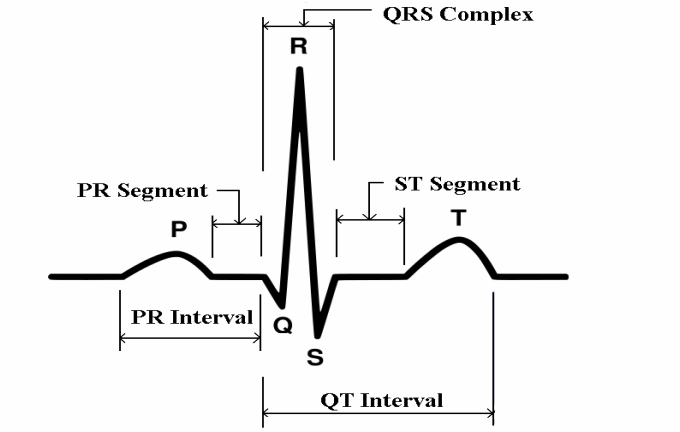

Fig.1 ECG Signal

Numerous QRS detection algorithms such as derivative based algorithms, algorithms based on digital filters, wavelet transform, length and energy transform, artificial neural networks, genetic algorithm, 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 complex is present at a given instant in the signal.

SVMs based classification methods represents a major development in pattern recognition research. Two innovations of SVMs are responsible for the success of these methods, 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.

This paper is structured as follows: ECG signal preprocessing is described in section II. Section III 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 IV. The experimental results and discussion of the proposed algorithm are provided in section V.

II. Preprocessing Of ECG Signal

A raw ECG signal of a subject 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 are 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 and these are clustered into two classes, namely QRS and nonQRS 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 nonQRS region.

The probability, $P_i(\mathrm{x})$ of slope at each sampling instant belonging to each of the two classes is calculated using (1).

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

$i = 1, 2;\ \mathrm{x} = 1, 2, \ldots..,\ s$

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 nonQRS classes is calculated using (2). These entropies are then normalized.

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

$i = 1, 2;\ \mathrm{x} = 1,2,\ldots., s$

Thus, from a single filtered ECG signal, two normalized entropy curves, one from the QRS entropies, and other from the nonQRS entropies are obtained. Similar procedure is applied for remaining leads of a subject and for all the subjects from the CSE ECG database.

Fig. 2 shows the results of the preprocessing stage of lead V_5 of record MO1_20 of CSE ECG database. As depicted in Fig.2(b), the preprocessor removes noise and base line wander present in the raw ECG signal. Fig. 2(c) and (d) shows curve for QRS and nonQRS entropy respectively. In QRS region, the lower value of QRS entropy shows lower uncertainty or higher certainty of the occurrence of QRS complex, similarly higher value of nonQRS entropy shows higher uncertainty of nonQRS or high certainty of QRS complex. Thus, in gross, indicating the presence of QRS region.

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

$$y_i((\mathbf{w}.\mathbf{x}_i)+b) \geq 1 \quad (3)$$

$i = 1, \ldots\ldots, l$

In many practical situations, a separating hyperplane does not exist. To allow for possibilities of violating (3), slack variables, ξ_i are introduced like

$$\xi_i \geq 0, \quad (4)$$

$i = 1, \ldots\ldots, l$

to get

$$y_i((\mathbf{w}.\mathbf{x}_i)+b) \geq 1-\xi_i \quad (5)$$

$i = 1, \ldots\ldots, l$

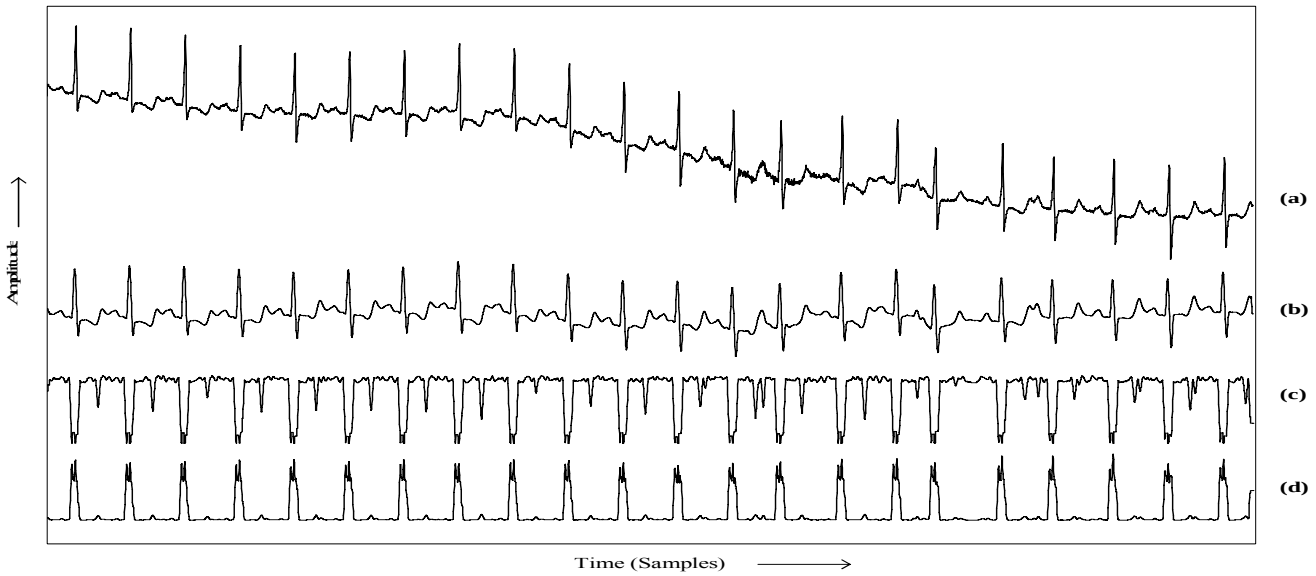

Fig.2 Preprocessing of ECG Signal (a) Raw ECG of lead V_5 of record MO1_20 of CSE ECG database, (b) Filtered ECG Signal, (c) Entropy QRS, (d) Entropy nonQRS

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

Minimize: $$\Phi(\mathbf{w},\xi) = (\mathbf{w}.\mathbf{w}) + C\sum_{i=1}^{l}\xi_i \qquad (6)$$

subject to constraints (4) and (5).

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:

$$f(\mathbf{x}) = sgn\left[\sum_{i=1}^{l} y_i\alpha_i(\mathbf{x}.\mathbf{x}_i) + b\right] \qquad (7)$$

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].

The training set consists of normalized entropy values of different leads of certain portions of fourteen ECGs covering a wide variety of QRS morphologies. The training set consists of 9707 samples in all.

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.

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. 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 of QRS detection. 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=1, γ = 0.2 and ν= -0.1 are obtained with the cross validation accuracy of 99.44%.

B. Performance Evaluation

The evaluation of the performance of the proposed algorithm for QRS detection is done using 1500, single-lead ECG records from the CSE ECG library [31]. This library contains a variety of pathological cases. Every record picked from CSE ECG database is of 10s duration sampled at 500Hz thus giving 5000 samples. Detection is said to be false positive if nonQRS wave is detected as a QRS complex and it is said to be false negative if the algorithm fails to detect the QRS complex. 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 nonQRS regions after preprocessing.

The algorithm, when tested using the optimum values of the parameters (C=1, γ =0.2, ν= -0.1) gives detection rate of 99.68%. The percentage of false negative detection is 0.32 and the percentage of false positive detection is 2.28. The false positive detections are found mainly in the ECG records where the slopes of P and T wave are comparable with that of QRS-complexes.

The performance of the proposed algorithm with the QRS detection rate of 99.68% is found to be better than the detection rate of other algorithms (99.38% to 99.6%) tested on the same database [11, 32, 33, 34, 35, 36].

Fig.3 shows results obtained at the preprocessing stage and QRS detection of lead L_2 of record MO1_026. As depicted in Fig.3 (b), the preprocessor removes noise and base line wander present in the signal. The P and T waves are not prominent in this case. It can be seen from Fig. 3 (c) and (d) that in the QRS region, the entropy belonging to QRS class is low i.e. uncertainty of the occurrence of QRS is low or in other words certainty of the occurrence of QRS region is high. Similarly, in this region entropy belonging to nonQRS is high i.e. uncertainty of the occurrence of nonQRS is high or in other words certainty of nonQRS is low. Hence all the thirteen QRS complexes are correctly identified by the SVM as shown in Fig. 3 (d).

Fig.4 shows QRS detection of lead L_1 of record MO1_040, where the entire QRS complex are correctly detected by the SVM.

Fig.5 and Fig.6 shows QRS detection of lead V_6 of record MO1_106 and record MO1_021 respectively. In these cases, T-waves are peaky, therefore entropy belonging to QRS complex in the region of T-wave is also low showing certainty of QRS complex, but due to low value of nonQRS entropy, these T-waves are not detected as QRS complexes by the SVM thereby reducing the false positives.

VI. Conclusion

In this paper, QRS detector using SVM is proposed and applied to CSE ECG database. 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 a input to a system that allows automatic cardiac diagnosis. The test results are consistent and encouraging. The successful detection depends strongly on the quality of the learning set (selection of cases), data representation and the choice of Kernel functions.

Acknowledgment

The authors wish to acknowledge All India Council for Technical Education (AICTE), New Delhi for providing research grant vide project no: 8022/RID/NPROJ/ RPS-10/2003-04 titled, Development of computer based techniques for identification of wave complexes and analysis of multi-lead ECG.

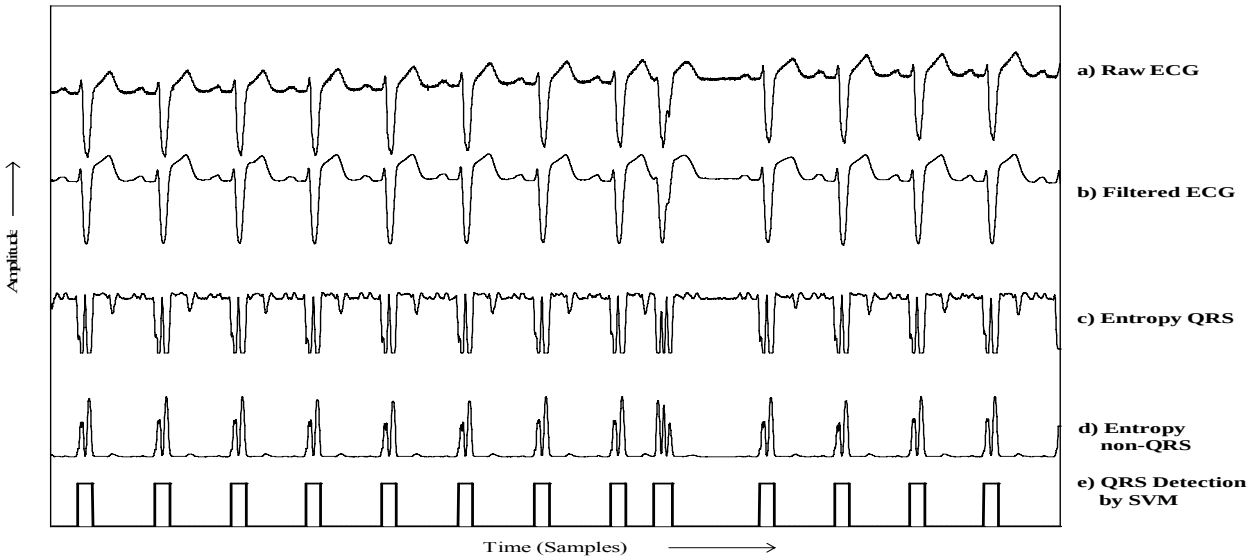

Fig.3 QRS detection of lead L2 for record MO1_026 of CSE ECG database

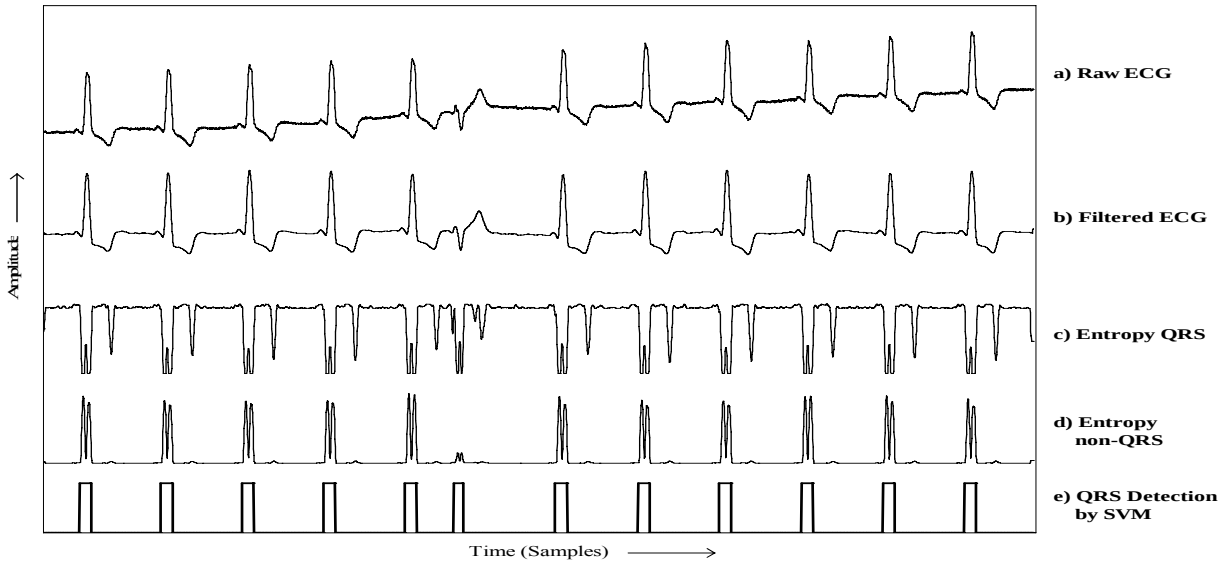

Fig. 4 QRS detection of lead L_1 for record MO1_040 of CSE ECG database

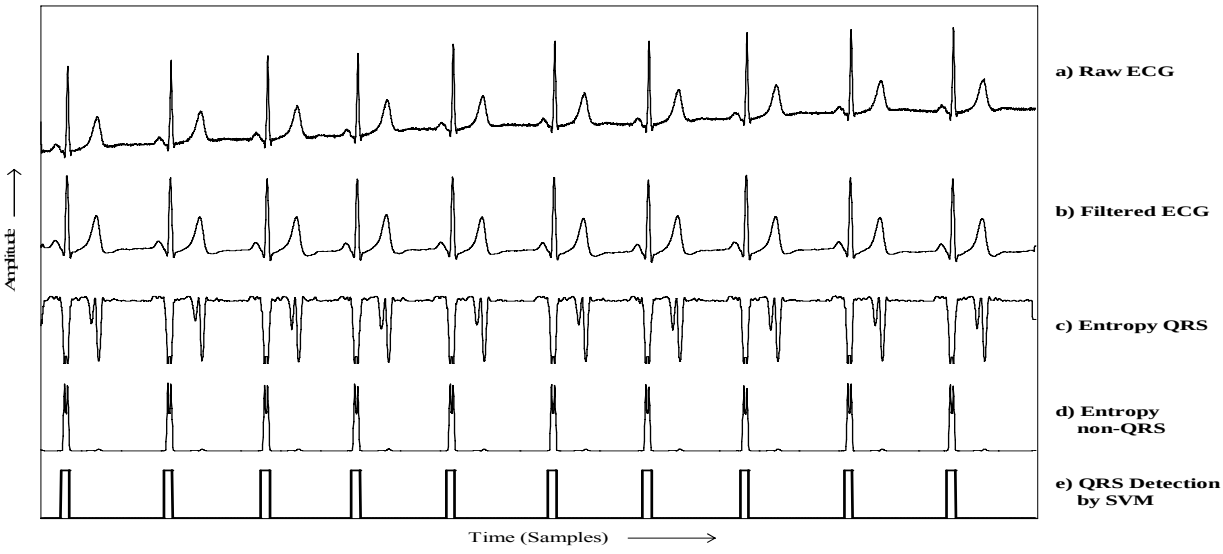

Fig. 5 QRS detection of lead V_6 of record MO1_106 of CSE ECG database

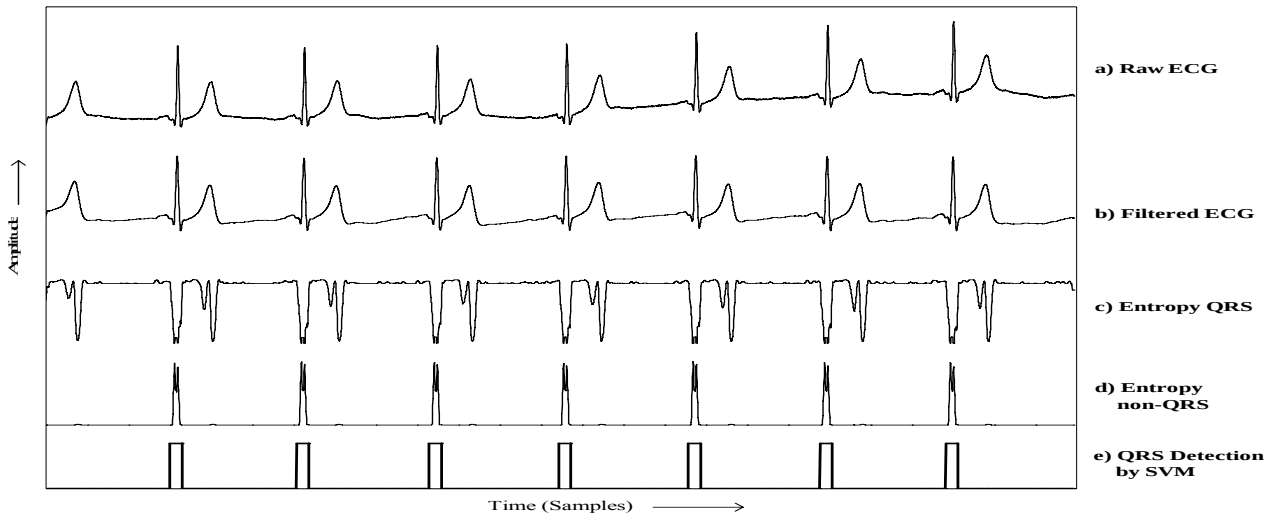

Fig. 6 QRS detection of lead V_6 of record MO1_021 of CSE ECG database

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