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Localization of QRS Complexes in Single Lead ECG

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ABSTRACT
The electrocardiogram (ECG) is graphical recording or display of the time variant voltages produced by the myocardium during the cardiac cycle. In recent years, computer aided ECG interpretation is playing an increasing role in assisting cardiologists in diagnosis and treatment of heart anomalies. The normal electrocardiogram consists of P, QRS and T wave associated with each beat, which reflects the rhythmic electrical depolarization and repolarization of the heart. Automatic localization of these ECG wave components is an important step in cardiac disease diagnosis. The first step in automated ECG analysis is the localization of QRS complexes. So, significant amount of research has focused on the development of algorithms for the accurate localization of the QRS complexes. This paper represents an algorithm for the automatic localization of the QRS complexes in single lead ECG signal based on geometric property of the ECG data. The algorithm is validated using lead L1 of 125 records covering a wide variety of QRS morphologies from the standard CSE ECG library. A detection rate of 96.03% is achieved. The algorithm is capable of localizing all the morphologies of the QRS complexes. The percentage of false positive and false negative observed is low.

Categories and Subject Descriptors
I 5.2 [Pattern Recognition]: Design Methodology, Classifier design and evaluation.

General Terms
Algorithm

Keywords
ECG, QRS complex, Optimal Hyperplane

1 INTRODUCTION
Electrocardiography (ECG) has basic role in cardiology since it consist of effective, simple, noninvasive, low-cost procedure for the diagnosis of cardiovascular disorder that have high epidemiological incidence and are very relevant for their impact on patient life and on social cost. The ECG, however, is nonlinear signal generated form nonlinear system, the human body. It is usually recorded with surface electrodes on the chest. It is record of heart electrical activity, with number of segments corresponding to the depolarization and subsequent repolarization of various region of the heart muscle. As displayed in Fig.1 ECG is characterized by wave sequence of P, QRS and T wave. The QRS complex is defined by rapid positive going transition from Q-wave to the R-wave, immediately followed by rapid negative going transition from R-wave to S-wave making up the high frequency spike, caused by ventricular depolarization of the human heart.

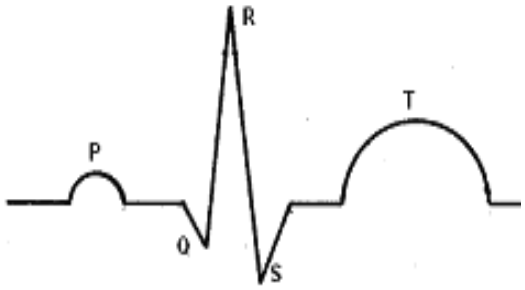

Figure 1 ECG Waveform and its Component

Online ECG processing system requires a reliable and fast QRS complex detection algorithm. After the QRS complex has been identified, the heart rate may be calculated, the ST segment may be examined for evidence of ischemia, or the waveform may be classified as normal or abnormal. A large amount of superimposed noise often comes along with ECG signal. Such a noise is basically composed by baseline wander, high frequency muscle burst and power line interference. In addition, the wave shapes and amplitude of some artifacts are fairly typical for QRS complexes. This QRS like artifact are difficult to deal with and can degrade the overall QRS-detector performance. The overall QRS detection procedure is divided in two stages, 1. pre-processing stage, 2. decision stage. The first stage enhances the QRS complex by reducing contribution of non-correlated noise. The second stage detects enhanced QRS occurrences.

The problem of QRS detection is addressed by many researchers. Recently Discrete Wavelet transform [1], Artificial Neural Network [2], Neural Network based Adaptive matched filtering [3], Genetic Algorithm and Multicriteria Decision Analysis [4], Support Vector Machine [5] etc. are applied for accurate identification of QRS complexes. Here the authors have suggested simple method based on generation of optimal classifier for pattern recognition is presented in this paper for the detection of QRS complexes in single lead ECG.

2 OPTIMAL CLASSIFIER

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Classification is problem of generating decision boundaries that can successfully distinguish the various classes in the feature space. The feature space is generally unbounded and continuous in nature. However, if the bounding information can be derived from the training patterns and if the space is discretized to sufficiently small interval in each dimension then the classification problem can be handled within the framework of MATLAB. The methodology to find a near-optimal classifier is described below.

Step 1: We consider fixed number of lines (say H) to denote a decision boundary in a two-dimensional feature space x_1-x_2. The value of H varies from problem to problem, depending upon the number as well as nature of the classes.

Step 2*:* Let us assume that there are tr training patterns available. Then in this step maximum and minimum values of each of the two features X_1 and X_2 are computed. Let these be Max_1, Min_1, Max_2, Min_2 for the features X_1 and X_2 respectively. Then the rectangle enclosing the sample points is given by the vertices (Min_1, Min_2), (Min_1, Max_2), (Max_1, Min_2), (Max_1, Max_2). Fig.2 shows an example. The rectangle represents the search space for the possible lines which may be considered as candidates for the formation of the decision boundary.

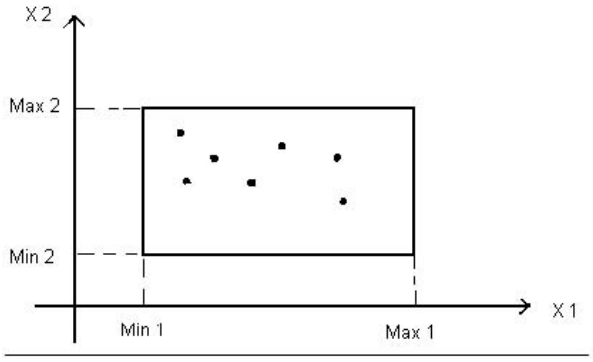

Figure 2 Training Patterns and enclosing rectangle

Step 3: To separate two closest point of the data set, which may belong to two different classes, by a line in at least one direction, a distance, $dist$ is computed as follows:

Let A represent the training data set. Then we define,

$$dist = \min \{ dist(x, y) \mid x \in A, y \in A, x \neq y \} \quad (1)$$

Where *dist(x,y)* denotes the Euclidean distance between points x and y. So the separation between two consecutive parallel lines, in any direction, is taken to be $dist$ /2. Thus, the maximum number of parallel lines max_ lines,

$$\text{max\_lines} = \left[\frac{diag}{dist} * 2 \right] \quad (2)$$

One way of representing line is by the equation

$$x_1 \cos\alpha + x_2 \sin\alpha = d \quad (3)$$

Here α is the angle between X_1-axis and the unit normal to the line: d is the perpendicular distance of the normal from the origin.

Step 4: The entire feature space will be spanned if the angle α is allowed to vary in the range from 0 to π radians. The angle space is discretized to sufficiently small intervals as $0, \delta\pi, 2\delta\pi, ..., n\delta\pi$. The number of discrete angles considered is then equal to $n+1$, and $\delta = 1/n$. An angle α can thus be specified by number angle in the range $[0, n]$ such that,

$$\alpha = angle * \delta\pi \quad (4)$$

Step 5: Once the angle α is fixed, the orientation of the line becomes fixed. For a given orientation, the perpendicular distance of the two lines passing through the base points

(Min_1, Min_2) and *(Max_1, Min_2)* of the enclosing rectangle, from the origin are computed from (3). Among these, the one with the minimum value $d_{\min}$, is selected as the base line. In other word, all the lines with $d < d_{\min}$, are automatically discarded from the search space. The other end is a parallel line at perpendicular of $d_{\min} + \max\_lines * (dist/2)$ from the origin. Therefore any line at distance $offset$ from the base line can be specified by number p in the range $[0, \max\_lines]$ such that,

$$[offset = p * dist/2] \quad (5)$$

The perpendicular distance d of the line from the origin is therefore,

$$d = d_{\min} + offset \quad (6)$$

Step 6: For each line the parameter α and d are retrieved. For each training pattern point (x_1^k, x_2^k) k =1, 2….*tr,* the sign with respect to line, i.e. the sign of the expression,

$$\cos\alpha x_1^k + \sin\alpha x_2^k - d \quad (7)$$

found. The sign is digitized as 1(0) if the point lies on the positive (negative) side of the line. The process is repeated for each of the lines and the line with minimum of the miss-classification is regarded as optimum hyper plane.

2.1 PROCEDURE FOR QRS DETECTION

Step 1: A raw digital single lead ECG signal of a patient is acquired. Fig.3 (a) shows raw signal of lead I of record MO1_020.

Step 2: Raw ECG signal 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 [7] 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 $(\mu/\pi)*f_s$,

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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 [8] is used to remove 50Hz power line interference. Fig. 3 (b) displays the filtered ECG signal after removal of power line interference and base line wander.

Step 3*:* The feature signal is obtained by calculating square of the slope of the filtered ECG signal at each sampling instant. The feature signal is generated to enhance the QRS complexes while suppressing other components like P and T waves. Fig.3(c) displays feature signal.

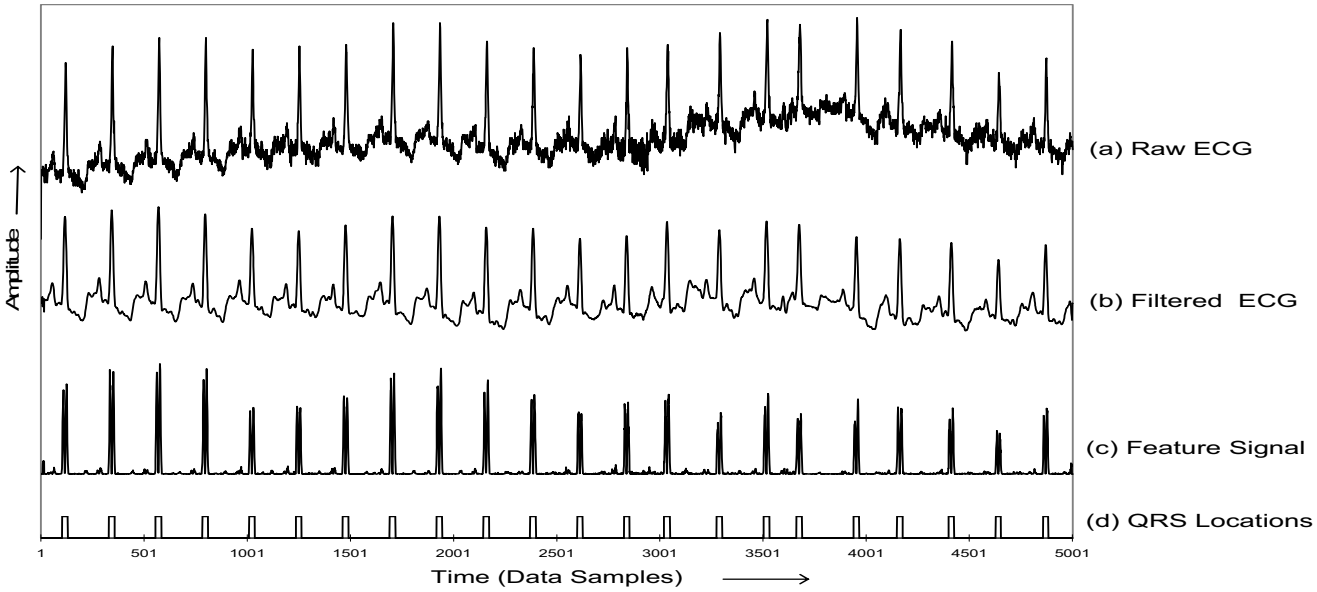

Figure 3. Results obtained at each step for record MO1_020

Step 4: Certain portions of the different ECG signals picked from the standard CSE ECG database covering wide variety of QRS complexes are used to form the training set. Steps 1 to Step 3 are repeated. Thus, the training set consists of feature signal belonging to portions of the ECG signal selected for training. An output of 1 is marked or labeled if the sample belongs to the QRS cluster and 0 for the non-QRS cluster.

Step 5: An Optimal classifier is calculated applying the procedure described in section2.

Step 6*:* During testing again for each record, Step 1 to 3 are repeated to generate feature signal. The membership of the feature signal, at given sampling instant, is found i.e. whether it belong to QRS or non-QRS domain and accordingly it is labeled as 1 or 0 respectively. It is observed that continuous train of 1's and 0's is obtained in the QRS and non-QRS region respectively.

Step 7: A continues train of 1's is 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 complex and the other ones are discarded. The locations of the QRS complexes are shown by the curve Fig.3 (d). The average pulse width criterion is incorporated because in some cases, when the P or T waves are peaky in nature, the trains of 1's are obtained in the P or T-wave region but of smaller duration compared to that of QRS complex. In order to differentiate between trains of labels of 1's for QRS complex and peaky P or T waves, an average duration of all the trains of labels of 1's is calculated. Those trains of labels of 1's whose duration is greater than average pulse duration are picked up as QRS complexes and those whose duration is smaller than the average pulse duration are discarded. Thus, average pulse duration criterion reduces the number of false positive detections.

3 RESULT AND DISCUSSION

The evaluation of the performance of the proposed algorithm for QRS detection is done using single lead, 125 original ECG recordings for picked from the CSE multi-lead ECG library [9].The CSE ECG database is developed to evaluate the performance of the ECG analysis software. It consists of a wide variety of pathological cases. Every record of the CSE ECG database is of 10 seconds duration sampled at 500Hzs thus provides 5000 samples. Detection is said to be true positive if the algorithm correctly detect the QRS complex, it is said to be false positive if 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. A significant detection rate of 96.03% is achieved using the proposed algorithm. False positive detections are obtained in the cases having peaky P or T-waves. False negative detections are obtained in the cases of non-prominent QRS complexes. Fig. 4 shows ECG signal of record MO1_099 and beneath it a square wave representing the locations of the QRS complexes as detected by the algorithm. 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 are accurately identified by the algorithm. The algorithm correctly identifies all the morphologies of the QRS complexes.

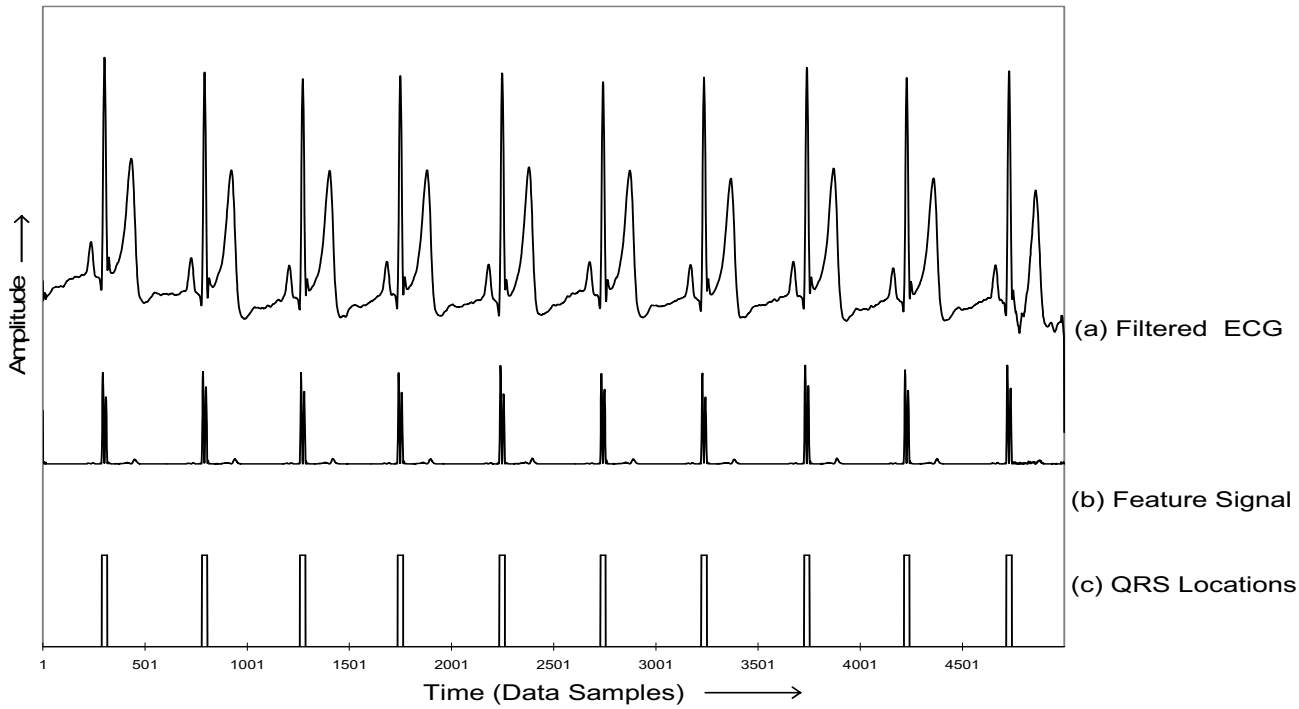

Figure 4. QRS detection for record MO1_099

4 CONCLUSION

A simple method for QRS detection in single lead ECG is presented in this paper. The algorithm is tested against the 125 records from the CSE ECG database. Significant detection rate is achieved. The information 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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