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BIOMEDICAL SIGNAL PROCESSING USING SVM

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Abstract

This paper presents a novel approach for biomedical signal processing using Support Vector Machine (SVM). Bioelectrical signals express the electrical functionality of different organs in the human body. The Electrocardiogram, also called ECG signal, is one important signal among all bioelectrical signals. ECG is characterized by a recurrent wave sequence of P, QRS and T- wave associated with each beat. The automatic detection of ECG waves is important to cardiac disease diagnosis. SVM is used as a classifier for the automatic detection of ECG waves. The performance of the algorithm is evaluated using original simultaneously recorded 12-lead ECG recordings from the standard CSE ECG database. Significant detection rate is achieved.

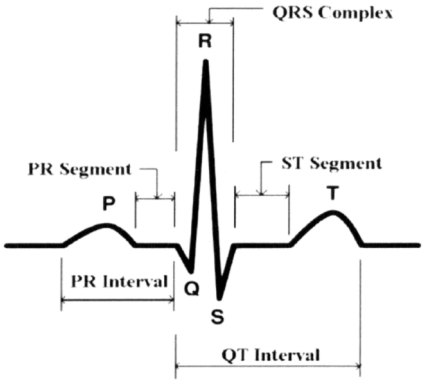

Fig.1 ECG signal

1 Introduction

The Electrocardiogram (ECG) is quite an important tool to find out the functional status of the heart. The ECG pattern consists of a recurrent wave sequence of P, QRS and T- wave associated with each beat. The automatic detection of ECG waves is important to cardiac disease diagnosis. In a clinical setting, such as intensive care units, it is essential for automated systems to accurately detect and classify ECG wave components. 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, the first deflection, termed the P-wave is due to the depolarization of the atria. The large QRS-complex is due to the depolarization the ventricles. This is the complex with highest amplitude and it is easy to detect. Numerous methods are reported in literature for the detection of QRS-complex [15]. The last deflection is T-wave corresponds to the ventricular repolarization of the heart. Reliable detection of P and T wave is more difficult than QRS complex detection for several reasons including low amplitudes, low signal-to-noise ratio, amplitude and morphological variability and possible overlapping of the P wave with T wave or the QRS complex. The P wave may be even absent from some ECG recordings.

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 into 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. [3] described a successful use of SVMs applied to gene expression data for the task of classifying unseen genes. Dehmeshki et al. [7] used SVM for the classification of lung data. Chu et al. [6] 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 [1, 2, 13, 14, 18, 20, 21], where in component wave detection is accomplished by using some other technique. SVM is applied in the present work for the detection of QRS complex, P and T waves in the ECG signal.

2 Support vector machine

SVM is a new paradigm of learning system. The technique of SVM, developed by Vapnik [26], 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 $y_i \in \{-1,+1\}$. For a linearly separable classification problem, the construction of a hyperplane is $\mathbf{w}^T\mathbf{x} + b = 0$ so that the margin between the hyperplane and the nearest point is maximized and can be posed as the following quadratic optimization problem:

$$\min_{\mathbf{w}} \frac{1}{2}(\mathbf{w}^T\mathbf{w}) \tag{1}$$

subject to $y_i((\mathbf{w}^T\mathbf{x}_i)+b \geq 1, \quad i = 1, ..., l.$ (2)

Equation (2) forces a rescaling on (w, b) so that the point nearest to the hyperplane has a distance of $(1/\|w\|)$ [4].

In many practical situations, a separating hyperplane does not exist. To allow for possibilities of violating (2), slack variables, ξ_i are introduced like

$$\xi_i \geq 0, \quad i = 1, ..., l. \tag{3}$$

to get

$$y_i((\mathbf{w}^T\mathbf{x}_i)+b) \geq 1-\xi_i, \quad i = 1, ..., l. \tag{4}$$

The optimization problem now becomes as follows:

$$\min_{\mathbf{w},\xi} \frac{1}{2}(\mathbf{w}^T\mathbf{w}) + C\sum_{i=1}^{l}\xi_i \tag{5}$$

subject to constraints (3) and (4).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. By introducing Lagrange multipliers α_i and using Karush-Kuhn-Tucker theorem of optimization theory [4], the solution is given by;

$$\mathbf{w} = \sum_{i=1}^{l} y_i\alpha_i\mathbf{x}_i \tag{6}$$

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 boundary. All other training examples with corresponding zero α_i values are now rendered irrelevant and automatically satisfy constraint (5) with $\xi_i = 0$.

The hyperplane decision function for the vector $\mathbf{x}$ can be written as follows:

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

By replacing the inner product $(\mathbf{x}^T\mathbf{x}_i)$ with kernel function $K(\mathbf{x}, \mathbf{x}_i)$; the input data are mapped to a higher dimensional space [4]. It is then in this higher dimensional space that a separating hyperplane is constructed to maximize the margin.

3 Algorithm

This section describes an algorithm developed for the detection of QRS complex, P and T waves in simultaneously recorded 12-lead ECG signal. SVM is used as a classifier. Fig. 2 displays the result obtained at each step for record MO1_015 and the results are explained using lead V2.

Step 1: A raw digital 12-lead simultaneously recorded ECG signal of a patient is acquired. Fig. 2(a) shows raw ECG signal of a lead of 12-lead ECG.

Step 2: A 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 [25] 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 [8] is used to remove 50Hz power line interference. Fig. 2(b) displays the filtered ECG signal after removal of power line interference and base line wander.

Step 3: The slope at every sampling instant is calculated to enhance the signal in the region of QRS complex. These slope values are then normalized. This way a set of twelve normalized slope curves is obtained, one for each lead. The slope is used as an important criterion because slope of the signal is much more in the region of QRS complex than in the other region as displayed in Fig. 2(c).

Step 4: The input to the support vector classifier is a set of vectors $\mathbf{x}_i$ containing twelve normalized slope values, one from each of the twelve leads of ECG at a particular sampling instant. During the training of SVM, a sliding window is moved forward by one sampling instant over the normalized slope curves. When the window lies in the region of QRS complex, the desired output of the SVM is set to 1 and when it lies in the other region, the desired output is set to -1. The SVM is trained on a set of training data covering wide variety of ECG signals with different morphologies of QRS complex picked from CSE ECG database.

Step 5: On testing, normalized value of twelve slopes, 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 slopes, 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 QRS region and -1 for the remaining region. The 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 as detected by SVM are shown by the curve Fig. 2(d).

Step 6: The QRS complexes detected by the SVM are removed from the ECG signal by replacing them by a base line. The ECG signal without QRS complexes is displayed in Fig. 2(e).

Step 7: The ECG signal without QRS complexes (Fig. 2(e)) is further processed for the detection of T waves. The three main steps, namely slope calculation and normalization (step 3), training of SVM (step 4), and testing of SVM (step 5) are repeated for the detection of T waves. Slope is used as a important discriminating feature because slope of the ECG signal is more in the region of T waves than in the other region as shown in Fig. 2(f). The locations of the T wave are shown by the curve Fig. 2(g).

Step 8: The T waves are removed from the QRS-less ECG signal shown in Fig. 2(e), by replacing the T waves by a base line for further processing i. e. for the detection of P waves. The signal displayed in Fig. 2(h) is without QRS complex and T waves.

Step 9: Again step 3 to step 5 are repeated on QRS and T waves removed ECG signal for the detection of P waves. Slope is again used as a important discriminating feature because slope of the signal is much more in the P wave region than in the other region of the signal as displayed in Fig. 2(i).

Step 9: Fig. 2(j) shows the obtained locations of the P wave. SVM is thus used as a classifier for the detection of ECG components.

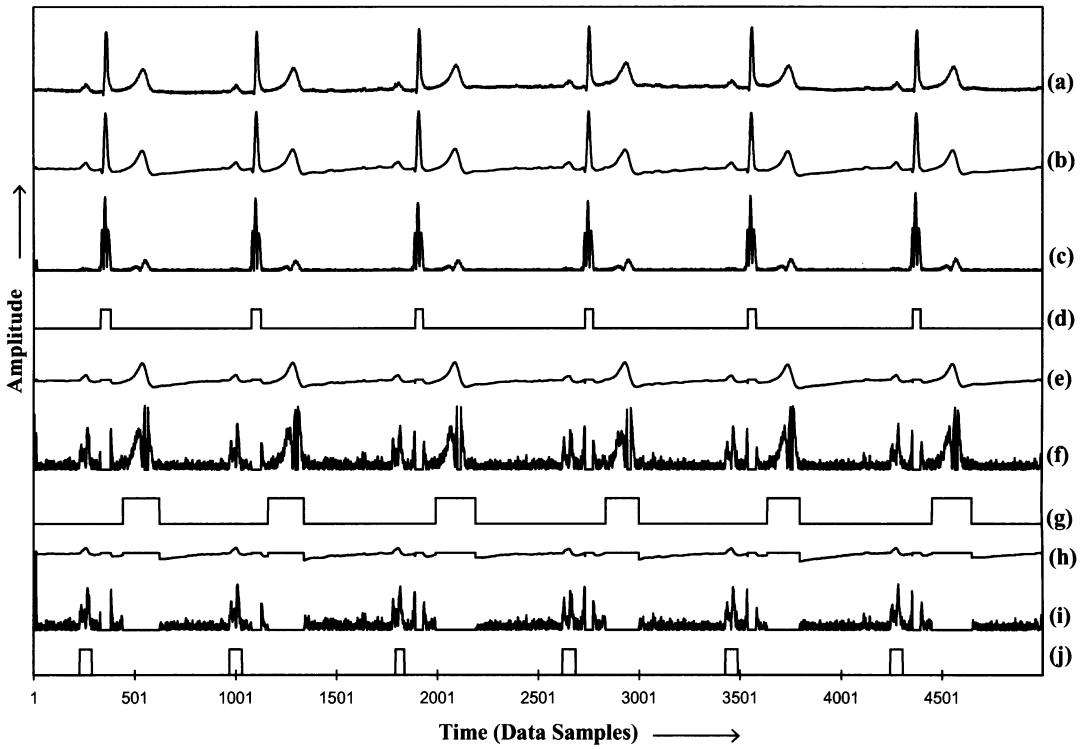

Fig. 2 Results obtained at each step of the algorithm, (a) Raw ECG, (b) Filtered ECG, (c) Slope of the ECG signal, (d) QRS locations, (e) ECG signal without QRS, (f) Slope of the ECG signal without QRS, (g) T wave locations, (h) ECG signal without QRS and T waves, (i) Slope of the ECG signal without QRS and T waves, (j) P waves locations.

4 Implementation

Implementation of SVM for the detection of QRS complex, T-waves, and P waves in ECG signal is done by using LIBSVM software [5]. 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 [19].

In the present problem of QRS complex, T and P wave 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 [17]. The type of kernel function, its parameters and margin-loss trade-off C should be

determined to find the optimal solution. It is not known beforehand which values of C, the type of kernel function and its parameter are the best for this problem of ECG pattern recognition. The objective is to obtain best kernel function, its parameters and margin-loss trade-off C so that the classifier can accurately predict unknown data (testing data). In the present study four- fold cross- validation approach is used to select the kernel function, to tune its parameters and margin-loss trade-off C [12]. 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 best generalization performance is achieved with the sigmoid kernel function. There are three free parameters namely γ, ν of the sigmoid kernel function and margin-loss trade-off C, that should be determined to find the optimal solution. The optimum values of these parameters are displayed in Table 1.

Wave	C	γ	ν	Training instances	Cross validation accuracy
QRS Complex	2	2	-0.1	9877	99.34%
T wave	2	3	-0.1	9460	99.01%
P wave	2	3	-0.1	8220	96.23%

Table 1 Optimum value of various parameters with the cross validation accuracy

5 Results and Discussions

The validation of the proposed algorithm for QRS complex detection is done using 50, simultaneously recorded, 12-lead ECG records of dataset 3 of CSE multi-lead measurement library [27]. This library contains original 12-lead simultaneous ECG recordings covering a wide variety of pathological cases. It should be noted here that the CSE library contains a high percentage of pathological variety of ECG signals, and there are some wave components 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 algorithm, when tested using the optimum values of the parameters gives detection rate of 99.8% for QRS complex, 92.13% for T waves, and 83.58% for P-waves. The algorithm is capable of detecting all the types of QRS, P and T-wave morphologies. It also detects the P and T wave after the last detected QRS complex. The comparison of other algorithms with the proposed algorithm using SVM for QRS detection tested on the CSE ECG database is given in Table 2. Table 3 displays comparison of the proposed algorithm for P and T wave detection with other algorithms.

Fig. 3 illustrates the effectiveness of the algorithm for the detection of QRS complex, P and T waves. The performance of the algorithm for the record MO1_119 is displayed in which there is a wide variety of QRS complex, P and T wave morphologies. In leads L2, L3, and aVF, T-waves are taller than the QRS complexes. In lead aVR, P and T-waves are inverted and in lead aVL, the amplitude of P and T-waves is very small. The SVM successfully detects all these QRS complexes, P and T-waves as shown in Fig.3

Reference	Method	Detection rate
Proposed Algorithm	Support vector machine	99.75%
Gritzali[10]	Length and energy transformation	99.60%
Kyrkos et al. [16]	Time recursive Prediction technique	99.00%
Trahanias, and Skordalalkis [23]	Bottom up approach	98.49%
Trahanias [24]	Mathematical morphology	99.38%

Table 2 Comparison of proposed SVM based algorithm with other QRS detection algorithm using CSE database.

Reference	Method	Database used for testing	Limitations
Proposed Algorithm	Support vector machine (12-lead detection)	CSE database	-
Goutas et al. [9]	Digital fractional order differentiation (single-lead detection)	Segments from MIT/BIH database	Not suitable for biphasic T waves
Sun et al. [22]	MMD transform (single-lead detection)	Lead L2,MIT/BIH database, QT database	False detections in biphasic T waves
Gritzali [11]	Length transformation (single-lead / multi-lead detection)	CSE database	Cannot detect P and T waves after the last detected QRS complex

Table 3 Comparison of proposed SVM based algorithm for P and T wave detection with other algorithms

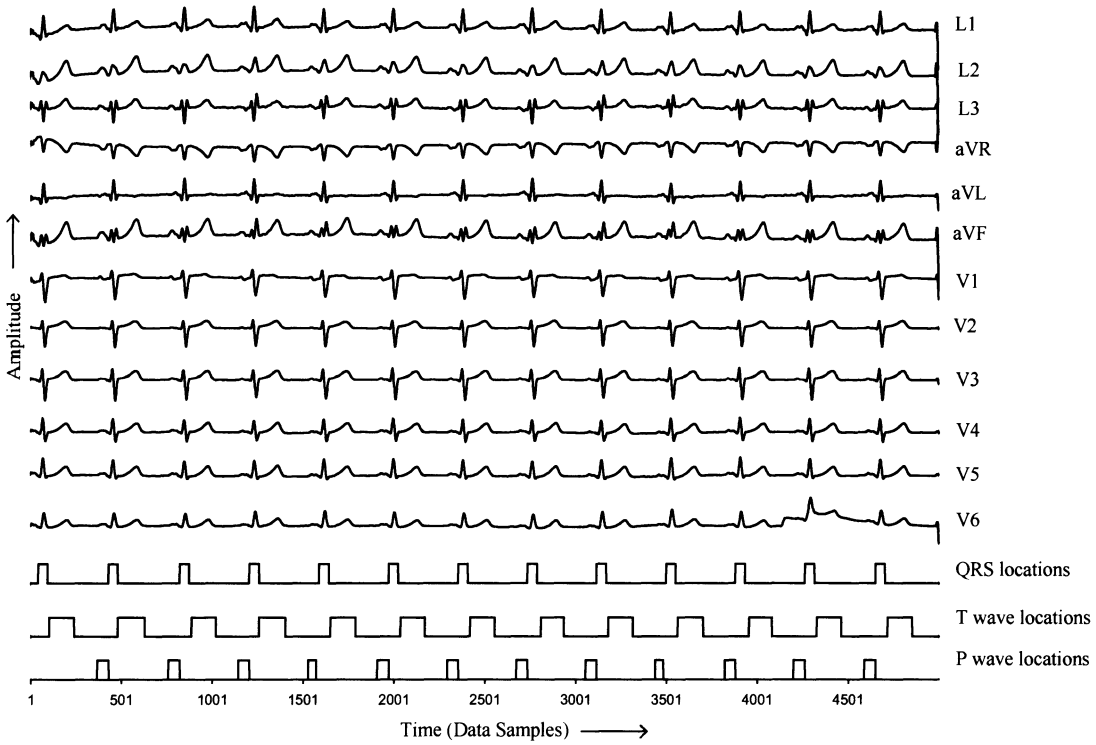

Fig. 3 QRS Complex, P and T-wave detection for record MO1_116 of CSE ECG database

6. Conclusions

This paper presents a new method for the detection of QRS complex, P and T-waves in simultaneously recorded 12-lead ECG signal using support vector classifier. The method has been exhaustively tested using the CSE ECG database covering a wide variety of QRS complex, P and T-wave morphologies. A significant detection rate is obtained. The proposed method accurately detects normal, inverted and biphasic P and T-waves. 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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