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# Identification of QRS complexes in 12-lead electrocardiogram

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**Abstract**

A method for the detection of QRS complexes in 12-lead electrocardiogram (ECG) using support vector machine (SVM) is presented in this paper. Digital filtering techniques are used to remove base line wander and power line interference. SVM is used for the identification of QRS complexes in the processed signal. The performance of the algorithm is evaluated against the standard CSE ECG database. The results indicated that the algorithm achieved 99.75% of the identification rate. The percentage of false positive and false negative is 1.61% and 0.26%, respectively. The performance of the proposed algorithm is found to be better than published results of the other QRS detectors tested on the same database. The proposed method functions reliably even under the conditions of poor signal quality in the ECG data.


*Keywords:* ECG; QRS complex; SVM

## 1. Introduction

Electrocardiogram (ECG) is an important tool, which provides useful information about the 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, 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 the literature. Kohler, Henning, and Orglmeister (2002) described and compared the performance of all these QRS detectors. Recently, few other methods based on pattern recognition (Mehta, Sexana, & Verma, 1996), Hilbert transform (Benitez, Gaydecki, Zaidi, & Fitzpatrick, 2001), wavelet transform (Saxena, Kumar, & Hamde, 2002), neuro-fuzzy approach (Engin, 2004), filtering technique (Israel, Irvine, Cheng, Wiederbold, & Wiederhold, 2005), first derivative (Arzeno, Poon, & Deng, 2006), curve length concept (Paoletti & Marchesi, 2006), moving-averaging incorporating with wavelet denoising (Chen, Chen, & Chan, 2006), etc., are proposed for the detection of QRS complexes. Christov et al. (2006) gave a comparative study of morphological and time-frequency ECG descriptors for heartbeat

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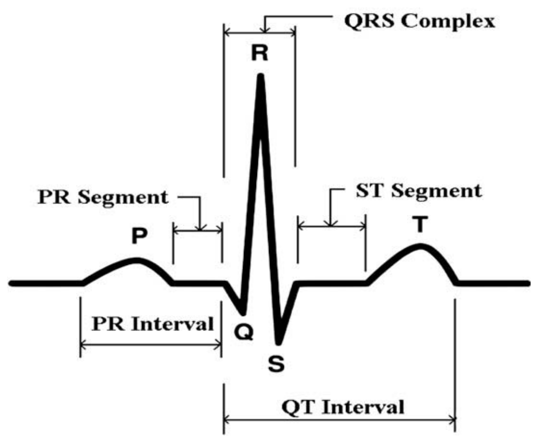


Fig. 1. ECG Signal.

classification. Most of these QRS detectors are single 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 (Gritzali, 1988). 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.

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. (1999) described a successful use of SVMs applied to gene expression data for the task of classifying unseen genes. Dehmeshki, Chen, Casique, and Karakoy (2004) used SVM for the classification of lung data. Chu, Jin, and Wang (2005) 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 Roig, Galiano, Chorro-Gasco, and Cebrian, 2000; Jankowski et al., 2003; Jankowski and Oreziak, 2003; Osowski, Hoai, and Markiewicz, 2004; Acir, 2005; Song, Lee, Cho, Lee, and Yoo, 2005; Acir, 2006, 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 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. Implementation of SVM for a given problem of QRS detection is discussed in Section 3. The experimental results and discussion of the proposed algorithm are provided in Section 4.

## 2. Support vector machine

SVM is a new paradigm of learning system. The technique of SVM, developed by Vapnik (1998), 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 support vectors.

Consider a set of training examples $(\mathbf{x}_1,y_1), \ldots ..,(\mathbf{x}_l,y_l)$, 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:

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

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

Eq. (2) forces a rescaling on (w, $b$) so that the point nearest to the hyperplane has a distance of $(1/\|w\|)$ Burges, 1998.

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

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

to get

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

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 the minimization of the classification error.

By introducing Lagrange multipliers $\alpha_i$ and using Karush–Kuhn–Tucker theorem of optimization theory, 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 $\alpha_i$ 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 $\alpha_i$ values are now rendered irrelevant and automatically satisfy constraint (4) with $\xi_i = 0$.