



Support vector machine-based arrhythmia classification using reduced features of heart rate variability signal

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Summary

Objective: This paper presents an effective cardiac arrhythmia classification algorithm using the heart rate variability (HRV) signal. The proposed algorithm is based on the generalized discriminant analysis (GDA) feature reduction scheme and the support vector machine (SVM) classifier.

Methodology: Initially 15 different features are extracted from the input HRV signal by means of linear and nonlinear methods. These features are then reduced to only five features by the GDA technique. This not only reduces the number of the input features but also increases the classification accuracy by selecting most discriminating features. Finally, the SVM combined with the one-against-all strategy is used to classify the HRV signals.

Results: The proposed GDA- and SVM-based cardiac arrhythmia classification algorithm is applied to input HRV signals, obtained from the MIT-BIH arrhythmia database, to discriminate six different types of cardiac arrhythmia. In particular, the HRV signals representing the six different types of arrhythmia classes including *normal sinus rhythm*, *premature ventricular contraction*, *atrial fibrillation*, *sick sinus syndrome*, *ventricular fibrillation* and *2° heart block* are classified with an accuracy of 98.94%, 98.96%, 98.53%, 98.51%, 100% and 100%, respectively, which are better than any other previously reported results.

Conclusion: An effective cardiac arrhythmia classification algorithm is presented. A main advantage of the proposed algorithm, compared to the approaches which use the ECG signal itself is the fact that it is completely based on the HRV (R–R interval) signal which can be extracted from even a very noisy ECG signal with a relatively high

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accuracy. Moreover, the usage of the HRV signal leads to an effective reduction of the processing time, which provides an online arrhythmia classification system. A main drawback of the proposed algorithm is however that some arrhythmia types such as left bundle branch block and right bundle branch block beats cannot be detected using only the features extracted from the HRV signal.

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1. Introduction

Heart diseases are a major cause of mortality in the developed countries. Many different instruments and methods are developed and being daily used to analyze the heart behavior. One of the relatively new methods to assess the heart activity and to discriminate different cardiac abnormalities is to analyse the so-called heart rate variability (HRV) signal. HRV signal, which is generated from electrocardiogram (ECG) by calculating the inter-beat intervals, is a nonlinear and nonstationary signal that represents the autonomic activity of the nervous system and the way it influences the cardiovascular system. Hence, measurement and analysis of the heart rate variations is a non-invasive tool for assessing both the autonomic nervous system and the cardiovascular autonomic regulatory system. Furthermore, it can provide useful information about the current and/or the future heart deficiencies [1]. Therefore, HRV analysis can be considered as an important diagnostic tool in cardiology.

Several methods have been proposed in the literature for automatic cardiac arrhythmia detection and classification. Some examples of the techniques used include: threshold-crossing intervals [2], neural networks [3–10], wavelet transforms [11], wavelet analysis combined with radial basis function neural networks [12], support vector machines [13], Bayesian classifiers [14], fuzzy logic combined with the Markov models [15], fuzzy equivalence relations [16], and the rule-based algorithms [17]. Most of these studies [2–6, 11–13] are based on the analysis of the ECG signal itself. In most methods, the various features of the ECG signal including the morphological features are extracted and used for classification of the cardiac arrhythmias. This is a time-consuming procedure and the results are very sensitive to the amount of the noise.

An alternative approach would be to extract the HRV signal from the ECG signal first by recording the R–R time intervals and then processing the HRV signal instead. This is a more robust method since the R–R time intervals are less affected by the noise. Different HRV signal analysis methods for cardiac arrhythmia detection and classification were introduced in the past. Tsipouras and Fotiadis [8] proposed an algorithm based on both time and

time–frequency analysis of the HRV signal using a set of neural networks. Their method could only classify the input ECG segments as “normal” or “arrhythmic” segments without the ability to identify the type of the arrhythmia. Acharya et al. [16] employed a multilayer perceptron (MLP) together with a fuzzy classifier for arrhythmia classification using HRV signal. They could classify the input ECG segments into one of the four different arrhythmia classes. In [17], Tsipouras et al. proposed a knowledge-based method for arrhythmia classification into four different categories. The main drawback of their algorithm was the fact that the atrial fibrillation, which is an important life-threatening arrhythmia, was excluded from the ECG database.

In this paper a new arrhythmia classification algorithm is proposed which is able to effectively identify six different and more frequently occurring types of cardiac arrhythmia. These arrhythmias are namely the normal sinus rhythm (NSR), the premature ventricular contraction (PVC), the atrial fibrillation (AF), the sick sinus syndrome (SSS), the ventricular fibrillation (VF) and the 2° heart block (BII). The proposed algorithm is based on the two kernel learning machines of the *generalized discriminant analysis* (GDA) and the *support vector machine* (SVM). By cascading SVM with GDA, the input features will be nonlinearly mapped twice by radial basis function (RBF). As a result, a linear optimal separating hyperplane can be found with the largest margin of separation between each pair of arrhythmia classes in the implicit dot product feature space.

GDA is a data transformation technique which was first introduced by Baudat and Anouar [18]. It can be considered as a kind of generalization to the well-known *linear discriminant analysis* (LDA) algorithm and has become a promising feature extraction scheme [19–24] in recent years. The main steps in GDA are to map the input data into a convenient higher dimensional feature space F first and then to perform the LDA algorithm on the F instead of the original input space. By GDA therefore, both dimensionality reduction of the input feature space and selection of the useful discriminating features can be achieved simultaneously.

SVM, which was first proposed by Vapnik [25], has been considered as an effective classification

scheme in many pattern recognition problems recently [22–24,26,27]. It is often reported that SVM provides better classification results than other widely used methods such as the neural network classifiers [28,29]. This is partly because SVM aims to obtain the optimal answer using the available information and in the same time it shows better generalization ability on the unseen data.

In continue the details of the proposed algorithm for cardiac arrhythmia classification from the HRV signal is presented. Section 2 provides the overall block diagram of the proposed algorithm together with the details of each block. The results of the application of the proposed algorithm to the MIT-BIH arrhythmia database are presented in Section 3. Section 4, compares the results obtained by the proposed algorithm to those obtained by the other previously reported techniques. This is followed by a discussion on the results and the methods. Finally, Section 5 concludes the paper.

2. Materials and methods

2.1. Database

The HRV data used in this work is generated from the ECG signals provided by the MIT-BIH Arrhythmia Database [30]. The database was created in 1980 as a reference standard for serving all those who are conducting a research on the cardiac arrhythmia detection and classification problem [31].

The MIT-BIH Arrhythmia Database includes 48 ECG recordings each of length 30 min with a total of about 109,000 R–R intervals. The ECG signals were band-pass-filtered in the frequency range of 0.1–100 Hz and were sampled with a sampling frequency of 360 Hz. Each of the about 109,000 beats was manually annotated by at least two cardiologists working independently. Their annotations were compared, consensus on disagreements was obtained, and the reference annotation files were prepared [31]. The reference annotation files include beat, rhythm, and signal quality annotations. Due to the lack of the VF data in the MIT-BIH arrhythmia database, which is needed in the current study, the Creighton University Ventricular Tachyarrhythmia Database was added to the MIT-BIH data as the VF arrhythmia class after resampling it at a rate of 360 Hz.

Finally, a total number of 1367 ECG segments each with 32 R–R intervals were selected from the above-mentioned database and used in this work, which contains all six different arrhythmia classes considered in this study. The specialists defined rhythm annotations for each segment were also considered along with the segments.

2.2. The proposed algorithm

The block diagram of the proposed algorithm is demonstrated in Fig. 1. As seen, it comprises the four steps of preprocessing, feature extraction, GDA-based feature reduction and SVM-based arrhythmia classification. In continue, each block is described in more details.

2.2.1. Preprocessing

As a first step, it is necessary to extract the HRV signals from the ECG signals within the database. In general, this process can be affected by many interfering signals such as the mains 50 Hz, the interferences from electromyogram (EMG) signals and also the baseline wandering. The interfering signals are effectively eliminated from the input ECG signal using a 5–15 Hz bandpass filter. Furthermore, the cubic splines are used for baseline approximation, which is then subtracted from the signal [32].

Next, the tachograms are extracted from the filtered ECG signals as follows. Initially, using the Hamilton and Tompkins algorithm [33,34], a point within the QRS complex is detected (QRS point). Afterwards, the main wave of the QRS complex, i.e., the R wave, is identified by locating the maximum absolute value of the signal within the time window [QRS–280 ms, QRS + 120 ms]. The HRV signal is then constructed by measuring the time intervals between the successive R waves (R–R intervals). Plotting the R–R intervals against the time indices provides the so-called tachograms. The tachograms are then divided into small segments each containing 32 R–R intervals and characterized using the database rhythm annotation. It must be noted that the resulting tachograms are sequences of unevenly sampled beat-to-beat intervals. Therefore, for the case of the frequency domain analysis in the forthcoming Section 2.2.2, the cubic spline interpolation method is used at a sampling rate of 4 Hz to produce an evenly sampled data. This resampling procedure

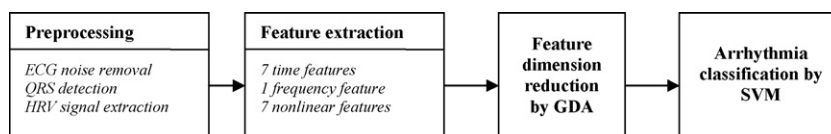


Figure 1 Block diagram of the proposed arrhythmia classification algorithm.

is necessary prior to using the well-known methods of power spectral density (PSD) estimation which are only applicable to the evenly sampled signals.

2.2.2. Feature extraction

The next step in the block diagram is the feature extraction step. In general, the cardiovascular system, hence the HRV signals, demonstrates both linear and nonlinear behavior. Different linear and nonlinear parameters are defined and used for HRV signal description. In this work, a combination of both linear and nonlinear features of the HRV signal is considered. Time and frequency domain features are among the standard linear measures of the HRV signals which are strongly recommended in a special report published by the Task Force of the European Society of Cardiology and North American Society of Pacing and Electrophysiology in 1996 [1]. As in most previous works, these features are used in the current study.

2.2.2.1. Linear analysis: time domain features. Seven commonly used time domain parameters of the HRV signal which are also considered in this work are as follows:

Mean: This refers to the mean value of the 32 R–R intervals within each segment.

RMSSD: This refers to the root mean square successive difference of the 32 R–R intervals in each segment.

SDNN: This refers to the standard deviation of the 32 R–R intervals within each segment.

SDSD: This refers to the standard deviation of differences between the adjacent R–R intervals within each segment.

pNN50, pNN10, pNN5: These refer to the number of successive difference of intervals which differ by more than 50, 10 and 5 ms, respectively, divided by 32, the total number of the R–R intervals within each segment.

2.2.2.2. Linear analysis: frequency domain features. Although the time domain parameters are computationally effective but they lack the ability to discriminate between the sympathetic and parasympathetic contents of the HRV signal [35]. As the most popular linear technique used in the HRV signal analysis, however, the frequency domain analysis of the HRV signal has the ability to discriminate between the two. In fact, it is generally accepted that the spectral power in the high-frequency (HF) band (0.15–0.4 Hz) of the HRV signal reflects the respiratory sinus arrhythmia (RSA) and thus cardiac vagal activity. On the other hand, the low-frequency (LF) band (0.04–0.15 Hz), is related to the baroreceptor control and is mediated by both vagal and sympathetic systems [1,7]. In this work, the ratio of the LF and HF bands power (LF/HF) is used as the frequency domain feature of the HRV signal.

2.2.2.3. Nonlinear analysis. Seven different nonlinear parameters of the HRV signal are used in this work, which are listed and described in continue. **SD1/SD2:** Let us consider the HRV signal as a time series of the R–R intervals which is denoted by $RR(i)$. Now, if each interval $RR(n+1)$ is plotted as a function of the previous interval $RR(n)$, then the resulting plot is known as the Poincaré plot, which is a relatively new tool for HRV signal analysis. A useful feature of this tool is that it does not require the HRV to be considered as a stationary signal [36]. Poincaré plot can be seen as a graphical representation of the correlation between the successive R–R intervals. This plot can be quantitatively analyzed by calculating the standard deviations of the distances of the points $RR(i)$ from the lines $y = x$ and $y = x + 2RR_m$, where RR_m is the mean of all $RR(i)$ values. These standard deviations are denoted by SD_1 and SD_2 , respectively. In fact, SD_1 represents the fast beat-to-beat variability, while SD_2 describes the relatively long-term variability in the HRV signal [37]. The ratio SD_1/SD_2 is usually used to describe the relation between the two components.

ApEn: Approximate entropy (ApEn) is a measure of unpredictability of the fluctuations in a time series, and reflects the likelihood that particular patterns of observations will not be followed by additional similar observations. A time series containing many repetitive patterns has a relatively small ApEn, while a more complex (i.e., less predictable) process has a relatively high ApEn [38]. We have used the method proposed in [39] for calculating ApEn for each HRV segment by setting the pattern length $m = 2$ and the measure of similarity $r = 20\%$ of the standard deviation of the segment, as proposed in [40].

SpEn: Similar to ApEn, spectral entropy (SpEn) quantifies the complexity of the input time series (HRV segment) but in the frequency domain [41]. The Shannon's channel entropy is used in this work to obtain an estimate of the spectral entropy of the process as

$$H = - \sum_f p_f \log(p_f) \quad (1)$$

where p_f is the value of the probability density function (PDF) of the process at frequency f [7]. Heuristically, the entropy can be interpreted as a measure of uncertainty about the event at frequency f .

LLE: Lyapunov exponent is a measure of how fast two initially nearby points on a trajectory will

diverge from each other as the system evolves, hence providing useful information about the system's dependency on initial conditions [42]. A positive Lyapunov exponent strongly indicates that the system is a chaotic one [43,44]. Although an m -dimensional system has m Lyapunov exponents, however, in most applications it is sufficient to obtain only the average largest Lyapunov exponent (LLE) as follows. First, a starting point is selected within the reconstructed phase space of the system and then all those points residing within a neighborhood of a predetermined radius ε from the starting point are determined. Next, the mean distances between the trajectory of the initial point and the trajectories of the neighboring points are calculated as the system evolves. By plotting the logarithm of the above-mentioned mean values against the time index, the slope of the resulting line provides the LLE. To remove the dependency of the calculated values to the starting point, this procedure is repeated for different starting points and the average is taken as the average LLE [45] used as a feature to quantify the chaotic behavior of the HRV signal.

DFA: The detrended fluctuation analysis (DFA) is a useful parameter to quantify the fractal scaling properties of the R–R intervals. This technique is a modification to the root-mean-square analysis of the random walks applied to nonstationary signals [46]. For the detrended fluctuation analysis of the HRV signal, the R–R time series (of total length N) is integrated using the following equation first:

$$y(k) = \sum_{i=1}^k (RR(i) - RR_m) \quad (2)$$

where $y(k)$ is the k th value of the integrated series, $RR(i)$ is the i th inter-beat interval and RR_m is the average inter-beat interval over the entire series. Then, the integrated time series is divided into windows of equal length n . In each window of length n , a least-square line is fitted to the R–R interval data (representing the trend in that window). The y coordinate of the straight line segments are denoted by $y_n(k)$. Next, the integrated time series within each window n is detrended. The root-mean-square fluctuation of this integrated and detrended time series is then calculated as

$$F(n) = \sqrt{\frac{1}{N} \sum_{k=1}^N [y(k) - y_n(k)]^2} \quad (3)$$

This computation is repeated over all window sizes (time scales) to obtain the relationship between $F(n)$ and the window size n (i.e., the number of beats within the observation window). $F(n)$ is usually plotted against the observation win-

dow size n on a log–log scale. Typically, $F(n)$ increases with the window size. The fluctuation in small windows can be characterized by a scaling exponent (self similarity factor), α , which represents the slope of the line relating $\log F(n)$ to $\log n$ [35].

Sequential trend analysis: Sequential trend analysis of the HRV signal evaluates not only the sympathetic–parasympathetic balance but also provides the spectral analysis of the signal without the necessity to consider the signal is stationary. To perform the sequential trend analysis, it is necessary to plot $\Delta RR(n)$ against $\Delta RR(n+1)$ and divide the plane into four quadrants. The points located in the $+/+$ quadrant indicate two consecutive interval increments, which means the heart rate is decreasing and the ones in the $-/-$ quadrant indicate two consecutive interval decrements, which means the heart rate is increasing. In this work the density of the points within the $-/-$ and $+/+$ quadrants are used as two features that measure the sympathetic and parasympathetic activities, respectively [36].

2.2.3. Feature dimension reduction by GDA

Having defined the above-mentioned linear and nonlinear features, due to the large variations in the HRV patterns of various arrhythmia classes, there is usually a considerable overlap between some of these classes in the feature space. For example, the SSS and NSR classes demonstrate a large overlap with each other making it difficult to distinguish between the two. In this situation, a feature transformation mechanism that can minimize the within-class scatter and maximize the between-class scatter will be very beneficial. GDA [18] is such a transform which is employed in this work.

GDA is a nonlinear extension to the ordinary LDA. The input training data is mapped by a kernel function to a high-dimensional feature space, where different classes of objects are supposed to be linearly separable. The LDA scheme is then applied to the mapped data, where it searches for those vectors that best discriminate among the classes rather than those vectors that best describe the data [47]. In fact, the goal of the LDA is to seek a transformation matrix that maximizes the ratio of the between-class scatter to the within-class scatter. Furthermore, given a number of independent features which describe the data, LDA creates a linear combination of the features that yields the largest mean differences of the desired classes [48]. As a result, if there are N classes in the data set, the dimension of feature space can be reduced to $N - 1$.

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