Arrhythmia classification based on multi-domain feature extraction

Li Yin, Fumin Chen, Qi Zhang, Xu Ma
State Key Laboratory for Manufacturing Systems Engineering, Xi’an Jiaotong University, Xi’an 710049, China
missyin@stu.xjtu.edu.cn

Abstract: Arrhythmia is a common abnormality of cardiac electrical activity. Arrhythmia classification has enormous significance for the clinical diagnosis of cardiovascular diseases. In this study, a method of multi-domain electrocardiogram feature extraction was put forward as to classify arrhythmia precisely. The RR intervals were extracted as time domain feature. The fifth level approximation coefficients of wavelet decomposition were adopted to represent frequency domain feature. Besides, the sample entropy values of six wavelet coefficients were employed as nonlinear feature. These three features were fed to classifier for automated diagnosis. Furthermore, ten-fold cross-validation scheme was adopted to train and test classifier whose parameters were optimized by genetic algorithm. In this study, eight classes of the most frequently occurring arrhythmia from MIT-BIH arrhythmia database were validated. The result turned out that the SVM classifier yields an average accuracy of 99.70%. Compared with the existing methods, the proposed method shows better results.

1. Introduction
Arrhythmia refers to the abnormal rhythm or frequency of the heart beat caused by the disorder in the origin or conduction of cardiac activities. Many cardiovascular diseases are often accompanied by arrhythmia at the beginning of the diseases, and severe arrhythmias can endanger the lives of patients. Therefore, detecting arrhythmia is of great significance to prevent heart disease and sudden cardiac death [1]. Electrocardiogram (ECG) can reflect the periodicity of cardiac activity, each cycle of which corresponds to a heartbeat, called a beat. The type of beat is a significant evidence for detecting cardiovascular diseases [2]. On account of various arrhythmia types and ever-changing ECG waveforms, the automatic classification for ECG beats, especially for ECG monitoring generating a large amount of data, can dramatically decrease the workload of doctors so as to improve the diagnostic efficiency.

For the automatic classification of arrhythmias, feature extraction is a critical step. Many methods have been put forward in the past. Generally, traditional approaches are usually based on time-domain features including heartbeat intervals, duration (QRS, QT, PR, etc.) and amplitude. Due to the complexity of ECG waveform and easy to be interfered, the accuracy of pure time domain feature extraction was low, resulting in inaccuracy of classification [3-5]. Providing time and frequency representation of signals, wavelet analysis is applicable to non-stationary signals. In recent years, it has been widely used as an effective tool to classify arrhythmia [6-8]. Other nonlinear features have been applied to the ECG feature extraction process. For example, Li et al. [9] characterized the signal using approximate entropy of each wavelet packet decomposition’s frequency band. Kamath compared the differences between the average Teager energy of ECG beats in frequency and time domains [10].
Higher order spectral (HOS) was also considered as an effective feature to distinguish different beats [11,12].

Although the above methods have achieved good results, they just combined features in frequency and time domains or used a single non-linear feature, while multi-domain feature can more fully reflect the complex characteristics hidden in ECG signals [13]. In consequence, a multi-domain feature extraction method, which combined time and frequency domains as well as nonlinear feature was presented in this study, namely RR intervals, the approximation coefficients of 5-level wavelet decomposition and the sample entropy of each sub-band of wavelet decomposition were combined as feature vector finally input into the classifier to realize automatic classification of arrhythmia.

2. Methods

The flow of arrhythmia classification is displayed in Fig.1, and the details will be explained in the subsequent paragraphs.

![Flow diagram of arrhythmia classification](image)

**Fig.1 Flow diagram of arrhythmia classification**

2.1. MIT-BIH arrhythmia database

Experimental data is from MIT-BIH arrhythmia database containing 48 ECG records from 47 patients. Each record also includes two leads. The first is MLII contained by every record, and it is one of the most commonly used leads for diagnosing heart disease. MLII provides the ECG signals for experiment [14]. Tab.1 provides a certain number of eight arrhythmia beat types and their numbers

| Class                          | Symbol | Number |
|-------------------------------|--------|--------|
| Normal beat                   | N      | 20000  |
| Paced beat                    | /      | 6900   |
| Left bundle branch block beat | L      | 7018   |
| Fusion of ventricular and normal beat | F | 750   |
| Atrial premature beat         | A      | 2566   |
| Right bundle branch block beat| R      | 6943   |
| Ventricular flutter wave      | !      | 472    |
| Premature ventricular contraction | V  | 6734   |
| Total                         |        | 51383  |

2.2. Preprocessing

ECG signal is a very weak biological signal. The wavelet threshold method used in literature [15] was adopted to denoise the noise mixed into the signal during the acquisition process of signals. The QRS complex detection of the denoised ECG signals was performed using a wavelet transform based method proposed by Li, searching for the zero crossing point between the maximum and minimum pairs of the
wavelet transform modulus in a certain scale or several scales, namely the R-wave peak point [16]. 165 sampling points after the R point and 95 sampling points before the R point, including the R point itself, namely a total of 261 sampling points formed a waveform segment as a beat for subsequent analysis. Fig.2 displays the waveform of single beat randomly selected from each type of arrhythmia after preprocessing.

2.3. Feature extraction

(1) RR intervals

RR interval a kind of effective time-domain feature refers to the time interval between adjacent beats. Making use of the positioned R point, the following four RR intervals were obtained for each beat: Pre_RR, the duration from the occurrence of previous R point to the current R point; Post_RR: the time duration from the occurrence of current R point to the next R point; Local_RR: average of the first 10 Post_RR intervals of the current R point; Ave_RR: mean of all Post_RR intervals for the first 5 minutes of the current R point [17].

(2) Approximation coefficients

With multi-resolution properties, wavelet transform can reflect the time-frequency characteristics of non-stationary signals [8]. The db6 wavelet base was chosen to carry out 5-level decomposition of the beats obtained above.18-dimensional approximation coefficients was selected as the frequency domain feature, for the reason that it can better reflect the general law of the beats.

(3) Sample entropy

Sample entropy (SamEn) measures the complexity of time series by measuring the probability of producing a new pattern in the signal. Namely the greater the chance that the new pattern generates, the greater complexity of the series will become. SampEn was applied to diagnose pathological conditions and assess complexity of physiological time series [18-20]. Therefore, the sample entropy of six wavelet coefficients was taken as nonlinear feature. The algorithmic steps for SampEn are as follows [18]:

Suppose a time series of length N a(n)={a(1),a(2),...,a(N)} and a set of m-dimensional vectors \( Y(i)=[a(i),a(i+1),...,a(i+m-1)] \), \( i=1,2,...,N-m+1 \). And \( d[Y_{m+1}(j),Y_{m+1}(i)] \) represents the maximum of the difference’s absolute value between the corresponding elements where \( j \neq i \). Then SampEn is expressed as:

\[
\text{SampEn} = -\ln \frac{A}{B}
\]

Where A is the number of vectors with dimension \( m+1 \) that satisfy the condition \( d[Y_{m+1}(j),Y_{m+1}(i)] < r \), and B is the number of vectors with dimension \( m \) that satisfy the condition \( d[Y_m(j),Y_m(i)] < r \).

Parameter ‘r’ called similar tolerance, ‘m’ called embedding dimension and usually the ‘m’ has a value of 2 and ‘r’ equals 0.2 times of the target sequence’s standard deviation.

(4) Feature combination
The 4-dimensional RR intervals, the 18-dimensional wavelet approximation coefficients and the 6-dimensional sample entropy obtained by the above were combined into 28-dimensional feature vector. They were randomly selected from each type of ECG beats. As is shown in Fig.3, the feature vectors of different types of beats are distinguished from each other.

2.4. Classification and evaluation
The 28-dimensional feature vector obtained above was fed into SVM classifier with radial basis function (RBF) as kernel function to get classification results. All classification results can be divided into four types: TN (True Negative), FN (False Negative), TP (True Positive), FP (False Positive). The following three statistical indicators are adopted to assess the classification performance [21]:

- Positive Predictive Accuracy, namely Accuracy = TP/(TP+FP) ×100 %;
- Specificity = TN/(TN+FP) ×100 %;
- Sensitivity = TP/(TP+FN) ×100 %.

3. Results and Discussions
Adopting the method proposed in the previous section, after ECG signal was preprocessed, all beats were decomposed into 5 levels by db6 mother wavelet, and the 18-dimensional approximation coefficients were applied as the frequency domain feature. The sample entropy of the six sub-bands obtained by wavelet decomposition was calculated as nonlinear feature. In addition, 4 RR intervals were taken as time domain feature. These three features constituted a 28-dimensional feature vector. After being normalized, the vector was fed to SVM-RBF for classification. Two parameters of SVM-RBF, namely the kernel parameter δ and penalty factor C optimized by genetic algorithm(GA) exert a huge impact on the performance of the classifier [23]. Ten-fold cross-validation scheme was adopted to train and test the classifier whose overall performance was evaluated by the mean of evaluation indicators in 10 folds.

![Fig.3 Feature vectors of eight types of beats](image)

![Fig.4 Three indicators of SVM-RBF in ten folds](image)
The performance of SVM-RBF in each cross-validations is shown in Fig.4. It can be observed that three indicators of SVM-RBF are all above 99.6% in each fold. With \( C = 15.2972, \delta = 16.0635 \), it yields an average sensitivity, specificity and accuracy of 99.68%, 99.96% and 99.70%, respectively. Fig.5 shows the fitness curve of GA.

Besides the results of each fold, the classification results for each arrhythmia type are also important. Tab.3 provides the mean values of the three indicators of 10 folds for each type of arrhythmia by SVM-RBF classifier. Fig.6, the histogram of the data in Tab.3, provides the classification results for eight types of arrhythmia. It can be seen that the three indicators of all types are superior to 95%, especially three indicators of ‘N’, ‘R’, ‘L’ and ‘/’ more than 99.9%.

Tab.3 Classification result for eight types of beats

|         | N     | V     | R     | L     |  /    | A     | F     | !     |
|---------|-------|-------|-------|-------|-------|-------|-------|-------|
| Average accuracy(%) | 99.9584 | 98.5641 | 99.9169 | 99.9357 | 99.9129 | 98.9867 | 98.3336 | 99.7778 |
| Average sensitivity(%) | 99.9410 | 99.2318 | 99.9321 | 99.9156 | 99.9036 | 99.2584 | 95.1422 | 96.6690 |
| Average specificity(%) | 99.9484 | 99.7874 | 99.9871 | 99.9896 | 99.9841 | 99.9507 | 99.9727 | 99.9977 |

Fig.6 Histogram of classification results for 8 types of arrhythmia beats
Tab.4 summarizes the comparison among the proposed method and several other methods using MIT-BIH database. It is obvious that the arrhythmia classification method proposed in this study yields better accuracy. Furthermore, it can also classify eight types of arrhythmia.

| Literature      | Features              | Classifier   | Classes | Accuracy | Sensitivity | Specificity |
|-----------------|-----------------------|--------------|---------|----------|-------------|-------------|
| Martis [6]      | DWT, ICA              | PNN          | 5       | 99.28%   | 97.97%      | 99.83%      |
| Li [10]         | approximate entropy   | SVM-RBF      | 5       | 97.78%   | /           | /           |
| Kamath [11]     | Teager energy         | fuzzy C-means clustering | 5 | 98.83%   | 98.83%      | /           |
| Elhaj [23]      | PCA, DWT, ICA, HOS    | NN           | 5       | 98.90%   | 98.91%      | 97.85%      |
| Alickovic [24]  | statistical features of DWT | Random forest | 7 | 99.33%   | /           | /           |
| Proposed        | RR intervals, DWT, SampEn | SVM-RBF        | 8       | 99.70%   | 99.68%      | 99.96%      |

4. Conclusion
A multi-domain feature combination method was proposed: four RR intervals for time domain, approximation coefficients of 5-layer wavelet decomposition in frequency domain and approximate entropy of each wavelet coefficient for nonlinear feature. It can classify eight arrhythmia types in MIT-BIH database effectively, with an average accuracy of 99.70%.

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