Diagnosis of AF Based on Time and Frequency Features by using a Hierarchical Classifier

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Abstract

Early diagnosis of Atrial Fibrillation (AF) could be benefited from automatic analysis of a short single-lead ECG recording that can be collected easily by a portable device. Due to the limitations of both quantity and quality of the signal, it is challenging to distinguish AF from a broad taxonomy of rhythms. This paper presents a new method which classifies the recordings of single lead ECGs by combined time and time-frequency features. The time features of a recording are represented by some characteristics of its RR intervals and Poincare plot, while the time-frequency features are extracted from its representative beat waveforms by Matching Pursuits algorithm. A set of methods are adopted in the process to eliminate the effects of noise. With the features extracted, a hierarchical classifier is trained based on the CinC Challenge 2017 dataset to classify the recordings into four classes: normal sinus rhythm, AF, other rhythm and too noisy to classify. The final score of our work in the CinC Challenge 2017 is 0.78.

1. Introduction

Atrial Fibrillation, considered the most common sustained cardiac arrhythmia, has become a growing and serious global health problem [1]. The early diagnosis of AF is still a problem, because it may be asymptomatic and episodic [2]. Currently, the emerging lightweight, unobtrusive and low-cost single-lead ECG monitoring technology creates opportunities for solving this problem [3]. In view of the huge volume of data to be produced, automatic technologies capable of classifying a variety of cardiac rhythms is necessary for a practicable system.

Two categories of AF detection methods, the atrial activity analysis-based and the ventricular response analysis-based, catch most of research interests. The atrial activity analysis-based methods utilize the absence of P waves or the presence of f waves for a diagnosis [4–6]. The performance of this kind of method highly depend on the signal quality, which is hard to be guaranteed in the practice. While the ventricular response analysis-based methods are based on the variability of RR intervals [7, 8]. Although these kind of methods have robust noise resistance, the diagnostic accuracy is inadequate when a wide variety of rhythms need to be dealt with, because the information conveyed by RR intervals is limited.

In this study, we try to classify the short-time single-lead ECG records into four categories: normal sinus rhythm, AF, other rhythm and too noisy to classify. The dataset is from CinC challenge 2017 [9], which is collected by the AliveCor device. As noise contamination and a broad taxonomy of rhythms are two features of this dataset, neither of the methods mentioned above can achieve a satisfied diagnostic accuracy by itself. In view of this, we synthesize both the atrial activity features and ventricular response features in our method. The features for classification are constituted by: (a) time features of RR intervals, representing the ventricular activity, and (b) time-frequency features of representative beat waveform, representing both atrial and ventricular activities. In the process of feature extraction, some methods, such as slide-window energy analysis and signal averaging, are adopted to eliminate the effects of noise.

2. Methods

2.1. Preprocessing

The goal of preprocessing is to eliminate the effects of noise in the signal. The low-frequency noise, or baseline wander, is extracted by a moving averaging filter, and then is subtracted from the original signal. The residual noise

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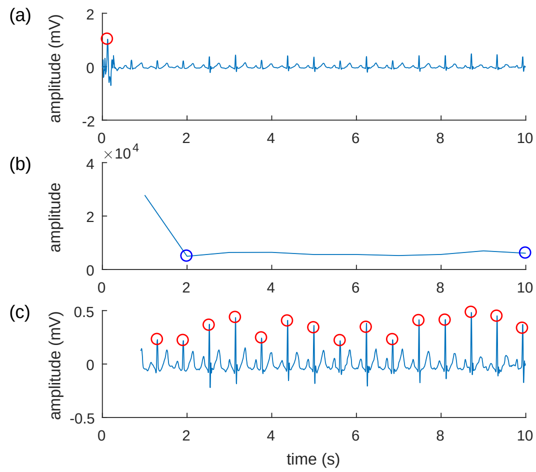

Figure 1. Effects of noise in the transition period on the R peaks detection of Pan-Tompkins algorithm. (a) An ECG record with noisy transition part. (b) The sliding window energies of the record. (c) The signal with noisy transition part cut away. Red circles represent detected R peaks by using Pan-Tompkins algorithm. Blue circles represent the midpoints of the first and last remaining windows respectively.

is further reduced by using wavelet transform denoising [10]. Even after this process, some noise still remains in the signal and disturbs the subsequent analysis. In particular, noise with a high energy in the transition part of an ECG signal will dramatically distort the performance of Pan-Tompkins algorithm [11] which is widely used to detect R peaks in ECG. An intuitional example is shown in Fig. 1(a), where the high noise peak prevents the algorithm from detecting the real R peaks in the main body of the signal.

To solve this problem, we design a simple method based on sliding window energies to cut away the noisy transition period. The window size in our design is 2 seconds, which is wide enough to prevent the energy wave from fluctuating drastically at R peaks. Adjacent windows have an overlap of 1 seconds with each other to achieve a higher resolution. Our method tries to find the first window whose energy is not higher than the median of the subsequent windows. If the window exists, its preceding windows are regarded too noisy and cut away. As shown in Fig. 1, this method effectively improves the performance of Pan-Tompkins algorithm on signals with a noisy transition part.

2.2. Representative beats of a record

A representative beat of a record is the average of some kind of heartbeat waveforms in the records. The representative beat has many good features: 1) it is relevant to a wide variety of cardiac diseases; 2) it has good resistance against the noise; 3) it is easier to handle than the original beats, because typically only one or two kinds of beats appear in a short record ($\leq 60s$). In this study, we use representative beats to derive some features for the classification of cardiac rhythms.

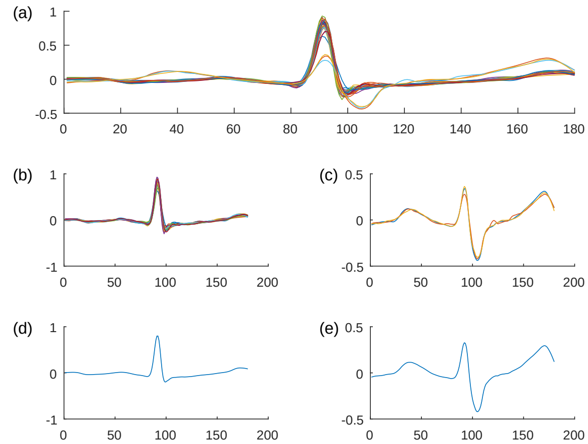

Figure 2. Original beats, grouped beats and representative beats of a record. (a) Original beats. (b) Beats of group 1. (c) Beats of group 2. (d) Representative beat of group 1. (e) Representative beat of group 2.

The first step to obtain the representative beats of a record is extracting all beats in the record. We set a beat as a segment of the ECG with midpoint at the R peak and span of 0.6s. Given the position of R peaks, it is straightforward to extract the beats. As mentioned above, the Pan-Tompkins algorithm is used in our study to detect the R peaks.

With the beats in a record extracted, we group them based on their Pearson correlation coefficients between each other. Compared with Euclidean distance, Pearson correlation coefficient appears to have a stronger noise resistance. Let $P_{i,j}$ denote the Pearson correlation coefficients between beat i and beat j, we define the distance between these two beats as $D_{i,j} = 1 - P_{i,j}$. Based on the distance matrix, the DBSCAN algorithm [12] is used to group these beats. The two parameters, namely $MinPts$ and Eps, of the DBSCAN algorithm is set to 2 and 0.1 respectively in our implementation.

After the beats grouped, the representative beat of each group is obtained from averaging of all beats in the group. An example of the representative beats extraction is shown in Fig. 2. This record has two distinctly different representative beats, which is generally a mark of arrhythmia.

A noteworthy fact is that a fraction of signals in the database of CinC challenge 2017 are inverted, which will affect the R peak detection and, further, the beat extraction. In our study, we design a method to check if a record is inverted based on the representative beats. Firstly, a reference beat dictionary is constructed from representative beats of a subset of the database, where the inverted beats are reversed manually. Then, for each record to be deal with, two sets of representative beats are extracted respectively from the original signal and its revered version. Finally, the set, as well as its corresponding signal, with a higher maximum Pearson correlation coefficient between its beats and the beats in the reference dictionary is regarded as non-inverted.

2.3. Time features of RR intervals

Features of RR intervals constitute an important part of our feature set for the rhythm classification. Such features in our study can be further divided into two categories: characteristics of RR intervals and characteristics of Poincare plot. They are all extracted from the time field as listed in Table 1. The standard deviation of RR intervals is normalized as follows:

$$nSTD := \frac{1}{\mu}\sqrt{\frac{1}{N}\sum_{i=1}^{N}(I_i - \mu)^2}$$

, where μ is the mean RR interval of the record, I_i is the ith RR interval of the record. The characteristics of Poincare plot are extracted according to the study of Park et al. [8]. For a stronger noise resistance, we also add the median stepping increment of inter-beat intervals to our feature vector.

Table 1. List of RR intervals features.

Feature type	Feature name
Characteristics of RR intervals	Maximum Minimum Median Normalized standard deviation
Characteristics of Poincare plot	Number of clusters Mean stepping increment Median stepping increment Dispersion of points around diagonal line

Table 2. List of time-frequency features of a record.

Feature name	Feature size
MP coefficients of 1st representative beats	30
MP coefficients of 2nd representative beats	30
MP residual of 1st representative beats	1
MP residual of 2nd representative beats	1

2.4. Time-frequency features of beat waveforms

To overcome the limitation of RR interval features, features of beat waveforms are incorporated in our study. In view of the nonstationarity of ECG signals, time-frequency analysis is especially suitable for the feature extraction. We extract these features from the representative beats by using the Matching Pursuits (MP) algorithm, which have been proved effective to extract the time-frequency features of beat waveforms [13]. Most of the ECG records as stated above have only one or two representative beats. Records with more than two representative beats are very few and mostly a result of noise contamination. Consequently, at most two representative beats will be analyzed to extract the time-frequency features.

To use the MP algorithm, a dictionary is needed to provide unitary waveforms for the heartbeat approximations. Typically, an over-complete dictionary, such as wavelet packets, is used. However, the coefficients of MP algorithm based on such a dictionary are too many (about 200 for beats in our study) to constitute a compact feature vector. Therefore, we build a small dictionary with the top-30 unit waveforms ranked according to the average l^1 norm of their coefficients across the representative beats of a set of normal sinus rhythm records. With this dictionary, the representative beats of the two biggest beat groups in each records are decomposed by the MP algorithm. The produced coefficients and residuals constitute a part of the feature vector, as shown in Table 2. If only one representative beat exists in a records, the features of the second representative beat will copy that of the first representative beat.

2.5. Classifier structure

Our classifier is in a hierarchical structure: a Noisy-checking Classifier to check if a record is too noisy to classify, and a Rhythm Classifier to classify records by rhythm, as shown in Fig. 3. Both the classifiers are based on the bagged decision trees model. The features for the Noisy-checking Classifier are composed of the remaining proportion after noisy transition part removed, mean Pearson correlation coefficients between beats, and the RR-intervals features stated above. The features for the Rhythm Classifier are composed of the RR-intervals features and the heartbeat time-frequency features stated above.

3. Results and conclusions

The classifier is trained based on the CinC challenge 2017 dataset. Due to the unbalanced data, the records of AF, other rhythms and noisy are oversampled according to the ADASYN method [14]. The trained classifier is evalu-

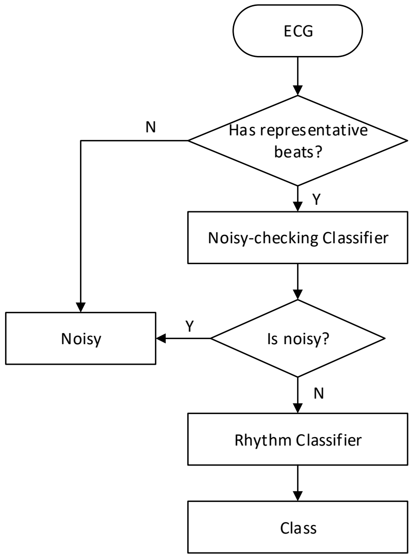

Figure 3. Structure of the classifier.

ated by the test set. The F_1 scores [9] for normal rhythm, AF and other rhythms on 1000 records (27.3%) of the test set are 0.91, 0.80 and 0.73 respectively. The overall score [9] on the whole test set is 0.78. In conclusion, we proposed a new method for AF detection based on short-time single-lead ECGs.

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