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A Combination Method of Improved Impulse Rejection Filter and Template Matching for Identification of Anomalous Intervals in RR Sequences

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Abstract

Anomalous intervals in RR sequences of electrocardiogram (ECG) introduce practical problems in heart rate variability (HRV) analysis, trauma evaluation, and other clinical applications where ECG artifact rejection is important. Impulse rejection filters (IRFs) have been used to identify anomalous intervals. However, traditional IRFs do not consider the influence of non-stationary time series of RR intervals, and cannot effectively identify anomalous intervals caused by ECG morphology changes. This study therefore improves the traditional IRF method, develops an ECG morphology feature-based template matching method, and develops a combination method of improved IRF and template matching for better identification of anomalous intervals in RR sequences. Four methods (IRF, improved IRF, template matching, and the combination method of improved IRF and template matching) are applied to the MIT-BIH arrhythmia database. 43 RR sequences that contain 30368 normal intervals and 2760 anomalous intervals are analyzed. Sensitivity and specificity analyses are performed to quantify identification performance. The sensitivity and specificity values are 86.1% and 87.0% for IRF, 92.3% and 94.9% for improved IRF, 90.7% and 95.5% for template matching, and 98.5% and 99.2% for the combination method, respectively. The results verify that the combination method is suitable for the identification of anomalous RR intervals.

Keywords: Anomalous intervals, Electrocardiogram, Heart rate variability, Impulse rejection filter, Template matching

1. Introduction

Sequences of electrocardiogram (ECG) RR intervals introduce practical problems in heart rate variability (HRV) analysis [1-3], trauma evaluation [4], and other clinical applications [5,6]. The presence of anomalous intervals confounds traditional ECG analysis and leads to erroneous results [1]. Sethuraman et al. reported that anomalous intervals led to inaccurate HRV calculations in approximately 36% of trauma patients, and that these errors can be caused by a single anomalous interval [7]. Therefore, accurately identifying anomalous RR intervals is clinically important.

Several methods for identifying anomalous intervals have been reported and tested [8-11]. Lippman et al. assessed and compared deletion, linear or cubic spline interpolation, and

nonlinear predictive interpolation methods for anomalous interval correction [10]. McNames et al. reported a nonlinear impulse rejection filter (IRF) for removing anomalous intervals [11]. The simulation results by McNames et al. and a subsequent study by Thuraisingham [1] demonstrated the validity of this method. Wen et al. used trend correlation of the heart timing signal to detect anomalous intervals and found that their methods improved power spectral density estimation in HRV analysis [12].

Since the aforementioned methods mainly focus on the time-span information of RR intervals, reasonable identification performance can be achieved with good ECG signal quality. However, these methods do not consider ECG morphology feature changes, resulting in incorrect anomalous identification caused by artifacts or ventricular ectopic beats [13]. In addition, the traditional IRF has two main limitations in practical application [14]. Firstly, it does not consider the influence of non-stationary time series of RR intervals. The anomalous interval is often characterized by a sharp transient. However, if

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there is a non-stationary trend, it is difficult to distinguish an anomalous interval from normal intervals due to their small difference. Secondly, it is difficult to pre-define an appropriate threshold for ECG signals.

Therefore, this study improves the traditional IRF method, and develops an ECG morphology feature-based template matching method, and develops a combination method of the improved IRF and template matching methods for better identification of anomalous intervals in RR sequences.

2. Materials and methods

2.1 Raw RR sequence acquisition

ECG recordings from the MIT-BIH arrhythmia database were used [15]. The database contains 48 ECG recordings, each having two ECG signals of 30-min duration. Four paced recordings (recording numbers 102, 104, 107, and 217, respectively) and a recording from serious arrhythmia (recording number 232) were excluded in this study. For each ECG recording, the first 10 min of the signals were used for method development since it is generally accepted that 5 to 10 min of an ECG signal is adequate to achieve accurate short-time HRV analysis [3,8].

Next, the wavelet transform modulus maxima (WTMM) method was applied to automatically detect the R wave peaks of the ECG recordings [16]. The RR interval calculated from two consecutive R wave peaks was used to form the raw RR sequence. In total, 43 raw RR sequences were constructed with the number of sample points ranging from 506 (recording number 117) to 1131 (recording number 215).

2.2 Classification of anomalous intervals

Raw RR sequences often contain some anomalous intervals caused by the incorrect detection of the R peak [17]. The incorrect detection can be a false negative (FN) if a true beat is undetected due to a low amplitude of the R-wave, or a false positive (FP) if a beat is falsely detected due to a high amplitude of the T-wave or noisy ECG signals. Figures 1(a) and (b) show examples of the two types of anomalous interval. They are referred to as simply FN anomalous interval and FP anomalous interval. The intervals from the sinus beats are referred to as normal intervals (N).

Ectopic beats, including the supra-ventricular ectopic beat (sVEB, originating from the atria or the atrioventricular node) and the ventricular ectopic beat (VEB, originating from the ventricle), can also lead to anomalous RR intervals. These two types of ectopic beat have distinctly different ECG morphologies. Usually, the morphological features of the sVEB are similar to those of a sinus beat, whereas the VEB has higher amplitude of the R peak. To classify the anomalous RR intervals caused by the two types of ectopic beat, the outcome of the automatic R peak detection using the WTMM method was compared with a cardiologist's annotations. If the beats annotated as atrial premature beat (AP), aberrated atrial premature beat (aAP), nodal premature beat (NP), and supra-ventricular premature beat (SP) were correctly detected by the

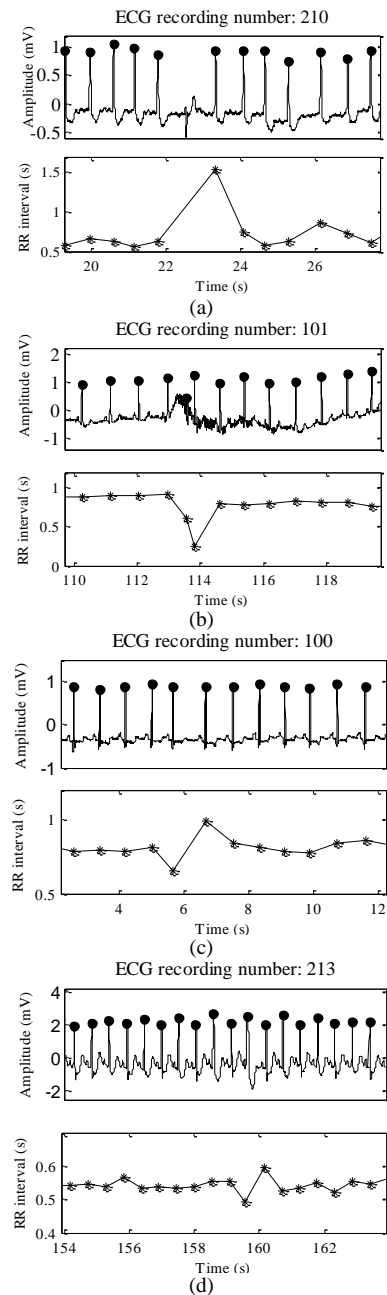


Figure 1. Examples of four types of anomalous interval in ECG RR sequences. (a) FN anomalous interval: a true beat is undetected. (b) FP anomalous interval: a beat is falsely detected. (c) sVEB anomalous interval caused by supra-ventricular ectopic beats, and (d) VEB anomalous interval caused by ventricular ectopic beats. In each sub-figure, the upper panel shows an ECG recording segment, and the lower panel shows the constructed raw RR sequence after the R-wave peaks have been detected.

WTMM method, these corresponding RR intervals were counted as sVEB anomalous intervals. Similarly, if the beats annotated as premature ventricular contraction (PVC) and ventricular escape beat (VE) were correctly detected by the WTMM method, their RR intervals were classified as VEB anomalous intervals. Figures 1(c) and (d) show the examples of sVEB and VEB anomalous intervals.

In total, there were 33128 RR intervals (30368 normal intervals and 2760 anomalous intervals) from the 43 recordings selected from the MIT-BIH arrhythmia database. Among these anomalous intervals, there were 92, 156, 301, and 2211 FN, FP, sVEB, and VEB anomalous intervals, respectively.

2.3 Impulse rejection filter

The IRF was proposed by McNames et al. for removing ectopic beats. Anomalous intervals are detected by the following nonlinear filter [11]:

$$D(n) = \frac{|x(n) - x_m|}{1.483 \times \text{med}\{|x(n) - x_m|\}} \quad (1)$$

where $\text{med}\{*\}$ is a median operator applied to the entire RR sequence, and x_m is the median value of the RR intervals, i.e. $x_m = \text{med}\{x(n)\}$.

A user-specified threshold τ is then selected. If the value of $D(n)$ is larger than the defined τ , the corresponding interval is recognized as an anomalous interval. The threshold τ is usually set to a constant value between 2 and 4.

2.4 Improved impulse rejection filter method

With the traditional IRF method, the selection of threshold τ is arbitrary and impractical, especially when the quality of an ECG recording is poor. To overcome the limitations described in the previous section, the sliding window and signal enhancement techniques are implemented in this study. The details of the improved IRF method are described below.

- (1) The WTMM method is used to detect the R wave peaks of an ECG recording. The raw RR sequence $RR = \{RR_1, RR_2, \dots, RR_N\}$ is then constructed.
- (2) The raw RR sequence is divided into several segments using a sliding window. The segmentation operation will minimize the influence of non-stationary composition in the RR sequence. If sliding window m is too large, the suppression effect for the non-stationary composition is weakened. If m is too small, normal RR intervals can be falsely identified as anomalous intervals. So a sliding window of $m = 50$ was selected for segmentation based on a retrospective analysis of the identification results. Each segmented RR sequence had a 50% overlap with the adjacent one. The initial two segmented RR sequences are:

$$R_1 = [RR_1 \ RR_2 \ \dots \ RR_{50}], R_2 = [RR_{26} \ RR_{27} \ \dots \ RR_{75}] \quad (2)$$

The IRF of each segmented RR sequence R_i was then calculated as:

$$d_i(j) = \frac{|R_i(j) - \text{med}\{R_i\}|}{1.483 \times \text{med}\{|R_i(j) - \text{med}\{R_i\}|\}} \quad (3)$$

where $\text{med}\{*\}$ is a median operator and $j = 1, 2, \dots, 50$.

- (3) The signal enhancement defined in Eq. (4) is applied to highlight the output differences between the normal and anomalous intervals.

$$D_i(j) = d_i(j)^k \times \log_2 d_i(j)^k \quad (4)$$

where k is the enhancement coefficient. If $k > 1$, the difference between two consecutive RR intervals is enlarged. In this study,

k was set to 3 since it effectively magnified the difference between two consecutive RR intervals.

- (4) The threshold τ is set to 100. The selection of τ was determined from the receiver operating characteristic (ROC) curve analysis. The details were described in our previously published study [14]. The sensitivity and specificity were calculated for a range of τ values (from 30 to 500). The threshold which yielded the maximum sum of sensitivity and specificity was selected.
- (5) Anomalous intervals are identified with $D_i(j) > 100$.

2.5 Template matching method

A template matching technique, a shape-based matching of ECG morphology features, was developed.

- (1) R-wave peaks are firstly detected using the WTMM method. The raw RR sequence was formed and expressed as: $RR = \{RR_1, RR_2, \dots, RR_N\}$.
- (2) The mean RR interval is predicted from the raw RR sequence. With $m = 10$, m consecutive RR_i values are chosen to form a segmented RR sequence $X_m(i) = \{RR_i, RR_{i+1}, \dots, RR_{i+m-1}\}$, where $i = 1, 2, \dots, N-m+1$.

Let σ_i denote the standard deviation of $X_m(i)$, which forms a $N-m+1$ dimension vector $\sigma = [\sigma_1, \sigma_2, \dots, \sigma_{N-m+1}]$. Let k denote the position of the minimal σ_i and $Rate$ denote the mean value of the segmented RR sequence $X_m(k) = \{RR_k, RR_{k+1}, \dots, RR_{k+m-1}\}$. In statistics, $Rate$ represents the mean RR interval.

- (3) An ECG template is constructed. Each RR_k in $X_m(k)$ corresponds to one ECG recording segment. Let x_k denote the ECG recording segment. x_k is enlarged or shortened to have a uniform length, i.e., the length of $Rate$. Then, the mean value vector of all x_k , named $Rmean$, is calculated and used as an ECG template.
- (4) The correlation between the constructed ECG template and the ECG recording segment is calculated. For the raw RR sequence $RR = \{RR_1, RR_2, \dots, RR_N\}$, let $Recg_j$ denote the ECG segment corresponding to the interval of RR_j ($j = 1, 2, \dots, N-1$). The correlation between $Rmean$ and $Recg_j$ is calculated as:

$$R_j(0) = \left[\sum_{m=1}^{N_j} Rmean(m) Recg_j(m) \right] / N \quad (5)$$

where N_j is the length of $Recg_j$.

- (5) Anomalous intervals are identified. If the morphology of the ECG recording segment does not match the ECG template, $R_j(0)$ is a small value close to 0; if the morphology of the ECG recording segment well matches the ECG template, $R_j(0)$ is close to 1. Identification criteria ($R_j(0) < \text{threshold } \tau$) are then applied to detect anomalous intervals. The determination of threshold τ was also based on ROC curve analysis. By setting τ from 0.4 to 1, it was found that $\tau = 0.9$ yielded the maximum sum of sensitivity and specificity.

2.6 A combination method of improved IRF and template matching

Improved IRF takes into account the time-span information

and template matching method can detect ECG morphological changes, so a method based on their combination is expected to perform well in identifying anomalous intervals. The RR interval will be determined as an anomalous interval if one of these two determination criteria can be met: 1) $D_i(j) \geq 100$ and $R_j(0) \leq 0.93$, or 2) $D_i(j) \geq 50$ and $R_j(0) \leq 0.9$.

2.7 Evaluation of the four methods for identification of anomalous intervals

The four methods (IRF, improved IRF, template matching, and the combination method of improved IRF and template matching) for the identification of anomalous intervals were applied to the 43 RR sequences from the MIT-BIH arrhythmia database. The identification outcomes of the identified anomalous intervals are referred to as simply A1, A2, N1, and N2. A1: the total number of anomalous intervals that are falsely identified as normal intervals; A2: the total number of anomalous intervals that are truly identified as anomalous intervals; N1: the total number of normal intervals that are truly identified as normal intervals; N2: the total number of normal intervals that are falsely identified as anomalous intervals.

Finally, the sensitivity and specificity were calculated for the four methods as follows:

$$\text{sensitivity} = A2/(A1+A2) \times 100\% \quad (6)$$

$$\text{specificity} = N1/(N1+N2) \times 100\% \quad (7)$$

3. Results

3.1 Performance of the four methods

Figure 2 shows the identification outcomes for four types of anomalous interval. As shown in Figs. 2(a) to (c), the improved IRF method had the best performance in identifying FN, FP, and sVEB anomalous intervals. However, it failed to identify the VEB anomalous interval, as shown in Fig. 2(d), which did not introduce a large change in the RR interval. However, this failed identification by the improved IRF method was corrected by the template matching method, which is sensitive to ECG morphology feature changes. Therefore, the combination method of the improved IRF and template matching can identify all types of anomalous interval.

3.2 Evaluation results

The total numbers of identified anomalous intervals for the four methods are shown in Table 1. The identification sensitivity and specificity are also given. The improved IRF achieved a better sensitivity and specificity than those of the traditional IRF (92.3% vs. 86.1% for sensitivity, 94.9% vs. 87.0% for specificity). This confirms that the identification of anomalous intervals can be improved by taking into account the influence of the non-stationary trend and by using the signal enhancement technique. Table 1 clearly shows that the combination method produced the best results, with sensitivity and specificity values of 98.5% and 99.2%, respectively.

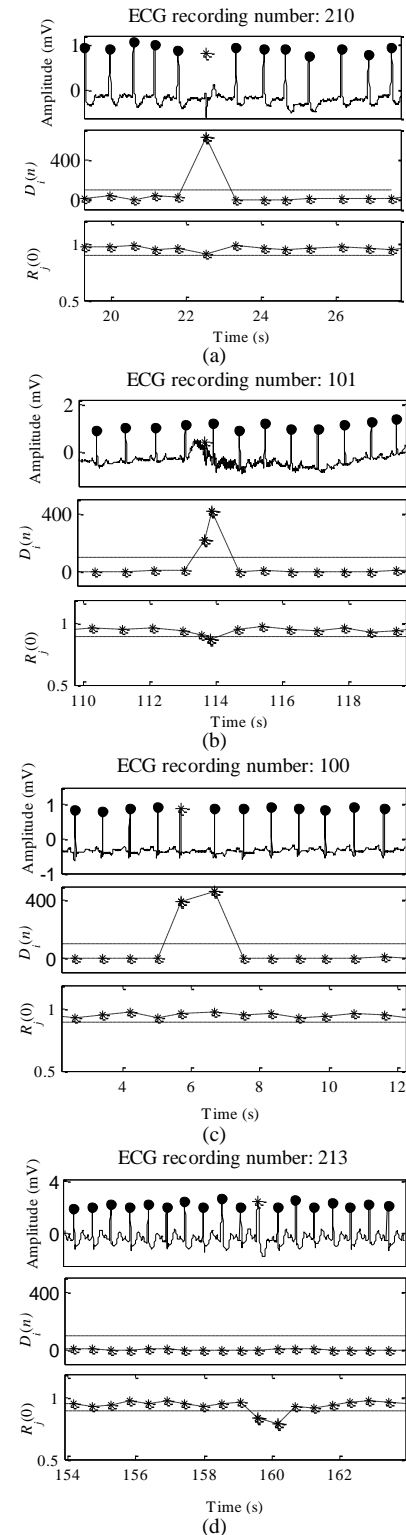


Figure 2. Identification outcomes for four types of anomalous interval for the improved IRF and template matching methods. (a) FN, (b) FP, (c) sVEB, and (d) VEB. In each sub-figure, the upper panel shows an ECG recording segment. The middle panel shows the output $D_i(j)$ of the improved IRF and the lower panel shows the output $R_j(0)$ of the template matching method. The horizontal dashed lines are the thresholds of 100 and 0.9, respectively, for the improved IRF and template matching method.

Table 1. Number of identified anomalous intervals and the evaluation results for the four identification methods.

Methods	Identification results				Evaluation results	
	A1	A2	N1	N2	Sensitivity (%)	Specificity (%)
IRF method	384	2376	26427	3941	86.1	87.0
Improved IRF	214	2546	28811	1557	92.3	94.9
Template matching	257	2503	28987	1381	90.7	95.5
Combination method	41	2719	30125	243	98.5	99.2

(A1: anomalous interval→normal interval; A2: anomalous interval→ anomalous interval; N1: normal interval→normal interval; N2: normal interval→anomalous interval).

4. Conclusion

The identification of anomalous intervals in RR sequences is essential in clinical applications where RR intervals are needed for analysis. The traditional identification methods of anomalous intervals mainly focus on the time-span information of RR intervals [8,10,11], and do not consider the influence of non-stationary time series of RR intervals. In this study, an improved IRF method that uses a sliding window and signal enhancement techniques was proposed. It overcomes the limitations of the traditional IRF and can effectively identify several types of anomalous interval (FN, FP, and sVEB), but it is not sensitive to anomalous intervals caused by ECG morphology feature changes.

In real clinics, anomalous RR intervals caused by ECG morphology feature changes (VEB or noisy ECG recording) occur frequently, and it is therefore clinically useful to identify them. For this purpose, a template matching method was developed, and combined with the improved IRF method. Results show that the combination method is suitable for the identification of anomalous intervals.

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