Postprint of Automated J-Wave Detection Based on Linear and Nonlinear Feature Fusion

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Date: 2018-05-24T00:00:00+00:00

Abstract

Clinical studies have demonstrated that the J-wave can serve as a high-risk early warning indicator for certain cardiac diseases. To address the problem that current J-wave diagnosis by physicians relies solely on empirical recognition, which is prone to misdiagnosis, this paper proposes an automatic J-wave recognition method from a signal processing perspective. The method extracts energy features and high-order cumulant features from electrocardiogram data after extreme-point symmetric mode decomposition, fuses linear and nonlinear features, employs principal component analysis for feature dimensionality reduction, and finally utilizes a support vector machine optimized by the artificial bee colony algorithm for classification, thereby achieving automatic J-wave recognition. Comparative experimental results demonstrate that the proposed method achieves an average accuracy of 97.3% and can effectively identify J-waves.

Full Text

Preamble

Automatic Recognition of J Wave Based on Combination of Linear and Nonlinear Features

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Abstract: Clinical studies have demonstrated that the J wave can serve as a high-risk early warning indicator for certain cardiac diseases. Current clinical diagnosis of J waves relies primarily on physicians' experiential judgment, which is prone to misdiagnosis. To address this limitation, we propose an automatic J wave identification method from a signal processing perspective. This method extracts energy features following extreme-point symmetric mode decomposition

(ESMD) of electrocardiogram (ECG) data and higher-order statistics (HOS) features, thereby fusing linear and nonlinear characteristics. Principal component analysis (PCA) is employed for feature dimensionality reduction, and an artificial bee colony (ABC) algorithm-optimized support vector machine (SVM) is used for classification to achieve automatic J wave recognition. Comparative experimental results demonstrate that the proposed method achieves an average accuracy of 97.3%, enabling effective J wave identification.

Keywords: J wave; extreme-point symmetric mode decomposition; higher-order statistics; artificial bee colony algorithm; support vector machine

0 Introduction

The J point represents the junction between the QRS complex and the ST segment on an ECG signal, marking the end of ventricular depolarization and the beginning of repolarization [1]. When the J point deviates from the baseline, appearing as a sharp peak, hump, or notch with amplitude 0.1 mV and duration 20 ms, this deflection is identified as a J wave [2,3]. Clinical research indicates that when J wave amplitude exceeds 0.1 mV accompanied by ST segment changes, it can trigger fatal myocardial infarction, malignant arrhythmia, or even sudden cardiac death [4,5]. Currently, clinicians diagnose J waves through visual assessment of their size and duration on ECGs combined with patients' clinical manifestations. This subjective, experience-based approach frequently leads to misdiagnosis and missed diagnoses. Consequently, automatic J wave recognition could facilitate timely diagnosis and effectively reduce J wave-related mortality.

To achieve automatic J wave identification, this study investigates J waves from a signal processing perspective by extracting both linear and nonlinear features from ECG data. An artificial bee colony algorithm-optimized support vector machine is then employed for classification. The automatic recognition results can assist physicians in formulating optimal diagnostic and treatment plans based on patients' clinical conditions.

1 Data Preparation and Preprocessing

We obtained a substantial collection of paper-based ECG recordings containing J waves from the Shanxi Provincial Hospital ECG database. High-resolution scanners converted these paper records into digital images, which were then processed using image processing techniques including Hough transform, K-means clustering, and curve fitting to achieve digitization. The specific procedure is as follows:

First, tilt correction was performed using Hough transform to detect background grid lines in the ECG paper, calculating the tilt angle from line slopes for rotational correction. Next, pixel clustering separated black ECG signal pixels from red background grid pixels based on their similarity, employing K-means clustering for this segmentation. Interference removal eliminated pixels corresponding to lead markers and reference voltages by selecting connected components with small areas from the binary image. Finally, curve fitting read the coordinates of ECG pixel points, interpolated missing points, and fitted the data to obtain complete digitized ECG signals.

From the digitized data, we selected 40 normal ECG recordings and 40 J wave-containing recordings at a 250 Hz sampling rate, with each record lasting 2 minutes, labeling them as type N and type J respectively. Due to various interference factors, ECG data typically contains multiple noise components [6]. Since ECG frequency spectra are primarily concentrated between 1 Hz and 40 Hz, we applied second-order Butterworth filters with cutoff frequencies of 1 Hz and 40 Hz to remove baseline drift and power-line interference.

2 Methodology

Our approach extracts linear and nonlinear features from preprocessed ECG data. Linear features are obtained through extreme-point symmetric mode decomposition (ESMD), which decomposes the signal into intrinsic mode functions (IMFs). Nonlinear features are extracted using higher-order statistics (HOS). These features are fused and dimensionality-reduced via principal component analysis (PCA) before being input into an artificial bee colony algorithm-optimized support vector machine (ABC-SVM) for classification. The overall algorithm framework is illustrated in [Figure 1: see original paper].

2.1 Linear Features

We employ ESMD to extract linear features from ECG data, specifically the energy features of decomposed IMFs [7,8]. Current time-frequency analysis methods for ECG data primarily include wavelet transform and empirical mode decomposition (EMD). While wavelet transform demonstrates good analytical performance for ECG classification, it is non-adaptive and its effectiveness heavily depends on wavelet function selection. Once initialized, the same wavelet basis must be applied globally, making optimal analysis difficult. EMD is an adaptive signal processing method that decomposes signals into different time-scale components from low to high frequency based on intrinsic fluctuation patterns, making it more suitable for ECG analysis.

ESMD improves upon EMD by modifying the envelope interpolation method, replacing EMD’ s cubic spline interpolation with internal pole symmetric interpolation and endowing the residual component with physical meaning. Through least squares optimization, the residual becomes an “adaptive global mean curve” that determines optimal decomposition. This effectively resolves the mode mixing problem in EMD [9].

The ESMD decomposition procedure is as follows: identify all extrema (maxima and minima) in the original ECG data; connect adjacent extrema with line segments, mark their midpoints, and add boundary midpoints; construct interpolation curves through these midpoints and compute their average; repeat screening until the standard deviation falls below a permitted error or maximum iterations are reached to obtain the first IMF; repeat the process on the residual sequence until it becomes monotonic or contains insufficient extrema, yielding multiple IMFs and a final trend term.

A key improvement in ESMD is that maximum screening iterations are determined by the adaptive global mean curve. Before decomposition, the number of remaining poles M must be set, which determines the possible curvature of trend term r and its ability to reflect data trends. For boundary interpolation requirements, $M \geq 4$. If M is too large, modal resolution decreases. We set $M = 4$ in this study. By plotting σ_0 against K and identifying the K value corresponding to the minimum σ_0, we determine the optimal screening count. As shown in [Figure 2: see original paper], the minimum occurs at $K = 36$, yielding the decomposition result displayed in [Figure 3: see original paper] with 7 IMFs and one trend term.

Based on ECG waveform characteristics, each IMF carries specific physiological meaning: the first two components c_1 and c_2 represent the highest-frequency QRS complex; c_3 begins to include P wave components; c_4 adds T wave components; c_5 and c_6 represent low-frequency superposition of P, QRS, and T waves; c_7 reflects larger time-scale cardiac regulatory rhythms. The trend term r, as the adaptive global mean curve, effectively captures ECG signal trends, as shown in [Figure 4: see original paper].

The energy vector is computed as follows: after ESMD decomposition, calculate energies E_i for each IMF component c_i and E_r for trend term r using $E_i = \sum_{t=1}^{2000} c_i^2(t)$ and $E_r = \sum_{t=1}^{2000} r^2(t)$. The energy vector $V = [E_1, E_2, \dots, E_r]$ is then normalized to $V' = [p_1, p_2, \dots, p_r]$, where $p_i = E_i / \sum_{j=1}^{r+1} E_j$ represents the proportion of each component' s energy in the total ECG energy. Vector components from p_1 to p_r correspond to progressively lower frequencies, yielding 8 linear features. [Figure 5: see original paper] compares energy vector distributions between type N and type J ECGs, showing type N energy decreasing from high to low frequency with concentration in high-frequency components, while type J exhibits peak energy at p_3.

2.2 Nonlinear Features

Linear features cannot capture subtle signal variations or nonlinear relationships between parameters. Therefore, we extract HOS features to mine J wave information [11]. Specifically, we compute third-order moments (third-order cumulants) as features:

$$C_3(m, n) = E[x(i)x(i + m)x(i + n)]$$

where $E[\cdot]$ denotes statistical expectation and m, n are time-delay parameters.

[Figure 6: see original paper] and [Figure 7: see original paper] display third-order cumulants and their contours for normal and J wave-containing ECGs, respectively, demonstrating clear discriminability. We extract 40 third-order cumulant features as nonlinear characteristics.

2.3 PCA Dimensionality Reduction

To reduce computational complexity, we employ PCA for feature reduction. This transforms high-dimensional initial features via a transformation matrix into lower-dimensional new feature vectors that retain primary information [12]. We fuse 8 linear features (IMF energies) with 40 nonlinear features (HOS) to obtain 48 feature vectors, then apply PCA to select the top 12 principal components for classifier training and testing.

2.4 ABC-SVM

SVM exhibits strong generalization capability for small-sample conditions, making it suitable for J wave ECG classification [13]. The SVM objective is to find an optimal hyperplane that effectively separates type N and type J ECG data:

$$f(x) = \omega^T \Phi(x) + b$$

where ω is the weight vector and b is the bias term. The optimal hyperplane is obtained by solving:

$$\min_{\omega,b,\xi} \frac{1}{2}\|\omega\|^2 + C\sum_{i=1}^{n}\xi_i$$

subject to $y_i(\omega^T\Phi(x_i) + b) \geq 1 - \xi_i$ and $\xi_i \geq 0$, where ξ_i are slack variables and C is the penalty factor. Through Lagrangian transformation, this becomes a convex quadratic programming problem:

$$\max_{\alpha} \sum_{i=1}^{n}\alpha_i - \frac{1}{2}\sum_{i=1}^{n}\sum_{j=1}^{n}\alpha_i\alpha_j y_i y_j K(x_i, x_j)$$

subject to $\sum_{i=1}^{n}\alpha_i y_i = 0$ and $0 \leq \alpha_i \leq C$. The solution yields $\omega = \sum_{i=1}^{n}\alpha_i y_i \Phi(x_i)$, and the classification function becomes:

$$f(x) = \operatorname{sgn}\left(\sum_{i=1}^{n}\alpha_i y_i K(x_i, x) + b\right)$$

We select the radial basis function (RBF) kernel $K(x, x') = \exp(-\|x - x'\|^2/(2\sigma^2))$ due to its single parameter optimization requirement. The ABC algorithm optimizes kernel width γ and penalty factor C to establish the J wave recognition model [14]. The optimization process involves: (a) determining colony size and scout bee proportion; (b) randomly selecting A parameter combinations (C, γ) as food sources; (c) evaluating source quality, with scouts searching or following high-quality sources; (d) local search around selected sources; (e) reallocating bees based on updated quality assessments; and (f) iterating until optimal parameters are found.

3 Experimental Results

3.1 Evaluation Metrics

We evaluate J wave recognition performance using sensitivity (Se), specificity (Sp), and accuracy (Ac). Se represents the correct identification rate for type J ECGs, Sp for type N ECGs, and Ac for overall correct classification of both types.

3.2 Results Analysis

Our dataset comprises 80 ECG recordings (40 normal, 40 with J waves), each 2 minutes long, totaling approximately 10,400 heartbeats. Five-fold cross-validation was employed: the dataset was divided into five disjoint subsets, with four used for training (8,320 beats) and one for testing (2,080 beats). This process was repeated five times, with average performance metrics reported.

We compared four approaches: ESMD+ABC-SVM, HOS+ABC-SVM, fused features+SVM, and our proposed method. SVM parameters (C, γ) for each method are listed in , with average performance results shown in .

The ESMD+ABC-SVM method achieved average Se, Sp, and Ac of 92.7%, 90.1%, and 93.8%, respectively. HOS+ABC-SVM improved these to 95.6%, 95.4%, and 96.3%. Fusing ESMD and HOS features with ABC-SVM yielded the highest performance: 96.7% Se, 96.8% Sp, and 97.3% Ac. Compared to fused features+SVM without ABC optimization, ABC-SVM improved Se, Sp, and Ac by 2.2%, 3.2%, and 2.1%, respectively.

We further compared our method with two existing J wave detection approaches. Clark et al. [15] used morphological and geometric features, which have limitations in detecting only certain J wave patterns. Wang et al. [16] proposed an fPCA and J-score method for 12-lead ECGs, but with high computational complexity and suboptimal test results. As shown in , our method outperforms both alternatives, demonstrating superior J wave recognition capability.

4 Conclusion

This paper presents an automatic J wave recognition technique that comprehensively extracts ECG features by fusing ESMD-based energy features with nonlinear higher-order cumulant features. After PCA dimensionality reduction, an ABC-optimized SVM classifier achieves accurate and efficient J wave identification. Experimental results demonstrate 97.3% average accuracy, providing valuable assistance for clinical cardiac disease diagnosis.

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Note: Figure translations are in progress. See original paper for figures.