

An ECG Signal Classification Method Based on Encoded Feature Reduction and Machine Learning

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Abstract

The electrocardiogram (ECG) signal generated during the heart's beating cycle is a weak, low-frequency biosignal resulting from the potential difference across the cell membranes of cardiac cells. The electrocardiogram (ECG), which displays the heart's activity over time and variations detected by external electrodes, is an effective tool for identifying cardiac abnormalities, as different waveforms correspond to distinct heart activities. The wavelet packet transform has been utilized to classify ECG signals, and the misclassification rate can be significantly reduced through data reduction and the extraction of classification features. The application of machine learning in medical diagnosis, especially ECG signal classification, represents a novel, popular, and effective approach to assist physicians in diagnosing cardiac diseases. The objective of this paper is to provide a reliable diagnostic tool for the early detection and differentiation of arrhythmias, congestive heart failure, and normal sinus rhythm, thereby enhancing the prevention and differentiation of heart diseases. Experimental results indicate that the machine learning classification method based on wavelet packet transform can substantially improve classification accuracy and offer an effective solution for the automated analysis of ECG signals.

Keywords

Classification of electrocardiographic diseases, Electrocardiogram; feature extraction, machine learning, wavelet packet transform.

1. Introduction

Every day, countless signals are generated to transmit information among individuals, taking various forms such as images and sounds. In medicine, signals emitted by the body are often utilized to diagnose critical diseases. One such signal is the electrocardiogram (ECG), which reflects the heart's activity as it pumps blood through the blood vessels, nourishing all tissues with each heartbeat. The heart's rhythm is initiated by the pacemaker cells, with the atria and ventricles responding in succession, accompanied by bioelectrical changes that form the ECG signal. This signal is a weak, low-frequency biosignal, representing the potential difference generated by the cell membranes of human heart cells, with a frequency range of 0.05 Hz to 100 Hz. The specific process involves the atrial and ventricular muscles being in a "polarized state" due to the significant difference in the concentration of extracellular ions (including potassium, sodium, calcium, and others) in the space between the atrial and ventricular muscles at rest. This polarized state is temporarily disrupted by excitation from the pacemaker cells, a phenomenon referred to as "depolarization" in medical terminology. This depolarization generates the electrical activity of the heart. The ECG is a well-established technique for the diagnosis of heart-related diseases. It not only obtains images of the heart over time, but also includes changes in the external electrodes attached to the skin, and can be used to detect various abnormalities of the heart, such as arrhythmia and heart failure, etc. The depolarization of the atrial myocardium is shown as a P-wave and that of the ventricular myocardium as a cluster of QRS-waves in the ECG signal, and the T-wave represents the potential change of the

ventricular repolarization process with low amplitude, and U-wave is located in the wake of the T-wave, representing the posterior ventricle. The wave is located after the T-wave and represents the subsequent potential of the ventricle, and its amplitude is lower than that of the T wave and sometimes not obvious. The U-wave is located after the T-wave and represents the subsequent potential of the ventricle. As shown in 0 Classic One Cardiac Cycle Waveforms Classic One Cardiac Cycle Waveforms, after a depolarization, the myocardium returns to its original polarization state, a process known as repolarization. Inpatients with abnormal heartbeats, the waveforms in the ECG signals are clearly abnormal. Various computerized methods have been developed to analyze ECG signals. Among these, wavelet packet transform (WPT)-based signal processing techniques have been employed to classify ECG signals. As the number of wavelet decomposition levels increases, the resolution in the frequency domain improves. At each level of signal decomposition, both high-frequency and low-frequency subbands are further decomposed. A cost function is minimized, and an optimal decomposition path is computed to analyze the original signal. The versatile application of wavelet bases not only facilitates signal classification but also demonstrates significant effectiveness in biological signal denoising and data compression[5]. Therefore, selecting the appropriate decomposition function during the signal classification process is crucial for recognizing subtle neural activity patterns, which is essential for the diagnosis and prevention of diseases.

With the advancement of human society and the fields of science and technology, the innovative application of machine learning in medical diagnosis has emerged as a promising approach to assist physicians in diagnosing heart-related diseases. This innovative and effective method aids physicians in diagnosing heart-related diseases, particularly in the analysis and processing of ECG signals. Previous studies have indicated that 90% of cardiac diseases can be detected early with some degree of intervention. This capability is highly beneficial for disease prevention. The wavelet packet transform, a widely used technique for feature extraction in machine learning, is an emerging method for processing nonstationary signals. It serves as an ideal tool for analyzing signals in both the time and frequency domains. Utilizing both domains to analyze ECG signals can effectively identify anomalies, thereby facilitating the early detection of cardiovascular diseases in humans. Additionally, classifiers trained through machine learning not only demonstrate high classification speed but also achieve remarkable accuracy, making this approach highly regarded in the field.

In this paper, we aim to present a method for classifying Arrhythmia (ARR), Congestive Heart Failure (CHF), and Normal Sinus Rhythm (NSR) within a dataset. The paper is organized into four main sections. The second section focuses on feature extraction and transformation of the signals. The third section describes a machine learning classification method used to classify the decomposed signals, while the fourth section addresses the accuracy of the classification and draws conclusions.

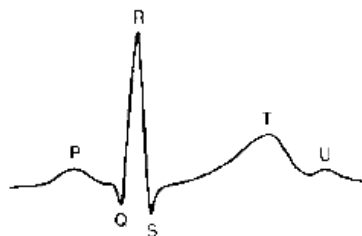


Fig.1 Classic One Cardiac Cycle Waveforms Organization of the Text

2. Feature Extraction Based on improved Wavelet Packet

To date, auxiliary medical tools like ECG electrocardiograms cannot directly detect cardiac abnormalities. In actual medical diagnosis, ECG serves only as an adjunct and cannot directly confirm conditions such as heart failure; the final interpretation still requires a cardiologist's

diagnosis. Nevertheless, the integration of ECG technology with emerging machine learning techniques can enhance diagnostic efficiency and significantly reduce the burden on physicians, while remaining crucial for identifying other cardiac abnormalities.

The ECGdata dataset used in the classification experiments of this paper originates from PhysioNet, an open-access online resource platform in the United States. Users can freely access raw data and analysis tools from PhysioBank and PhysioToolkit, providing significant convenience for researchers studying ECG signals. Specifically, ECGdata comprises 162 electrocardiogram recordings sourced from three PhysioNet databases: the MIT-BIH Arrhythmia Database, the BIDMC Congestive Heart Failure Database, and the MIT-BIH Normal Sinus Rhythm Database. This comprises 96 records from patients with arrhythmias, 30 records from patients with congestive heart failure, and 36 records from patients with normal sinus rhythm. The entire experiment was conducted using the commercial mathematical software MATLAB 2012b. Data in MAT format is directly usable within MATLAB, the software employed in this study. ECGdata is a structure array containing two fields: data and labels. The data field is a 162×65536 matrix, where each row represents an ECG recording sampled at 128 Hz. while 'labels' is a 162×1 diagnostic label vector containing one of three values: ARR, CHF, or NSR. After loading the data, a helper function 'helperRandomSplit' designed in MATLAB randomly splits the dataset into two groups in a 7:3 ratio for training and testing, respectively, with corresponding label splits. During this process, 70% of the data in each class is randomly assigned to the training set, while the remaining 30% is allocated to the test set. Each row in both the training and test sets corresponds to an ECG signal, and each element in the training and test labels contains the class label for the corresponding row. At this point, the training and test sets are finalized. The training set contains 113 records, and the test set contains 49 records. After splitting, the training data accounts for 69.75% (113/162) of the total data. Now, reviewing our previous operations: the ARR class accounts for 59.26% (96/162) of the total data, CHF accounted for 18.52% (30/162), and NSR accounted for 22.22% (36/162). After verification, the percentage distribution of each class in both the training and test sets matches the overall class distribution in the dataset.

After completing data processing, we will begin feature extraction operations on these data, enabling classification based on these features. First, the helper function helper Plot Random Records plots the first few thousand samples from four randomly selected records in ECGdata, as shown in 0, accepting ECGdata and a random seed as inputs. The initial seed is set to 14 to ensure at least one record from each category is plotted. Here, ECGdata serves as the sole input parameter. By repeatedly executing helperPlotRandomRecords, we gain a clearer and more comprehensive understanding of the various ECG signal waveforms associated with each category, as illustrated in 0. When extracting features for classification from each signal, we first divide the signal into eight segments before performing extraction, with each segment lasting approximately one minute. The extracted features primarily comprise three types: fourth-order autoregressive (AR) model coefficients, Shannon entropy values (SE) from fourth-order maximum overlap discrete wavelet packet transform (MODWPT), and multifractal wavelet waveguide estimation of fractal estimates and singular spectra.

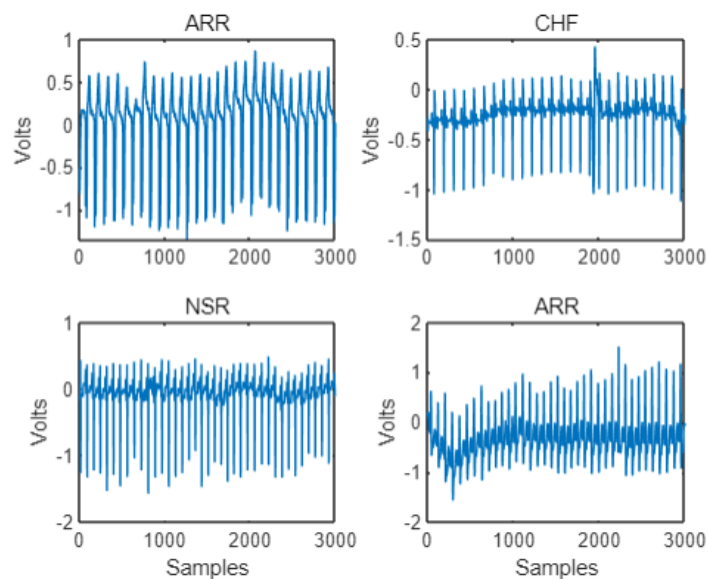


Fig.2 ECG Signal Category Representation Diagram

We should note that when processing electrocardiogram signals, the principle of simplicity should be followed to avoid excessive parameters causing unnecessary interference. The wavelet transform is a later-developed mathematical tool derived from the short-time Fourier transform. It decomposes signals into components of different frequencies based on varying wavelet basis functions, enabling multi-scale observation of signals—a form of multi-scale analysis. Common wavelet basis functions include Haar wavelets, dbN wavelets, and symN wavelets, where N denotes the wavelet order. Given the db2 wavelet basis function's superior symmetry, compact support, and minimal phase distortion, this paper employs the db2 wavelet basis function to decompose signals into multiple scales.

Furthermore, when extracting wavelet variance estimates at different scales for each signal across its entire length, unbiased wavelet variance estimation is required, ensuring at least one wavelet coefficient remains unaffected by boundary conditions. For a signal length of 2^{16} (65,536) time units using the db2 wavelet basis function, this operation results in the signal being decomposed into 14 levels.

The features extracted above were selected based on published research demonstrating their effectiveness in ECG waveform classification. However, this does not imply that only these three features are significant in the waveform, nor does it indicate that other features are ineffective for classification.

We should note that when processing electrocardiogram signals, the principle of simplicity should be followed to avoid excessive parameters causing unnecessary interference. The wavelet transform is a later-developed mathematical tool derived from the short-time Fourier transform [21]. It decomposes signals into components of different frequencies based on varying wavelet basis functions, enabling multi-scale observation of signals—a form of multi-scale analysis. Common wavelet basis functions include Haar wavelets, dbN wavelets, and symN wavelets, where N denotes the wavelet order. Given the db2 wavelet basis function's superior symmetry, compact support, and minimal phase distortion, this paper employs the db2 wavelet basis function to decompose signals into multiple scales.

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Following the above processing, the AR coefficients for each window are estimated using the Burg method. The Burg method enhances model accuracy and stability—particularly with limited or small datasets—by simultaneously accounting for both forward and backward prediction errors. In, the authors employed model order selection to determine the AR model that provided the optimal fit for ECG waveforms in similar classification problems.

Random forest is an ensemble learning method based on decision trees in machine learning. Its fundamental principle involves constructing multiple decision trees trained on different subsets of the data to derive the final prediction result.

In the literature, Shannon entropy—an information-theoretic metric—was computed at the terminal nodes of wavelet packet trees. This paper combines Shannon entropy with a random forest classifier. Here, we employ MODWPT up to the fourth level.

Shannon entropy serves to measure the uncertainty of a random variable. Selecting features with low Shannon entropy for constructing the random forest classifier reduces the impact of irrelevant or redundant features on the model, thereby enhancing its performance and efficiency. From an information-theoretic perspective, Shannon entropy aids in explaining the decision-making process of the random forest model, revealing how it classifies by reducing uncertainty.

From a machine learning perspective, feature selection based on Shannon entropy aids in constructing more compact and efficient random forest models. By selecting only features highly correlated with the target variable—i.e., the classification feature vector—it reduces the risk of model overfitting and enhances our understanding of its internal mechanisms.

The Shannon entropy definition based on the non-sampling wavelet packet transform (UWPT) is shown in Equation (1):

$$SE_j = -\sum_{k=1}^N p_{j,k} * \log p_{j,k} \quad (1)$$

where N represents the number of corresponding coefficients in node j , and also denotes the normalized square of the wavelet packet coefficient in the j th terminal node.

Additionally, we employ two fractal measures estimated via wavelet decomposition (i.e., high-frequency and low-frequency subbands) . as features, a common approach in signal processing. We utilize the singular spectral width obtained from DWTleader as a metric for the multifractal properties of ECG signals. We also employed the second cumulants of the scaling exponents. Scaling exponents describe power-law distributions within signals at different resolutions based on scaling. The second cumulants roughly indicate deviations of scaling exponents from linearity. We can use modwtvar to obtain the wavelet variance across the entire signal. Wavelet variance serves to measure signal variability proportionally, or equivalently, to measure variability within frequency intervals of the octave band.

$$V_j = \frac{1}{N_j} \sum_{k=1}^{N_j} (d_{j,k} - \bar{d}_j)^2 \quad (2)$$

Here, $d_{j,k}$ denotes the k th wavelet coefficient at the j th scale, $\bar{d}_j$ represents the mean of the wavelet coefficients at the j th scale, and N_j indicates the number of wavelet coefficients at the j th scale. The wavelet variance is estimated through calculation.

After obtaining these features, our designed helper function `helperExtractFeatures` calculates them and concatenates them into feature vectors for each signal. Since the dataset is split into

training and test sets at a 7:3 ratio, the features are similarly divided into trainFeatures and testFeatures, forming matrices of dimensions 113×190 and 49×190 respectively. Each row of these matrices represents the feature vector for the corresponding ECG data in trainData and testData.

The Holder index range map reflects the smoothness or singularity of a signal—particularly non-stationary signals—around a specific point. Different cardiac conditions may alter the Holder index range in ECG data. For instance, ARR may cause changes in the Holder index of P waves or T waves. By calculating and analyzing Holder index range plots of ECG data across different time periods or leads, and extracting relevant features, valuable insights can be provided for early diagnosis, condition assessment, and classification of cardiac diseases. This assists physicians in making more accurate clinical judgments.

The Holder index range correlation diagram for the three signal types is shown in Fig.3.

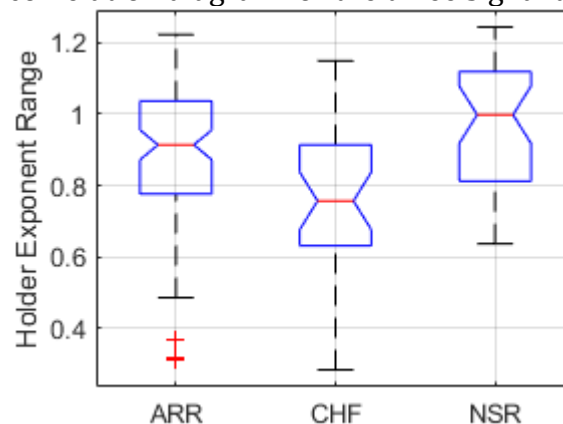


Fig.3 Box-and-Whisker Plots of Holder Index Ranges for Three Types of ECG Signals

When creating classification feature vectors, these data points are reduced from 2^{16} samples to 190-element vectors. This significant reduction in data volume is not an end in itself, but rather aims to condense the data into a smaller set of features that capture differences between categories. This enables the classifier to accurately separate signals. The feature indices constituting both trainFeatures and testFeatures are contained within the structure array features. We can certainly use these indices to explore features by group. For example, we can examine the range of the Holder index in the singular spectrum during the first time window to plot ECG signal images across the entire dataset.

We can also perform a one-way ANOVA on a specific feature to confirm what is shown in the block diagram: the ranges for the ARR and NSR groups are significantly larger than those for the CHF group, and the between-group variation is clearly greater than the within-group variation, as shown in Table 1. In the ANOVA in table 1, SS, df, and MS represent the sum of squares, degrees of freedom, and mean square, respectively.

Table 1. Analysis of Variance Table

Source	SS	Df	MS	F	p-value
Group	0.55664	2	0.27832	7.14	0.0011
Error	6.20009	159	0.3899		
Total	6.75673	161			

For example, consider the variance differences across three groups in the second-lowest frequency (second-largest scale) wavelet subband. If we perform variance analysis on this feature, we find that the NSR group exhibits significantly lower variance in this subband compared to the ARR and CHF groups, indicating more concentrated data and reduced fluctuations. The CHF group exhibits the highest median wavelet variance and the most outliers,

indicating greater data variability. The ARR group's data variability falls between these two extremes, as shown in Fig.4.

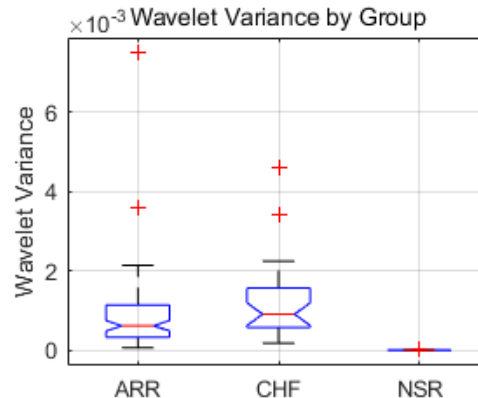


Fig.4 Box-and-Whisker Plots of Wavelet Variance Data for Three Types of ECG Signals

The above explanation describes how a single feature is used to separate classes, but relying on just one feature is far from sufficient. Our goal is to obtain a sufficiently representative set of classification feature vectors from the feature vectors and train a classifier capable of distinguishing the three classes: ARR, NSR, and CHF.

After these numerous steps, the data has been refined into classification feature vectors corresponding to each signal. The next step is to classify the ECG signals using these feature vectors. We can use the Classification Learner application to rapidly evaluate a large number of classifiers. In this experiment, we employed a multi-class Support Vector Machine (SVM) with a quadratic kernel to perform two analyses.

Cross-validation is a commonly used model evaluation method in machine learning and data analysis. Five-fold cross-validation enables more thorough utilization of data. This is because, during each iteration, while the majority of data is used for model training, every sample has an opportunity to serve as validation data for better model assessment. Therefore, we ultimately chose to use five-fold cross-validation across the entire dataset to estimate the misclassification rate and confusion matrix.

The confusion matrix summarizes prediction results for classification problems. Its core technique involves aggregating counts of correct and incorrect predictions, segmented by category, to reveal where the classification model experiences confusion during prediction. Final estimation yielded a five-fold classification error rate of 8.02% (corresponding to an accuracy rate of 91.98%). The confusion matrix (confmatCV) reveals which data points were misclassified, while the grouporder function provides the group sequence. Results indicate that in the test set: - 2 cases in the ARR group were misclassified as CHF - 8 cases in the CHF group were misclassified as ARR, with 1 case misclassified as NSR - 2 cases in the NSR group were misclassified as ARR.

3. Experimental Results

In the classification task of this paper, precision is calculated by dividing the number of correct positive results by the total number of positive results. Recall is defined as the number of correctly labeled instances divided by the total number of instances in a given class. Accuracy reflects our desire for strong performance in both precision and recall. For example, suppose we have a classifier that labels every record as ARR. In this case, the recall for the ARR class would be 1 (100%). This would result in all records belonging to the ARR class being labeled as ARR, leading to very low precision.

This occurs because our classifier labels all records as ARR. Thus, for a precision of 96/162 (0.5926), there would be 66 false positives. The F1 score is the harmonic mean of precision and

recall, providing a single metric that reflects the classifier's performance in both recall and precision.

Additionally, we employ the helper function `helperPrecisionCall` to compute precision, recall, and F1 scores for the three classes. By examining the code in the helper function section, we can observe how this function calculates precision, recall, and F1 scores based on the confusion matrix. As shown in Table 2, we observe that both the ARR and NSR classes exhibit excellent precision and recall rates, while the CHF class demonstrates a notably lower recall rate.

Table 2. Original Classification Evaluation Indicator Table

	Precision	Recall	F1_Score
ARR	90.385	97.917	94
CHF	91.304	70	79.245
NSR	97.143	94.444	95.775

In the subsequent steps, we will only fit the multi-class quadratic SVM to the training dataset and then use this model to predict the test dataset. The test set contains 49 data records.

To obtain the confusion matrix, we first determine the number of correctly predicted cases. The classification accuracy for the test dataset is approximately 98%. The confusion matrix indicates that one CHF record was misclassified as NSR in the predictions. The subsequent steps, similar to those performed in the cross-validation analysis, aim to obtain the precision, recall, and F1 score for the test set (the table requires a title), as shown in Table 3.

Table 3. Classification Evaluation Metrics Table After SVM Fitting Only

	Precision	Recall	F1_Score
ARR	100	100	100
CHF	100	88.889	94.118
NSR	91.667	100	95.652

Based on the preceding analysis, two questions naturally arise. They are: Is feature extraction necessary to achieve good classification results? Is a classifier required? Can these features separate the three categories without a classifier? To address the first question, we need to repeat the cross-validation process on the original time series data. We should note that applying SVM to a matrix of dimensions 162×65536 (2^{16}) incurs significant computational cost. After completing the calculations, the results are presented in Table 4.

Table 4 Classification Evaluation Metrics Table Following Repeated Cross-Validation Processes

	Precision	Recall	F1_Score
ARR	64	100	78.049
CHF	100	13.333	23.529
NSR	100	22.222	36.364

The results indicate that the misclassification rate of the original time series data is 33.3%. We recalculated their precision, recall, and F1 scores. Based on the data analysis, we observe that the F1 scores for both the CHF group (23.52) and the NSR group (36.36) are notably low. Additionally, we need to obtain the Discrete Fourier Transform (DFT) coefficients for each signal to perform frequency domain analysis. Since the data is real-valued, we can leverage the property that the amplitude spectrum of the Fourier transform of a real function is an even function to achieve some data reduction using DFT. Here, we employed DFT amplitude to reduce the misclassification rate to 19.13%. Although the misclassification rate decreased, it remained more than double the error rate achieved with the 190 features above, as shown in Table 5.

Table 5. Classified Evaluation Indicator Table After Data Reduction

	Precision	Recall	F1_Score
ARR	64	100	78.049
CHF	100	13.333	23.529
NSR	100	22.222	36.364

The above analysis indicates that the accuracy of a classifier's classification depends on the careful selection of features.

To address the issue of classifier effectiveness, we attempted clustering data using only the classification feature vectors. The k-means clustering algorithm is a widely used unsupervised learning method. Gap statistics also serve as an effective approach in machine learning for determining the number of clusters within a dataset. Using both methods, we can determine the optimal number of clusters and cluster assignments. Our data may have between 1 and 6 clusters. Gap statistics indicate that the optimal number of clusters is 3. However, if we examine the number of records in each of the three clusters, we find that k-means clustering based on classification feature vectors performs poorly in separating the three diagnostic categories, as shown in Table 6.

Table 6 Number of Results for Separating Three Diagnostic Categories Using k-means Clustering Based on Classification Feature Vectors

Ans=3*1
61
74
27

Now, let's review our data: there are 96 individuals in the ARR category, 30 in the CHF category, and 36 in the NSR category.

4. Conclusion

The differentiation between ARR, NSR, and CHF holds significant importance in cardiology and plays a crucial role in preventing human diseases. This paper proposes a small-to-medium-sized model that employs wavelet analysis to extract wavelet features from electrocardiogram (ECG) signals. From these features, selected classification features are chosen to form a classification feature vector. Following data reduction, the ECG signals are ultimately classified into three categories using the machine learning SVM algorithm. The model's advantage lies in its ability to significantly reduce both data volume and computational load through feature extraction while capturing multiple distinctions between ARR, CHF, and NSR classes, as demonstrated by cross-validation results and the SVM classifier's performance on the test set. This experiment further demonstrates that applying SVM directly to raw ECG signals yields poor performance, and the same result occurs without clustering the classification feature vectors using SVM. In other words, neither the classifier nor the data features alone are sufficient to separate the three categories. However, when data reduction is performed using feature extraction techniques before applying the classifier, the three categories are well-separated. This demonstrates that extracting classification feature vectors from data enhances computational efficiency by transforming data into a more manageable form, thereby providing more detailed investigation opportunities for subsequent classification tasks.

Since all records in the MIT-BIH database originate from European subjects, to broaden its applicability, future clinical research should focus not only on accurately classifying the three

ECG signals but also on achieving more efficient and rapid classification while improving model generalization performance.

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