

# Classification of Ventricular Arrhythmia using a Support Vector Machine based on Morphological Features

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**Abstract** — This paper proposes a method for the classification of ventricular arrhythmia using support vector machines (SVM). The features used in the SVMs were extracted automatically based on morphological information. Three different features were extracted: RR interval, QRS slope, and QRS shape similarity. Then, the SVM was used to classify five different electrocardiogram (ECG) heartbeat episodes. The Gaussian Radial Basis Function was utilized for the kernel function because the ECG beat episodes were treated as a non-linear pattern. The sensitivity of the classification used for the five beat episodes was 93.16%.

## I. INTRODUCTION

Many people have suffered from various illnesses. Arrhythmia is one of the critical diseases, especially ventricular arrhythmia, which is a significant symptom of heart attack, and arrhythmia detection and classification have been become important work. Researchers have attempted to classify arrhythmia using many different tools, including a fuzzy clustering neural network [1], an adaptive neural network [2], AR modeling [3], wavelet transform [4], the time-frequency method [5], particle swarm optimization [6], and higher-order spectral techniques [7]. These approaches have achieved remarkable results, but most of the related methods included a heavy calculation cost or had to be manually calculated for extracting features.

In this work, we propose that ventricular arrhythmia using SVM should be classified with a morphological feature vector that extracts automatically and simply. As the QRS complex has the most information on the ventricular arrhythmia [2], we extracted the feature from the QRS complex. The proposed approach was validated by the MIT-BIH and Creighton University database and yielded reliable classification accuracy.

This paper is organized into five sections. A preprocessing stage of ECG data is presented in Section II. In Section III, we describe how to extract the features. Section IV presents the Support Vector Machine (SVM) briefly. In Section V, we discuss the results of our proposed method. Finally, the conclusion is discussed.

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## II. ECG DATA PREPROCESS

All of the ECG data was obtained from the Creighton University Ventricular Tachycardia database and various MIT-BIH databases comprised of Normal Sinus Rhythm, Malignant Ventricular Arrhythmia, and Supraventricular Arrhythmia. The sampling frequencies of the ECG data were 128 Hz or 250 Hz. The ECG record has an annotation file that was used to identify an ECG beat. We selected five different types of heart rhythms, such as normal sinus rhythm (NSR), supraventricular tachycardia (SVT), ventricular tachycardia (VT), ventricular flutter (VFL), and ventricular fibrillation (VFib) from the records kept by Creighton University or the MIT-BIH database.

In the preprocessing step, first, each ECG record was resampled. The ECG records had been sampled at different rates; therefore we needed to normalize the ECG sampling frequency. In this paper, all of the ECG records had been resampled with a 200Hz sampling frequency. We must show a QRS complex because the objective of this paper is ventricular arrhythmia classification, and the component of ECG of QRS complex clearly shows up to 200Hz sampled ECG records. Each record was separated into four-second segments after the process of resampling was completed. For this paper, we obtained four-second segments from each ECG record and automatically distinguished the QRS complex. The duration of 4 seconds refers to the real-world time expended on ECG data collection. In record of 60 beats per minute (bpm) NSR, number of QRS complex appears approximately 3 during 4 seconds. If the data collection took less than 4 seconds, it then lacked information on the QRS complex required for decisions and if it took more than 4 seconds, the data was provided too late to formulate decisions on the proper treatment. Finally, each segmented ECG underwent filtering, such as a 2-40 Hz bandpass filter, and correction of baseline drift or shift (1). This correction uses a 500 ms window of the ECG segment and subtracts the average of the window from each value of the window. This process continued until the end of the ECG segment.

## III. FEATURE EXTRACTION

The feature extraction is a core process utilized for the recognition of heart rhythm. For a good recognition, a well-extracted feature is required. We extracted a feature from the QRS complex based on morphological information. These features offer physiologically meaningful information. Three of these features were selected to classify the ventricular arrhythmia, and these features are QRS slope, and QRS shape similarity.

### A. QRS Detection

Detection of the QRS complex should be conducted because this process affects the feature extraction process a great deal after the preprocess is concluded. The QRS detection process is comprised of the following sequence. 1) The ECG segment is separated into two parts, with one being above the baseline (the positive part) and the other being under the baseline (the negative part). 2) The process of adaptive threshold peak detection is applied to these two parts. 3) We defined the peak of the positive part as 1 and the peak of the negative part as -1. 4) The sequence of [-1 1 -1] was established, means of QRS location, and the performance results of QRS detection are given in Fig. 1. This algorithm is modified from [8]. In [8], a threshold was determined adaptively, but it was only good for PhotoPlethysmoGraphic (PPG). So, to apply this method properly for ECG, we added a feedback variable, and then (1) was drawn.

$$thr_k = thr_{k-1} + \beta \frac{peak_{n-1} + thr_{k-1} - \sigma_{ECG}}{F_s} \quad (1)$$

In (1)  $thr_k$ ,  $\beta$ ,  $peak_{n-1}$ ,  $\sigma_{ECG}$  and  $F_s$  signify k-th slope threshold, slope changing rate, previous peak amplitude, standard deviation of the four-second segments, and sampling frequency. The  $thr_{k-1}$  of a second term is operated as a feedback factor and this factor make a threshold slope to exponential shape.

### B. RR Interval

In a normal situation, the human heart does not beat at a fast rate. In cases of tachycardia, flutter, and fibrillation, the RR interval is shorter than a normal beat, however. The P and T wave are combined or disappeared. This feature represents a ventricular pacing status.

### C. QRS Complex Slope

A ventricular conduction problem leads to the gradual slope of QR and RS, a means of expanding QS width. Typical symptoms of this problem include tachycardia, flutter, and fibrillation. The NSR and the SVT have a steep incline. In this paper, which considers two parts of slope, such as QR and RS, the conductivity was calculated by averaging the slope value of QR and RS.

### D. QRS Complex Shape

The shape of the QRS complex is a significant factor in classifying ventricular arrhythmia. The QRS shape of NSR, SVT, monomorphic VT, and VFL show a similar pattern, compared with the shape of the QRS' own segment. In this paper, cross correlation was used to measure the similarity of the QRS shape at each four-second segment. A method of obtaining a stable score on how QRS shape is matched is described in the following sequence. 1) The first QRS shape is converted into a reference template. 2) A cross correlation is performed with each QRS shape. 3) The latter process is conducted again until every QRS shape has been selected as a reference template. 4) The median value of the cross correlation represents the stable score of the QRS shape.

## IV. ECG CLASSIFICATION

A Support Vector Machine (SVM) is a powerful classification tool proposed by C. Cortes and V. Vapnik [9].

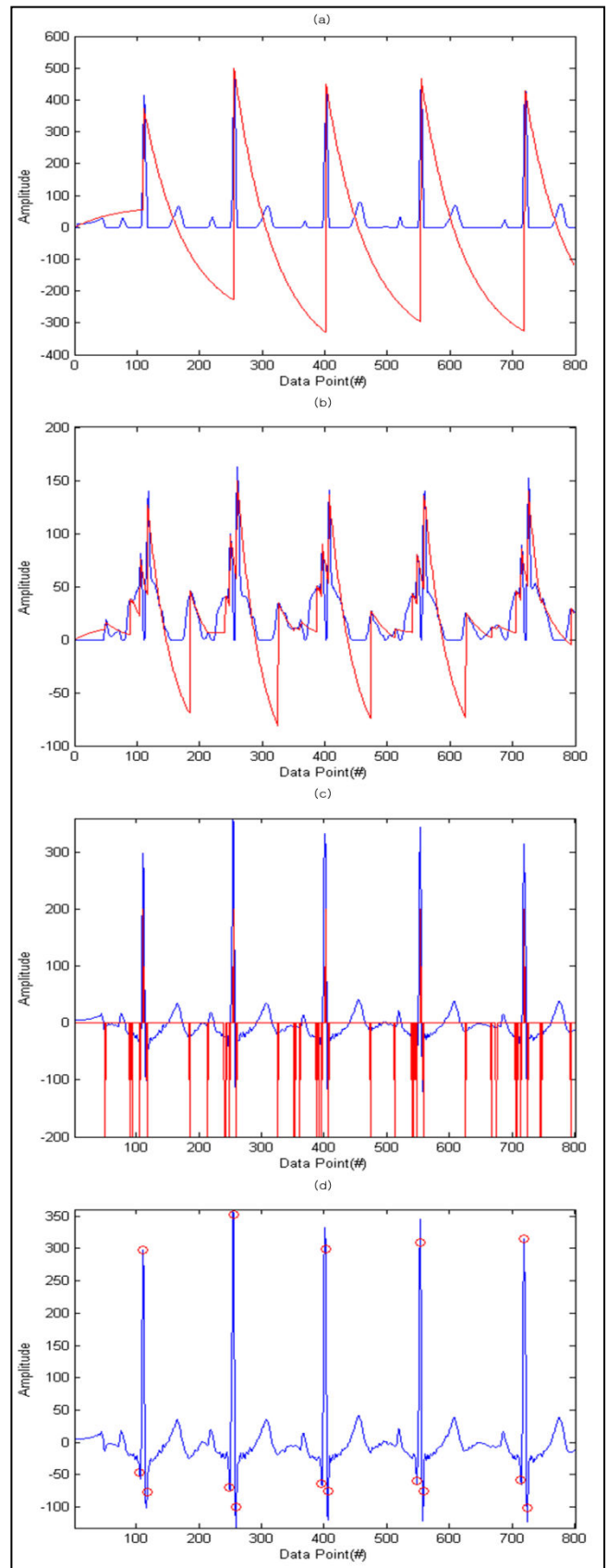


Figure 1. The detection process for the QRS segment: (a) the positive part of ECG; (b) the negative part of ECG; (c) QRS (-1 1 -1) sequence; and (d) detection of QRS segment; the red line in (a) and (b) is adaptive threshold line and in (c) is detected peak location

TABLE I. THE RESULTS OF CROSS-VALIDATION

Class Type	NSR	SVT	VT	VFL	VFib
Cross-Validation Accuracy (%)	96.3	95.06	92.59	91.36	88.27
C	128	32	8	16	4
Gamma	1	4	1	4	0.5

The concept behind this method is the maximization of a margin of two groups, whereas a typical classifier minimizes a misclassification. The SVM separates input data  $X$  into two classes. When the decision hyperplane  $d(x)$  conducts this separation,  $X$  determines whether  $d(x) > 0$  or  $d(x) < 0$ .

A classification problem generally occurs when there is a non-linear class boundary. It is a very hard to separate classes into two groups, so a feature space is transformed to a higher dimension space. As a result of this transformation, we can utilize a more simple support vector classifier. The method of increasing dimension creates a problem, however: an increased calculation cost. To solve this problem, the kernel trick was proposed. Using a kernel function, we can calculate 3D vectors as 2D vectors. The SVM should optimize the hyperplane. To perform this optimization, the following objective function should be solved [10].

$$L(\alpha) = \sum_i^N \alpha_i - \frac{1}{2} \sum_i^N \sum_j^N \alpha_i \alpha_j y_i y_j K(x_i, x_j), \quad (2)$$

$$\sum_i^N \alpha_i y_i = 0, \quad (3)$$

$$0 \leq \alpha_i \leq C, i = 1, \dots, n \quad (4)$$

The objective of this equation was to maximize (2) in conditions of (3) and (4). A linear classifier is easier to use in analysis or calculation than a non-linear classifier, but in this work, the distribution pattern of the groups is not clearly linear. In this case, we used a non-linear SVM, which necessitated a kernel function. In this work, a Gaussian Radial Basis Function (RBF) was utilized as the SVM kernel function represented by (5). The RBF kernel is commonly used in unknown data distribution.

$$K(x, x') = e^{-\|x-x'\|^2/2\sigma^2} \quad (5)$$

$$d(X) = \sum_{X_i \in SVS} \alpha_i y_i K(X_i, X) + b \quad (6)$$

As when using SVM, a two-step process must be conducted. One is a training step. The other is a classifying step. In the training step, when input vector come into (2), the vector  $\alpha$ , which is maximizing the (1), is obtained. This vector creates a discriminant function given in (6). In the classifying step, a new input vector is determined by the discriminant function. The SVM method is basically a binary classification tool, but we have five classes of data and thus could classify just two.

To solve this problem, two methods, called one against one (OAO) and one against all (OAA), were developed, and we applied OAA to this work, and this method was discussed in [9]. The OAA, named "winner takes all," sorts all of the classes into the same group except one, a reference class, and then a one binary classifier can be made. If the  $k$  classes

TABLE II. THE RESULTS OF CLASSIFICATION

Class Type	NSR	SVT	VT	VFL	VFib
NSR	63	0	0	0	0
SVT	0	5	0	0	0
VT	0	0	20	3	4
VFL	0	0	2	23	0
VFib	0	0	1	1	39
Sensitivity(%)	100	100	74.07	92	95.12
Specificity(%)	100	100	97.76	97.06	96.67

existed, total  $k$  binary classifiers would be created.

## V. RESULTS & DISCUSSION

In this experiment, we used ECG data extracted from Creighton University and the MIT-BIH database. We included five types of ECG beat episodes: NSR, SVT, VT, VFL, and VFib. These five episode types are called ventricular arrhythmias except the NSR. Unfortunately, these episodes are not all the same because arrhythmia episodes arise variably and do not have to be sustained for 4 seconds. For this reason, the segment of SVT and VFL could not be extracted from the ECG record easily. To establish a training data set, we chose 50% of each beat episode and left out those used for the test set. The total number of data was 323, while that of the training set was 162. Another 161 data had been used in the test set data.

We needed to select two parameters,  $C$  and  $\gamma = \frac{1}{2\sigma^2}$  for optimal classification. To find these two parameters optimally, we had to perform a cross-validation. Then, we took the best of  $C$  and  $\gamma$ . In this work, the five classes exist, and cross-validation should be performed five times. Table I shows the results of cross-validation.

The results of SVM classification are shown in Table II. This table represents the correct classified number, misclassified number, and accuracy of each heartbeat class. The NSR and SVT were 100% classified, but some VT, VFL, and VFib were misclassified. The three VT data were misclassified as VFL, and four VT data were misclassified as VFib. For VFL, two data were classified to VT. Each bit of VFib data was classified as VT or VFL. The QRS complex of NSR and SVT had a very similar morphology, and the SVT's RR interval was commonly shorter than that of NSR. This is a why good distinguish result appeared between NSR and SVT. The polymorphic VT, VFL, and VFib resembled each other, as well. VT consists of two types: monomorphic and polymorphic. The monomorphic VT has a very simple type of beat shape, and stable QRS complex shape with wide QRS width and fast beat rate. This morphological characteristic is very similar to VFL. In contrast, the polymorphic VT is characterized by a variable QRS complex, like VFib. These facts explain why this morphological approach does not perfectly classify ventricular arrhythmia.

## VI. CONCLUSION

The objective of this study was to apply morphological-based SVM classifications to ventricular arrhythmias, such as NSR, SVT, VT, VFL, and VFib. The three classification features were extracted through the

automatic QRS complex detection method. In computer simulation, our proposed method has a successful result of recognition and 93.16% sensitivity. Future research might aim to increase the number of each heartbeat data point and find a morphological feature to obtain greater accuracy.

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