

# The Prediction of Ventricular Fibrillation based upon HRV Signal Using Combination of Genetic Algorithm and Neural Networks

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## Abstract

*Nowadays ventricular fibrillation has become one of the most serious cardiac rhythm disturbance in the world. It is worth predicting this problem and also achieving valuable chance for clinical therapy. At the time of happening VF some symptoms in heart rate variability (HRV) signal are apparent, which can be used to predict VF. Before happening VF, finding these symptoms are cumbersome and this problem leads to the fact that the proposed approach becomes weaker because it is desirable to reduce the time of prediction. In this study, an algorithm with the purpose of predicting VF is presented, which is based on extracting linear, frequency and non-linear features from HRV signal. Extracted features are validated through the use of t-test, and useful features*

*are extracted by means of genetic algorithm (GA) and neural networks. Target function of GA is selected by considering the linear combination with positive rate of accuracy, sensitivity, specialty and negative rate in number of features. The most significant achievement of this study is taking no notice of frequency features of HRV signal, which represents the stress level and also relaxation of patient before happening VF. Moreover, the obtained results of this study are compared based on k-fold test and has achieved the accuracy of 96.67% in accordance with the non-linear features.*

*Keywords: Ventricular Fibrillation, Heart Rate Variability, Genetic algorithm, Neural network, Prediction*

## Introduction

Early detection of life threatening arrhythmias is important for successive defibrillation therapy.

Ventricular fibrillation (VF) created by myocardial ischemia is one of the main factors of death related to cardiovascular diseases. In other words, sudden cardiac death (SCD) is the result of millions of death worldwide and has no important symptoms earlier than one hour before occurrence (Przystup, Przystup, Bujnowski, & Wtorek, 2014). It is to be noted that VF is the most common reason for SDD and also leads to death in most cases and consequently prognosis of this disease in one minute before occurrence can be

very precious (Riasi, 2013). This is mainly because VF is inherently a probabilistic event that can be affected under certain pathophysiological and routine situations (Arini, Bonomini, & Valentinuzzi, 2010). Heart rate variability (HRV) is the temporal variation between sequences of consecutive heartbeats (Reed, Robertson, & Addison, 2005). The most important problems of VF are as follows: the occurrence of VF has the clear symptoms related to HRV and ECG, which can be used with the aim of predicting this discomfort. However, before happening VF, finding these symptoms are cumbersome and this problem leads to the fact that the proposed approach becomes

weaker because it is desirable to reduce the time of prediction. Authors in (Reed et al., 2005) investigated the relationship between Heart rate variability measurements and the prediction of ventricular arrhythmias as a review paper. Moreover, authors in (Asl, Sharafat, & Setarehdan, 2012) studied the classification of arrhythmias including VF and PVC and also normal rhythms based on the detailed analysis of HRV. Furthermore, authors in (Nabina N Rawther, April 2015) designed an algorithm correspond to multiresolution wavelet analysis using temporal and wavelet features of Electrocardiogram and Phonocardiogram along with Electrocardiogram-Phonocardiogram relationships was designed so as to increase the efficiency of the heart diagnostics. Authors in (Zhuang et al., 2008) investigated two nonlinear complexity measures based on entropy: approximate entropy (ApEn) and sample entropy (SampEn) as well as two time linear indices: the mean RR interval (the average of time intervals between consecutive R-waves) and the standard deviation of RR intervals were used for short-term forecasting of VT-VF occurrence. Moreover, authors in (Joo, Choi, & Huh, 2012) proposed a classifier that can predict VTA events using artificial neural networks (ANNs) trained with parameters from heart rate variability (HRV) analysis. Altogether, to the best of our knowledge the lack of investigating features based on ability to separate is the main disadvantage of previous studies. In this paper, using GA and determination of the superior chromosome leads to solving this problem.

### Proposed method

All databases that are utilized in this paper are spontaneous ventricular arrhythmias databases based on [Medtronic company](http://www.medtronic.com), which are available in <https://physionet.org>. These databases have 135 pair of RR interval, which are recorded using an ICD that placed in 78 patients' body. The R wave in EGM signal is identified using an amplifier, which is

regulated automatically. All the data are divided into two parts i.e. Prevt and Prevf. Prevt data consists of 106 records corresponding to patients and also Prevf consists of 29 records. There is another group of data in these database, which its name is MR and are called control group. MR group consists of records corresponding to Prevt and Prevf patients, when these patients do not have any heart attack. At the end of each recorded signal there is a place that related to start of VF and VT, in other words the label of data is there. Figure 1 shows the HRV signal of a patient when VF attack happens to them. in figure 2 the HRV signal of patient is shown when there is no complication.

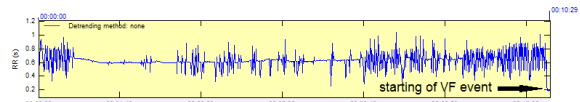


Figure 1: The HRV signal of a patient when VF attack happens

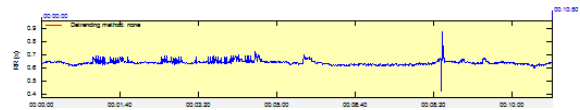


Figure 2: The HRV signal of a patient when there is no complication

### The horizon of prediction

In type 1, 10 seconds before complication is identified, and then 1 minute is moved back. In other words, the time of 1 minute before 10 to 70 seconds until happening of VF is investigated with the purpose of investigating desirable features in this period. Figure 3 shows the extracted HRV signal of patient in this period. In type 2 extracted features only consist of features that are in interval between 70th-130th second. In other words, in this method the horizon of prediction is considered at 70 seconds before occurrence of complication. Figure 4 shows HRV signal related to this situation. Moreover, the extracted features in type 3 consist of differences between extracted features in type 1 and type 2.

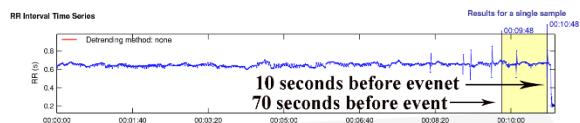


Figure 3: The extracted signal in type 1 (Short time prediction)

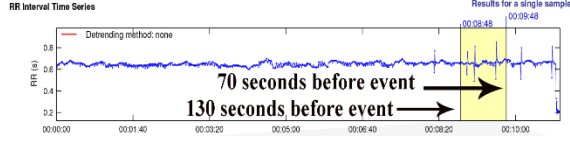


Figure 4: The extracted signal in type 2 (Long time prediction)

In this paper, the following features are extracted, and then investigated using statistical methods:

SampEn, D2, Alpha-1, Alpha-2, Lmean, Lmax, REC, Mean\_RR, std\_RR, RMS\_SD, NN50, PNN50, DET, TINN, LF, HF, VLF, SD1, SD2, APEN, ShannonEN.

### The evaluation of features based on statistical methods

Performing Kolmogorov–Smirnov test on specified features that consist of linear features, non-linear features, TINN, PNN50, NN50, mean\_RR, frequency features, DIV, SampEn, APEN, DFA.alpha, DFA.alfa1, SD2, D2 and SD1 results in the fact that all of them have a normal distribution and other features do not have this property and are abnormal. T-test is utilized with the aim of evaluating the normal features and Mann–Whitney test is utilized with the purpose of evaluating abnormal features. It should be noted that the VLF, HF and DIV parameters do not have the ability to separate these two groups, because p-value for them are less than 0.05. Finally, the dimensions of features are decreased to 22 using taking no notice of these three parameters.

### The evaluation of results based on GA

In order to select superior features genetic algorithm and neural network classifications are employed simultaneously. The dimensions of each classifier were different in each type of proposed method. The initial parameters in the proposed algorithm are as follows:

#### The cost function

$$Cost_i = w_1 \times (1 - Accuracy_i) + w_2 \times (1 - Sensitivity_i) + w_3 \times (1 - Specificity_i) + w_4 + \frac{L_i}{N}$$

At first, 20 chromosomes with 22 genes that randomly get the value of 0 or 1 are selected, and then genetic mutation operation, chromosomal combination operation and calculating their worthiness are implemented, and after 50 iterations a chromosome that had the best result in cost function was chosen as the superior chromosome. It is to be noted that this operation is implemented for each type and each classifier separately. The sensitivity coefficient, specialty coefficient and accuracy coefficient are considered 0.4, 0.19 and 0.4 respectively. Moreover, the probability of equivalent mutation was 0.6% for GA. In order to decrease the number of features target function are designed based on the number of features. After extracting features for both groups of healthy and unhealthy people, in order to make data matrix each person is placed in a row and each feature is placed in a column. The dimensions of data matrix for type 1 and 2 of proposed method are similar and equivalent to  $58 \times 22$ , and for type 3 are  $116 \times 22$ . Considering the fact the average state is a special case of type 3 and the similar results for these two states were achieved, the average state does not consider as a new type. In order to classify, data learning process is performed using 10-fold cross validation. Stop benchmark of network is getting default validation error, which is under the test validation learning error.

### The results of classification for two different methods

For type 3, the best specificity, accuracy and sensitivity are derived from KNN classifier at the time of using GA. In this type, using KNN classifier leads to achieving the best results for sensitivity, specificity and accuracy. The GA algorithm in this situation using selection of 13 features improved the values of results to 96.97%. The selected features in this type are according to table 1. It is to be noted that the most significant achievement of this study is taking no notice of frequency features of HRV signal, which represents the stress level and also relaxation of patient

before occurrence of VF. The main reason of ignoring these features is that HRV is a rhythm-based signal and consequently the features that are based on beat have the less effectiveness in comparison with other features.

Table 1: The selected features according to type 3

Feature	Sensitivity	Specificity	Accuracy
All feature	94%	75.76%	84.88%
PCA	87.88%	78.79%	83.33%
GA	96.97%	96.97%	96.97%

Considering the fact that the results of all types at the time of using GA had the best performance in comparison with other methods, in the following chart the results of each classifier for each type based on sensitivity, specificity and accuracy for GA are shown in detail.

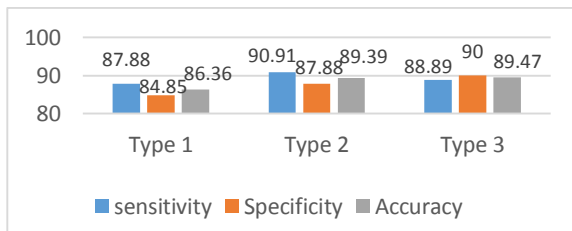


Figure 5: The results of each classifier for each type

MLP classifier similar to two previous classifiers in type 3 had the best ability to separation using GA. In this type, GA utilized 13 features with the purpose of classifying data.

## Conclusion

Altogether, the most significant results of this study are as follows: Investigating intervals between 70th-130th seconds and 10th-70th before the occurrence of VF leads to the fact that the accuracy of prediction has an ascending order. The best answer was at type 3, which was the differences between two intervals.

The results of our study showed that KNN classifier could possess the best accuracy for prediction of data on ventricular fibrillation, and considering the fast performance of this algorithm leads to the fact that it will fasten the speed of prediction.

In this study, using GA and type 3 of proposed method leads to achieving features in the highest level of accuracy, which were included linear, non-linear. Finally, it should be noted that the most achievement of our study is taking no notice of frequency features related to HRV signal

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