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Early detection of sudden cardiac death using Poincaré plots and recurrence plot-based features from HRV signals

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Abstract: In this paper we present a method to predict sudden cardiac death (SCD) based on the heart rate variability (HRV) signal and recurrence plots and Poincaré plot-extracted features. This work is a challenge since it is aimed to devise a method to predict SCD 5 min before its onset. The method consists of four steps: preprocessing, feature extraction, feature reduction, and classification. In the first step, the QRS complexes are detected from the electrocardiogram signal and then the HRV signal is extracted. In the second step, the recurrence plot of the HRV signal and Poincaré plot-extracted features are obtained. Four features from the recurrence plot and three features from the Poincaré plot are extracted. The features are recurrence rate, determinism, entropy and averaged diagonal line length, and SD1, SD2, and SD1/SD2. In the next step, these features are reduced to one feature by the linear discriminant analysis technique. Finally, K-nearest neighbor and support vector machine-based classifiers are used to classify the HRV signals. We use two databases, the MIT/BIH Sudden Cardiac Death Database and PhysioBank Normal Sinus Rhythm Database. We manage to predict SCD occurrence 5 min before the SCD with accuracy of over 92%.

Key words: Sudden cardiac arrest, heart rate variability, support vector machine, k-nearest neighbor, recurrence plot, Poincaré plot

1. Introduction

Abnormality in heart rhythm (arrhythmia) can cause sudden cardiac death (SCD) [1–3]. SCD causes thousands of adult deaths in the United States each year [4,5]. Despite the reduction in deaths from heart diseases in the last 20 years [6–9], SCD is responsible for half of all deaths from cardiovascular diseases [10–15]. When the electrical system of the heart becomes irregular, SCD will occur. One of the signs of SCD is ventricular fibrillation (VF) [16]. Arrhythmias like VF occur because for various reasons such as diabetes, alcohol, and smoking [17,18]. Today invasive and noninvasive techniques are the main ways of predicting the risk of SCD [19–24]. In recent years genetic factors have been added to the previous SCD risk factors [3]. Electrocardiograms (ECGs) are among the best ways to diagnose heart diseases. There is a QRS complex in each ECG signal, which consists of three waves named Q, R, and S. Invariant heart rate (HR) is the beat-to-beat variation and shows a failure in heart function [25]. Heart rate variability (HRV) is the distance between the R waves from beat to beat, also known as the RR interval. Recently researchers have focused on nonlinear methods that are extracted from the HRV signal because of their performance [26]. Bilgin et al. [27] presented a method that provides new indexes for ventricular tachyarrhythmia diseases. In their study they showed that some subbands over LF and HF base-bands have lower energy values than other subbands for ventricular tachyarrhythmia datasets. In another

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study, Bilgin et al. [28] described a VLF band with determination of dominant subbands in order to evaluate ventricular tachyarrhythmia diseases. Voss et al. [29] proposed a method by using time and frequency features from ECG and HRV signals of 35 healthy people and 26 cardiac patients after myocardial infarction (they were divided into a low-risk group and high-risk group). They used nonlinear methods and renormalized entropy. They found 96% separation between healthy people and high-risk patients using nonlinear methods. The time domain and frequency domain parameters had less than 90% accuracy. They found complete 100% separation between the two groups by using the combination of features from all domains and a stepwise discriminant function. La Rovere et al. [30] extracted time and frequency domain parameters and features from HRV signals to study their usage in SCD prediction. Their results showed that the short-term low-frequency power of HRV during controlled breathing is a perfect predictor of sudden cardiac death in chronic heart failure patients. Shen et al. [31] developed a personal cardiac homecare system to predict SCD 2 min before SCD occurrence. They used features from ECG and HRV signals of 20 health people and 23 SCD patients and found 87.5% separation between healthy people and SCD patients using wavelet analysis and short-term HRV analysis. Finally, features were determined and used in artificial neural networks. The accuracy of SCD prediction by using the least mean square, decision-based neural network, and backpropagation neural network was 67.44%, 58.14%, and 55.81%, respectively. Elias et al. [32] extracted linear (MNN, SDNN, RMSSD, SDSD, pNN50, low frequency (LF), high frequency (HF), very low frequency (VLF), and ratio of LF and HF bands power) and time-frequency (TF) (average energy from the HRV signal) features to study their usage in SCD prediction. They used features from HRV signals of 35 healthy people and 35 cardiac patients. They claimed that the results could predict SCD with an accuracy of 74.36% and 73.87% using linear features, and 99.16%, and 96.04% for TF features using MLP and KNN classifiers respectively for the first 1-min interval. They likewise reported 72.38% and 69.35% accuracy for the linear method and 91.23% and 89.27% for the TF method using MLP and KNN classifiers, respectively, for the 2-min interval before SCD onset. George et al. [33] used nonlinear methods (Poincaré plot, DFA, Hurst's exponent, approximate entropy), geometrical methods (triangular index), frequency analysis methods (power in LF and HF bands), and statistical methods (pNN50, RMSSD, SDSD, SDNN) in HRV analysis. They used features from HRV signals of 40 patients with ischemic heart failure (high and low risk). The accuracy of classification was 87.5% by using SVM with the RBF kernel and 85% by using random forest classifiers.

In this study, some features, based on our previous experiences, are extracted from HRV signals. Initially, 3 Poincaré plot analysis and 4 recurrence plot features are extracted from each HRV sample of healthy and cardiac patients. A Poincaré plot is a plot with an axis of current RR intervals versus previous RR intervals. The Poincaré plot is usually used to quantify self-similarity [34]. A recurrence plot is a graph that is suitable for the analysis of physiological signals. After the feature extraction process, a linear discriminant analysis (LDA) method is used to select the most discriminating feature. A feature vector is used for prediction of SCD occurrence using a support vector machine (SVM) and the K-nearest neighbor (KNN) method. To get the best performance, different numbers of nearest neighbors and kernel functions (RBF and polynomial) are tested in the KNN and SVM classifiers [35]. We could reach 5 min of prediction before SCD occurrence and this is a tipping point in this field. This work has been implemented in MATLAB 8.4 software.

2. Materials and methods

Two databases were used in this study: the MIT/BIH SCD database and the PhysioBank Normal Sinus Rhythm database [36].

We used a database consisting of 59 ECG signals from 23 cardiac patients (18 to 89 years old) with a sampling rate of 250 Hz. The number of healthy controls was 36, with 18 healthy people with lead I and 18 with lead II (20 to 50 years old and 128 Hz sampling rate). In this study, the HRV signals derived from lead II of patients and lead I and lead II for healthy people were used. In order to maintain accuracy, the ECGs from the patients were downsampled (from 250 Hz to 125 Hz to match the normal ECGs). The HRV signals of three patients were eliminated from the SCD database since they did not have ventricular fibrillation (V) episodes, and no signal from the normal database was discarded since it was without abnormalities. To evaluate the performance of our method in separating cardiac patients from healthy people, feature vectors were extracted from the fourth and fifth 1-min segments of the signals before SCD occurrence.

The block diagram of our process to predict the cardiac patients and healthy people is shown in Figure 1.

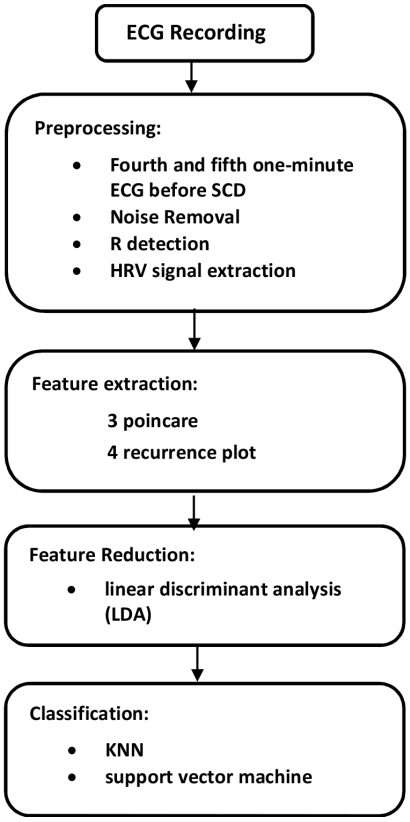

Figure 1. The block diagram of our process to predict cardiac patients and healthy subjects.

Figure 2 shows the data segmentation of a cardiac patient (2 min before SCD).

2.1. Preprocessing

We divided the ECG signal into specified time intervals (first 1 min, up to the fifth 1 min before SCD). These time intervals were used as ECG signals of patients. For healthy subjects random 1-min intervals were selected from a 1-h recording. First, noise reduction for healthy and patient ECG signals was done. Low frequencies in baseline wander (because of DC drift) and high frequencies in power line interference (because of AC power noise) were removed. To remove the baseline drift both healthy and patient ECG signals were filtered with a

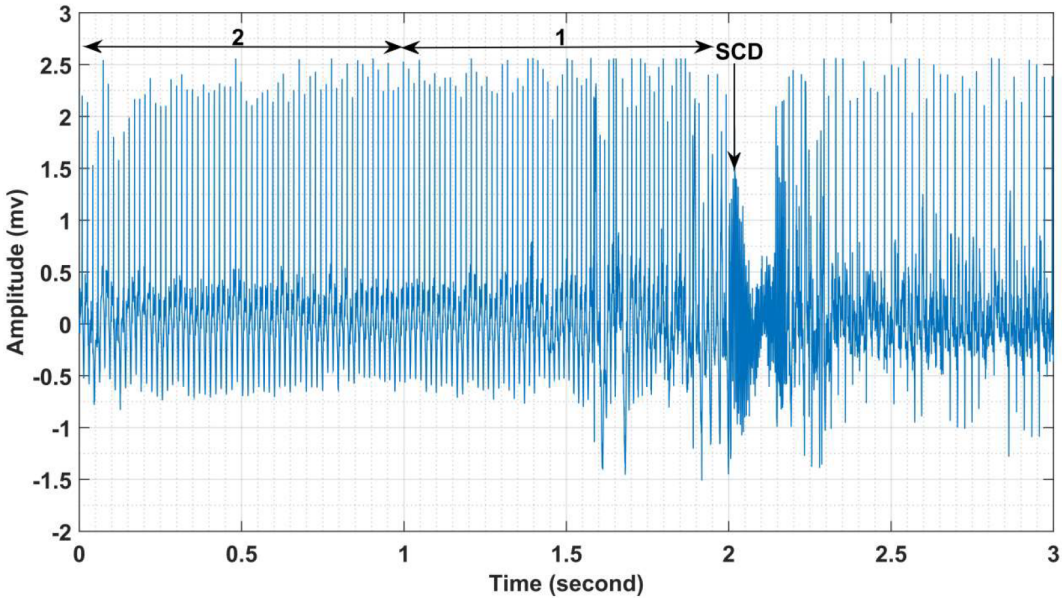

Figure 2. Data segmentation of a cardiac patient. Number 1 shows the first minute of the ECG signal before SCD started. Number 2 denotes the second minute (2 min) before SCD started.

moving-average filter. With the moving average filter, an array of raw (noisy) data $[y_1, y_2, \ldots, y_N]$ can be converted to a new array of smoothed data. The smoothing process is like a low-pass filter response:

$$y_s(i) = \frac{1}{2N+1} \sum_{k=-N}^{N} y(i+k). \tag{1}$$

In this equation, $y_s(i)$ is the smoothed value of the ith data point, and N denotes the number of data neighbors on each side of $y_s(i)$. The number 2N+1 is usually used as the window size. We apply a two-stage moving average filter on each ECG signal. First, signals move through a moving average filter with window size of 1/3 signal length, and then this prefiltered signal moves through a moving average filter with window size of 2/3 signal length. The drift of the signal will be removed by subtracting the output of this filter from original data [37]. A median filter with a notch filter is used to remove the power line frequency [38]. The median filter is a nonlinear digital filter. The mathematical concept of median is used to describe the middle of the data. Like the moving average filter, we apply a two-stage median filter on each ECG signal. First, signals move through the median filter with window size of 1/3 signal length, and then this prefiltered signal moves through a median filter with window size of 2/3 signal length. The median filter thus uses both past and future values for predicting the current point. We can describe the operation of the median filter as follows:

$$y_p(n) = median(x(n+M1).....x(n).....x(n-M2)), \tag{2}$$

where:

$$median(x_1....x_N) = \begin{cases} x_{\left(\frac{N+1}{2}\right)} & N \quad \text{odd} \\ \frac{1}{2}\left(x_{\left(\frac{N}{2}\right)} + x_{\left(\frac{N}{2}+1\right)}\right) & N \quad \text{even} \end{cases} \tag{3}$$

and where $x_{(n)}$ is the nth smallest of the values x_1 through x_N. For the notch filter we use the following formula [39]:

$$y_k(n) = \frac{1}{2}[(1+a_2)\,x(n) - 2a_1 x(n-1) + (1+a_2)\,x(n-2)]$$

$$+a_1 y(n-1) - a_2 y(n-2), \tag{4}$$

where:

$$a_1 = \frac{2\cos(\omega_0)}{1+\tan(\frac{\Omega}{2})},$$

$$a_2 = \frac{1-\tan\left(\frac{\Omega}{2}\right)}{1+\tan\left(\frac{\Omega}{2}\right)} \tag{5}$$

In Eqs. (3) and (4), x(n) is the input signal and y_k(n) is the output of the notch filter. ω_0 and Ω are the notch frequency and 3-dB rejection bandwidth, respectively.

We used filtered signals in all procedures. The Pan–Tompkins [40] algorithm is used for detection of the QRS-complex, and especially the R wave, and then we could determine the RR-intervals and HRV signal (the RR-interval between two consecutive beats). After these processes the HRV signal is ready to have features extracted from it. The HRV signals of a patient and a healthy person are shown in Figure 3.

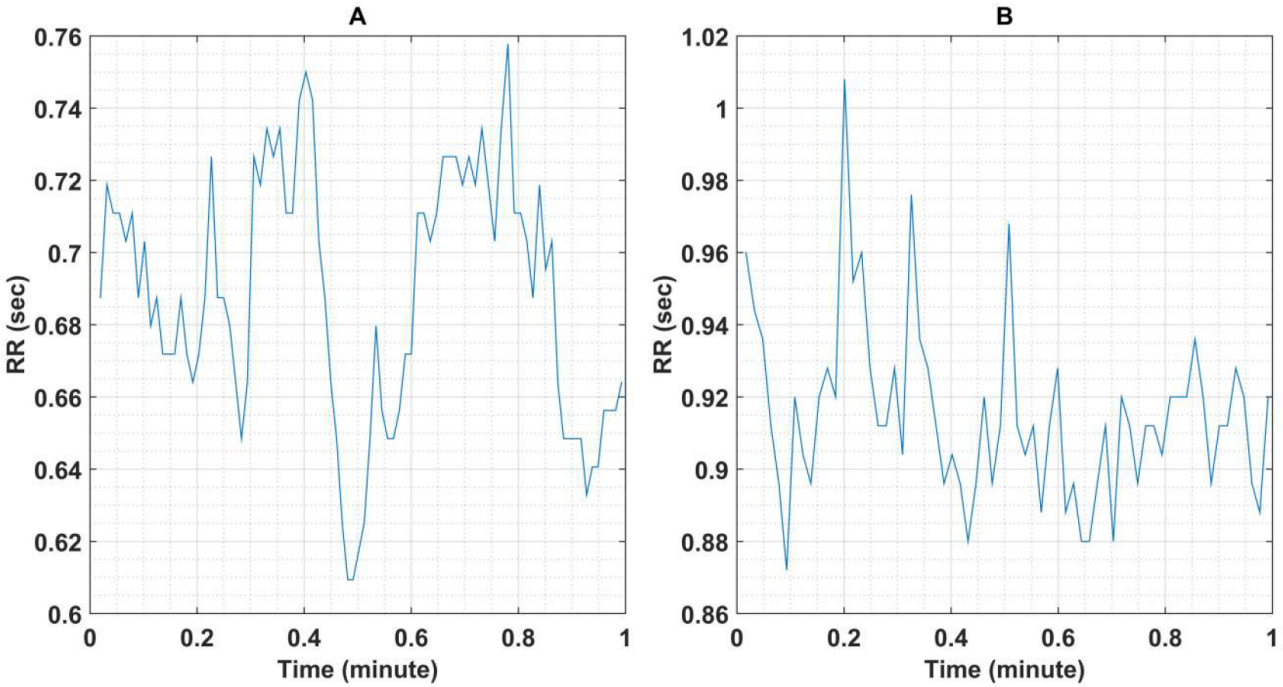

Figure 3. (A) HRV of a healthy person, (B) HRV of a person just before SCD onset.

2.2. Feature extraction

In this step, we attempt to extract the features from HRV signals, which can be used as a predictor of SCD. For HRV signals, the linear methods are simple and features can be extracted by time and frequency domain

analysis for each episode. Nonlinear analysis can show HRV irregularities better than linear analysis in dynamic systems [41]. In this study, we extracted 7 features (according to our previous experiences) from HRV signals. These features are recurrence rate, determinism, entropy and averaged diagonal line length from the recurrence plot (RP), and SD1, SD2, and SD1/SD2 from the Poincaré plot, which are described in the next sections.

2.3. Poincaré plot-extracted features

The Poincaré plot is a method that does not require the HRV signal to be stationary [42]. A Poincaré plot is a graphical diagram to show the correlation $RR_{(n+1)}$ as a function of $RR_{(n)}$ where $\mathrm{RR}_{(i)}$ is the beat-to-beat interval and R corresponds to the peak of the QRS complex for each beat in the ECG signal. The Poincaré plot was drawn by calculating standard deviations of the distances of $RR(i)$ from the lines $y = x$ and $y = -x + 2RR_m$, where RR_m is the mean of all $RR(i)$. These standard deviations are called SD1 and SD2. Another feature that we used was SD1/SD2. Figure 4 shows the Poincaré plot of a normal HRV.

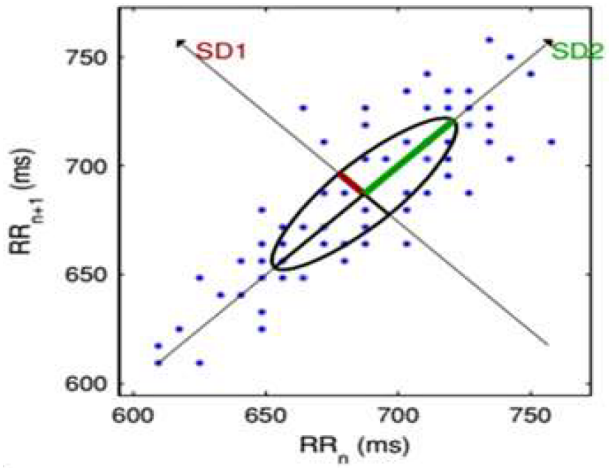

Figure 4. Poincar plot of the normal HRV (record 16265).

2.4. Recurrence plot

In recent years features like entropy and Lyapunov exponents are considered as good features for time series [43]. The RP is a tool for analysis that was introduced in the late 1980s [44]. RP is a visualization (or a graph) of a square matrix, in which the matrix elements correspond to those times at which a state of a dynamical system recurs (columns and rows correspond to a certain pair of times). Technically, the RP reveals all the times when the phase space trajectory of the dynamical system roughly visits the same area in the phase space. The RP is suitable for the analysis of physiological signals, which are often nonstationary [45].

2.5. Feature dimension reduction by LDA

The reason to use LDA is to perform dimensionality reduction [22]. The projection can be written as:

$$Y = \mathbf{W}^t x, \tag{6}$$

where W is the weight matrix and x is the feature vector. The weights are estimated to maximize the differences between the means of classes and to minimize the differences within the same class. Generally, classes with

large dissimilarities will have larger weights. As a result, if there are C classes, the dimension of the feature can be reduced extremely to C – 1. In this paper, numbers of original features have been reduced to one feature by means of the LDA technique.

2.6. Classification

In this work we used two classifiers, the K-nearest neighbor (KNN) and support vector machine (SVM), to differentiate between healthy subjects and patients. To evaluate the performance of classifiers, a ten-fold cross-validation method is used. The 56 ECG signals are divided into ten parts and the numbers of signals in parts are equal unless in two or three groups. One part was used to test the classifier and nine parts were used to train the classifier. This process was repeated ten times for each different test set, and the average performance for accuracy, sensitivity, and specificity was calculated. In order to increase the accuracy, we repeated each of the ten processes twenty times.

2.7. K-nearest neighbor

This classifier stores labeled feature vectors and calculates the minimum distance between stored and new feature vectors [46,47].

The basic steps of the KNN algorithm are:

- To compute the distances between all samples that have already been classified into clusters;
- To find the k samples with the smallest distance values;
- To approve new data.

A new sample will be added (classified) to the largest cluster out of k selected samples. We tested the values of k from 1 to 25 to make a comparison with [48] and we found that k = 5 and k = 15 get the best results with the KNN classifier for 4 min and 5 min before SCD, respectively. We show three k values (5, 15, 25) to reduce the complexity of tables.

2.8. Support vector machine

This classifier is a supervised learning method that is an extension of nonlinear models of the generalized portrait algorithm. The SVM algorithm is based on statistical learning theory [49,50]. The goal of regression is to determine the best model from a set of models (named estimating functions) to approximate future values accurately. The generic support vector regression estimating function is:

$$f(x) = (w \cdot \Phi(x)) + b, \tag{7}$$

where $w \subset R^n$, $b \subset R$ and Φ is a nonlinear function that maps x into a higher dimensional space. The weight vector (w) can be written as:

$$w = \sum_{i=1}^{l} (\alpha_i - \alpha_i^*)\Phi(x_i). \tag{8}$$

By substituting Eq. (4) into Eq. (3), the generic equation can be rewritten as:

$$f(x) = \sum_{i=1}^{l} (\alpha_i - \alpha_i^*)(\Phi(x_i) \cdot \Phi(x)) + b$$

$$= \sum_{i=1}^{l} (\alpha_i - \alpha_i^*)k(x_i.x) + b. \tag{9}$$

In this equation, the function $k(x_i x)$ is replaced with the dot product and known as the kernel function. The choice of kernel functions and kernel parameters usually depends on the application. Some of the useful kernel functions are radial basis functions (RBFs) and polynomial kernel functions. The formulas of these kernel functions are shown below, respectively:

$$exp\left\{\frac{-|x-x_i|^2}{2\sigma^2}\right\}, \tag{10}$$

$$\left[(x*x_i)+1\right]^d. \tag{11}$$

In this work, RBFs and polynomial kernel functions were used with different sigma values (σ = 0.8, 1, 1.2) and orders (d = 1, 2, 3), respectively.

3. Results and discussion

The RR, DET, ENTR, and L are described below [51].

RR: Recurrence rate; the percentage of recurrence points in an RP corresponds to the correlation sum.

$$RR = \frac{1}{M^2}\sum_{i.j=1}^{M} R_{i.j} \tag{12}$$

Here $R_{i,j}$ is to visualize the phase space trajectory by its recurrences and M is the dimension of the recurrence matrix. The optimum value for the embedding dimension, based on the criterion of the percentage of false nearest neighbors being minimum, is m = 4 for the proper state space reconstruction of the RR-interval segments.

DET: Determinism, the percentage of recurrence points that form diagonal lines.

$$DET = \frac{\sum_{l=l_{min}}^{M} lp(l)}{\sum_{i.j}^{M} R_{i.j}} \tag{13}$$

Here $p(l)$ is the number of diagonal structures whose length is l and $l_{min} = 2$ is used.

ENTR: Entropy, the Shannon entropy of the probability distribution of the diagonal line lengths $p(l)$.

$$ENTR = -\sum_{l=l_{min}}^{M} P(l)\, lnP(l) \tag{14}$$

Here $P(l)$ is the probability density of the diagonal structure whose length is l and it is defined as $p(l)/\mathrm{sum}(p(l))$.

L: Averaged diagonal line length, the average length of the diagonal lines.

$$L = \frac{\sum_{l=l_{min}}^{M} lp(l)}{\sum_{l=l_{min}}^{M} p(l)} \tag{15}$$

The best delay for signals such as HRV is 1 [52].

Tables 1 and 2 summarize the performance of the two classifiers for 4 min and 5 min before SCD. The features are used as input of LDA to reduce the numbers of original features and to enhance the performance of the proposed algorithm, and then we use SVM and KNN classifiers for classification. We have evaluated the performance of the classifiers with different kernels and k, such as polynomials with order 1, 2, and 3 and RBFs with different sigma values (σ = 0.8, 1, 1.2) for the SVM classifier and we tested values of k from 1 to 25 and found that k = 5 and k = 15 get the best results in the KNN classifier for 4 min and 5 min before SCD, respectively. We show three k values (5, 15, 25) to reduce the complexity of the tables.

Table 1. Performance of the two classifiers for 4 min before SCD.

Classifier	Sn (%)	Sp (%)	Acc (%)
KNN_5.00	83.25	95.41	91.07
KNN_15.00	75.00	97.22	89.28
KNN_25.00	75.00	97.22	89.28
SVM_poly_1.00	83.25	97.22	92.23
SVM_poly_2.00	80.50	97.22	91.25
SVM_poly_3.00	78.50	97.22	90.53
SVM_rbf_0.80	85.00	95.27	91.60
SVM_rbf_1.00	84.75	96.25	92.14
SVM_rbf_1.20	84.25	96.80	92.32

Table 2. Performance of the two classifiers for 5 min before SCD.

Classifier	Sn (%)	Sp (%)	Acc (%)
KNN_5.00	85.75	94.72	91.51
KNN_15.00	90.00	96.38	94.10
KNN_25.00	84.75	97.22	92.76
SVM_poly_1.00	90.00	93.33	92.14
SVM_poly_2.00	90.00	94.30	92.76
SVM_poly_3.00	89.25	95.13	93.03
SVM_rbf_0.80	90.00	91.80	91.16
SVM_rbf_1.00	90.00	92.36	91.51
SVM_rbf_1.20	90.00	92.91	91.87

Tables 3 and 4 present the mean and standard deviation (SD) of the features extracted using the Poincaré plot and RP techniques from the fourth and fifth 1-min data of patient and healthy HRV signals. SD1 and SD2 represent the standard deviations extracted from Poincaré plots.

Table 3. The mean and standard deviation of features extracted from the fourth 1 min before SCD onset and 1 min of normal HRV.

Features	SCD		Normal	
	Mean	SD	Mean	SD
SD1	0.12	0.08	0.03	0.02
SD2	0.15	0.11	0.07	0.03
SD1/SD2	0.94	0.34	0.41	0.17
RR	0.45	0.17	0.39	0.09
DET	0.93	0.04	0.95	0.02
ENTR	1.96	0.36	2.04	0.23
L	6.38	2.02	6.27	1.32

Table 4. The mean and standard deviation of features extracted from the fifth 1 min before SCD onset and 1 min of normal HRV.

Features	SCD		Normal	
	Mean	SD	Mean	SD
SD1	0.10	0.08	0.02	0.02
SD2	0.10	0.09	0.06	0.03
SD1/SD2	1.11	0.39	0.39	0.16
RR	0.47	0.16	0.42	0.09
DET	0.93	0.04	0.95	0.01
ENTR	1.94	0.31	2.06	0.21
L	6.30	1.73	6.26	1.38

It is shown in Tables 3 and 4 that the values of the RR, DET, and L parameters vary for healthy subjects and cardiac patients in time intervals, but the value of the ENTR parameter is lower for patients compared to healthy subjects. The values of SD1, SD2, and SD1/SD2 are lower for healthy subjects as compared to cardiac patients.

Voss et al. [29], La Rovere et al. [30], Shen et al. [31], Elias et al. [32], and George et al. [33] reported the results for times of less than 4 min before SCD occurrence and they were described in detail in Section 1.

Elias et al. [53] predicted SCD up to 4 min before SCD occurrence by using nonlinear and TF analysis of HRV signals. They extracted average energy as TF features and of Poincare plots and DFA as nonlinear features from HRV signals. They used KNN and MLP classifiers. Their results presented accuracy of 83.96% for the fourth 1 min before SCD onset. Rajendra et al. [48] proposed a method using discrete wavelet transform and nonlinear analysis of ECG signals. They segmented the ECG signal 4 min before SCD occurrence. For each time interval, nonlinear features were extracted from the composed signal with the discrete wavelet transform, and then the KNN and SVM classifiers were used for separating cardiac patients from healthy subjects. They proposed an accuracy of 92.11% (SVM) for 4 min before SCD onset. Our method can predict SCD occurrence 4 and 5 min before SCD onset with an accuracy of 92.14% (SVM) and 94.10% (KNN), respectively. This result is 1 min more than in previous works. This gives clinicians time to attend to patients within these 5 min. Another advantage of our work is that we did not change the original HRV signal parameters by eliminating ectopic beats or other detrending methods. Table 5 shows a summary of previous studies to predict SCD using ECG signal analysis.

Table 5. Summary of previous studies to predict sudden cardiac death using ECG signal analysis.

Features	No. of features	Classifier	Accuracy (4 and 5 min before SCD)
Combined linear, nonlinear, and TF methods [53]	Linear time domain (5), linear frequency domain (4), TF (11), and nonlinear (4)	KNN, MLP	4 min before = 83.96%
Nonlinear methods [48]	Nonlinear features (18), Sudden Cardiac Death Index	DT, SVM	4 min before = 92.11% (SVM)
This work	Poincaré plot features (3), recurrence plot features (4)	SVM, KNN with LDA	4 min before = 92.14% (SVM) 5 min before = 94.10% (KNN)

The time of the process from removing the noise of the ECG signal to get the classification results in the

worst case, with SVM classifier with polynomial kernel and order 3 (SVM_poly_3), is 1.38 s for one person with an Intel core i7, 2.70 GHz processor and MATLAB 8.4 software.

4. Conclusion

In this work, we presented a method to predict SCD 4 min and 5 min before SCD occurrence with an accuracy of 92.14% (SVM) and 94.10% (KNN), respectively. We used features derived from HRV signals. The LDA algorithm was used to identify the optimal feature for SCD prediction. The best feature was then fed into the SVM and KNN classifiers for prediction. The results showed that the prediction rate of this method is better than those of other studies with improvement in the SCD prediction rate. Our method showed better performance in 4 min before SCD occurrence in comparison to other studies. Moreover, we were able to extend the interval to 5 min for the first time and get good results before SCD.

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