A Machine Learning Method to Predict Sudden Cardiac Death Using Heart Rate Variability Signals

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Abstract

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Sudden Cardiac Death (SCD) is a sudden and unexpected death due to a cardiovascular cause occurring within one hour of symptoms onset. In this research, two combined schemes are proposed with the intention of predicting SCD by analyzing 16 minutes (at eight successive intervals of 2 minutes) of Heart Rate Variability (HRV) signals from a normal population and subjects at risk of SCD. In the first procedure, Ensemble Empirical Mode Decomposition (EEMD) approach is implemented on extracted HRV signals for decomposing them into different Intrinsic Mode Functions (IMFs). Subsequently, four entropy parameters, including Distribution Entropy, Sample Entropy, Fuzzy Entropy, and Rényi Entropy, are computed from the first three IMFs obtained. Then, a searching selection approach is applied to identify the best features for classification in feature space. Afterward, the classification is applied separately to each feature; then, the best distinguishing feature is selected based on the value of classification accuracy it returns. The most discriminating feature is thus combined with the other individual features to construct the best group combination. Eventually, these selected features are fed into various classifiers, such as Multilayer Perceptron (MLP), Support Vector Machine (SVM) and K-Nearest Neighbors (kNN), for the classification process. In the second procedure, the Empirical Mode Decomposition (EMD) method is utilized. Compared with well-performing methods, the two proposed schemes can predict subjects at risk of SCD up to 16 minutes earlier. The EEMD-based scheme demonstrates remarkable performance with an accuracy of 94.7%, 90.8%, 92.1%, 96.1%, 85.5%, 89.5%, 85.5% and 86.8% for the 1^{st} 2-min to 8^{th} 2-min before SCD onset, respectively. The results illustrate the significant capacity of the proposed method for predicting sudden cardiac death as compared with the previous studies, along with reducing the complexity of the study.

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Chapter 1: Introduction

1.1 Research Motivation

Sudden cardiac death (SCD) is an abrupt and unexpected death due to a lethal change in heart rhythm leading to loss of heart function, which is responsible for half of all heart disease deaths, often occurs with no warning [1–3]. SCD accounts for nearly 325,000 deaths in the US and 700,000 in Europe annually [4, 5]. Among young people (aged 35 years or younger), SCD has an incidence rate of approximately 5-37 events per one million person-year and occurs more frequently in men [6, 7]. People experiencing any type of heart diseases such as heart failure (HF), coronary artery disease (CAD), myocardial infarction (MI), and transient ischemia, have a higher SCD risk [2–6]. Based on a review on estimating deaths from cardiovascular diseases, ventricular fibrillation (VF), which is a life-threatening heart rhythm in which the ventricles quiver uselessly, is a leading cause of total and cardiovascular mortality [4]. Accordingly, for people who have experienced VF previously, early detection of unanticipated SCD would be crucial for treatment and subsequently improved survival. In addition, Ventricular Arrhythmias (VA) have been reported as the leading causes of SCD in both groups with previously diagnosed or even undiagnosed cardiovascular abnormality [8–10]. Also, Left Ventricular Hypertrophy (LVH) is an independent risk factor in adult patients, accounting for cardiovascular diseases leading to SCD. There are pieces of evidence that individuals with longstanding hypertension often have LVH problem [11]. Accordingly, SCD could be prevented on condition that a bystander applies an automated external defibrillator (AED) just quickly after cardiac arrest onset. The short time after SCA onset is vital since the restoration of heart rhythm would effectively increase the survival chance. Public Access Defibrillation (PAD) policies have been passed to support the programs on the public's access to such preventive devices [12, 13].

1.2 Background and Research Significance

Electrocardiogram (ECG) and Heart Rate Variability (HRV) signals have been utilized by researchers worldwide as predictor factors for SCD probability. The mentioned signals are the clinical markers that could expose cardiac problems which may result in SCD. For instance, HRV signal, measured by the variation in the beat-to-beat intervals which is the time of two successive R-wave within ECG signals [14], is an independent predictor of mortality after myocardial infarction (MI)[15]. Sudden Cardiac Arrest (SCA) could be the first and last heart condition to be diagnosed in a person, which continues to claim millions of people's lives around the world; consequently, early detection of SCD has increasingly being investigated. However, the accessible methods for prediction and prevention of SCD still need improvements to achieve a desirable efficiency and cost-effectiveness. The methods that have been implemented for analysis of HRV signals are classical linear methods (time domain and frequency domain), time-frequency (TF), and nonlinear methods. Lower statistics for HRV signal, such as standard deviation (SD) of the mean sinus R–R intervals (SDANN) and mean of SD, are detected in SCD class rather than that of normal people [16]. Also, some researches have demonstrated that compared to the classic methods for HRV signal analysis, the nonlinear method had more ability to find complexities underlying the HRV signals due to the non-stationary and nonlinear characteristics of these signals [17].

Van Hoogenhuyze et al. determined two HRV measures from 24-h holter records of 69 patients [18]. They studied standard deviation (SD) of the mean sinus R–R intervals (SDANN) for successive 5-minute periods over 24 hours, and mean of SD of R-R for successive 5-min periods over 24 hours. Their results suggested that a spectrum of HRV is relatively higher in normal young subjects rather than in SCD patients. Moreover, Ebrahimzadeh et al. [19] employed a total of 20 features, such as 11 features in the time-frequency (TF) and 9 from classical methods (5 in time domain and 4 in frequency domain). After applying Principal Component Analysis (PCA) on the features vector, they were

fed to a Multilayer Perceptron (MLP) classifier for first 1-min of ECG signal before SCD occurrence, reporting the accuracy of 99.16% and 74.36%, respectively by TF and classical linear methods. In another study by the same research group, they proposed a number of features in non-linear and time-frequency domains in HRV signals, being able to increase the classifier's robust for distinguishing the HRV signals of SCD patients and normal individuals, in such a way, HRV signal classes were classified with high accuracy of 99.43% and 97.86%, respectively for 1^{st} 1-min and 2^{nd} 1-min interval prior to SCD onset [20].

In a study by Sheela et al., the HRV signal before SCD have been investigated to classify SCD patients from normal patients with an average accuracy of 88% on the basis of time domain and frequency domain features, and applying Support Vector Machine (SVM) classifier [21]. The algorithms built by combining nonlinear features and wavelet transform have been performed on HRV signals, confirming the ability to predict SCD 4 minutes before its onset [15, 22]. Nevertheless, finding a suitable basis function selection of wavelet transforms for the signals analyzed was not easy since the basic function was not adaptive to decomposed signals. The EEMD and EMD methods are adaptive signal decomposition approaches that decompose the signals into IMFs without prior knowledge according only to the characteristics of the signals itself. These methods are significantly applicable in the area nonlinear and non-stationary signal analysis [23]. Such decomposition methods have shown their capacity in various applications, such as the classification of ECG heartbeats [19], detection of shockable ventricular arrhythmia [24], and automated identification of congestive heart failure [25]. A study [20] used a total of 24 features extracted from HRV signals for SCD prediction, including 5 time domain features, 4 frequency domain features, 11 time-frequency domain features and 4 nonlinear features. A strategy of local feature subset selection was utilized since the number of extracted features was large relatively, whereas a small amount of data is available. So, this strategy was able to elicit different features with significant information in different intervals from 24 combined features.

To improve the early prediction of SCD, two prediction schemes are proposed in this

research based on nonlinear decomposition methods and entropy features. A flowchart of the proposed method is displayed in Figure 1.1 on the next page. EEMD and EMD are performed on the HRV signals for 16 minutes to obtain the first three levels of IMF; and entropy parameters such as Distribution Entropy (DisEn), Sample Entropy (SamEn), Fuzzy Entropy (FuEn) and Rényi Entropy (RenEn), are computed from the three IMFs obtained. Furthermore, the features with crucial information are used various classifiers, i.e., Support Vector Machine (SVM), Multilayer Perceptron (MLP), and k-Nearest Neighbor (kNN), to distinguish normal people from patients at risk of SCD.

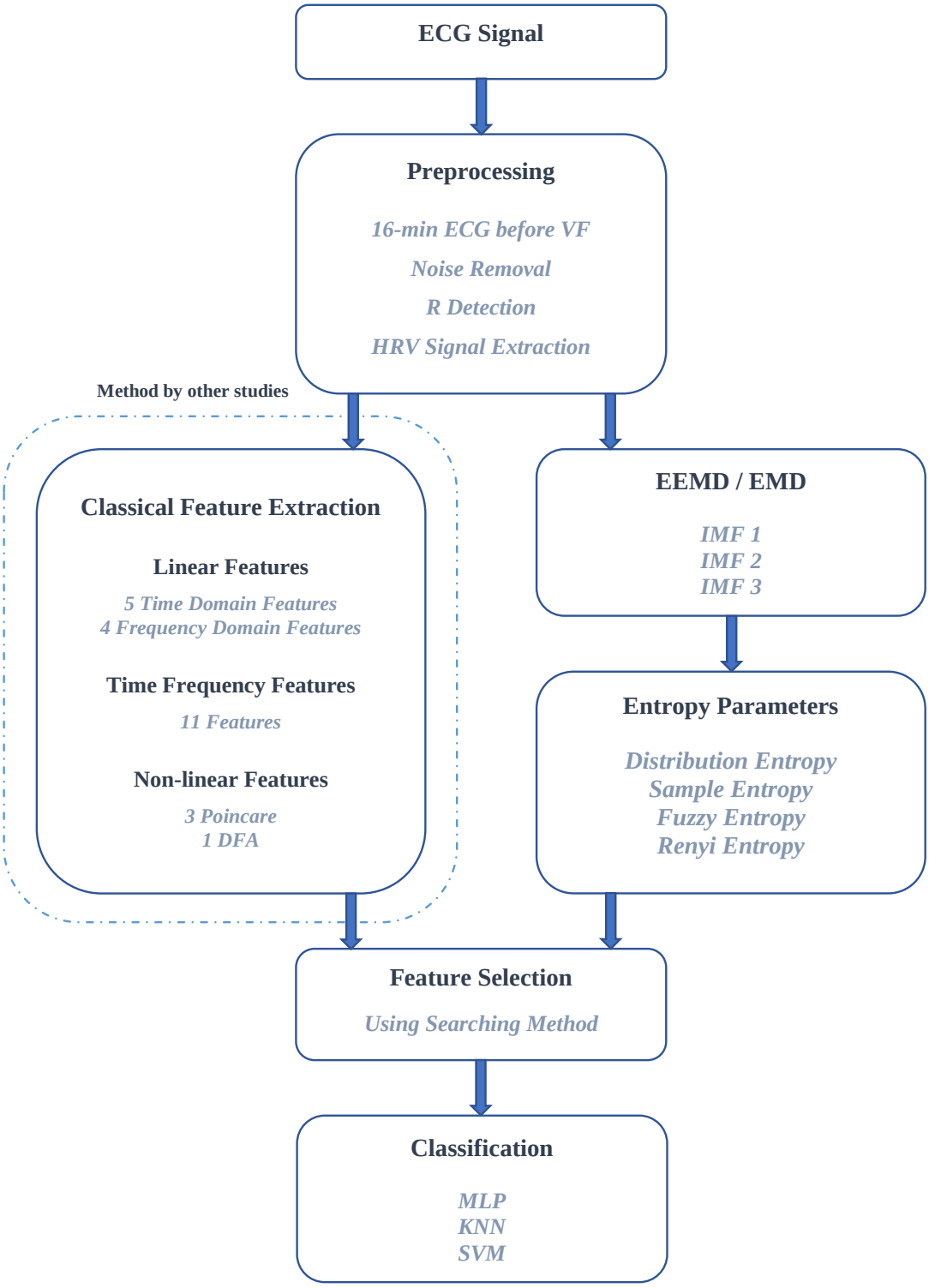

Figure 1.1: The research process

Chapter 2: Materials and Methods

2.1 Data Acquisition

The open access data "Normal Sinus Rhythm" and "Sudden Cardiac Death Holter" provided by the MIT-BIH Database are utilized as the target assessments. This database contains 18 normal subjects (13 female and 5 male, aged 20-50) and 23 SCD subjects (Table 2.1). From the 23 SCD subjects, only 20 patients (8 female, 10 male and 2 unknown, aged 18-89) are used for the analysis since ECG signals of three subjects did not show any VF episodes. Each ECG signal has two leads (SCD subjects with leads II, III and normal subjects with leads I, II). Having some of the patients with two channels, both of relevant ECG signals are considered as the input observations. Thus, considering normal subjects and patients, there is a total of 76 ECG signals to analyze. Each normal subject ECG signal and SCD subject signal are sampled at 128 HZ and 250 HZ, respectively. In order to have consistent sampling between the two classes, all the ECG signals are resampled at 360 HZ.

Table 2.1: Dataset based on gender and age distribution for both classes

		Gender			**Age**	
	Total	Male	Female	Unknown	Range	Mean $\pm$ σ
SCD	**23**	13	8	2	18-79	60.31 ± 21.07
Normal	**18**	5	13	-	20-50	34.33 ± 8.44

2.2 Preprocessing and HRV Signal Extraction

The ECG signals of 16 minutes before VF onset extracted from 24 hours of ECG recordings of the SCD patients are used in order to simulate the electrical activity of the heart during that period before SCD. For the healthy subjects, the 16-min duration of ECG signals

are chosen randomly. ECG signal collection contains interference from various noises including baseline wander due to respiration containing low frequency components (<0.5HZ) and power line interference containing high frequency components (>50Hz). First, noise reduction in ECG signals is done. All ECG signals are filtered by a moving-average filter to remove the baseline wander, in such a way, the first and second stage averaging window lengths are set to be 1/3 and 2/3 of the length of the input signal in samples, respectively.Then, power-line frequency is removed from the median-filtered ECG with a notch filter. Figure 2.1 on page 7 shows the filtered ECG signal of a normal subject. The filtered ECG signals are used as input data in all subsequent processing.

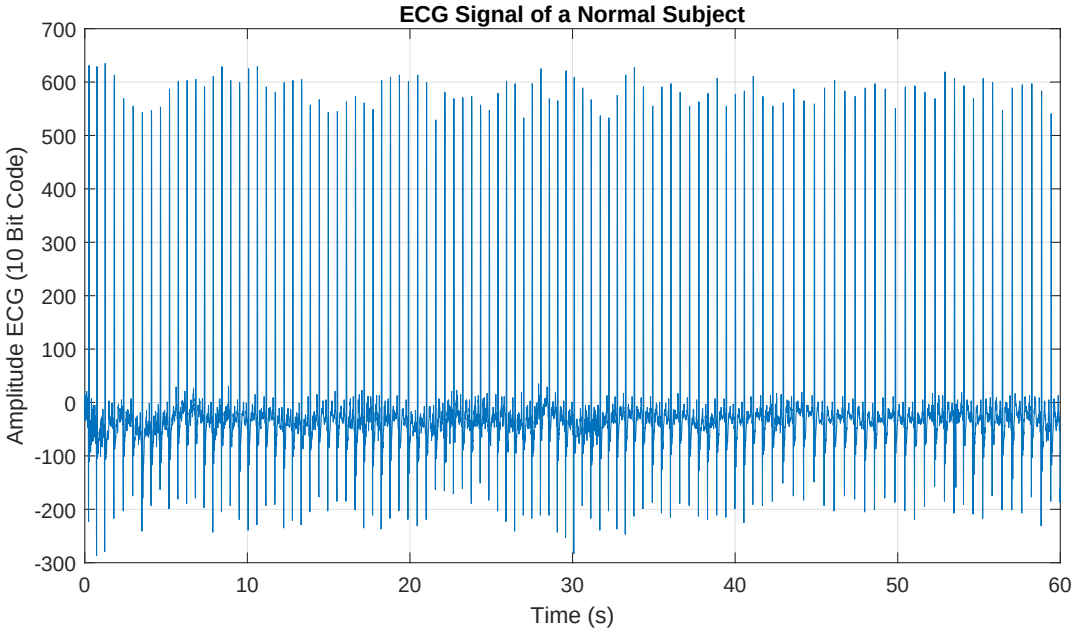

Figure 2.1: One minute of an original ECG signal after noise removal

The denoised ECG signals are subjected to the Pan-Tompkins algorithm for QRS complex detection [26], and thereupon the corresponding HRV signals are determined. In this research, the HRV signals at 16 minutes prior to SCD are uniformly divided into eight 2-min intervals (i.e., 1st 2-min, 2nd 2-min, 3rd 2-min, etc.). Correspondingly, 16-min duration of HRV signals chosen randomly but are similarly partitioned into eight 2-min intervals for normal subjects, now the preprocessed HRV signal is prepared for feature extraction. The

HRV signal of a normal person is represented in Figure 2.2.

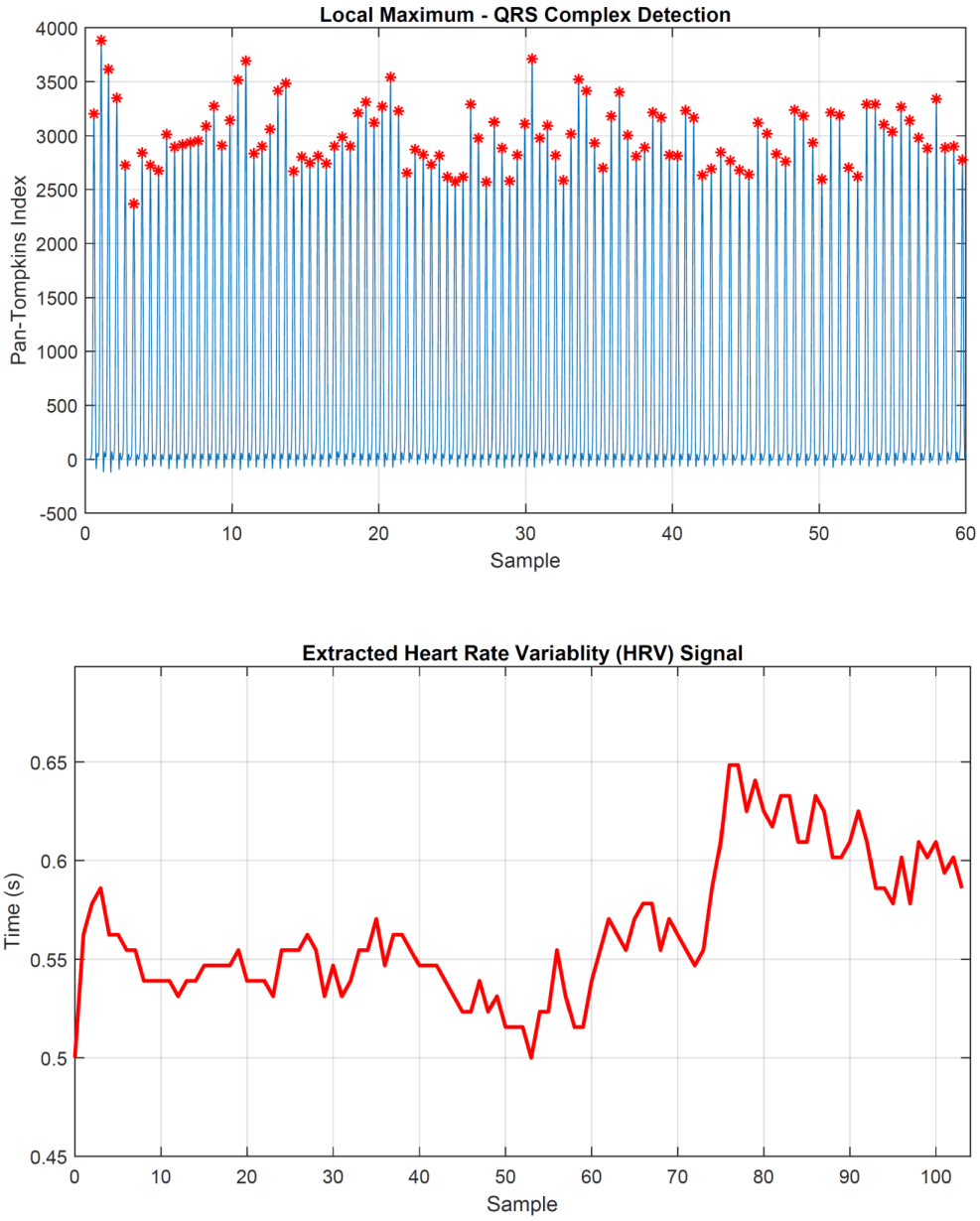

Figure 2.2: (a) QRS complex detection (b) Resulting HRV signal

2.3 EMD

Empirical Mode Decomposition (EMD) is a method of breaking down a signal without leaving the time domain [27]. This method is an adaptive signal decomposition approach that decompose the signals into IMFs without prior knowledge according only to the

characteristics of the signals itself. These methods are significantly applicable in the area nonlinear and non-stationary signal analysis such as for natural signals, in other words, EMD's significant value is to have the capability of detecting local information hidden in the signal [23, 28]. Obtaining IMFs from bio-signals is significant when natural processes often have multiple causes, and each may happen at specific time intervals. In order to apply EMD method on the signal, we start the processing by setting $r_0 = x(n)$ and $k = 1$, where n is a sample in HRV signal. The procedure to calculate the k^{th} IMF is explained in the following [28],

a) First, let $b_k(i-1)$ equal to r_0, with $i = 1$ for the start

b) All the local extremum points are computed

c) The local extrema are interpolated based on a cubic spline function to find the corresponding lower and upper envelopes (e^k_{min} and e^k_{max})

d) The mean defined by $m_k(i-1) = (e^k_{min} + e^k_{max})/2$ is computed

e) Let $b_k(i) = b_k(i-1) - m_k(i-1)$

f) The expression $D = \sum_{n=1}^{N} \left| \frac{b_k(i-1) - b_k(i)}{b_k(i-1)} \right|^2$ is calculated, when D is less than a threshold given previously, set $IMF_k = b_k(i)$ when $b_k(i)$ is an IMF (n is the number of samples in total), otherwise the process returns to loop step b, but with $i = i+1$. Now, the term r_{k+1} equal to $r_k - IMF_k$ is defined. If r_{k+1} has two extrema at least, we would go back to number b, otherwise r_{k+1} is the residue.

$$x(n) = \sum_{k=1}^{K} IMF_k + r_{k+1} \tag{2.1}$$

2.4 EEMD

EEMD is the modified EMD signal decomposition method through adding White Gaussian noise that evenly distributes the whole time-frequency space to a signal. With this method, the mode mixing phenomenon of EMD, that is an IMF including different amplitude

oscillations or parallel oscillations reside in different IMFs, is effectively avoided [29]. In order to initialize applying EEMD method on a signal $x(n)$, White Gaussian noises $N^i(n)$, $(i = 0, 1, \cdots, L)$ are added with different standard deviations [28]. In the next step, each ensemble signal $x(n)$ is subjected to EMD process to compute IMFs $a_k^i(n)$, $(k = 0, 1, \cdots, K)$. Then, the k^{th} IMF of the ensemble signal $x_i(n)$ is calculated as follows,

$$\overline{IMF_k} = \frac{1}{L}\sum_{i=1}^{L} a_k^i(n) \tag{2.2}$$

In the present work, EEMD and EMD (D = 0.2 by trial and error) are individually used to decompose each HRV signal segment of 2-min intervals into several IMFs for the subsequent extracting of corresponding features. Considering the tolerable level of reconstruction error and the total number of features extracted in the following, we use the first three IMFs in both EEMD and EMD. Figure 2.3 on next page depicts the decomposition of the first 2-min HRV signal interval from normal subjects and patients with SCD using EEMD.

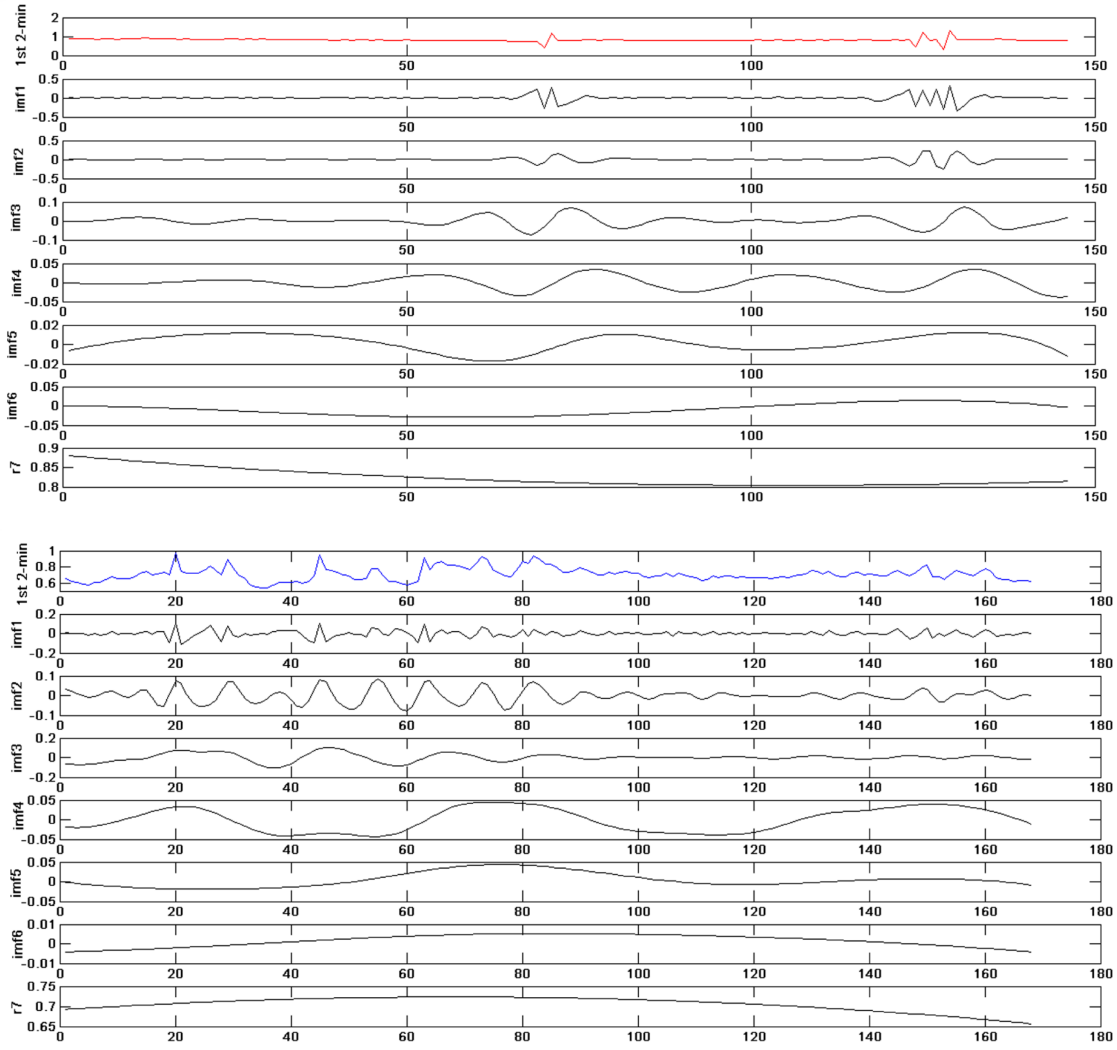

Figure 2.3: Decomposed 1st 2-min interval of HRV signal into IMFs for (a) SCD sample and (b) normal sample

2.5 Entropy Feature Extraction

The cardiovascular system has non-stationary behaviors. Besides, this system is more complex than a linear system. Accordingly, in this study, two non-linear analyses are employed to illustrate the non-linear dynamical characteristics in the HRV signal. Generally, non-linear analysis is recognized for their ability to describe the biological process more effectively. A review by Devi et al. [30] has shown that various nonlinear techniques have been extended to study various cardiac arrhythmia. Overall, four entropy parameters, called

DisEn, SamEn, FuEn, and RenEn are applied to the first three levels of IMFs obtained from nonlinear decomposition (EEMD and EMD) for detecting abnormalities within prone-to-SCD HRV signals.

2.6 Entropy Feature Parameters

2.6.1 Rényi Entropy (RenEn)

This entropy parameter has the ability to evaluate the spectral complexity in time series. Having this property, has made this entropy being useful and applicable for analyzing HRV signal [31, 32]. This entropy is defined by [28],

$$R_x = \frac{1}{1-q}\log_2\left(\sum_{i=1}^{n} P_i^q\right) \qquad q > 0 \ , \ q \neq 1 \tag{2.3}$$

Where P_i is the value of probability density function at frequency i, in this work q (Rényi quadratic entropy) $= 2$ is used [33].

2.6.2 Sample Entropy (SamEn)

This entropy assesses the presence of unpredictability within a time series and overcomes the shortcomings of approximation entropy that highly depends on the given data length and is short of relative consistency; a small SamEn means a signal varying rhythmically [34]. For $\{x(i),\ \ i = 1,\cdots,N\}$, construct a-dimensional vectors $X_i = \{x(i), x(i+1),\cdots,x(i+a-1)\}$, where we have $1 \leq i \leq N-a+1$. The definition of sample entropy is,

$$S_x = -\ln\frac{A^{a+1}}{B^a} \tag{2.4}$$

The term B^a is computed as below,

$$B^a = (N-a)^{-1}\sum_{i=1}^{N-a} C_r^a(i) \tag{2.5}$$

Where $C_r^a(i) = N^a(i)/(N-a+1)$ for $i = 1, \cdots, N-a+1$. $N^a(i)$ is the number that meets the conditions, such that $d[X_i, X_j] \leq r$. Expression $d[X_i, X_j]$ $(i \neq j)$ is defined as the maximum distance between vectors X_i and X_j. Similarly, A^{a+1} is computed for the $(a+1)$-dimensional vectors as,

$$A^{a+1} = (N-a)^{-1} \sum_{i=1}^{N-a} C_r^{a+1}(i) \tag{2.6}$$

Here, B is the probability that reveals the total number of m-dimensional matched vectors, and likewise A is computed for (m+1)-dimensional vectors. In this work, $a = 2$ and $r = 0.15 * SD$ are used [34].

2.6.3 Fuzzy Entropy (FuEn)

This entropy is defined to quantify the complexity of time series, accordingly increase in the complexity within HRV signal would result in a larger value of Fuzzy Entropy [28, 35]. Considering a time series $x(i)$ of length N, a-dimensional vectors are constructed as

$$X_i = \{x(i), x(i+1), \cdots, x(i+a-1)\} - a^{-1} \sum_{k=0}^{a-1} x(i+k),\ 1 \leq i \leq N-a+1 \tag{2.7}$$

Fuzzy entropy is calculated by

$$F_x = -\ln(\phi^{a+1}/\phi^a) \tag{2.8}$$

Where ϕ^a is computed as

$$\phi^a = \frac{1}{N-a} \sum_{i=1}^{N-a} \left(\frac{1}{N-a-1} \sum_{j=1, j\neq i}^{N-a} D_{ij}^a \right),\ D_{ij}^a = \exp(-(d_{ij}^a)^p/r) \tag{2.9}$$

The power p and tolerance r are given in advance. The similarity degree $d_i^a j$ is the maximum distance between vectors X_i and $X_j (i \neq j)$. Then, similarly, compute ϕ^{a+1} for $(a+1)$-dimensional vectors. Here, we use the following values, $a = 2$, $r = 0.15 * SD$ and $p = 2$ [36].

2.6.4 Distribution Entropy (DisEn)

This entropy is computed on the basis of the empirical probability distribution function (ePDF) of vector-to-vector distances from a given time series and has the reliable capacity to measure complexity of short-term RR interval data [37]. For time series $x(i)$ with length N, a-dimensional vectors are formed such as $X_i = \{x(i), x(i+1), \cdots, x(i+a-1)\}$, where $1 \leq i \leq N-a$. The formulation of Distribution Entropy is defined as below,

$$D_x = -\sum_{b=1}^{M} P_b \log_2(P_b) \tag{2.10}$$

The term P_b is the probability, where its index $b = 1, 2, \cdots, M$. The steps to calculate P_b is as follows. First, we need to compute distance matrix $D = \{d_{ij}\}$, where d_{ij} is the maximum distance between vectors X_i and X_j with $1 \leq i$ and $j \leq N-a$. Then, the probability density is measured by applying the histogram method to the distance matrix D. M denotes bins of the histogram, where $a = 2$ and $M = 512$ are used here [38]. The entropy parameters mentioned above quantify the complexity and randomness within HRV signals derived of normal and SCD patients [28].

2.7 Feature Selection

There is a total of 12 entropy features (four entropy parameters are computed from the first three IMFs) obtained from the above steps; however, all the acquired features are not crucial in distinguishing normal and SCD classes. In any classification task, some of the extracted features might be excess; thus, they would increase the running time of the method and weaken its performance. In this way, the selection of the best possible discriminator features plays an important role when constructing classifiers. A searching selection approach is applied to identify the best features for classification in feature space. In such a way, first, the classification is applied separately to each feature. The best distinguishing feature is selected based on the value of classification accuracy it returns. This feature are combined with the

other individual features and thus the best group combination are produced. The optimal feature space is achieved when the minimum number of features results in the highest classification accuracy (i.e., when adding a new feature does not increase the classification accuracy, see Section 2.9). In other words, the feature grouping process stops when adding a new feature decreases the classification accuracy. The training process in each step is done only using the training data after performing the feature selection, afterward, the best combination of features is determined. Then, testing session is done using the remaining sample.

2.8 Classification

In this study, utilizing three classifier methods are intended for the classification. The k-Nearest Neighbor (kNN), Multilayer Perceptron (MLP) and Support Vector Machine (SVM) with three well known kernels (Linear, Gaussian, and Quadratic), are applied to distinguish ECG signals of normal subjects from those susceptible to SCD. The mentioned classifiers are implemented as described in Ref [39]. Moreover, with the aim of testing the performance of above-mentioned classifiers, the 10-fold cross-validation method is employed. Accordingly, the classifier with the highest accuracy and minimum number of features is selected. At each stage, 10% of the observations is selected as the testing data and the other remaining 90% as the training data. The whole processing is done ten times, and meanwhile, the error of trained model is calculated in each iteration, finally the average of that is reported.

2.9 Evaluation

The confusion matrix, as a predictive analytical tool, is used to calculate sensitivity, specificity, and accuracy for evaluating the performance of the proposed method in classification of SCD cases. Utilizing this metric, we can analyze how well our classifier has performed on the dataset. In the equations (2.11) to (2.13), the following terminology is used: TP

(True Positives) refers to correctly predicted SCDs, TN (True Negatives) refers to correctly predicted non-SCDs, FN (False Negatives) refers to incorrectly predicted non-SCDs, ultimately FP (False Positives) refers to incorrectly predicted SCDs. Then, the above-mentioned metrics are calculated as demonstrated as follows. Accuracy (ACC) is the ratio of correct predictions to the total predictions,

$$ACC = \frac{TP + TN}{TP + TN + FN + FP} \tag{2.11}$$

Sensitivity, Recall or True Positive Rate (TPR) is the ratio of true positives to the total positives.

$$TPR = \frac{TP}{P} = \frac{TP}{TP + FN} \tag{2.12}$$

Specificity or True Negative Rate (TNR) is the ratio of true negatives to the total negatives.

$$TNR = \frac{TN}{N} = \frac{TN}{TN + FP} \tag{2.13}$$

Chapter 3: Results

Table 3.1 represents the values (mean and SD) of the different features acquired by applying the EEMD-based method for the first 2-min interval of HRV signals for both groups. R1, R2, and R3 represent the RenEn features extracted from the first to third IMF obtained from EEMD decomposition. This notation also applies to other entropy features (SamEn, FuEn, and DisEn), for example, F3 represents the FuEn features extracted from the third IMF obtained from the EEMD decomposition. The features are fed into three different classifiers (MLP, KNN, and SVM) for having the highest possible accuracy.

Table 3.1: Entropy features based on EEMD from HRV signals of normal and SCD subjects in 1st 2-min before SCD onset

Feature	Normal		SCD	
	Mean	**SD**	**Mean**	**SD**
D1	0.32184	0.13014	0.63499	0.19257
D2	0.31507	0.11322	0.52663	0.16893
S1	1.64896	0.52571	0.81399	0.61183
F1	0.88601	0.28848	0.53068	0.32372
D3	0.32304	0.10115	0.43872	0.14783
R1	12.67906	1.43455	11.6301	1.49677
R3	8.93022	1.30001	9.87756	1.45206
R2	11.06330	1.43788	11.8445	1.41445
S2	0.53054	0.16235	0.44830	0.20974
F3	0.42805	0.06743	0.39619	0.14159
F1	0.90270	0.33615	0.80586	0.50435
S3	0.58508	0.10475	0.54997	0.20542

Figure 3.1, and Tables 3.2 and 3.3 show classification performances using different classifiers for normal and SCD HRV signals at the 1st 2-min before SCD onset. It is explicit on Figure 3.1 that in distinguishing the HRV signals of normal and SCD subjects, the highest accuracy of 94.7% is achieved by implementing the SVM classifier with only eight entropy

features. Table 3.4 shows the maximum accuracies achieved based on EEMD/EMD for all eight intervals (i.e., 1st 2-min, 2nd 2-min, $\cdots$, 8th 2-min) using different classifiers with a different number of features. It is mentionable that the highest accuracy achieved by EEMD is 96.1% with sensitivity of 93% and specificity of 100% are achieved via the KNN classifier with usage of only six entropy features for the classification of normal and SCD subjects from the 4th 2-min HRV signal (Table 3.4).

Table 3.2: Classification with highest accuracy using different classifiers based on EEMD method for both classes of HRV signals at 1st 2-min interval

Classifier	Features	TP	TN	FP	FN	Accuracy	Sensitivity	Specificity
KNN	4	36	32	4	4	89.5%	90%	88.9%
SVM (Linear)	8	35	32	5	4	88.2%	89.7%	86.5%
SVM (Quadratic)	8	38	34	2	2	94.7%	95%	94.4%
SVM (Gaussian)	8	37	31	3	5	89.5%	88.1%	91.2%
MLP	2	35	32	5	4	88.2%	89.7%	86.5%

Table 3.3: Number of features versus accuracy using various classifiers for normal and SCD HRV signals at 1st 2-min before SCD onset

		Number of Features					
		2	**4**	**6**	**8**	**10**	**12**
Accuracy (%)	**MLP**	88.2	87	85	85.2	85	84
	KNN	84.2	89.5	88.8	88	87.4	87.9
	SVM	83	83.5	93	94.7	94	93.5

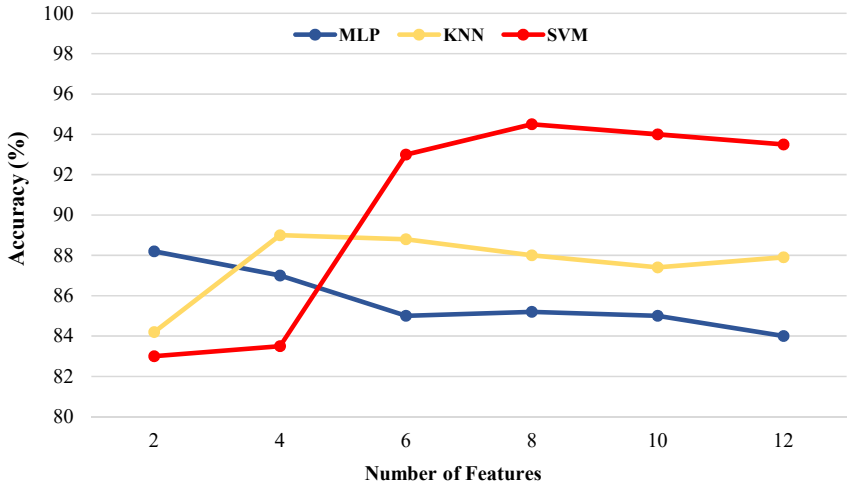

Figure 3.1: Plot of number of features versus accuracy using various classifiers for normal and SCD HRV signals 1st 2-min before SCD onset

Figure 3.2 depicts the comparison of classification results obtained from the methods based on EEMD and EMD. It is obvious that the performance of the EEMD-based method is superior to that of the EMD-based method. The reason is that, in EEMD method, the mode mixing phenomenon is removed in the process of signal decomposition in comparison with that in EMD. EEMD has more band limited and concentrated component, and thus more capacity for deciphering the hidden information in the signals for classification.

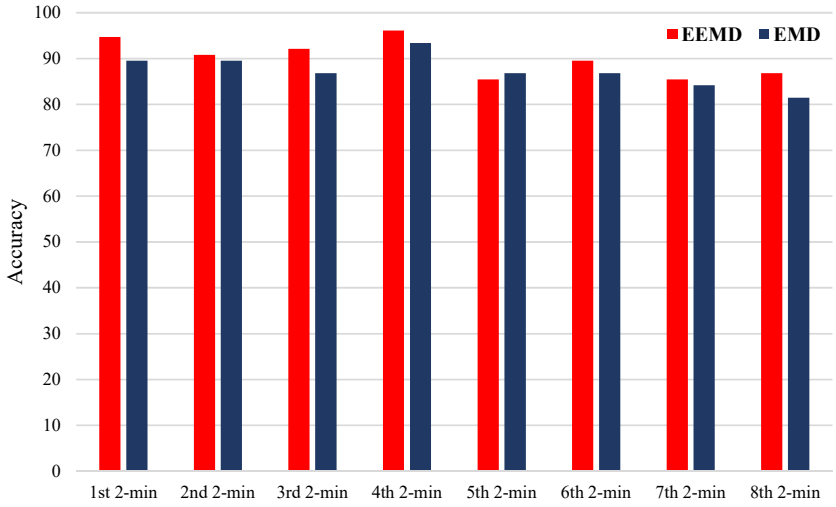

Figure 3.2: Comparison of accuracies of the two algorithms (EMD and EEMD) within 16 minutes

Table 3.4: The maximum accuracy obtained by using the EEMD/EMD based method

(a) The results of EEMD-based method

Classifiers	Features	TP	TN	FP	FN	Accuracy	Sensitivity	Specificity
1st 2-min (SVM Quadratic)	8	38	34	2	2	94.7%	95%	94.4%
2nd 2-min (MLP)	5	38	31	2	5	90.8%	88.4%	94%
3rd 2-min (KNN)	5	38	32	2	4	92.1%	90.5%	94.1%
4th 2-min (KNN)	6	40	33	0	3	96.1%	93%	100%
5th 2-min (SVM Quadratic)	5	32	33	8	3	85.5%	86.5%	80.5%
6th 2-min (SVM Quadratic)	3	35	33	5	3	89.5%	92.1%	86.8%
7th 2-min (MLP)	3	33	32	4	7	85.5%	82.5%	88.9%
8th 2-min (SVM Quadratic)	3	32	34	2	8	86.8%	80%	94.4%

(b) The results of EMD-based method

Classifiers	Features	TP	TN	FP	FN	Accuracy	Sensitivity	Specificity
1st 2-min SVM (Quadratic)	5	36	32	4	4	89.5%	90%	88.9%
2nd 2-min (SVM Linear)	3	36	32	4	4	89.5%	90%	88.9%
3rd 2-min (KNN)	5	37	29	3	7	86.8%	84.1%	90.6%
4th 2-min (KNN)	5	39	32	1	4	93.4%	90.7%	97%
5th 2-min (SVM Quadratic)	3	35	31	5	5	86.8%	87.5%	86.1%
6th 2-min (SVM Quadratic)	5	34	32	6	4	86.8%	89.5%	84.2%
7th 2-min (SVM Quadratic)	5	33	31	5	7	84.2%	82.5%	86.1%
8th 2-min (SVM Quadratic)	5	32	30	6	8	81.5%	80%	83.3%

Figure 3.3 illustrates that the prediction accuracy based on the EEMD method beyond 16 minutes before the SCD incident has decreased perceptibly below 85%. This threshold is chosen here as a proper criterion for increasing the confidence in the matter of classifying the subjects inputted. For example, the accuracy for the prediction of SCD is 63.6% and 66.2%, respectively 28 minutes and 30 minutes before onset. Conceivably, the proposed approach shows less capability for prediction of the potential heart attack that may happen in the long run rather than a closer time. In other words, we can claim that SCD is predictable using the present approach with more than 85% accuracy up to 16 minutes earlier.

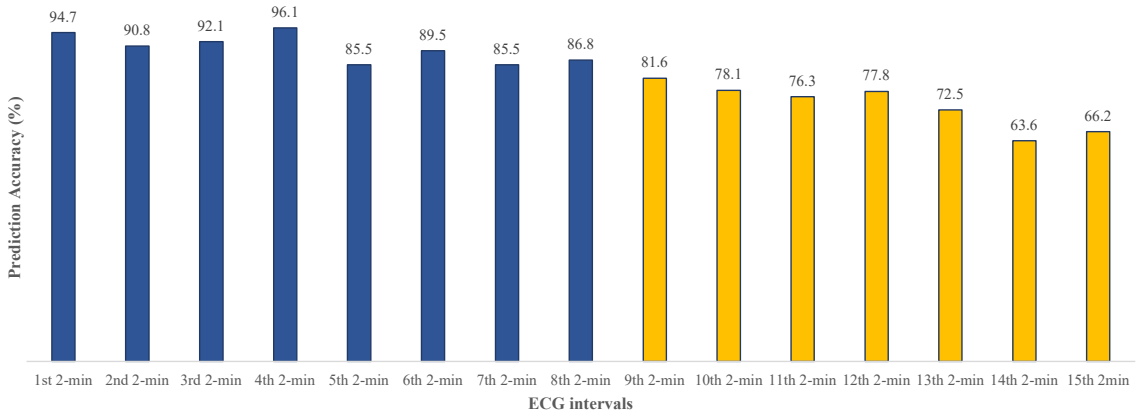

Figure 3.3: Comparison of accuracies for prediction of SCD onset using different intervals of ECG signals

Chapter 4: Discussion

The dataset were split into two sets as the training set and the testing set. Employing 10-fold cross validation procedure, around 90% of samples (68 ECG signals) are taken as the training set to determine the best combination of the features. The remaining samples (8 ECG signals) are selected as the testing set, which are applied to evaluate the efficiency of the trained model. Given that there are signals from two leads available for each person as an independent observation; in order to prevent the correlation of the results and lack of bias in network training, both two channels from an individual are used in either a training set or the testing set. Namely, a channel of each person is not put in the training set when another one is in the testing set. Table 4.2 represents the results by previous studies with two different prediction time intervals (1-min and 2-min). The reason behind selecting 2-min intervals in this study was a trade-off between having good prediction resolutions concurrently with having a valid set of extracted features. Although increasing the length of intervals would improve the accuracy, besides it decreases the prediction resolution. Additionally, selecting smaller intervals rather than two minutes make the credibility of the feature set disputable.

In the researches on HRVs of one-minute interval, the approach by Ref [19] has shown an improved performance for SCD prediction with accuracy of 99.16% and 91.23% for the first and the second minutes respectively prior to onset. Through a classical linear method and Wigner–Ville transform based time-frequency method, a total of 20 features were extracted. They developed a novel algorithm, which had the ability to predict SCD risk four minutes early by employing 24 features on the basis of combining classical linear, time-frequency, and nonlinear methods. For the first 1 to 4 min before onset, the accuracies of 99.73%, 96.52%, 90.36%, and 83.93% were achieved [20]. Recurrence Quantification Analysis and Discrete Wavelet Transform were performed on normal and SCD risk HRV signals to acquire nonlinear features from HRV signals in these studies, demonstrating an ability of predicting

SCD 4 minutes prior to its occurrence. Ebrahimzadeh et al. employed 24 features in diverse processing domains and the approach to local feature subset selection for detecting SCD 12 min early with an average accuracy of 89.70% [40]. Table 4.2 describes that the prediction time of most studies is 4 minutes before the incident. The prediction time of individual studies is extended from 4 minutes to 12 minutes, but using more features (24 features) is unsuitable for a limited number of samples. In comparison to other studies on HRV of 2-min interval for SCD detection (Table 4.2), the proposed methods using fewer features whilst can extend the prediction time from 4 minutes to 16 minutes. The proposed method based on EEMD achieved accuracies 94.7%, 90.8%, 92.1%, 96.1%, 85.5%, 89.5%, 85.5%, and 86.8% for the 1^{st} 2-min to the 8^{th} 2-min interval before onset, respectively (Table 3.4). Although while one study [41] achieved 96.36% accuracy using an SVM classifier 1st 2-min before SCD occurrence, they used a total of 34 features from different domains for classification, where the number of features is nearly three times that in our proposed method. Evaluating the performance of this approach adopting 10-fold cross validation algorithm makes this proposed method more robust. It is noteworthy that the proposed EEMD-based method obtained an average accuracy as high as 90.13% 16 minutes before SCD occurrence, which is higher than the 89.7% achieved in Ref [40].

Table 4.1: SCD prediction using ECG/HRV Signals of 1-min intervals

Article	Data	No. of Features	Method	Classification	Results (Accuracy)
Ebrahimzadeh et al. [19]	35 Normal, 35 SCD (HRV)	20	Linear and Nonlinear Methods Time Domain Features 5 Frequency Domain Features 4 Time-Frequency Domain Features 11	KNN, MLP	99.16% (1st 1 min before) 91.23% (2nd 1 min before)
Ebrahimzadeh et al. [20]	35 Normal, 35 SCD (HRV)	24	Linear and Nonlinear Methods Time Domain Features 5 Frequency Domain Features 4 Time-Frequency Domain Features 11 Nonlinear Features 4	KNN MPNN (Multilayer Perceptron Neural Network)	99.73% (1st 1 min before) 96.52% (2nd 1 min before) 90.36% (3rd 1 min before) 83.93% (4th 1 min before)
Acharya et al. [15]	18 Normal, 20 SCD (ECG)	18	DWT and Nonlinear Methods Nonlinear Features 6	KNN, SVM DT (Decision Tree)	92.1% (1st 1 min before) 98.7% (2nd 1 min before) 93.4% (3rd 1 min before) 92.1% (4th 1 min before)
Acharya et al. [22]	18 Normal, 20 SCD (HRV)	10	Recuurence Quantification Analysis, Nonlinear Methods RQA Parameters 10	KNN, SVM, DT, PNN	92.1% (1st 1 min before) 86.8% (2nd 1 min before) 81.5% (3rd 1 min before) 86.8% (4th 1 min before)
Mirhoseini et al. [42]	18 Normal, 19 SCD (HRV)	22	Linear and Nonlinear Methods Time Domain Features 5 Frequency Domain Features 4 Time-Frequency Domain Features 10 Nonlinear Features 3	SVM	83.24% (1st 1 min before)
Fujita et al. [43]	18 Normal, 20 SCD (HRV)	9	Wavelet Transform, Nonlinear Methods Nonlineare Features 9	KNN, SVM, DT	97.3% (1st 1 min before) 89.4% (2nd 1 min before) 89.4% (3rd 1 min before) 94.7% (4th 1 min before)
Ebrahimzadeh et al. [40]	35 Normal, 35 SCD (HRV)	24	Linear and Nonlinear Methods Time Domain Features 5 Frequency Domain Features 4 Time-Frequency Domain Features 11 Nonlinear Features 4	MLP	Average 89.7% (12 min before)

Table 4.2: SCD prediction using ECG/HRV Signals of 2-min intervals

Article	Data	No. of Features	Method	Classification	Results (Accuracy)
Shen et al. [11]	20 Normal, 23 SCD (HRV)	4	Nonlinear Methods Time-Frequency Domain Features 4	ANN (Artificial Neural Networks) BP (Back Propagation)	Wavelet Method: 87.5% (1st 2 min before) HRV Analysis: 67.4% (1^{st} 2 min before)
Murukesan et al. [41]	18 Normal, 20 SCD (HRV)	34	Linear and Nonlinear Methods Poincare Plot Analysis Time Domain Features 15 Frequency Domain Features 13 Nonlinear Features 6	SVM, PNN	SVM: 96.36% (1st 2 min before) PNN: 93.64% (1^{st} 2 min before)
Current Research	18 Normal, 20 SCD (HRV)	12	EMD, EEMD and Nonlinear Methods Nonlinear Features 4	KNN, MLP, SVM	EEMD 94.7% (1^{st} 2 min before) 90.8% (2^{nd} 2 min before) 92.1% (3^{rd} 2 min before) 96.1% (4^{th} 2 min before) 85.5% (5^{th} 2 min before) 89.5% (6^{th} 2 min before) 85.5% (7^{th} 2 min before) 86.8% (8^{th} 2 min before) Average 90.13% (16 min before incidence)

Chapter 5: Conclusion

In this research, an algorithms are proposed based on nonlinear decomposition methods (EEMD and EMD) by employing four entropy parameters (DisEn, SamEn, FuEn, and RenEn). This method shows the capability of early predicting of SCD occurrence up to 16 minutes in advance with a higher accuracy even when using relatively small amounts of features extracted from HRV signals. The prediction results of the EEMD-based algorithm show accuracies of 94.7%, 90.8%, 92.1%, 96.1%, 85.5%, 89.5%, 85.5%, and 86.8% for the first 2-min to the eighth 2-min respectively. Hence, the proposed EEMD-based algorithm could be incorporated into a telemonitoring system for patients at risk of SCD, especially outside of the hospital. Its promising ability to provide warning signals 16 minutes prior to SCD onset saves many more lives undeniably. The limitation of this work is the small available data set. The EEMD-based algorithm used with a large data set is of great necessity before its implementation for the clinical purpose.

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