B. TECH. PROJECT REPORT

On

Sliding-Mode Singular Spectrum Analysis for Sleep Apnea Detection using ECG signals

BY

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Sliding-Mode Singular Spectrum Analysis for Sleep Apnea Detection using ECG signals

A PROJECT REPORT

Submitted in partial fulfillment of the requirements for the award of the degrees

of
BACHELOR OF TECHNOLOGY
in
ELECTRICAL ENGINEERING

Submitted by:
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Guided by:
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CANDIDATE'S DECLARATION

We hereby declare that the project entitled **"Sliding-Mode Singular Spectrum Analysis for Sleep Apnea Detection using ECG signals"** submitted in partial fulfillment for the award of the degree of Bachelor of Technology in 'Electrical Engineering' completed under the supervision of **Dr. Ram Bilas Pachori, Professor, Electrical Engineering,** IIT Indore is an authentic work.

Further, I declare that I have not submitted this work for the award of any other degree elsewhere.

Himali Singh

CERTIFICATE by BTP Guide

It is certified that the above statement made by the students is correct to the best of my knowledge.

Dr. Ram Bilas Pachori

Professor,

Discipline of Electrical Engineering

IIT Indore

Preface

This report on **"Sliding-Mode Singular Spectrum Analysis for Sleep Apnea Detection using ECG signals"** is prepared under the guidance of **Dr. Ram Bilas Pachori**, Professor, Discipline of Electrical Engineering, IIT Indore.

Through this report, I have presented an automatic system for detection of sleep apnea using electrocardiogram (ECG) signals. The Sliding-mode Singular Spectrum Analysis (SM-SSA) decomposition technique is a key step in the proposed method. This computer-aided detection system can prove to a great help for the clinicians in diagnosing sleep apnea.

I have tried to the best of my abilities and knowledge to explain the proposed method in a lucid manner. The results obtained with the present work are also included in this report. I have also added the comparison of the present work with some of the existing works in this direction.

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Abstract

This project work aims at developing a novel automated system for sleep apnea detection using the electrocardiogram (ECG) signals. Sleep apnea is characterized by repetitive interruption of breathing during sleep. The diagnosis of sleep apnea involves a polysomnograhy test which itself is an invasive and expensive procedure. Hence, there is a need for low-cost automated systems for the detection of sleep apnea to aid the clinicians. This work aims to develop such an automated system based on a recently developed data-driven Sliding-mode Singular Spectrum analysis (SM-SSA) technique. The heart rate variability (HRV) and ECG-derived respiratory (EDR) signals extracted from the ECG signal quantify the information about the cardio-pulmonary activity. These signals can provide more information for the apnea event as compared to the ECG signal itself. The SM-SSA provides the reconstructed components (RCs) of the HRV and EDR signals. The features such as mean and standard deviation values of instantaneous amplitude (IA) and instantaneous frequency (IF) are extracted from each RC of both HRV and EDR signals. Stacked autoencoder based deep neural network (SAE-DNN) classifier and support vector machine (SVM) classifier with radial basis function (RBF) kernel are considered to classify apnea and normal episodes using the proposed features. A sensitivity of 82.45% and specificity of 79.72% is obtained which is higher than that for some of the existing features for sleep apnea detection.

Keywords: EDR signal, HRV signal, SM-SSA, SAE-DNN, SVM-RBF.

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List of Abbreviations

AHI	Apnea/hyponea index
AM-FM	Amplitude and frequency modulated
AROC	Area under receiver operating characteristic
autoSSA	Automated SSA algorithm
CSA	Central sleep apnea
ECG	Electrocardiogram
EDR	ECG-derived respiration signal
EEG	Electroencephalogram
HRV	Heart-rate variability
HTSA	Hilbert transform separation algorithm
IA	Instantaneous amplitude
IF	Instantaneous frequency
OSA	Obstructive sleep apnea
PC	Principal component
PCA	Principal component analysis
RC	Reconstructed component
SAE-DNN	Stacked autoencoder based deep neural network
SM-SSA	Sliding-mode singular spectrum analysis
SSA	Singular spectrum analysis
SVD	Singular value decomposition
SVM-RBF	Support vector machine with radial basis kernel function

Chapter 1:

Introduction

1.1 Sleep apnea and its diagnosis

Sleep is an essential physiological activity in our daily lives. A normal person needs at least seven hours of healthy sleep in a day to rejuvenate the body and function normally [1]. One of the common disorders that affect the quality of sleep is sleep apnea. In sleep apnea, there is repetitive cessation of breathing during sleep [2]. This reduces the breathing rate and blood oxygen levels [3]. The respiratory event characterized by partial blockage of airflow is termed as hypopnea [4]. Sleep apnea syndrome is classified as obstructive, central and mixed apnea [4]. Obstruction of the upper airway causes obstructive sleep apnea (OSA) while central sleep apnea (CSA) is a neurological condition causing loss of respiratory efforts [5]. Mixed sleep apnea has both OSA and CSA characteristics. Sleep apnea is accompanied by sleepiness during the day, headache, reduced learning ability and loss of concentration [6].

Apnea-hypopnea index (AHI) is a standard criterion to quantify sleep apnea. AHI is defined as the average number of apnea/ hypopnea events per hour of sleep [7]. The OSA is considered to be severe when the AHI parameter is above 30 while that between 5 and 15 is termed as mild OSA. The AHI below 30 indicates moderate OSA [8]. The sleep apnea is commonly treated using the continuous positive airway pressure (CPAP) device [9]. The CPAP provides a constant flow of air pressure in the throat to avoid obstruction in breathing. The diagnosis of sleep apnea requires an expensive and invasive polysomnography test. It requires simultaneous recording and monitoring of various signals such as electroencephalogram (EEG), oxygen saturation, blood pressure, electrooculogram (EOG), electromyogram (EMG), etc. [10, 11]. The patient is made to sleep in sleep laboratories with dedicated systems and personnel. The highly uncomfortable and inconvenient procedure itself degrades the quality of sleep. Hence, there is a need for low-cost, simpler and automated systems for the detection of sleep apnea.

1.2 Literature survey

In literature, several automated techniques have been proposed for sleep apnea detection. The use of various physiological signals, signal decomposition techniques and features followed by different classifiers has been studied for the detection of sleep apnea [6, 12-31]. The Fourier decomposition method (FDM) based multiresolution analysis is used to extract modes or intrinsic band functions (IBFs) of both HRV and EDR signals in [6]. Among various physiological signals used like saturation of peripheral oxygen (SpO_2) [15], pulse oximetry signals [16] and ECG, ECG and its derived signals are considered to be most reliable. Authors in [17] used ECG morphological patterns like the RR-time series and the area of the QRS-complex. The apnea and non-apnea classification was done using the bivariate time varying autoregressive model. The recurrence quantification analysis (RQA) features from heart rate variability (HRV) signal are proposed with classifiers as the artificial neural network (ANN) and support vector machine (SVM) in [18]. The ECG signal is decomposed into intrinsic mode functions (IMFs) using the empirical mode decomposition (EMD) technique in [19]. Higher-order statistical features are extracted from these IMFs and classified using extreme learning machine (ELM). Nonlinear features such as Hurst exponent, approximate entropy, correlation dimension, fractal dimension, etc. extracted from the ECG signal are classified with ANN classifier to detect sleep apnea [20]. Similarly, in [21], wavelet transform based features are computed from both HRV and ECG derived respiratory (EDR) signal and classified using SVM classifier. The energy and fuzzy entropy features are used to quantify the information related to apneic event. The tunable-Q wavelet transform (TQWT) evaluates the subbands of ECG signal in [23]. The centered correntropy of these subbands are used as input features for classification. Moreover, hidden Markov models (HMMs) are proposed for detection of sleep apnea in [24, 26]. In addition to HMM, authors in [26] used sparse autoencoder to learn features from the ECG signal. Authors in [25] developed a non-parametric kernel density based approach for classification of apnea and normal ECG segments. In [27], components from principal component analysis (PCA) of EDR signal provide apnea related information. Spectral and statistical features are considered to compare the classification performance of neural networks for sleep apnea detection [28]. The neural networks considered are multilayer perceptron network and probabilistic neural network. Authors in [29] suggested convolutional neural network (CNN) for sleep apnea detection.

1.3 Motivation

From the literature, it is evident that the use of HRV and EDR signals in the detection of sleep apnea has proved to be better than the ECG signal itself. The aim of this study is to develop an automated system for the detection of sleep apnea using sliding mode singular spectrum analysis (SM-SSA) of the HRV and EDR signals.

SM-SSA is a recently developed data-driven technique. It aims to provide amplitude and frequency modulated (AM-FM) based components of a non-stationary signal. The SM-SSA approach for decomposition of the input signal into reconstructed components (RCs) is a modification of singular spectrum analysis (SSA) technique [32-34]. The SM-SSA is a data-driven technique without any assumption about the basis functions. This technique has shown better decomposition results than SSA for the separation of mono-components from non-stationary signals [32,34]. Sleep apnea event causes variations in the HRV and EDR signals' characteristics [35]. Hence, it is expected that the RCs extracted from the HRV and EDR signals using SM-SSA will be able to represent these apneic pathological variations.

Recently, different deep learning approaches have been proposed for various classification problems of biomedical interest [28, 29, 34, 36, 37]. The use of SAE-DNN as classifier for sleep stages has been investigated in [36]. The SVM classifier has been widely used in biomedical research problems. In [2, 38], SVM is used for sleep apnea detection itself while in [39, 40], SVM is proposed for sleep stage classification using EEG signals.

1.4 Objective

The objective of this project is to develop a novel automated method for the detection of sleep apnea based on the SM-SSA decomposition technique. The features are extracted from the RCs obtained from SM-SSA and their performance is evaluated using SAE-DNN classifier and SVM-RBF classifier independently.

1.5 Organization of the report

The remaining portion of this report is organized as follows: The database used in this study is briefly described in chapter 2. Chapter 3 describes the proposed methodology along with the description of SM-SSA and the classifiers in detail. The results of the study are discussed in chapter 4. Finally, chapter 5 draws conclusions of this report and provides the future scope.

Chapter 2:

Database description

In this work, the 'Apnea-ECG' database is used to validate the proposed methodology [42,43]. This database is available online for research purpose at Physionet [66]. The database consists of 70 single-lead ECG recordings of approximately 8 hours duration each sampled at the sampling frequency of 100 Hz. The apnea events recorded in the dataset are either obstructive or mixed. The AHI value of the subjects in these recordings varies from 0 to 83. Out of the 70 recordings, 35 recordings have been annotated minute-by-minute as apnea or normal by an expert. The annotations were provided on the basis of simultaneously recorded respiration and oxygen saturation signals. The segments classified as apnea also included the segments with hypopnea characteristics. From the number of apnea/hypopnea events per hour, each recording was classified as "apnea", "borderline" and "normal". Recordings with at least 60 minutes of AHI ten or more and at least 100 minutes of apnea events were classified as clinically significant apnea cases. Similarly, recordings labeled as borderline case had at least 60 minutes of AHI five or

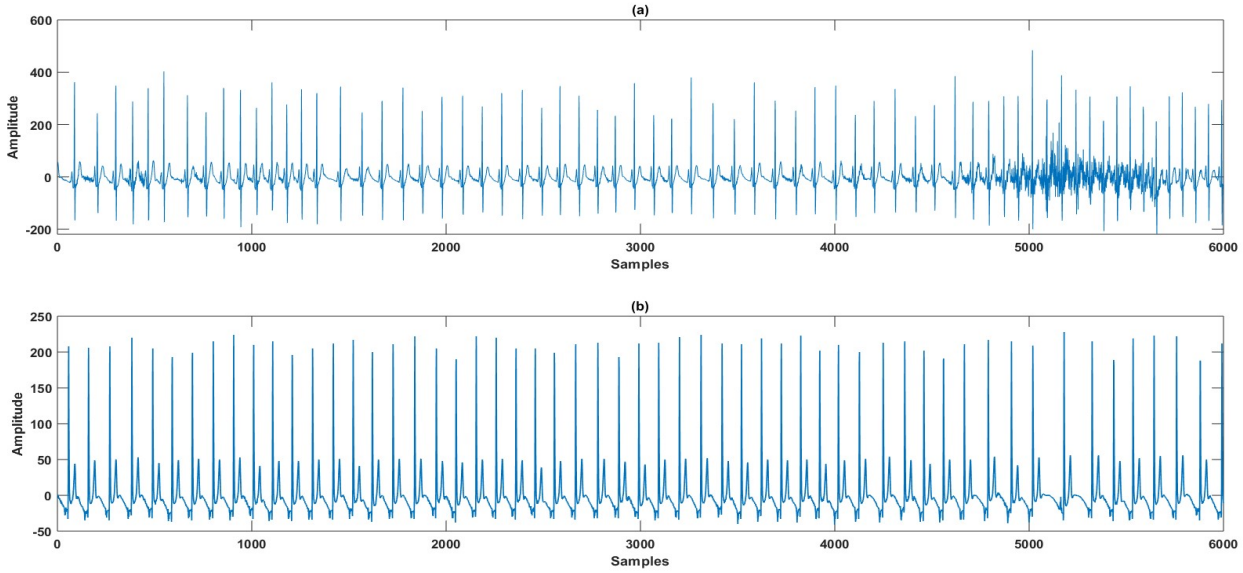

Figure 2.1 Plots of one minute ECG segments for (a) Apnea class, (b) Normal class

more and apnea events between 5 and 99. Fewer than 5 minutes of apnea were considered to be normal. Out of the 35 annotated recordings, 20 belonged to apnea class, 5 belonged to borderline class and 10 belonged to the normal class. From this database, we have considered only the recordings for which the minute-by minute annotations were available. These included 35 single-lead ECG records.

In the present work, the proposed methodology has been developed to classify one-minute ECG segments as apnea or normal. The ECG recordings are first segmented into 1 minute epochs i.e. 6000 samples each and classified as apnea or non-apnea using the annotation files available. The ECG signals and the corresponding annotation files are downloaded and read using the WFDB toolbox of MATLAB 2018a. A total of 6,509 apnea and 10,442 non-apnea minutes are considered. The ECG signal segments for both apnea and normal classes are shown in Figs. 2.1(a) and 2.1(b) respectively.

Chapter 3:

Methodology

In this project, the heart rate variability HRV and ECG-derived respiration (EDR) signals are first extracted from the ECG segments based on Pan Tomkin's algorithm [44] and principal component analysis (PCA) based method [45] respectively. The SM-SSA provides the RCs of both HRV and EDR signals. The SM-SSA extracts AM-FM components from non-stationary signals. The information in AM-FM based component is represented in the time-varying amplitude and frequency of the component. To extract these variations in amplitude and frequency, the instantaneous amplitude (IA) and instantaneous frequency (IF) of the RCs are evaluated using the Hilbert transform separation algorithm (HTSA). Mean and standard deviation of both IA and IF for each RC obtained after decomposition of HRV and EDR signals are used as input features for the classifiers. Using these features, different feature sets are formulated, namely, the HRV features, the EDR features and the HRV and EDR (HRV and EDR) features together. All different feature sets are fed to both SAE-DNN classifier and SVM-RBF classifier separately to classify apnea and normal ECG segments. The entire approach for detection of sleep apnea is briefly outlined in the block diagram given in Fig 3.1.

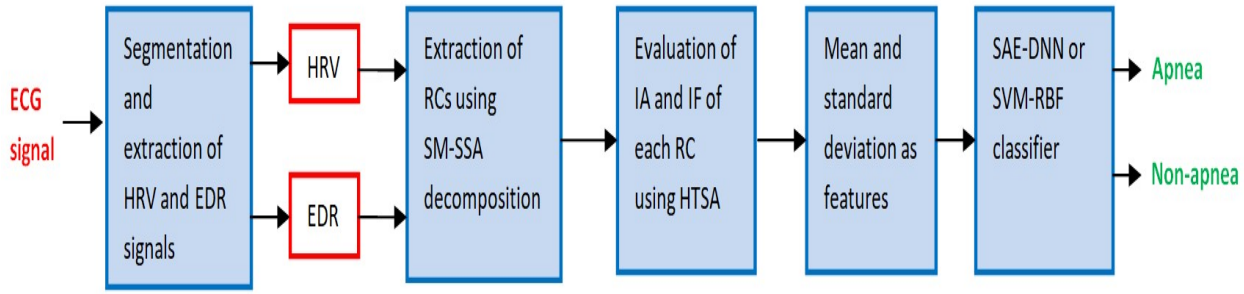

Figure 3.1 Block diagram representation of the proposed approach for sleep apnea detection

3.1 HRV and EDR signals extraction

3.1.1 HRV signal extraction

The HRV signal measures the variations in the beat-to-beat interval of the heartbeats. Also known as RR variability, it is obtained by the detecting the R peaks in the ECG signal. The Pan Tomkin's algorithm [44] is the most commonly used method to detect QRS complexes in an ECG signal in real time. An ECG beat with the QRS complex is represented in Fig. 3.2. The Pan Tomkin's algorithm uses a series of filters to highlight the frequency content of the QRS complex in ECG signal. Squaring of the signals amplifies the QRS peaks which are finally detected by applying a adaptive threshold to the local peaks of the filtered signal. First, a bandpass filter with bandwidth about 5-15 Hz increases the signal to noise ratio of the ECG signal and reduces the noise due to baseline wander, power line interference and P wave and T wave frequency content. A derivative filter is used to extract the information about the slope of the QRS complex followed by squaring of the filtered signal. Squaring helps to enhance the dominant R peaks in the signal. A moving window integration filter provides the information of the duration of the QRS complex. Finally, local peaks are evaluated from the integrated signal and simultaneously classified as R peak or noise peak using an adaptive threshold. The entire QRS detection algorithm is summarized in the block diagram shown in Fig. 3.3. The HRV signal extracted for apnea and normal classes is shown in Figs. 3.6 (a) and 3.6 (g) respectively.

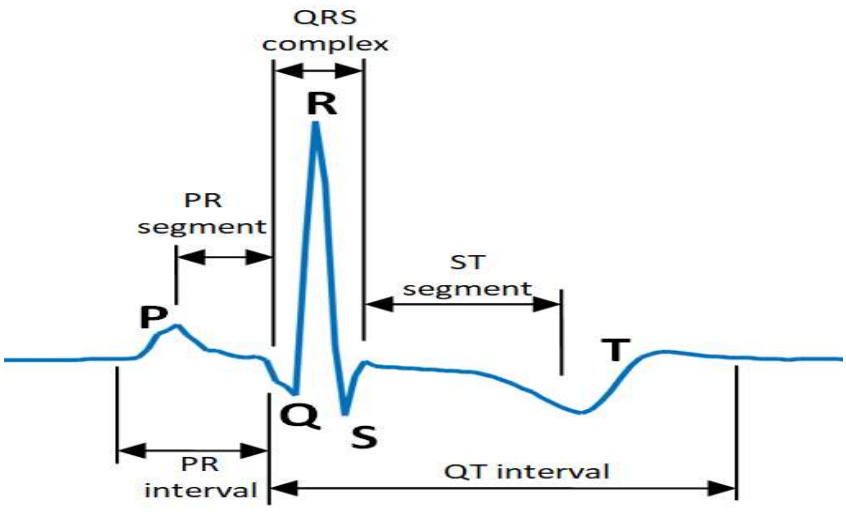

Figure 3.2 ECG beat showing P wave, QRS complex and T wave

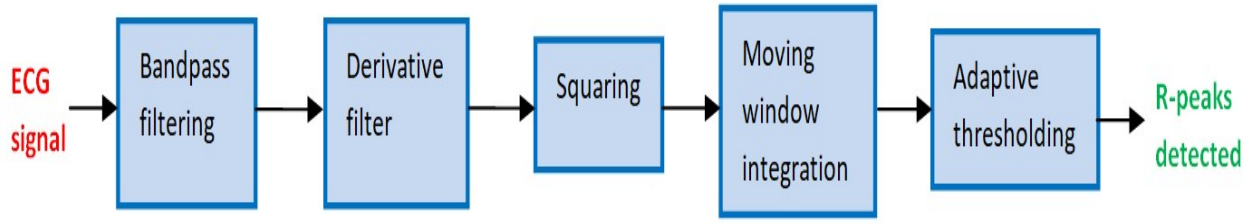

Figure 3.3 Block diagram representing the Pan Tomkin's algorithm for QRS detection

3.1.2 EDR signal extraction

Respiration induces changes in the ECG morphology due to changes in the anatomical position of the heart with respect to the ECG electrodes. This respiratory information is extracted from the beat-to-beat variations of the ECG signal as EDR signal. Different signal processing techniques have been developed to derive the EDR signal. In this work, we have used a PCA based approach proposed in [45] to extract the EDR signal.

PCA is a technique to convert a set of correlated variables into a set of linearly uncorrelated variables using an orthogonal transformation. First, the covariance matrix *Cov* is constructed from the *m* random variables *x*. An orthogonal matrix *T* of size *m X m* is formulated with rows being the eigenvectors of *Cov*. The principal components (PCs) of *x* are then defined by [67],

$$Z = Tx \tag{3.1}$$

where *Z* is the vector of *m* PCs.

For EDR extraction, first the R peaks are detected using the standard Pan Tomkin's algorithm [44]. Considering a window of 30 samples before each R-peak and 50 samples after each R-peak, an ECG beat matrix is formed. The PCA technique applied to this ECG beat matrix provides as many PCs as the number of beats analyzed. Out of these, the first three PCs which capture most of the variability due to respiration are considered to derive the EDR signal. The EDR signal extracted for apnea and normal class is shown in Figs. 3.7 (a) and 3.7 (g) respectively.

3.2 Sliding-mode singular spectrum analysis (SM-SSA)

The SM-SSA is a data-driven technique to decompose a non-stationary signal into AM-FM based components known as reconstructed components (RCs) [32]. It has been effectively applied for the analysis of EEG signals recently [34]. The number of RCs in SM-SSA is preassigned. In SM-SSA, SSA is applied to each frame considering a sliding window instead of the whole signal directly.

The steps involved in evaluating RCs from the input signal *s(n)* using the automated SSA (autoSSA) algorithm are described as follows:

1) First, a trajectory matrix X is formulated from the input signal with the parameter embedding dimension L given by,

$$X = \begin{bmatrix} s(1) & s(2) & \cdots & s(K) \\ s(2) & s(3) & \cdots & s(K+1) \\ \vdots & \vdots & \cdots & \vdots \\ s(L) & s(L+1) & \ldots & s(N) \end{bmatrix} \tag{3.2}$$

where $K=N-L+1$ and N is the length of the input signal. The trajectory matrix is a Hankel matrix, a matrix with each ascending skew-diagonal from left to right as constant. The embedding dimension is an important parameter which determines the decomposition of signal using SSA and SM-SSA. It ranges from 2 to N-1 [32].

2) X with rank $R \leq \min(L, K)$ is decomposed as a sum of weighted orthogonal matrices using singular value decomposition (SVD) which is given by,

$$X = USV^T = \sum_{i=1}^{R} X_i \text{ with } X_i = \sigma_i u_i v_i^T \tag{3.3}$$

where $S = \text{diag}(\sigma_1,\sigma_2,\ldots,\sigma_R)$, σ_i are the singular values sorted in descending order, u_i,v_i and σ_i are termed as the i^{th} left eigenvector, i^{th} right eigenvector, and i^{th} singular value of matrix X respectively. X_i is the i^{th} matrix obtained from 'i' number of left eigenvector, right eigenvector and singular value. The energy contribution of each eigentriple (u_i,v_i,σ_i) is proportional to σ_i^2. Here, the eigendecomposition of covariance matrix $C = XX^T$ is used to obtain SVD expansion of X.

3) Next, in autoSSA, diagonal averaging is used to obtain the elementary components from each X_i. Ideally, if X_i is a perfect Hankel matrix, it will correspond to a trajectory matrix of a time series which will be a component of the input signal. But with real world

signals, X_i is almost Hankel. Diagonal averaging or Hankelization provides a time series s_i whose trajectory matrix is closest to X_i in least-squares sense. These time series are termed as the elementary components of the input signal. The diagonal averaging is of X_is is given by,

$$s_i(n) = \begin{cases} \frac{1}{n}\sum_{\mathrm{m}=1}^{n} \mathrm{x}(\mathrm{m}, \mathrm{n}-\mathrm{m}+1) & \text{for } 1 \le \mathrm{m} \le \mathrm{L} \\ \frac{1}{L}\sum_{\mathrm{m}=1}^{\mathrm{L}} \mathrm{x}(\mathrm{m}, \mathrm{n}-\mathrm{m}+1) & \text{for } \mathrm{L} \le \mathrm{m} \le \mathrm{K} \\ \frac{1}{N-n+1}\sum_{m=n-K+1}^{L} x(m, n-m+1) & for\ K+1 \le m \le N \end{cases} \quad (3.4)$$

4) The last step involves the grouping of the elementary components in *r* distinct clusters. This clustering is done using the agglomerative hierarchical clustering technique. In agglomerative clustering, each data point is initially considered as an individual cluster. At each iteration, similar clusters are merged until the required number of clusters is obtained. Here, the number of clusters is taken as *r* i.e. the preassigned number of RCs. Finally, summing up of each cluster provides the required reconstructed components (RCs).

Similarly, the evaluation of RCs using SM-SSA is explained in the following steps:

1) A sliding window of length *W* (an odd integer) is considered with step size or samples between two adjacent frames as δ. The number of RCs for each sample is assigned in a vector *r(n)* of same length as the input *s(n)* i.e. *N*.
2) With the frame index *p* varying from 1 to *N-W+1* and increment δ, the center of the frame is calculated as $n_c = p + \frac{W-1}{2}$ and the end of the frame as $n_e = p\text{-}W+1$.
3) Using the autoSSA algorithm and embedding dimension as '*L*', the current RCs are evaluated for each frame.
4) For the first position of the sliding window i.e. *p=1*, the estimated components are directly assigned with the RCs extracted from autoSSA for the sample range *[1, n_c]*. For the next positions i.e. *p>1*, the current components provided by autoSSA are matched with the previously estimated components considering the delay δ. The matching is done through minimization of correlation distance measure given by [32],

$$d(x,y) = \frac{|<x,y>|}{\|x\|\|y\|} \tag{3.5}$$

with inner product $<x,y> = x^T y$ and $L2 - norm\ \|x\| = \sqrt{< x,x >}$. A variable J stores the previously associated components to avoid the association of one component more than once. If the number of components increases, the current component is associated with a non-affected estimated component while if the number remains same or decreases, all the current components are associated with the previously estimated components. For the last position of the frame index i.e. $p = N\text{-}W\text{+}1$, all the samples in $[n_c, W]$ are stored in their corresponding associated components.

In this work, we have extracted five RCs from both HRV and EDR signals. The optimum values of the embedding dimension L and window length W is obtained using grid search approach based on the average accuracy of classification. The variation of accuracy with different window length and embedding dimension for both HRV and EDR signals is shown in Figs. 3.4 and 3.5 respectively. For both HRV and EDR signals, the embedding dimension is taken as 5 samples. A window length of 21 samples and 15 samples for HRV and EDR signals respectively gives highest classification accuracy. Fig. 3.6 shows the plots of RCs obtained from the HRV signal for both apnea and normal classes. Similarly, Fig. 3.7 shows the plots of RCs obtained from the EDR signal for both apnea and normal classes.

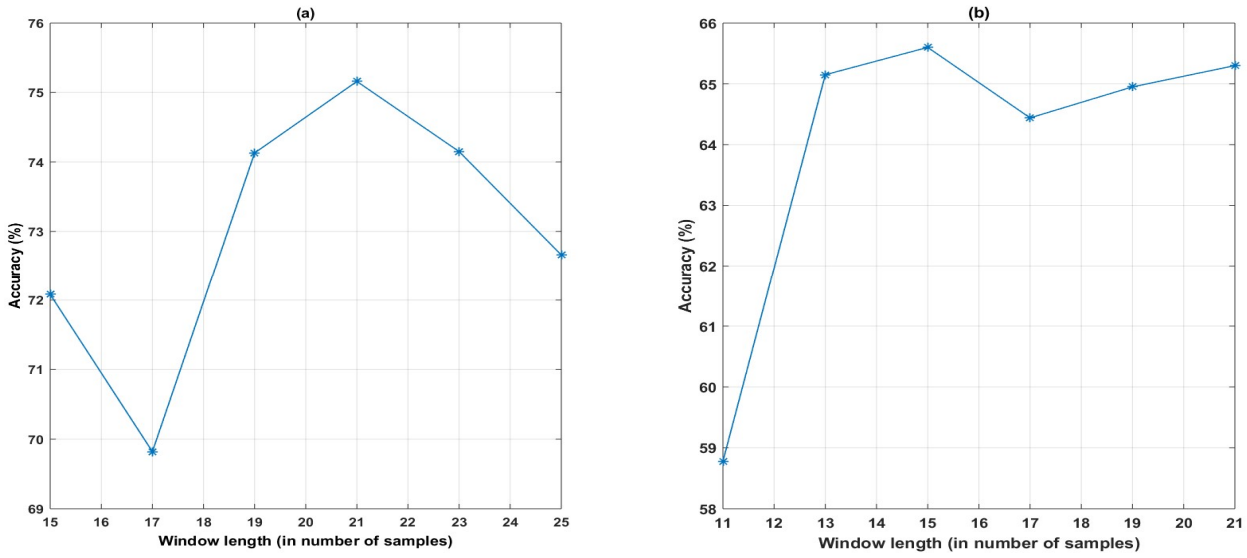

Figure 3.4 Variation of accuracy with different window length for (a) HRV, (b) EDR

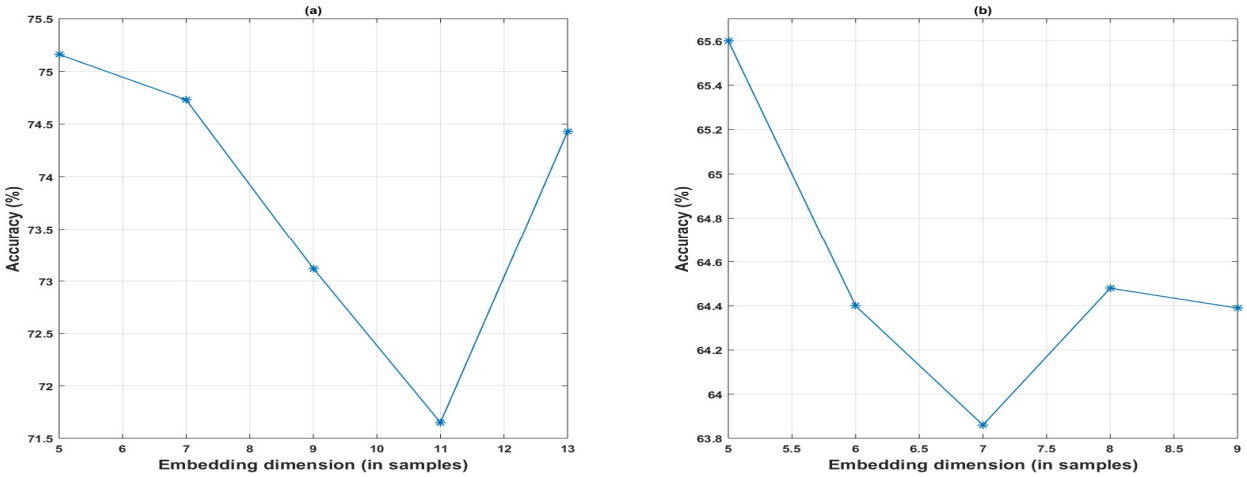

Figure 3.5 Variation of accuracy with different embedding dimension for (a) HRV, (b) EDR

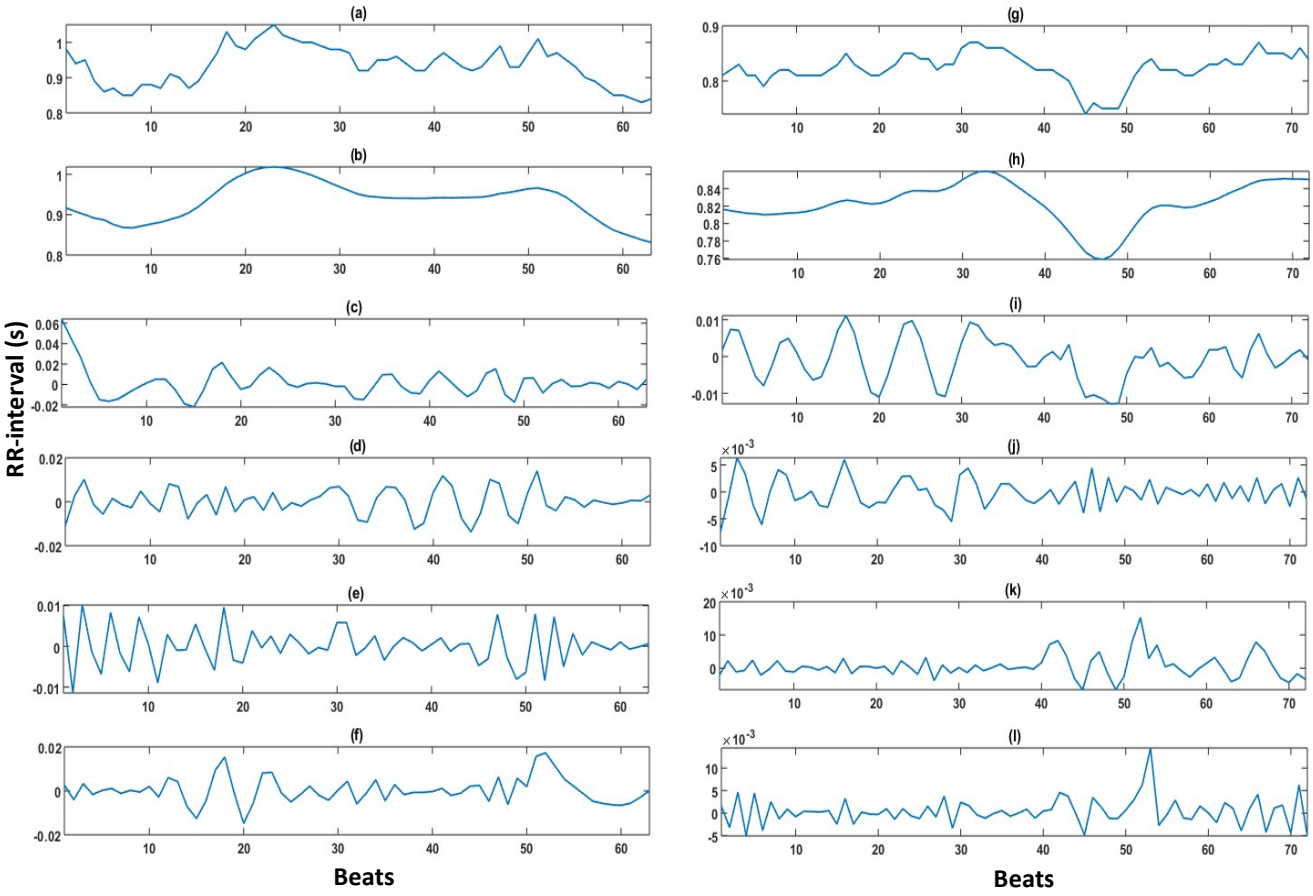

Figure 3.6 Plots of RCs obtained from HRV signal; (a) HRV signal for apnea class, (b)-(f) Five RCs obtained for apnea class, (g) HRV signal for normal class, (h)-(l) Five RCs obtained for normal class

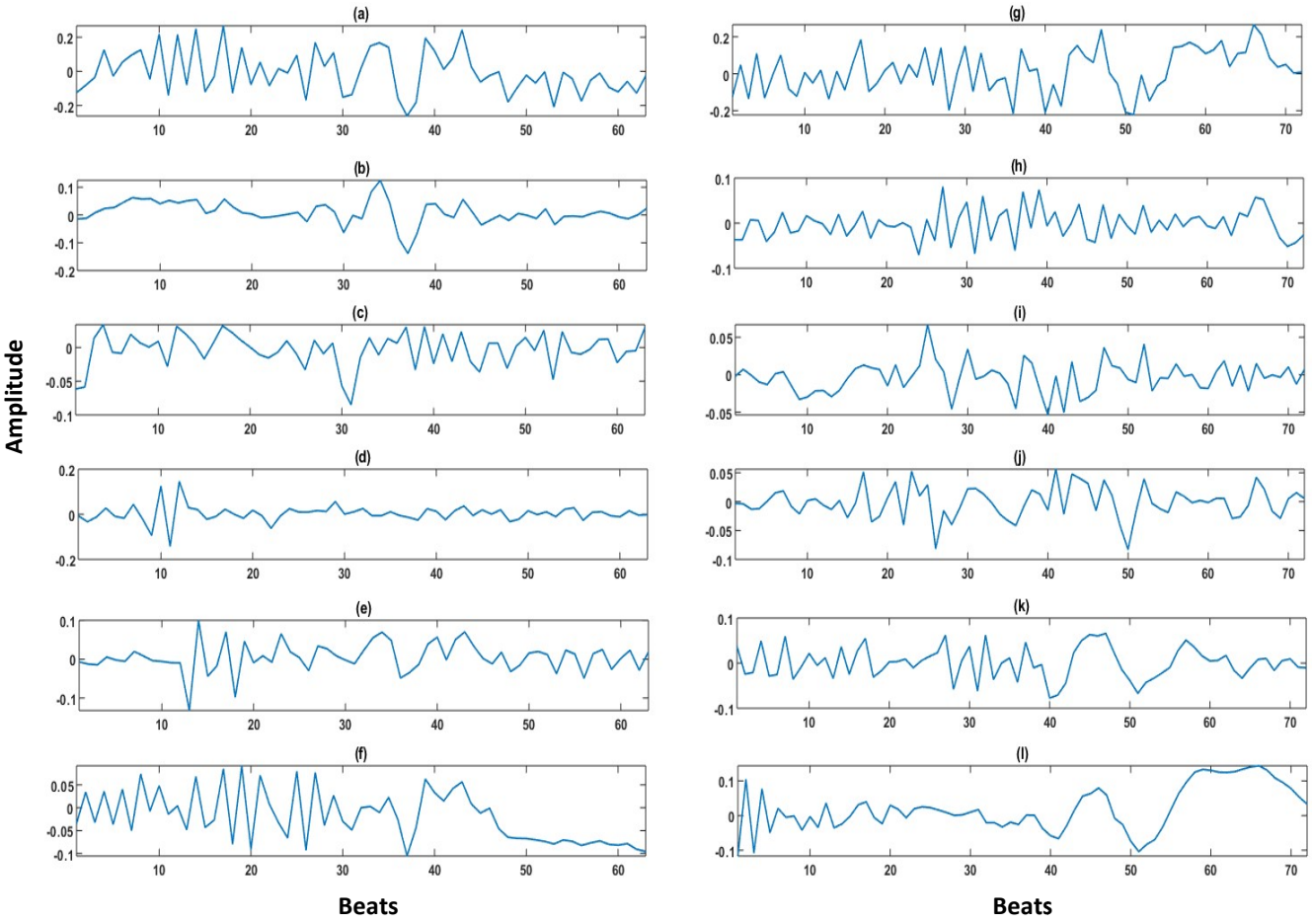

Figure 3.7 Plots of RCs obtained from EDR signal; (a) EDR signal for apnea class, (b)-(f) Five RCs obtained for apnea class, (g) EDR signal for normal class, (h)-(l) Five RCs obtained for normal class

3.3 Hilbert transform separation algorithm (HTSA)

In this work, the IA and IF are evaluated for each RC from both HRV and EDR signals using HTSA. In general, a real-valued AM-FM signal is given by,

$$s(t) = A(t)\cos\left(\omega_c t + \omega_m \int_0^t q(\tau)\, d\tau + \varphi(0)\right) = A(t)\cos\big(\varphi(t)\big) \tag{3.6}$$

with instantaneous phase define as $\varphi(t) = \omega_c t + \omega_m \int_0^t q(\tau)\, d\tau + \varphi(0)$.

Here, *A(t)* is the IA signal varying with time and the instantaneous angular frequency signal is given by,

$$\omega_i = \frac{d\varphi}{dt}(t) = \omega_c + \omega_m q(t) \tag{3.7}$$

Here, *q(t)* ϵ*[-1, 1]* is the frequency modulating signal, ω_c is the carrier frequency, $\varphi(0)$ is an arbitrary phase offset and $\omega_m \epsilon[0, \omega_c]$ is the maximum frequency deviation.

The Hilbert transform of any signal *s(t)* is defined as [46],

$$\hat{s}(t) = s(t) * \frac{1}{\pi t} \tag{3.8}$$

where '*' denotes the convolution operation and the Fourier transform is given as

$$\hat{S}(\omega) = -j\, sgn(\omega)\, S(\omega) \tag{3.9}$$

where *S(ω)* is the Fourier transform of *s(t).*

An analytic signal is defined as,

$$z(t) = s(t) + j\hat{s}(t) = m(t)\exp[j\theta(t)] \tag{3.10}$$

The modulus of *z(t)* i.e. *m(t)* and derivative of phase $\dot{\theta}(t)$ are an approximate estimate for the amplitude envelope and instantaneous angular frequency of *s(t)*. Hence, the HTSA can be summarized in the following two equations [41]:

$$m(t) = \sqrt{s^2(t) + \hat{s}^2(t)} \approx |A(t)| \tag{3.11}$$

$$\text{and } \dot{\theta}(t) = \frac{d}{dt}\left(arctan\left[\frac{\hat{s}(t)}{s(t)}\right]\right) \approx \omega_i(t). \tag{3.12}$$

In present study, the HTSA is implemented using MATLAB's inbuilt function *hilbert()*.

3.4 Feature extraction

In this study, statistical features are used to classify apnea and normal ECG episodes. Mean and standard deviation of both IA and IF of all the RCs obtained from HRV and EDR signals is considered. Both mean and standard deviation are calculated using *mean()* and *std()* functions of

MATLAB respectively. These features are fed as input features to the SAE-DNN and SVM-RBF classifiers. Both the classifiers are explained briefly in the following sections.

3.5 Classifiers

In this work, SAE-DNN [48] and SVM-RBF [47] classifiers are used independently for the classification purpose. Both the classifiers are implemented in MATLAB 2018a using its different inbuilt functions.

3.5.1 SAE-DNN classifier

The SAE-DNN classifier is formed by stacking of autoencoders [48]. The stacked autoencoder based classifier has been used for sleep stage classification and other classification problems [36,49]. The feature matrix for any classification is denoted as $F \in R^{m \times N}$, m is the number of ECG segments and N is total number of features used for classification. The F matrix has 'm' number of instances with $F = [f_v]_{v=1}^{m}$ and $f_v \in R^N$. The class label for v^{th} instance is denoted by [10] or [01] for apnea and non-apnea classes, respectively. The architecture of the SAE-DNN classifier for EDR feature set is shown in Fig. 3.8 (b).

Autoencoders are deep neural networks with same number of neurons at the input and output layers. It consists of an encoding i.e. input and hidden layers and a decoding (output) layer. The hidden layer evaluates the hidden features from the input feature set as $H = f(Wz + b)$. At the decoding layer, the hidden features are converted to output feature vector as,

$$z\ddot{A} = f\left(W\ddot{A}H + b\ddot{A}\right). \tag{3.13}$$

where W and $W\ddot{A}$, b and $b\ddot{A}$ represent the weight matrices and the bias values for the encoder and decoder layers respectively. Here, the activation function $f(.)$ used is the sigmoid activation function given by,

$$\sigma(k) = \frac{1}{1+e^{-k}}. \tag{3.14}$$

The input feature vector z and output feature vector $z\ddot{A}$ are same in an autoencoder and the cost function for the same is given by,

$$J = \frac{1}{v}\sum_{i=1}^{v}\left\|z_i - z\ddot{A}_i\right\|_2^2 + \frac{\lambda}{2}\|W\|_2^2. \quad (3.15)$$

After evaluating the encoding part weight matrix, the decoding part weight matrix is calculated as $W\ddot{A} = W^T$. The encoding layer maps the data into a latent space with reduction in dimension. The decoding layer produces an output as close as possible to the input data using the new latent space representation. Thus, by training an autoencoder, we can get a reduced representation of the input features with minimum loss of information. The autoencoders can be used to learn features for further classification purpose. In SAE-DNN, sparse autoencoders are used to derive the hidden layers' features.

In this work, the SAE-DNN classifier used consists of an input layer, two hidden layers and a softmax classifier layer. The greedy layer-wise training method is used for evaluation of the weight matrix and bias values of both the autoencoders followed by fine-tuning using backpropagation algorithm to optimize the trained model. The number of hidden neurons in each hidden layer is an important parameter which affects the performance of the classifier. The grid search approach based on classification accuracy is used to find the optimum size of the hidden layers for different input feature vectors. The number of neurons in different layers for HRV feature set and EDR feature set are *(20, 15, 5, 2)* and *(20, 15, 10, 2)* respectively. Similarly, for HRV and EDR feature set, the number of neurons is *(40, 30, 15, 2).*

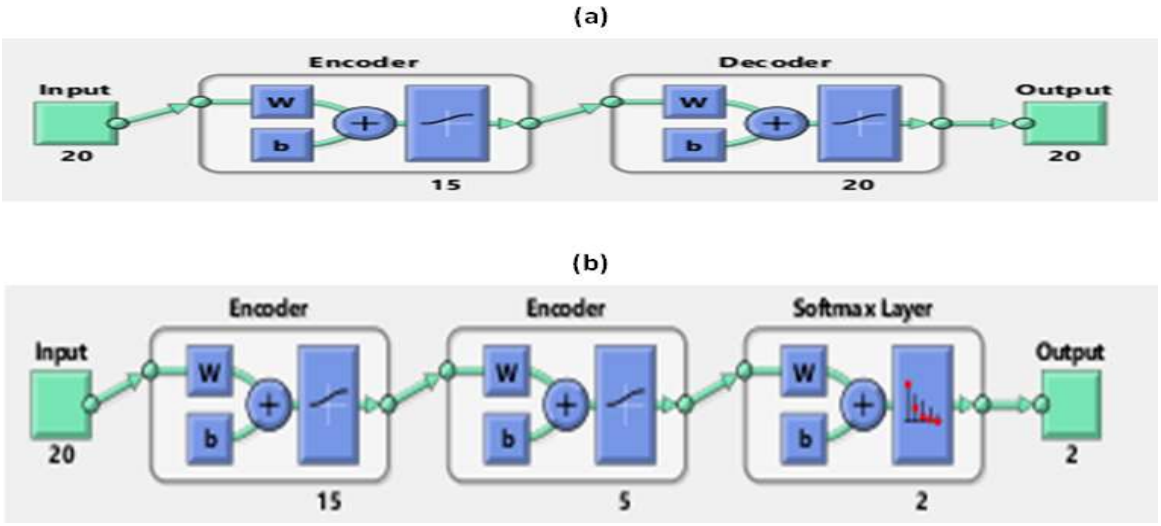

Figure 3.8 SAE-DNN classifier (a) Extraction of hidden layer from autoencoders, (b) architecture of SAE-DNN classifier for sleep apnea detection

3.5.2 SVM-RBF classifier

The support vector machine (SVM) classifier is a binary classification algorithm [47]. The class labels for the test instances are obtained using weight vector (*W*), bias value (*B*) and the kernel function $K(I_i, I_{test})$. During the training phase, the parameters *W* and *B* are evaluated. In this study, we have used radial basis function (RBF) as the kernel function for the SVM classifier given by,

$$K = e^{\frac{\|I_{test} - I_i\|^2}{2\sigma^2}}. \tag{3.16}$$

The feature matrix is formulated with rows as the number of features for each instance and columns as the number of instances and is denoted as $Y \epsilon R^{rxq}$. While training with the feature matrix, the objective of SVM is to estimate the optimal decision boundary by formulating the optimization problem [47],

$$\min_{W,B,E} \frac{W^T W}{2} + \alpha \sum_{i=1}^{q} E_i \tag{3.17}$$

such that $t_i(W^T \varphi(I_i) + B) \geq 1 - E_i, E_i \geq 0$, where α is the regularization parameter for assigning membership to error $E_i = t_i - \widehat{t_i}$, where t_i and $\widehat{t_i}$ are the actual and predicted class labels for i^{th} training instance. This optimization problem can be solved using Lagrangian given by,

$$max_\gamma J(\gamma) = \sum_{i=1}^{q} \gamma_i - \frac{1}{2} \sum_{i=1}^{q} \sum_{j=1}^{q} \gamma_i \gamma_j y_i y_j K(I_i, I_j). \tag{3.18}$$

For testing, the class label for each test instance (I_{test}) is computed as,

$$t_{test} = sgn\left[\sum_{i=1}^{q} \gamma_i y_i K(I_i, I_{test}) + B\right]. \tag{3.19}$$

We have used the inbuilt MATLAB 2018a functions for implementing SVM classifier with kernel scale set as 'auto'. The function selects an appropriate scale of the kernel using a heuristic procedure.

Chapter 4:

Results and Discussion

4.1 Statistical Analysis of features

In this section, the statistical analysis of the proposed features is presented. Fig. 4.1 depicts the boxplots for all the HRV features extracted. Similarly, Fig. 4.2 shows the boxplots for all the EDR features extracted. The proposed features have distinct median, lower quartile and upper quartile values for apnea and normal classes. The mean and standard deviation (std) of the proposed HRV features for apnea and normal classes are tabulated in Table 4.1. In Table 4.2, the mean and standard deviation of EDR features for both the classes are tabulated. It is observed that the standard deviation values of the IF and IA of the RCs have higher values for the apnea class as compared to the normal class. Similarly, the mean of IA and IF of the RCs have higher values for the normal class than that for the apnea class. In the event of sleep apnea, the obstruction of airway causes fluctuations in blood pressure which modulates the HRV signal [52]. Simultaneously, the EDR signal characteristics changes due to interruption in breathing [53, 54]. These variations are reflected in distinct mean and standard deviation values of the IF and IA of the RCs for apnea and normal classes. Using the Student's t-test approach [55], the p-values of the proposed features are evaluated. The p-value represents the probability that the results from the sample data occurred by chance. Lower p-values indicate effectiveness of the features. The independent two-sample t-test is performed using ttest2 command of MATLAB 2018a. A total of 19 HRV features and 16 EDR features have p-values less than 0.001. These small p-values establish the significance of the proposed features for sleep apnea detection.

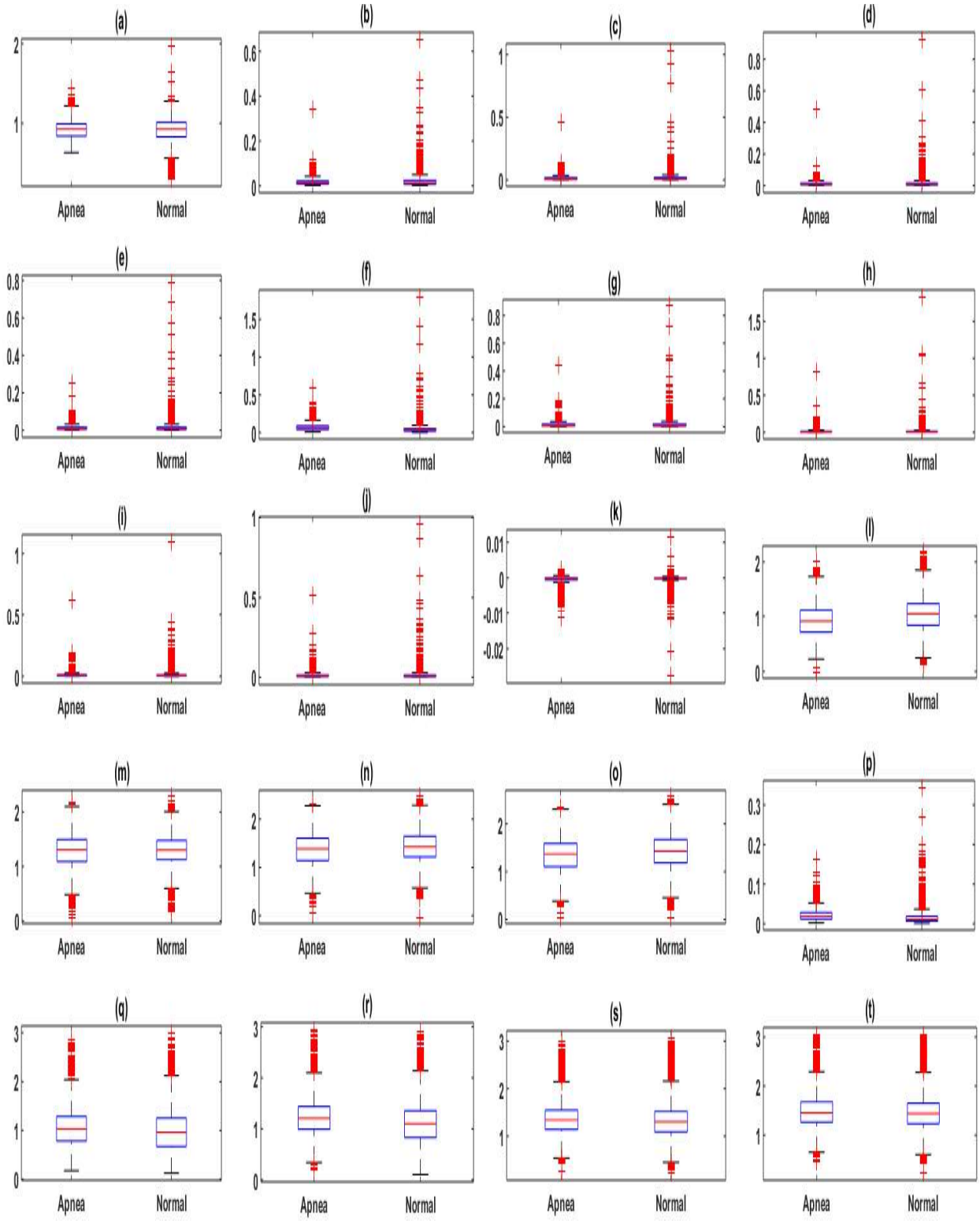

Figure 4.1 Boxplots of features extracted from HRV signal for (a)-(e) mean of IA, (f)-(j) standard deviation of IA, (k)-(o) mean of IF, (p)-(t) standard deviation of IF

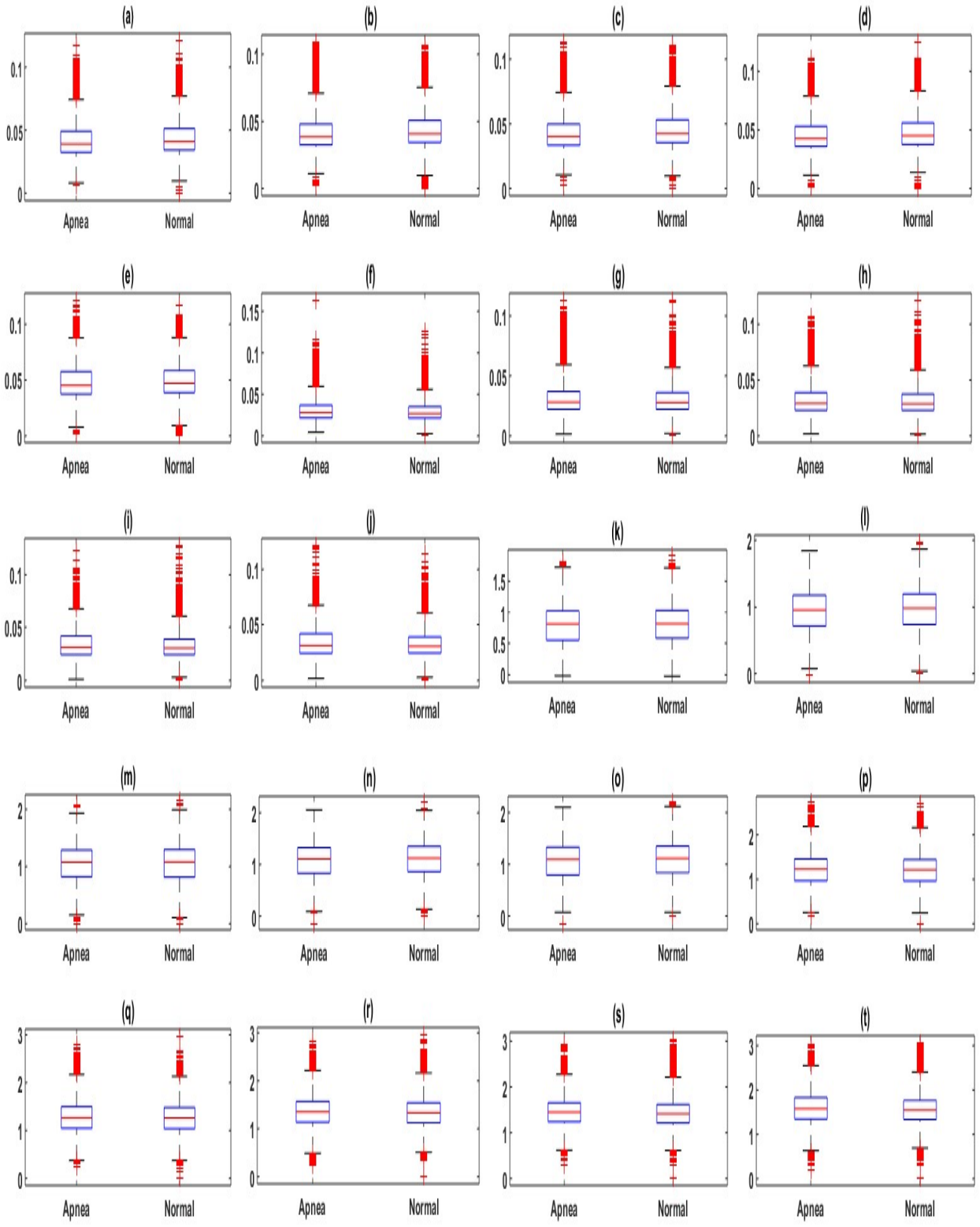

Figure 4.2 Boxplots of features extracted from EDR signal for (a)-(e) mean of IA, (f)-(j) standard deviation of IA, (k)-(o) mean of IF, (p)-(t) standard deviation of IF

Table 4.1 Mean (μ) and standard deviation (σ) of the HRV features for apnea and normal classes

HRV feature	Apnea (μ±σ)	Normal (μ±σ)	p-value (ttest)
Mean of IA of RC1	0.9197±0.1082	0.9208±0.1313	p=0.5457
Mean of IA of RC2	0.0162±0.0119	0.0201±0.0232	p<0.001
Mean of IA of RC3	0.0125±0.0110	0.0174±0.0273	p<0.001
Mean of IA of RC4	0.0117±0.0111	0.0153±0.0240	p<0.001
Mean of IA of RC5	0.0117±0.0102	0.0153±0.0247	p<0.001
Std of IA of RC1	0.0703±0.0420	0.0415±0.0450	p<0.001
Std of IA of RC2	0.0138±0.0138	0.0148±0.0225	p<0.001
Std of IA of RC3	0.0107±0.0162	0.0124±0.0302	p<0.001
Std of IA of RC4	0.0102±0.0138	0.0115±0.0239	p<0.001
Std of IA of RC5	0.0101±0.0134	0.0117±0.0239	p<0.001
Mean of IF of RC1	-0.000354±0.00074	-0.00019±0.00073	p<0.001
Mean of IF of RC2	0.9297±0.2873	1.0470±0.2884	p<0.001
Mean of IF of RC3	1.2885±0.2968	1.3037±0.2652	p<0.001
Mean of IF of RC4	1.3598±0.3343	1.4291±0.3252	p<0.001
Mean of IF of RC5	1.3402±0.3526	1.4241±0.3595	p<0.001
Std of IF of RC1	0.0221±0.0143	0.0152±0.0141	p<0.001
Std of IF of RC2	1.0490±0.3576	0.9780±0.4016	p<0.001
Std of IF of RC3	1.2249±0.3448	1.0953±0.3934	p<0.001
Std of IF of RC4	1.3597±0.3225	1.3136±0.3324	p<0.001
Std of IF of RC5	1.4849±0.3303	1.4542±0.3304	p<0.001

Table 4.2 Mean (μ) and standard deviation (σ) of the EDR features for apnea and normal classes

EDR feature	Apnea (μ±σ)	Normal (μ±σ)	p-value (ttest)
Mean of IA of RC1	0.0434±0.0162	0.0444±0.0148	p<0.001
Mean of IA of RC2	0.0428±0.0158	0.0442±0.0145	p<0.001
Mean of IA of RC3	0.0441±0.0157	0.0458±0.0148	p<0.001
Mean of IA of RC4	0.0468±0.0159	0.0480±0.0147	p<0.001
Mean of IA of RC5	0.0492±0.0164	0.0497±0.0154	p=0.0276
Std of IA of RC1	0.0315±0.0146	0.0300±0.0125	p<0.001
Std of IA of RC2	0.0317±0.0141	0.0305±0.0121	p<0.001
Std of IA of RC3	0.0326±0.0140	0.0315±0.0123	p<0.001
Std of IA of RC4	0.0347±0.0149	0.0329±0.0126	p<0.001
Std of IA of RC5	0.0349±0.0147	0.0330±0.0123	p<0.001
Mean of IF of RC1	0.7949±0.3164	0.8115±0.3103	p<0.001
Mean of IF of RC2	0.9363±0.3295	0.9628±0.3227	p<0.001
Mean of IF of RC3	1.0411±0.3416	1.0482±0.3373	p=0.1811
Mean of IF of RC4	1.0633±0.3619	1.0927±0.3497	p<0.001
Mean of IF of RC5	1.0534±0.3732	1.0869±0.3607	p<0.001
Std of IF of RC1	1.2181±0.3605	1.2001±0.3507	p=0.0013
Std of IF of RC2	1.2763±0.3465	1.2615±0.3336	p=0.0057
Std of IF of RC3	1.3621±0.3382	1.3362±0.3199	p<0.001
Std of IF of RC4	1.4554±0.3356	1.4222±0.3210	p<0.001
Std of IF of RC5	1.5911±0.3728	1.5540±0.3389	p<0.001

4.2 Performance comparison of classifiers

The performance of SAE-DNN and SVM-RBF classifiers is evaluated with three different feature sets i.e. HRV features, EDR features and HRV&EDR features together. The performance is compared based on accuracy (Acc), sensitivity (Se) and specificity (Sp) parameters [50,51]. These parameters are defined in terms of true positives (TP), true negatives (TN), false positives (FP) and false negatives (FN) as follows,

$$\text{Accuracy} = \frac{TP+TN}{TP+TN+FP+FN} \times 100\% \quad (4.1)$$

$$\text{Sensitivity} = \frac{TP}{TP+F} \times 100\% \quad (4.2)$$

$$\text{Specificity} = \frac{TN}{TN+FP} \times 100\% \, . \quad (4.3)$$

Using the unbalanced training dataset, the average accuracy, sensitivity and specificity are calculated with k-fold cross validation approach with 'k' as 10. In k-fold cross validation approach, the entire dataset is divided into k subsets. In each iteration, one of the k subsets is used as the test set/ validation set and the model is trained with the remaining k-1 subsets. This process is repeated for all the subsets. The average classification parameters obtained from SAE-DNN and SVM-RBF classifiers with different feature sets is tabulated in Table 4.3. The best classification performance is obtained with the SVM-RBF classifier using both HRV and EDR features together. An average accuracy of 79.05%, sensitivity of 69.61% and specificity of 84.92% is obtained. It is observed that the HRV features individually performed better than the EDR features for both the classifiers.

Table 4.3 Performance of classifiers with unbalanced dataset and 10-fold cross-validation

Signal	**SAE-DNN classifier**			**SVM-RBF classifier**		
	Accuracy (%)	**Sensitivity (%)**	**Specificity (%)**	**Accuracy (%)**	**Sensitivity (%)**	**Specificity (%)**
HRV	75.16±2.191	60.1±5.312	84.59±1.003	77.61±0.602	65.56±1.974	85.1±0.951
EDR	65.6±1.083	38.27±10.00	82.59±4.894	65.97±0.700	37.61±1.677	83.62±0.661
HRV + EDR	77.15±1.796	65.29±3.794	84.56±1.469	79.05±0.813	69.61±1.482	84.92±1.117

Classifier training with balanced dataset is suggested for detection of heart failure and sleep apnea in [62] and [63] respectively. Motivated from this, both the classifiers are also trained with balanced datasets which has equal number of instances for both the classes. The average performance parameters are obtained with hold-out cross-validation approach. In hold-out method, a part of the dataset is used for testing purpose and the remaining part is used for training the model. In this work, 10% of the balanced dataset is used for testing and 90% is used for training. The results with balanced dataset are tabulated in Table 4.4. The SVM-RBF classifier provided the best classification results with accuracy of 81.06%, sensitivity of 82.45% and specificity of 79.72%. The use of balanced training dataset significantly increased the sensitivity values for the SAE-DNN classifier from 65.29% to 79.01%. With balanced training dataset, the performance of HRV features and HRV and EDR features together is comparable for the SVM-RBF classifier. On the other hand, the performance of the SAE-DNN classifier improved significantly with the use of EDR features with HRV features.

Table 4.4 Performance of classifiers with balanced dataset and hold-out cross-validation

Signal	**SAE-DNN classifier**			**SVM-RBF classifier**		
	Accuracy (%)	**Sensitivity (%)**	**Specificity (%)**	**Accuracy (%)**	**Sensitivity (%)**	**Specificity (%)**
HRV	75.95±1.621	76.59±2.227	75.33±1.928	81.32±0.667	82.8±0.621	79.82±1.26
EDR	64.49±0.963	62.35±2.401	66.62±1.848	69.43±0.709	69.53±1.081	69.36±1.925
HRV + EDR	77.65±1.507	79.01±1.727	76.3±1.779	81.06±0.709	82.45±0.735	79.72±1.397

The performance of the proposed method is also evaluated with subject-specific cross-validation approach as shown in Table 4.5. In this method, data from one subject/patient is used for testing and the remaining dataset is used in training. The process is repeated for all the subjects and the average parameters are calculated. It is also known as the leave-one-out cross-validation approach. Using subject-specific cross-validation with HRV and EDR features as the input feature set, higher accuracy values are obtained with SVM-RBF classifier while higher sensitivity values are obtained with SAE-DNN classifier.

Table 4.5 Performance of classifiers with different datasets and cross-validation approaches

Cross-validation Schemes	SAE-DNN classifier			SVM-RBF classifier		
	Accuracy (%)	Sensitivity (%)	Specificity (%)	Accuracy (%)	Sensitivity (%)	Specificity (%)
10-fold cross validation on unbalanced dataset	77.15±1.79	65.29±3.79	84.56±1.47	79.05±0.81	69.61±1.48	84.92±1.11
10-fold cross validation on balanced dataset	77.65±1.51	79.01±1.73	76.3±1.78	81.06±0.71	82.45±0.73	79.72±1.39
Subject-specific cross validation	74.76±12.02	63.48±27.47	79.91±10.61	76.12±12.92	62.87±29.01	81.53±10.10

The area under the receiver operating characteristic (AROC) is evaluated for the quantification of the classification performance of different feature sets and classifiers. These values are tabulated in Table 4.6. AROC value is equal to the probability that a classifier will rank a randomly chosen positive instance higher than a randomly chosen negative instance when using normalized units. A perfect binary classifier has an AROC value of 1. Larger AROC values represent better classification performance. The highest AROC value is obtained with SVM-RBF classifier using both HRV and EDR features together. The results obtained show that the SM-SSA is effective in capturing the information related to apnea event in the RCs obtained.

Table 4.6 AROC values for SAE-DNN and SVM-RBF classifiers with different feature sets

Signal	Area under ROC	
	SAE-DNN classifier ($\mu\pm\sigma$)	SVM-RBF classifier ($\mu\pm\sigma$)
HRV	0.7176±0.0481	0.7654±0.0055
EDR	0.6190±0.0195	0.6357±0.0097
HRV+EDR	0.7496±0.031	0.7800±0.0095

4.3 Comparison with existing works

The results obtained with the proposed method are compared with some of the existing works for detection of sleep apnea using ECG signals. The comparison is presented in Table 4.7. Authors in [57] used cardio-pulmonary (CP) features based on Fourier transform and reported sensitivity and specificity values of 66.8% and 72.9% respectively. The proposed method has shown better performance than Fourier transform based CP features. Varon et al. in [58] reported a sensitivity of 88.84% and specificity of 83.29% using statistical features from both HRV and EDR signals. The least squares SVM (LS-SVM) is used as classifier. The CP features are extracted from EDR and HRV signals in [59] and classified using a logistic regression classifier. Authors reported a sensitivity of 81.90% and specificity of 91.50%. In [38], wavelet-based features are used and sensitivity of 94.40% and specificity of 98.80% is achieved. The method in [38] reported better results than the proposed approach but they have used a different ECG database in their study. Authors in [61] introduced Hilbert-Huang transform (HHT) for sleep apnea detection. They have reported a sensitivity of 73.1% and specificity of 71.2%. The method proposed in present study has performed better than HHT based method using balanced dataset. However, in [61], the performance is not evaluated with subject-specific cross-validation approach. Using fuzzy entropy and energy features, a sensitivity of 78.02% and specificity of 74.64% is reported in [6]. The proposed method performed better than the features in [6] with balanced training dataset.

The sensitivity and specificity values obtained in the present work are lower than that reported for some of the existing works. However, in this study, all 35 annotated recordings are used. The performance is evaluated with both subject-specific cross-validation approach and 10-fold cross-validation approach. Also, the results are evaluated using both unbalanced and balanced training datasets.

Table 4.7 Comparison of the performance of proposed method with existing systems for sleep apnea detection

Approaches (Features and classifier)	Sensitivity (%)	Specificity (%)	Database and validation methods
CP features extracted using Fourier transform and threshold classifier [57]	66.80	72.90	Apnea-ECG (hold-out)
Statistical features extracted from HRV and EDR signals and LS-SVM classifier [58]	88.84	83.29	Apnea-ECG (leave-one-out)
Cross-spectral features using EDR and HRV signals and Logistic Regression [59]	81.90	91.50	Apnea-ECG (leave-one-out)
Wavelet transform based feature extraction and SVM [38]	94.40	98.80	SRU-database [38] (leave-one-out)
Different features extracted from EDR and HRV signals and ELM classifier [60]	76.30	87.32	Apnea-ECG (leave-one-out)
CP features using HHT and threshold classifier [61]	73.10	71.20	Apnea-ECG (hold-out)
Features extracted from IBFs of both EDR and HRV signals, and KELM [6]	78.02	74.64	Apnea-ECG (10-fold)
Proposed features (Statistical features from IA and IF of RCs of both EDR and HRV signals) and SVM-RBF	82.45	79.42	Apnea-ECG (10-fold)
Proposed features and SAE-DNN	63.48	79.91	Apnea-ECG (leave-one-out)

Chapter 5:

Conclusions and Future work

5.1 Conclusions

In this work, we have proposed a novel method based on SM-SSA for detection of sleep apnea. The SM-SSA is used to evaluate RCs from both HRV and EDR signals. The IA and IF of these RCs are calculated using HTSA. These IAs and IFs extract the information related to sleep apnea from the variations in HRV and EDR signals. Statistical features such as mean and standard deviation are used to quantify this information. Based on these input features, The ECG segments are classified as apnea and normal using SVM-RBF and SAE-DNN classifiers. The proposed method achieved the highest classification accuracy of 81.06% with sensitivity of 82.45% and specificity of 79.72% using both HRV and EDR features together and SVM-RBF as the classifier.

The advantages of this study are as follows:

1. The recently developed SM-SSA technique is introduced for the analysis of HRV and EDR signals for sleep apnea detection.
2. Changes in IA and IF of the extracted RCs are used to capture the information about the various physiological variations during the apnea event.
3. The application of both SAE-DNN and SVM-RBF classifiers is investigated for the classification of apnea and non-apnea ECG signals.

5.2 Future work

In future, more robust features can be used to extract information from the RCs obtained using SM-SSA. Some of these features are entropy based features, energy based features, spectral features and other higher order statistical features. Recently, different neural networks have been proposed in literature as classifiers for sleep apnea detection [34, 37, 64, 65]. The use of these classifiers like recurrent neural networks (RNNs) and convolutional neural networks (CNNs) can also be investigated to develop improved sleep apnea detection methods.

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1. H. Singh, R. K. Tripathy and R. B. Pachori, “An Intelligent System for the Detection of Sleep Apnea using Heart Beat Interval and ECG Derived Respiration Signals,” IEEE Journal of Biomedical and Health Informatics (under review).