

# Detecting Types of Sleep Apneas through Nonlinear Features of Electrocardiogram and Electroencephalogram Signals

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Received: 05 April 2021 / Accepted: 14 May 2021

## Abstract

**Purpose:** Sleep apnea is a common disease among women, and mainly men. The most dangerous complication of this disorder is heart stroke. Other complications include insufficient sleep and resulting daytime tiredness and illness that affect the individual's activities during the day, disrupt their life. Therefore, identifying this disease is important.

**Materials and Methods:** We used Electroencephalogram (EEG) and Electrocardiogram (ECG) channels from the data of 25 patients with sleep apnea, for each type of sleep apnea, 8 nonlinear-like features, including fractal dimension, correlation dimension, certainty, recurrence rate, mean diagonal lines, the entropy of recursive quantification analysis, sample Entropy, and Shannon entropy were extracted. Then, feature matrices were sorted using principal component analysis in the order of linear combination of features, and the 20 selected features were chosen, normalized using common methods, and fed to different classifiers. Two 5-class and 2-class classification methods were assessed. In the 5-classification, three classifiers were used; the support vector machine, k-nearest neighbor, and multilayer perceptron.

**Results:** The results showed that the highest mean validity, accuracy, sensitivity, and specificity for the SVM classifier was 88.45%, 88.35%, 88.33%, and 88.32%, respectively. In the 2-class approach, in addition to the mentioned classifiers, linear discriminant analysis, Bayes, and majority voting were used, and each class was considered against all classes. The highest average validity, average accuracy, average sensitivity, average specificity using the majority rule voting was 94.35%, 94.30%, 94.32%, and 94.15% respectively.

**Conclusion:** When the results of classifiers are combined with the majority voting method, the validity of identifying the classes increases. The average validity for this method was obtained at 94.42%, which was higher than several other studies. It is recommended that databases with a larger sample size be used. This would lead to increased reliability of the proposed analysis method. Moreover, using novel deep-learning-based methods could help obtain better results.

**Keywords:** Sleep Apnea; Electrocardiogram; Electroencephalogram; Nonlinear Features; Classification.

## 1. Introduction

### 1.1. Background

Sleep apnea is a severe medical condition in which the patient repeatedly experiences short apneas during sleep. Sleep apnea is a common disease among women, and mainly men [1], developed due to wrong lifestyle (inactivity and being overweight, high-lipid diet, and stress) in individuals and has an increasing trend. The most dangerous complication of this disorder is heart stroke. Other complications include insufficient sleep and resulting daytime tiredness and illness that affect the individual's activities during the day, disrupt their schedules, and lower their quality of life. Therefore, identifying this disease is important [2].

Detecting any of these disorders could lead to proper therapeutic measures.

There are four types of sleep apnea: Obstructive Sleep Apnea (OSA) [3], Central Sleep Apnea (CSA), mixed sleep apnea, and hypopnea [4]. OSA is a recurrent and serious sleep disorder leading to complete obstruction of the upper air tract and the relaxation of throat muscles, finally obstructing the airway during sleep. OSA symptoms include morning headaches and loud snoring. CSA is also known as Cheyne-Stokes respiration [5], a sleep disorder in which respiration starts and repeatedly stops during sleep. The brain stops transmitting signals to the breathing muscles. CAS may also develop as a result of heart failure and stroke. The most prevalent sleep disorder is obstructive sleep apnea. Another type of sleep apnea is mixed sleep apnea which is a mixture of OSA and CSA [2] and [5].

### 1.2. Contribution and Paper Organization

The objective of the present study was to detect different types of sleep apnea by extracting the chaotic features and machine learning-based methods from ECG and EEG signals.

Diagnosing sleep apnea is a tedious procedure that needs time, effort, and high expertise [6]. It has been proved that ECG [7] and EEG help diagnose sleep apnea [1] and [8]. There are different process methods to identify the disorder out of patients' EEG and ECG signals. Among these methods, the non-linear methods may be better choices compared to other methods due to the non-linear nature of these signals. It is recommended in this study

that different sleep apnea disorders be identified by extracting nonlinear features.

In this work, after extracting a 30-second segment of two EEG and ECG channels from the data of 25 patients with sleep apnea in the University College Dublin Sleep Apnea Database, for each type of sleep apnea, eight nonlinear-like features, including Fractal Dimension (FD), Correlation Dimension (CD), certainty, recurrence rate, mean diagonal lines, the entropy of Recursive Quantification Analysis (RQA), sample Entropy, and Shannon entropy were extracted. Then, feature matrices were sorted using Principal Component Analysis (PCA) in the order linear combination of features, and the 20 selected features were chosen, normalized using common methods, and fed to different classifiers. Two 5-class and 2-class classification methods were assessed. In the 5-classification, three classifiers were used; the Support Vector Machine (SVM), k-Nearest Neighbor (K-NN), and Multilayer Perceptron (MLP). Eighty percent of the samples were used to train classification and 20% to test. Ultimately, four criteria, namely, validity, accuracy, specificity, and sensitivity, were calculated in 100 repetitions, and the mean and standard deviation values were reported for them. The present study results showed that the highest mean validity, accuracy, sensitivity, and specificity for the SVM classifier was 88.45%, 88.35%, 88.33%, and 88.32%, respectively. In the 2-class approach, in addition to the mentioned classifiers, Linear Discriminant Analysis (LDA), Bayes, and majority voting were used, and each class was considered against all classes. The highest average validity, average accuracy, average sensitivity, average specificity using the majority rule voting was 94.35%, 94.30%, 94.32%, and 94.15%, respectively.

Using artificial intelligence-based methods could help understand the influencing mechanisms in developing sleep apnea. Therefore, it would be possible to select the proper treatment for these patients at the right time, which is a fervent hope of medicine.

## 2. Materials and Methods

### 2.1. Database

In this study, EEG and ECG signals of the University College Dublin Sleep Apnea Database were used (from physionet.org) (Figures 1, 2). This database consists of two EEG channels (C3-A1 and C4-A1) and one ECG

channel (abdominal V2), which is recorded from 25 patients (21 male and four female) suspected of sleep apnea. The mean age in these patients was 50 years (with a standard deviation of 10), and the mean BMI index was 31.6 kg/m<sup>2</sup> (standard deviation of 4). These recordings were collected at St. Vincent's University Hospital Sleep Disorders Clinic, under the direction of Prof. Walter McNicholas.

Dr. Liam Doherty, Dr. Silke Ryan, and Dr. John Garvey collected and assembled the clinical and demographic information, and Ms. Patricia Boyle was responsible for polysomnogram scoring and annotation.

Eric Chua was responsible for de-identification and electronic archiving of records [9]. Onset time and duration of respiratory events (obstructive, central, mixed apneas and hypopneas, and periodic breathing episodes) were annotated by the same sleep technologist (see the \_respevt.txt files [9]). Terms used in these files include:

- 1st column-Time of occurrence (time of day)
- 2nd column
  - HYP – Hypopnea
  - C – Central

- O – Obstructive
- M - Mixed
- 3rd column - Periodic breathing (PB)/ Cheynes-Stokes (CS)
- 9th & 10th columns - Bradycardia/ Tachycardia

## 2.2. The Proposed Method

A 30-second segment of two EEG signal channels and an ECG channel is available for 5000 samples to detect sleep apnea. Linear and non-linear features are extracted from each channel, which is later explained.

### 2.2.1. Sample Entropy (SampEn)

SE is considered as an effective method for investigating different types of time series data. A lower SE value indicates a high frequency of similarity in time series [10] For a time series of length n, Sample Entropy (m,r,n) can be defined as the negative logarithm of conditional probability that two sequences are similar for m point [11] within a tolerance value r, excluding any self-matches. The Equation 1 can be represented according to [10]:

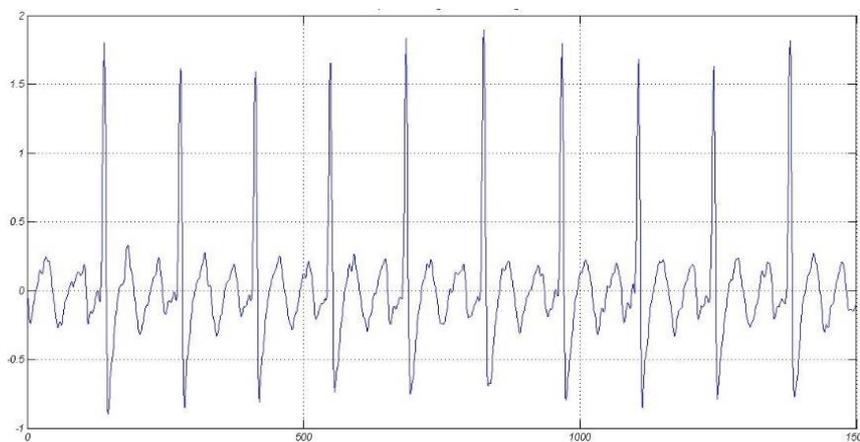


Figure 1. Sample of ECG signal after filtering

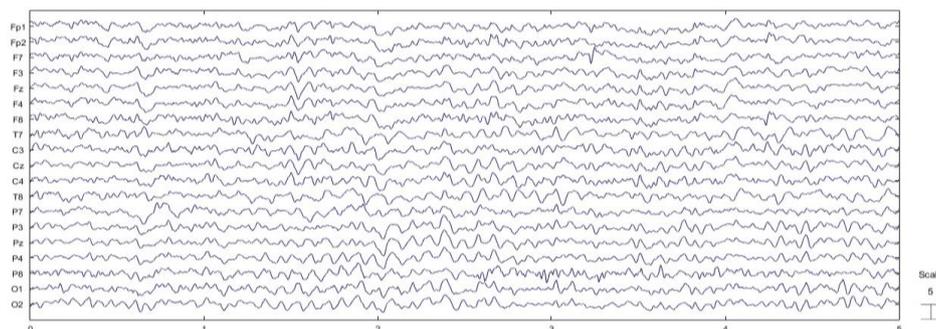


Figure 2. Sample of EEG signals after filtering

$$SampEn(m,r) = \lim_{N \rightarrow \infty} \left\{ -\ln \left[ \frac{A^m(r)}{B^m(r)} \right] \right\} \quad (1)$$

Where, m is the length of sequences to be compared, r is the tolerance value for accepting matches, n is the length of original data, and A and B are defined as follow (Equation 2):

$$A = \left\{ \frac{(n-m-1)(n-m)}{2} \right\} A^m(r) \quad (2)$$

$$B = \left\{ \frac{(n-m-1)(n-m)}{2} \right\} B^m(r)$$

Where,  $A^m(r)$ , is the probability that the two sequences match for  $m + 1$  points, and  $B^m(r)$  is the probability that the two sequences match for m points. Each SE value indicates relative consistency with respect to any value of (m,r). That is, if a record has a lower SE value than another record for a part of fixed m and r values, it will be lower for any part of fixed m and r values [11]. SE is independent of the data length and shows an elimination of self-matching. In order to approximate the conditional probabilities of matches, SE uses a point-wise approach [10].

### 2.2.2. Correlation Dimension

The correlation dimension is expected to give information on the minimum number of dynamic variables needed to model the underlying system and it can be obtained as follows [12].

Similarly as in the calculation of approximate and sample entropies, form length m vectors  $u_j$  (Equation 3):

$$u_j = (RR_j, RR_{j+\tau}, \dots, RR_{j+m-1}) \quad (3)$$

$$j = 1, 2, \dots, N - m + 1$$

and calculate the number of vectors  $u_k$  for which  $d(u_j, u_k) \leq r$ , that is (Equation 4):

$$C_j^m(r) = \frac{\text{nbr of } \{u_k | d(u_j, u_k) \leq r\}}{N - m + 1} \quad (4)$$

Where the distance function  $d(u_j, u_k)$  is now defined as (Equation 5):

$$d(u_j, u_k) = \sqrt{\sum_{l=1}^m (u_j(l) - u_k(l))^2} \quad (5)$$

Next, an average of the term  $C_j^m(r)$  is taken (Equation 6):

$$C^m(r) = \frac{1}{N - m + 1} \sum_{j=1}^{N-m+1} C_j^m(r) \quad (6)$$

Which is the so-called correlation integral. The correlation dimension  $D_2$  is defined as the limit value (Equation 7):

$$D_2(m) = \lim_{r \rightarrow 0} \lim_{N \rightarrow \infty} \frac{\log C^m(r)}{\log r} \quad (7)$$

In practice this limit value is approximated by the slope of the regression curve  $(\log r, \log C^m(r))$  [13]. The slope is calculated from the linear part of the log-log plot (see Figure 3). The slope of the regression curves tend to saturate on the finite value of  $D_2$  when m is increased. In the software, a default value of  $m=1$  was selected for the embedding.

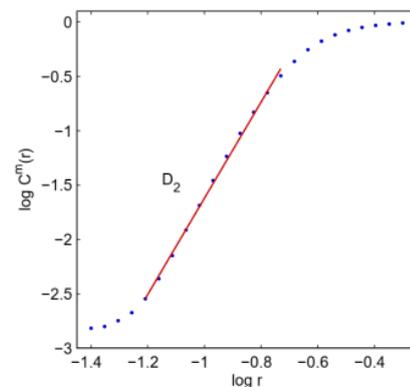


Figure 3. Approximation of the correlation dimension  $D_2$  from the  $(\log r, \log C^m(r))$  plot

### 2.2.3. Recurrence Plot (RP)

Yet another approach, included in the software, for analyzing the complexity of the time series is the so-called Recurrence Plot (RP) analysis. In this approach, vectors (Equation 8):

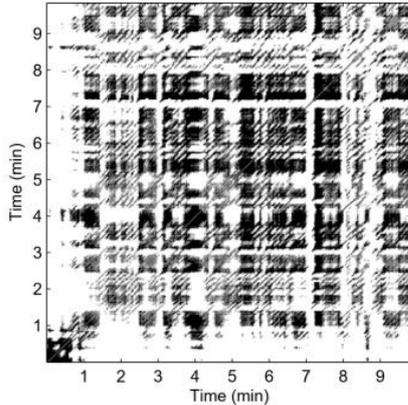
$$u_j = (RR_j, RR_{j+\tau}, \dots, RR_{j+(m-1)\tau}) \quad (8)$$

$$j = 1, 2, \dots, N - (m - 1)\tau$$

Where m is the embedding dimension and  $\tau$  the embedding lag. The vectors  $u_j$  then represent the RR interval time series as a trajectory in m dimensional space. A recurrence plot is a symmetrical  $[N-(m-1)\tau] \times [N-(m-1)\tau]$  matrix of zeros and ones. The element in the j'th row and k'th column of the RP matrix, i.e.  $RP(j,k)$ , is 1 if the point  $u_j$  on the trajectory is close to point  $u_k$ . That is (Equation 9):

$$RP(j,k) = \begin{cases} 1, & d(u_j - u_k) \leq r \\ 0, & o.w \end{cases} \quad (9)$$

Where  $d(u_j - u_k)$  is the Euclidean distance (see above) and  $r$  is a fixed threshold. The structure of the RP matrix usually shows short line segments of ones parallel to the main diagonal. The lengths of these diagonal lines describe the duration of which the two points are close to each other. An example RP for heart rate variability time series is presented in Figure 4.



**Figure 4.** Recurrence plot matrix for HRV time series (black = 1 and white = 0) [14]

The first quantitative measure of RP is the Recurrence Rate (REC) which is simply the ratio of ones and zeros in the RP matrix. The number of elements in the RP matrix for  $\tau=1$  is equal to  $N-m+1$  and the recurrence rate is simply given as (Equation 10):

$$REC = \frac{1}{(N - m + 1)} \sum_{j,k=1}^{N-m+1} RP(j,k) \quad (10)$$

The recurrence rate can also be calculated separately for each diagonal parallel to the line-of-identity (main diagonal). The trend of REC as a function of the time distance between these diagonals and the line-of-identity describes the fading of the recurrences for points further away.

The rest of the RP measures consider the lengths of the diagonal lines. A threshold  $l_{min} = 2$  is used for excluding the diagonal lines formed by tangential motion of the trajectory. The maximum line length is denoted  $l_{max}$  and its inverse, the divergence (Equation 11),

$$DIV = \frac{1}{l_{max}} \quad (11)$$

has been shown to correlate with the largest positive Lyapunov exponent [15]. The average diagonal line length, on the other hand, is obtained as (Equation 12):

$$l_{mean} = \frac{\sum_{l=l_{min}}^{l_{max}} l N_l}{\sum_{l=l_{min}}^{l_{max}} N_l} \quad (12)$$

where  $N_l$  is the number of length  $l$  lines. The determinism of the time series is measured by the variable (Equation 13):

$$DET = \frac{\sum_{l=l_{min}}^{l_{max}} l N_l}{\sum_{j,k=1}^{N-m+1} RP(j,k)} \quad (13)$$

Finally, the Shannon information entropy of the line length distribution is defined as (Equation 14):

$$shanEn = - \sum_{l=l_{min}}^{l_{max}} n_l \ln n_l \quad (14)$$

Where  $n_l$  is the number of length  $l$  lines divided by the total number of lines, that is (Equation 15):

$$n_l = \frac{N_l}{\sum_{l'=l_{min}}^{l_{max}} N_{l'}} \quad (15)$$

### 2.2.4. Fractal Dimension (FD)

A fractal is a geometric shape that can be split into smaller parts. Each shows a reduced version of the original shape. FD could be calculated through a set of points using different methods, which are different in terms of validity, sensitivity to the used points, and the time required for calculation. Higuchi's Fractal Dimension (HFD) is usually used to find the FD of the EEG signal. Higuchi introduced a useful algorithm to analyze discrete-time sequences to obtain a consistent and accurate FD. EEG signal is assumed as a time series of  $x(1), x(2), \dots, x(n)$ . The time series of  $x_m^k$  could be shown as Equation 16.

$$x_m^k = \left\{ x(m), x(m+k), x(m+2k), \dots, x\left(m + \left\lceil \frac{N-m}{k} \right\rceil k\right) \right\} \quad (16)$$

Where  $m= 1,2,\dots,k$ .  $m$  represents the initial time value, and  $k$  indicates the discrete-time interval between points. The length  $L_m(k)$  for each time series  $K$  or curves  $x_m^k$  can be defined as follows (Equation 17):

$$L_m(k) = \frac{\sum_{i=1}^{\lceil a \rceil} |x(m+ik) - x(m+(i-1)k)| (N-1)}{\lceil a \rceil k} \quad (17)$$

Where  $n$  is the total length of  $x$  time series. The mean length of the curve  $L_m(k)$  for each  $k$  is defined as the average of the  $L_m(k)$  for all  $m$  values. Thus, an array of average values of  $L_m(k)$  is obtained. A graph of  $\log(L_m(k))$  is plotted against  $\log(1/k)$ , and FD is estimated as the slope of the line that fits the pairs  $\{\ln[L(k)], \ln(1/k)\}$  in a least-squares sense. In other words, FD could be defined as  $\log(L_m(k))/\log(1/k)$ .

### 2.2.5. Dimensionality-Reduction using Principle Component Analysis

PCA is one of the most famous dimensionality-reduction methods. The idea of PCA originated because if data are described with many features, then useful data will be present in only a few features. Therefore, we intend to find the correlation between variables in PCA so that if there is a correlation between the variables, dimensionality-reduction will be significant. We look for the direction of greatest variance in PCA in data with large dimensions to store them in a subspace with smaller dimensions. The storage method should be in a way that most of the data is saved. We had a matrix of 5000 in 24 attributes, we know that this method ranks the attributes in one step according to the values with more variance, and in the next step we select some superior attributes, thus sorting the attributes and reducing the dimension. Here, from the 24 properties extracted in the previous step, the top 20 linear combinations are selected. Finally we have a 5000 by 20 matrix.

### 2.2.6. Normalizing

The extracted features are in different numerical ranges; before classification, the features should be set in the same range. For this purpose, four normalization methods were used. There are different methods for feature normalization, including Z normalization, min-max normalization, Softmax normalization, and decimal normalization. After testing with each of the methods, the method which reported more optimal results in the classification was chosen as the selected method [16,17].

### 2.2.7. Classification

Two 5-class and 2-class classification methods were assessed. In the 5-class approach, we have four apnea types, obstructive, central, mixed, hypopnea, and non-apnea classes, and in the 2-class approach, a class is compared against others which are repeated five times for each class. In the 5-class approach, the K-NN, MSVM, and MLP [18] were used. In the 2-class approach, Bayes, LDA, and a new mixed method called Majority Voting (MV) were used that are discussed in this section.

### 2.2.8. Evaluation of Results

As stated earlier, there are two 5-class, and 2-class classification approaches. Each classifier was trained,

tested, (Test and train data for each repetition is "randperm") and evaluated 100 times in each approach, and the mean results were reported. The main criteria studied in this article was the error of each classifier, like the validity, accuracy, specificity, and sensitivity.

The equations are written for the 5-class approach ( $j=5$ , class counter); in the 2-class approach,  $j$  was equal to 2. In the 5-class approach, the equation parameters are defined as follow:

$TP_i$  are the values correctly classified in the  $i$  class.

$TN_i$  are the values correctly classified in other classes.

$FN_i$  are the values incorrectly classified in the class.

$FP_i$  are the values correctly classified in other classes.

In the 2-class approach, assuming the understudy class as the positive class and others and negative classes, then:

TP: The number of positive classes which are correctly detected as positive classes.

TN: The number of negative classes which are correctly detected as negative classes.

FN: The number of negative classes which are incorrectly detected as positive classes.

FP: The number of positive classes which are incorrectly detected as negative classes.

In 5 classes we defined the  $TP_i$ ,  $TN_i$ ,  $FN_i$  and  $FP_i$  for each class. We mentioned the classification accuracy for each class.

The samples of Confusion matrixes formation for 2-class approach:

$$\text{Confusion matrix} = \begin{bmatrix} TP & FP \\ FN & TN \end{bmatrix}$$

$$\text{MLP} = \begin{bmatrix} 0.43 & 0.03 \\ 0.09 & 0.44 \end{bmatrix}$$

$$\text{K-NN} = \begin{bmatrix} 0.39 & 0.09 \\ 0.11 & 0.41 \end{bmatrix}$$

$$\text{SVM} = \begin{bmatrix} 0.45 & 0.05 \\ 0.04 & 0.46 \end{bmatrix}$$

$$\text{Bayes} = \begin{bmatrix} 0.38 & 0.12 \\ 0.14 & 0.36 \end{bmatrix}$$

$$\text{LDA} = \begin{bmatrix} 0.40 & 0.09 \\ 0.10 & 0.41 \end{bmatrix}$$

$$\text{Majority Voting} = \begin{bmatrix} 0.46 & 0.03 \\ 0.04 & 0.47 \end{bmatrix}$$

### 3. Results

In this article, four apnea classes, i.e., obstructive, central, mixed, hypopnea, and a non-apnea class, were available. The samples were divided into two groups of training and test.

Eighty percent of samples were grouped in the training group and 20% in the test group. The classification was conducted 100 times, and in the end, the mean and SD of the evaluation indices were calculated and reported. In one step, classification was conducted as 5-class using SVM with linear kernel, MLP, and KNN. In the other step, the classification was conducted as a 2-class approach using these three classifiers and LDA, Bayes, and majority voting. The SVM classifier results with the linear kernel in the 5-class and 2-class approach are shown in Figure 5 and Figure 6, respectively.

According to Figure 5, using MSVM, the highest validity was obtained. The mean and SD of this method were 88.45% and 2.17%, respectively. Then MLP and KNN obtained a validity of 84.52% and 82.30%. As shown in Figure 6, SVM detected the OSA class with a higher validity (93.72%). Non-apnea class compared with others, hypopnea compared with others, central apnea class compared to others, and mixed apnea placed next.

The KNN classifier is evaluated for different values of K from 4 to 10, and the Euclidean distance criterion is considered, and finally the mean values and standard deviation of the evaluation criterion are obtained. The best KNN accuracy is obtained for the value of K = 7.

The best performance for diagnosing apnea for both 5-class and 2-class classification approaches is obtained from ECG and EEG signals per 7 neurons in the occipital layer.

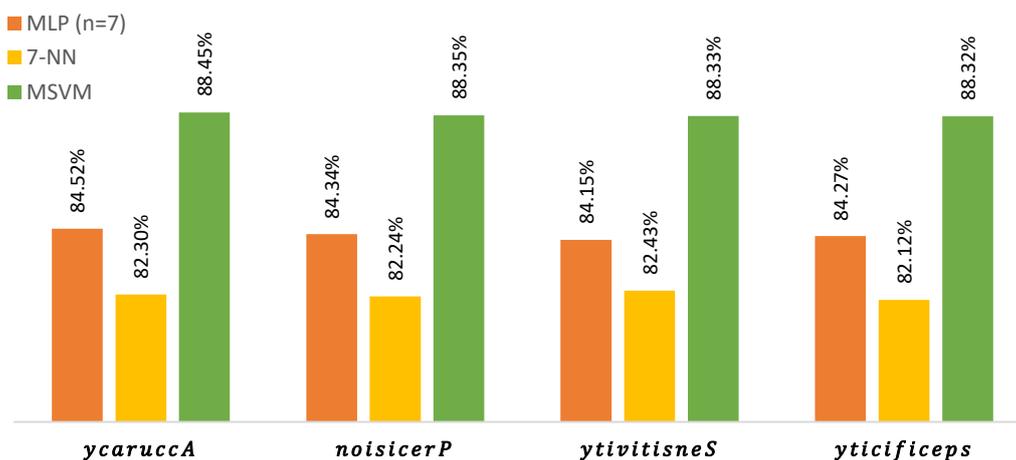


Figure 5. The results of sleep apnea types classification through ECG and EEG signals using KNN, MLP, and linear SVM in a 5-class approach

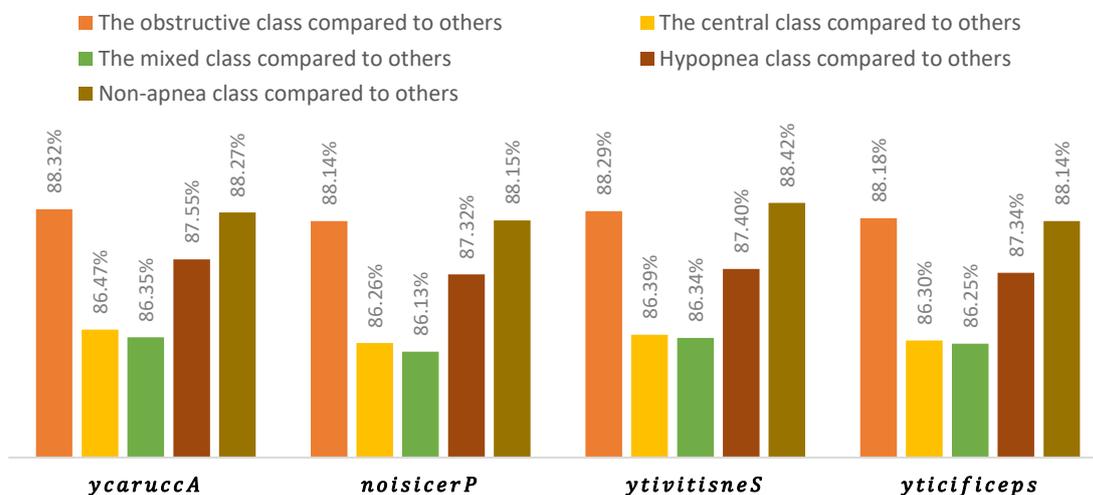


Figure 6. The results of sleep apnea types classification through ECG and EEG signals using SVM in a 2-class approach

The KNN classifier was evaluated for K values from 4 to 10; Euclidean distance was considered; and ultimately, the mean and standard deviation of the understudy criterion was obtained. The highest validity of KNN was obtained in K=7, and the results are shown in the Figure 7.

According to Figure 7, in the KNN method (K=7), the highest mean and standard deviation was obtained at 87.65% and 2.32 for the OSA class compared with others. Then, other classes are similar to the result of MLP and SVM.

For MLP, a hidden layer with several variable neurons in this layer and an output layer with five neurons were considered for the 5-class mode in this layer. In problem 2, the number of output layer neurons was 1. The number of input layer neurons was 20 (the selected features in PCA). This classification was conducted using the neural

network toolbox of Matlab. The best diagnostic performance of apnea apneic disorders in both 5-class and 2-class approaches was yielded for ECG and EEG signals for seven neurons in hidden layers. The results are shown in Figure 7, Figure 8 for 5-class and 2-class modes, respectively. As shown in Figure 8, MLP detected OSA class with a higher validity (88.32%). Non-apnea class compared with others, hypopnea compared with others, central apnea class compared to others, and mixed apnea placed next.

The classification results of different apnea and non-apnea classes for features extracted from ECG and EEG in the 5-class and 2-class approach using Bayes, LDA, and majority voting are reported in Figure 9 until 11.

According to Figure 9, the highest average validity and standard deviation of 2-class classification of OSA

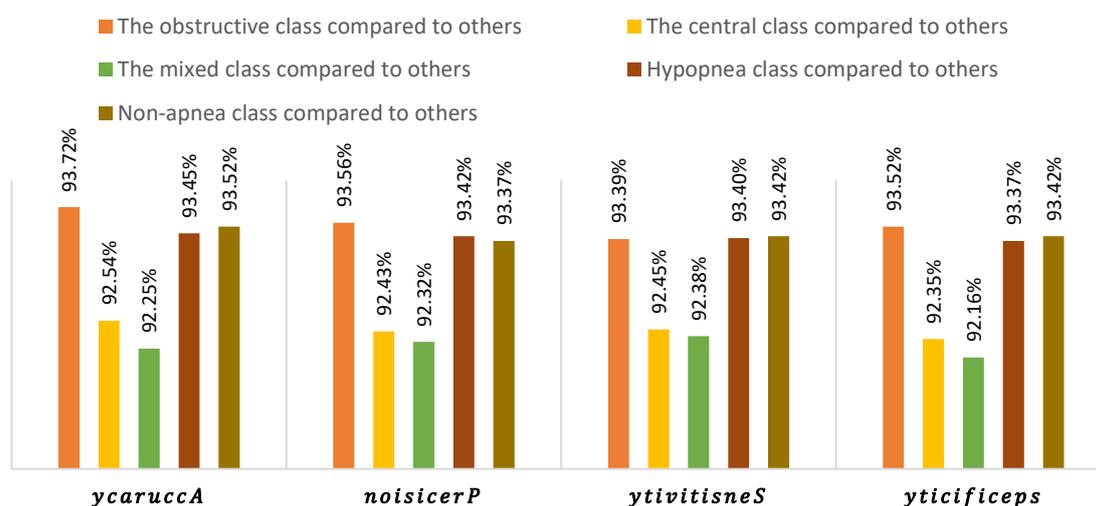


Figure 7. The results of sleep apnea types classification through ECG and EEG signals using KNN (K=7) in a 2-class approach

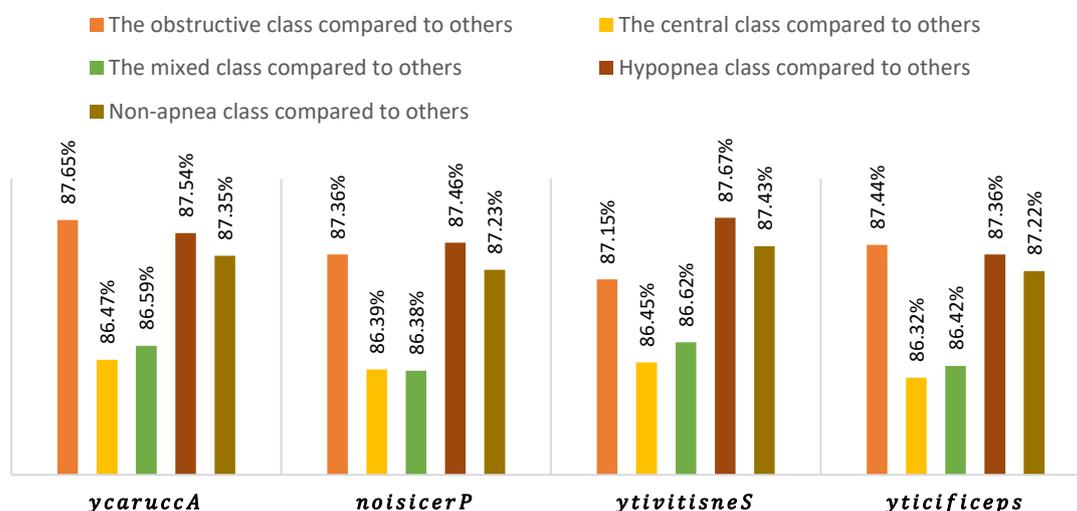


Figure 8. The results of sleep apnea types classification through ECG and EEG signals using MLP in a 2-class approach

and other classes were obtained  $86.62 \pm 2.32\%$  for Bayes. The validity of other classes was slightly lower.

and other classes were obtained  $94.42 \pm 2.32\%$  for majority voting. The validity of other classes was slightly lower.

According to Figure 11, the highest average validity and standard deviation of 2-class classification of OSA

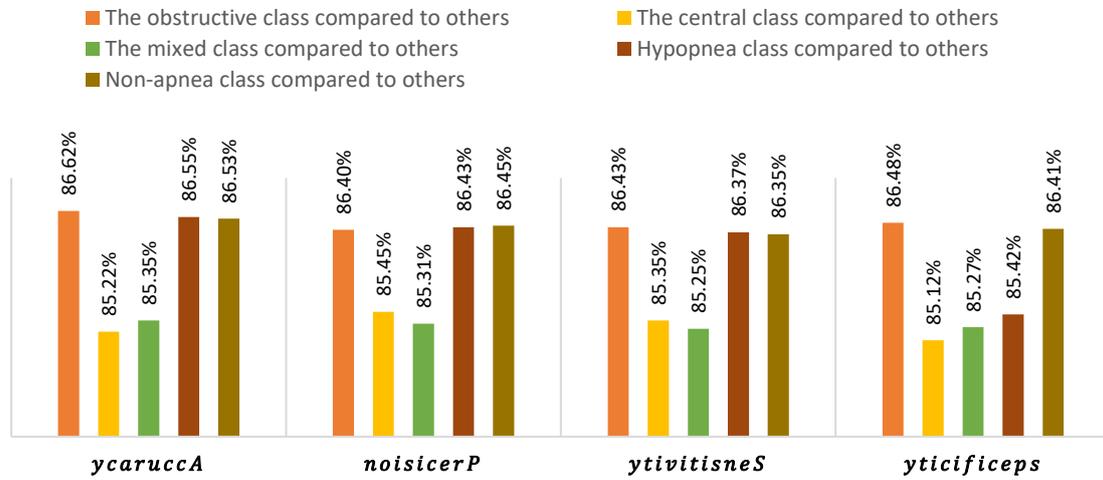


Figure 9. The results of sleep apnea types classification through ECG and EEG signals using Bayes in 2-class approach

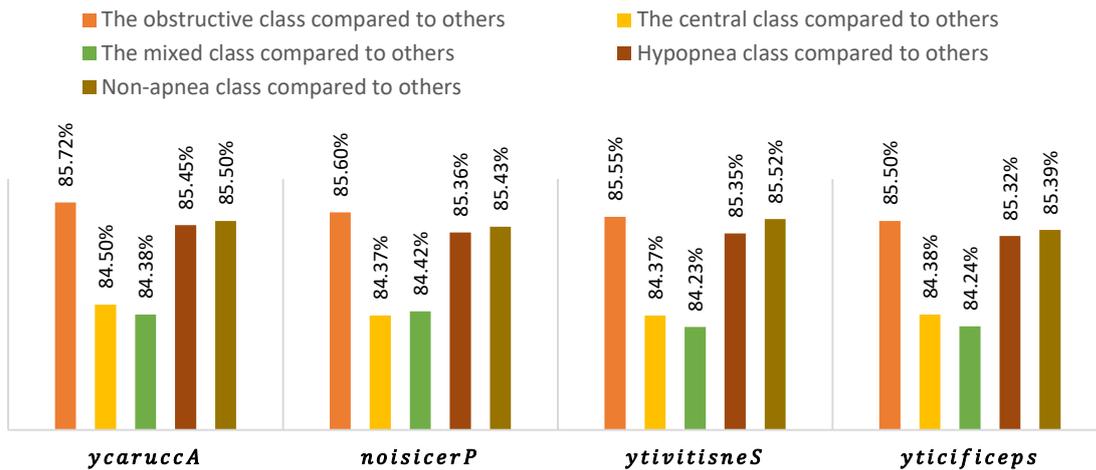


Figure 10. The results of sleep apnea types classification through ECG and EEG signals using LDA in a 2-class approach

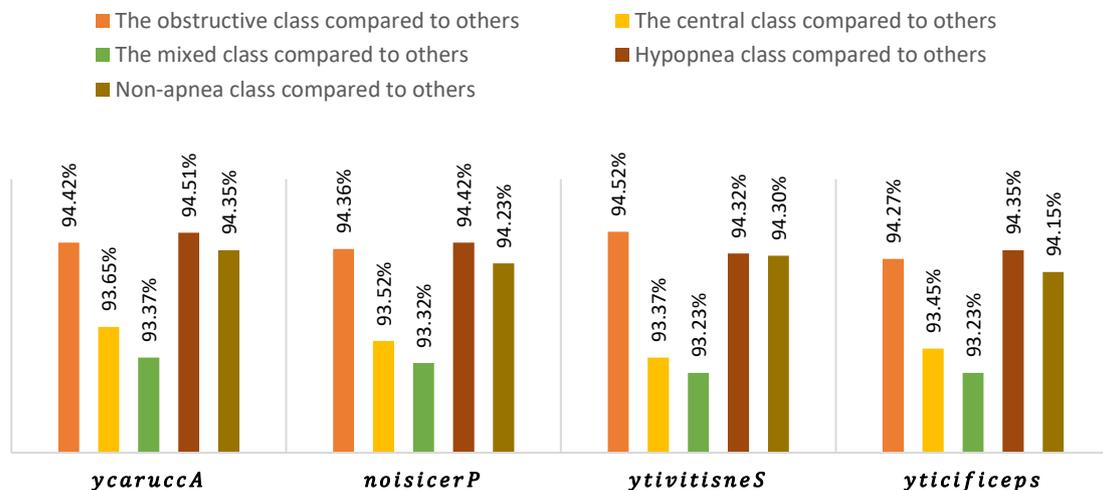


Figure 11. The classification results of sleep apnea types through ECG and EEG signals using majority voting in a 2-class approach

## 4. Discussion

The objective of the present study was to detect different sleep apneas, i.e., obstructive, central, mixed, and hypopnea classes from a non-apnea class, using the data obtained from nonlinear features of ECG and EEG. It was assumed that using these two signals and extracting nonlinear features would improve the final results. In addition to the extracted features, the dimension reduction method of PCA was also used. Also, in addition to a slight reduction of feature dimension, the features were sorted in terms of superiority. Then, using the common methods, the features were normalized. Then, the classification was conducted using two approaches. In the first approach, three MLP, MSVM, and KNN classifiers (for different parameters) solved the problem as a 5-class. In the second approach, the problem was solved using these classifiers and three other methods as a 2-class. Meaning that the OSA class was first compared with other classes, then the central apnea class, and then other classes. The three binary methods used here, in addition to the mentioned classifier was LDA, Bayes, and majority voting.

Comparing the classifiers used in the 5-class approach, the highest average validity was obtained for SVM (88.45%) and MLP (84.52%). The average validity for the KNN classifier was slightly lower (82.30%).

We know that SVM is one of the most potent classifying methods in machine learning and the results of the present study approved the superiority of this method over MLP and KNN. In the 2-class approach, the highest validity was for the majority voting method and when the sleep apnea class was compared with other classes. Mean validity, specificity, accuracy, and sensitivity for this method were 94.42%, 94.27%, 94.36%, and 94.52%, respectively. Moreover, the results of comparing OSA class with others, hypopnea class with others, and non-apnea with others were relatively similar and slightly higher than central apnea compared with others and mixed apnea with others.

Table 1 summarizes the results of the present study results with other studies on classifying apnea. As observed, the highest average validity for 5-class classification of different apnea and non-apnea types in this study was 88.45%. The used data and methods are different in terms of the number of the classes. In these studies, different apnea types were not studied, and two classes, i.e., obstructive apnea and non-apnea, are studied. The

reason for using obstructive sleep apnea in this study was its higher prevalence. Central and mixed sleep apnea occur less frequently; therefore, recording patients with these two apnea types is usually challenging, and the obstructive class is usually studied. Our results in the 2-class approach were higher than [1, 8, 19-25] and lower than seven other articles. The lower accuracy of about 1.5% could be attributed to the superiority of the deep-learning method (convolutional network) compared with machine learning used in this study. Moreover, the data are not the same that affect the results [3, 5, 6, 26-29], all of them had higher validity than the present study, used EEG or ECG sleep apnea, but the present article used EEG in addition to ECG. Given that the processing method is relatively the same as the present article (NN, KNN, and SVM), it can be said that adding this signal did not improve the results.

As observed, there are different methods available to detect sleep apnea, mainly features based on time, frequency, non-linear domain, and machine learning methods (PCA, MLP, KNN, SVM, etc.) and deep learning (RNN, CNN, etc.). Machine learning methods are more common than deep learning because they do not require powerful hardware and big data. SVM would be used in the present article to detect the disorder. As shown in the table, the studies using this classifier yielded a result of over 90%.

The article structure is designed as follows:

Section 2 is dedicated to introducing the proposed method and the understudy database. The simulation results are reported in Section 3. In Section 4, the proposed method is discussed and compared with other relevant studies. The conclusion and recommendations are given in Section 5.

## 5. Conclusion

The present study results showed that the highest mean validity, accuracy, sensitivity, and specificity for the SVM classifier was 88.45%, 88.35%, 88.33%, and 88.32%, respectively. In the 2-class approach, in addition to the mentioned classifiers, LDA, Bayes, and majority voting were used, and each class was considered against all classes. The highest average validity, average accuracy, average sensitivity, average specificity using the majority rule voting was 94.35%, 94.30%, 94.32%, and 94.15%, respectively.

**Table 1.** The comparison of the thesis's results with those of recent studies

Reference	Type of Data	Analysis Method	Results
[1]	EEG	Extracting frequency bands, entropy, variance, energy ANN, SVM, KNN	Accuracy: 99 % Sensitivity: 90 % Specificity: 100%
[3]	ECG	Common time features, frequency and non-linear, ANN classifier	Accuracy: 96%
[4]	ECG	Bi-spectrum analysis, higher-order spectrum-based feature	Accuracy: 95.57 % Specificity: 92.51 % Sensitivity: 98.64%
[5]	ECG	Common time features of variable-length epochs, SVM	Accuracy: 95%
[6]	ECG - SpO <sub>2</sub>	Common time features, ANN	Accuracy: 98.3%
[8]	ECG - EDR	SRE, K-means SVM	Accuracy: 78.07% Sensitivity: 78.01% Specificity: 78.13%
[19]	ECG	Common time features	Accuracy: 83 % Specificity: 75 % Sensitivity: 88%
[20]	ECG	Tunable-Q wave transform, statistical feature, classifier RSUBoost	Accuracy: 91.94% Sensitivity: 90.35% Specificity: 92.67%
[21]	ECG	HRV, features in the time and frequency domain	Specificity: 92.54% Sensitivity: 90.85% Accuracy: 91.67%
[22]	ECG	TQWT filterbanks, entropy, central correlation MLP. Booster, random forest	Accuracy: 92.78% Sensitivity: 93.91% Specificity: 90.95%
[23]	ECG	Phasic entropy, energy logarithm, BAWFB, LS-SVM	Accuracy: 90.11% Sensitivity: 90.87% Specificity: 88.88%
[24]	ECG	BAWFB, phasic entropy Energy logarithm, KNN, decision tree Linear Discriminant Analysis, regression logistic, SVM	Accuracy: 90.87% Sensitivity: 92.43% Specificity: 88.33% (F1 criterion) 92.61
[25]	ECG and respiration	Spectrum entropy, interquartile energy, and limit, VMD. KNN, PCA, LDA	Accuracy: 87.5%
[26]	EEG	Detrended fluctuation analysis, SVM	Accuracy: 95.01%
[27]	ECG	Common features of HRV, recursive neural network	Accuracy: 97.8%
[28]	ECG	CNN	Precision: 96% recall: 96% (F1 criterion) 96%
[29]	EEG	Extraction of frequency bands with wavelet transform, SVM	Accuracy: 98%

Reference	Type of Data	Analysis Method	Results
[30]	ECG and respiration	Symbolic dynamic, alphabetical entropy, sample entropy, Approximate/phasic entropy, SVM, ANN, KNN GentleBoost and RUSBoost	Accuracy: 93.26%
Our Article	EEG - ECG	Sample entropy, Shannon entropy, certainty, mean length Diagonal lines, recurrence rate, entropy, CD LSA, MLP, KNN, SVM, FD, Bayes Majority voting	94.42% the correctness) of the majotablerity (vote Accuracy: 94.36% Sensitivity: 94.52% Specificity: 94.27%

The objective of the present study was to identify sleep apnea classes using nonlinear features and machine learning methods. The preprocessed EEG and ECG signals of patients with sleep apnea in each sleep apnea class (obstructive, central, mixed, and hypopnea) was processed using nonlinear methods, and then after normalizing, the superior linear combination of these features was given to powerful machine learning classifiers in two 5-class and 2-class approaches. The study results showed when the results of classifiers are combined with the majority voting method, the validity of identifying the classes increases. The average validity for this method was obtained at 94.42%, which was higher than several other studies. It is recommended that databases with a larger sample size be used. This would lead to increased reliability of the proposed analysis method. Moreover, using novel deep-learning-based methods could help obtain better results. Today with the development of hardware technologies, using novel machine-learning-based methods is increasing. It is recommended that these novel methods be used to improve the results of classifying different sleep apnea classes.

## Acknowledgements

This research did not receive any specific grant from funding agencies in the public, commercial, or nonprofit sectors.

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