Towards Improvement of Sleep Apnea Identification using Multi-feature Analysis from Screening of Non-overlapping Single Lead ECG

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Abstract—Sleep apnea is not easy to diagnose. Electrocardiography (ECG) signals are broadly used to identify and analyze different types of sleep disorders. For detection of sleep apnea, the multi-feature analysis is an encouraging means to assist recognize the characteristic non-overlapping apnea and non-apnea events. This study consists of the following steps: 1) segmenting non-overlapping apnea and non-apnea events, (2) investigating beat by beat of ECG signal to identify and calculate RR interval, (3) feature extraction to deeply based time, frequency, and non-linear analysis approach, and (4) classifying apnea and non-apnea using the various kernel of support vector. To address this issue, we created an optimal SVM model classifier to investigate the utility of patterns in predicting apnea and non-apnea occurrences. Our system with RBF kernel function of SVM is achieved to have an area under the curve (AUC), the classification accuracy (CA), F1 score, precision, the recall of 0.836, 0.851, 0.85, 0.86, 0.851 respectively in labelling ECG signal into apnea or non-apnea events.

Index Terms—ECG, sleep disorder, sleep apnea, SVM, multifeature analysis

I. INTRODUCTION

Sleep is a type of human rest. Sleep quality has an impact on the freshness and normalcy of human organs. The human body will refresh body cells. Therefore, it is important to preserve sleep quality. People are less concerned about their health and quality of life because of technological advancements and modern lives. In the long term, the standard of living, to some extent, will be influenced by sleep patterns. Some potential factors can disrupt the sleep pattern like lack of sleep, depression, snoring disorders, fatigue, wrong sleeping position, uncomfortable place, and sleeping environment. Obstructive sleep apnea-hypopnea syndrome (OSAHS) is a chronic sleeping disorder. OSAHS is distinguished by a respiratory system blockage, leading people to wake up frequently throughout the night and deteriorating their physical condition during the day. These problems can lead to more serious disease in the human heart. The most extreme conditions will result in hypertension, stroke, and other cardiovascular issues [1]. Someone with short sleep duration and poor-quality sleep is strongly associated with weight gain compared to those who have enough sleep, For the first time, this study provides a systematic review of the literature as well as quantitative estimates of the cross-sectional associations between sleep duration and obesity (or measures of obesity) in population-based studies of children and adults from around the world. Obesity is associated with an increased risk of being a short sleeper, both in childhood and in adulthood. A pooled regression analysis in adults also suggests that losing one hour of sleep per day is associated with an increase in body mass index. It weighs about 1.4 kg for a person of about 178 cm height with short sleep duration had the potential to be overweight [2].

The clinical sleep centre is the site of the study of sleep, and the problem is using polysomnography (PSG). PSG is a quantitative measure to analyze sleep disorders. Even other equipment with the same function will always use PSG as a comparison, the gold standard used by the hospital. PSG usually consists of several electrodes and more complicated, electroencephalography (EEG) electrodes to record electrical activity in the brain, two electrodes for electrooculography (EOG) to record the movement of the eyeball, three electromyography (EMG) which are usually attached to the legs to record movement during sleep, electrocardiography (ECG) electrodes to record heart activity and some sensors to record oxygen saturation [3], [4], [5], thoracic and abdominal respiratory and respiratory movements [6], [7]. Heart rate variability has been used in research on biological cues for the identification of sleep problems [8], [9]. These studies focused on extracting sleep stages are extracted based on three-band time-frequency localized and wavelet filter bank from a single lead EEG [10]. This approach is also using 30 seconds of ECG signals to get features based on time series decomposition of RR into intrinsic mode functions (IMFs) on EEG signals [11]. Other studies use a combination of several non-linear features, features obtained from the frequency domain and phase reconstruction of ECG signals to detect sleep apnea [12]. Alternative investigation of Obstructive Sleep Apnea (OSA) screening using wavelet bicoherence from snore signals [13]. An extraction process based on internal RR variations uses the wavelet decomposition process [14]. This technique has been used to assess the severity of OSA by analyzing the morphology of the pQRSt waves from an

ECG signal [15]. Another approach employs time-varying autoregressive modeling to account for differences in HRV between normal and epileptic patients [16]. Furthermore, the characteristics of intrinsic band functions are derived from EDR and HRV observations [17]. The combination feature set from RR interval, systolic blood pressure and diastolic blood pressure from beats of the signal using Laquerre expansion approach [18].

To get maximum results during the extraction process, an examination of the signal's acquisition and preprocessing steps is required. However, the analysis should not degrade the signal's characteristics or reject valuable clinical information. Several studies associated to preprocessing ECG signals include sinusoidal modelling to reduce or even eliminate disturbing signal parts such as power line interference and signal wandering noise [19]. The results of the extraction procedure are heavily influenced by signal wandering. The action of reducing or eliminating will be beneficial as is done with ECG signals using linear regression techniques [20]. Another study, reduce noise in ECG signals using the low-pass filter FIR method by adjusting the window values that vary so that the results are more efficient [21]. An alternative strategy using Hilbert transform to eliminate baseline wander ECG signals has been carried out [22]. Moreover, eliminating at the same time unwanted signal and signal to wandering using the wavelet transform with a multi adaptive [23].

Several approaches for diagnosing sleep disorders were started several years ago, including employing support vector machine (SVM) and other classifiers to classify five cases of sleep disorders [10]. Estimated slow wave sleep based on the variation of RR interval to identify OSA and healthy patients [24]. In another study, the difference between normal and apnea is recognized using a bootstrap aggregating classifier based on spectral and statistical features of the ECG signal [25]. Moreover, another approach to detect OSA using SVM [26], [27]. Other Classify strategy based on the Unable-Q factor wavelet transform to recognize sleep apnea using RUSboosted [4]. In recent years, research leading to the uses of deep learning to detect OSA has developed rapidly. Advanced deep learning research that uses data learning techniques automatically to get set features using deep learning as alternate method uses six convolution layers using one Dimension Convolutional Neural Network [28] without specifying set features. One of the last publication uses RNN deep learning from ECG derived feature values [29]. However, there are some limitations to the studies that have been carried out. The ectopic beats, arrhythmic events, missing data and noise effects, causes corrupt data along the QRS interval. There are inconsistencies in the absolute and relative frequency band values. Therefore, the possible loss of clinical information is critical. The deviation of potential loss may lead to unpredictable results that are not easy to interpret. The loss of clinical information causes difficulties and inaccuracies in the diagnosis of signal patterns in individuals with sleep disorders. To distinguish between apnea and non-apnea signaling patterns, a tool is therefore required for a more in-depth investigation of ECG morphology, QRS intervals, and periodic patterns of ECG signals.

In this study, to obtain the set features that have characteristics that are compatible with the ECG signal pattern in sleep disorder patients, we combined five approaches obtained from the time domain, frequency domain and other non-linear analysis techniques to get the best features. These approaches are statistical RR interval approach, Poincare plot, FFT spectrum, AR spectrum and detrended fluctuation analysis. This combination resulted in 17 features and those features were then re-processed using the relief feature selection method by selecting relevant features and contributing to getting classification results with high accuracy values. Subsequently, in this research, we proposed five important features and used various kernel models of SVM to categorize apnea and non-apnea segments.

The objective of this research: (1) Investigation of sleep disorder signal from single lead ECG recordings based on multi-feature analysis, namely time, frequency and non-linear approach; (2) Evaluation of feature value based on characteristic QRS morphologies to obtain the most important and significant feature to predict potential sleep disorder; (3) Evaluation of feature selection method to reduce complexity and computation time without losing the clinical pieces of information; and (4) Applying various kernel model of SVM to classify apnea events and non-apnea events.

II. DATA DESCRIPTION AND METHODS

2.1. ECG-Apnea Recordings

The Apnea-ECG recordings utilized in the experiment are provided by the physionet database [30]. The recordings were acquired from single-lead ECG at a sampling rate of 100Hz and 16-bit resolution. There are 70 recordings with a length of 7 – 10 hours and labelled by the clinical expert, namely apnea-non-apnea events. The experiment used several labels with the index of a01-a20. This study used 343 non-overlapping recordings for the precision of evaluation and classification process. The non-overlapping signals have durations of ± 20 minutes. Fig. 1(a) displays two non-overlapping segmented signals, namely non-apnea events for label a01N and Fig. 1(b) shows two non-overlapping segmented signals, namely apnea events (±16 minutes) for label a01A. Each record has been marked as apnea and non-apnea events by a clinical expert. In some recordings, there may be additional signals such as the influence of spO2, oxygen saturation, and respiratory so that the recording pattern becomes not easy to process again.

2.2. Pre-processing

ECG-apnea recordings will be divided into groups based on need. The segmented data will further improve the quality of the recorded signal, as shown in Fig. 2 To reduce some of the effects of noise, the signal will be reconstructed during pre-processing, such as the effect of noise power source, noise medical instrumentations and other influences that make the quality of the ECG signal damaged. The noise-induced ECG signal imperfection will have a substantial impact on the detection of ECG waves. Moreover, contaminate ECG signals with noise and other signals will interpret very difficultly. The block diagram developed in this study is presented in Fig. 3 In the first stage, the data was obtained by chopping the signal after it had been confirmed by a medical specialist to obtain the apnea signal and the non-apnea signal.
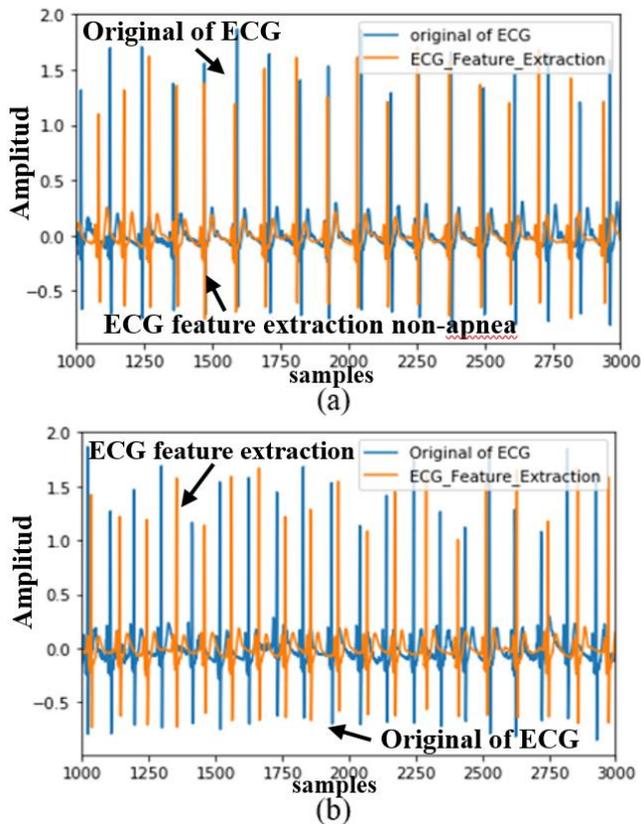
Fig.1. An example of non-apnea event (a) and apnea event(b) of ECG signal segments

The segmentation was performed without overlapping to guarantee that no interference could disrupt the feature extraction process. The second stage involved obtaining features that matched the ECG signal pattern of patients with sleep problems. These features were derived using a variety of methods, one of which was analyzing the statistical value of the adjacent R wave intervals or commonly known as calculating heart rate variability. With this approach, several features can be obtained, including RRmean, RRstd, heart rate std, triangular interpolation of RR intervals and root mean square of the successive differences. These parameters can then be used to determine whether there are differences in the mean and standard deviation across apnea and non-apnea patients. Those difference will then be utilized to determine which features are significant and useful for increasing classification accuracy.

The following step involved further reducing the generated features to shorten the computation time and reduce feature complexity caused by the components that did not relate to the sleep disturbance signal pattern. In the final step, the collection of features was divided into two groups: those whose characteristics resembled the signal pattern for apnea and those of other groups, which resembled the signal pattern for non-apnea. Most of the ECG recordings from dataset have been intensively pre-processed with some approaches to eliminate noise. The recordings of ECG with label a16N have robust heart rate variability. There is a small spike that could reduce the heart rate minute by minute and therefore, the RR intervals will change while comparing successive values of beats. The ECG signal to be retrieved must be flawlessly pre-processed and free of signal deterioration or noise interference.
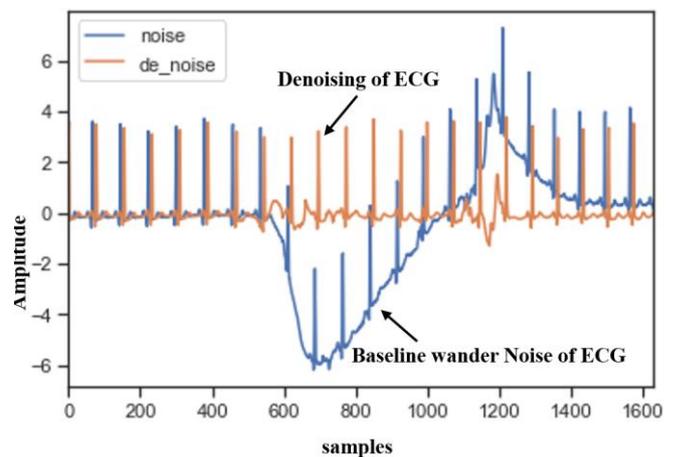

Fig. 2. Original of ECG event with noise and de-noising and baseline wander removing

If not done appropriately, this could result in a signal loss of clinical information. The loss means that clinical experts will have trouble diagnosing. Because of incorrect medical treatment, an incomplete diagnosis will do the patient harm. ECG signal segment discloses differences between two non-overlapping signals. Table. II shows the variation of the histogram of apnea events and non-apnea events. The comparison of the different recordings to find the best feature extraction process and the best feature value. The comparison of data distribution features based on quantitative evaluation reveals that there is a considerable difference in the pattern of the ECG signals linked with any changes that occur because of periodic failures and unanticipated construction. The non-apnea event has a heart rate mean of 84 BPM and a standard deviation of 5.2 BPM over 1242 beats. Besides, the non-apnea event has a heart rate mean of 77 BPM and a standard variation of 8 BPM over 1278 beats.

2.3. Extraction of ECG features

This section will detail our feature extraction scheme. After segmenting the data, it will be extracted. The method of feature extraction is utilized to obtain features that will be used to define the many problems associated with sleep apnea based on variations in patterns between apnea and non-apnea. The recognition of the pattern will further assist the clinical expert in diagnosing and determining further steps to take preventive action. Based on the experiment features tests are categorized into five approaches: (i) statistical RR interval features, (ii) Poincare plot features, (iii) FFT spectrum, (iv) AR spectrum, and (v) detrended fluctuation analysis approach. The following sections define the different features, are as follows: The test produces 17 features including RRmean, RRstd, heart rate std, RMSSD, TINN (statistical of HRV parameters), SD1, SD2 (Poincare plot parameters), VLF power, LF power, HF power (FFT spectrum and AR spectrum parameters), alpha1, residue1, alpha2 and residue2 (detrended fluctuation analysis parameters). Table I demonstrates the values of the mean and standard deviations for apnea and non-apnea, which have a lower feature value compared with the feature value of apnea (* mark). This difference indicates that these features are highly relevant for input on the next process, namely the feature selection and the classification processes. Furthermore, the comparison shown in Table I between groups showed that the decrease in the temporal and spectral
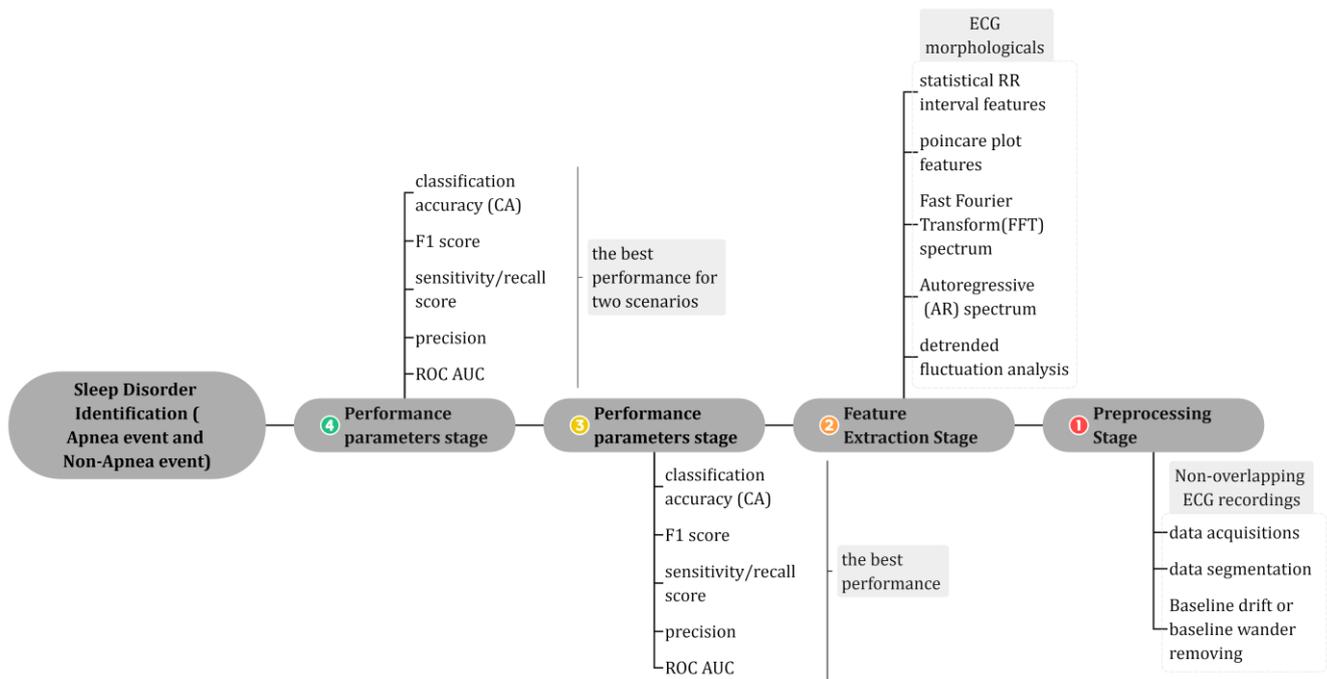
Fig. 3. A Framework of the Proposed Approach

component parameters of apnea events resulted differently from non-apnea events. For instance, non-apnea events show significant difference feature value in RR mean (ms),

TABLE I
THE FEATURE VALUE FOR APNEA AND NON-APNEA

features	recordings of apnea (Mean (±standard deviation))	recordings of non-apnea (Mean (±standard deviation))
RR mean (ms)	904(±93)	866(±115)*
RR std (ms)	92(±48)	65(±41)*
heart rate std(BPM)	7.3(±5.5)	5.4(±2.8)*
RMSSD(ms)	87(±65)	77(±61)*
TINN(ms)	263.2(±98.3)	150.2(±62.5)*
SD1(ms)	61(±46)	55(±43)*
SD2(ms)	128(±60)	91(±46)*
VLF power_fft spectrum(ms2)	3953(±5532)	1204(±2103)*
LF power_fft spectrum(ms2)	4061(±5076)	2370(±3623)*
HF power_fft spectrum(ms2)	2630(±4334)	2159.8±3887.1)*
VLF power_ar spectrum(ms2)	6789(±7740)	2277(±4466)*
LF power_ar spectrum(ms2)	7135(±7545)	4502(±6909)*
HF power_ar spectrum(ms2)	4225(±6248)	3839(±5909)*
Alpha1	1.2612(±0.3187)	0.9373(±0.2608)*
Residue1	0.0004641 (±0.0004756)	0.0005333 (±0.0006675)
Alpha2	0.4615 (±0.2246)	0.7060 (±0.2425)

RR std (ms), Heart rate std (Beats per minute), RMSSD (ms), TINN (ms), SD1 (ms), SD2 (ms), VLF power (ms2), LF power (ms2), HF power (ms2), VLF power (ms2), LF power (ms2) and HF power (ms2), while this difference is only observed during some period of short and long duration for apnea and non-apnea events. It is well known that the

behavior of the thirteen features for non-apnea events corresponds to the lower feature value than feature value of apnea events, and their periodic pattern of ECG signals for sleep disorder is strong enough to be noticed by the model proposed. Additionally, this behavior is seen in the nonlinear analysis parameters as one of the five other features that were chosen for the analysis. For apnea events, the non-linear parameters exhibit a range of slope value alpha1, and alpha2 of 1.2612 and 0.4615, respectively. The slope value for non-apnea is 0.9373 and 0.7060 respectively. The short-long scaling of the ECG signal is indicated by the slope of the line. The alpha1 is a marker for the short duration of the ECG signal based on the local trend of the signal. The alpha2 is displayed for the long duration of the ECG signal based on the local trend of the signal result. Slope value that is more than 0.5 means that the signal has a similarity with the original signal with the smallest error value.

```
1  Start;
2  input: Non-overlapping ECG signals (x);
3
4  Calculate: RR(i), RR(average);
5  Calculate: integrated time-series (y(k));
6  Segmentation of y(k) with windowsize(n);
7  signal trending(yn(k)) with regression;
8  calculate: approximation error(e(k));
9  Calculate: RMS approximation error (F(n));
10
11 Output: plot log F(n) to log(n);
12 Features Value: alpha1, residue1, alpha2,
     residue2;
13
14 Finish;
```

CODE SNIPPET. 1. Pseudo code for calculating fractal scaling from RR interval

The variabilities result of these nonlinear dynamics methods using detrended fluctuation analysis [31] could have the

quantitative approach to investigate the irregularity of heart rate in the time and frequency of the signal. Here, we propose the fluctuation analysis approach is strongly related to the value of approximation error and successively attained the value of $F(n)$ and the value of the slope alpha (α). The procedure is summarized step by step to explore a nonlinear approach, which has the following Code Snippet 1 structure. The Code Snippet. 1 is the pseudo code for the process to determine signal slope to demonstrate the DFA approach to analyzing self-similarity for short-range ECG-apnea signal.

2.4. Feature Selection

The classification phase can be applied in all areas of life, including its use in the medical field. Moreover, there are many algorithms used to perform classification techniques. To obtain valid and efficient classification results, researchers have even performed a variety of methods such as improvement of the preprocessing phase, modification of feature extraction scheme and finding the feasible of feature selection phases. All processes aim to produce features that are dominant and influential during the classification process. Further features selected will be used to build a model based on five selected features. Also, the selection process of this feature will shorten the process of building the model and the process of classification. In this study, based on feature extraction results, there are 17 features derived from 5 feature sets. Further, 17 features are done by the ranking process using scoring analysis of variance. This scoring method will be constructive to reduce the problem of feature space, which is always a constraint in generating the classification process. Furthermore, features that have a dominant value will be selected to be the main feature that will be used later when forming the model for the classification process. In Fig. 4, the dominant features of scoring features are TINN, SD2, VLF, alpha1, and alpha2.
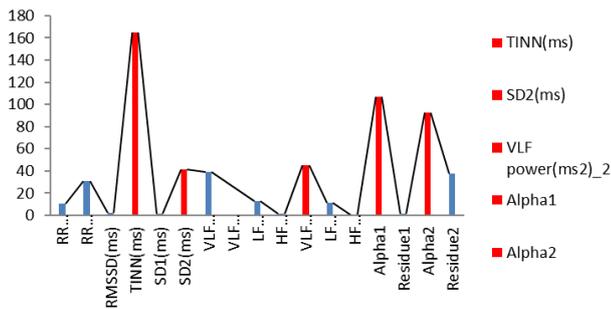

Fig. 4. The result of the scoring method to select five important features

2.5. Various Kernel of Support Vector Machine (SVM) Classifier

The concept of the SVM classification method is to maximize the hyperplane to get the best point to separate the two classes. The best point is obtained by measuring the distance between the hyperplane and the closest data from each class. Previous studies have used SVM to differentiate apnea and non-apnea [32], [33], [34]. In this study, we used 4 type kernels to test the similarity of two vectors in high dimensional space such as SVM with linear kernel, SVM with the polynomial kernel, SVM with sigmoid kernel and SVM with RBF kernel [34]. In SVM, the goal is to find a

hyperplane that separates the data with the minimum error. The use of different kernels is to get different approaches so that the problem can be quickly solved and known according to the characteristics of each kernel. The kernel method is basically mapping data into a higher dimensional by expecting that the data will be more easily separated or more structured in that space so that the best hyperline can be determined by a clear separation between two classes. The experiment with varying SVM is to ensure getting the best hyperline and support vector according to the characteristics of the data to be classified. Using the right kernel with the right dataset is one of the key elements in the success or failure of implementing the kernel in an SVM.

III. RESULTS AND ANALYSIS

We explain the details of our experiments, offer the results, and discuss their advantages. Fig 4 gives the result of the hypothesis. It can be seen that all the features display the difference between apnea and non-apnea. The selective feature method possesses a good discriminatory capability to classify apnea and non-apnea signal segments. The data distribution on alpha1 features indicates how often data with certain feature values appear in the data. For alpha1, the feature value of 0.8205-1.2016 has the number apnea events of 47 and non-apnea events of 90. This shows the probabilities for apnea events is 0.343 ± 0.079 (mean $\pm$ SD) and for non-apnea events is 0.657 ± 0.079 (mean $\pm$ SD). Moreover, for TINN, the feature value < 179.5 has 28 apnea events and 138 non-apnea events. It shows the probabilities for apnea events is 0.169 ± 0.057 (mean $\pm$ SD) and non-apnea events is 0.831 ± 0.057 (mean $\pm$ SD). Distribution of feature value for VLF power is < 179.5 and the number of occurrences of apnea events is 124 and non-apnea events is 177. It shows the probabilities for apnea events is 0.412 ± 0.056 and non-apnea events is 0.588 ± 0.056. The Alpha 2 has feature value is 0.42-0.78, and the number of incidences of apnea events is 71 and non-apnea events is 95. It shows the probabilities for apnea events is 0.428 ± 0.075 and non-apnea events is 0.572 ± 0.075. Besides, it presents the distribution of feature value for SD2 as < 95.5 and the number of incidences of apnea events is 58 and non-apnea events is 122. The SD2 feature also shows the value of the probabilities for apnea events is 0.341 ± 0.071 and non-apnea events is 0.659 ± 0.071. Many kernels that can be utilized to obtain hyperplanes that match the characteristics of datasets have helped the development of SVM in recent years. Such kernel functions can make class separation better and more structured. The selection of kernel functions depends on the desired model. The mapping function with a specific limit will not make the dimension space impossible. Table III displays various parameter settings for each kernel, as well as the available alternatives and recommended values for obtaining the most accurate model. The SVM kernel parameter values are determined by optimizing the training model. A suitable model is less time consuming and reduces complexity accuracy of 0.851, while the SVM with sigmoid kernel achieved the highest area under the curve (AUC) of 0.7250. The RBF kernel's trainable parameters are 0.001 optimization parameters with an iteration limit of 100. As a result, the average performance of the dataset was taken into account in the selection of optimal architecture

No	Variable Feature	Frequency	Probabilities (mean ± SD)
1	**Alpha1**		
	with class ≤ 0.8205	Apnea:10; Non-apnea:64	Apnea:0.220±0.090 Non-apnea:0.780±0.090
	with class 0.8205 - 1.2016	Apnea:47; Non-apnea:90	Apnea:0.343±0.079 Non-apnea:0.657±0.079
	with class 1.2016 – 1.5828	Apnea:71; Non-apnea:27	Apnea:0.724±0.088 Non-apnea:0.276±0.088
	with class ≥ 1.5828	Apnea:24; Non-apnea:2	Apnea:0.343±0.079 Non-apnea:0.657±0.079
2	**TINN**		
	with class ≤ 179.5	Apnea:28; Non-apnea:138	Apnea:0.169±0.057 Non-apnea:0.831±0.057
	with class 179.5 – 311.9	Apnea:93; Non-apnea:39	Apnea:0.705±0.078 Non-apnea:0.295±0.078
	with class 311.9 – 444.3	Apnea:30; Non-apnea:6	Apnea:0.833±0.122 Non-apnea:0.167±1.22
	with class ≥ 444.3	Apnea:9; Non-apnea:0	Apnea:- Non-apnea:-
3	**Alpha2**		
	with class ≤ 0.42	Apnea:76; Non-apnea:21	Apnea:0.784±0.082 Non-apnea:0.216±0.082
	with class 0.42– 0.78	Apnea:71; Non-apnea:95	Apnea:0.428±0.075 Non-apnea:0.572±0.075
	with class 0.78 – 1.14	Apnea:12; Non-apnea:57	Apnea:0.174±0.089 Non-apnea:0.826±0.089
	with class ≥ 1.14	Apnea:1; Non-apnea:10	Apnea: 0.091±0.170 Non-apnea: 0.909±0.1770
4	**VLF_power**		
	with class ≤ 8783	Apnea:124; Non-apnea:177	Apnea:0.412±0.056 Non-apnea:0.588±0.056
	with class 8783 – 17522	Apnea:20; Non-apnea:2	Apnea:0.909±0.120 Non-apnea:0.091±0.120
	with class 17522 – 26261	Apnea:8; Non-apnea:2	Apnea:0.800±0.248 Non-apnea:0.200±0.248
	with class ≥ 26261	Apnea:8; Non-apnea:2	Apnea:0.800±0.248 Non-apnea:0.200±0.248
5	**SD2**		
	with class ≤ 95.5	Apnea:58; Non-apnea:112	Apnea:0.341±0.071 Non-apnea:0.659±0.071
	with class 95.5 – 167	Apnea:63; Non-apnea:57	Apnea:0.525±0.089 Non-apnea:0.475±0.089
	with class 167 – 238.5	Apnea:26; Non-apnea:13	Apnea:0.667±0.148 Non-apnea:0.333±0.148
	with class ≥ 238.5	Apnea:13; Non-apnea:1	Apnea:0.929±0.135 Non-apnea:0.071±0.135

for the SVM model. Table IV shows the specifics of classification performance obtained using various SVM kernels. The performance of the SVM classifier was evaluated using four metrics: area under the curve (AUC), classification accuracy (CA), F1, Precision, and Recall. According to the classification results, the SVM with RBF kernel earned the greatest classification.

In this section, an SVM classifies two datasets of different classes by finding out the maximum hyperplane margin which separates two classes. To map the input space to a high dimensional feature space, we can use the mapping function or better known as the kernel function. An SVM has several kernel functions, including linear, RBF, sigmoid and polynomial kernel functions [35]. In this work, we used all the kernel functions to detect the non-overlapping ECG signal segment using five feature values.

TABLE III
HERE ARE THE PARAMETERS OF VARIOUS SVM KERNELS

parameters	SVM linear	SVM polynomial	SVM rbf	SVM sigmoid
Setting cost	1	-	-	-
Regression loss	0.1	-	-	-
Optimization parameters (tolerance)	0.001	0.001	0.001	0.001
Optimization parameters (iteration limit)	100	100	100	100
Setting g, c, d	-	g=auto, c=0.00, d=0.3	g=auto	g=auto, c=0.00, d=0.3

TABLE IV
PERFORMANCE COMPARISON OF VARIOUS SVM KERNELS FOR CLASSIFICATION

kernels	The best performance evaluation				
	AUC	F1 score	Precision	Recall	CA
SVM rbf	0.836	**0.850**	**0.860**	**0.851**	**0.851**
SVM polynomial	0.836	0.782	0.782	0.782	0.782
SVM linear	0.711	0.782	0.782	0.782	0.782
SVM sigmoid	**0.841**	0.770	0.770	0.770	0.770

Based on the observed that the SVM that uses the RBF kernel has the best classification accuracy among others, It is observed that the SVM that uses the RBF kernel has the best classification accuracy among others. Based on the SVM model with a linear kernel generated, our system can predict apnea recordings of 103 records accurately and accurately predict non-apnea by 166 records. Predictions with the SVM model using a polynomial kernel, its performance can predict 50 apnea recordings correctly and predict 180 non-apnea records. SVM kernel with RBF kernel can accurately predict apnea records as much as 113 and predict non-apnea recordings precisely as much as 162. Other kernel models, namely sigmoid, have the exact prediction ability of 116 for apnea recordings and 137 for non-apnea recordings. Therefore, to measure using one measure of performance, the best is the SVM model with the RBF kernel. In addition, the value of accuracy is to compare data that are correctly classified as non-apnea and apnea with the overall data.

TABLE V
PERFORMANCE COMPARISON CUMULATIVE STUDY OF PREVIOUS WORK CONDUCTED ON THE PHYSIONET APNEA-ECG DATABASE

Authors	Feature extraction technique	Decision	Methods	Accuracy value(%)
Gutta et al[36]	Manual or handcraft feature	OSA	HMM	82.33
Singh et al[37]	automatic or learned feature	OSA	DNN	85
Singh et al [38]	Manual or handcraft feature	Normal and apnea	SVM	sensitivity: 82.45, and specificity: 79.72
Li et al [39]	Manual or handcraft feature	OSA	decision fusion method	85
Viswabhargav et al [40]	Manual or handcraft feature	Normal and apnea	SVM with radial basis function (RBF) kernel	78.07
Pombo et al [41]	Manual or handcraft feature	Normal and apnea	SVM	61.61 using 84 features, and 70.94 using 20 features
Our work	Manual or handcraft feature	Normal and apnea	SVM with RBF	85.1

There are several objectives to be achieved in comparing several feature extraction and selection techniques from several previous studies. The accurate performances of these classifiers and our work are presented in Table V. There are indeed other techniques that produce high accuracy today, namely deep learning. Deep learning performs the feature extraction process automatically. One of them uses the convolution technique through configuration with various approaches, but its use is basically an unknown process when extracting features such as a black box. This approach makes the process non-transparent so that it is not known which features have the dominant role, in which part of the process the most plays a role and how much important information is lost or useless and still requires very large data to create a model that produces optimal results. Therefore, the study of manual feature extraction is still sufficient to make it continue to grow. These studies also provide a variety of approaches such as studies based on the number of features, selection methods, number of leads, data duration, preprocessing techniques, and data acquisition.

IV. CONCLUSION

In this study, we developed a machine learning model that uses multi-feature analysis from screening of non-overlapping single lead ECG. We employ statistical and spectral moment to generate 17 different features such as statistics of HRV parameters, Poincare plot, FFT spectrum, AR spectrum, and detrended fluctuation analysis parameters to predict the risk of sleep disorder among patients. In this study, besides submitting a feature selection process. The experiment is designed to test multiple classification models to see which one performs the best. The dominating characteristics are then used for classification using SVM classifiers with various kernels such as RBF kernel of SVM, Linear kernel of SVM, polynomial kernel of SVM, and sigmoid kernel of SVM. The suggested method produces the best-performing kernel, the RBF kernel of SVM, with an AUC of 0.836, classification accuracy (CA) of 0.851, F1 of 0.85, the precision of 0.86, and recall of 0.851. This method demonstrates that multi-feature analysis with feature selection can assist a clinical expert in obtaining suspected sleep disorder screening, particularly when used for individual testing at home. Besides, these approaches can provide a more efficient, timeless consuming, and cost-effective tool to evaluate the performance of sleep study investigation.

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