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**Abstract:** Sleep disorders are challenging to diagnose. The complexity of records obtained from ECG recordings is required manual inspection by experienced medical practitioners. Meanwhile, ECG records are still widely used to diagnose heart problems during sleep. To resolve the issue, the multifractal analysis is a promising means to help identify the characteristic non-overlapping apnea and non-apnea events based on signal behaviour and QRS morphologies. Therefore, we propose a novel approach to develop automatic classification sleep disorder to minimalize visual inspection and manual scoring. The new features set have been extracted, which are eventually being used as inputs space to a support vector machine (SVM). Through examine the feature set, we designed an optimum SVM model classifier to explore the usability of patterns to predict corresponding apnea and non-apnea events. Hence, our approach model with RBF kernel of SVM is achieved to have accuracy, sensitivity, specificity of 92.16%, 88.24%, 94.12% respectively.

**Keywords**: ECG classification, Multifractal, Sleep disorder, SVM kernel, ECG apnea

## 1. Introduction

Sleep is one of the human rest phases. Sleep quality has an impact on freshness and normality of the human organs. The human body will refresh body cells. Therefore, it is crucial to maintain the sleep quality. The development of technology and modern lifestyle make people pay less attention to health and quality ways of life. In the long term, the quality of life, to some extents, will be determined by sleep pattern. Some potential factors can disrupt the sleep pattern like Sleeplessness, depression, snoring disorders, fatigue, worst sleeping position, uncomfortable place, and sleeping environment. Obstructive sleep apnea-hypopnea syndrome (OSAHS) is a chronic sleep disorder condition. OSAHS is characterized by a recurrent recurrence of the respiratory tract so that people often wake up throughout the night and make the body condition during the day become weak. These conditions can lead to a more severe problem in the human heart. The most severe conditions will cause hypertension, stroke and other heart problems [1]. Someone with short sleep duration and poor quality sleep is strongly associated with weight gain compared to those who have enough sleep, in a study shows children (89%) and adults (55%) with short sleep duration had the potential to be overweight [2]. Sleep problems may be treated and diagnosed individually or in the hospital. The site usually has equipment for the evaluation of sleep symptoms. Polysomnography (PSG) is among them. For the initial screening, PSG is a useful and gold standard for comparison by the hospital. However, there are weaknesses including the element of subjectivity in performing evaluations is qualitative and relies heavily on assessment experience. Naturally, varying levels of experience contribute to various evaluations. Besides that, there can also be variations in diagnosis due to human errors due to the presence of human interference in visual inspection. PSG usually consists of several electrodes. During test, many wire and channel are attaching on some of body. These conditions are very complicated cause to comprehensive monitoring of the many biophysiological signals. For example, the electroencephalography (EEG) electrodes to record electrical activity in the brain, the electrooculography (EOG) to record the movement of the eyeball. Besides that, the electromyography (EMG) which are usually attached to the legs to record movement during sleep. and the electrocardiography (ECG) electrodes to record heart activity and some sensors to record oxygen saturation [3-5], thoracic and abdominal respiratory and respiratory movements [6-7]. Research on biological signals for the overview of sleep disorders include the use of heart rate variability [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 [9]. 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 [8]. Other studies use a combination of several nonlinear features, features obtained from the frequency domain and phase reconstruction of ECG signals to detect sleep apnea [10]. Alternative investigation of OSA screening using wavelet bicoherence from snore signals [11]. An extraction process based on internal RR variations uses the wavelet decomposition process [12]. This technique has been utilizing the morphology of the pQRSt waves from the ECG signal to get four groups of feature sets to identify the severity of OSA [13]. Other approach using dissimilarity between normal patients and epilepsy patients based on HRV using time-varying autoregressive modelling [14]. In addition, the features of intrinsic band functions come from EDR and HRV measurements [15]. The feature value obtains from Q wavelet to sub bandwidth ECG signals [16]. The combination feature set from RR interval, systolic blood pressure and diastolic blood pressure from beats of the signal using Laquerre expansion approach [17].

In order to get maximum results during the extraction process, an analysis of the acquisition and preprocessing stages of the signal is needed. However, the analysis should not damage the characteristics of the signal. Besides that, the process is without eliminating the desired clinical information. Several studies related to preprocessing ECG signals include sinusoidal modelling to eliminate disturbing signal parts such as power line interference and signal wandering noise [18]. Signal wandering is very influential on the results of the extraction process. The action of reducing or eliminating will be beneficial as is done with ECG signals using linear regression techniques [19]. Another research, by changing the variance in window values to make the results more accurate, minimize noise for ECG signals using the low pass filter FIR method [20]. Different approach use Hilbert transform to eliminate baseline wander ECG signals has been carried out [21]. Moreover, eliminating at the same time for unwanted and wandering the signal using the wavelet transform with a multi adaptive [22].

Various methods for detecting sleep disorders were commenced several years ago, including classifying five cases in sleep disorders using support vector machine (SVM) and other classifiers approach [9]. Estimated slow wave sleep based on the variation of RR interval to identify OSA and healthy patients [23]. Another research classifies normal and apnea variations, based on the features of spectral analysis and the statistical value of ECG signal, using the bootstrap aggregation classifier[24]. Moreover, another approach to detect OSA using SVM [7, 25]. Other classify method to detect sleep apnea using RUSboosted based on the feature set of the Unable-Q factor wavelet transform [4]. In recent years, research leading to the use of deep learning to detect OSA has developed rapidly. The advanced deep learning research that uses data learning techniques automatically to get set features using deep learning [26]. An alternate method that uses six convolution layer using one Dimension Convolutional Neural Network [27] without specifying set features. One of the last publication using RNN deep learning from ECG derived feature values [28]. Though, these methods require an enormous dataset and cannot understand the significance of the pattern of a feature.

However, there are some limitations to the studies that have been carried out. These approach does not reconstruct the complexity of ECG signals as a result of degradation during data acquisition and preprocessing stages. Besides that, the ectopic beats, arrhythmic events, missing data and noise effects, which causes the corrupt data along with the QRS interval and there are irregularities in the absolute and relative values of the frequency band so that the potential loss of clinical information is significant. The deviation of potential loss from the following requirements may lead to unpredictable results that are difficult to interpret. The lost clinical information makes difficulties and errors in the diagnosis of signal patterns in patients with sleep disorders. Therefore, a tool is needed for a more in-depth analysis of ECG morphology, QRS intervals and periodic patterns of ECG signals to get the difference between apnea and non-apnea signalling patterns.

Throughout this research, we merged two methods obtained from nonlinear to get the best features that correspond to the ECG signal pattern throughout patients with sleep disorders. These approaches are monofractal and multifractal analysis. The combination of these methods is to obtain ten features. In order to make the most of the training and testing process, the assessment scenario is conducted in a variety of approaches, such as find out the suitable method for selecting a feature, setting the parameters to develop the appropriate model, and evaluate the system using some or all of the features. To achieving an appropriate diagnosis and treatment based on different signal behaviour and QRS morphology phenomenon, precise sleep scores are deemed to be a critical part of that process. The conventional method of visual scoring is still the most acceptable approach to date. However, it involves the interpretation of the various signals by visual data. Automatic scoring is, therefore seen as an effective approach and minimize manual inspection for human error prevention.

The contributions of the research are: (1). The investigation of robustness and complexity ECG recordings only from single lead ECG with duration more than ten-minute segments; (2). Employed less amount feature to obtain a significant advantage for the classification with decreasing the time of training and testing; (3). The screening process of ECG to obtain acceptable pattern distinctions between apnea and non-apnea based on signal behaviour and QRS morphologies using multifractal analysis; (4). Applying the optimization parameters to the automatic correction of hyperplane using the various kernel of SVM; (5). To develop real time classification sleep disorder to minimalize visual inspection and manual scoring apnea and non-apnea events by the medical employee.

## 2. Data Description and Methods

### 2.1 ECG-Apnea Recordings

The physionet database provides the dataset used in the experiment[29]. The recordings were acquisition at sampling rate 100Hz and 16-bit resolution from single-lead ECG. There are seventy recordings available on the dataset with a normal length of 7 – 10 hours. The only 35 recordings that were scored by the clinical experts, namely apnea and non-apnea events. For the experiment, the dataset consists of nineteen recordings from nineteen subjects with annotated severe apnea indication (apnea/hypopnea index (AHI≥15). The demographics cover different sex, age, height and weight. All subjects were male, with an average age of 52.11 years, the average height of 176.16 cm and an average bodyweight of 95.53 kg. This study was used 502 non-overlapping recordings with an average duration of 13.10 minutes in length. The distribution of recording is 61.75% of apnea events and 38.25% of non-apnea events. To measure the performance of the proposed framework, the non-overlapping ECG signals are divided into two categories, namely the training set and testing set. Fig. 3(a) shows the non-overlapping segmented signals, namely non-apnea event and apnea event. Each record has been marked apnea and non-apnea by a clinical expert. In some recordings, there may be additional signals such as the influence of spO2, oxygen saturation, respiratory so that the recording pattern becomes not easy to process.

### 2.2 Preprocessing

ECG-apnea recordings from the physionet database have a very long duration ranging from 7 to 8 hours. For testing purposes, then the data will be segmented according to the need. The segmented data will further improve the quality of the recorded signal. The removing noise contaminated as shown in Fig 3(b). In this process, the signal will be reconstructed to eliminate some of the effects of noise, such as the effect of noise power line interference, the effect of noise medical equipment and other influences that make the morphological quality of the ECG signal imperfect. The ECG signal imperfection caused by the noise will significantly affect the detection process of ECG waves. Moreover, contaminate ECG signals with noise and other signals will interpret very difficult.

The block diagram proposed in this research is as shown in Fig 2. The first stage, the data was acquired the signal following the annotation that has been validated by the medical expert to get the apnea signal and the non-apnea signal. The second stage, the automatically removed noise interference employ to deducting baseline wander and noise eliminating. These schemes used to ensure there was no interference and would potentially disturb QRS waves detection based on RR interval extraction. Third, the segmentation process was carried out without overlapping noticed by an expert. In addition, Preprocessing and QRS detection implies to refinement the segmented signal by adjusting QRS frequency range, QRSonset, QRSoffset, and bandpass filter setting for fiducial point of other waves. The third stage, features are extracted from fractal analysis to get features that had similarities with the ECG signal pattern of patients with sleep disorders. Besides that, features were obtained from a variety of approaches to deeply investigation, one of which was by calculating the statistical value of QRS morphologies, including QRS amplitude and QRS width. These parameters can then be known whether there are differences in mean and standard deviation between apnea and non-apnea. The next stage, the normalization process involves for all data to transforming a specific range of feature value to meet machine learning requirement. These approach resulting features were further to reduce feature complexity due to the parts that were not relevant to the sleep disorder signal pattern and bias elimination of unbalance dataset. The last stage was to classify the collection of features into two classes, namely the class whose features have similarities with the signal pattern for apnea and the other classes which had similarities with the signal pattern for non-apnea.

Most of ECG data set recordings are intensively preprocessed using some approaches to noise elimination. The recordings of ECG have robust heart rate variability. There is a small spike to reducing the heart rate minute by minute and therefore, takings changes of RR intervals while comparing successive values of beats. The ECG signal to be extracted must be cleared of signal disruption or noise interference in the preprocessing ideal. In case this is not done carefully, it will cause a signal to lose clinical information. The loss means that clinical experts will have difficulty diagnosing. An incomplete diagnosis will harm the patient because of erroneous medical treatment.

Fig. 1 shows the graph frequency distribution of data point for apnea event and non-apnea event. With the clear observations that are disclosed differences both of them. The non-apnea event (label: ECG_a16N) has heart rate mean of 82 BPM and heart rate standard deviation of 6.8 BPM through the length of 1523 beats. The apnea event (label: ECG_a16A) has heart rate mean of 72 BPM and heart rate standard deviation of 4.8 BPM through the length of 997 beats. Table 1 shown the characteristic of all features for non-apnea and apnea events. In order to a deeper investigation of the different characteristic of the signal based on occur variabilities of successive R waves of QRS complex were calculated. In summary, the apnea ECG recordings contain RR mean of 743 milliseconds, RR standard deviations of 120 milliseconds, QRS amplitude mean of 2.3 millivolts, QRS amplitude standard deviations of 1.6 millivolts, QRS width mean of 110 milliseconds, and QRS width standard deviations of 63 milliseconds. Conversely, a non-apnea recording has RR mean of 839 milliseconds, RR standard deviations of 52 milliseconds, QRS amplitude mean of 3 millivolts, QRS amplitude standard deviations of 1.7 millivolts, QRS width mean of 110 milliseconds, and QRS width standard deviations of 72 milliseconds.

Furthermore, the comparison of each feature with p-value is computed based on raw of ECG recordings and observed statistic distribution. These logarithmic deviations are used to obtain features with distributions more rapidly to normal. Based on the quantitative evaluation, the data distribution characteristics comparison shows that there is a significant difference in the pattern of the ECG signals associated with any changes that occur as a result of periodic failures and unexpected construction. These can be observed in Table 1 shows it was found that the features with p-values lower than 0.05 for the distinction between apnea and non-apnea were a feature of alpha1, a feature of alpha2, a feature of residue2, a feature of hqmin, a feature of hqmid, a feature of Dqmax, and a feature of hqmaxhqmin. The significant level was very useful to optimization the classifier to improve the performance parameters.

### 2.3 Feature extraction process

In this section, the main aim of the proposed approach is an assessment of best practice to combine the fractal structure based on a short and long range of sleep disorder ECG signals using the feature set from fractal analysis methods. The feature extraction scheme will help medical. The feature extraction scheme will help the medical practitioner to constructs the variation fractal scaling of ECG signals during sleep automatically. The data that has been segmented will then be extracted. Feature extraction is a process to obtain features that will be used to describe the different characteristics of sleep apnea abnormalities based on differences in patterns between apnea and non-apnea. The recognized of pattern will further assist the clinical expert in diagnosing and determining further steps to take preventive action. Based on the experiment features set are categorized into two approaches, namely monofractal analysis feature set, and multifractal feature set.

The fractal analysis aims to determine the periodic pattern of a signal at a certain period so that the fractal structure can be recognized based on variations in signal fluctuations. Recognition of biomedical signal patterns using the Fractal Structure Approach provides another point of view for differences in patterns between the two classes. It is noted that biomedical signals are essentially visible, but important information such as the amplitude and width of the QRS complex is extremely difficult to capture If only conventional methods are employed.
The biomedical signals also have a very high degree invariant scale and continuously repeated. Therefore, it is very practical to analyze various physiological signals using the spectrum analysis method, specifically signals with an indication of sleep disorders. The flow chart for the monofractal analysis stage is schematically illustrated in Fig. 4.

### 2.4 Extraction using detrended signal

Observations on a signal, particularly biomedical signals with a dynamic invariant dimension, frequently neglect tiny or robust sections. Meanwhile, these small 37s are often only described in the form of calculating the average value, standard deviation, maximum value, minimum value, and median value. That approach is not enough, especially for observations on signals of very long duration. Therefore, another approach is needed that is able to describe a signal through fractal structure analysis to calculate the estimat49 low-exponent power as a representation of the scale invariant structure of the biomedical signal. 37

The Monofractal analysis technique, or more well known as detrended fluctuation analysis (DFA), is used to analyze time series data [31-32]. The variability of the nonlinear dynamic approaches using DFA may provide the quantitative technique for analyzing the heart rate variability in the signal time-frequency series. The DFA 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). In order to get a slope, we apply a DFA approach [32]. The experimental is summarized as step by step to explore this model could be viewed as a nonlinear approach, which has the following format:

1) Define the segmented profile of signal y(i) of length N:

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$$y(i) = \sum_{k=1}^{i} RR(i) - RR(ave), i = 1, \dots, N \quad (1)$$

RR(i) is RR interval of the $i$th, and RR ($ave$) is mean of RR interval of profile.

2) 41mented y(i) through the length of the signal. Calculate the local trend by a least square fit, and and determine of variance v, v=1.

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$$Ft^2(\text{v}) = \frac{1}{t}\sum_{i=1}^{t}[\text{y}(\text{v}-1)\text{t}+\text{i}) - p_v(\text{i})] \quad (2)$$

3) Root-mean-square is calculated by:

$$F(t) = \left[\frac{1}{2Nt} = \sum_{v=1}^{2Nt} Ft^2(\text{v})\right] \quad (3)$$

4) 36thermore, repeat procedure 2 and 3 to obtain the log F(n) and log n correlations.

In Fig. 2 presents the flow chart for the process to determine signal slope to demonstrate the DFA approach to analyzing self-similarity for short-range ECG-apnea signal. As explained previously, the resulting slope has a statistical meaning. Therefore, through this monofractal analysis, the correlation between raw signal and local trending can be correlated. The results of the calculation will mean correlated for long range structure if the value of the slope is 0.5-1, on the contrary to the slope 0-0.5 means anti-correlated [33] for short range structure.

### 2.5 Extraction using multifractal

The monofractal analysis seems to be clarified earlier in order to detect a signal fractal structure, not only to obtain the slope of a signal but also to obtain certain parameters in the context of a multifractal width structure. The ECG signals that are invariant on the fractal structure scale are closely related to the changes that occur due to impulses from the heart while working. The process for multifractal analysis stage is schematically illustrated in Fig. 5.

In addition, the fractal structure invariant can also be caused by weight and age factors of a patient and noise [34]. The use of MFDFA in biomedical time and heart rate analyses is useful for estimating the low exponent power of a signal[36-37]. The multifractal parameters in the form of slope and width are extremely helpful in certain studies in the analysis or determination of signal differences.

In order to achieve features that are important to the classifiers, the study of the ECG records using multifractal spectrum to detect subtle morphology changes and heart rate variability expressed in width parameters will be proposed. As mentioned previously, the width parameter is represented by several related features, namely Dq and hq. Based on the MFDFA approach in time series[35] the fractal dimension (Dq) is obtained based on the conversion of Hq (slope) to the scaling exponent (tq) in the monofractal analysis by Eq. (6). The monofractal parameter is calculated by Eq. (1), Eq. (2), and Eq. (3), while q order by Eq. (4). These processes are the basic of the experiment by multifractal analysis. In order to calculate the fractal dimension (Dq), four steps are implemented and described as follow.

$$Fq(t) = \left\{\frac{1}{2Nt} = \sum_{v=1}^{2Nt}[Ft^2(\text{v})][[Ft^2(\text{v})]^{q/2}\right\}^{1/q} \quad (4)$$

$$F_q(t) \sim t^{h(q)} \quad (5)$$

Even though, in the DFA approach, hq parameter does not depend on changes in $q$. However, the hq parameter of MFDFA process is affected by the value of q because of the nature of $Ft^2$(v) scaling behaviour for all values of q.

$$t(q) = qh(q) - 1 \quad (6)$$

Whereas, the Dq is obtained by Eq. (7).

$$D(q) = \frac{t(q)}{q-1} = \frac{qh(q)-1}{q-1} \quad (7)$$

Consequently, that every change in the parameter q will affect the fractal dimension (Dq).

### 2.6 Various Kernel of Support Vector Machine

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 [32-34]. In this study, we used four 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 [39]. 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 hyperplane can be determined by a clear separation between two classes. The experiment with varying SVM is to ensure getting the best hyperplane 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. The basic knowledge about the kernel as the following equations: linear kernel denoted by Eq. (8); polynomial kernel formulated by Eq. (9); rbf kernel formulated by Eq. (10), and sigmoid kernel formulated by Eq. (11).

$$K(x, y) = x^T y \quad (8)$$

$$K(x, y) = (\gamma . x^T y + \mathrm{r})^d, \gamma > 0 \quad (9)$$

$$K(x, y) = exp\|x - y\|^2 / 2\sigma^2 \quad (10)$$

$$K(x, y) = \tanh(\gamma . x^T y + r \quad (11)$$

Where, r, d, and γ are specific kernel parameters.

## 3. Results

In this section, we elucidate the details of our experiments, present the results and discourse about their advantages.

### 3.1 Analysis of local trending

The local trending signal is basically to obtain the feature value of slope and feature value of residue fluctuation for each segment. These slope values are the result of fitting in the raw signal profile based on the regression line. The slope value is represented in the alpha1 and residue1 parameters which represent the results of the first fitting. In the other part, the results of the second fitting are represented in the form of alpha2 and residue2 parameters. Fig. 6(a) shows the result of the local trending process on the apnea indication signal with a segment duration of 10 minutes 40 seconds (64090 data points). The results of the fitting in the apnea indication profile using the DFA analysis show the feature value of slope with the alpha1 parameter of 1.336 and residue1 value of 0.00067. While the results of the second fitting in the profile, the nonlinear parameters show a range of slope value namely alpha2, residue2 of 0.15, 0.00016, respectively. As can be seen in the bottom graph in Fig. 6 (b) shows the results of local trending on the signal profile with a non-apnea indication. The profile length in 8 minutes 40 seconds and the number of sample 52090 data points. It is clear from the figure that the result shows the parameters slope alpha1, residue1 of 0.695, 0.00049, respectively. Besides that, the result of the second fitting show slope of alpha2, residue2 of 0.64, 0.00179 respectively. The short-long scaling of the ECG signal is represented to the slope of the line. The alpha1 is indicators for the short duration of the ECG signal based on the local trend of the signal result. The alpha2 is indicators 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 or in other words, has the smallest error value. The main difference between these measures to identify apnea characteristic from the non-apnea event. The root squares of the differences between the profile and the fits are used to calculate the fluctuation function in step 3 of the DFA approach. Therefore, based on the experimental results show that the profile that is trending will produce a large slope so that any changes due to fluctuations in the signal will affect the overall the root mean square (RMS) error. The results confirm that the monofractal analysis could yield better investigate the behaviour of the signal than the conventional approaches.

### 3.2 Analysis of multifractal spectrum

This section describes MFDFA to the analysis of the signal. The MFDFA approach is used to learn more about structure fractals. The multifractal time series have local fluctuations with both extremely small and large magnitudes that is absent in the monofractal time series. Fig. 6(c) shows trending results to obtain fractal scaling such as Dq and HQ on apnea indication profile. The profile has a duration of 14 minutes 59 seconds and which correspond to the segments by a number of samples of 90000 data points. Based on the results confirm that the features have feature value for the parameters Dqmin, hqmin, hqmid, Dqmax, hqmax, hqmaxhqmin of -0.68544, 1.6677, 0.57913, 0.5966, 0.044191, 1.6235 respectively. Whereas in Fig. 6 (d) shows the results of fractal scaling for the signal profile with an indication of non-apnea with the number of samples of 72000 data points. The profile has a duration of 11 minutes 59 seconds in length. The results confirm that the calculation of feature value for parameters Dqmin, hqmin, hqmid, Dqmax, hqmax, hqmaxhqmin of -0.49536, 1.2342, 0.46088, 0.5644, 0.12182, 1.1123 respectively. Both of the experiment results provide an explanation that the MFDFA method in the signal profile is a reflection of the temporal variation in the structure time domain. These results are visualized in the width and shape of multifractal. Furthermore, the fractal spectrum has a smaller range that makes the fractal structure more stable, whereas a broad spectrum range represents the fractal structure of the slow fluctuation. The results conclude that the multifractal analysis could yield appropriately to investigate fractal scaling in spectrum than the other approaches.

### 3.3 Statistical analysis

The set of features has functions and influences when used for the classification process. The feature capability can be measured by testing its significance level so that the differences between the two classes can be seen based on the features fed in the input classifier. Ten features obtained from the monofractal feature set (4 features) and multifractal feature set (6 features) were presented with a various feature value and were score on their abilities to identify the pattern of sleep disorder for non-apnea events and apnea events. The scaling fractal with monofractal and multifractal structures is fundamentally different in the study of a signal, as each measures the RMS and determine slopes. One of the differences between the two is that the MFDFA approach is very useful when performing local signal trends that are robust small and large magnitudes. In general, significance levels are represented in terms of forms $p<0.05$. The p-value is considered as a probability in interpreting the two samples tested. The test results are compared with the null hypothesis as the basis of an assumption. Therefore, if the p-value is below the assumption, it can be concluded that the feature has a different distribution, but conversely, if the p-value is above the assumption, then the distribution is identical. The results of the distribution p-value are tabulated in Table 1. The results of these experiments confirm that the significance test is known to have significant differences between the two classes. More specifically, this strategy may lead to affect the classification process. Therefore, the distribution of feature values generated at the time of feature extraction needs to be recognized in deeply. To obtain the normally distributed is a feature scaling by calculating the mean and standard deviation of each feature value. Furthermore, standard deviations are used as standard scores which make a normal distribution yield the standard normal distribution. The preprocessing technique with scaling properties makes every feature has potentially contributed to improving accuracy. To appropriately use this approach, the applied z-score for each feature value is normalized scoring and then calculated as follows:

$$z = \frac{x-\mu}{\sigma} \tag{12}$$

Whereas, z is the standard score, x denotes the value to be standardized, $\mu$ is mean, and $\sigma$ denotes the standard deviation.

In Fig. 7 shows the result of the standard normal distribution using z-score for the selective feature, namely alpha1, alpha2, hqmin, hqmax, and hqmaxhqmin. hqmaxhqmin. It can be seen that if a frequency distribution is normally distributed, the probability of a score occurring by standardizing the scores can be calculated. As mentioned in the graph of the standard normal distribution, the data distribution on alpha1 features indicates how often data with certain values appear in the data. For instance, the alpha1 of non-apnea event has the mean and standard deviation of 0.57, 0.77 respectively, the feature value of $\geq$ -0.75 and $<$ -0.5 has the number of occurrences of apnea events being 21 and non-apnea events being 18 (total 39 or 7.77% overall). The other hand, for the alpha1 of apnea event, has the mean and standard deviation of 0.35, 0.96 respectively, the feature value of $\geq 0.25$ and $< 0.5$ has the number of occurrences of apnea events being 29 and non-apnea events being 12(total 41 or 8.17% overall). Moreover, for alpha2 of the apnea event, the feature value of $\geq$ -0.5 and $<$ -0.25 has the number of occurrences of apnea events being 34 and non-apnea events being 13 (total 47 or 9.36% overall). Whereas, the alpha2 of non-apnea event has the feature value of $\geq 0.25$ and $< 0.5$ with the number of occurrences of apnea events being 19 and non-apnea events being 23, and also has the feature value of $\geq 0.5$ and $< 0.75$ with the number of occurrences of apnea events being 13 and nonapnea events being 19 (total 74 or 14.74% overall). It shows the probabilities for apnea events $-0.34 \pm 0.88$ (mean $\pm$ SD) and non-apnea events $0.55 \pm 0.94$ (mean $\pm$ SD). The distribution of hqmin feature value for apnea with $-0.5 \geq$ hqmin$< 0$ has the number of occurrences of apnea events being 40 and non-apnea events being 29 (total 69 or 13.75% overall), and the feature value for non-apnea with $0 \geq$ hqmin$< 0.5$ has the number of occurrences of apnea events being 53 and non-apnea events being 35 (total 88 or 17.53% overall). It shows the probabilities for apnea events $0.15 \pm 1.00$ and non-apnea events $-0.25 \pm 0.95$. The distribution of hqmax feature value for apnea with $0 \geq$ hqmax$< 0.5$ has the number of occurrences of apnea events being 64 and non-apnea events being 43 (total 107 or 21.31% overall), and the feature value for non-apnea with $-0.5 \geq$ hqmax$< 0$ has the number of occurrences of apnea events being 101 and non-apnea events being 53 (total 154 or 30.68% overall). The apnea event has the mean and standard deviation of -0.03, 0.99 respectively, and apnea event has the mean and standard deviation of 0.05, 1.00, respectively. The last distribution for apnea event with hqmaxhqmin feature value of $\geq 0$ and $< 0.5$ has the number of occurrences of apnea events being 51 and non-apnea events being 37 (total 88 or 17.53% overall). And for the non-apnea event has feature value of $\geq$ -0.5 and $< 0$ with the number of occurrences of apnea events being 39 and non-apnea events being 46 (total 85 or 16.93% overall). It also shows the probabilities for apnea events and nonapnea events $0.15 \pm 1.00$, $0.23 \pm 0.95$, respectively. The fact that the results testing using the z-scores is very useful in making decisions about the distribution of datasets. Therefore, the characteristics of each feature set in generating feature values greatly affect the distribution of datasets in each class. The significance of the differences in each class determines the success in each dataset training process to get the desired optimization model

### 3.4 SVM Classifier and Performance Evaluation

In recent years, the development of SVM has been supported by many kernels that can be used to obtain hyperplane that matches the characteristics of datasets so that 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 2 shows some parameter settings for each kernel, the available options related to the recommended values for getting the model with the best accuracy. The values of SVM kernel parameters based on the optimizing training model. The test results confirm that empirically the performance of the classifier with kernel variations is quite promising. In this study, we trained our model using training set to fit the optimization parameters by 90%, then for tuning the parameters using the validation set by 20% out of 90% of the training set, and used testing set to assess the performance of the classifier by 10%.

The specifics of the classification performance obtained using various SVM kernel are presented in Table 3. three measures, namely, accuracy, sensitivity, and specificity were used to assess the performance of the SVM classifier. The classification result is observed that the SVM with RBF kernel achieved the highest classification accuracy of 92.16% and highest specificity of 94.12%. The SVM with polynomial kernel achieved a sensitivity of 93.75%. More specifically, the trainable parameters of the RBF kernel are optimization parameters with the optimization setting of c=1.0, and gamma=1.0. As clearly described previously that the results testing of the standard normal distribution produced will cause many feature values that can contribute as input to machine learning to get high accuracy.

As the appropriate model is being tested on testing set. The SVM applied to the single lead of ECG signal had an average sensitivity of 85.74% ± 7.16%, specificity of 83.63% ± 9.91% and accuracy of 83.19% ± 6.79%. In order to implement, the specificity parameter is the most important metric because it measures the ability of the algorithm to detect apnea patients. It does not classify a patient as non-apnea when is apnea. Based on the confusion matrix observed that the SVM that uses the RBF kernel has the best classification accuracy and specificity among others of 92.16%, 9412% respectively. Some of these differences are described by the fact that the comparison between the kernels. The difference of kernel has an effect on the accuracy. Specifically, the accuracy of the linear kernel, sigmoid kernel, and polynomial kernel is reduced by 8%, 11.96%, and 15.92% respectively compared by RBF kernel. Therefore, it is clear from the table that an RBF kernel outperforms the other kernels. Related to calibration curve in Fig. 8 shows the predicted probabilities on SVM linear and SVM RBF was appropriate in line of perfectly calibrated. With the result that both obtained the optimal values of accuracy. Conversely, the SVM sigmoid kernel and SVM polynomial has worst predicted probabilities with accuracy lower than other kernels of 80.20% and 76.24 respectively.

## 4. Discussion

The main aim of this study is to improve sleep disorders in real time for reducing visual inspection and manual evaluation. It is because visual examination takes time and acceptance discrepancies rely on the skills of medical staff. To carry out a deeply describe on preprocessing stage, feature extraction stage, and classification method, this study is more exploit sleep scoring with the examination single lead ECG with complexity and robustness in more than ten minutes length, the new features are proposed to boost the efficiency of the algorithm for classification to the obtained acceptable pattern to clear distinctions between apnea and non-apnea based on trending signal behaviour and characteristic of QRS morphologies using fractal analysis, and the last one is to attained proper optimal parameter to improve the large margin of SVM hyperplane. As described in the previous section, it is very clear that solving the sleep disorder classification case using the feature set of fractal analysis has improved performance. This improvement is better than use based only on the feature set of the variability of time and frequency domain. Besides that, the improvement is obtained using only limited features but is able to provide high differences between the two classes so that the algorithm works more optimally. A performance comparison the articles that report various researchers for classification on apnea ECG physionet is presented in Table 4.

The explaining the first contribution, fractal analysis based on monofractal and multifractal are frequently adopted to nonlinear behaviour of ECG signals. However, the application is still individually to solve cases related to the fractal structure in the presence of dynamic forms. However, monofractal analysis techniques have been used for a long time[30], but its application is still reliable to solve problems related to correlation in time series with the nonlinear phenomenon. In the case of detection or classification of sleep disorders, the use of extraction methods with investigative techniques using fractal analysis, especially in monofractal analysis alone or in combination has never existed. The previous research has focused more on analytical approaches based on time-frequency domains and their derivatives [41-42]. In fact, the characteristics of sleep disorders are not only recognized by the pattern based on the occurrence of ECG wave morphology, namely p wave, QRS wave, and t wave. However, we can know the periodic pattern of sleep disorder through signal behaviour based on dynamism so that it can be obtained and calculated the resulting parameters. In the present study, we attempted the combine mono-fractal and multifractal analysis to explore the dynamic of the ECG signal by examining the obtained feature set for the diagnosis of sleep disorder. The experimental results are very clear that the two approaches are able to recognize signal patterns and result in improved performance of the classification method.

The second contribution is related to the number of features and the feature extraction method chosen. As previously stated, ECG recording analysis for patients with indications of sleep disorder is widely used for assessment. One of the most widely used diagnostic tools is based on the calculation of heart rate variability (HRV)[7] with 28 features that represent the variability of power in mean and standard deviation. In addition, through HRV many features that can be used like analysis of the energy and fuzzy entropy feature of intrinsic band function with total features of 12, and 1-minute length of segment[15]. The results of the SVM kernel rbf classification in this study are sensitivity, specificity, and accuracy of 79.70%, 73.35%, 76.58, respectively. The results of the performance evaluation are quite promising and can still be improved by other approaches. The other studies with a higher number of features, 32 features derived from the combination of time domain analysis of HRV, ECG respiration, and cardiopulmonary coupling in one minute length from single lead of ECG[42], the results confirm that the combination approach presented an accuracy of 89.8%, the specificity of 92.9%, and the sensitivity of 84.7%. The performance measures have improved compared to previous related research, but with more features analyzed will have an impact on the complexity of the computational process, allow the loss of clinical information, and do not yet represent all the information related to the pattern of ECG signal for the sleep disorder. The other studies have presented a real time sleep apnea detection by applying a feature selection method to an algorithm, 39 out of 150 features can be reduced. Furthermore, various schemes are implemented to obtain performance improvements, including testing by combining ECG and SpO2 records in one-minute, individual testing, ECG only, SpO2 only. The scheme was quite successful with sensitivity, specificity, and accuracy are all around 81% and 82% [43]. Other studies with significant improvements in the three evaluation parameters were found to be in the range above 90%[44], the improvement not only in the extraction method but also in the preprocessing stage with reducing error of the result of RR interval detection using a local medial filter modification focused on abnormal RR intervals.

This approach can provide more efficient of time-consuming to examine and lest cost study and compare the performance of sleep home study and PSG laboratory.

Another contribution is how the application of the effects of optimization of different kernels of SVM so as to enhance the efficiency of classification methods. Finally, the proposed method comparison can provide other alternatives in producing computer-based tools to minimize visual inspection and manual scoring by medical employees. The results of the experiment show that the problem in the classification process is the distribution of data on apnea events and non-apnea events is not balanced. However, choosing the right classification method is quite able to reduce the effect of the imbalance of the dataset. The facts show that the algorithm is better at detecting both classes with sensitivity and specificity levels in the range above 88%. In general, could be concluded that the effectiveness of feature set successfully and affectively exploits the difference of pattern of apnea and non-apnea events is deeply complex and dynamical information changes during sleep.

## 5. Conclusion

Attention to sleep quality will provide long-term benefits. Sleep profoundly is essential for health and as necessary as healthy food and adequate exercise. We report that ECG-apnea recordings of the patients with different segmentation for preprocessing and extraction process. We employ the monofractal and the multifractal analysis to generate 10 different features such as alpha1, residue1, alpha2, residue2, Dqmin, hqmin, hqmid, Dqmax, hqmax, and hqmaxhqmin. The experiment is directed using various classification models in order to find out which one emerges as the best performing. The dominant features are then used for the classification using SVM classifier with different kernels such as RBF kernel of SVM, Linear kernel of SVM, a polynomial kernel of SVM and sigmoid kernel of SVM. The proposed method yields the best-performing kernel is the RBF kernel of SVM with a classification accuracy of 92.16%, sensitivity of 88.24%, and the specificity of 94.12%.

This approach shows that multi-feature analysis with fractal analysis is a capable means to assist a clinical expert in getting potential sleep disorder screening, mainly when applied to home sleep testing. For future work, we are planning to develop a real-time assessment that can detect the level of severity based on apnea-hypopnea index (AHI), special treatments for investigation obstructive sleep apnea-hypopnea syndrome (OSAHS) using a single electrode and using a minimal feature set.

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