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An Explainable AI Approach Towards Automatic Sleep Apnea Detection Based on ECG Signal

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Abstract

Sleep apnea is a serious abnormal sleep condition that deals with breathing pauses during a patient's sleep, which may cause serious health concerns if not treated. This study gives an approach for diagnosing sleep apnea using explainable AI methods applied to single-lead ECG readings. The process includes extracting features from ECG readings and using models such as Multilayer Perceptron (MLP), Support Vector Machine (SVM), Gradient Boosting (GB), and Long Short-Term Memory (LSTM) networks to detect apnea events. We focus on improving the interpretability of our models by employing ante-hoc and post-hoc Explainable Artificial Intelligence (XAI) techniques such as Decision Trees and Local Interpretable Model-agnostic Explanations (LIME), which provide an improved understanding of the decision-making procedure. Experimental results demonstrate that our technique works effectively, with the suggested models recognizing apnea episodes using time windows with high accuracy on the Apnea ECG database. Incorporating LIME strengthens the prediction of the Machine Learning model, making it an impressive tool for medical decision support. This study illustrates the potential of explainability tools to design reliable, interpretable, and explainable machine learning models for detecting sleep apnea, with a chance of expanding these approaches to other medical applications. This approach provides insight into the critical features contributing to sleep apnea detection.

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Keywords: Explainable AI; LIME(Local Interpretable Model Agnostic Explanation); Machine learning.

1. Introduction

Sleep Apnea (SA) also called Obstructive sleep apnea (OSA) is an abnormal condition during sleep that mostly occurs because of lifestyle habits and sleep disorder in which a patient finds difficulty breathing. In the population, an estimated 4% of men and 2% of women are seriously affected [1]. The muscles responsible for breathing become paralyzed to produce damage to the hippocampal zone in the human brain and other serious consequences [2]. Early identification and diagnosis are essential for sleep apnea to be effectively treated and the associated health risks to be avoided. Untreated SA can develop serious healthcare situations for instance diabetes, cardiac disease, stroke, hypertension, or high blood pressure. The apnea-hypopnea index (AHI) is a measurement index for estimating the intensity of the SA by estimating the amount of apnea existence per hour of sleep [3]. $AHI \geq 5$ indicates an abnormality,

while $0 \leq \text{AHI} < 5$ is considered normal [4]. The cardiac rate and Supply of blood to its muscles are evaluated and measured using electrocardiography (ECG). Furthermore, thorax, stomachic, and auricular indications from respiration or sleeping can aid in detecting SA. As a result, numerous electrodes are applied to the subject's scalp and body. Because numerous sensors are bonded to the SA individual for collecting information, SA identification via PSG (Polysomnography) is expensive and challenging. Furthermore, especially for experts, analyzing an extensive quantity of data is a tedious and exhausting task. As a result, it would be beneficial to have a technique that is inexpensive, simple to operate less complex, and provides a convenient method while remaining precisely correct [3]. Several techniques in this area have been investigated, including a study of snoring sounds, oximetry for pulse measurement, and ECG (electrocardiography). Respiratory problems related to sleep significantly affect the rate of heartbeat, blood pressure, and various additional ECG parameters. The Analysis of the ECG record can calculate the interrupted breaths throughout sleep, which aids in computing the apnea score. As a result, a trustworthy substitute for the PSG has been shown in recent research to be a low-cost, safe single-lead ECG that provides accurate data on the cardiac activity impacted by sleep apnea. Heart rate typically decreases during an apneic episode, and then rises towards the finish of the episode. The availability of these apneic instances causes an unexpected change in the frequency pattern of the ECG signal. As an outcome, the method of analyzing ECG to detect SA is rapidly gaining popularity among several academic societies. ECG signals also serve as a practical and affordable approach [5]. Several machine-learning approaches have been advised for detecting Sleep Apnea. These approaches rely on physiological measurement data like single-lead ECG signals, snoring, and breathing signals. Time, frequency, and nonlinear domain interpretation can reveal physiologic modifications in the ECG signal throughout SA. As an outcome, the majority of these different studies centered on mining time-related i.e. temporal, spectral, and nonstationary features from physiological data. A lot of different supervised learning techniques have been used in those feature extractions to enhance SA detection capability [6][7]. These automated sleep apnea identification algorithms have received a lot of recognition and have illustrated positive outcomes in identifying SA based on physiological signals; however, there is one noticeable gap: the uninterpretable nature of machine learning. The black-box aspect of machine learning approaches, typically taking an input, generating an outcome, and not explaining the model's conclusion, is one of the main causes of concern. The explainable artificial intelligence approach provides insights into the inside mechanisms and outcomes provided by machine learning algorithms. XAI approaches are classified as ante-hoc and post-hoc. The ante-hoc approach is largely concerned with creating algorithms that can intrinsically explain themselves, such as rule-based methods. The post-hoc model then focuses on interpreting the outputs of the inputs. These methods enhance the explainability of different AI algorithms and operate separately from the model. One widely used method in this field is Local Interpretable Model-Agnostic (LIME). Because of its simplicity, it is commonly employed and is going to be used in this research. Python package of LIME is available to use directly, which means it is simple to use [8]. In this study, our focus is to utilize XAI approaches for diagnosing sleep disorders after processing ECG signals and extracting features from raw patient data. The primary goal of this investigation is to use an explainable AI method for detecting SA to ensure anyone who uses it can trust the results. The rest of the paper is structured as follows: In Section 2, related work is summarized. The suggested methodology is described in Section 3, together with its theoretical framework and implementation procedures. The use and implementation of explainable artificial intelligence (XAI) techniques are described in Section 4. The results of XAI are presented and discussed in Section 5. The paper is finally concluded in Section 6 with a review of the results along with ideas for future research.

2. Related Work

Several researches have been published in the literature that use AI approaches, specifically, to diagnose and treat sleep apnea syndrome. This study describes a few of them.

Global recognition has been established for polysomnography (PSG) as a valuable tool for SA identification [9]. For the period of the night, individuals must be placed on numerous electrodes to accumulate recordings, and they must then depend upon professionals to physically categorize their information [10]. This method is not only overpriced, but it also might impact the subjects' sleep patterns, which might disturb the findings even more. Single-lead signal-based approaches are gaining important interest. Examples include respiration signals, blood oxygen saturation, photoplethysmography, snoring, electrocardiogram (ECG) [11], and other similar techniques. ECGs provide an enormous amount of breathing information and are easier to gather than other signals. According to studies, ECGs

can show SA events [12]. SA and heart rate fluctuations have a significant connection [13] [14]. RR intervals derived from ECGs are going to show specific fluctuations in the frequency of SA actions [15].

Machine learning algorithms such as Support Vector Machine, Independent Component Analysis, Principal Component Analysis, and Linear Discriminant Analysis, among others, have recently gained popularity for detecting SA [9]. Researchers suggested an SVM-based SA detection approach that extracts R-R interval and R peak amplitude features [16]. Song et al. [17] used multiple fundamentally common classifiers, which include Linear Discriminant Analysis, Support Vector Machine, logistic regression, and K-nearest neighbors, and afterward considered time dependence to create an HMM-based identification method. A previous study developed a Fast Fourier technique and SVM for accurate identification of SA. Such machine-learning approaches regularly demand hand-crafted feature development and have limited presentation [18].

Cheng et al. [19] extracted features from ECG signals which were gathered via the physionet.org open-access database, and developed an OSA identification technique using a deep learning Recurrent Neural Network method. Wang et al. [20] identified sleep apnea using an enhanced LeNet-5 convolutional neural network. Sharan et al. [21] investigated the implementation of a single-dimensional Convolutional Neural Network to detect sleep syndromes. Faust et al. [22] developed a deep-learning approach for categorizing apnea or non-apnea. They developed a test arrangement that receives RR time frame signals and determines the fact that particular sections of signal indicate sleep apnea symptoms. Bahrami et al. [23] designed and experimented with multiple deep-learning approaches for the identification of sleep apnea through a single-lead ECG signal, they implemented CNN(LeNet) and DRNNs (LSTM, bidirectional LSTM, and gated recurrent unit). A weighted-loss time-dependent (WLTD) model of classification and a multi-scale dilation attention single-dimensional convolutional neural network were the foundations of Shen et al.'s [24] proposed OSA identification technique. In a novel approach to SA classification of ECG signals, Almutairi et al. [25] suggested deep learning techniques for extracting features from the ECG records and categorizing them as well. Although these techniques are based on deep learning for SA identification producing favorable outcomes, there is further opportunity for improvement.

Wearable technology has been attracting a lot of interest recently and is being used in many different industries, including blood pressure tracking, pulse tracking, and hazard prevention systems. A wearable gadget is worn on the skin or affixed to it. As a result, SA detection using wearable technology is also possible based on gathered ECG signals [26]. To detect SA, pressure sensor gadgets are frequently integrated into pillows. Users wouldn't be contacted, and professional advice is also not required. Such gadgets are designed to be utilized by one person and are highly susceptible to damage. A smart pillow using a pressure sensor was created by Veiga et al. [27] to monitor the quality of sleep. Ali et al. [28] proposed a without effort flexible pillow made up of six air bladders. This smart pillow can not only identify Sleep Apnea, but it can also effortlessly modify an individual's resting posture or observe an attack and change the pillow settings accordingly. If the individual fails to bounce back due to an active Apnea attack, it will sound a siren. Although, pressure-based gadgets are aware of their environments. The lack of openness in existing machine learning algorithms for sleep apnea detection makes it challenging for doctors or patients to understand or trust their predictions. Our suggested model outperforms existing artificial intelligence models in the identification of sleep apnea with trust and transparency using explainability, demonstrating higher accuracy and interpretability over previous techniques.

3. Proposed Methodology

Figure 1 depicts the methodology followed in this research. First, the ECG records are pre-processed, and then the signals are passed through a bandpass filter to remove unwanted frequency components, ensuring only relevant cardiac information is retained. The filtered signals are then segmented into smaller, manageable portions, allowing for more precise feature extraction. The extracted features are subsequently fed into machine learning algorithms for classification, with an explainable AI (XAI) model providing transparent insights into the results. Finally, the explanations generated by the XAI model undergo a thorough evaluation to assess their accuracy and relevance.

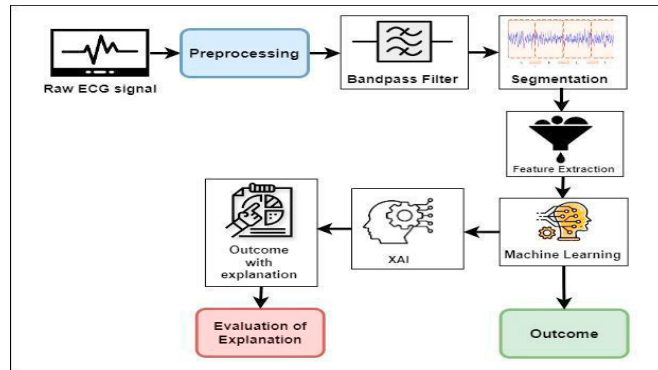


Fig 1. A flow-chart illustration for explainable machine learning models.

4. Implementation

1. Dataset

The common and extensively utilized Physio Net Apnea-ECG database, made available by Dr. Thomas Penzel at Philipps University in Marburg, Germany, was used in this study [29]. Male and female participants ranging from the ages of 27 and 63 are encompassed in the Physio Net Apnea-ECG dataset. The 1-minute ECG window was labeled as either "SA" or "Normal" without any differentiation between hypopnea or apnea. In addition, the AHI value was used to divide these ECG signals into three different classes (A, B, and C). The definition of class C involves the normalization of AHI values to 5 or lower. Apnea is defined as level A if the AHI value is above 10. Those records that had an AHI value of 5 or higher throughout sleep were classified as class B (boundary line sleep apnea). Single-lead ECG recordings from seventy subjects are included in the dataset. The recorded ECG signals are split into two groups, each comprising 35 individuals, the released set and the withheld set. Training samples are twenty in A, five in B, and ten in C, and Testing samples are thirty-five in X. Model building and monitoring are typically accomplished using released sets, while withheld sets are employed for model testing.

2. Pre-processing and Feature extraction

Prior research has demonstrated that important information regarding the existence of SA can be found in the ECG signals' period of RR and R-peak frequencies [17]. Therefore, the ECG signal is pre-processed to take out the RR time frames and R-peak frequencies. The original ECG record is notable for having a lot of distortion. To reduce this noise before processing, we employed a FIR bandpass filtering technique, setting the low frequency to 3 Hz and the high frequency to 45 Hz. The RR time frame is the period between 2 adjacent R peaks [15]. The R peaks are found with the help of the Hamilton approach [29], and the RR intervals are then determined using the R peaks that have been identified.

Twelve features derived from intervals of RR and six features derived from R-peak frequencies are put together to create the feature vector. Six of the 12 RR interval features are in the time domain, though the remaining six are in the frequency domain. The average of RR intervals (ARR), average heart rates (AHR), standard deviation of RR intervals (SDR), root mean square of differences between successive RR intervals (RMS), number of most adjacent RR intervals that are above 50 milliseconds (NRR50), and NRR50 divided by the total number of RR intervals (pNRR50) are the six time-domain features [30] [31]. in which N is a count of intervals of the RR and RR(n) is the value of the n'th RR interval. To analyze the next six frequency features, we initially compute power spectral density (PSD) through the Welch method using a fast Fourier transform ($N = 256$) [32]. Next, we derive 6 features by examining the strength of every individual frequency component: extremely lower frequency, lower frequency (0.04~0.15 Hz), higher frequency (0.15~0.4 Hz), the ratio of lower and higher frequency, the ratio of lower frequency and lower frequency with higher-frequency, and the ratio of higher frequency and lower frequency with higher frequency from R peaks amplitudes to build the model. Hence, apart from the RR intervals' frequency features, Additionally, using the R-peak amplitudes, we derive the six frequency features (ELF, LF, HF, LF/ (LF + HF), and HF/ (LF + HF)) needed to build

the model. After extracting the features, we normalize them using the following formula due to the significant differences in their distributions [33]. here σ is the feature's standard deviation and \bar{x} denotes the feature's average.

$$x^* = \frac{x - \bar{x}}{\sigma}$$

This study also utilized a moving time window concept that helps the classifier to include temporal data from ECG recordings [33]. This method involves taking a sequence of consecutive ECG windows inside a temporal window. By considering multiple windows simultaneously, the model can efficiently learn and take advantage of the temporal dependencies present in the ECG record. To collect the temporal dependence from ECG data, features from past windows, along with the features of the current window are considered as input to the model. Here we have used a time window size of 5 (1 current window, and 5 previous windows). Figure 2 demonstrates the method to pick the time window.

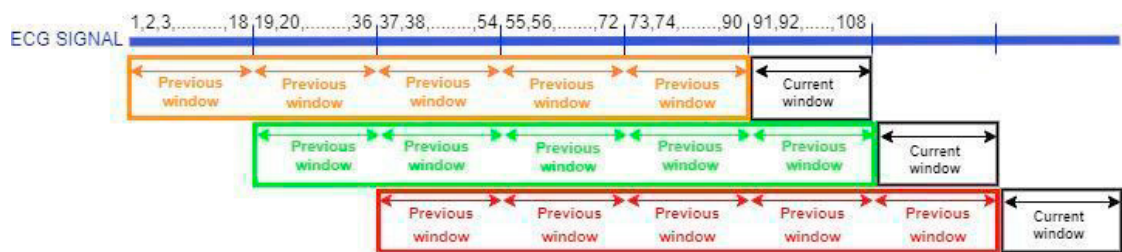


Fig 2. Illustration of time window selection used in the study.

3. Detection of sleep apnea using various classifiers

- 3.1. *MLP (Multilayer Perceptron)*: A feedforward ANN with at least three layers—an input layer, hidden layers, and an output layer—is called a multilayer perceptron. In this study, the Multilayer Perceptron (MLP) classifier was set up with certain parameters to enhance its ability to identify sleep apnea based on ECG signals. We used an L2 regularization with an alpha value of 1 to avoid overfitting caused by high weights being penalized. To balance the training time while providing the model enough opportunity to derive knowledge from data used for training, the model was given a maximum of 1000 iterations. These parameters were used to train and assess the MLP classifier, which resulted in an appropriate balance between learning ability and generalization, and precise identification of sleep apnea activities. To evaluate the successful outcome of the model, key performance metrics such as accuracy, sensitivity, and specificity have been calculated from the confusion matrix.
- 3.2. *SVM (Support Vector Machine)*: SVM learning is a frequently used binary classification algorithm (often referred to as supervised learning) [34]. We standardized both training and test datasets to pre-process the single-lead ECG signals. The training data in this SVM model is mapped into kernel space using a linear kernel function in our implementation. The proposed model's training approach consists of five stages: data input, pre-processing of data, extraction of features, SVM model training, and SA detection. The SVM classifier's performance was verified on the test dataset, and it accomplished a remarkable accuracy score. We conducted a general evaluation of the estimates made by the model applying a confusion matrix, from which we created significant performance pointers such as accuracy, sensitivity (sn), and specificity (sp).
- 3.3. *LSTM (Long Short-Term Memory)*: This research investigates the usage of networks grounded on Long Short-Term Memory (LSTM) to accomplish automatic sleep apnea identification employing single-lead electrocardiogram (ECG) signals [1]. To evaluate the time-series individual's ECG signals while sleeping, we use this model inspired by LSTMs' effectiveness in diagnosing temporal relationships in sequential data [35]. A sequential LSTM model is employed in our suggested model. LSTM layers are divided by dropout layers, which are a regularization approach to evade overfitting during training. Utilizing a sigmoid activation function, the last layer predicts binary outcomes (apnea or no apnea) by utilizing the identified features. Using

the testing dataset that has not been viewed, the built LSTM model is validated. We evaluate the effectiveness of the model using a confusion matrix, similar to the SVM method. Key constraints such as accuracy, sensitivity, and specificity are measured to ensure a thorough review.

- 3.4. *GB (Gradient Boosting)*: The use of Gradient Boosting classification techniques for automated sleep apnea identification with single-lead electrocardiogram data. Gradient Boosting is an effective ensemble learning approach that utilizes numerous weak learners (decision trees) to produce a more powerful learner [36]. Both training and testing datasets are standardized using a common scaler. After the data has been pre-processed, it will be input into the Gradient Boosting classifier, which is set up with 100 decision trees, a 0.1 learning rate, and a maximum depth of three. A segment of the data is applied for the model training, and another set of data is employed for evaluating it.
- 3.5. *Performance of the models*: The performance of the models is evaluated on metrics like specificity, accuracy, and sensitivity. Sensitivity (Recall) is the percentage of correctly detected true positives ($\text{True Positive} / (\text{True Positive} + \text{False Negative})$). Specificity is the percentage of successfully detected true negatives ($\text{True Negative} / (\text{True Negative} + \text{False Positive})$). The percentage of actual findings (both positive and negative) out of all predictions ($(\text{True Positive} + \text{True Negative}) / (\text{True Positive} + \text{True Negative} + \text{False Positive} + \text{False Negative})$) indicates the accuracy model. Table 1. represents the performance of various AI models (MLP, SVM, GB, LSTM). Performance comparison of various models using ROC-AUC curves is shown in Figure 3. The True Positive Rate (Sensitivity) vs the False Positive Rate for four models—MLP, SVM, LSTM, and GB—are compared on the ROC (Receiver Operating Characteristic) curve. The AUC (Area Under the Curve) results show that every model performs effectively, while the MLP model outperforms the others. Table 2. displays a comparison with state-of-the-art models. Our suggested model achieved better

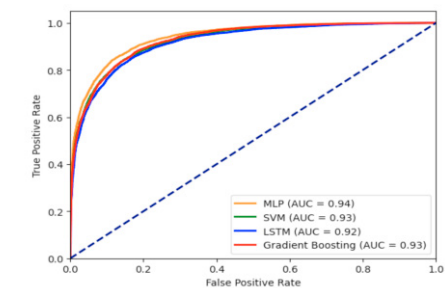


Fig 3. ROC-AUC Curves for Different Models.

than the others.

Table 1. Performance of various models.

Models	Accuracy	Sensitivity	Specificity
MLP	0.868	0.824	0.895
SVM	0.853	0.803	0.883
GB	0.853	0.793	0.891
LSTM	0.846	0.768	0.895

Table 2. Comparison with the state-of-the-art models.

References	Methodology	Accuracy (%)
[3]	MLP without a time window	85.1
[6]	LSTM without a time window	82.5
[5]	GB without a time window	75.2
[17]	SVM without a time window	73.8
Proposed approach	MLP with a time window	86.8

4. Explainable AI

Explainability through XAI should be integrated into classification methods developed using machine learning, as these algorithms are inherently black-box and largely uninterpretable. This is particularly crucial in situations of greatest risk when the algorithm's output must be sufficiently trusted to prevent unfavorable outcomes. It was discovered that there are two possible XAI implementation systems: post-hoc and ante-hoc. Explainability is employed in ante-hoc and post-hoc systems to give users confidence in their judgments, derived from the results of machine learning techniques with explanation. In this study, we have used a decision tree and LIME as explanation methods.

4.4.1 Ante-hoc: Ante-hoc explainability includes machine learning algorithms, such as decision trees and K nearest neighbor, that are already nearly interpretable using "glass-box" methods [37].

Decision Tree: The testing dataset was categorized using a decision tree classification algorithm, which is a tree-like arrangement used to build a model utilizing a training database [38]. As an ante-hoc model, the Decision Tree model provides visible decision-making pathways that are easy to understand. This provides for a better understanding of how certain factors influence the identification of sleep apnea occurrences. Figure 4 represents the decision tree output.

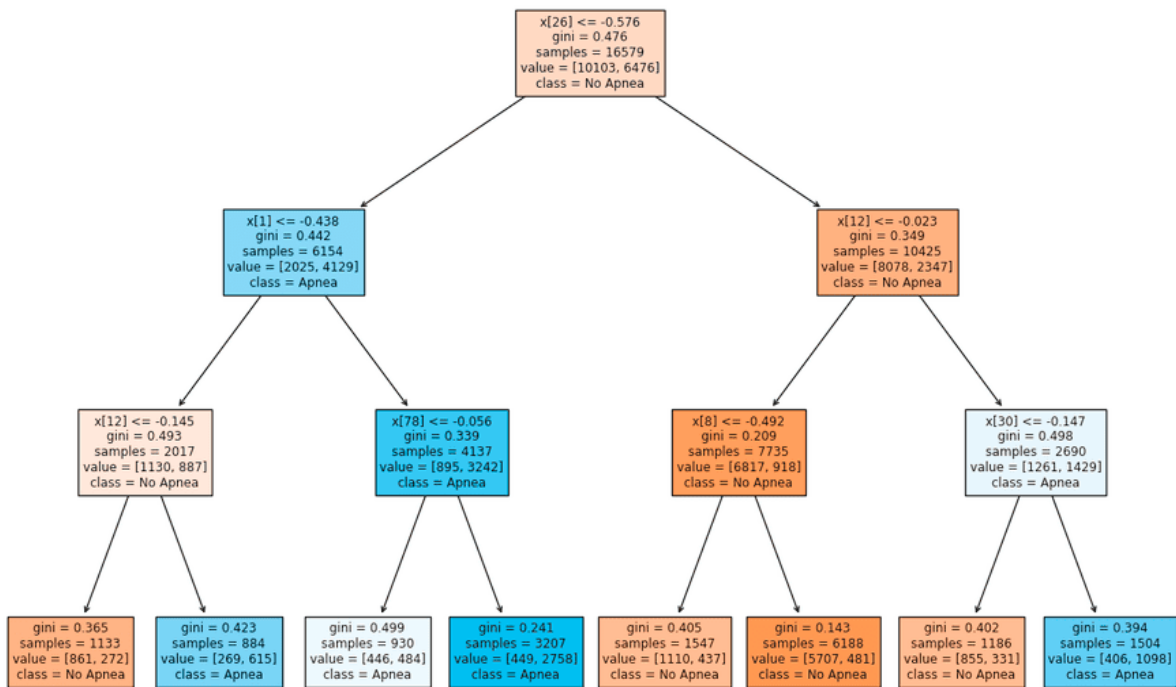


Fig 4. Decision tree, Orange nodes have No Apnea, and blue nodes are normal nodes.

4.2.2 Post-hoc: To enhance understanding of the procedure of making decisions and output generation of an Artificial Intelligence model, post-hoc explainability approaches include analyzing and explaining the outcome generation mechanism of the model after it has generated predictions. The most popular post-hoc technique is LIME (Local Interpretable Model-Agnostic Explanations) to calculate the importance of several characteristics for a particular result [39]. The Random Forest model yields results that may be interpreted by humans using the LIME approach, which stands for Local Interpretable Model Agnostic Explanation. LIME computes explanations for a single sample instance, a feature known as local explanation. Instead of the complete dataset, they are given for each case. Experiments were

conducted to evaluate the explanations for both SA and non-SA classes. Figure 5 shows the LIME output (Non-SA). These graphs represent the contribution of features, which show the top 6 features.

5. Explainable AI Results

The PhysioNet Apnea-ECG database has not been used in any research that uses explainable artificial intelligence (XAI) to detect sleep apnea. In this study, XAI models are applied to AI models to interpret the outcome provided by the ML models that are trained on features from 5-time windows of one-minute duration and one current window of 1 minute as suggested by [33]. 18 features were extracted from each time window and thus there are 108 features. As shown in Figure 5 the top features identified by LIME and the decision tree top features are Feature 8, Feature 12, Feature 26, Feature 30, Feature 48, Feature 66, Feature 68, etc. The features identified by XAI techniques are mostly from previous windows rather than the current window. Thus, the explanation provided by XAI models supports the idea proposed by [33].

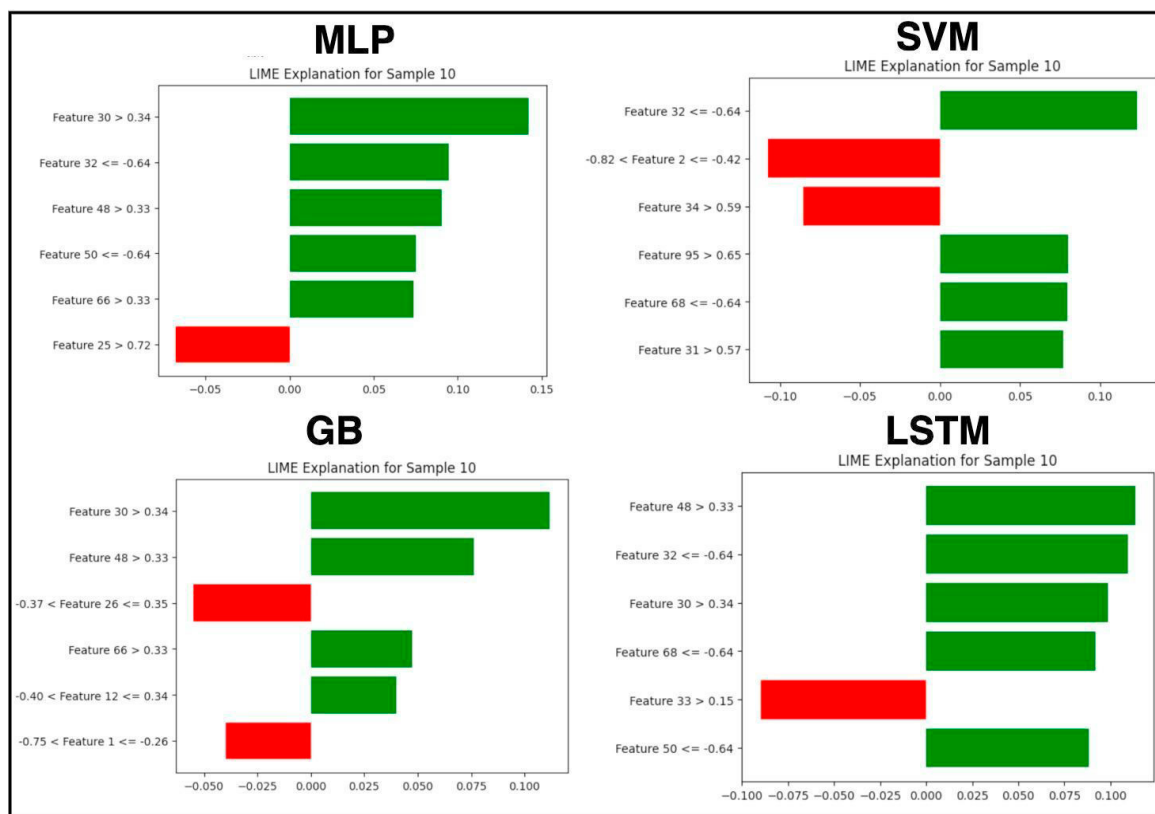


Fig 5. LIME explanation of ML model.

6. Conclusion and Future Scope

In this work, we investigated the utilization of several machine learning and explainable AI techniques to identify sleep apnea from single-lead ECG signals. The suggested technique comprised extracting relevant features and then training models to categorize between apnea and non-apnea events correctly. Experimental findings show that the proposed models were executed effectively with an accuracy of 86.8%. Further, LIME is used to provide an understanding of how the model makes decisions. This transparency is critical for establishing confidence and assuring that model predictions can be explained and verified in practice. The performance evaluation shows that our models outperform other AI models in the detection of sleep apnea, achieving high accuracy and interpretability. Clinical trust

is dependent on prediction transparency, which was further improved with the integration of LIME. Future work could focus on improving these models by investigating additional features and incorporating different datasets.

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