

Sleep Apnea sub-type detection from Polysomnography signals

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Abstract—One of the most common sleep-related disorder is Obstructive Sleep Apnea Syndrome (OSAS). Increased upper airway resistance during sleep causes partial or full airflow interruptions. In stroke patients, severe OSAS increases the risk of mortality, neurological impairments, functional result after rehabilitation, and uncontrolled hypertension, making OSAS identification and treatment crucial. Polysomnography is the best OSAS test. In this work, it is proposed to use PSG signals to identify different sub-types of OSAS. Although many works have been done to detect OSAS but no work has been done till now to detect the sub-types of OSAS. It is of great medical importance to find out the sub-types of OSAS in order to plan proper treatment and diagnosis for the patient. Technically, it is more challenging to detect sub-types rather than just detecting the presence of OSAS. Deep learning architectures find use in extracting features from PSG signals. They further enhance learning to classify the 4 different categories of sleep apnea. Results demonstrate that a mean accuracy of 94.26% is achieved with the proposed methodology.

Index Terms—sleep apnea, polysomnography, deep learning, classification, signal processing

I. INTRODUCTION

Sleep Apnea (SA) is a condition characterized by the intermittent interruption or decrease in the flow of air during sleep [1]. The condition is distinguished by the occurrence of Obstructive Sleep Apnea (OSA), which is defined as either complete or partial obstruction of the upper airways, or Central Apnea, which is characterized by a reduction or cessation of the respiratory motor output of the medulla. These conditions can occur individually or in combination. Two respiratory episodes that can be detected in SA include complete cessation of respiration, also known as apnea, and decreased airflow, referred to as hypopnea [2]. These occurrences result in reduced oxygen levels (known as hypercapnia), as well as increased activity of sympathetic nerve, variations in heart rate and blood pressure. The physiological changes mentioned above have an impact on the sleep cycle of patients, leading to brain arousal, disturbance in different sleep stages, and fragmentation of sleep [3]. According to [1], the prevalence of SA among middle-aged individuals is approximately 10%. Despite the great incidence of this illness, a significant number of patients remain ignorant of the impact that SA has on their breathing pattern. Consequently, a considerable number of individuals refrain from pursuing expert medical assistance.

Numerous scholarly investigations have been conducted to explore the morbidity associated with SA. The findings of these studies indicate that the failure to promptly diagnose and treat SA can lead to various adverse effects, including daytime drowsiness [4], cognitive impairment [5], cardiovascular conditions such as hypertension [6], coronary artery disease [7], stroke and metabolic disorders like diabetes [8]. Hence, the timely identification of SA is imperative in mitigating subsequent difficulties. In this work, it is proposed to detect the type of Apnea such as Hypopnea, Apnea-central, Apnea-Obstructive and Apnea-Mixed from the polysomnography signals measured from patients during their sleep. The remaining part of this paper is organized as follows. We first discuss the related works (Sec. II) in this field explaining the progress and shortcomings of current works. Then in Sec. III we discuss our approach in detail followed by our results in Sec. IV. We then conclude and discuss what can be done in future in Sec. V.

II. RELATED WORK

The majority of research on single-lead OSA (Obstructive Sleep Apnea) detection utilizes Electrocardiogram (ECG) based signals and pulse oximetry. Information extraction techniques, such as analyzing data in time and frequency domains, are used to accurately identify patterns and trends that can help determine and forecast the occurrence of OSA. A synthesis of previous studies conducted on the Physionet Apnea-ECG database [9] utilizing 35 withheld and 35 released Lead-II ECG signals To detect OSA from ECG signals, Changyue Song et al. [10] used Discriminative Hidden Markov Model (HMM). Nonetheless, this did not provide any indication regarding the degree of severity of the OSA episode. The outcome is restricted to a Boolean value without any further explanation. Li et al. [11] conducted an additional investigation employing DNN and HMM with a single-lead ECG signal. The efficacy of the method was enhanced by various classifiers, including support vector machines (SVM), ANN, and HMM. Conversely, this research is limited by the absence of disease detection and classification. Qi Shen et al. [12] utilized a methodology that involved the use of a multiscale dilation attention 1-D convolutional neural network model, a multiscale feature extraction algorithm, and classifiers with weighted loss and time-dependence (WLTD). Regrettably, the network

model encountered significant challenges in its attempt to autonomously extricate features from the initial ECG data, thereby requiring considerable manual intervention.

The polysomnography (PSG) [13] diagnostic procedure is considered the benchmark for SA diagnosis. Electrocardiogram (ECG), electroencephalogram, electromyogram, pulse oximetry, airflow measurement, and respiratory effort are all utilized in PSG to examine sleep and respiration parameters. Very few strategies for diagnosing SA with PSG have been proposed and implemented [14]–[16].

Until now, most of the works have been done using ECG signals available from the Apnea-ECG dataset, but recently a new dataset consisting of stroke unit recordings OSAS detection (OSASUD) [17] have been released that contains not only ECG data, but also PSG and other derived data like heart rate and oxygen saturation (SpO₂) for 30 patients. Data of the patient spans for several hours and thus provides a rich and varied information for studying OSA. Hence, it is now possible to use this vast data repository to create better sleep apnea detection algorithms.

The main objective in this work is to detect the presence or absence of apnea and to classify the type of apnea detected.

III. METHODOLOGY

In this section the details regarding the preparation of data and the procedure attempted for classification is discussed. First, the description of the dataset is made followed by the challenges present in the data and the way to approach is presented. Finally, the training of deep learning model and classification of the different types of apnea from the normal class is projected.

A. Dataset

OSASUD dataset [17] has been utilized in the proposed experiment. Thirty patients hospitalized to the stroke unit of the Clinical Neurology Unit of the Udine University Hospital for a suspected cerebrovascular event (ischemic stroke, transient ischemic attack, or hemorrhagic stroke) between August 2019 and July 2020 are included in this dataset. The following criteria were used to exclude patients from the study: age < 18 years, inadequate adherence to standard monitoring and/or PSG, aphasia severe enough to hinder understanding the study protocol and/or informed consent expression, and a high risk of alcohol or drug withdrawal syndrome. Patients conducted simultaneous recording of photoplethysmography (PPG), electrocardiogram (ECG), and photoplethysmography (PSG) overnight after providing informed consent. Vital signs such as heart rate (HR), Respiratory Rate per minute (RR) and premature ventricular contractions per minute (PVC) were derived from the ECG recordings for each patient. Oxygen saturation (SpO₂) level were derived from the PPG. Apart from these vital signs, the dataset also has several hours of recording of PPG signal (frequency 80Hz), ECG signals from three lead sources with frequency 80Hz each and five PSG signals (abdomen, flow, position, snore and thorax). PSG signal of flow was sampled at 20Hz while the remaining PSG signals

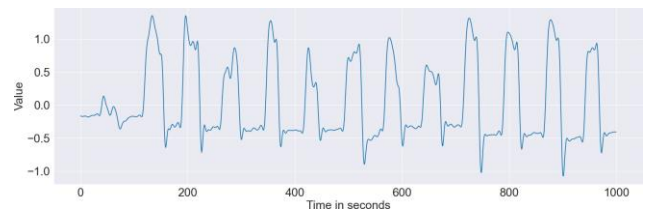


Fig. 1: PSG signal of 2000 seconds

were sampled at 10Hz. Annotation for each second of the data is provided. Each second is annotated with one of the five labels - central apnea, obstructive apnea, mixed apnea, hypopnea or normal. The first four levels denote the presence of some type of sleep apnea while the normal label denotes that the signal for that particular second has no apnea. In this work, the authors have used PSG signals. Clinically, the reference standard for diagnosing SA is PSG, which is also an effective method for monitoring sleep conditions. [18]. A representative of the PSG signal from one of the samples in the dataset is shown in Fig. 1. Further details regarding the sensors and patient demographics can be found from the original paper [17].

B. Data pre-processing

The authors have applied a variety of pre-processing techniques to each type of data. The details of which are given below-

1) *Data cleaning*: After analysing the data, many missing values were found in the dataset. Whenever a missing data value is found in any of the features (vital signs, PPG, ECG and PSG signals), the missing value along with the corresponding data were removed for all other features such that the total number of seconds of data remains same for all the features.

2) *Outlier detection and removal*: Outliers were detected in all the features. A value x is considered an outlier if $x - \mu > 2\sigma$ where μ and σ are the mean and standard deviation of that particular feature to which x belongs to. It is observed that 14% of vital signs and PSG data are outliers while 8% of ECG and PPG data are outliers. Hence a total of 14% data from the dataset were removed.

3) *Windowing*: In order to provide contextual information to the classification model, re-structure of the data was needed into fixed length windows containing a few seconds of data and an associated label for that window. Let the total number of seconds for which the clean and outlier removed data is available be N . Initially each vital sign feature in the data was organised as a 1D array of size N where each element corresponds to one second data and each element has an associated label. The PPG data was organised as a 2D array of size $N \times 80$ as each second has 80 data values (sampled at 80Hz). The ECG data of each lead was also organised as a 2D array of size $N \times 80$ as the sampling frequency was 80. The PSG data was also organised as a 2D array of size $N \times 10$ ($N \times 20$ in case of PSG flow).

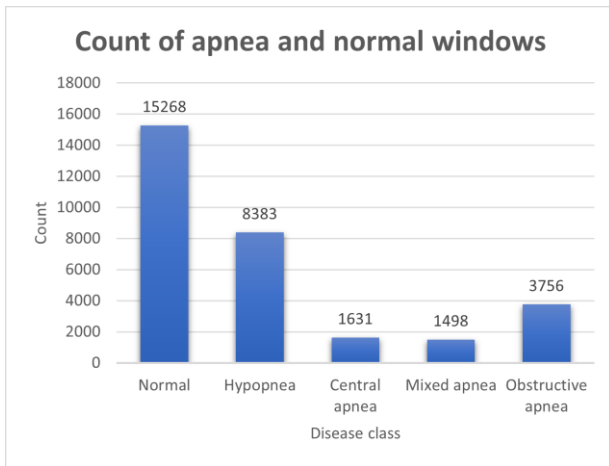


Fig. 2: Count of each individual classes in the dataset after windowing

These arrays were divided with N seconds into M windows of 60 seconds each. But windows were carefully selected by searching for a particular second of data that was labelled as one of the apnea class, then taking 30 seconds after and 29 seconds before that data point and considered it as one window. A sliding window of 60 seconds was created for windows belonging to the normal class (having no apnea labels) and checked whether any value in that 60 second window has any label other than normal. The normal class window was chosen that satisfies the above criteria. Hence, after windowing, each vital sign feature was represented by a $M \times 60$ matrix. The PPG feature was represented by a $M \times 60 \times 80$ matrix. Each ECG feature was represented by a $M \times 60 \times 80$ matrix whereas the other PSG features were represented by a $M \times 60 \times 10$ matrix.

4) *Class distribution*: After extracting windows from the data, it was found that windows belonging to normal class are much higher in number than the apnea classes. The total number of windows belonging to all of the apnea classes is 15268 while the number of normal windows is 61242. To mitigate this class imbalance normal windows were discarded and random selection of 15268 windows were done in order to balance the normal and apnea classes. Since, the number of data samples were relatively high, no data augmentation techniques were applied. The count of each individual apnea classes is shown in Fig. 2.

C. Deep learning model

In order to learn from this huge amount of data, a convolutional neural network (CNN) is trained. CNNs have been widely utilized in the realm of artificial intelligence (AI) in recent years [19]. The approach is a deep neural network that replicates the complex hierarchical organization of human vision. It has been effectively utilized in tasks such as image classification, natural language processing (NLP), and speech recognition [20]–[22]. CNN is utilized for developing sophisti-

TABLE I: Mapping of class labels to class names

Class Label	Class Name
0	Normal
1	Central apnea
2	Mixed apnea
3	Obstructive apnea
4	Hypopnea

cated signal analysis techniques because to its effectiveness in automatic feature extraction [23], [24]. An instance of CNN was employed by Kiranyaz et al. (2015) for the purpose of ECG categorization. In this case, the classification model was constructed using a straightforward and efficient implementation of a CNN called LeNet-5 [25].

1) *Modified LeNet-5*: The LeNet-5 model, as originally presented by [25], was specifically developed to address the task of character recognition. The architecture had an input layer, two convolutional layers, two fully connected layers, two max pooling layers, and an output layer, totaling seven layers. The specifics of every layer are outlined in LeCun's publication from 2015. In contrast to character recognition task, the time series utilized in this study consisted of one-dimensional data, which presents a notable distinction from the two-dimensional character recognition tasks. In contrast to the vast number of training samples often used in character or picture classification, the data sets included in this work were very limited, hence heightening the potential for overfitting. The feature maps, convolution layer strides, and fully-connected layer nodes in conventional LeNet-5 may not be appropriate for this particular scene. Hence, the modified LeNet-5 architecture from [26] was adopted for this task. They used 1D convolutional layers instead of 2D and used dropout layers to prevent overfitting. The overall model architecture is shown in Fig. 3.

2) *Loss Function*: The loss function in deep learning algorithms is an essential element that measures the difference between the projected outputs produced by the neural network and the actual values of the target in a given dataset. A loss function quantifies the performance of a neural network model in classification tasks. The goal is to minimize the loss value generated by the loss function.

In this work the categorical cross entropy loss function was used, which is one of the most popular loss functions for classification tasks and has been used in many research works [26], [27]. Formally, a set of M windows $\{X_i, y_i\}_{i=1}^M$ are taken, where X_i is the original window containing signal data and y_i is a class label of the window i.e., 0,1,2,3 or 4, the meanings of which are given in table I. The categorical cross entropy function is used to calculate the disparity between the predicted label \hat{y}_i and the actual label y_i .

$$J(\omega, b) \triangleq -\frac{1}{M} \sum_{l=1}^M y_{l,1} \log \hat{y}_{l,1} + \dots + y_{l,K} \log \hat{y}_{l,K} \quad (1)$$

where ω and b represent the weights and biases of modified LeNet-5 network layers, respectively. K is the number of class

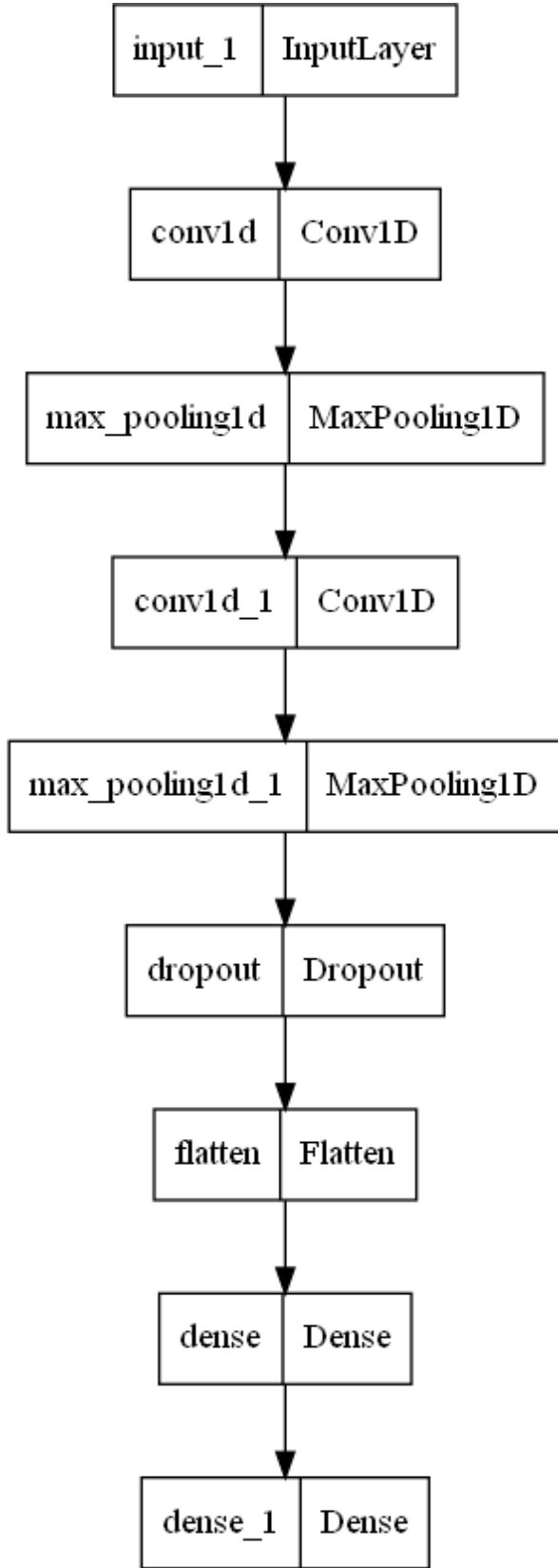


Fig. 3: Architecture of modified LeNet-5 adjusted for learning from time series data

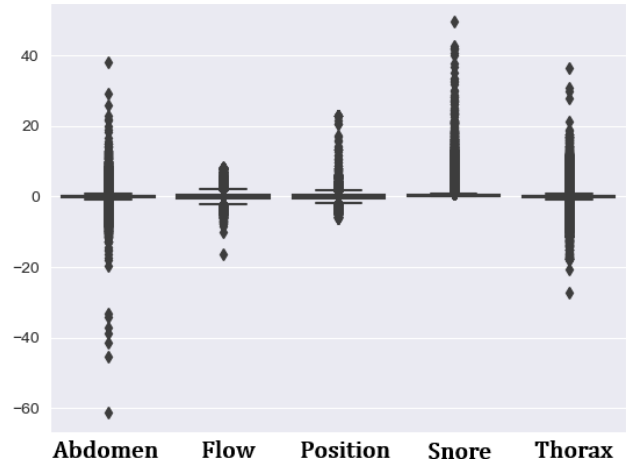


Fig. 4: Outliers marked as dots above and below the 75th and 25th percentile of each signal respectively

category ($K = 5$ in this case) and $\hat{y}_{l,k}$ corresponds to the softmax value of the k^{th} class category, defined as:

$$\hat{y}_{l,k} = \text{softmax}(z_k) = \frac{e^{z_k}}{\sum_{j=1}^K e^{z_j}} \quad (2)$$

IV. RESULTS AND DISCUSSION

In this section, the outcomes of experiments are shown. Among several data pre processing techniques as described in III-B the removal of outliers had a major impact on accuracy of the model and is briefly discussed in the following part. Before that a discussion on the evaluation metrics is provided, followed by the impact of outlier removal and finally the classification performance will be discussed in detail.

A. Evaluation metrics

The model performance was assessed using the following metrics: specificity (Sp), sensitivity (Sn), accuracy (Acc), and area under the curve (AUC), as demonstrated by the majority of other publications [26], [28]. They are defined below-

$$\text{specificity} = \frac{TN}{TN + FP}$$

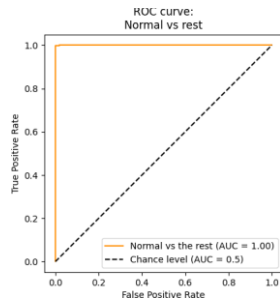
$$\text{sensitivity} = \frac{TP}{TP + FN}$$

$$\text{accuracy} = \frac{TP + TN}{TP + TN + FP + FN}$$

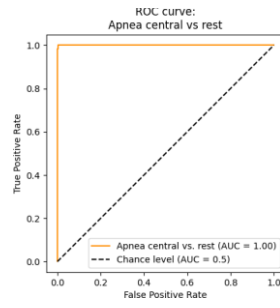
where FP , TP , FN and TN stands for 'false positive' and 'true positive', 'false negative' and 'true negative', respectively.

B. Impact of outlier removal

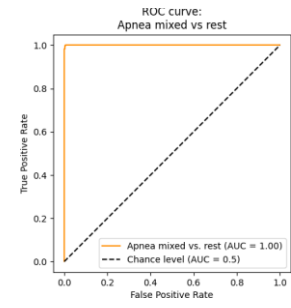
As mentioned in Sec. III-B2, PSG signals had around 14% outliers. The outliers can be visually portrayed in the box plots of each PSG signal in Fig. 4. Table II shows the accuracy of the model with and without outliers.



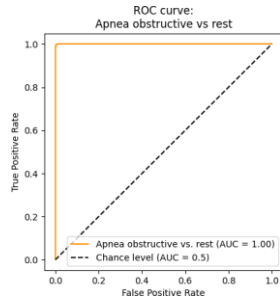
(a) ROC curve of Normal class



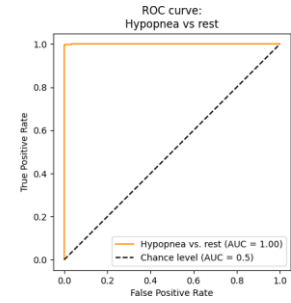
(b) ROC curve of Apnea central class



(c) ROC curve of Apnea mixed class



(d) ROC curve of Apnea obstructive class



(e) ROC curve of Hypopnea class

Fig. 5: ROC curve for the five classes

C. Model performance

The results of the performance of the proposed model is shown in Table III. Fairly good results have been achieved using only PSG data.

Very few works have used PSG data for SA detection. Hence, comparison with other baseline DL models is shown in Table IV. Model complexity and kernel size affects the overall accuracy of the model. The first model (CNN) is a very basic CNN model with only one 1D Convolutional Layer and two fully connected (FC) layers. The convolutional layer had kernel size 5. For the second comparison, the modified LeNet5 was used but with kernel size 3 (K3) for all of its convolutional layers. When compared to the same architecture with kernel size 5 (K5), it can be seen that even the kernel size is a crucial aspect for the model to learn properly. The kernel size determines features from how many times frames of data points are being extracted at a time. A smaller kernel size will extract too little features which may not be enough to learn the differences among various classes, while a bigger kernel size may extract ambiguous features as the receptive field will be too large. Hence, an optimal kernel size needs to be determined. The final proposed model uses kernel size 5.

No work was found that have done multi class classification of SA. [28] have done binary classification, i.e., to detect

whether a person has sleep apnea or not using PSG and SpO2 data. From Table III, accuracy of the first row indicates how well the model is able to detect normal class and its corresponding precision value (0.981) supports the fact that the model has indeed able to learn the distinction among normal vs. other classes and the corresponding accuracy is not null accuracy. Hence, the accuracy value (97%) of normal class can be considered as the binary classification accuracy which is marginally better than the accuracy of [28]. After extensive literature search it was found that none of the works have done multi-class classification to detect the different types of apnea. Hence, comparative results with other works cannot be shown due to lack of experiments regarding multi-class SA detection in the literature. The Receiver Operating Characteristic (ROC) for each of the class is shown in Fig. 5.

V. CONCLUSION

This work presents a DL framework for detection of different types of SA based on CNNs using only PSG data. The DL framework is based on a modified LeNet5 CNN architecture adjusted for 1D signal data. This method demonstrated higher performance and generated state-of-the-art findings using a public dataset gathered from real-life settings. Its average accuracy was 94.26%.

In future it is proposed to incorporate more types of signals like ECG, PPG available in the dataset and also other derived data like SpO2 and heart beat data to further improve detection performance. Also, attempts need to be made to increase the number of samples of classes having less data to ensure all the classes are balanced using data augmentation techniques.

TABLE II: Accuracy of the model with and without outliers

Configuration	Accuracy %
With outliers	82.48
Without outliers	94.26

TABLE III: Results of the proposed model for detection of different types of Sleep Apnea. Class values are given in Table I

Class	Precision	Recall	F1 Score	Sensitivity	Specificity	Accuracy
0	0.981	0.973	0.977	0.97	0.98	0.97
1	0.952	0.892	0.921	0.908	0.997	0.908
2	0.961	0.927	0.944	0.912	0.998	0.912
3	0.946	0.942	0.944	0.96	0.991	0.96
4	0.929	0.962	0.945	0.962	0.974	0.963
Mean	0.954	0.939	0.946	0.942	0.982	0.9426

TABLE IV: Comparing the accuracy of each class for the proposed model with other deep learning models.

	CNN	Modified LeNet5-K3	Modified LeNet5-K5
0	0.78	0.963	0.97
1	0.712	0.88	0.908
2	0.723	0.897	0.912
3	0.756	0.93	0.96
4	0.764	0.951	0.962
Mean	0.747	0.924	0.942

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