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An Analytics of Sleep Apnea Classification using Caswideresnet Algorithm

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Abstract:

Sleep apnea is a common yet serious sleep disorder that affects millions of individuals worldwide. Timely and accurate detection of sleep apnea can significantly improve patient outcomes and quality of life. In this study, we propose an advanced approach for sleep apnea classification and prediction using the CasWideResNet algorithm. Our methodology includes preprocessing steps such as Z-score normalization to standardize the data and improve algorithm performance. Additionally, we employ an improved Pan-Tompkins algorithm for feature selection, which helps in identifying relevant features from physiological signals such as electrocardiogram (ECG) and oxygen saturation (SpO2) data. The CasWideResNet algorithm, known for its deep learning capabilities, is utilized for the classification and prediction tasks. This algorithm leverages the power of deep convolutional neural networks (CNNs) to automatically learn discriminative features from the input data and make accurate predictions. By integrating Z-score normalization, improved feature selection, and the CasWideResNet algorithm, our proposed system aims to achieve high accuracy in detecting and predicting sleep apnea episodes. We evaluate the performance of our approach using a comprehensive dataset containing a diverse range of sleep apnea cases. Our results demonstrate the effectiveness of Z-score normalization in improving data quality and the role of the improved Pan-Tompkins algorithm in selecting informative features.

Keywords: CasWideResNet, classification, deep learning, prediction, Sleep apnea.

I. Introduction

Disruptions to the sleep cycle have a significant impact on people's well-being and health. One of the most common sleep disorders is obstructive sleep apnea (OSA), which happens repeatedly while sleep [1]. The blockage of the upper airway causes a ten-second pause in breathing in patients with OSA. The person gets up and keeps breathing since their oxygen saturation drops when they stop breathing [2]. The severity of sleep apnea syndrome can be evaluated using many metrics, one of which is the apnea and hypopnea index (AHI) [3]. A high number of episodes each hour is used to calculate the AHI. An hourly episode frequency for a moderate OSA patient ranges from five to fifteen times [4]. Patients with mild symptoms had 15 or less episodes per hour, whereas those with severe symptoms have 30 or more episodes per hour [5-6]. Fatigue, sadness, and memory difficulties are all consequences of this issue, which has a profound impact on people's daily lives [7-8]. Stroke, arrhythmia, and myocardial interaction are all increased risks in moderate to severe OSA patients when they sleep. Consequently, a critical concern in this situation is the detection or prediction of OSA episodes [9-10]. All forms of sleep apnea can be reliably diagnosed using polysomnography. Electroencephalogram (EEG), electrocardiogram (ECG), respiration (Resp) signal, blood oxygen level, and eye movement data make up the polysomnogram (PSG) signal [11, 12]. Under the guidance of a sleep expert, this signal is captured throughout the night from individuals who are suspected of having a sleep disturbance. The expert has the option of using online monitoring or offline observation to identify sleep episodes. However, the professional finds this technique challenging. As say, it's a tedious process that demands undivided attention [13–14].

Adults can have sleep apnea syndrome (SAS) when their airways momentarily constrict while they sleep, preventing air from reaching their lungs [15]. If this happens, cannot be able to breathe for almost ten seconds. One typical adverse effect is a drop in blood oxygen saturation, which might cause to wake up from sleep just to breathe [16]. It is believed that intermittent hypoxia generated by repeated obstructive events that happen during sleep triggers an oxidative stress response and activates oxygen free radicals [17]. The most common pattern of sleep-associated hypoxia (SAS) events, based on whether the patient shows signs of respiratory effort, is known as Obstructive Sleep Apnea (OSA) and occurs when the air flow completely stops during a patient's sleep [18]. When these two symptoms occur simultaneously, it's called mixed sleep apnea (MSA). In this condition, the patient has a central respiratory arrest followed by an obstructive ventilator effort very quickly thereafter. Hypopnea, which occurs when part of the airway is partly obstructed, also lowers oxygen supply to the lungs and produces shallow, slow breathing [19–20].

The main contribution of the paper is:

- Dataset preprocessing using Zscore Normalization
- Feature Selection using improved Pan–Tompkins Algorithm
- Classification and Prediction using caswideResnet Algorithm

1.1 Motivation of the paper

The motivation behind this paper is to address the critical need for timely and accurate detection of sleep apnea, a widespread and serious sleep disorder impacting millions globally. By proposing an advanced approach that integrates cutting-edge techniques like Z-score normalization for data standardization, improved feature selection using the Pan-Tompkins algorithm, and the deep learning capabilities of CasWideResNet, we aim to significantly enhance the accuracy and efficacy of sleep apnea classification and prediction. This work is driven by the potential to improve patient outcomes and quality of life through more precise and efficient diagnosis and management of sleep apnea episodes.

II. Background study

Ahmed, S. et al. [1] The author found that by combining the most relevant questions, diagnostic accuracy for pediatric OSA can be increased, as part of these authors effort to study the predictive validity of affordable and simple test protocols like questionnaires. By using feature selection approaches, the authors were able to construct a new survey that outperformed the old ones in terms of accuracy. Dong, Q. et al. [4] these authors research introduces a technique for identifying OSA using a convolutional neural network. A variety of augmentation techniques were investigated for the validating dataset, in addition to the conventional data augmentation for the training dataset. Improving identification accuracy was possible with the help of representation learning. Increasing the size of the neural network and the quantity of labelled datasets can further enhance the accuracy. Learning, M. U. S. M. [8] the findings show that self-reported symptoms and readily accessible characteristics for modeling provide excellent results when using a machine learning technique to predict OSA. As a quick and inexpensive supplementary tool, it might be used by doctors or medical personnel to assess individuals at high risk of OSA. Manoochehri, Z. et al. [10] while comparing the two models that were examined, the C5.0 algorithm outperformed LRM, which had an accuracy of 0.737 and a specificity of 0.78, compared to another model. So, instead of using PSG, C5.0 decision trees can be utilized to diagnose OSA patients. Mencar, C. et al. [12] Early screening and diagnosis of OSAS was essential for the use of an efficient treatment for treating the illness. This can be achieved by addressing a current important research topic on how to categorize individuals with a probable diagnosis of OSAS based on the severity of their illness. Onargan, A. et al. [14] The goal of this study was to create a signal processing method that could use multi-channel EEG data to distinguish between individuals with apnea and healthy controls. The "EMD" method, a multivariate extension of the popular signal separation technique, was used for the EEG signal analysis. Phan, H. et al. [16] the author provide a multi-task convolutional neural network (CNN) architecture for automated sleep staging, which combines categorization and prediction. The goal of the framework, which was driven by the interdependence of sleep epochs, was to classify an input epoch and forecast its neighbors' labels in the context output all at once.

Table 1: Comparison table for sleep apnea prediction methods

Author	**Year**	**Methodology**	**Advantage**	**Limitation**
Alimardani, M., & de Moor, G.	2021	SVM	The advantage of this study lies in its use of EEG signals to not only detect apnea episodes but also classify their severity and types accurately.	The research has certain limitations, one of which is that it only used 25 apnea patients whose EEG data were taken.
Johnson et al.	2020	Sleep apnea prediction model developed for African Americans	Develops a tailored prediction model for sleep apnea in a specific demographic group, improving accuracy and relevance of diagnostic tools.	Can lack generalizability to other populations or ethnicities, requires validation in diverse cohorts.
Mazzotti et al.	2019	Symptom	Determines which	Focuses on symptom

		subtypes of obstructive sleep apnea predict incidence of cardiovascular outcomes	subtypes of sleep apnea symptoms are associated with worse cardiovascular outcomes; this information can then be used to develop more tailored interventions.	subtypes and cardiovascular outcomes, cannot cover all aspects of sleep apnea diagnosis and management.
Taghizadegan et al.	2021	Obstructive sleep apnea event prediction using recurrence plots and CNNs	Utilizes recurrence plots and CNNs for predicting obstructive sleep apnea events, providing a data-driven approach for event detection.	Relies on specific signal processing and machine learning techniques, can require expertise for implementation and interpretation.
Alimardani & de Moor	2021	Automatic Classification of Sleep Apnea Type and Severity using EEG Signals	Provides an automated approach for classifying sleep apnea types and severity using EEG signals, aiding in accurate diagnosis and management.	Limited to EEG-based classification, cannot capture all aspects of sleep apnea diagnosis such as respiratory events.

2.1 Problem definition

The problem addressed in this study is the need for improved methods of detecting and predicting sleep apnea. Despite being a common and serious sleep disorder with significant impact on patient outcomes and quality of life, accurate detection remains a challenge. The study aims to develop an advanced approach using the CasWideResNet algorithm, combined with Z-score normalization and an improved Pan-Tompkins algorithm for feature selection, to enhance the accuracy of sleep apnea classification and prediction.

III. Materials and methods

Research papers and reports often include in this section that details the procedures used to gather data. The research process is described in great detail so that readers can comprehend and carry out the same experiment or study. If the study’s findings are to be believed and replicated, this part is crucial.

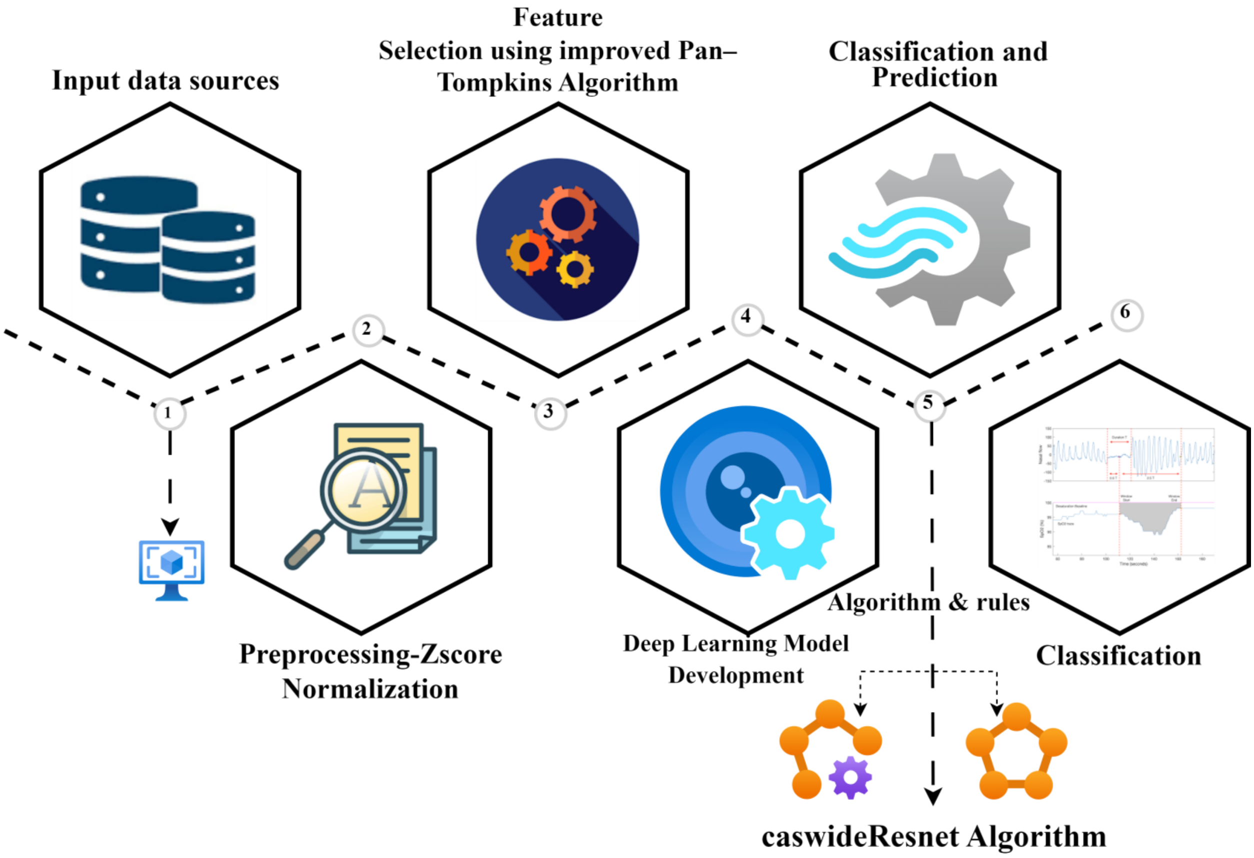

Figure 1: Overall architecture

3.1 Dataset collection

The dataset was collected from Kaggle website https://www.kaggle.com/competitions/sleepapneadetection

3.2 Preprocessing-Zscore Normalization

Data pre-processing is cleaning up the raw data before using it. Simply said, data obtained from various input characteristics is often obtained in an unusable raw format, making analysis a challenging task. Therefore, certain procedures are followed to transform the data into an accurate dataset. Data pre-processing is the name given to this procedure. Data that is inconsistent, noisy, or missing values is common in real-world datasets, making it difficult to analyze them further.

Using the Z-score Normalized Data Pre-processing model, we conduct missing value analysis to improve the outcomes of this work. To fill in the blanks in the database, our study makes use of Z-Score Normalized Data Pre-processing. Using the formula score deviation/standard deviation in a database, it is also used to standardize scores on the same scale. Here we can get the number of standard deviations for the provided data point from the mean. A schematic of the Z-score normalized data preparation model is shown in Fig. 2.

It is composed of thirteen characteristics, denoted as 'n', where 'n'= 13', and each component belongs to one of three distinct categories, '$T = T1, T2, T3$', which are objective, examination, and subjective, respectively.

$$PVM = \begin{bmatrix} P_{11} & P_{12} & P_{13} & P_{1n} \\ P_{21} & P_{22} & P_{23} & P_{2n} \\ \cdots & \cdots & \cdots & \cdots \\ P_{m1} & P_{m2} & P_{m3} & P_{mn} \end{bmatrix} \text{---------} (1)$$

For instance, according to Eq. (1), the first row of the data set for patient number "1" is represented by the values of features "i" for the feature "i" associated with patient number "1," and the subsequent rows are labeled "P11, P12, P13, and P1n."

Standard deviation of features

$$(\sigma) = \sqrt{\frac{\sum_{i=1}^{n}(F_i - \mu_i)}{n}} \text{-----------------} (2)$$

Each feature's value 'Fi'and the mean of features μ_i'relative to the total number of features n' are used to estimate the standard deviation of the overall patient vector matrix, as shown in Eq. (3). After that, we can estimate each feature's log-transformed Z-score function using the formula below.

$$Z - score(LT) = \frac{1n(F_{ij}) - 1n(\mu_i)}{\sigma[1n(F_i)]} \text{---------------} (3)$$

As a general rule, if the length is smaller than the maximum limit, then the Z-score is at least one standard deviation higher than the mean. After normalizing the data, log transformed Z-scores are shown below in pseudo code form.

The goal of pre-processing the raw information for sleep apnea disease with enhanced accuracy and speed to predict heart disease stays the same as in the previous method. Here, the missing values are filled in using Z-score log-transformation as part of the pre-processing. After that, we assess the lower and higher limits using the initialized lower and upper thresholds, and we normalize the log-transformed Z-score function. Lastly, this is used to standardize the various patient characteristics and convert them to the same magnitude. Using this method helps improve the accuracy and speed of heart disease prediction by ensuring that the findings are independent on the data's size; this is because the algorithm's sole function is to reject the quantity.

Data normalization is a preprocessing step that involves decomposing data into its component numerical properties in order to provide a range of acceptable values. Normalization via decimal scaling, z-score normalization and min-max normalization are some of the most common approaches used for this purpose. Equation 4 shows how Z-score normalization expands the previously unknown range of values for the v_i attribute from E to$v$.

$$v' = \frac{v_i - E_i}{std(E)} \text{------------------} (4)$$

Description:

v' = outcome of the standardization parameter

v = the attribute's value that has to be normalized

E_i = the average worth of the property

$std(E)$ = characteristic of standard deviation E

3.3 Feature Selection using improved Pan–Tompkins Algorithm

One method for processing data is the enhanced Pan-Tompkins algorithm, which is mainly used for the purpose of detecting QRS complexes in ECG signals. By improving the feature extraction process or adding new preprocessing stages, it improves upon the original Pan-Tompkins technique. In order to perform tasks such as arrhythmia diagnosis or heart rate variability analysis, this enhanced algorithm's feature selection process entails selecting the most useful features retrieved from the ECG signal.

The first step was to use the Butterworth band-pass filter to limit the ECG signal to a frequency range of 5–15 Hz. A five-point derivative was used to distinguish the signal, and subsequently, it was squared one point at a time after filtering. Afterwards, an integrated energy signal was generated from the squared ECG signal. The QRS peaks in the filtered ECG signal and the integrated energy signal were identified using two sets of adaptive thresholds. The peaks were re-detected using optimization thereafter. To start recognising a T wave, had to make sure the RR interval wasn't more than 360 ms. The missing beats were located using a searching back technique in cases where the RR interval was greater than the RR interval missed limit (RRML). Because they were derived from the operating signal and noise peak levels seen in the continuously processed signals, the thresholds thereafter adjust themselves to match the signal's properties. Iterative peak level estimator was used to compute the signal and noise peak levels in this approach. It is necessary to determine whether a freshly discovered peak is signal or noise before proceeding. The detection threshold was determined using Equation (5).

$DT = NPL + TC \times (QRSPL - NPL)$ ------------- (5)

The detection threshold (DT), noise peak level (NPL), threshold coefficient (TC), and QRS signal peak level (QRSPL) are all defined here. With this method, TC equals 0.25.

Afterwards, in order to rule out the chance of a false alarm, a 200 ms refractory blanking technique was used. The next step was to identify the QRS locations by calculating the peak points across all detections.

$y[n] = x[n] - x[n - N]$ ------------ (6)

where:

- $x[n]$ is the input signal.
- $y[n]$ is the differentiated output signal.
- N is the time delay for differentiation, typically chosen as 5 samples.

$y_{squared}[n] = y[n]^2$ ------------------ (7)

Where $y_{squared}[n]$ represents the squared output of the differentiation step.

$y_{integrated}[n] = \sum_{i=n-M}^{n} Y_{squared}[i]$ ---------------- (8)

where:

- $y_{integrated}[n]$ is the integrated output signal.
- MM is the integration window size, typically chosen as 30 to 150 samples.

3.4 Classification and Prediction using caswideResnet Algorithm

The CasWideResNet algorithm is a deep learning model designed for ECG signal classification and prediction tasks, particularly in the context of cancer detection and diagnosis from medical data like ECG. It leverages ResNet architecture with cascading layers to effectively capture intricate patterns and features within the ECG signals. Classification involves categorizing signals into different classes, while prediction tasks can include estimating disease progression or treatment response based on ECG signal data.

It uses a label encoder to standardize the input, in particular. We substitute the labels without numbers with their numerical equivalents. Word counts, textual frequency, or TF-IDF can be transformed into an integer sequence or vector with a binary coefficient using the Tokenize tool.

The total number of times a certain token occurs in a particular content record is known as Tf, or token frequency. The proportion of token occurrences in the content record as a percentage of all tokens, as calculated in equation 9.

$\mathrm{tf}_{\mathrm{ij}} = \frac{\mathrm{n}_{\mathrm{ij}}}{\sum_{\mathrm{k}} \mathrm{n}_{\mathrm{ij}}}$------ (9)

Researchers in the field of statistics use the Inverse Data Frequency (idf) statistic to find the frequency with which unexpected tokens appear in historical data. Tokens that appear infrequently in the record document are more likely to be (10)

$\mathrm{df(w)} = \log\left(\frac{\mathrm{N}}{\mathrm{df_i}}\right)$ ------- (10)

By combining a word's TF score (3) with its IDF score (w) (4), we can get its TF-IDF score (w). To be more precise, I am referring to equation 11.

$\mathrm{W}_{\mathrm{i,j}} = \mathrm{tf}_{\mathrm{i,j}} \times \log\left(\frac{\mathrm{N}}{\mathrm{df_i}}\right)$ ------- (11)

$\mathrm{tf}_{\mathrm{i,j}}$= counting the occurrences of I in j
$\mathrm{df_i}$= records where I is the id value
N = the whole count of files

To begin training the model, the text to sequence tool is used to convert tokens into word sequences.

$\mathrm{argminU} \ \|\mathrm{D(N,X,T)} - \mathrm{D(N,X,T \cdot U)}\| + \lambda\Omega(\mathrm{U})$ ------- (12)

In line with what has been said so far, this structural optimization belongs to the class of problems called NP-hard due to its computational complexity of O(2n). It is well recognized that GAs garnered the most attention when applied to NP-hard problems. Thus, GA might be used to enhance the aforementioned design. One way to improve the architecture of a ResNet network is shown in Algorithm 1.

Consider the gene $vk(wij)$ as a switch that, when turned on, indicates whether the edges connecting nodes I and j are indeed linked. The only way for neurons I and j to be linked in ResNet is for $vk\ (Tij)$ to be set to 1. If it's not, the connection is destroyed.

In order to find an optimal network design, we evaluate each representation in equation 13 using the following evolution function.

$\mathrm{fitness} = \alpha\|\mathrm{D(N,X,T)} - \mathrm{D(N,X,T \cdot U)}\| + \lambda\Omega(\mathrm{U})$ ------ (13)

$\Omega(\mathrm{U}) = 1 - \frac{\sum_{\mathrm{k=1}}^{\mathrm{N}} \mathrm{u_k}}{\mathrm{N}}$ ------- (14)

Where and are weight-changing adaptive parameters that provide a search pressure between the loss function and the network's architecture in equation 15.

$z1 = |D(N, X, T) - D(N, X, T \cdot U)|$ ------- (15)

$z2 = \Omega(U)$ ----- (16)

$a = \frac{r}{\Sigma_1^{max} - z_1^{min}}$ ------- (17)

$r = \frac{1-r}{z_2^{max} - z_2^{min}}$ ------ (18)

Since the gene is either 1 or 0, when mutated it will become the latter (or 1).

From a methodology standpoint, GA operates as follows: in the present generation t, P(t) represents the parents and C(t) represents the offspring; the detailed implementation of GA is explained in Algorithm 1.

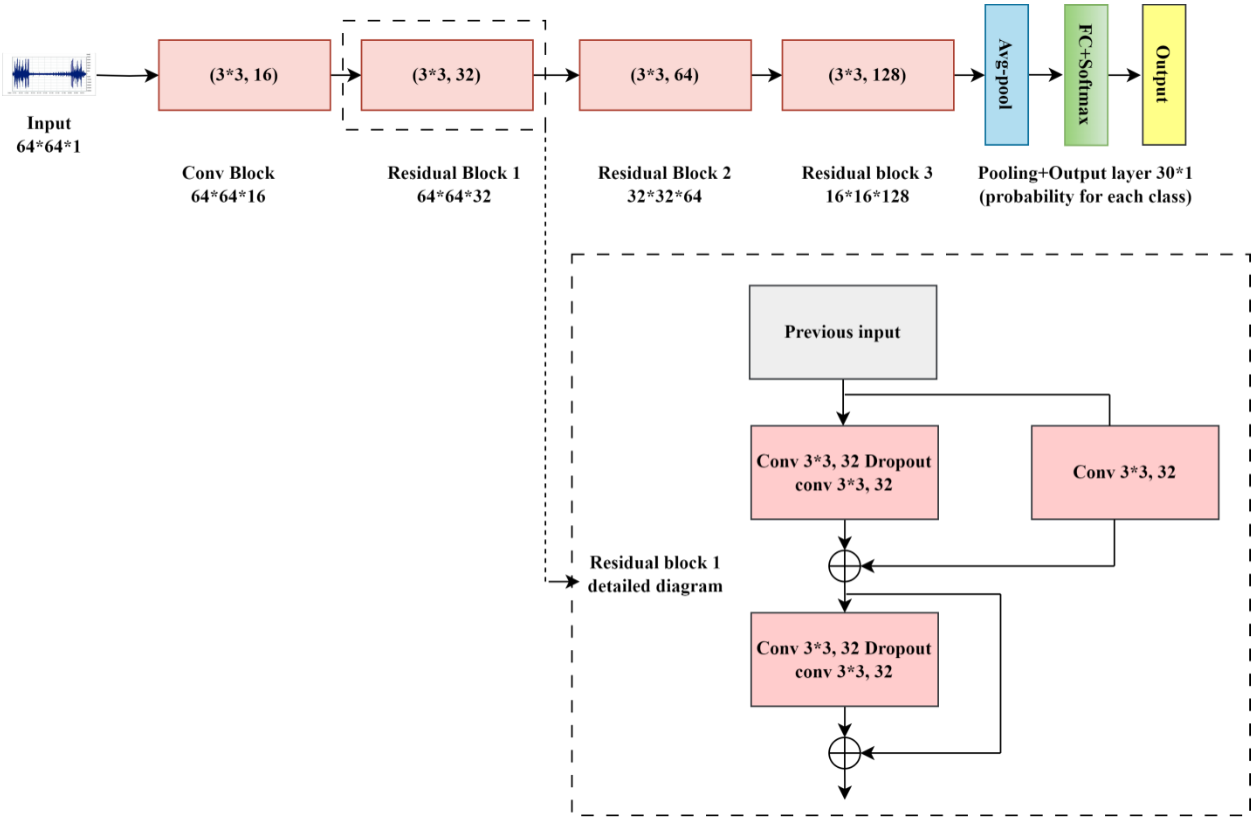

Figure 2: caswideResnet architecture

Algorithm 1: caswideResnet

Input:

- Preprocessed EEG signals from sleep apnea patients
- Label encoder for normalization
- Tokenizer for word-to-sequence conversion
- Transition matrix U for network structure optimization

Steps:

Algorithm:

1. Initialize the CasWideResNet model with a modified ResNet architecture suitable for sleep apnea classification.

$\Omega(U) = 1 - \frac{\sum_{k=1}^{N} u_k}{N}$

2. Preprocess the input EEG signals using the label encoder and tokenizer.
3. Apply TF-IDF transformation to the tokenized data to obtain word scores.
   $a = \frac{r}{\Sigma_1^{max} - Z_1^{min}}$
4. Train the CasWideResNet model using the preprocessed EEG data and the fitness function (equation 9) tailored for sleep apnea classification.

Optimize the network architecture using a genetic algorithm (GA) with the following steps:

- Generate an initial population of network structures (U) based on mutation rate and population size.
  $r = \frac{1-r}{Z_2^{max} - Z_2^{min}}$
- Evaluate the fitness of each network structure using the fitness function (equation 9) specific to sleep apnea classification.
- Select parent structures ($P(t)$) based on fitness scores and apply crossover and mutation to create child structures($C(t)$).

Output:

- Trained CasWideResNet model parameters
- Optimized network architecture (U)

IV. Results and discussion

The "Results and Discussion" section of a research paper or project report typically presents and analyzes the outcomes of the study or experiment. It serves as the core of the document where findings are interpreted, compared with existing literature, and implications are discussed. This section is crucial for understanding the significance of the research and its potential impact on the field.

4.1 Performance evaluation

$Accuracy = \frac{(TP + TN)}{(TP + FP + TN + FN)}$ ----------- (19)

$Precision = \frac{TP}{TP + FP}$ ------------ (20)

$Recall = \frac{TP}{TP + FN}$ -------------- (21)

$F1\,score = 2 * Precision * Recall / (Precision + Recall)$ --------- (22)

Table 2: Classification performance metrics comparison

	Algorithm	**Accuracy**	**Precision**	**Recall**	**F-measure**
Existing methods	Densenet	96.21	92.65	94.01	94.23
	VGG-16	97.35	93.87	95.10	95.07
	Resnet	98.11	95.32	96.75	97.14
Proposed methods	caswideResnet	99.62	97.11	97.84	98.21

The table 2 presents performance metrics for existing methods (Densenet, VGG-16, Resnet) and a proposed method (caswideResnet) across various evaluation criteria. Firstly, in terms of accuracy, caswideResnet outperforms all existing methods with an accuracy of 99.62%, showcasing its superior classification capability. When considering precision, which measures the ratio of correctly predicted positive instances, caswideResnet also exhibits the highest precision at 97.11%. Furthermore, in terms of recall (also known as sensitivity), which indicates the proportion of actual positive instances correctly identified, caswideResnet maintains a high value of 97.84%, highlighting its ability to capture most positive instances. Finally, the F-measure, which harmonizes precision and recall, demonstrates caswideResnet's robust performance with an F-measure of 98.21%, further underscoring its effectiveness in classification tasks compared to the existing methods.

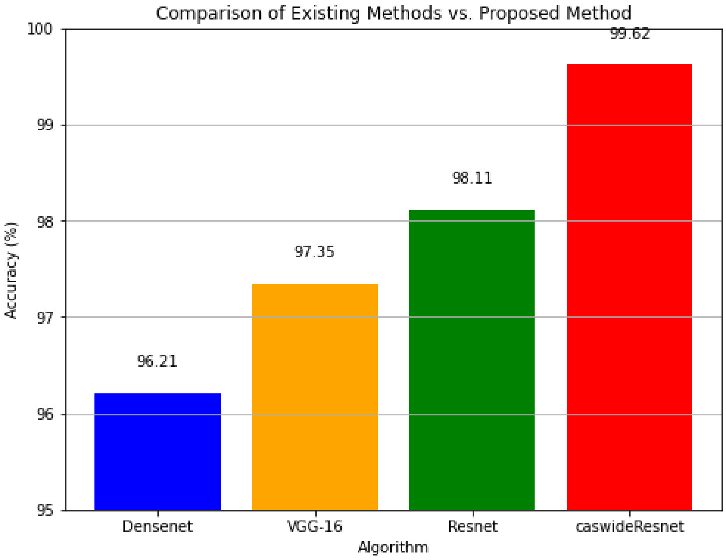

Figure 3: Accuracy comparison chart

A chart comparing accuracy is shown in figure 3. On one side, can see algorithms, and on the other, can see scores for accuracy.

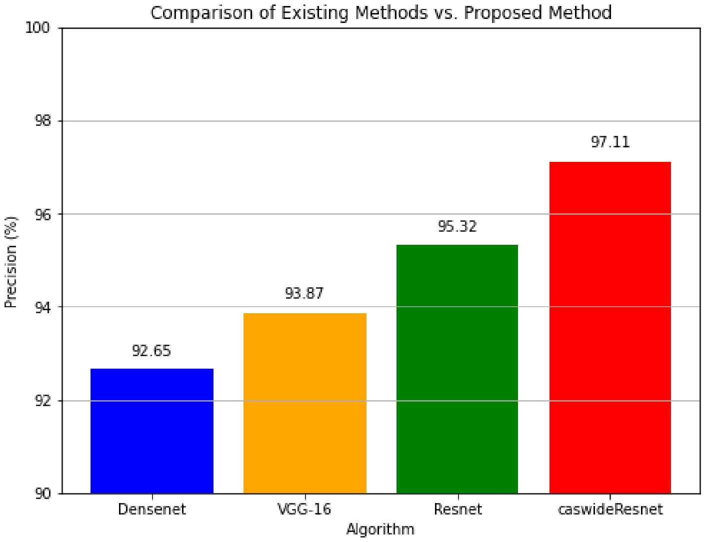

Figure 4: Precision values comparison chart

Figure 4 displays a chart comparing accuracy values. Algorithms are shown on the x-axis, while accuracy values are shown on the y-axis.

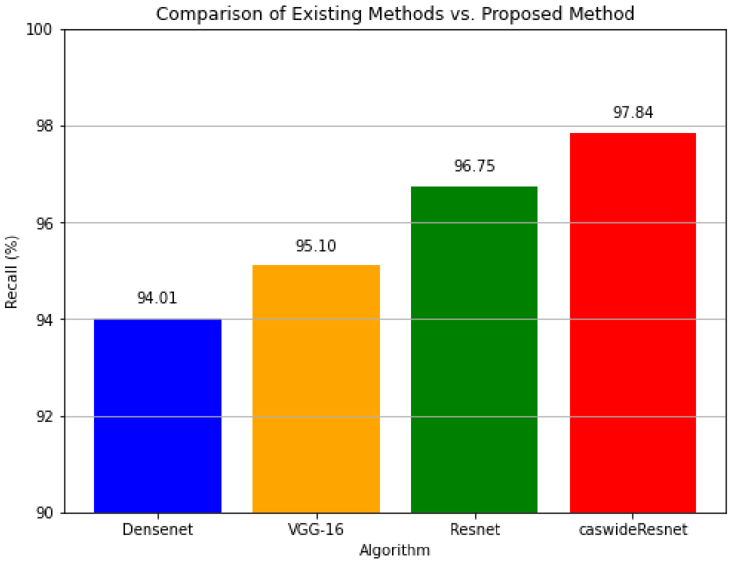

Figure 5: Recall comparison chart

Recall comparison table is shown in picture 5. Recall values are shown on the y-axis and algorithms are shown on the x-axis.

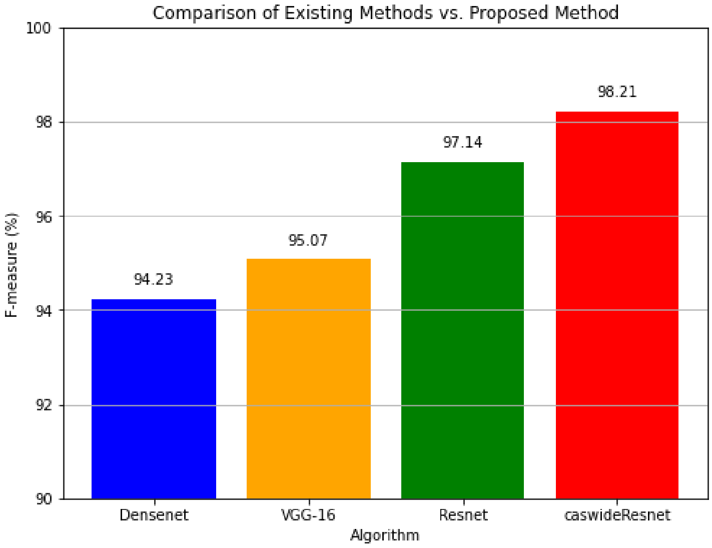

Figure 6: F-measure value comparison chart

Figure 6 displays a chart comparing F-measure values. On one side, we have algorithms, and on the other, we have the F-measure value.

V. Conclusion

In conclusion, our study presents a novel and effective approach for sleep apnea classification and prediction using the CasWideResNet algorithm. Through the integration of Z-score normalization for data standardization, improved Pan-Tompkins algorithm for feature selection, and the deep learning capabilities of CasWideResNet, we aimed to enhance the accuracy and reliability of sleep apnea detection and prediction. Our results on a diverse dataset affirm the effectiveness of these methodologies, showcasing improved data quality with Z-score normalization and the identification of relevant features crucial for accurate classification and prediction. Firstly, in terms of accuracy, caswideResnet outperforms all existing methods with an accuracy of 99.62%, showcasing its superior classification capability. This study contributes to advancing the field of sleep disorder diagnosis and highlights the potential of advanced algorithms in improving patient outcomes and quality of life through timely and accurate sleep apnea detection. Future research can further explore optimization strategies and real-time implementation of these algorithms in clinical settings to translate these findings into practical healthcare solutions.

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