Automated Sleep Apnea Prediction Using Deep Learning for Improved Health

Major Project Report

Submitted in Partial Fulfillment of the
Requirements for the Degree of

BACHELOR OF TECHNOLOGY
IN
INFORMATION AND COMMUNICATION TECHNOLOGY

By
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Under the Guidance of
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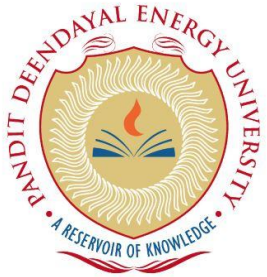

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May 2025

Certificate of Originality of Work

I hereby declare that the B.Tech. Project entitled **Automated Sleep Apnea Prediction Using Deep Learning for Improved Health** submitted by me for the partial fulfillment of the degree of Bachelor of Technology to the Department of Information and Communication Technology Engineering at the School of Technology, Pandit Deendayal Energy University, Gandhinagar, is the original record of the project work carried out by me under the supervision of Dr. Manish Kumar.

I also declare that this written submission adheres to the University guidelines for its originality, and proper citations and references have been included wherever required.

I also declare that I have maintained high academic honesty and integrity and have not falsified any data in my submission.

I also understand that violating any guidelines in this regard will attract disciplinary action by the institute.

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Designation of the Supervisor: Assistant Professor, Department of ECE

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Certificate from the Project Supervisor/Head

This is to certify that the Comprehensive Project Report entitled **Automated Sleep Apnea Prediction Using Deep Learning for Improved Health** submitted by **Patel Mitalikumari, Patel Het**, Roll No. **21BIT017, 21BIT279D** towards fractional compliance of the requirements for the award of a degree in Bachelor of Technology in the field of **Information and Communication Technology** Engineering from the **School of Technology**, Pandit Deendayal Energy University, Gandhinagar is a record of his efforts done under our supervision and assistance. The student's work has, in our judgment, attained a sufficient level to be accepted for assessment. To the best of our knowledge, the results of this significant project effort have not been submitted to any other University or Institution for the granting of any degree or certificate.

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Acknowledgement

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Patel Mitalikumari
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Abstract

A person with sleep apnea (SA), a dangerous and frequently disregarded sleep disorder, experiences frequent pauses in breathing while they are asleep. Poor sleep quality can result from this because it lowers oxygen levels in the body. Overnight polysomnography (PSG), which is costly and uncomfortable for patients, is the standard method of diagnosing this illness.

To make the diagnosis of sleep apnea more efficient and widely accessible, this study introduces an automated approach using deep learning techniques applied to ECG signals from the PhysioNet Apnea-ECG database. Prior to model training, the ECG data undergoes thorough preprocessing, including the extraction of RR intervals and normalization of signal amplitudes to ensure consistency.

Two deep learning architectures are developed and evaluated: a hybrid model combining Convolutional Neural Networks (CNN) with Bidirectional Long Short-Term Memory (BiLSTM), and a one-dimensional Residual Network (ResNet1D). The CNN+BiLSTM model achieved a training accuracy of 98.07% and a validation accuracy of 95.39%. Additionally, it recorded a ROC-AUC score of 0.96, highlighting its effectiveness, particularly in accurately detecting apnea events.

On the other hand, the ResNet1D model demonstrated slightly better overall accuracy, with training and validation accuracies of 98.94% and 96.10%, respectively. However, it tended to produce more false negatives, indicating a higher rate of missed apnea detections compared to the CNN+BiLSTM model.

Overall, both models showed good results in detecting sleep apnea. However, the CNN+BiLSTM model may be more reliable for medical use because it is better at catching actual apnea episodes. This study shows how deep learning can help improve the diagnosis of sleep disorders in a faster, easier, and non-invasive way.

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NOMENCLATURE

Term	Description
ECG	Electrocardiogram – records electrical activity of the heart.
CNN	Convolutional Neural Network – deep learning model for pattern recognition.
RR	RR Interval – time between successive R-waves in ECG, used in heart rate variability analysis.
AUC	Area Under the Curve – a performance metric for classification models.
EEG	Electroencephalogram – records electrical activity of the brain.
SA	Sleep Apnea – a sleep disorder involving pauses in breathing.
ROC	Receiver Operating Characteristic – a graph showing the diagnostic ability of a classifier.
OSA	Obstructive Sleep Apnea – a sleep disorder due to airway blockage.
REM	Rapid Eye Movement – sleep stage with vivid dreams and muscle atonia.
CSA	Central Sleep Apnea – a sleep disorder where breathing stops due to a lack of respiratory effort.
PSG	Polysomnography – a comprehensive sleep study used to diagnose sleep disorders.
BCE	Binary Cross Entropy – loss function used in binary classification.
NREM	Non-Rapid Eye Movement – sleep stages excluding REM, including deep sleep.
MSA	Mixed Sleep Apnea – a combination of OSA and CSA.
RRI	RR Interval – another term for heart beat interval (see RR).
HRV	Heart Rate Variability – variation in time intervals between heartbeats.
QRS	QRS Complex – ECG waveform representing ventricular depolarization.
SE	Standard Error – a statistical term representing estimation precision.

Chapter 1: Introduction

Sleep is one of the most essential and rejuvenating processes in human life. It's not just a time of rest, but a vital biological function that supports overall health and well-being. Unfortunately, various sleep disorders can disrupt the quality, timing, and duration of sleep, potentially leading to serious health issues. Among the many roles sleep plays, it significantly impacts our cognitive performance, helps consolidate memories, and supports emotional balance — all of which contribute to both mental and physical health. One common and often underdiagnosed sleep disorder is sleep apnea (SA). This condition is marked by repeated interruptions in breathing during sleep, which can lead to fragmented rest and decreased oxygen levels. Studies estimate that sleep apnea affects approximately 5% to 21% of the adult population [1]. Sleep itself consists of two major phases: Rapid Eye Movement (REM) sleep and Non-REM (NREM) sleep. REM sleep is associated with vivid dreams, increased brain activity, and elevated sympathetic nervous system responses, including fluctuations in heart rate and blood flow. In contrast, NREM sleep is generally more restorative, marked by a slower heart rate and reduced oxygen consumption. While sleep apnea can occur during any phase, it is particularly common during REM sleep due to the greater relaxation of the muscles that support the upper airway.

The medical industry has greatly benefited from advancements in machine learning and automated disease diagnosis, particularly in detecting and managing sleep disorders like sleep apnea. SA is a serious medical condition that negatively impacts health by causing breathing disturbances during sleep [2]. It is one of the main causes of mortality among infants and the elderly. SA is mainly characterized by the recurrent breathing roles that last for 10-20 seconds, leading to significant falls in the oxygen saturation level in the blood. This condition affects about 15% of men and 5% of women [3]. Repeated breathing disorders not only lead to sleep disorders but also increase the risk of severe health complications such as heart failure, stroke, seizures, and other neurological conditions.

Sleep apnea is generally classified into three primary types: obstructive sleep apnea (OSA), central sleep apnea (CSA), and mixed sleep apnea (MSA). Obstructive Sleep Apnea (OSA) is the most common type of sleep apnea and occurs when the upper airway repeatedly

becomes blocked during sleep. These blockages can cause drops in blood oxygen levels and, in more severe cases, may completely collapse the airway. People with OSA often wake up multiple times throughout the night as their body reacts to the lack of oxygen. Over time, this disruption in sleep and oxygen flow can contribute to serious health issues, including high blood pressure, heart disease, irregular heartbeat (arrhythmia), stroke, and other cardiovascular conditions. To evaluate the severity of sleep apnea, doctors use the Apnea-Hypopnea Index (AHI), which measures how many apnea (complete stoppage of breathing) and hypopnea (partial blockage) events occur per hour of sleep.

Late-night sleeping habits have been associated with heightened mortality risk due to a variety of contributing factors. Individuals who stay up late are more prone to engage in unhealthy behaviours such as smoking and excessive alcohol consumption, which negatively impact overall health. Moreover, their internal circadian rhythms often conflict with typical societal schedules, leading to chronic sleep deprivation and various health complications. Disruption of metabolic processes due to irregular sleep patterns further elevates the risk of conditions like cardiovascular diseases and diabetes. In the context of sleep-related disorders, Central Sleep Apnea (CSA) results from a failure of the brain to send appropriate respiratory signals, causing temporary pauses in breathing during sleep. These episodes lead to oxygen desaturation and fragmented sleep, posing serious health risks in severe cases. Mixed Sleep Apnea (MSA), which combines features of both Obstructive Sleep Apnea (OSA) and CSA, can result in decreased oxygen levels and insufficient airflow into the lungs. Frequent sleep interruptions in such patients are often caused by the brain's response to oxygen deficiency. OSA, especially prevalent among individuals with cardiovascular conditions, is linked to ailments such as heart failure, stroke, arrhythmias, coronary artery disease, and hypertension [7][8]. During CSA events, the impaired neural signaling disrupts respiratory muscle coordination, resulting in airflow cessation and lowered blood oxygen, which exacerbates sleep disturbances and can lead to severe medical consequences [9]. Electroencephalogram (EEG) signals are crucial in detecting Sleep Apnea (SA), as they capture vital information on brain activity that is essential for understanding and diagnosing sleep disorders.

Various studying algorithms can successfully extract those functions from EEG statistics, automating the system of detecting SA events. Most research utilizes indicators from Polysomnography (PSG) data for SA detection. Additionally, desaturation statistics, consisting of SaO_2 (oxygen saturation) and airflow indicators, can resource in identifying SA occasions. Analyzing time-area and frequency-area capabilities of desaturation statistics in addition helps check the intensity and severity of SA occasions.

1.1 Brief History of Sleep Apnea

The physiological understanding of sleep apnea began in the 1960s when researchers first noticed repeated airway blockages during sleep. Early on, it was often mistaken for conditions like narcolepsy due to symptoms such as excessive daytime sleepiness. By the 1970s, the term "Obstructive Sleep Apnea Syndrome" (OSAS) was introduced to describe sleep apnea caused by repeated upper airway collapse despite ongoing breathing effort.

In the 1980s, polysomnography (PSG) became the standard diagnostic tool, monitoring signals like EEG, ECG, oxygen levels, airflow, and breathing effort overnight to detect apneic events. Around the same time, the Apnea-Hypopnea Index (AHI) was established to gauge the severity of the disorder.

From the 1990s onward, research revealed strong links between sleep apnea and serious health issues such as hypertension, heart disease, stroke, metabolic problems, and cognitive decline. This shifted the view of sleep apnea from a minor annoyance to a major public health concern.

More recently, advances in signal processing, machine learning, and wearable technology have led to new, less invasive, and more affordable diagnostic methods. AI-driven analysis of biosignals like EEG, ECG, and oxygen saturation now enables accurate, automated detection of sleep apnea, reducing reliance on costly PSG tests. Additionally, home sleep testing and mobile health solutions have made diagnosis more accessible. Today, sleep apnea research spans multiple fields, aiming to improve early detection, personalized treatment, and long-term patient care.

1.2 Problem Statement

Sleep apnea is a common yet often overlooked sleep disorder that causes frequent pauses in breathing during sleep. These interruptions can lower blood oxygen levels and disrupt normal sleep cycles, leading to daytime fatigue and other health complications. While traditional diagnostic methods like overnight polysomnography offer accurate assessments, they are costly, time-consuming, and inconvenient for many patients. This highlights the growing need for a reliable, efficient, and automated system that can detect and classify sleep apnea events using physiological signals, making diagnosis more accessible and less burdensome.

1.3 Motivation

The rising number of sleep-related disorders and the serious health risks linked to sleep apnea highlight the need for early and accurate diagnosis. Recent progress in machine learning and signal processing has made it possible to create automated systems that can detect sleep apnea in real time. Using EEG signals, which carry detailed brain activity information, can help improve the precision and dependability of these detection systems.

1.4 Objective

Develop a deep learning model that can accurately identify and categorize sleep apnea episodes using physiological signals (such as EEG, ECG, and SpO_2) to allow for early diagnosis. The model aims to identify potential sleep apnea risks before severe symptoms arise, allowing timely intervention to prevent cardiovascular or metabolic complications.

Chapter 2: Literature Review & Problem Identification

2.1 Literature review

Many research efforts have focused on detecting sleep apnea using various machine learning and deep learning techniques. These studies often apply unique preprocessing strategies to the data, which play a crucial role in enhancing the accuracy and overall effectiveness of the models.

Table 1. Literature Survey on Sleep Apnea Detection

Author [citation]	Signal Type	Model	Accuracy
[10]	EEG	FCNN Bi-LSTM	93.25%
[11]	EEG	Linear Support Vector Machine (LSVM)	94.81%
[12]	EEG	Decision Tree	95.10%
[13]	EEG	Support Vector Machine	95%
[14]	EEG	Support Vector Machine	94.33%
[15]	ECG	1D CNN + LSTM + DNN	79.45%
[16]	ECG	Support Vector Machine	90.87%
[17]	EEG	Convolutional Neural Network	86.9%
[18]	EEG	Convolutional Neural Networks + Recurrent Neural Networks	82.9%
[19]	ECG	1-D Convolutional Neural Network	85.8%
[20]	ECG	Artificial Neural Networks + Support Vector Machine	82.12%
[21]	ECG	Deep residual neural network (LeNet-5 CNN)	94.4%
[22]	ECG	K-nearest neighbour classifier	87.5%

Table 1 summarizes recent studies on sleep apnea detection using EEG and ECG signals, highlighting the models used, achieved accuracy, and corresponding preprocessing techniques.

Mahmud et al. (2021) [10] used a hybrid Fully Connected Neural Network (FCNN) and Bi-LSTM model on EEG signals and achieved 93.25% accuracy. They employed Variational Mode Decomposition (VMD) to extract intrinsic mode functions from the EEG signals before classification. Alam et al. (2024) [11] used a Linear Support Vector Machine (LSVM) with energy-efficient FPGA implementation and obtained 94.81% accuracy. Their preprocessing included artifact removal, bandpass filtering, and normalization to extract relevant EEG frequency bands. Gupta et al. (2020) [12] achieved 95.10% accuracy using a Decision Tree classifier after preprocessing EEG signals with Discrete Wavelet Transform (DWT) to extract sub-band frequency features. Vimala et al. (2019) [13] used an SVM model with 95% accuracy, applying noise removal, bandpass filtering, and extracting statistical and spectral features from EEG signals. Wang et al. (2020) [14] also used SVM on EEG data, achieving 94.33% accuracy through EEG segmentation and FFT-based feature extraction.

Banluesombatkul et al. (2018) [15] achieved 79.45% accuracy using a hybrid model of 1D CNN, LSTM, and DNN on single-channel ECG data. Their preprocessing included denoising, R-peak detection, RR interval computation, and normalization. Sharma et al. (2019) [16] used an SVM model and achieved 90.87% accuracy by applying an Optimal Orthogonal Wavelet Filter Bank (OOWFB) to extract sub-band features from ECG signals. Vaquerizo-Villar et al. (2023) [17] employed a Convolutional Neural Network (CNN) model on EEG with 86.9% accuracy. Their preprocessing involved filtering, normalization, and epoch segmentation. Korkalainen et al. (2019) [18] combined CNN and Recurrent Neural Networks (RNNs), achieving 82.9% accuracy after applying Z-score normalization, resampling, artifact rejection, and windowing the EEG time-series data. ECG-based studies have also shown promising results Yeh et al. (2022) [19] used a 1D CNN model with 85.8% accuracy after decomposing ECG into subbands using filter banks and extracting features such as spectral energy.

Pinho et al. (2019) [20] combined Artificial Neural Networks (ANNs) and SVM, achieving 82.12% accuracy using feature selection techniques following signal denoising. Wang et al. (2019) [21] proposed a deep residual network (LeNet-5 CNN) with 94.4% accuracy based on RR intervals obtained through R-peak detection, followed by normalization and interpolation. Finally, Sharma and Sharma (2020) [22] used a K-nearest neighbour (KNN) classifier with 87.5% accuracy after applying VMD to ECG signals and extracting entropy-based features.

Overall, these studies demonstrate the importance of tailored preprocessing techniques such as filtering, wavelet decomposition, VMD, RR interval extraction, normalization, and segmentation in boosting model accuracy for sleep apnea detection using physiological signals.

2.2 Problem Identification and Research Gaps

One of the primary issues in current sleep apnea classification research is the dependence on small-scale or highly specific datasets. Many studies utilize data collected under controlled conditions or from limited demographic groups, which affects the model's ability to generalize across diverse populations. This lack of diversity can lead to biased results and reduced performance in real-world applications. Without broader, multi-center datasets that capture a wide range of physiological and demographic variations, the practical utility and robustness of these models remain questionable.

In addition to data limitations, preprocessing methods significantly influence model performance and reliability. Common techniques such as Butterworth filtering are used to eliminate noise from EEG and ECG signals, while RR interval (RRI) analysis—derived from QRS detection—is crucial for evaluating heart rate variability. Discrete Wavelet Transform (DWT) is another frequently used method for time-frequency analysis, enabling the decomposition of signals into subbands to extract meaningful temporal and spectral features. However, inconsistencies in preprocessing standards across studies can make it

difficult to compare results or replicate findings, highlighting the need for more standardized and validated signal processing pipelines.

Moreover, deep learning models such as CNNs and LSTMs are popular for their ability to capture intricate patterns in physiological signals. However, they typically demand large datasets and significant computational power for effective training. Their performance can decline when applied to limited or imbalanced data. In contrast, traditional machine learning approaches, which are also used either independently or in hybrid frameworks, depend heavily on manually extracted features and are highly influenced by the quality of feature selection. Optimization methods such as Adam are commonly employed for training deep networks, yet alternative strategies that could enhance model performance are seldom investigated. This gap presents opportunities to explore novel optimization techniques and model architectures that could yield improved results in sleep apnea classification.

Chapter 3: Proposed Methodology

Figure 1 illustrates the proposed framework for detecting sleep apnea through software simulation. The process begins with collecting ECG signal samples, which are then carefully preprocessed to eliminate noise and other unwanted artifacts. Once cleaned, the data is divided into training and testing sets and formatted to suit the input requirements of deep learning models. Next, an advanced deep learning model that integrates attention mechanisms is trained to effectively distinguish between apnea and non-apnea events. The model's performance is then assessed using validation and test datasets by measuring key metrics such as accuracy, sensitivity, and specificity. Additionally, a confusion matrix and detailed classification report are generated to provide deeper insights into the model's detection capabilities and any misclassification patterns. This comprehensive approach leverages deep learning to improve the accuracy and reliability of sleep apnea detection from ECG signals.

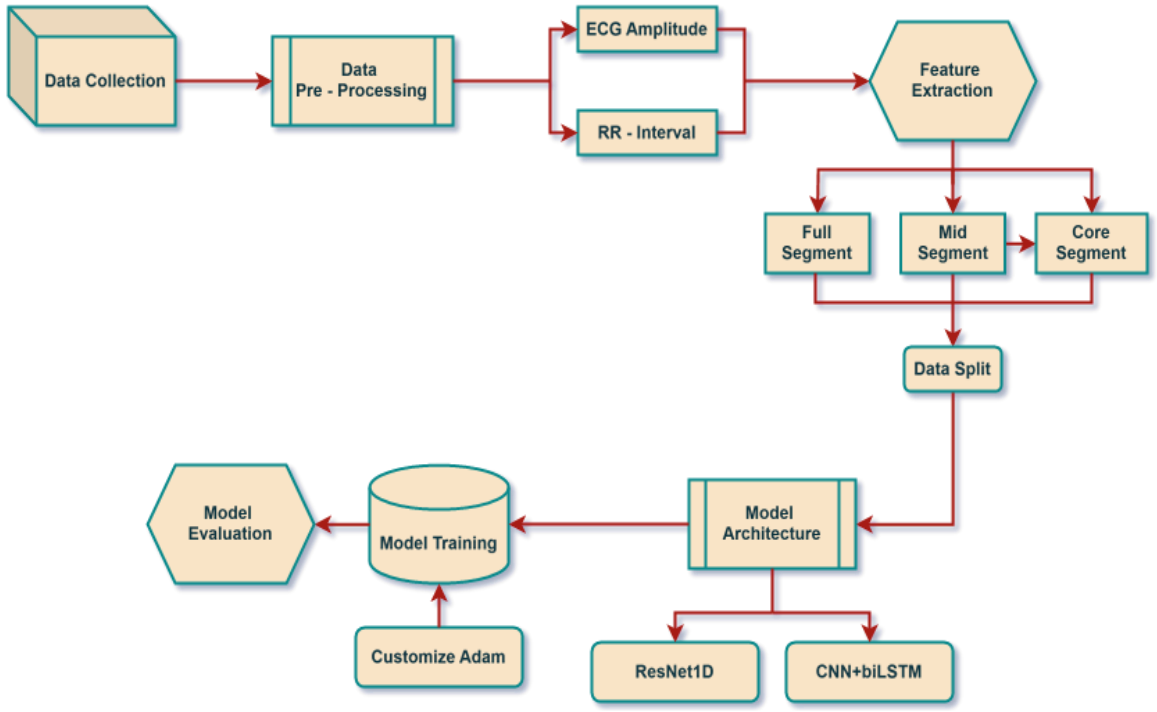

Fig 1. Proposed Overall Methodology Diagram

3.1 Dataset Description:

The Apnea-ECG Database, available on PhysioNet, consists of 70 ECG recordings. Each recording lasts roughly eight hours and is sampled at a frequency of 100 Hz. These recordings come with annotations marking the presence or absence of apnea events in one-minute segments. The dataset is divided evenly into two sets: a training set containing 35 records (labeled from a01 to a20, b01 to b05, and c01 to c10) and a testing set with 35 records (x01 through x35). The length of the recordings varies, generally ranging between just under 7 hours to approximately 10 hours. The PhysioNet dataset provides several file types critical for sleep apnea research. The .apn files are annotation files that indicate whether apnea is occurring during each minute of the recording, while the .dat files store the raw ECG signal data in binary format.

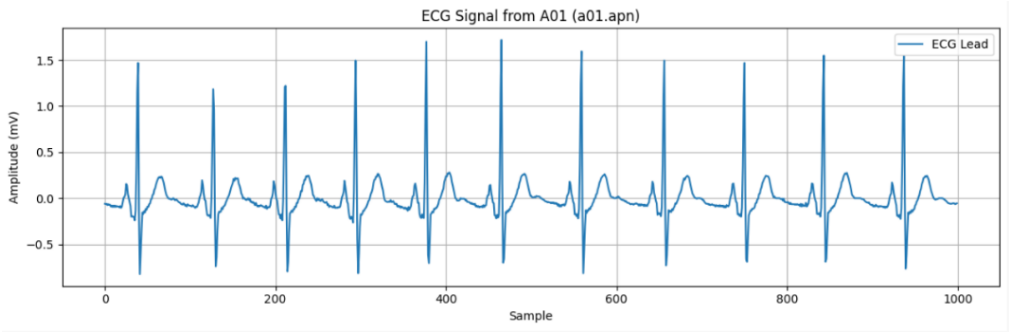

Fig 2. ECG signal segment from subject A01 (a01.apn)

Figure 2. ECG signal segment from subject A01 (a01.apn) showing characteristic QRS complexes. The vertical axis represents signal amplitude in millivolts (mV), and the horizontal axis represents the sample number.

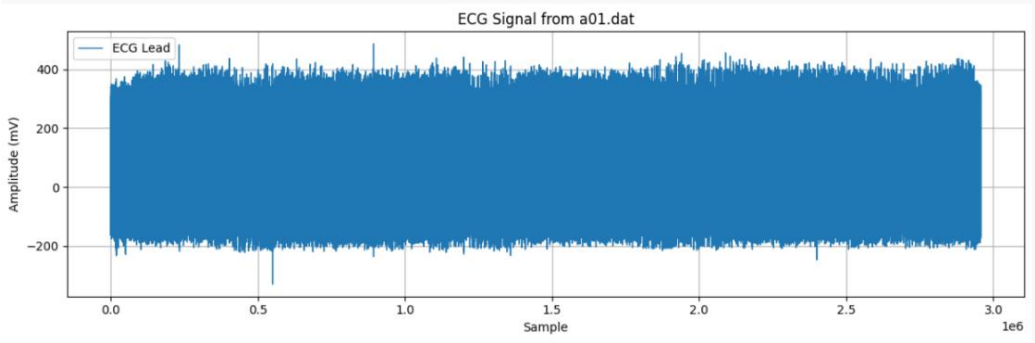

Fig 3. ECG signal from subject A01 (a01.dat)

Figure 3. Full-length ECG recording from subject A01 (file: *a01.dat*) displayed at high-resolution sampling. The vertical axis indicates the signal amplitude in millivolts (mV), while the horizontal axis denotes the sample number.

3.2 Data Pre-Processing:

Before feeding the signals into the CNN+BiLSTM model, proper data pre-processing is essential to ensure accurate learning. One important step is RR interval calculation, which measures the time difference between consecutive R-peaks in the ECG signal. These intervals are crucial for heart rate variability (HRV) analysis and can help detect irregular heart rhythms, such as those associated with sleep apnea.

R-peaks are typically detected using established algorithms such as the Pan-Tompkins method or Hamilton Segmented, and RR intervals are computed as:

$$\mathrm{RRI}_i = \frac{r_{i+1} - r_i}{f_s} \qquad \text{.....(1)}$$

Where:

- r_i : Time index (or sample index) of the iii-th R-peak
- f_s : Sampling frequency (in Hz)
- RRI_i : Time difference between two consecutive R-peaks (in seconds)

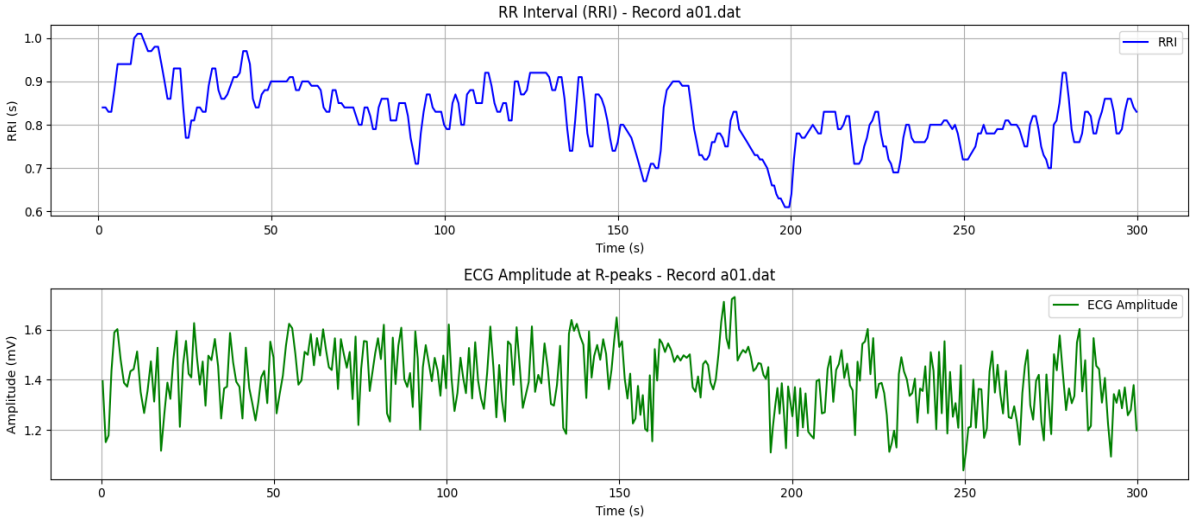

Fig 4. RR Interval and ECG Amplitude from record *a01.dat*

Figure 4 illustrates two key parameters derived from the ECG signal of record a01.dat. The top plot represents the RR Interval (RRI) over time, showing the duration between successive heartbeats in seconds. The bottom plot displays the ECG amplitude at R-peaks in millivolts, indicating the strength of the heart's electrical activity. Together, these plots help analyze heart rate variability and signal amplitude trends over 300 seconds.

Another vital preprocessing step is ECG amplitude normalization, which addresses variability introduced by factors such as electrode positioning and patient-specific differences. Normalization ensures that the model focuses on relative signal patterns rather than raw amplitude values. Common normalization techniques include:

- **Min-Max Scaling**:

$$x' = \frac{x - x_{min}}{x_{max} - x_{min}} \qquad \text{.....(2)}$$

- **Z-score Normalization**:

$$x' = \frac{x - \mu}{\sigma} \qquad \text{.....(3)}$$

To ensure consistent temporal alignment between different signal types (e.g., ECG and RR intervals), interpolation is applied. Since these signals may be unevenly sampled, methods such as linear interpolation or cubic spline interpolation are used to generate uniformly spaced time series. This step enhances compatibility and synchronization across modalities.

These preprocessing methods—R-peak detection, amplitude normalization, RR interval computation, and interpolation—clean up and organize the input data. This directly improves the accuracy and generalization of the model in the downstream sleep apnea classification task.

3.3 Feature Extraction

After preprocessing the signals, the interpolated ECG amplitude and RR interval signals are subjected to feature extraction to identify noteworthy patterns. The extracted features help the model distinguish between normal and apnea sleep stages.

Steps:

- Full-length Signal Pair Extraction:

$$\text{Feature}_1 = [\text{RRI}_{\text{interp}}, \text{AMPL}_{\text{interp}}]$$

- Middle Segment Extraction:

$$\text{Feature}_2 = RRI_{interp}[180:720],\ AMPL_{interp}[180:720]$$

- Center Segment Extraction:

$$\text{Feature}_3 = RRI_{interp}[360:540],\ AMPL_{interp}[360:540]$$

The model receives carefully extracted features from the time domain, frequency domain, and nonlinear analyses as inputs. The dataset is then split into 80% for training and 20% for validation to effectively evaluate the model's ability to classify sleep apnea. Incorporating these thoughtfully derived features greatly improves both the accuracy and the overall reliability of the classification.

3.4 Model Architecture

a) CNN+biLSTM Model

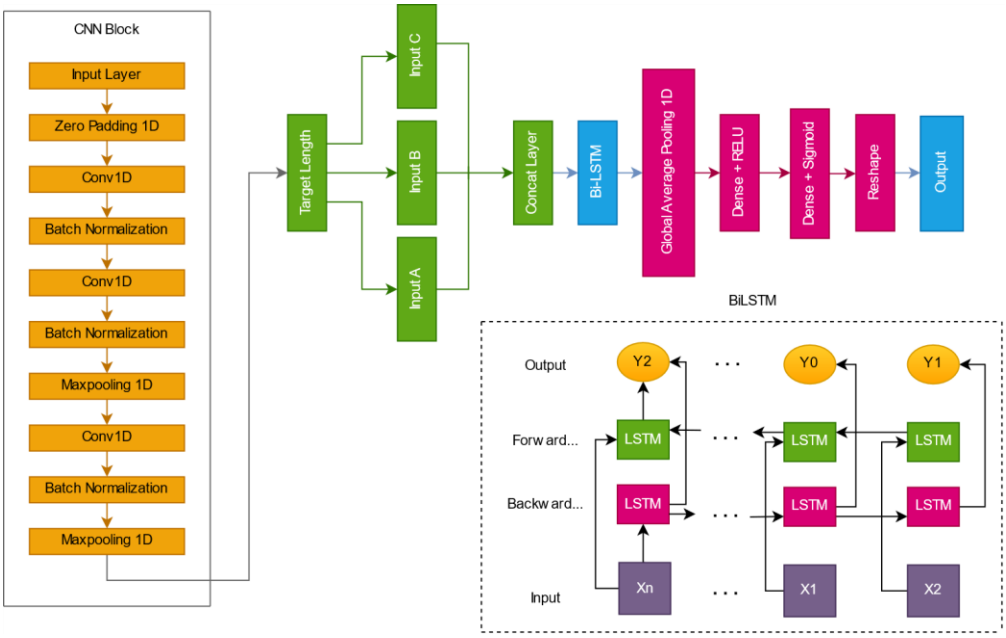

Fig 5. Model Architecture of CNN+biLSTM

Figure 5 represents the model architecture of CNN+BiLSTM, which is designed for analyzing time-series biomedical signals such as EEG and ECG. The CNN block for feature extraction, the data processing and concatenation step, the BiLSTM block for sequential pattern learning, and the classification block for prediction-making comprise the model's four primary components.

Table 2. Algorithm 1

Algorithm 1: Model Architecture

Step 1: Input

Three EEG channels: input_a, input_b, input_c

Shape: (T, F), where T = time steps, F = features

Step 2: CNN Feature Extraction (applied to each input)

- Zero-Padding to match target length
- Conv1D → BN → ReLU (Filters=16, Kernel=11)
- Conv1D → BN → ReLU (Filters=24, Kernel=11, Stride=2)
- MaxPooling1D (Pool=3)
- Conv1D → BN → ReLU (Filters=32, Kernel=11)
- MaxPooling1D (Pool=5)

Step 3: Feature Fusion + Sequential Learning

- Concatenate features from 3 channels
- BiLSTM (units=64, dropout=0.5, recurrent_dropout=0.2)

Step 4: Squeeze-and-Excitation Block

- GlobalAveragePooling1D
- Dense(128, ReLU) → Dense(128, Sigmoid)
- Reshape and multiply with BiLSTM output

Step 5: Classification Head

- GlobalAveragePooling1D
- Dropout(0.5)
- Dense(2, Softmax) → Output: [Class 0, Class 1]

Step 6: Training

- Optimizer: Adam, LR=0.001
- Loss: Weighted Categorical Crossentropy
- Epochs=50, Batch=32
- Split: Train 58%, Val 13%, Test 29%

End of Algorithm

CNN Block:

The CNN block extracts key features from the input signals. It begins with an Input Layer, followed by Zero Padding 1D, which ensures that the signal size remains consistent. The Conv1D layers detect important patterns, while Batch Normalization stabilizes learning and improves performance. MaxPooling 1D reduces the data size, retaining the most essential features. This sequence of convolution, normalization, and pooling is repeated to refine the feature representation before passing it to the next stage.

Data Processing and Concatenation

After feature extraction, the model processes multiple inputs (A, B, and C) representing different signal sources. The Target Length step ensures all inputs have the same sequence length for proper alignment. Then, the Concatenate Layer merges these inputs into a single representation, allowing the model to learn from all the available data simultaneously.

BiLSTM Block

The block in charge of learning patterns over time is called the BiLSTM (Bidirectional Long Short-Term Memory). In contrast to conventional LSTMs, BiLSTM can process data both forward (from the past to the present) and backward (from the present to the past). The model's ability to capture dependencies from both past and future time steps is enhanced by this bidirectional approach, which improves its efficacy for sequential data analysis. To increase accuracy and robustness, the outputs from both directions are combined.

Classification Block

The final stage of the model is classification. The Global Average Pooling 1D layer reduces the data size while preserving critical information. A Dense layer with ReLU activation further processes the extracted features. Another Dense layer with Sigmoid activation determines the final class, such as whether the sleep stage is normal or shows signs of apnea. The Reshape layer adjusts the output format before the final Output layer generates the prediction.

This CNN+BiLSTM model efficiently combines feature extraction, temporal pattern learning, and classification, making it highly suitable for sleep apnea detection using EEG and ECG signals.

b) ResNet1D Model (1D Residual Neural Network)

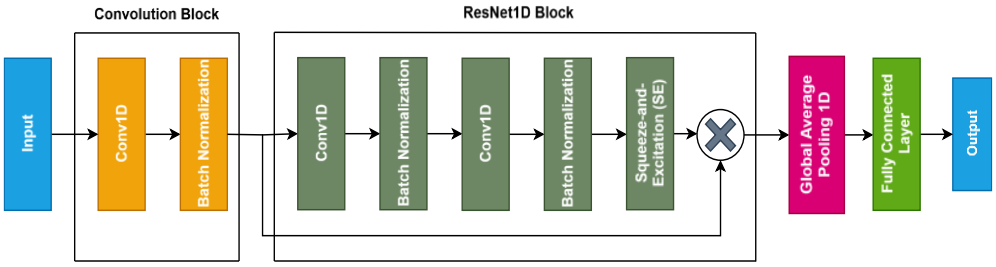

Fig 6. Model Architecture of ResNet-1D

Figure 6 represents the model architecture of ResNet1D, which is designed for analyzing time-series biomedical signals such as ECG and RR intervals. The model consists of four main parts: the Convolution Block for initial feature extraction, the ResNet1D Block with Squeeze-and-Excitation (SE) for deep feature learning and residual mapping, the Global Average Pooling block for dimensionality reduction, and the Classification Block that includes a fully connected layer to generate final predictions.

Table 3. Algorithm 2

Algorithm 2: Residual 1D CNN Model (ResNet1D)
Step 1: Input • Input EEG segment: input, shape = (T, F) **Step 2: Initial Convolution Layer** • Conv1D (Filters=16, Kernel=11, Stride=2, Padding='same') • Batch Normalization • ReLU Activation **Step 3: Residual Blocks** For each block: • Conv1D → BN → ReLU • Conv1D → BN • Add shortcut connection (adjust with Conv1D if shape mismatch) • ReLU Activation Blocks:

- Residual Block 1: Filters = 16
- Residual Block 2: Filters = 24
- Residual Block 3: Filters = 32

Step 4: Global Feature Aggregation

- GlobalAveragePooling1D
- Dropout(0.5)

Step 5: Output Layer

- Dense(2, Softmax) → Output: [Class 0, Class 1]

Step 6: Training Settings

- Optimizer: Adam
- Loss: Weighted Categorical Crossentropy
- Epochs = 50, Batch Size = 32

End of Algorithm

Input Block:

The model takes a 1D time-series signal as input, such as interpolated RR intervals and ECG amplitudes. These signals are essential for capturing temporal patterns related to physiological changes, such as those associated with sleep apnea.

Convolution Block:

This block consists of a 1D convolution layer followed by batch normalization. The convolution layer extracts local temporal features from the signal, while batch normalization normalizes the output to accelerate training and improve stability.

ResNet1D Block:

The core of the model is the ResNet1D block, which includes two convolutional layers, each followed by batch normalization. A Squeeze-and-Excitation (SE) mechanism is integrated to enhance important features by learning channel-wise dependencies. A skip connection adds the block's input directly to its output, enabling better gradient flow and reducing the risk of vanishing gradients during training.

Global Average Pooling Block:

This block applies global average pooling across the time dimension, converting each feature map into a single value. This reduces the feature dimensionality and

makes the model less sensitive to the temporal location of features, promoting generalization.

Fully Connected Layer and Output Block:

The pooled features are passed through a fully connected layer that maps them to the output classes. The final output layer produces the class probabilities, indicating the presence or absence of conditions like sleep apnea based on the input ECG signals.

3.5 Model Training:

To improve the training process, we use a customized Adam optimizer along with a Learning Rate Scheduler. These techniques help the model learn faster, stabilize training, and improve classification accuracy.

Customized Adam Optimizer:

For training the proposed CNN+BiLSTM model, we utilize a customized version of the Adam optimizer, referred to as CustomizeAdam. Adam (Adaptive Moment Estimation) is a sophisticated optimization algorithm widely used in deep learning due to its ability to combine the advantages of AdaGrad and RMSProp. It provides adaptive learning rates for each parameter by using first-moment (mean) and second-moment (variance) estimates of gradients, dynamically adjusting the learning rate to facilitate efficient and stable convergence. The customized version of Adam, CustomizeAdam, includes fine-tuned hyperparameters aimed at enhancing model performance, improving convergence, and ensuring greater stability, especially when dealing with complex signal patterns. This modified optimizer addresses potential pitfalls such as overfitting and instability, thereby improving the overall training dynamics of the CNN+BiLSTM model.

Learning Rate Scheduling

A Learning Rate Scheduler is incorporated to enhance model convergence and stability by dynamically modifying the learning rate throughout training. Instead of using a fixed learning rate, we employ a scheduling strategy to reduce the learning rate at predefined

intervals, preventing the optimizer from overshooting the optimal solution and ensuring fine-tuned weight updates.

Loss Function: Binary Cross-Entropy

Since our classification problem involves distinguishing between two classes (normal and apnea sleep stages), we employ binary cross-entropy (BCE) as the loss function. For binary classification tasks, BCE is widely used because it computes the discrepancy between the predicted and actual class probabilities.

The BCE loss function is defined as:

$$\mathcal{L} = -\frac{1}{N}\sum_{i=1}^{N}[y_i \log(\hat{y}_i) + (1 - y_i)\log(1 - \hat{y}_i)] \qquad \text{.....(4)}$$

Where:

- y_i represents the true class label (0 or 1),
- $\hat{y}_i$ is the predicted probability for class 1,
- N is the number of training samples.

3.6 Model Evaluation:

The model evaluation demonstrates strong performance in classifying sleep apnea and normal sleep stages. Classifier performance is assessed using several indicators that are obtained from the confusion matrix.

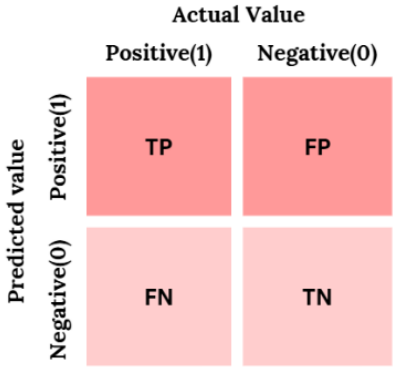

Figure 7: Confusion Matrix

Accuracy (Acc): It evaluates both correctly classified positive and negative samples to determine the model's overall accuracy. It's provided by:

$$Acc = \frac{TP}{TP+FP+TN+FN} \quad \text{……(5)}$$

Sensitivity/Recall (Sn): Sensitivity evaluates the percentage of true positives that are accurately detected. It is provided by:

$$Sn = \frac{TP}{TP+FN} \quad \text{……(6)}$$

Specificity (Sp): The percentage of true negatives that are accurately identified is known as specificity. It is provided by:

$$Sp = \frac{TN}{TN+FP} \quad \text{……..(7)}$$

Precision (Pr): It indicates how many of the positive predictions made by the model were true positives. It is given by:

$$Pr = \frac{TP}{TP+FP} \quad \text{…..……(8)}$$

F-measure (F1 score): Provides a single metric balancing precision and recall. It is given by:

$$F1 = \frac{2\times(Pr\times Sn)}{Pr+Sn} \quad \text{……..(9)}$$

Chapter 4: Results

4.1 Outcome of Proposed Methodology

a) Result using CNN+biLSTM model

Several modifications to the model architecture and training configuration were applied to evaluate the performance of the CNN+BiLSTM model for sleep apnea classification.

Table 4. Accuracy Variation with Different Changes in the CNN+biLSTM Model

Changes	Epoch	Train Acc.	Validation Acc
Add Batch Normalization (BiLSTM Dropout = 0.2)	50	98.53	96.47
BiLSTM Dropout = 0.3	50	98.49	95.42
CustomizeAdam	50	98.40	95.54
BiLSTM Dropout = 0.4	50	98.44	95.42
BiLSTM Dropout = 0.5	50	97.46	94.67
create_model(weight=1e-2)	50	97.56	95.27
batch_size=32 in Train the model	50	98.05	95.09
BiLSTM Dropout = 0.5	100	97.73	95.84
BiLSTM Dropout = 0.5	100	97.85	95.81
BiLSTM Dropout = 0.5	100	98.07	95.39

Table 4 presents the accuracy variation resulting from different modifications in the model architecture and hyperparameter tuning, particularly focusing on the CNN+BiLSTM model for sleep apnea classification. These results specifically reflect the scenario where a BiLSTM dropout rate of 0.5 is applied and the model is trained for 100 epochs. While higher accuracy was achieved at specific stages of training, noticeable fluctuations in the

validation accuracy curve suggested possible overfitting or instability in the model's ability to generalize effectively.

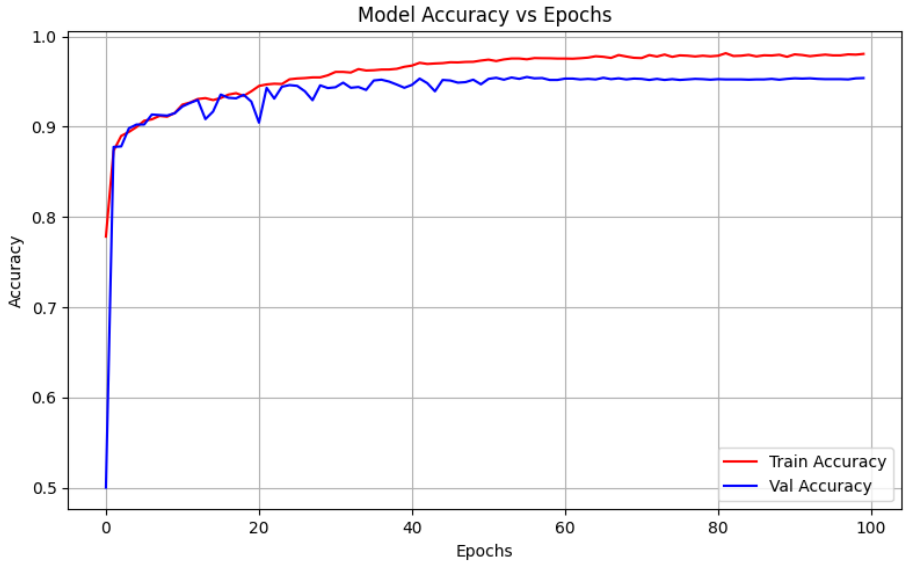

Fig 8. Model Accuracy vs Epochs

Figure 8 presents the accuracy versus epochs graph, highlighting the progression of training and validation accuracy over 100 epochs. At the start (epoch 1), the training accuracy is 0.7783, and the validation accuracy is 0.5003, reflecting the model's initial difficulty in generalizing. However, as training continues, both accuracies gradually improve. By epoch 100, the training accuracy climbs to 0.9807, and the validation accuracy reaches 0.9539, indicating successful learning and effective model performance.

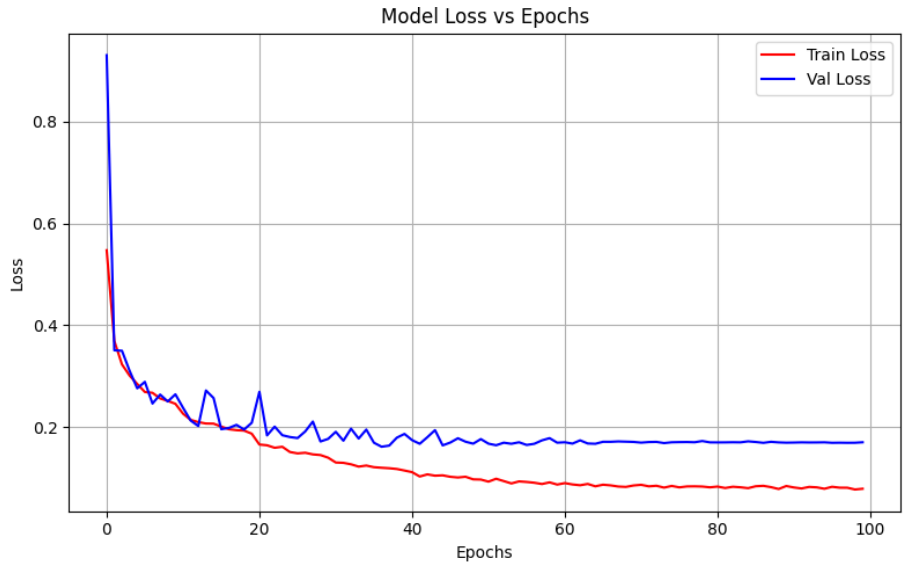

Fig 9. Model Loss vs Epochs

Figure 9 illustrates the variation in training and validation loss across 100 epochs. At the start of training, the model exhibits a training loss of 0.5473 and a higher validation loss of 0.9304, indicating initial difficulties in generalizing to unseen data. However, as training continues, both loss values decrease substantially. By the 100th epoch, the training loss declines to 0.0790, while the validation loss reduces to 0.1703, reflecting effective learning and enhanced model performance over time.

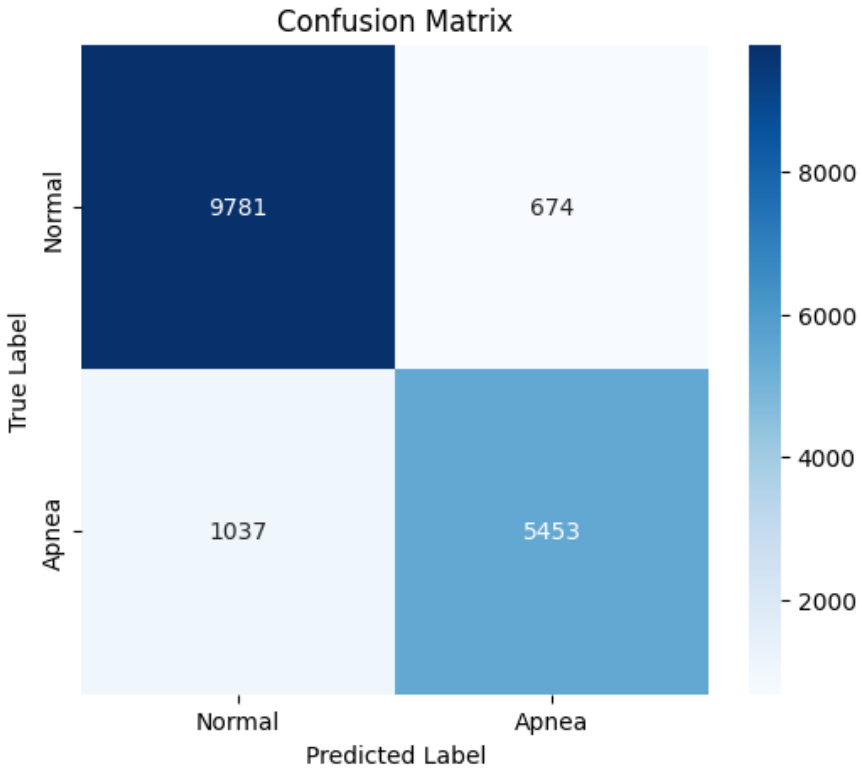

Fig 10. Confusion Matrix

Figure 10 shows the confusion matrix for the sleep apnea classification model, which helps evaluate its performance by comparing predicted and actual labels. The matrix indicates that 9781 Normal cases were correctly classified, while 674 Normal cases were misclassified as Apnea. Similarly, the model correctly identified 5453 Apnea cases, but 1037 Apnea cases were misclassified as Normal.

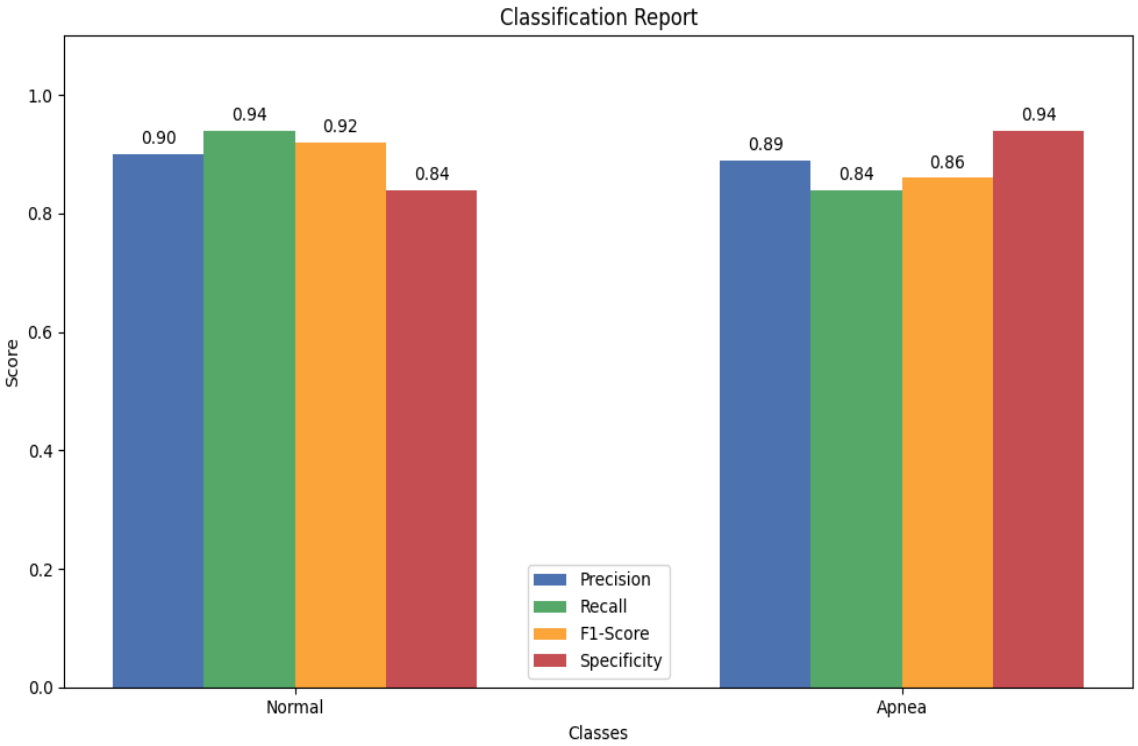

Fig 11. Classification Report of Sleep Apnea

The classification report in Figure 11 presents the performance of the sleep apnea detection model using four key metrics: Precision, Recall, F1-Score, and Specificity for both Normal and Apnea classes. The model shows high precision (0.90 for Normal and 0.89 for Apnea), indicating that most predicted cases are correct. Recall is higher for Normal (0.94) than Apnea (0.84), meaning the model correctly identifies more normal cases. The F1-Score, which provides a harmonic mean of Precision and Recall, is 0.92 for Normal and 0.86 for Apnea, indicating robust classification performance across both classes. Furthermore, the model demonstrates higher Specificity for Apnea (0.94) compared to Normal (0.84), suggesting it is more effective at correctly identifying apnea events. These results indicate that the model effectively classifies sleep stages with high accuracy and reliability.

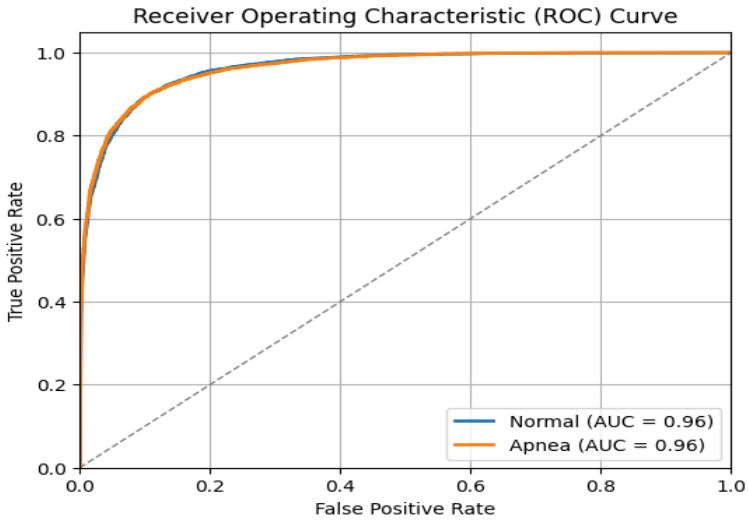

Fig 12. ROC curve

Figure 12 shows the Receiver Operating Characteristic (ROC) curve for the sleep apnea classification model. The curve helps measure how well the model separates normal and apnea sleep stages. The Area Under the Curve (AUC) is 0.96 for both classes, meaning the model performs very well. A higher AUC value (closer to 1) shows that the model can correctly classify normal and apnea stages. The dashed diagonal line in the ROC curve represents random classification performance (AUC = 0.5). The model's ROC curve lies significantly above this line, indicating strong discriminatory ability and high classification accuracy.

b) Results using the ResNet-1D model

Several modifications were applied to the model architecture and training configuration to evaluate the performance of the ResNet-1D model for sleep apnea classification.

Table 5. Accuracy Variation with Different Changes

Changes	Epoch	Train Acc.	Validation Acc
Add Batch Normalization (BiLSTM Dropout = 0.2)	50	98.43	96.78
BiLSTM Dropout = 0.3	50	98.29	95.21

CustomizeAdam	50	98.10	95.99
BiLSTM Dropout = 0.4	50	98.54	95.91
BiLSTM Dropout = 0.5	50	97.76	94.68
create_model(weight=1e-2)	50	97.46	95.98
batch_size=32 in Train the model	50	98.95	95.07
BiLSTM Dropout = 0.5	100	97.93	95.83
BiLSTM Dropout = 0.5	100	97.25	95.89
BiLSTM Dropout = 0.5	100	98.94	96.10

Table 5 presents the accuracy variation resulting from different modifications in the model architecture and hyperparameter tuning, specifically for the ResNet1D model applied to sleep apnea classification. The model achieved a peak validation accuracy of 96.10% when optimized with tuned hyperparameters and trained over 100 epochs. While this configuration outperformed others in terms of overall accuracy, the corresponding validation accuracy plot exhibited noticeable fluctuations, indicating that the model, despite its strong performance, may have experienced occasional instability or overfitting during training.

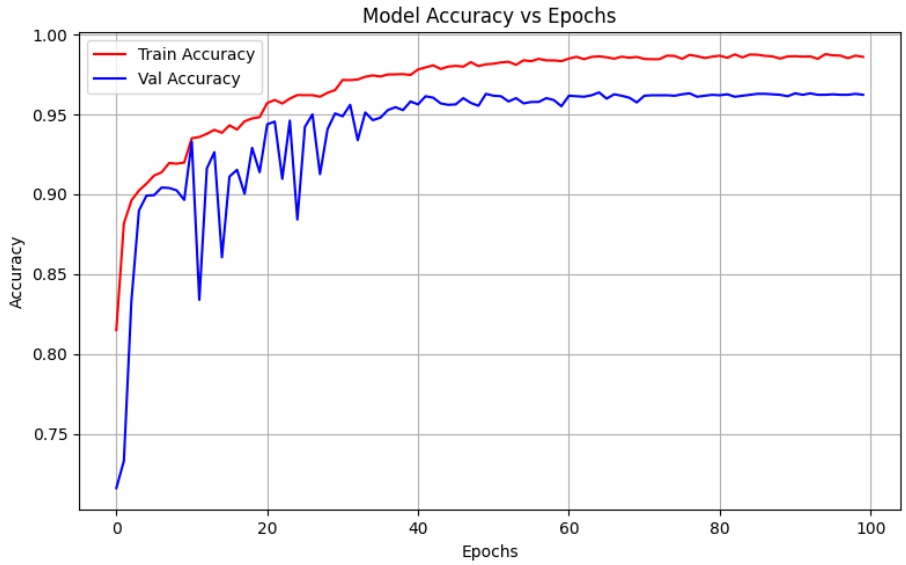

Fig 13. Model Accuracy vs Epochs

Figure 13 presents the graph of model accuracy versus epochs, highlighting the progression of training and validation accuracy over 100 epochs. At the first epoch, the training accuracy is 0.8546, whereas the validation accuracy is 0.7243, revealing an initial disparity in generalization performance between the training and validation datasets. As training continues, both accuracies improve significantly. The training accuracy steadily increases and reaches 0.9894 by epoch 100, while the validation accuracy also rises and stabilizes around 0.9610. Although the training accuracy is slightly higher, the close alignment of validation accuracy suggests that the model has learned well and generalizes effectively with minimal overfitting.

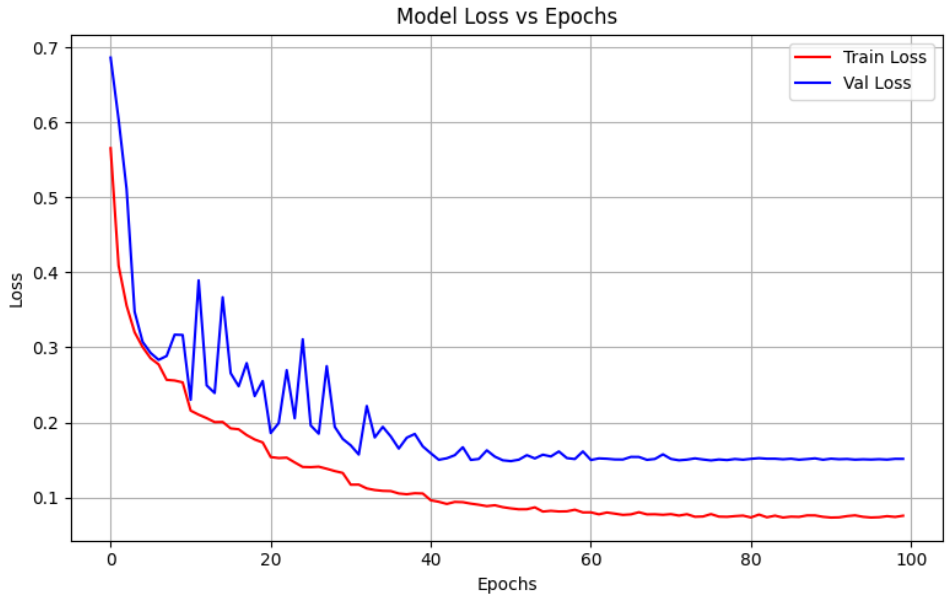

Fig 14. Model Loss vs Epochs

Figure 14 displays the model loss vs. epochs graph, showing how training and validation loss vary over 100 epochs. Initially, at epoch 1, the training loss is 0.5718, and the validation loss is 0.6812, indicating a high error rate at the start. As epochs progress, the training loss gradually decreases, reaching a low of 0.0716 at epoch 100. The validation loss also declines, though with some fluctuations, and stabilizes around 0.1472. The consistent gap between training and validation loss suggests that while the model has minimized training error, there may be slight overfitting, as reflected by the relatively higher validation loss.

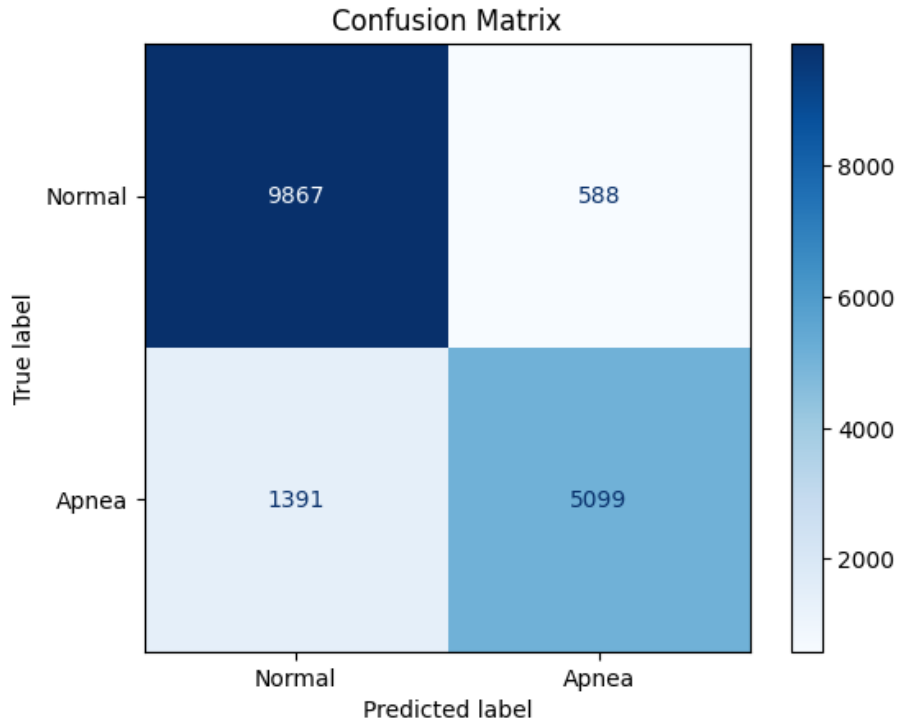

Fig 15. Confusion Matrix of the Classification Model

Figure 15 shows the confusion matrix of the model used for classifying Normal and Apnea events. The matrix provides a summary of prediction results on the validation dataset. Out of all instances labeled as Normal, the model correctly predicted 9867 as Normal (true negatives), while 588 were incorrectly classified as Apnea (false positives). For the Apnea class, the model correctly identified 5099 cases (true positives), but misclassified 1391 Apnea events as Normal (false negatives). These findings demonstrate that the model effectively differentiates between the two classes, showing greater accuracy in identifying Normal cases. However, the number of false negatives (1391) suggests that some Apnea episodes are missed, which could be critical in medical applications. Overall, the confusion matrix reflects a strong classification performance with scope for improvement in sensitivity for Apnea detection.

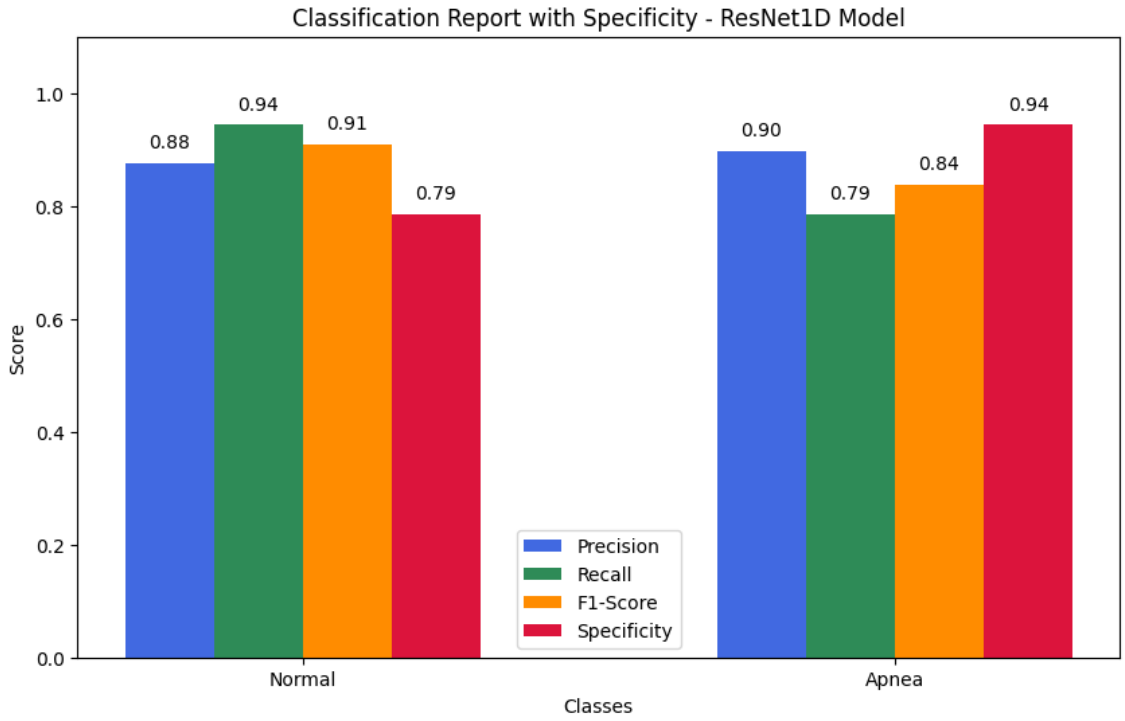

Fig 16. Classification Report with Specificity – ResNet1D Model

Figure 16 displays the classification report for the ResNet1D model, outlining key metrics such as precision, recall, F1-score, and specificity for both Normal and Apnea classes. For the Normal class, the model attained a precision of 0.88, a recall of 0.94, an F1-score of 0.91, and a specificity of 0.79, indicating a strong ability to accurately recognize Normal instances, particularly evident in the high recall and F1-score. In the case of the Apnea class, the model achieved a precision of 0.90, a recall of 0.79, an F1-score of 0.84, and a specificity of 0.94. These results suggest that while the model is highly specific in identifying Apnea events, it tends to miss some actual Apnea occurrences, as shown by the lower recall. Overall, the model demonstrates consistent and dependable performance across both classes, though enhancing recall for Apnea could further improve its usefulness in clinical settings.

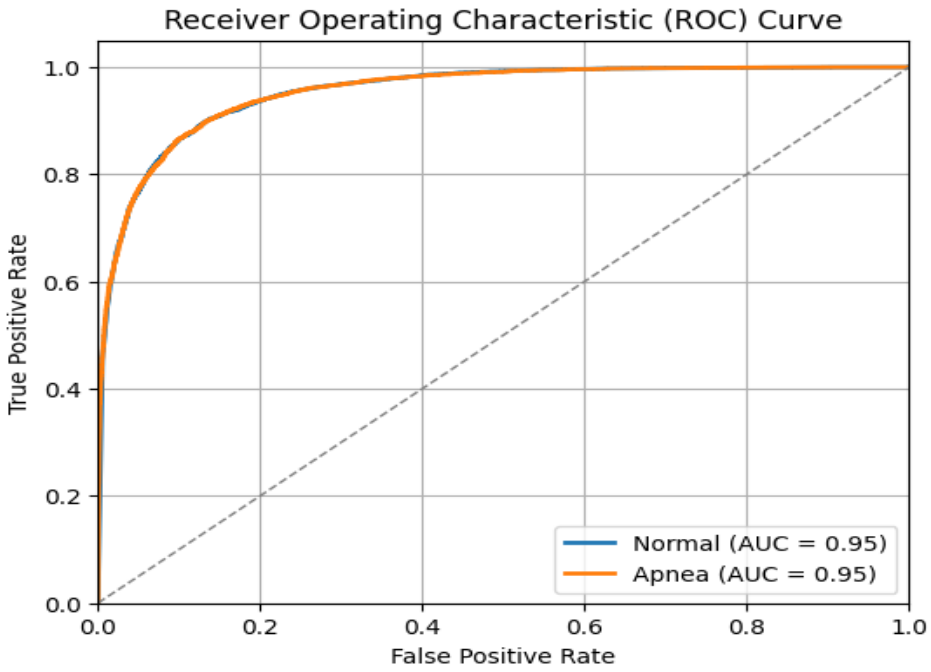

Fig 17. Receiver Operating Characteristic (ROC) Curve

Figure 17 displays the Receiver Operating Characteristic (ROC) curve for the ResNet1D model, highlighting its classification performance for both Normal and Apnea categories. The ROC curve plots sensitivity (true positive rate) against the false positive rate, offering a clear view of the model's ability to distinguish between the two classes. With an Area Under the Curve (AUC) of 0.95 for each class, the model demonstrates strong discriminative power. While an AUC of 1.0 reflects ideal performance and 0.5 indicates random prediction, the high AUC values achieved here confirm the model's effectiveness in accurately identifying Apnea events, even in the presence of imbalanced or overlapping data.

4.2 Discussion

The results obtained from the CNN+biLSTM and ResNet1D models for sleep apnea show that both achieved high accuracy in classifying sleep apnea events, but with notable differences in generalization and sensitivity.

The CNN+BiLSTM model underwent several architectural enhancements and regularization strategies, including the integration of batch normalization and a BiLSTM

dropout rate of 0.2, which led to a peak validation accuracy of 96.47%, demonstrating effective mitigation of overfitting. The accuracy trends (Fig. 8) indicated a steady rise throughout training, culminating in a training accuracy of 98.07% and a validation accuracy of 95.39% at epoch 100. However, fluctuations in the validation accuracy curve suggested occasional training instability, possibly due to overfitting on complex temporal features. The loss plot (Fig. 9) supported this observation, as the training loss decreased more substantially than the validation loss, ending at 0.0790 (training) and 0.1703 (validation), respectively, which still indicated good convergence. Analysis of the confusion matrix (Fig. 10) and classification report (Fig. 11) showed that the model achieved higher recall for the Normal class (0.94) compared to Apnea (0.84), with a moderate number of apnea events being missed. Nonetheless, the model maintained high precision and F1-scores across both classes, indicating balanced performance. The ROC curve (Fig. 12) yielded an AUC of 0.96, confirming excellent discriminative capability between the two classes.

In comparison, the ResNet1D model, designed to learn hierarchical temporal features, achieved a slightly higher validation accuracy of 96.10% under optimal settings that included batch normalization and a dropout rate of 0.5 over 100 training epochs. The accuracy progression (Fig. 13) exhibited smoother convergence with reduced fluctuation and strong alignment between training and validation curves, indicating more stable training behavior. The corresponding loss plot (Fig. 14) confirmed this, although the validation loss of 0.1472 remained slightly higher than the training loss of 0.0716, suggesting mild overfitting. The confusion matrix (Fig. 15) revealed a greater number of false negatives (1391 Apnea cases misclassified as Normal) than in the CNN+BiLSTM model, which may be problematic in clinical applications where detecting apnea events is critical. As detailed in the classification report (Fig. 16), the model exhibited better precision for Apnea (0.90) but lower recall (0.79) compared to CNN+BiLSTM, highlighting a trade-off between specificity and sensitivity. Despite this, the model achieved an AUC of 0.95 (Fig. 17), confirming strong overall classification performance.

Although both models demonstrated outstanding classification performance and robustness across key evaluation metrics, they showed distinct strengths that make them suitable for

different application contexts. The CNN+BiLSTM model exhibited better sensitivity for Apnea detection, achieving higher recall, which is particularly valuable in clinical settings where minimizing false negatives is critical to ensure timely diagnosis and intervention. Its balanced performance across precision, recall, and F1-score for both classes highlights its clinical reliability. In contrast, the ResNet1D model delivered more stable training behavior and higher precision, suggesting fewer false alarms, which may be advantageous in automated monitoring systems where excessive alerts can lead to alarm fatigue. However, this came at the cost of a slightly lower recall for Apnea events, indicating a higher rate of missed detections.

In summary, while both models are highly effective, the CNN+BiLSTM model offers greater clinical utility due to its superior recall and balanced detection of both Apnea and Normal events. The ResNet1D model, with its higher precision and training efficiency, may be better suited for environments where the priority is to reduce false positives, even if it risks overlooking some Apnea events.

Chapter 5: Conclusions and Future Scope

5.1 Conclusion

This study successfully developed and evaluated deep learning-based models—CNN+BiLSTM and ResNet1D—for automated detection of sleep apnea using single-lead ECG signals from the PhysioNet Apnea-ECG dataset. The motivation for using ECG lies in its non-invasive, easily accessible nature, and its compatibility with wearable technology, making it highly suitable for real-time, at-home monitoring. Unlike EEG-based diagnostics that require elaborate setups and clinical environments, ECG offers a more practical and scalable solution.

Among the two models, ResNet1D achieved the highest classification accuracy of 96.10%, slightly outperforming the CNN+BiLSTM model, which achieved 95.39%. However, the CNN+BiLSTM model showed better performance in terms of recall and F1-score—metrics that are particularly critical in medical diagnostics where minimizing false negatives is essential to avoid missing apnea events. This highlights the trade-off between overall accuracy and sensitivity to minority class detection, a vital consideration in healthcare applications.

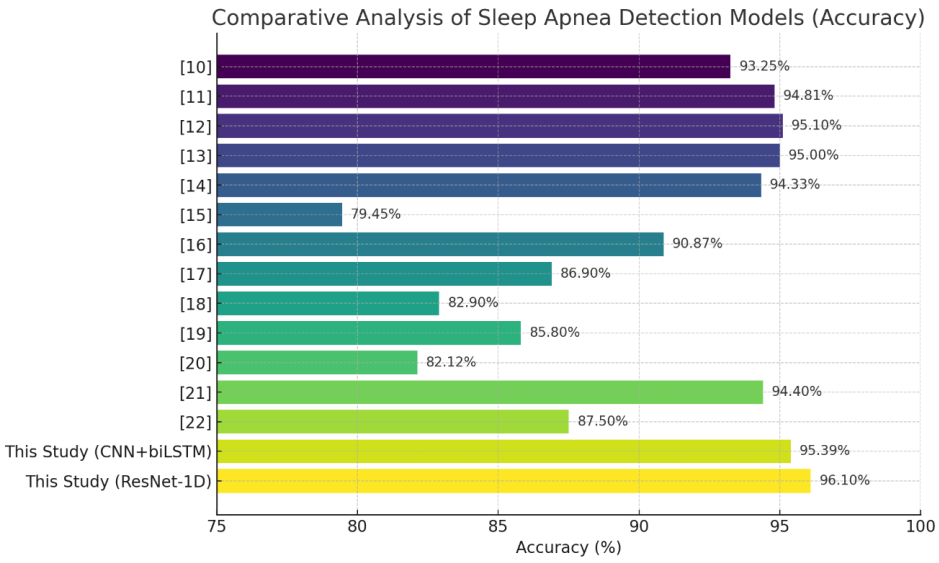

Fig 18. Comparative Analysis of Sleep Apnea Detection models

Figure 18 presents a comparative overview of our proposed models against other methods reported in the literature. Both the ResNet1D and CNN+BiLSTM models outperformed the majority of prior approaches in terms of accuracy, clearly demonstrating the advantage of advanced deep learning architectures combined with effective training strategies.

Several factors contributed to the superior performance of the proposed models:

- **End-to-end learning from raw ECG signals**: Unlike traditional methods that rely on handcrafted features, our models were able to automatically extract relevant patterns from raw ECG data, reducing the need for expert domain knowledge and manual feature engineering.
- **Use of advanced neural architectures**: The integration of convolutional layers for spatial feature extraction and BiLSTM layers for capturing temporal dependencies, along with residual connections in ResNet1D, significantly enhanced model capability.
- **Robust training strategies**: Custom learning rate scheduling, adaptive optimizers, and dropout regularization helped prevent overfitting and improved generalization to unseen data.

These findings confirm that single-lead ECG signals, when processed with robust deep learning techniques, can serve as a reliable and efficient alternative to traditional, more intrusive diagnostic methods like EEG. This opens the door for developing portable, user-friendly, and cost-effective sleep apnea monitoring systems that can be integrated into wearable health devices.

The proposed models also highlight the potential of deep learning to revolutionize healthcare by enabling more accessible, automated solutions for disease detection. As wearable health technology continues to evolve, the integration of such models could lead to significant improvements in early diagnosis, personalized care, and continuous health monitoring. Moreover, the application of these models to diverse populations and datasets could further enhance their generalizability, paving the way for widespread adoption of ECG-based sleep apnea detection systems in both clinical and home environments.

In conclusion, the proposed deep learning models not only demonstrate state-of-the-art performance on a benchmark dataset but also show strong potential for real-world applications in remote and continuous health monitoring. Future work could explore model deployment on embedded systems, integration with other physiological signals for multi-modal analysis, and validation on larger, more diverse datasets to ensure generalizability across populations.

5.2 Future Scope

This study highlights the promising potential for integrating automated sleep apnea detection models into real-world applications. A significant avenue for future research involves embedding the proposed CNN+BiLSTM and ResNet1D models into wearable devices, such as smartwatches or ECG patches. This integration would enable continuous, non-invasive monitoring of sleep patterns in home environments, making the detection of sleep apnea more accessible and convenient for individuals [23].

Additionally, incorporating multimodal physiological data, including SpO_2, respiratory signals, and EEG, into the models can further improve their robustness. By leveraging diverse signals, the models can better differentiate between normal sleep events and apnea events, thus reducing the rate of misclassification. Furthermore, the development of personalized models that adapt to individual physiological variations is crucial for improving detection accuracy across different populations. These models could account for various factors such as age, gender, and underlying health conditions, leading to a more reliable and user-centric approach to sleep apnea detection [24].

Future work should also prioritize clinical validation of the models, utilizing larger and more diverse datasets to ensure generalizability and reliability across different demographic groups and clinical conditions. This will be important for translating the proposed solutions into actual medical practice. Additionally, incorporating Explainable AI (XAI) techniques will be crucial to enhancing the transparency of the models' decision-making processes, fostering trust among healthcare professionals and patients. Techniques

such as saliency maps and attention mechanisms can help explain the factors influencing the model's predictions, which is particularly important for medical applications [25].

Moreover, the deployment of these models in telehealth platforms or mobile applications would expand their diagnostic reach, particularly in remote or underserved regions, where access to clinical sleep studies may be limited. These platforms could provide patients with real-time feedback and recommendations, enabling early intervention [26].

In addition to sleep apnea, the same deep learning architectures could be adapted to detect other sleep-related disorders, such as insomnia or restless leg syndrome, making the system more versatile. This would contribute to the development of a comprehensive, AI-driven sleep health monitoring solution, helping individuals manage and improve their overall sleep quality [27].

In conclusion, while significant progress has been made in using deep learning models for sleep apnea detection, there are still many exciting possibilities for future advancements. These include the integration of wearable devices, multimodal data, personalized models, clinical validation, and the expansion of the system to other sleep-related disorders, which together could revolutionize sleep health monitoring and management.

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