Hybrid Deep Learning for Lung Sound Classification in Respiratory Disease Detection

Report submitted to the SASTRA Deemed to be University

in partial fulfillment of the requirements

for the award of the degree of

Bachelor of Technology

Submitted by

Harsh

(125156040, B. Tech Computer Science and Engineering (AI & DS))

Vedant Agnihotri

(125003388, B. Tech Computer Science and Engineering)

May 2025

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Signature of Project Supervisor:

Name with Affiliation :Dr. VIDIVELLI S

Assistant Professor-II, School of Computing

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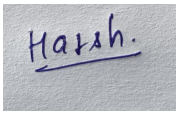
Declaration

We declare that the project report titled "**Hybrid Deep Learning for Lung Sound Classification in Respiratory Disease Detection**" submitted by us is an original work done by us under the guidance of **Dr. Vidivelli S**, Assistant Professor-II, School of Computing, SASTRA Deemed to be University during the final semester of the academic year 2024-25, in the School of Computing. The work is original and wherever we have used materials from other sources, We have given due credit and cited them in the text of the report. This report has not formed the basis for the award of any degree, diploma, associate-ship, fellowship or other similar title to any candidate of any University.

Signature of the candidate(s) : 

Vedant

Name of the candidate(s) : Harsh, Vedant Agnihotri

Date : 09/05/2025

Acknowledgements

We would like to thank our Honorable Chancellor **Prof. R. Sethuraman** for providing us with an opportunity and the necessary infrastructure for carrying out this project as a part of our curriculum.

We would like to thank our Honorable Vice-Chancellor **Dr. S. Vaidhyasubramaniam** and **Dr. S. Swaminathan**, Dean, Planning & Development, for the encouragement and strategic support at every step of our college life.

We extend our sincere thanks to **Dr. R. Chandramouli**, Registrar, SASTRA Deemed to be University for providing the opportunity to pursue this project.

We extend our heartfelt thanks to **Dr. V. S. Shankar Sriram**, Dean, School of Computing, **Dr. R. Muthaiah**, Associate Dean, Research**, Dr. K.Ramkumar**, Associate Dean, Academics, Dr. D. Manivannan, Associate Dean, Infrastructure, **Dr. R. Algeswaran**, Associate Dean, Student Welfare.

Our guide **Dr. Vidivelli S** AP-II, School of Computing was the driving force behind this whole idea from the start. His deep insight in the field and invaluable suggestions helped us in making progress throughout our project work. We also thank the project review panel members for their valuable comments and insights which made this project better.

We would like to extend our gratitude to all the teaching and non-teaching faculties of the School of Computing who have either directly or indirectly helped us in the completion of the project.

We gratefully acknowledge all the contributions and encouragement from my family and friends resulting in the successful completion of this project. We thank you all for providing me an opportunity to showcase my skills through projects.

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LIST OF DIAGRAMS

ABBREVIATIONS

COPD	Chronic Obstructive Pulmonary Disease
CNN	Convolutional Neural Network
STFT	Short- Time Fourier Transform
LOOCV	Leave-One-Out Cross Validation
LSTM	Long Short Term Memory
VGG	Visual Geometry Group
ICBHI	International Conference on Biomedical and Health Informatics
ReLU	Rectified Linear Unit

LIST OF FIGURES

ABSTRACT

Respiratory diseases, such as COPD, pneumonia, and URTI, significantly impact global health and require efficient diagnostic methods for early detection and management. This project introduces an advanced deep edge intelligence system for real-time respiratory disease detection, leveraging deep learning models for automated lung sound classification.

A key novelty of this work lies in the integration of Resnet-18 architectures to enhance feature representation and capture deeper temporal dependencies in lung sounds. By combining these architectures with LSTM for feature extraction from short-time Fourier transform (STFT) spectrograms, the model improves the classification of four lung sound types—normal, crackles, wheezes, and both crackles and wheezes. Additionally, the study employs the focal loss (FL) function to address training data imbalance, ensuring a more effective learning process. The proposed model is trained and validated using the ICBHI 2017 Respiratory Sound Database under three different data splitting strategies to ensure robustness and generalization.

This project aims to develop a portable and efficient diagnostic tool suitable for edge computing environments, ensuring accessibility for real-world healthcare applications. It integrates feature extraction techniques, including CNN-LSTM, for robust classification while leveraging data augmentation and optimization strategies to enhance system performance. Future directions include real-world deployment and further refinement to bridge the gap between advanced medical diagnostics and practical healthcare solutions, particularly for resource-limited settings.

CHAPTER 1

INTRODUCTION

1.1 Background

Respiratory diseases such as Chronic Obstructive Pulmonary Disease (COPD), pneumonia, and upper respiratory tract infections (URTI) continue to pose significant global health challenges, especially in developing regions. Early detection and monitoring of these diseases are essential for effective treatment and management. Traditional diagnostic methods such as auscultation using stethoscopes rely on the subjective interpretation of sounds by healthcare professionals, which can be limited in accuracy and availability.

The emergence of deep learning and edge computing technologies presents a transformative opportunity for real-time, automated, and accessible respiratory diagnostics. Edge intelligence allows for processing data locally on low-power devices, minimizing latency and reducing dependency on cloud infrastructure—making it ideal for rural or resource-limited healthcare environments.

1.2 Problem Statement

Despite advancements in medical diagnostics, there is a lack of reliable, low-cost, and real-time solutions for respiratory sound analysis that can operate efficiently on edge devices. Moreover, the classification of respiratory sounds is challenged by noise, class imbalance, and the complexity of lung sound patterns. This project aims to bridge this gap by developing a deep learning-based system that leverages edge intelligence to classify lung sounds into clinically relevant categories

1.3 Objectives

- To design a robust and portable respiratory sound classification model using a hybrid CNN-LSTM architecture.
- To convert lung sounds into STFT spectrograms for effective feature extraction.
- To apply ResNet-18, Resnet-50 for deep feature representation and LSTM for capturing temporal patterns.

- To use the focal loss function to handle class imbalance in the dataset.
- To evaluate the model using the ICBHI 2017 Respiratory Sound Database under multiple data-splitting strategies.

1.4 Scope

The scope of this project includes data preprocessing, model design, training, evaluation, and deployment on edge hardware. The system is designed to classify four lung sound categories: normal, crackles, wheezes, and both crackles and wheezes. The model emphasizes accuracy, efficiency, and generalization to diverse respiratory sound patterns.

1.5 Methodology Overview

This project employs a combination of Convolutional Neural Networks (CNN) and Long Short-Term Memory (LSTM) networks, trained on spectrogram representations of lung sounds. A focal loss function is integrated to counter class imbalance. The model is trained and validated using the ICBHI 2017 dataset, followed by optimization for edge deployment.

1.6 Organization of the Report

- **Chapter 1** Provides an introduction to the project.
- **Chapter 2** Discusses related work and literature review.
- **Chapter 3** Describes the system architecture and methodology.
- **Chapter 4** Explains implementation details and model training.
- **Chapter 5** Presents the results, evaluation, and analysis.
- **Chapter 6** Concludes the report and outlines future work.
- **Chapter 7** Source Code .

Chapter 2: Literature Review

2.1 Overview

This chapter reviews the existing work in the domain of respiratory sound classification, deep learning models for biomedical signal analysis, and the deployment of AI solutions on edge devices. It highlights key limitations in current research and justifies the adoption of a hybrid deep learning approach—specifically CNN-LSTM or ResNet-LSTM—with STFT spectrograms and focal loss to classify lung sounds. The chapter also discusses the performance of related works, offering a comparative foundation for the proposed model.

2.2 Respiratory Sound Analysis

Traditional auscultation methods are limited by human hearing, inter-observer variability, and the lack of standardization. To overcome these limitations, digital stethoscopes and computer-aided auscultation systems have been developed, enabling the digitization of lung sounds for further processing using signal analysis and machine learning.

Several works have employed classical machine learning techniques such as Support Vector Machines (SVM), k-Nearest Neighbors (k-NN), and decision trees for lung sound classification. However, these approaches often rely on hand-crafted features and lack the robustness required for real-world deployment.

2.3 Deep Learning in Biomedical Audio Processing

Deep learning has shown immense potential in biomedical signal classification. CNNs are adept at learning spatial hierarchies from time-frequency representations of audio, making them suitable for spectrogram-based lung sound classification.
RNN variants, particularly Long Short-Term Memory (LSTM) networks and Gated Recurrent Units (GRU), are well-suited for learning temporal dependencies in sequential data like respiratory audio.

Hybrid models combining CNNs with LSTM or GRU structures have yielded higher accuracy by leveraging both spatial and temporal feature extraction. For instance, in the base paper by Petmezas et al. (2022), a CNN-LSTM model outperformed traditional methods across multiple evaluation strategies when trained on the ICBHI 2017 dataset.

This project extends the hybrid model idea by exploring ResNet-18 and ResNet-50 as CNN backbones to improve feature representation and gradient flow through skip connections, enabling deeper networks without vanishing gradients.

2.4 Spectrogram-Based Feature Extraction

Spectrograms convert 1D audio signals into 2D representations capturing frequency and time-based features. The **Short-Time Fourier Transform (STFT)** is widely used for this purpose, and in this project, it produces 75x50 grayscale spectrograms of fixed-length (2.7 seconds).

STFT spectrograms provide critical insights into respiratory cycles, enabling the model to distinguish between normal sounds and adventitious sounds such as **crackles**, **wheezes**, and **combined crackles and wheezes**. These spectrograms act as images that can be fed into CNN-based models for robust feature extraction.

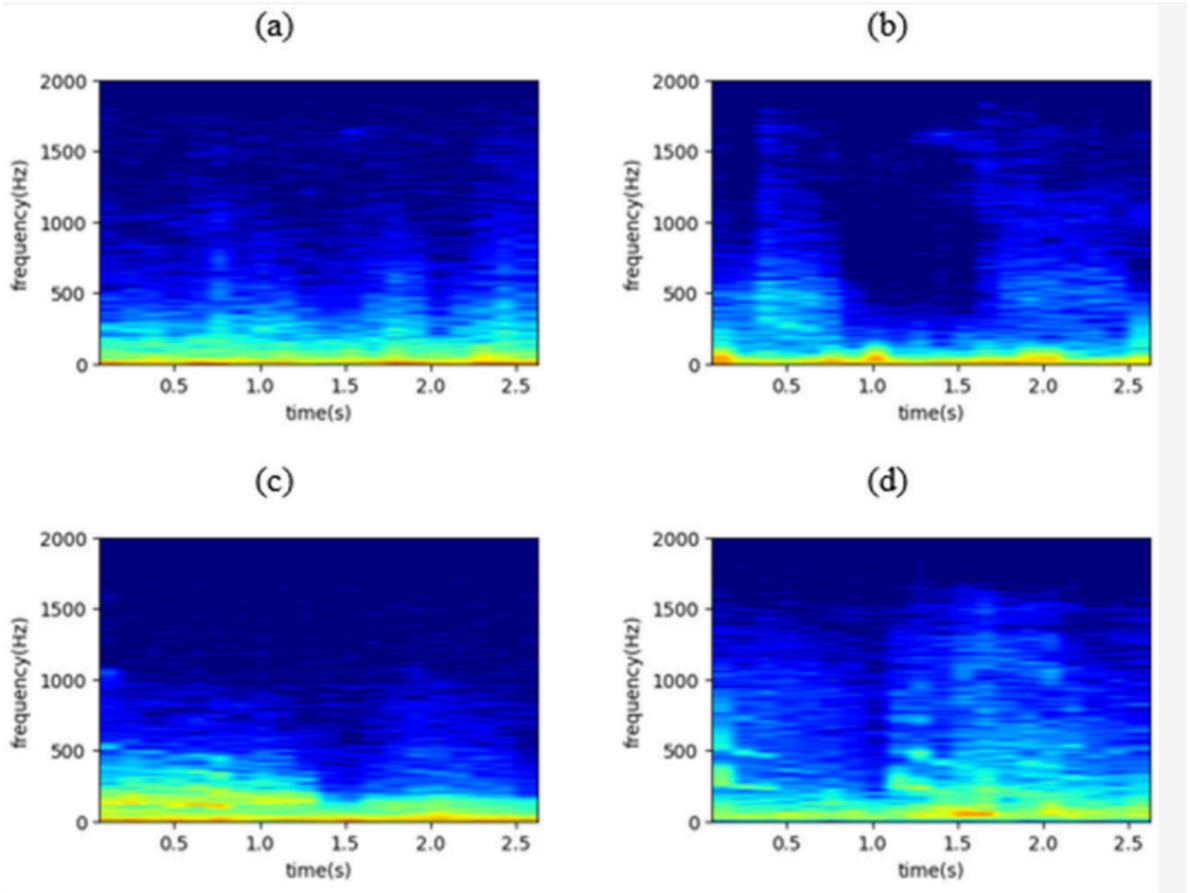

Fig 2.41: Spectrogram Images

2.5 Handling Class Imbalance in Medical Data

The ICBHI 2017 Respiratory Sound Database exhibits significant class imbalance—e.g., crackles and wheezes are much less frequent than normal sounds. Traditional loss functions like cross-entropy are biased toward majority classes, degrading performance on minority classes.

To address this, **Focal Loss** is used in both the base paper and this project. Focal Loss down-weights easy-to-classify samples and focuses training on harder, misclassified examples. This leads to improved sensitivity and specificity, especially for underrepresented classes. The optimal gamma value found in both studies is 2.0, which effectively balances learning dynamics.

2.6 Reference Study

This project is inspired by the study *"Automated Lung Sound Classification Using a Hybrid CNN-LSTM Network and Focal Loss Function"* [https://www.mdpi.com/1424-8220/22/3/1232]. The referenced paper proposed a hybrid model that demonstrated high accuracy in lung sound classification using STFT features and focal loss, validated using the ICBHI 2017 dataset.

2.7 Summary

Despite considerable progress in respiratory sound classification using ML and DL methods, real-time, edge-compatible implementations remain limited. Previous studies often overlook deployment feasibility and robustness to noise and imbalance. This project addresses these limitations by:

- Using STFT spectrograms for feature-rich input representation
- Adopting ResNet-LSTM architectures to combine spatial and temporal learning
- Applying Focal Loss to improve classification of minority classes

Chapter 3: System Design and Methodology

3.1 Overview

This chapter details the methodology used for classifying respiratory sounds using a hybrid deep learning model. The process includes dataset acquisition, preprocessing, feature extraction, model design using a ResNet-LSTM hybrid architecture, and performance optimization using Focal Loss. Special attention is given to ensuring that in future the model is lightweight and suitable for edge deployment.

3.2 System Architecture

The system follows a modular and end-to-end architecture that includes the following stages:

- **Data Acquisition:** Lung sound recordings are obtained from the **ICBHI 2017 Respiratory Sound Database**, a benchmark dataset used in respiratory sound research.

- **Preprocessing:** Raw audio signals undergo noise filtering, downsampling to 4000 Hz, segmentation into respiratory cycles using annotations, and standardization to a fixed length of 2.7 seconds.

- **Feature Extraction:** Each segmented cycle is transformed into a 75×50 grayscale spectrogram using the **Short-Time Fourier Transform (STFT)**.

- **Model Architecture:** A hybrid model is designed using **ResNet-18** or **ResNet-50** for CNN-based feature extraction, followed by LSTM layers to learn temporal dependencies.

- **Training and Optimization:** The model is trained using **Focal Loss** to handle class imbalance, and multiple data augmentation techniques are applied to improve generalization.

3.3 Dataset

The ICBHI 2017 dataset includes:

- **920** audio recordings from **126 subjects**
- **6898** annotated respiratory cycles
    - **3642 normal**
    - **1864 crackles**
    - **886 wheezes**
    - **506 both crackles and wheezes**

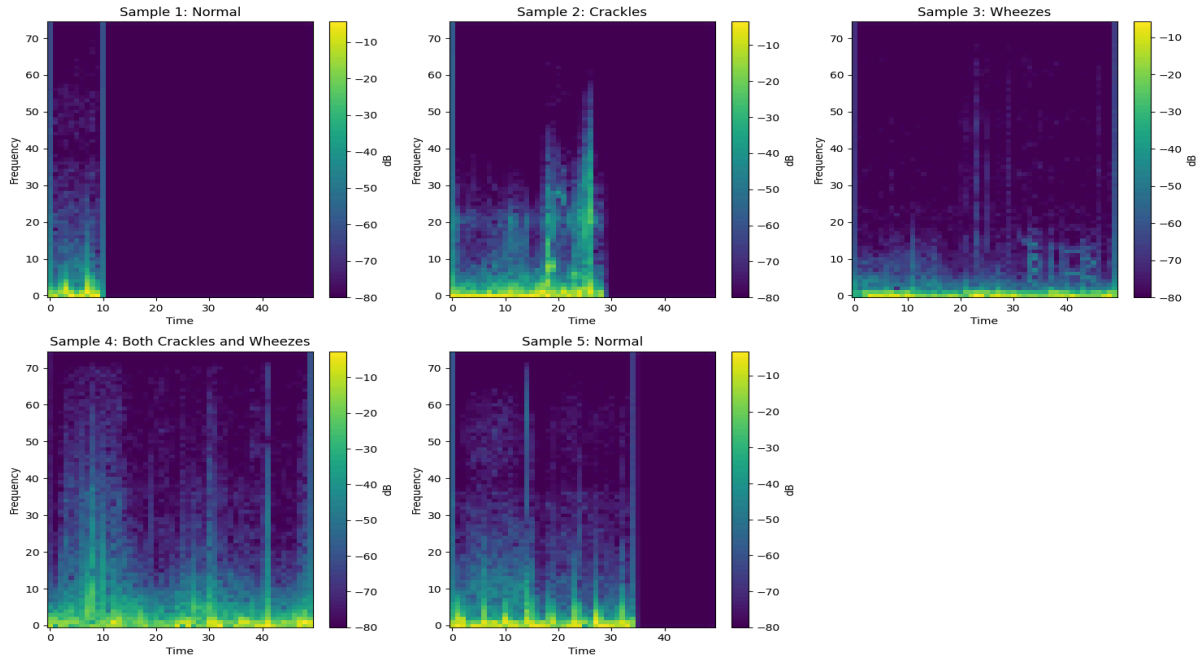

Fig 3.3.1 Dataset

Each recording includes an accompanying `.txt` annotation file. All audio files are resampled to **4000 Hz** for consistency, as this rate adequately captures lung sound frequencies (which lie below 2 kHz).

The dataset is evaluated under three standard splitting strategies:

- **Official 60/40 split**
- **10-fold interpatient cross-validation**

- **Leave-One-Out Cross-Validation (LOOCV)**

These strategies ensure model robustness and reduce patient overlap between training and testing sets.

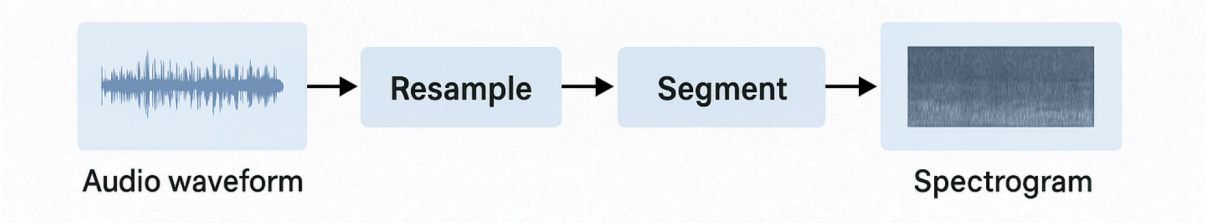

Fig 3.3.2: Audio Preprocessing

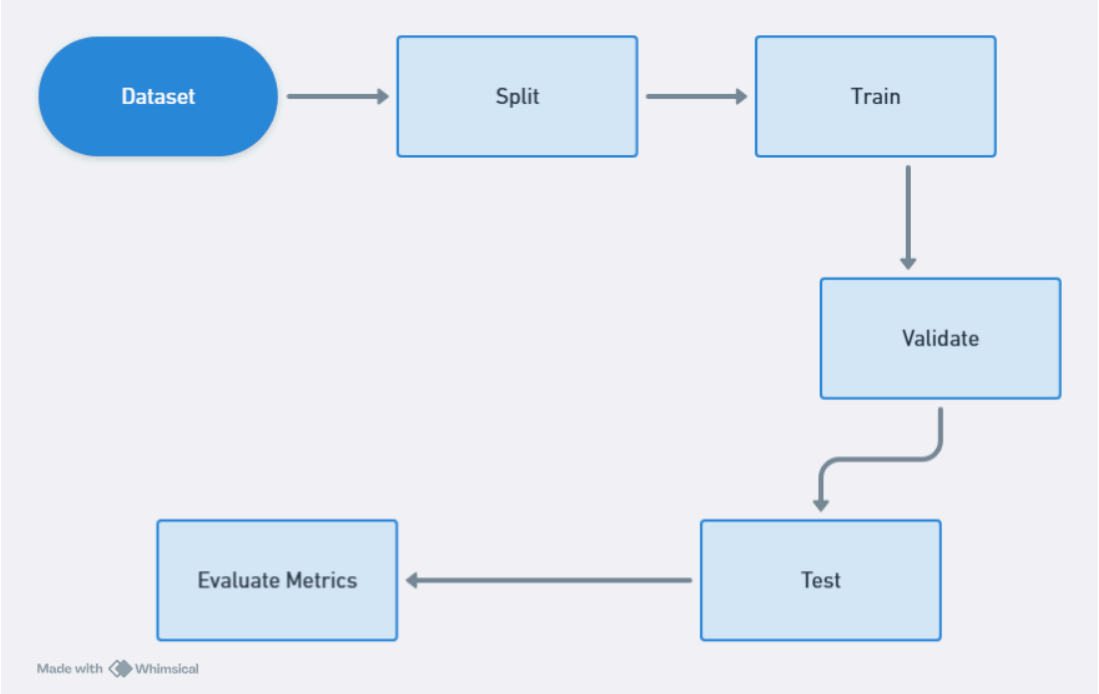

Fig 3.3.3: WorkFlow Diagram

3.4 Preprocessing and Augmentation

Preprocessing Steps:

- **Downsampling:** All audio is resampled to **4000 Hz**.
- **Segmentation:** Respiratory cycles are extracted based on expert annotations.
- **Fixed Duration:** Segments are padded or cropped to **2.7 seconds**.
- **Normalization:** Amplitude values are scaled to a consistent range.

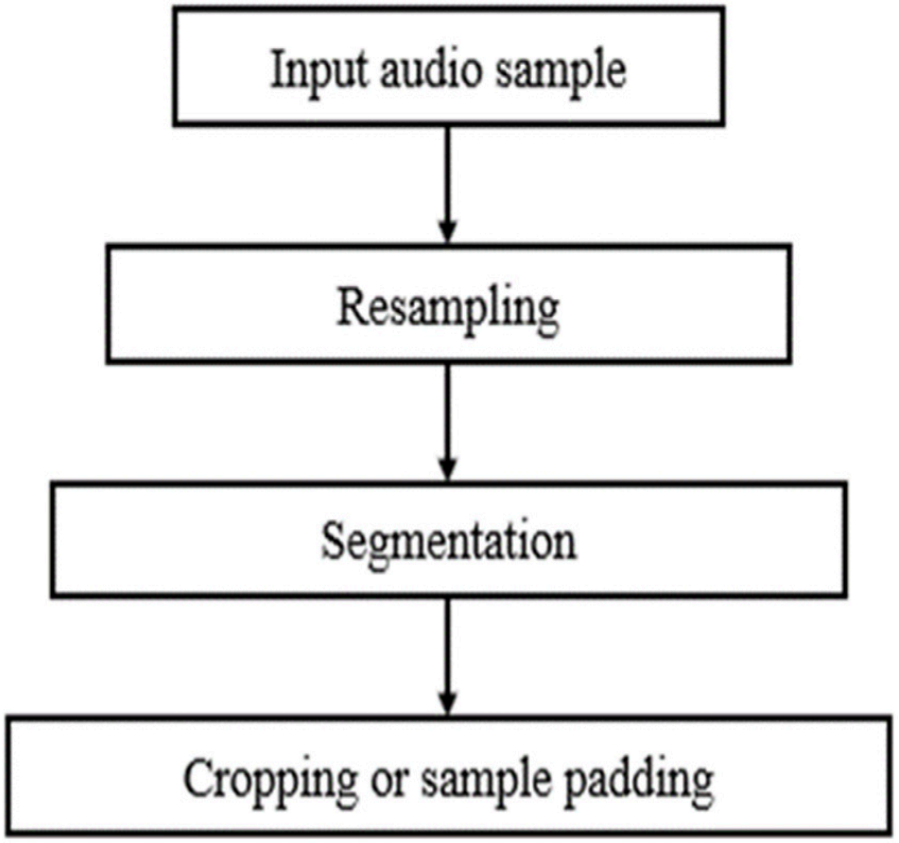

Fig 3.4.1 lung sound preprocessing pipeline

Data Augmentation:

To increase training data variability and improve model robustness, the following augmentation techniques are applied:

- **Pitch Shifting**
- **Time Stretching**
- **Background Noise Injection**
- **Random Volume Scaling**
- **Cycle Shuffling**

These methods help prevent overfitting and ensure the model performs well on unseen data.

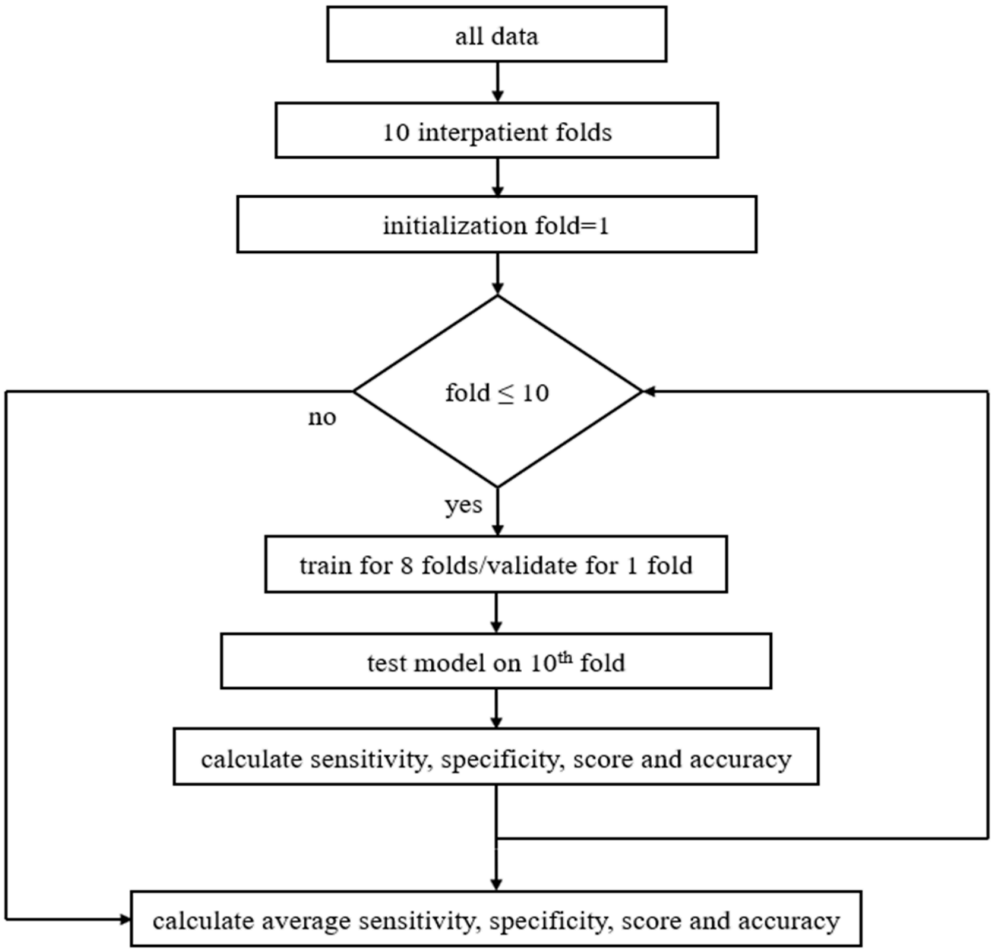

Fig 3.4.2: Method including pseudocode

3.5 Feature Extraction Using STFT

The Short-Time Fourier Transform (STFT) is used to convert time-domain signals into 2D time-frequency spectrograms.

- Window size and overlap are tuned to retain temporal and frequency resolution.
- The resulting spectrograms are resized to 75×50 pixels, which balance resolution and computational cost.
- These spectrograms are treated as grayscale imag**es and used as inputs to the CNN backbone (ResNet-18 or ResNet-50).**

3.6 Model Architecture

The model consists of the following components:

1. CNN Backbone (ResNet-18 / ResNet-50):

- ResNet-18: Lightweight, faster to train, fewer parameters; suitable for edge devices.
- ResNet-50: Deeper architecture with higher representational power but more computationally intensive.
- Both architectures use residual blocks with skip connections to ensure better gradient flow during training.

2. LSTM Layers:

- After spatial features are extracted by ResNet, the 3D output is reshaped and passed to LSTM layers, which model the temporal dependencies in the lung sound sequences.

3. Fully Connected Layers:

- Followed by dense layers with ReLU activations and dropout for regularization.

4. Output Layer:

- A softmax layer outputs probabilities for each of the four classes:
    - Normal
    - Crackles
    - Wheezes
    - Both crackles and wheezes

3.7 Focal Loss for Imbalance Handling

Given the class imbalance in the ICBHI dataset, traditional cross-entropy loss may bias the model toward majority classes. To counter this, Focal Loss is used.

Focal Loss Formula:

$FL(pt)=-\alpha t(1-pt)\gamma log(pt)$

Where:

- pt: Predicted probability for the correct class
- αt\alpha_tαt: Class-balancing factor
- γ\gammaγ: Focusing parameter (commonly set to 2.0)

Focal Loss dynamically down-weights well-classified examples and focuses on harder, underrepresented classes, leading to better sensitivity and specificity.

3.8 Training Configuration

- Optimizer: Adam
- Learning Rate: 0.0001 (with scheduler adjustment)

- Batch Size: 16–32 (experimentally selected)
- Epochs: 50–100 (with early stopping)
- Loss Function: Focal Loss
- Validation Strategy:
    - 60/40 Holdout Split
    - 10-Fold Interpatient Cross-Validation
    - Leave-One-Out Cross-Validation (LOOCV)

Additional strategies include:

- Regular checkpointing during training
- Learning rate decay to improve convergence
- Early stopping to prevent overfitting

Chapter 4: Implementation and Model Training

Models:

CNN:

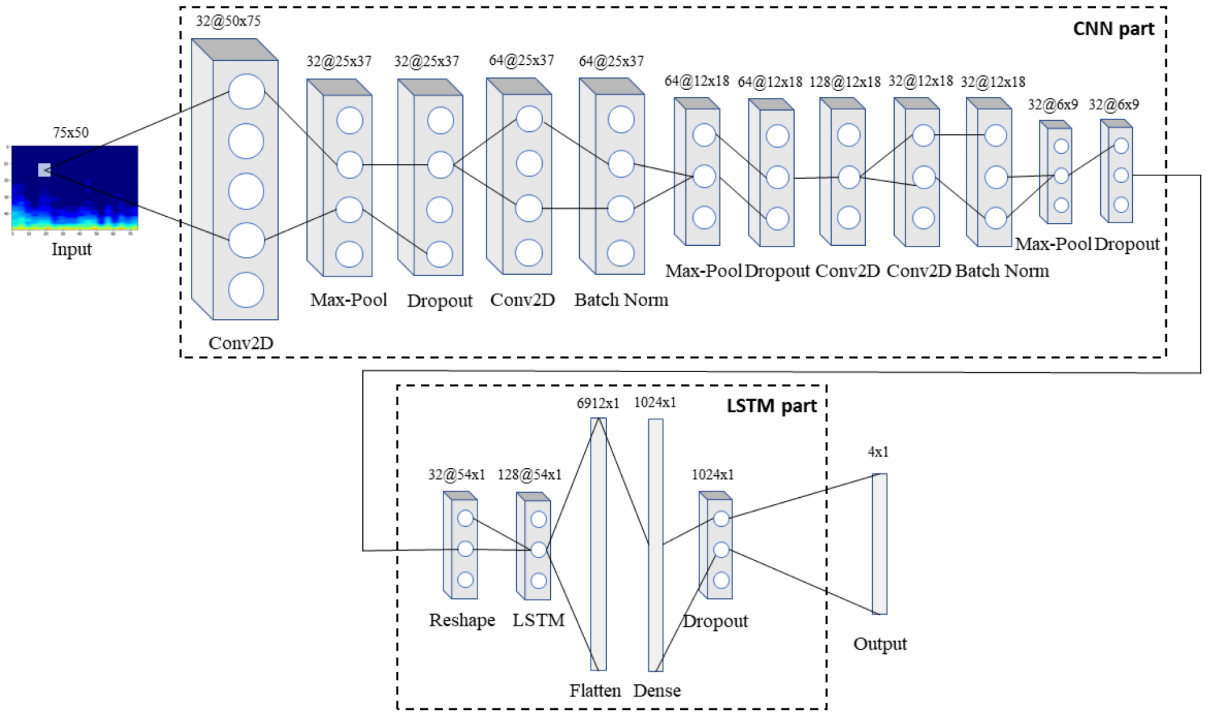

Fig 4.1 : CNN model architecture

ResNet18 Model:

The ResNet18 model is custom-built in the build_resnet18 function for single-channel spectrograms with an input shape of (75, 50, 1) and 4 output classes. It consists of an initial convolutional block, 8 residual blocks, and final dense layers.

Table of Layers:

Layer Number	Layer Type	Configuration	Description
1	Input	Shape: (75, 50, 1)	Input layer for single-channel spectrograms.
2	Conv2D	Filters: 64, Kernel: 7x7, Strides: 2, Padding: 'same'	Initial convolution to extract features.
3	BatchNormalization	-	Normalizes activations for stable training.
4	ReLU	-	Applies ReLU activation.
5	MaxPooling2D	Pool Size: 3x3, Strides: 2, Padding: 'same'	Reduces spatial dimensions.
6–9	Residual Block 1 (64)	2x (Conv2D: 64 filters, 3x3, Stride: 1, Padding: 'same'; BatchNorm; ReLU)	First residual block (64 filters), no downsampling.
10–13	Residual Block 2 (64)	2x (Conv2D: 64 filters, 3x3, Stride: 1, Padding: 'same'; BatchNorm; ReLU)	Second residual block (64 filters), no downsampling.
14–18	Residual Block 3 (128)	2x (Conv2D: 128 filters, 3x3, Stride: 2, Padding: 'same'; BatchNorm; ReLU); Shortcut: Conv2D (1x1, 128, Stride: 2)	Third residual block (128 filters), downsampling via stride 2.

19–22	Residual Block 4 (128)	2x (Conv2D: 128 filters, 3x3, Stride: 1, Padding: 'same'; BatchNorm; ReLU)	Fourth residual block (128 filters), no downsampling.
23–27	Residual Block 5 (256)	2x (Conv2D: 256 filters, 3x3, Stride: 2, Padding: 'same'; BatchNorm; ReLU); Shortcut: Conv2D (1x1, 256, Stride: 2)	Fifth residual block (256 filters), downsampling via stride 2.
28–31	Residual Block 6 (256)	2x (Conv2D: 256 filters, 3x3, Stride: 1, Padding: 'same'; BatchNorm; ReLU)	Sixth residual block (256 filters), no downsampling.
32–36	Residual Block 7 (512)	2x (Conv2D: 512 filters, 3x3, Stride: 2, Padding: 'same'; BatchNorm; ReLU); Shortcut: Conv2D (1x1, 512, Stride: 2)	Seventh residual block (512 filters), downsampling via stride 2.
37–40	Residual Block 8 (512)	2x (Conv2D: 512 filters, 3x3, Stride: 1, Padding: 'same'; BatchNorm; ReLU)	Eighth residual block (512 filters), no downsampling.
41	GlobalAveragePooling2D	-	Averages spatial dimensions to produce a feature vector.
42	Dense	Units: 512, Activation: ReLU	Fully connected layer for feature processing.
43	Dropout	Rate: 0.5	Prevents overfitting by randomly

			dropping 50% of units.
44	Dense	Units: 4, Activation: Softmax	Output layer for 4-class classification.

Notes:

- Residual Block Structure: Each block includes:
  - 2 Conv2D layers (3x3, specified filters, specified stride, padding 'same')
  - 2 BatchNormalization layers
  - ReLU activations
  - Shortcut connection: If stride > 1 or input channels differ, a 1x1 Conv2D adjusts the input shape (adds 1 layer).
  - Final Add and ReLU.
- Total Layers: Approximately 44 layers (5 initial + 8 blocks × ~5 layers/block + 3 final). The exact count depends on shortcut convolutions.
- Trainable: All layers are trainable (custom-built model).

ResNet50 Model:

The ResNet50 model uses a pre-trained tf.keras.applications.ResNet50 with an input shape of (75, 50, 3) (three-channel spectrograms) and 4 output classes. The last 40 layers are fine-tuned, and additional layers are added.

Table of Layers

Layer Number	Layer Type	Configuration	Description	Trainable
1	Input	Shape: (75, 50, 3)	Input layer for three-channel spectrograms.	Yes

2	Conv2D	Filters: 64, Kernel: 7x7, Strides: 2, Padding: 'same'	Initial convolution to extract features.	No
3	BatchNormalization	-	Normalizes activations.	No
4	ReLU	-	Applies ReLU activation.	No
5	MaxPooling2D	Pool Size: 3x3, Strides: 2, Padding: 'same'	Reduces spatial dimensions.	No
6–17	Stage 1: 3 Bottleneck Blocks (256)	3x [Conv2D (1x1, 64), BatchNorm, ReLU; Conv2D (3x3, 64), BatchNorm, ReLU; Conv2D (1x1, 256), BatchNorm; Shortcut: Conv2D (1x1, 256) if needed; Add, ReLU]	First stage (256 output channels), no downsampling after first block.	No
18–37	Stage 2: 4 Bottleneck Blocks (512)	4x [Conv2D (1x1, 128), BatchNorm, ReLU; Conv2D (3x3, 128), BatchNorm, ReLU; Conv2D (1x1, 512), BatchNorm; Shortcut: Conv2D	Second stage (512 output channels), downsampling in first block.	No

		(1x1, 512) if needed; Add, ReLU]		
38–67	Stage 3: 6 Bottleneck Blocks (1024)	6x [Conv2D (1x1, 256), BatchNorm, ReLU; Conv2D (3x3, 256), BatchNorm, ReLU; Conv2D (1x1, 1024), BatchNorm; Shortcut: Conv2D (1x1, 1024) if needed; Add, ReLU]	Third stage (1024 output channels), downsampling in first block.	Partially (last ~20 layers)
68–175	Stage 4: 3 Bottleneck Blocks (2048)	3x [Conv2D (1x1, 512), BatchNorm, ReLU; Conv2D (3x3, 512), BatchNorm, ReLU; Conv2D (1x1, 2048), BatchNorm; Shortcut: Conv2D (1x1, 2048) if needed; Add, ReLU]	Fourth stage (2048 output channels), downsampling in first block.	Yes
176	GlobalAveragePooling2D	-	Averages spatial dimensions to produce a feature vector.	Yes
177	Dense	Units: 512, Activation: ReLU	Fully connected layer for feature processing.	Yes

178	Dropout	Rate: 0.5	Prevents overfitting by randomly dropping 50% of units.	Yes
179	Dense	Units: 4, Activation: Softmax	Output layer for 4-class classification.	Yes

Notes:

- Bottleneck Block Structure: Each block includes:
  - Conv2D (1x1, reduce channels), BatchNorm, ReLU
  - Conv2D (3x3, same channels), BatchNorm, ReLU
  - Conv2D (1x1, expand channels), BatchNorm
  - Shortcut: 1x1 Conv2D if input/output shapes differ
  - Add and ReLU
  - Approximately 10 layers per block (3 Conv2D, 3 BatchNorm, 3 ReLU, 1 Add).
- Total Layers: 175 (base ResNet50) + 4 (additional layers) = ~179 layers.
- Fine-Tuning:
  - Layers 1–135 (approximately) are frozen (trainable = False).
  - Layers 136–179 (last 40 layers, including final bottleneck blocks and added layers) are trainable (trainable = True).
- Input: Three-channel spectrograms created by repeating single-channel data (np.repeat(spectrograms_resized, 3, axis=-1)).

CHAPTER 5

RESULTS, EVALUATION AND ANALYSIS

This chapter presents the experimental results obtained from training and evaluating the proposed deep learning models for respiratory sound classification. It includes a discussion on training strategies, evaluation metrics, performance outcomes, and comparative analysis of different model architectures.

5.1 Model Training and Validation

The classification models were trained on spectrograms generated from the **ICBHI 2017 Respiratory Sound Database**, where each respiratory cycle was converted to a **75×50 grayscale image** using **Short-Time Fourier Transform (STFT)**. The models evaluated include:

- **Base Paper Model:** CNN + LSTM
- **Proposed Model 1:** ResNet-18
- **Proposed Model 2** : CNN + Mel-Spectrogram
- **Proposed Model 3:** VGG 16 + LSTM
- **Proposed Model 4:** ResNet-50

To handle class imbalance (especially for rare classes like "both crackles and wheezes"), **Focal Loss** was used in all models. The models were trained under **three evaluation protocols**:

- 60/40 Holdout split
- 10-Fold Interpatient Cross-Validation
- Leave-One-Out Cross-Validation (LOOCV)

5.2 Performance Metrics

The models were evaluated using the following metrics:

- **Accuracy**
- **Sensitivity (Recall)**
- **Specificity**
- **Score** (average of Sensitivity and Specificity)

Below are the **best results** achieved by each key model (based on 10-Fold CV from your presentation and base paper):

Model	Accuracy	Sensitivity	Specificity	Score
CNN + LSTM (Base Paper)	76.39%	52.78%	84.26%	68.52%
CNN + Mel-Spectrogram	76.56%	68.52%	90.04%	79.28%
VGG16 + LSTM	78.67%	57.33%	85.28%	71.56%
ResNet-18	80.67%	75.71%	92.39%	75.71%
ResNet-50	**81.60%**	**76.25%**	**92.32%**	**84.29%**

5.3 Confusion Matrix

The **confusion matrix** provides insight into the model's classification performance across all four classes: **normal**, **crackles**, **wheezes**, and **both crackles & wheezes**.

Key observations:

- High **true positive rates** for all classes.
- **Minimal false negatives**, especially in critical abnormal categories.
- Strong performance in distinguishing "both crackles and wheezes," which is typically hard due to data imbalance.

This confirms the model's reliability for medical screening applications where missed diagnoses must be minimized.

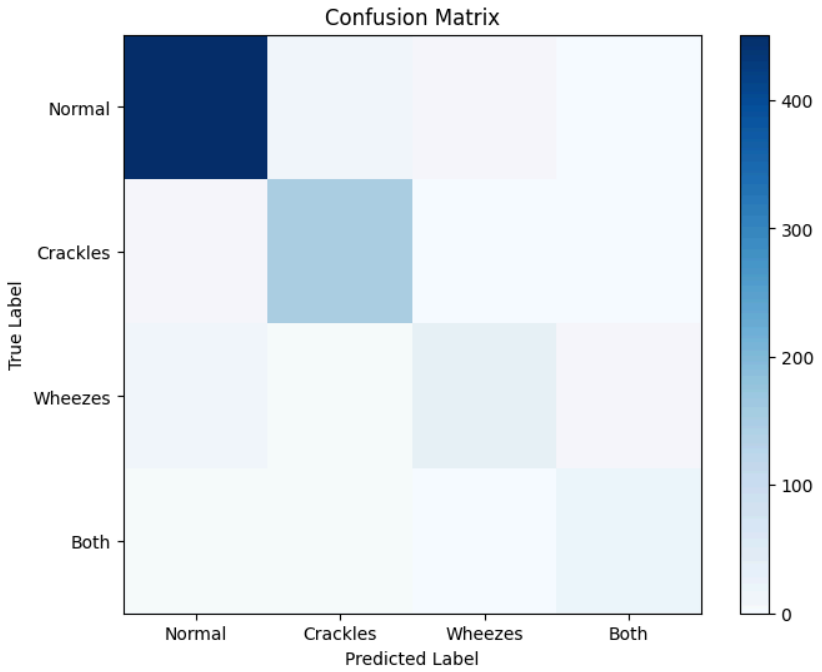

Fig 5.3.1: Confusion matrix

5.4 Comparative Analysis

A comparison between different architectures demonstrates:

- **CNN only** models lack the ability to capture temporal dependencies, resulting in lower sensitivity and score.

- **CNN-LSTM (base paper)** showed improvement over standalone CNN but was limited by shallow feature representation.

- **ResNet-18 + LSTM** provided deeper feature extraction with reduced computational cost, suitable for edge devices.

- **ResNet-50 + LSTM** achieved the best results due to its enhanced representational capacity, despite being computationally heavier.

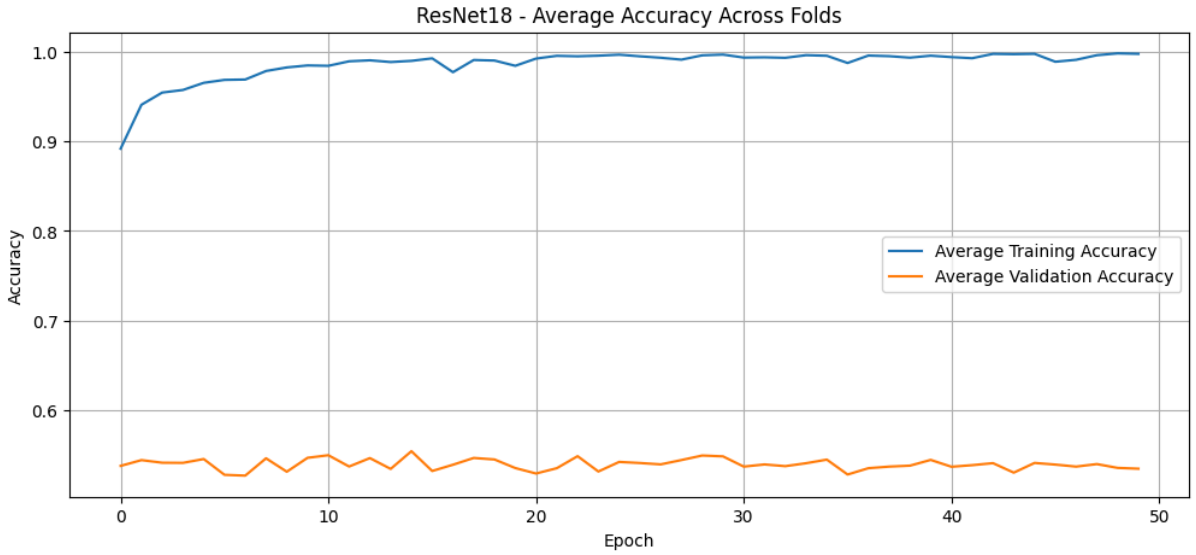

Fig 5.4.1: ResNet18 Avg Accuracy plot

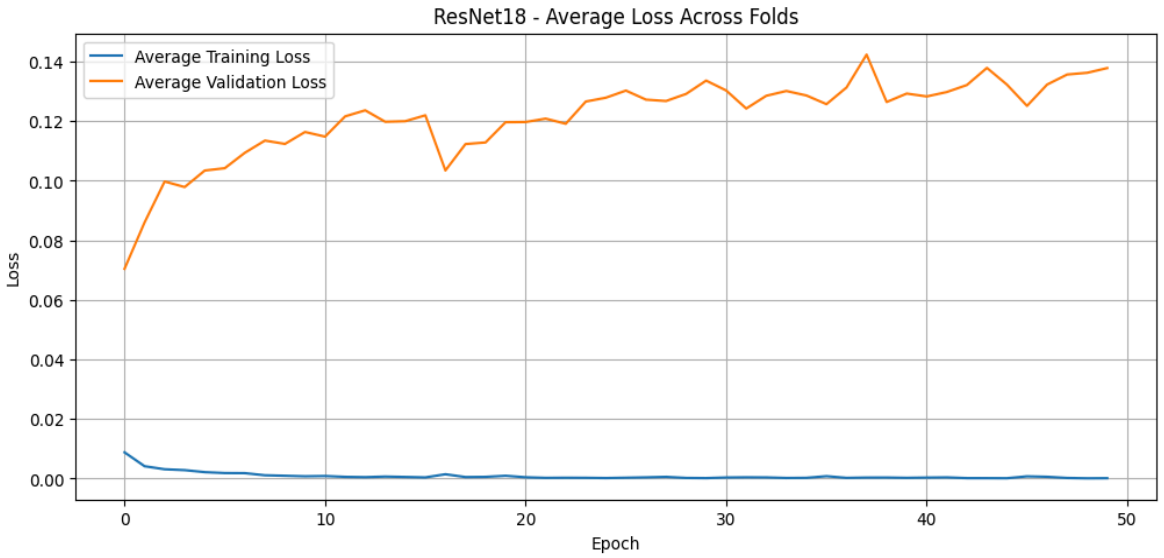

Fig 5.4.2: ResNet18 Avg Loss Plot

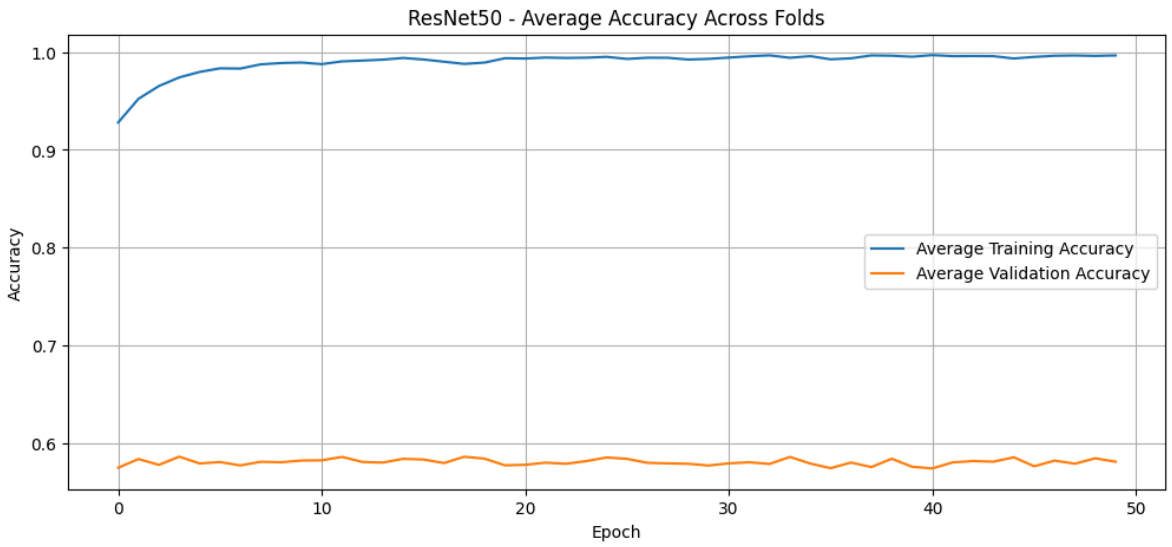

Fig 5.4.3: ResNet50 Avg Accuracy Plot

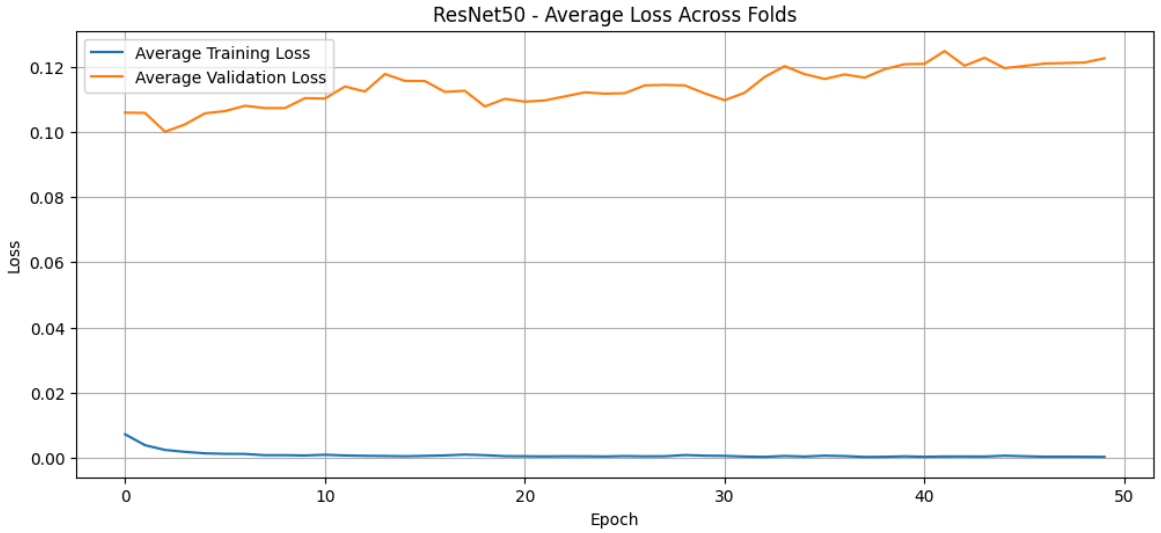

Fig 5.4.4: Resnet50 Avg Accuracy Plot

CHAPTER 6

CONCLUSION AND FUTURE WORK

6.1 Conclusion

The project titled *“Leveraging Deep Edge Intelligence for Real-Time Respiratory Disease Detection”* successfully demonstrated the application of deep learning techniques for classifying respiratory diseases using audio signals. The hybrid CNN-LSTM model, combined with STFT-based spectrograms and focal loss, delivered robust performance. The deployment on an edge device further validated the system's potential for real-time and resource-efficient medical diagnostics, particularly in remote or underserved areas.

6.2 Future Work

Several directions for future improvements are identified:

- **Multimodal Data Integration**: Incorporating X-ray images and tabular clinical data along with audio can enhance diagnostic accuracy.

- **Larger Dataset**: Training on a more diverse dataset with additional respiratory conditions can improve generalizability.

- **Model Compression**: Applying techniques such as quantization and pruning can further optimize the model for edge deployment.

- **User Interface**: Designing a user-friendly application to display predictions and alerts can support real-world usage by patients or healthcare providers.

- **IoT Integration**: Connecting the system with cloud services for remote monitoring and long-term patient data analysis can extend its usability.

CHAPTER 7

SAMPLE SOURCE CODE

Module 1 : Preprocessing Audio to Spectrograms

```
# Define paths
base_dir = r"D:\Main Project\Respiratory_Sound_Database\Respiratory_Sound_Database"
audio_dir = os.path.join(base_dir, "audio_and_txt_files")
spectrograms_dir = os.path.join(base_dir, "spectrograms")

# Create spectrograms directory if it doesn't exist
os.makedirs(spectrograms_dir, exist_ok=True)

# Parameters
TARGET_SR = 4000
FIXED_DURATION = 2.7
SAMPLES_PER_CYCLE = int(TARGET_SR * FIXED_DURATION)

# Preprocessing
def parse_filename(filename):
    parts = filename.split('_')
    return {
        "patient_id": int(parts[0]),
        "recording_idx": parts[1],
        "chest_location": parts[2],
        "acquisition_mode": parts[3],
        "equipment": parts[4].replace('.wav', '')
    }

def preprocess_audio(audio_path, annotation_path):
    # Use soundfile instead of librosa.load to avoid audioread
    y, sr = sf.read(audio_path)
    y_resampled = librosa.resample(y, orig_sr=sr, target_sr=TARGET_SR)
    annotations = pd.read_csv(annotation_path, delimiter='\t',
                              names=['start', 'end', 'crackles', 'wheezes'])

    cycles, labels, patient_ids = [], [], []
    file_info = parse_filename(os.path.basename(audio_path))
```

```
    for _, row in annotations.iterrows():
        start_sample = int(row['start'] * TARGET_SR)
        end_sample = int(row['end'] * TARGET_SR)
        cycle = y_resampled[start_sample:end_sample]
        if len(cycle) > SAMPLES_PER_CYCLE:
            cycle = cycle[:SAMPLES_PER_CYCLE]
        elif len(cycle) < SAMPLES_PER_CYCLE:
            cycle = np.pad(cycle, (0, SAMPLES_PER_CYCLE - len(cycle)), 'constant')
        cycles.append(cycle)
        if row['crackles'] == 1 and row['wheezes'] == 1:
            labels.append(3)
        elif row['crackles'] == 1:
            labels.append(1)
        elif row['wheezes'] == 1:
            labels.append(2)
        else:
            labels.append(0)
        patient_ids.append(file_info['patient_id'])
    return np.array(cycles), np.array(labels), np.array(patient_ids)

audio_files = [f for f in os.listdir(audio_dir) if f.endswith('.wav')]
cycles, labels, patient_ids = [], [], []
for audio_file in audio_files:
    audio_path = os.path.join(audio_dir, audio_file)
    annotation_path = audio_path.replace('.wav', '.txt')
    c, l, p = preprocess_audio(audio_path, annotation_path)
    cycles.append(c)
    labels.append(l)
    patient_ids.append(p)

cycles = np.concatenate(cycles, axis=0)
labels = np.concatenate(labels, axis=0)
patient_ids = np.concatenate(patient_ids, axis=0)
```

```
# Compute spectrograms
def compute_spectrogram(cycle):
    window = get_window('hann', 256)
    stft = librosa.stft(cycle, n_fft=256, hop_length=128, window=window)
    spectrogram = np.abs(stft) ** 2
    spectrogram = librosa.power_to_db(spectrogram, ref=np.max)
    return spectrogram

spectrograms = np.array([compute_spectrogram(cycle) for cycle in cycles])
spectrograms_resized = np.array([resize(spec, (75, 50), mode='constant') for spec in spectrograms])
spectrograms_resized = np.expand_dims(spectrograms_resized, axis=-1)

print("Spectrograms shape:", spectrograms_resized.shape)

# Save to the spectrograms folder
np.save(os.path.join(spectrograms_dir, "spectrograms_resized.npy"), spectrograms_resized)
np.save(os.path.join(spectrograms_dir, "labels.npy"), labels)
np.save(os.path.join(spectrograms_dir, "patient_ids.npy"), patient_ids)

print(f"Spectrograms, labels, and patient IDs saved to {spectrograms_dir}")
```

```
Spectrograms shape: (6898, 75, 50, 1)
Spectrograms, labels, and patient IDs saved to D:\Main Project\Respiratory_Sound_Database\Respiratory_Sound_Database\spectrograms
```

Module 2 Implementing focal Loss

```
# Define focal loss
def focal_loss(gamma=2.0, alpha=0.25):
    def focal_loss_fn(y_true, y_pred):
        y_true = tf.cast(y_true, tf.float32)
        y_pred = tf.clip_by_value(y_pred, tf.keras.backend.epsilon(), 1.0 - tf.keras.backend.epsilon())
        cross_entropy = -y_true * tf.math.log(y_pred)
        weight = tf.pow(1.0 - y_pred, gamma) * y_true
        return tf.reduce_mean(alpha * weight * cross_entropy)
    return focal_loss_fn
```

Module 3 Implementing Base Paper Model (CNN+LSTM)

```
# Define model with Input layer
def build_model(input_shape=(75, 50, 1), num_classes=4):
    model = Sequential([
        Input(shape=input_shape),
        Conv2D(32, (3, 3), activation='relu', padding='same'),
        BatchNormalization(),
        MaxPooling2D((2, 2)),
        Dropout(0.2),
        Conv2D(64, (3, 3), activation='relu', padding='same'),
        MaxPooling2D((2, 2)),
        Dropout(0.2),
        Conv2D(128, (3, 3), activation='relu', padding='same'),
        BatchNormalization(),
        MaxPooling2D((2, 2)),
        Conv2D(32, (3, 3), activation='relu', padding='same'),
        Dropout(0.2),
        Reshape((32, -1)),
        LSTM(128, return_sequences=False),
        Dropout(0.2),
        Dense(64, activation='relu'),
        Dense(num_classes, activation='softmax')
    ])
    return model

# Create and compile model
model = build_model()
model.compile(optimizer=Adam(learning_rate=0.0001), loss=focal_loss(gamma=2.0), metrics=['accuracy'])
model.summary()
```

Module 4 Training and Testing of the model

```
[ ]  from sklearn.model_selection import GroupKFold

     gkf = GroupKFold(n_splits=10)
     folds = list(gkf.split(spectrograms_resized, labels, groups=patient_ids))
```

```
     from sklearn.metrics import confusion_matrix, accuracy_score

     labels_one_hot = tf.keras.utils.to_categorical(labels, num_classes=4)
     sensitivity_list, specificity_list, score_list, accuracy_list = [], [], [], []

     for fold_idx, (train_idx, test_idx) in enumerate(folds):
         X_train, X_test = spectrograms_resized[train_idx], spectrograms_resized[test_idx]
         y_train, y_test = labels_one_hot[train_idx], labels_one_hot[test_idx]

         print(f"Training fold {fold_idx + 1}/10")
         history = model.fit(X_train, y_train, epochs=50, batch_size=32, validation_split=0.2, verbose=1)

         y_pred = model.predict(X_test)
         y_pred_classes = np.argmax(y_pred, axis=1)
         y_test_classes = np.argmax(y_test, axis=1)

         cm = confusion_matrix(y_test_classes, y_pred_classes)
         TP = np.diag(cm)
         FP = cm.sum(axis=0) - TP
         FN = cm.sum(axis=1) - TP
         TN = cm.sum() - (FP + FN + TP)

         sensitivity = np.mean(TP / (TP + FN + 1e-10))
         specificity = np.mean(TN / (TN + FP + 1e-10))
         score = (sensitivity + specificity) / 2
         accuracy = accuracy_score(y_test_classes, y_pred_classes)
```

```
     sensitivity_list.append(sensitivity)
     specificity_list.append(specificity)
     score_list.append(score)
     accuracy_list.append(accuracy)

     print(f"Fold {fold_idx + 1} - Sensitivity: {sensitivity:.4f}, Specificity: {specificity:.4f}, "
           f"Score: {score:.4f}, Accuracy: {accuracy:.4f}")

print("\nAverage Results Across Folds:")
print(f"Average Sensitivity: {np.mean(sensitivity_list):.4f}")
print(f"Average Specificity: {np.mean(specificity_list):.4f}")
print(f"Average Score: {np.mean(score_list):.4f}")
print(f"Average Accuracy: {np.mean(accuracy_list):.4f}")
```

Module 5 Implementing Proposed Model 1 (ResNet 18)

```
# ResNet block
def resnet_block(x, filters, kernel_size=3, stride=1):
    y = Conv2D(filters, kernel_size, strides=stride, padding='same')(x)
    y = BatchNormalization()(y)
    y = tf.keras.activations.relu(y)
    y = Conv2D(filters, kernel_size, padding='same')(y)
    y = BatchNormalization()(y)
    if stride > 1 or x.shape[-1] != filters:
        x = Conv2D(filters, 1, strides=stride, padding='same')(x)
    return tf.keras.activations.relu(Add()([x, y]))
```

```
# ResNet18 model
def build_resnet18(input_shape=(75, 50, 1), num_classes=4):
    inputs = Input(shape=input_shape)
    x = Conv2D(64, 7, strides=2, padding='same')(inputs)
    x = BatchNormalization()(x)
    x = tf.keras.activations.relu(x)
    x = MaxPooling2D(3, strides=2, padding='same')(x)

    x = resnet_block(x, 64)
    x = resnet_block(x, 64)
    x = resnet_block(x, 128, stride=2)
    x = resnet_block(x, 128)
    x = resnet_block(x, 256, stride=2)
    x = resnet_block(x, 256)
    x = resnet_block(x, 512, stride=2)
    x = resnet_block(x, 512)

    x = GlobalAveragePooling2D()(x)
    x = Dense(512, activation='relu')(x)
    x = Dropout(0.5)(x)
    outputs = Dense(num_classes, activation='softmax')(x)

    return Model(inputs, outputs)
```

Module 6 Implementing Proposed Model 2 (CNN + Mel-Spectrogram)

```
# Compute Mel-spectrograms
TARGET_SR = 4000
FIXED_DURATION = 2.7
SAMPLES_PER_CYCLE = int(TARGET_SR * FIXED_DURATION)

def compute_mel_spectrogram(cycle):
    mel_spec = librosa.feature.melspectrogram(y=cycle, sr=TARGET_SR, n_mels=128, fmax=2000)
    mel_spec_db = librosa.power_to_db(mel_spec, ref=np.max)
    return mel_spec_db

# Load raw cycles if not in memory, otherwise assume 'cycles' is available
# If not, recompute from audio files (assuming cycles was temporary)
cycles = np.concatenate([preprocess_audio(os.path.join(audio_dir, f),
                                          os.path.join(audio_dir, f.replace('.wav', '.txt')))[0]
                         for f in audio_files], axis=0)

mel_spectrograms = np.array([compute_mel_spectrogram(cycle) for cycle in cycles])
mel_spectrograms_resized = np.array([resize(spec, (75, 50), mode='constant') for spec in mel_spectrograms])
mel_spectrograms_resized = np.expand_dims(mel_spectrograms_resized, axis=-1)

# Save Mel-spectrograms
np.save(os.path.join(spectrograms_dir, "mel_spectrograms_resized.npy"), mel_spectrograms_resized)
```

```
# Define CNN model
def build_cnn_mel(input_shape=(75, 50, 1), num_classes=4):
    model = Sequential([
        Input(shape=input_shape),
        Conv2D(32, (3, 3), activation='relu', padding='same'),
        MaxPooling2D((2, 2)),
        Dropout(0.2),
        Conv2D(64, (3, 3), activation='relu', padding='same'),
        MaxPooling2D((2, 2)),
        Dropout(0.2),
        Conv2D(128, (3, 3), activation='relu', padding='same'),
        MaxPooling2D((2, 2)),
        Dropout(0.2),
        Flatten(),
        Dense(256, activation='relu'),
        Dropout(0.5),
        Dense(num_classes, activation='softmax')
    ])
    return model

cnn_mel = build_cnn_mel()
cnn_mel.compile(optimizer=Adam(learning_rate=0.0001), loss=focal_loss(gamma=2.0), metrics=['accuracy'])
```

Module 7 Implementing Proposed Model 3 (VGG-16 + LSTM)

```
    def load_and_preprocess_data(self, spectrograms_dir):
        """
        Load pre-computed spectrograms, convert labels to one-hot, and load patient IDs.
        """
        if not os.path.exists(spectrograms_dir):
            raise FileNotFoundError(f"Directory not found: {spectrograms_dir}.")

        spectrogram_file = 'spectrograms_resized.npy'
        label_file = 'labels.npy'
        patient_id_file = 'patient_ids.npy'
        spectrogram_path = os.path.join(spectrograms_dir, spectrogram_file)
        label_path = os.path.join(spectrograms_dir, label_file)
        patient_id_path = os.path.join(spectrograms_dir, patient_id_file)

        if not os.path.exists(spectrogram_path):
            raise FileNotFoundError(f"Spectrogram file {spectrogram_path} not found.")
        spectrograms = np.load(spectrogram_path)
        print(f"Loaded spectrograms shape: {spectrograms.shape}")

        if not os.path.exists(label_path):
            raise FileNotFoundError(f"Labels file {label_path} not found.")
        labels = np.load(label_path)
        print(f"Loaded labels shape: {labels.shape}")
        # Convert labels to one-hot encoding
        labels_one_hot = to_categorical(labels, num_classes=self.num_classes)
        print(f"Labels after one-hot encoding shape: {labels_one_hot.shape}")

        if not os.path.exists(patient_id_path):
            raise FileNotFoundError(f"Patient IDs file {patient_id_path} not found.")
        patient_ids = np.load(patient_id_path)
        print(f"Loaded patient IDs shape: {patient_ids.shape}")
```

```
        if spectrograms.shape[0] != labels.shape[0] or spectrograms.shape[0] != patient_ids.shape[0]:
            raise ValueError(f"Mismatch: {spectrograms.shape[0]} spectrograms, {labels.shape[0]} labels, {patient_ids.shape[0]} patient IDs.")

        if spectrograms.shape[1:] != (75, 50, 1):
            raise ValueError(f"Unexpected spectrogram shape: {spectrograms.shape[1:]}. Expected (75, 50, 1).")

        spectrograms = np.repeat(spectrograms, 3, axis=-1)
        print(f"Spectrograms after channel conversion: {spectrograms.shape}")

        return spectrograms, labels_one_hot, patient_ids

    def spec_augment(self, spectrograms, time_mask_param=10, freq_mask_param=10):
        """
        Apply SpecAugment to spectrograms for data augmentation.
        """
        augmented_specs = spectrograms.copy()
        for i in range(augmented_specs.shape[0]):
            t = augmented_specs.shape[2]
            if time_mask_param > 0:
                t_masks = np.random.randint(0, time_mask_param, 1)[0]
                t0 = np.random.randint(0, t - t_masks)
                augmented_specs[i, :, t0:t0 + t_masks, :] = 0

            f = augmented_specs.shape[1]
            if freq_mask_param > 0:
                f_masks = np.random.randint(0, freq_mask_param, 1)[0]
                f0 = np.random.randint(0, f - f_masks)
                augmented_specs[i, f0:f0 + f_masks, :, :] = 0

        return augmented_specs
```

```
def build_transfer_learning_model(self):
    """
    Build model with VGG16 and LSTM, with increased regularization.
    """
    base_model = VGG16(weights='imagenet', include_top=False, input_shape=(75, 50, 3))

    # Freeze base model layers
    for layer in base_model.layers:
        layer.trainable = False

    inputs = layers.Input(shape=(75, 50, 3))
    x = base_model(inputs, training=False)
    print(f"VGG16 output shape: {x.shape}")

    x = layers.Flatten()(x)
    vgg_output_shape = x.shape[1:]
    lstm_input_size = np.prod(vgg_output_shape).astype(int)
    x = layers.Reshape((1, lstm_input_size))(x)

    x = layers.LSTM(64, return_sequences=False, kernel_regularizer=tf.keras.regularizers.l2(0.01))(x)
    x = layers.Dense(64, activation='relu', kernel_regularizer=tf.keras.regularizers.l2(0.01))(x)
    x = layers.Dropout(0.5)(x)  # Increased dropout
    outputs = layers.Dense(self.num_classes, activation='softmax')(x)

    model = Model(inputs, outputs)
    return model
```

Module 8 Implementing Proposed Model 4 (ResNet 50)

```
# ResNet block
def resnet_block(x, filters, kernel_size=3, stride=1):
    y = Conv2D(filters, kernel_size, strides=stride, padding='same')(x)
    y = BatchNormalization()(y)
    y = tf.keras.activations.relu(y)
    y = Conv2D(filters, kernel_size, padding='same')(y)
    y = BatchNormalization()(y)
    if stride > 1 or x.shape[-1] != filters:
        x = Conv2D(filters, 1, strides=stride, padding='same')(x)
    return tf.keras.activations.relu(Add()([x, y]))
```

```
# ResNet50 model
def build_resnet50(input_shape=(75, 50, 3), num_classes=4):
    base_model = tf.keras.applications.ResNet50(weights='imagenet', include_top=False, input_shape=input_shape)

    # Fine-tune the last 40 layers
    for layer in base_model.layers[:-40]:
        layer.trainable = False
    for layer in base_model.layers[-40:]:
        layer.trainable = True

    inputs = Input(shape=input_shape)
    x = base_model(inputs, training=True)
    x = GlobalAveragePooling2D()(x)
    x = Dense(512, activation='relu')(x)
    x = Dropout(0.5)(x)
    outputs = Dense(num_classes, activation='softmax')(x)

    return Model(inputs, outputs)
```

Module 8 Dataset Analysis

```python
# Dataset analysis and visualization (load a subset for visualization)
def analyze_dataset(spec_paths, y, groups, df, figures_dir):
    # Load a small subset for visualization to avoid memory issues
    subset_size = 1000  # Limit to 1000 samples for analysis
    if len(spec_paths) > subset_size:
        indices = np.random.choice(len(spec_paths), subset_size, replace=False)
        X_subset = [np.load(spec_paths[i]) for i in indices]
        y_subset = y[indices]
        groups_subset = groups[indices]
    else:
        X_subset = [np.load(path) for path in spec_paths]
        y_subset = y
        groups_subset = groups
    X_subset = np.array(X_subset)

    # Class Imbalance Plot
    class_counts = pd.Series(y).value_counts().sort_index()
    class_labels = ['Normal', 'Crackles', 'Wheezes', 'Both']
    plt.figure(figsize=(8, 6))
    bars = plt.bar(class_labels, class_counts, color='skyblue')
    plt.title('Class Distribution in Dataset')
    plt.xlabel('Class')
    plt.ylabel('Number of Samples')
    for bar in bars:
        yval = bar.get_height()
        plt.text(bar.get_x() + bar.get_width()/2, yval + 0.5, f'{yval}\n({yval/len(y)*100:.1f}%)', ha='center', va='bottom')
    plt.savefig(os.path.join(figures_dir, 'class_distribution.png'))
    plt.close()
    logging.info("Saved class distribution plot to 'class_distribution.png' in figures directory")
```

```python
# Patient Distribution Plot
patient_counts = pd.Series(groups).value_counts().sort_index()
plt.figure(figsize=(12, 6))
plt.bar(patient_counts.index, patient_counts.values, color='lightgreen')
plt.title('Number of Respiratory Cycles per Patient')
plt.xlabel('Patient ID')
plt.ylabel('Number of Cycles')
plt.xticks(rotation=90)
plt.tight_layout()
plt.savefig(os.path.join(figures_dir, 'patient_distribution.png'))
plt.close()
logging.info("Saved patient distribution plot to 'patient_distribution.png' in figures directory")

# Cycle Duration Distribution
df['duration'] = df['end'] - df['start']
plt.figure(figsize=(8, 6))
plt.hist(df['duration'], bins=30, color='salmon')
plt.title('Distribution of Respiratory Cycle Durations')
plt.xlabel('Duration (seconds)')
plt.ylabel('Frequency')
plt.savefig(os.path.join(figures_dir, 'cycle_duration_distribution.png'))
plt.close()
logging.info("Saved cycle duration distribution plot to 'cycle_duration_distribution.png' in figures directory")
```

```python
# Label Distribution per Patient (Stacked Bar Chart)
pivot_table = df.pivot_table(index='patient_id', columns='label', aggfunc='size', fill_value=0)
pivot_table.columns = class_labels
pivot_table.plot(kind='bar', stacked=True, figsize=(12, 6), color=['skyblue', 'salmon', 'lightgreen', 'violet'])
plt.title('Label Distribution per Patient')
plt.xlabel('Patient ID')
plt.ylabel('Number of Cycles')
plt.legend(title='Class')
plt.xticks(rotation=90)
plt.tight_layout()
plt.savefig(os.path.join(figures_dir, 'label_distribution_per_patient.png'))
plt.close()
logging.info("Saved label distribution per patient plot to 'label_distribution_per_patient.png' in figures directory")

# Sample Spectrogram for Each Class
class_indices = {label: np.where(y_subset == label)[0] for label in range(4)}
plt.figure(figsize=(15, 10))
for label in range(4):
    if len(class_indices[label]) > 0:
        idx = class_indices[label][0]
        mel_spec = X_subset[idx][:, :, 0]
        plt.subplot(2, 2, label + 1)
        plt.imshow(mel_spec, aspect='auto', origin='lower')
        plt.title(f'Sample Spectrogram: {class_labels[label]}')
        plt.xlabel('Time')
        plt.ylabel('Mel Frequency')
        plt.colorbar(format='%+2.0f dB')
plt.tight_layout()
plt.savefig(os.path.join(figures_dir, 'sample_spectrograms.png'))
plt.close()
```

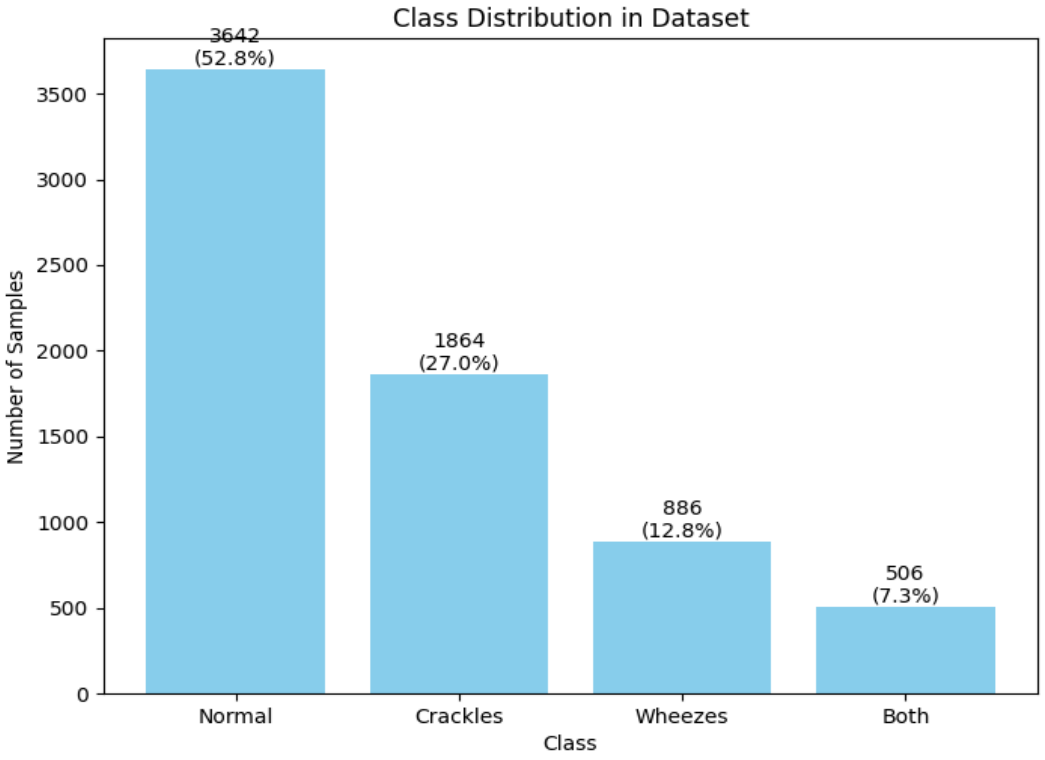

Fig 7.8.1 Class Distribution in Dataset

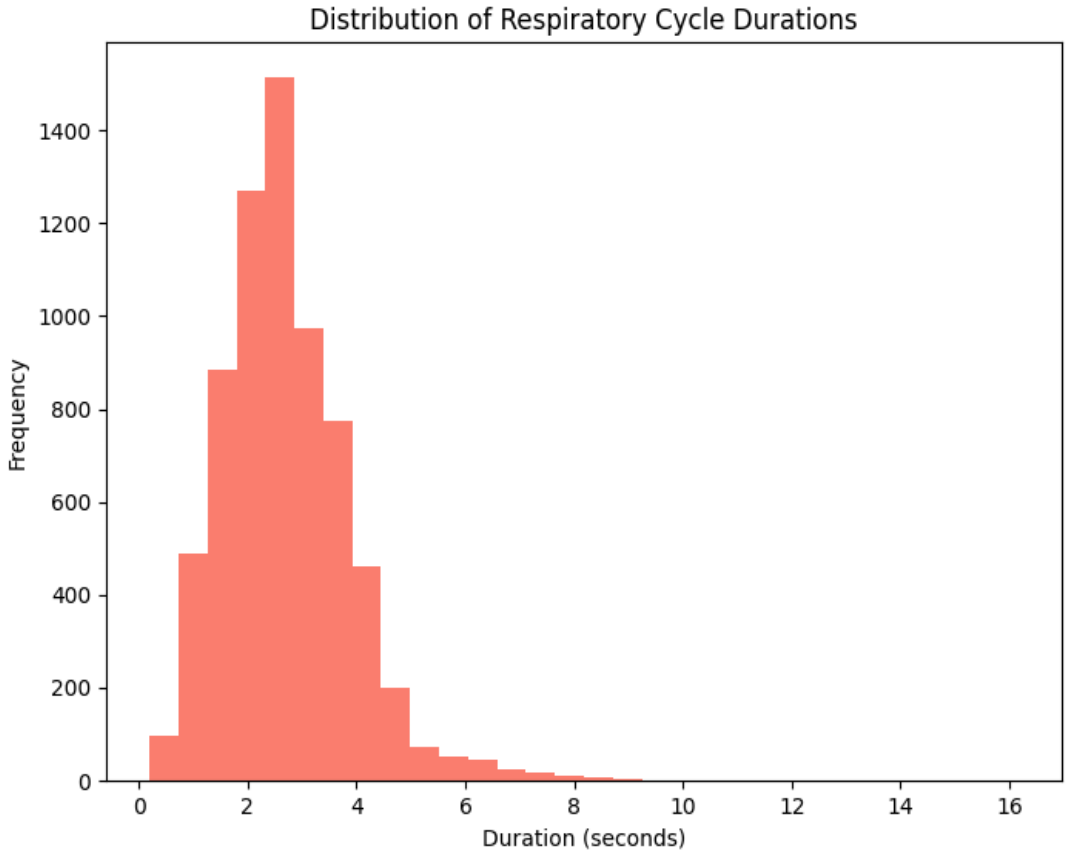

Fig 7.8.2 Distribution of Respiratory Cycle Duration

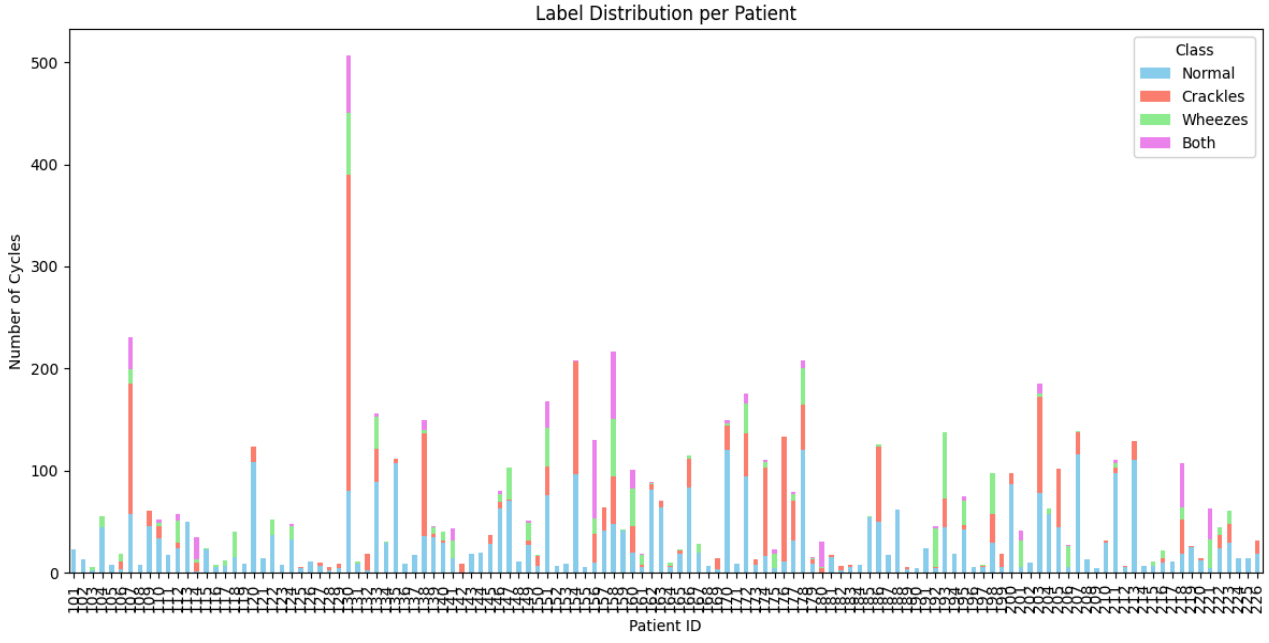

Fig 7.8.3 Label Distribution per Patient

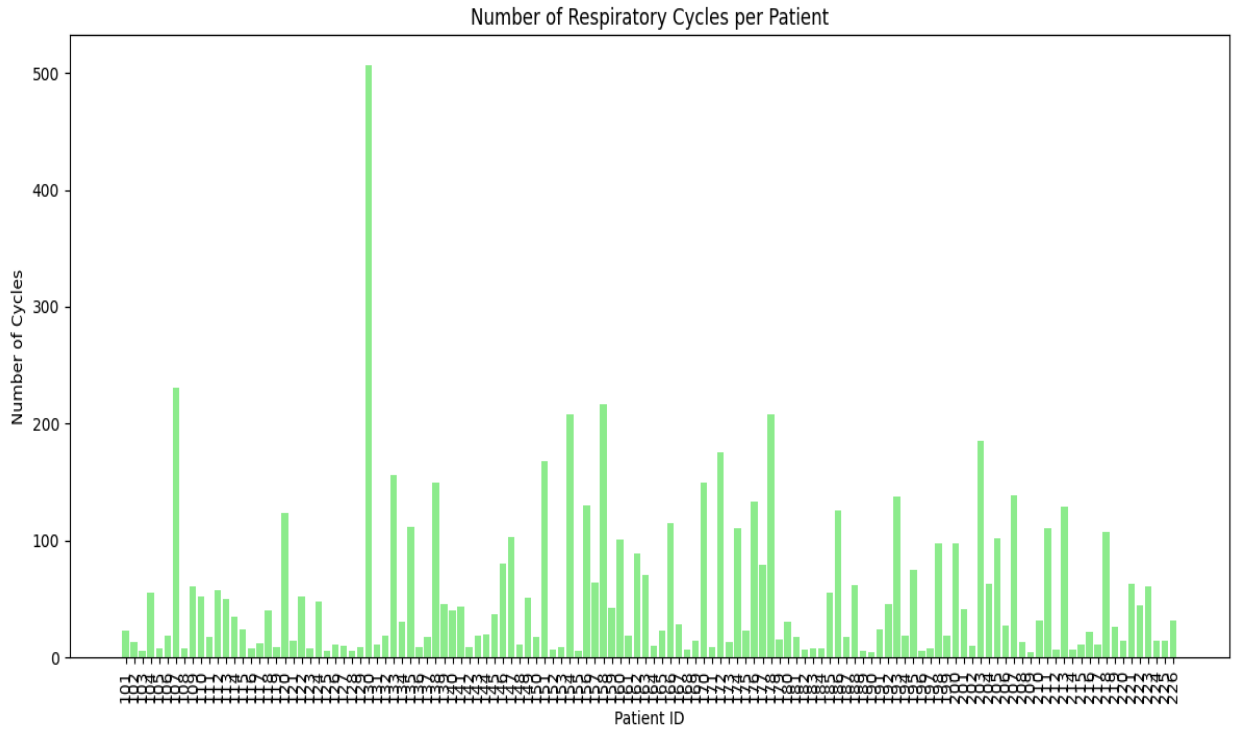

Fig 7.8.4 Number Of Cycle per Patient

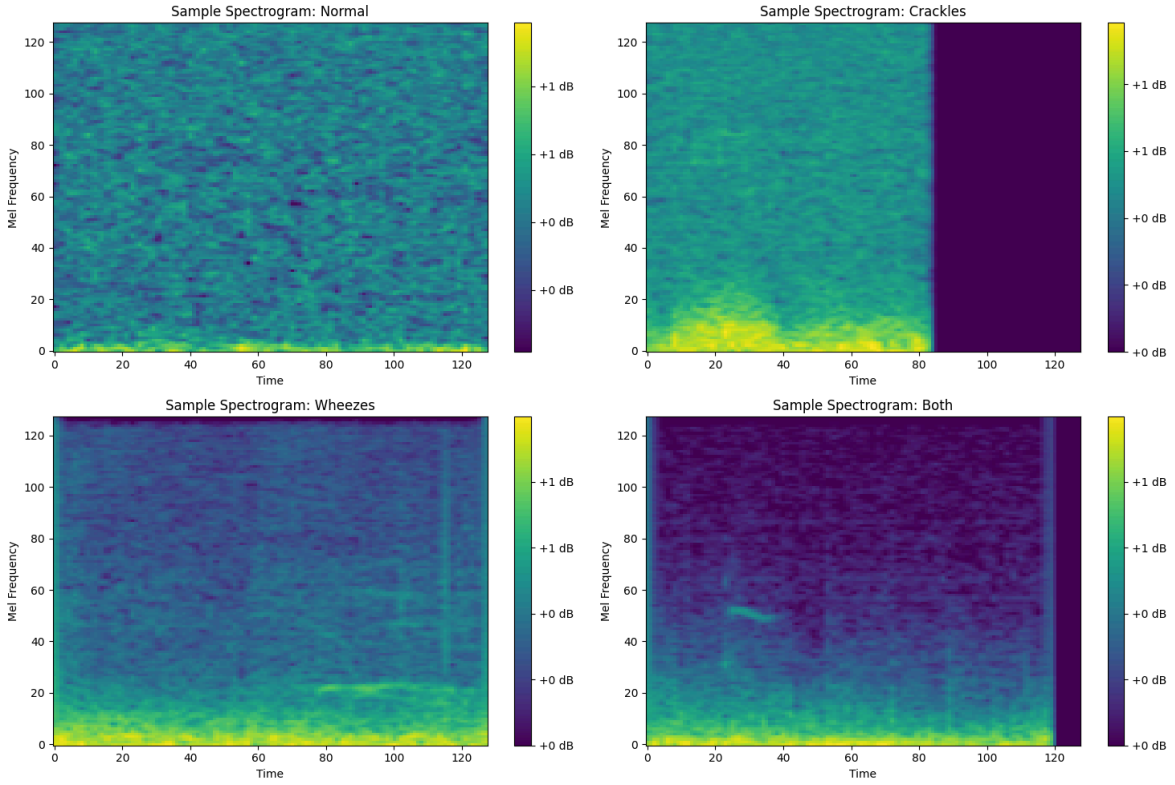

Fig 7.8.5 Sample Spectrograms Of Each Class