# Early Detection of Abnormal Lung Condition based on Deep Learning Model

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**Abstract:** Lung affecting diseases are most harmful because such diseases majorly cause death of the patient. Few diseases to mention are COVID-19, pneumonia, tuberculosis, cancer and asthma. These diseases have early symptoms of lung abnormalities. Hence, detection of these abnormalities can result in effective treatment and recovering of the patient at the early stage of the disease. Image processing based on deep learning techniques are popularly used for classification and analysis of huge data like medical images. In the proposed work, a deep learning model is designed to detect abnormal lung conditions for pneumonia, tuberculosis and COVID-19. In the proposed deep learning model, convolutional neural network is implemented for analysis of medical images. The segmentation of images is based on DenseNet algorithm. Various evaluation parameters are calculated for accurate detection. This approach is implemented to address the complex challenge of classifying abnormal lung images into multiple categories and effectively distinguish between pneumonia, tuberculosis, COVID-19 and normal lung conditions. Also, the implemented model presents significant value for healthcare providers by streamlining the diagnostic process and potentially expediting treatment decisions. The evaluation process sheds light on the model's performance in real-world scenarios, providing valuable insights for further optimization and clinical integration.

**Keywords:** Abnormal Lung Detection, Convolutional Neural Network (CNN), Image segmentation, Deep Learning (DL), DenseNet

## 1. Introduction

Lung diseases represent a significant global health concern, where pneumonia, Tuberculosis (TB), and COVID-19 being major contributors to morbidity and mortality worldwide. According to the World Health Organization (WHO), most recent data from 2018, there were 10.4 million cases of lung diseases, including pulmonary TB, and 1.6 million deaths globally attributed to these conditions. Early and accurate detection of these diseases is crucial for effective treatment and recovery of the patient. Traditional diagnostic methods often rely on radiological imaging, which can be time-consuming and subjective due to inter-observer variability. In recent years, Deep Learning (DL) techniques, a subset of Artificial Intelligence (AI), have shown promising results in automating and improving the accuracy of lung disease detection from medical images.

In DL models, particularly Convolutional Neural Network (CNN) have demonstrated exceptional capabilities in feature extraction and pattern recognition from complex and high-dimensional data, making them well-suited for analyzing medical images. The integration of deep learning techniques in lung disease detection holds great promise for revolutionizing diagnostic practices, offering potential improvements in accuracy, efficiency, and accessibility [1]. However, there remain challenges to be addressed, such as data scarcity, model interpretability, and generalizability across diverse populations. Continued research and collaboration between clinicians, researchers, and AI experts are essential to overcome challenges and to understand the potential of DL in advancing lung disease diagnosis and treatment. This work aims to explore and discuss the implementation of DL technique for lung disease detection, highlighting the advancements, challenges, and prospects in this rapidly evolving field.

Detection techniques for abnormal lung conditions for COVID-19, pneumonia, cancer, and TB have evolved significantly over the years, leveraging advancements in medical imaging, molecular biology, AI diagnostic systems, and other technologies. Here's an overview of each condition:

- *COVID-19*: The coronavirus SARS-CoV-2, which appeared in late 2019, is responsible for a disease that quickly escalated into a worldwide pandemic. It primarily affects the respiratory system, leading to symptoms such as fever, cough, and difficulty breathing. Diagnostic methods for COVID-19 include real time Reverse Transcription – Polymerase Chain (RT-PCR) tests for viral Ribonucleic Acid (RNA) detection, antigen tests for viral proteins, and imaging techniques like chest X-rays and computed tomography (CT) scans to identify characteristic lung abnormalities. As of 2024, there have been 704,753,890 confirmed cases of COVID-19 worldwide, with 7,010,681 deaths. The incidence and mortality rates vary across different regions and demographics [2].

- *Pneumonia*: Pneumonia is an inflammatory condition of the lungs, typically caused by bacterial, viral, or fungal infections. It can lead to symptoms such as cough, fever, and difficulty breathing. Diagnosis of pneumonia involves clinical evaluation, chest X-rays, CT scans, and laboratory tests such as sputum culture or blood tests to identify the causative pathogen. Pneumonia is a major contributor to illness and death globally, especially affecting children under five and the elderly. According to the WHO, pneumonia accounts for approximately 2.5 million deaths annually [3].

- *Tuberculosis*: TB spreads through the air when an infected person coughs or sneezes. Diagnosis of TB involves clinical evaluation, chest X-rays, sputum smear microscopy, Nucleic Acid Amplification Tests (NAATs), and culture-based methods to isolate the bacteria. TB is a global health threat. According to WHO, approximately 10 million tuberculosis cases and 1.4 million deaths were registered worldwide [4].

### 1.1 Relevance and Problem Definition

The proposed model have significant relevance with the field of healthcare and medical diagnostics. Some key points, highlighting its importance include early detection, reducing misdiagnosis, and effective diagnosis. The proposed model can transform the diagnostic practices and enhance patient care. Hence, the model addresses the global health challenges of lung diseases. It represents a promising intersection of healthcare, technology, and innovation, with the potential to make a profound impact on individual's life and public health on a broader scale.

The motivation is rooted in addressing the issue of rising healthcare costs as DL-based diagnostic tools can help streamline healthcare processes, potentially reducing costs for both patients and healthcare providers and helping with global health crises. Events such as the COVID-19 pandemic have highlighted the need for innovative and efficient diagnostic tools. DL-based diagnostics can enhance our preparedness for future health crises. Lung abnormalities, including cancer, pneumonia, TB, COVID-19, and other infections, are a significant public health concern. The timely and accurate detection of such abnormalities plays a crucial role in improving patient's recovery. Traditional diagnostic methods, based on manual interpretation of medical images like X-rays and CT scans, are time-consuming and may be subject to errors due to human factors. This work aims to develop a DL-based solution to address these challenges. Following are the objectives of the proposed model:

- *Automated Detection*: To develop a robust DL model capable of automatically detecting abnormal regions in lung images. This includes identifying tumors, nodules, or areas of infection.

- *Diagnostic Accuracy*: The model focuses on improving diagnostic accuracy by reducing the risk of human error in the interpretation of medical images. DL models are expected to provide consistent and precise results.

- *Large-Scale Analysis*: Healthcare institutions generate vast amount of medical image data daily. The DL model will efficiently analyze large datasets, making it feasible to diagnose lung abnormalities more rapidly than traditional manual examination.

- *User-Friendly Interface*: The DL model will be integrated into a user-friendly interface that is accessible to healthcare professionals and minimizes the need for extensive training.

### 1.2 Major Contributions

- An automated DL based model is proposed to predict early abnormalities of the lung that causes major and dangerous diseases like cancer, COVID-19 and TB.
- This work uses dense connectivity pattern based on Dense Convolutional Network. Here, each layer is connected to every other layer in a feed-forward fashion. This dense connectivity facilitates feature reuse and helps alleviate the vanishing-gradient problem. Hence, accuracy of the model is increased.
- Matthews Correlation Coefficient is used to predict large amount of imbalanced data. This provided deep learning of the abnormal structures of lung if affected by any disease.

## 2. Literature Survey

In recent years, DL techniques have shown promising outcomes in detecting abnormal lung structures associated with various diseases. This section explores various DL techniques employed for the detection of lung abnormalities in chest X-rays. The focus lies on four specific lung diseases: pneumonia, COVID-19, lung cancer, and tuberculosis.

For Pneumonia and COVID-19, in one study, the focus was on its detection using chest X-rays, employing logistic regression and a DenseNet-based deep learning model [5]. Although the deep learning model outperformed logistic regression slightly, the study emphasized the need for larger and more diverse datasets to enhance model performance effectively**.** Another study addressed the urgent need for efficient disease detection in the context of COVID-19 by proposing a CNN-Long Short-Term Memory (LSTM) approach for automatic COVID-19 diagnosis from X-rays [6]. In one study, the authors achieved a three-way classification (normal, pneumonia, COVID-19) with an impressive accuracy of 0.995 for COVID-19 detection using a combined Xception-ResNet50V2 network on a substantial dataset of over 11,000 images. Their innovative neural network achieved remarkable accuracy in detecting COVID-19 cases and demonstrated high performance across all classes, underlining its real-world effectiveness [3, 7]. Deep-CNN and Large-scale chest X-ray (ChestX-ray8) databases are also explored and used for weakly supervised learning for localizing disease regions in X-ray images. The ResNet (50 layers) gave better results than AlexNet, GoogleNet, Visual Geometry Group (VGG) model [8].

Research has also explored DL for lung cancer detection. One study utilized CT scans and a novel Fuzzy Particle Swarm Optimization (FPSO) based CNN for cancerous nodule localization and classification, demonstrating effectiveness and reduced computational complexity compared to other techniques [9]. In [10], DL combined with a genetic algorithm for lung nodule classification as malignant or benign, achieving promising results without explicit shape and texture feature computations. For lung cancer detection using CT scans, DL methods have been employed to localize cancerous nodules and classify cancer severity. Research utilizing FPSO-based CNN showcased superior performance in classification while optimizing computational complexity, representing a significant advancement in lung cancer detection.

Addressing TB, the DL techniques have been applied to improve TB detection from chest X-ray images, using a combination of deep learning, and segmentation [11]. By enhancing image quality through specific algorithms and employing transfer learning with pre-trained models, researchers achieved promising results in TB diagnosis, even with challenging image conditions. DL is also explored for the detection of tuberculosis patterns in chest X-ray images, demonstrating the feasibility of using DL for TB pattern detection [12].

The detailed study of detection techniques for pneumonia, COVID-19, lung cancer, and tuberculosis is carried out and a review is published in [13]. Readers can refer [13] for detailed literature review of the proposed model. The study infer that optimization of analysis of medical images can enhance the accurate detection of lung abnormalities. DL is popularly used as the model has mathematical background of convolution theory to support precise predictions.

## 3. Proposed Method

In this section, the procedural aspects required for DL model implementation is explained in detail. The dataset referred, data preparation, CNN architecture, parameters for data analysis, optimization methods and model saving procedure is explained as following:

### 3.1 Dataset

Here the datasets used for modeling are medical images indicating lung conditions, which are used to detect COVID-19, pneumonia, TB, and normal condition. The Covid-19 radiography database is made by a team of researchers from Qatar and Bangladesh. The dataset used for our study includes COVID-19 cases, both positive and negative, lung opacity cases, and pneumonia cases [14].

Similarly, a team of researchers from Qatar and Bangladesh, along with collaborators from Malaysia, developed the Tuberculosis (TB) Chest X-ray Database. This database contains chest X-ray images of both TB-positive cases and normal cases. There are 700 TB images publicly accessible and 2800 TB images [15].

### 3.2 Data Preparation

Data preparation was carried out for all the images as shown in Fig. 1. It consists of four steps as follows:

a. Increasing the contrast of all images using Histogram Equalization. This normalizes the intensity of images from different datasets.
b. Removing the noise from all images using Median Filtering with a window size of 3 × 3.
c. Resizing images to 28 × 28 pixels to match the input of the model used.
d. Normalizing image color based on mean and standard deviation of the ImageNet training set [16].

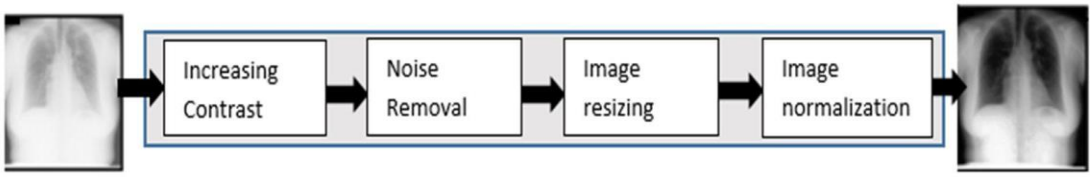


**Fig 1.** Data preparation process on an image [16]

### 3.3 CNN Architecture

Among all the convolutional neural network architectures like ResNet [17], and DenseNet [18], the model used in this research is the 121-layer Densely Connected Convolutional Networks (DenseNet-121) [19]. DenseNet stands for Dense Convolutional Network, and it's known for its dense connectivity pattern. In a DenseNet, each layer is connected to every other layer in a feed-forward fashion. This dense connectivity facilitates feature reuse and helps alleviate the vanishing-gradient problem.

#### 3.3.1 DenseNet

Deep Convolutional Networks (DCNNs) have become one of the most sought-after frameworks because of the deep convolutional and pooling layers [20]. DenseNet is a kind of CNN with dense feature connection that ensures complex information flow between its various layers [21]. The provided model employs transfer learning with DenseNet, a widely used pre-trained model for image classification tasks. DenseNet is chosen as the initial layer

within a Sequential model, serving the purpose of feature extraction. Unlike traditional architectures, DenseNet's dense connections between layers promote effective feature reuse and gradient flow during training. Following the DenseNet layer, a flattened layer is introduced to convert the multi-dimensional feature maps into a one-dimensional array, preparing them for input into subsequent fully connected dense layers.

In this implementation, four dense layers are sequentially stacked, progressively reducing dimensionality while augmenting the number of parameters. Each dense layer incorporates ReLU activation, enabling the model to learn intricate patterns and representations. The final dense layer is outfitted with softmax activation, generating probabilities for each class in the classification task. This ensures that the output values are appropriately normalized to represent class probabilities. The model summary provides comprehensive insights into its architecture, including the types of layers employed, their respective output shapes, and parameter counts. Notably, non-trainable parameters encompass the weights of the pre-trained DenseNet model, meticulously preserved during training to prevent their modification. In essence, this implementation harnesses transfer learning with DenseNet to proficiently extract features from input images, facilitating efficient classification. Such a strategy underscores a reliable methodology for leveraging pre-trained models in image classification tasks, thereby facilitating precise and effective outcomes.

The algorithm for implementing DenseNet architecture is as follows:-

Step 1: START
Step 2: Use a pre-trained convolutional base.
Step 3: Use the Flatten layer to convert the output of the convolutional base to a one-dimensional tensor.
Step 4: Create several densely connected layers with ReLU activation.
Step 5: Select an output layer with softmax activation for multi-class classification
Step 6: Choose the stochastic gradient descent optimizer and Adam optimizer to select the appropriate learning rate
Step 7: Train the model for 20 epochs
Step 8: END

### 3.4 Parameters

These parameters are commonly used metrics for evaluating the performance of classification models, particularly in the context of binary or multiclass classification tasks. Here's a brief explanation of each parameter:

a. *Precision*: A system is said to be precise if the system model produces accurate positive predictions. It is the ratio of the number of positive predictions of positive cases to the sum of positive and negative predictions of positive cases. Precision is crucial when the number of negative predictions is high [22]. In this context, the precision scores are 1 for COVID-19, 0.98 for pneumonia, 0.97 for tuberculosis, and 0.88 for normal images.
b. *Recall*: Also referred to as sensitivity, recall measures how effectively the model identifies all positive instances. It is crucial when it's important to capture all positive instances, even at the cost of some false positives. It is 0.88 for Covid-19, 0.95 for pneumonia, 0.98 for TB, and 0.99 for normal images [22].
c. *F1 score*: Precision considers all positive cases' predictions for precise results. Recall considers both positive and negative cases' predictions effective results. The F1 score is calculated by combining both precision and recall to have efficient output. It is the harmonic mean of both parameters. It is useful for evaluating models on imbalanced datasets where the class distribution is skewed [22]. Here it is 0.94 for COVID-19, 0.96 for pneumonia, 0.98 for TB, and 0.94 for normal images.
d. *Support*: Support indicates the number of occurrences of each class in the dataset. It provides insight into the distribution of classes and helps in understanding the reliability of the evaluation metrics. Classes with low support may indicate data imbalance or scarcity. It is 724 for COVID-19, 278 for pneumonia, 723 for normal, and 131 for TB.
e. *Matthews Correlation Coefficient*: The Matthews Correlation Coefficient (MCC) is a metric used in machine learning to assess the performance of binary classification models, especially when handling imbalanced datasets. The MCC considers the positive prediction of the positive case, positive prediction of the negative case, negative prediction of the positive case, and negative prediction of the negative case. Its value ranges from -1 to 1, where 1 signifies a perfect prediction, 0 signifies a random prediction, and -1 signifies complete disagreement between

prediction and observation [23]. Here, the positive prediction of negative cases and the negative prediction of positive cases are both risky outcomes because they will initiate an ill diagnosis of the patient. The formula for MCC is represented in Eq. 1.

$$MCC = \frac{PN \times PP - NN \times NP}{\sqrt{(PP+NP)(PP+NN)(PN+NP)(PN+NN)}} \quad \text{Eq. (1)}$$

where PP is a positive prediction for a positive case, PN is a positive prediction for a negative case, NP is a negative prediction for a positive case and NN is a negative prediction for a negative case.

### 3.5 Optimization Method

Optimization methods are fundamental components of training machine learning models. These methods are responsible for adjusting the parameters of the model iteratively during training to minimize a defined loss function. The objective is to find the optimal set of parameters that best fit the training data and generalize well to unseen data. In the provided code snippet, various optimization methods, and callbacks are implemented for training a neural network model using TensorFlow's Keras API. Here's an explanation of each component:

a. *Stochastic Gradient Descent (SGD)*: The SGD optimizer is imported from tensorflow.keras.optimizers. SGD is a popular optimization algorithm used to minimize the loss function during training by updating model parameters in a direction that reduces the loss [24]. In this implementation, SGD is configured with a learning rate of 0.01.
b. *Checkpoint Callback*: A checkpoint callback is created using ModelCheckpoint. This callback saves the model's weights during training at specific intervals or conditions [25]. In this case, the callback is configured to save only the weights (save_weights_only=True) to the specified checkpoint path (checkpoint_path). Additionally, verbose=1 indicates that progress updates will be displayed during training.
c. *Early Stopping Callback*: Another callback, EarlyStopping, is instantiated to monitor the validation loss during training. Early stopping prevents overfitting [26]. Parameters such as patience, min_delta, and restore_best_weights are provided to control the early stopping behavior. In this case, training will halt if the validation loss does not improve for 10 consecutive epochs (patience = 10), with a minimum required improvement of 0.001 (min_delta = 0.001). The restore_best_weights parameter ensures that the model's weights are restored to the best-performing ones on the validation set.

### 3.6 File format to save the model

The implementation includes functionality to save the trained model in HDF5 (.h5) format. The HDF5 format is a hierarchical data format commonly used for storing and managing large numerical datasets. In the context of deep learning, it serves as a standard format for saving and loading trained models in Keras. The .h5 file contains the model architecture, including the configuration of layers, as well as the trained weights and biases. Saving the model in HDF5 format allows for seamless reuse and deployment of the trained model in various applications, including further training, inference, and transfer learning.

### 3.7 Model Implementation

In this work, after training and evaluating the model, it is saved in both HDF5 and TensorFlow Lite formats using the model.save() function. The HDF5 format preserves the entire model architecture and weights, facilitating further analysis and modification if needed. On the other hand, the TensorFlow Lite conversion process involves additional steps to optimize the model for deployment on mobile and edge devices. This typically includes quantization (reducing the precision of weights and activations), pruning (removing unnecessary operations and parameters), and other optimizations tailored to the target platform.

a. *Data Preparation*: The code begins by downloading two datasets from Kaggle: the COVID-19 Radiography Database and the Tuberculosis (TB) Chest X-ray Dataset. These datasets contain chest X-ray images categorized

into different classes. The images are resized to a uniform size of 120x120 pixels and stored in lists along with their corresponding labels.

b. *Model Building*: The code constructs a deep learning model using transfer learning. Different pre-trained convolutional neural network (CNN) architectures, including VGG16, EfficientNetB0, EfficientNetB7, and ResNet50, are utilized as feature extractors. A fully connected neural network with dense layers is then added on top of the pre-trained CNN for classification. The model is compiled with various optimizers such as Adam and SGD, and the loss function is set to categorical cross-entropy.
c. *Model Training*: The training data is split into training, validation, and test sets using the train_test_split function. The model is trained on the training data with a specified batch size and number of epochs. Early stopping and model checkpoint callbacks are used to prevent overfitting and save the best model weights during training.
d. *Model Evaluation*: After training, the model is evaluated on the test set to assess its performance in terms of loss and accuracy. Additionally, classification metrics such as precision, recall, F1-score, support, and the Matthews correlation coefficient are calculated. A confusion matrix is generated to visualize the classification results.
e. *Results Visualization*: The predictions made by the model on the test set are visualized along with the corresponding actual labels using *matplotlib*. The model's training and validation accuracy and loss curves are plotted to analyze its training dynamics.

## 4. Results & Discussion

The architecture of the deep learning model is visualized using the plot_model function from Keras, which generates a graphical representation of the model's layers and their connections. Overall, the model demonstrates the end-to-end process of building, training, evaluating, and visualizing a deep learning model for chest X-ray image classification. The use of transfer learning with pre-trained CNN architectures allows for efficient feature extraction and classification, enabling the model to achieve high accuracy in identifying various chest diseases. The performance of the model in this study was evaluated using accuracy, precision, recall, F1-score, and support. The accuracy shows the degree to which the model correctly identified both positive and negative cases. The precision is a metric that measures the proportion of positive identifications that are correct. The Recall is a metric that measures how often a machine learning model correctly predicts the outcome. The F1 score is a metric in machine learning that evaluates a model's performance by balancing both precision and recall. The MCC for the given model is determined to be 0.9166. Table 1 displays the model testing parameters' scores for corresponding diseases using a multi-class single-stage classifier. The overall accuracy obtained for the model was 0.91.

**Table 1 Model performance evaluation using various performance metrics**

| Disease | Precision | Recall | F1 Score | Support |
|---|---|---|---|---|
| Covid-19 | 1 | 0.88 | 0.94 | 724 |
| Normal | 0.88 | 0.99 | 0.94 | 723 |
| Pneumonia | 0.98 | 0.95 | 0.96 | 278 |
| Tuberculosis | 0.97 | 0.98 | 0.98 | 131 |


**Fig 2.** Class wise performance comparison

Figure 2 depicts the graph of performance comparison using Precision, Recall and F1-score for Covid-19, Pneumonia, Tuberculosis and Normal classes. In Table 2, confusion matrix representing overall predictions is shown when evaluated using the testing data. Maximum value obtained on the diagonal of the matrix indicates the low error of the system and the model's efficiency to correctly identify the disease based on the x-ray image provided.

The model accuracy and model loss evolving with the progression of epochs during training and testing is measured and the graph is represented in Fig. 3. The trained dataset is compared with test data and the nature of the graph of test data is similar to that of trained data.

**Table 2 Confusion Matrix**

| | Covid-19 | Normal | Pneumonia | Tuberculosis |
|---|---|---|---|---|
| Covid-19 | 639 | 79 | 2 | 4 |
| Normal | 1 | 718 | 4 | 0 |
| Pneumonia | 0 | 15 | 263 | 0 |
| Tuberculosis | 2 | 0 | 0 | 129 |

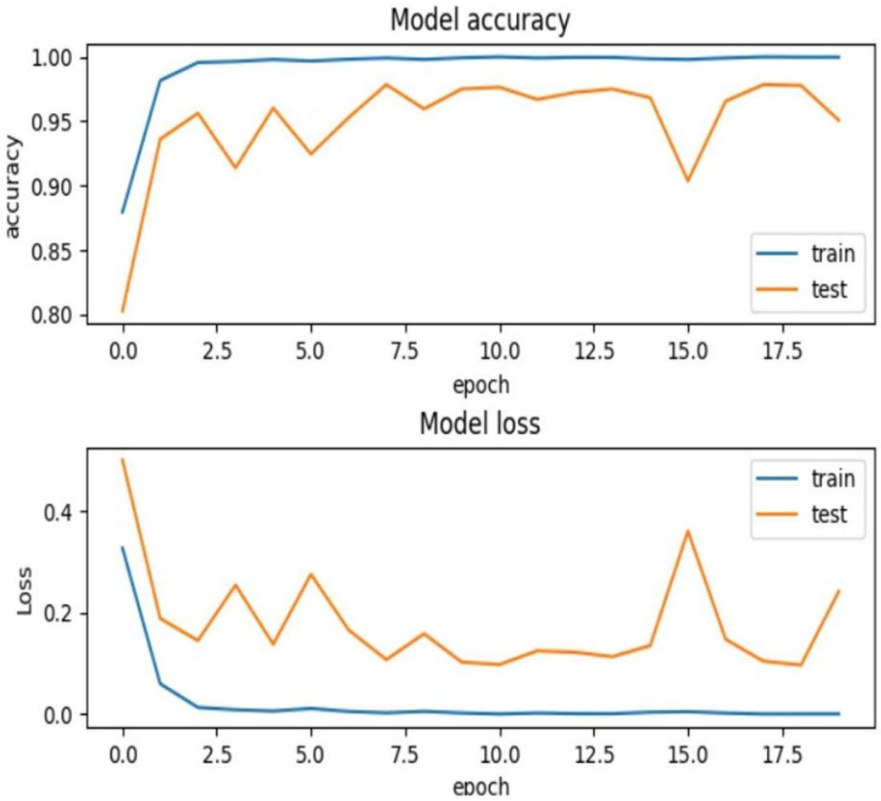


**Fig 3.** Model accuracy and model loss evolving with the progression of epochs during training and testing

Here, it is evident that the accuracy for the training data steadily increases with epochs and reaches saturation after a time. On the testing data, the accuracy takes an uneven course of path and forms local maximas and minimas.

From this optimal number of epochs for maximum accuracy of our model can be figured out. This illustrates class wise mean absolute error and root mean square error using a line chart of Normal, Covid-19, Pneumonia and Tuberculosis classes.

In Fig. 4, the error observed class wise are compared. The parameters calculated are the mean absolute error and root mean square error. The actual result and predicted result of few X-ray images of lungs used for testing the model's performance are depicted in Fig. 5.

It is seen that the model works efficiently, providing correct predictions as per the actual results. Hence, the proposed technique can be used for early detection of diseases.

Through this analysis, it is determined that the model achieved an accuracy of 94.23%. It means that the model accurately predicted the diagnosed disease of the lungs (if any) 9.423 out of 10 times.

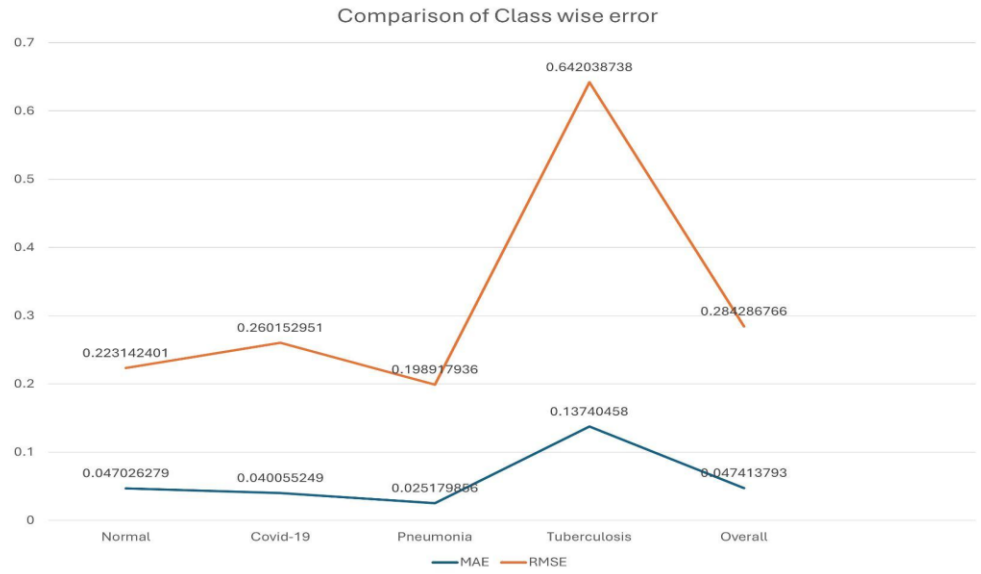


**Fig 4.** Class wise error comparison (mean absolute error and root mean square error)

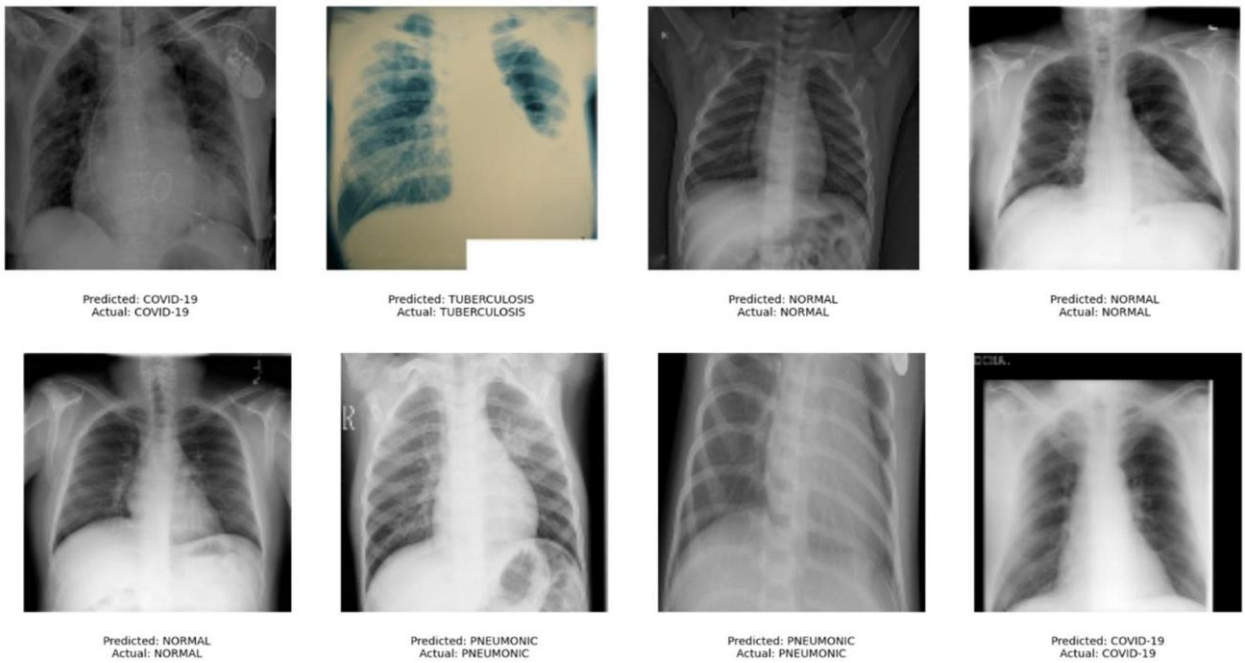


**Fig 5.** The predicted and actual results of images in the testing dataset

## 5. Conclusion

The model's ability to accurately classify chest X-ray images has promising implications for assisting healthcare professionals in efficiently diagnosing and managing respiratory diseases. By leveraging advanced deep learning

techniques, this study contributes to the broader efforts aimed at leveraging technology to augment and improve medical diagnosis and patient care.

The proposed work showcases the development and evaluation of a deep learning model for classifying chest X-ray images into distinct disease categories. The model exhibits a test accuracy of approximately 94.23% and a test loss of 0.2664 on the training dataset. These metrics, along with precision, recall, and F1-score analyses, underscore the model's efficacy in discerning between various respiratory conditions. However, it is noted that certain classes, such as COVID-19 and Pneumonia, may pose challenges for the model, as indicated by lower performance metrics compared to other classes. This observation suggests potential biases or difficulties in distinguishing between specific disease categories, warranting further investigation and refinement of the model architecture.

Future research endeavors could focus on the integration of the developed model into real-world healthcare settings and conducting clinical validation studies. Also, the further refinement and validation if warranted, the findings of this study hold promise for enhancing the efficiency and accuracy of respiratory disease diagnosis through automated image analysis methodologies.

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