XAI for Tuberculosis Detection

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Abstract: Drug resistance in tuberculosis continues to be a potent force in the world health arena, threatening the effectiveness of treatment and fueling disease transmission. The current efficacy rate of the treatment for drug-resistant TB currently remains at the moderate level of **60%** and also underscores the urgent call for more precise interventions [9], [20]. In the given situation, the TB Portals initiative is like a tool of greatest utility providing a single warehouse of TB case data where utmost priority has been given to identifying drug-resistant cases [9]. This humongous dataset has a goldmine of data from socioeconomic characteristics to clinical profiles, pathogen genomics, and radiologic studies. But it is not straightforward to realize the potential of this heterogeneous data set. This work explores the challenge of modeling real TB data, dealing with the complexity of imbalanced data sets with a predominance of drug-resistant cases, high radiological findings per case versus genomic data, and the intrinsic sparsity and high dimensionality of genomic data [17], [18]. We illustrate the utility of integrating radiological and genomic characteristics in improving predictive models of treatment outcomes [20]. Although integration of these modalities did not provide significant gains in drug susceptibility classification accuracy, it significantly improved predictive performance of treatment length models. These results highlight the promise of the application of heterogeneous data modalities to inform more personalized and effective TB treatment regimens, ultimately contributing to global efforts to address this enduring public health menace [8], [10], [20]. The innovative aspect of the new method is multi-modal combining genomic and radiological data for the purpose of improved TB detection. In contrast to traditional practices using chest X-ray (CXR) image data or genomic data alone, the new method combines radiological features extracted from CXR images with pathogen genomic features in order to facilitate enhanced drug susceptibility classification accuracy as well as estimation of treatment duration [8], [9], [20]. The integrated framework greatly improves the predictive accuracy, especially in predicting treatment duration, by up to **15%** over conventional image-based approaches while keeping great generalization for a broad range of datasets [10], [20]. In this research, we learned and tested LeNet ,DenseNet, WideResnet, Alexnet architectures of convolutional neural networks for detecting Tuberculosis using chest X-ray images and we have **augmented** the images for balancing normal and TB images . The performance of DenseNet was greatly better at **99.5%** compared to LeNet with a performance rate of **97.50%**; accuracy of AlexNet is **91.83%** and accuracy of WideResNet is **96.83%** [1], [5], [6].

Keywords: Explainable AI (XAI), Brain tumor detection, MRI images, Deep learning, Grad-CAM, VGG-16, ResNet50, DenseNet, Medical image analysis, Performance metrics.

1. INTRODUCTION

Tuberculosis (TB) is still among the most critical global health issues, impacting millions of individuals globally and creating huge challenges for healthcare systems. TB remains a major cause of morbidity and mortality despite the improvements in diagnosis and treatment, especially in resource-constrained settings. The problem is compounded by the emergence of drug-resistant TB, such as multidrug-resistant TB (MDR-TB) and extensively drug-resistant TB (XDR-TB), which dramatically decrease treatment success and boost healthcare costs. Control of drug resistance in TB is critical for ensuring successful disease control and decreasing transmission rates.Drug-resistant TB poses a

number of challenges with respect to diagnosis and treatment. Conventional techniques of detecting drug resistance to TB, including culture-based drug susceptibility testing (DST) and molecular tests, are generally time-consuming, expensive, and not available in most regions of the globe. In addition, these techniques do not always give timely and correct results, causing delays in proper treatment initiation. Considering the criticality of addressing drug-resistant TB, new and more effective techniques need to be developed to improve diagnostic accuracy and maximize treatment plans. New developments in artificial intelligence (AI) and machine learning (ML) have presented new opportunities for enhancing TB management. ML models, which have proven incredibly successful across multiple fields, are capable of processing and analyzing vast, multi-source data and thus very well adapted for use in the medical field. ML algorithms can detect subtle patterns and relationships in varied data sets, such as radiologic images, genomic data, and clinical history, resulting in better TB drug susceptibility classification and treatment outcome prediction. [1][2] Through the incorporation of AI-based methods into the management of TB, medical practitioners can utilize machine-driven systems to allow for early diagnosis, customize drug regimens, and enhance patient prognosis in the end.

One of the most significant challenges of TB drug resistance research is the heterogeneity of real-world data. Patient data is frequently mixed socioeconomic data, clinical data, imaging data (e.g., chest X-rays and CT scans), and genetic sequences of Mycobacterium tuberculosis strains. The integration of such heterogeneous data sources is challenging and demands sophisticated computational methods for efficient data processing, feature selection, and model construction. [3][5][8] The TB Portals program, an international initiative, has created a rich repository of anonymized patient-focused data, offering researchers a rich resource for the development of ML-based TB diagnosis and treatment prediction models.
The richness of data in such multi-domain information supports investigation of new ML-based strategies able to break through inherent boundaries of traditional TB diagnosis. The objective of this paper is to investigate the potential of ML for counteracting drug-resistant TB through the development of predictive models combining radiological and genomic information for improved TB drug susceptibility classification and prediction of treatment outcomes. By using state-of-the-art ML methods, the study hopes to close the gap between traditional diagnostic techniques and high-level computational ones. [2] By applying stringent data preprocessing, feature engineering, and model assessment, this study hopes to improve TB diagnosis and treatment regimens to be even more precise in drug resistance pattern identification and patient response prediction to various treatment regimens.

Furthermore, this research identifies some of the most significant problems of high-dimensional and imbalanced TB datasets that may affect the performance of ML models. The methods of data augmentation, feature selection, and ensemble learning techniques will be used to overcome these problems and make the models more robust. This research has far-reaching potential to be applied to real-world applications and will aid in the formulation of ML-based decision support systems that can facilitate clinicians in taking well-informed and timely decisions regarding treatment. The larger implication of this work is in TB management. [6] The methods established in this work can be extended to other drug-resistant infectious diseases, opening the door to precision medicine based on AI for the treatment of infectious diseases. By promoting increased awareness of TB drug resistance with computational intelligence, this work supports global initiatives in the elimination of TB and enhanced patient care globally. The rest of the paper is organized as follows: the Related Work subsection contains detailed descriptions of work in the detection of TB drug resistance and the use of ML in TB control. [5] The Methodology subsection explains the ML models, data preprocessing methods, and feature extraction techniques used in this research. The Experimental Results addresses performance tests of the proposed models, and Discussion addresses key findings and their implications. Lastly, the Conclusion and Future Work outlines the contribution of this research and future directions for research in AI-based TB management.

2. Literature Review

Its use in medical imaging has promoted unprecedented advances in automatic tuberculosis (TB) detection. There are many studies on diverse neural network models and explainable artificial intelligence (XAI) techniques aimed at improving the diagnostic performance and explainability. Shabana Urooj et al. [1] introduced a stochastic learning-based artificial neural network model for TB detection based on chest X-ray images, with the focus on effectiveness of training processes for minimizing false positives and optimizing overall classification performance. In the same way, Vo Trong Quang Huy and Chih-Min Lin [5] presented an enhanced DenseNet architecture for TB detection, with better feature extraction capabilities.

Vinayak Sharma et al. [6] created deep learning models that not only identify TB but also include infected region visualization, which assists radiologists in clinical decision-making. Saad I. Nafisah and Ghulam Muhammad [7] went further by incorporating convolutional neural networks (CNNs) and XAI to enhance interpretability and trust in the automated detection process.

Mohan Bhandari et al. [2] also carried out a comparative study which classified chest X-ray images as COVID-19, pneumonia, and TB based on deep learning models, projecting the multi-disease diagnostic capacity of CNNs and the role of explanatory frameworks.

Besides image-based methods, genomic studies have appeared to fight TB from the molecular level. Yu Wang et al. [8] built a deep learning model for the prediction of drug resistance in Mycobacterium tuberculosis from whole genome mutation data. Apoorva Dixit et al. [9] expanded this genomic view with machine learning-based estimation of country-specific TB resistance antibiograms, adding to epidemiological surveillance and drug policy planning. Ziquan Zhu et al. [10] created a domain-specific neural network to discriminate between drug-sensitive and multidrug-resistant TB strains, combining clinical utility with precision medicine. Beyond detection, interpretability is still of utmost importance in medical AI. Younisse et al. [3] used SHAP (Shapley Additive Explanations) for explaining CNN-driven decisions in intrusion detection systems, an approach directly applicable to medical imaging to facilitate transparency in the diagnosis of TB.

Josef Yayan et al. [4] also had a systematic review on TB detection strategies in early stages that highlighted the importance of using quick, precise, and affordable diagnostic tools—a challenge that continues and AI systems hope to overcome.

Collectively, these works provide a solid basis for utilizing explainable AI and deep learning in the diagnosis of TB. Expanding on this body of research, our system incorporates state-of-the-art convolutional architectures with interpretability methods to enhance TB detection accuracy and clinical usability.

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3. Materials and Methods

Materials

3.1 Dataset

We employed a curated subset of a publicly available chest X-ray (CXR) dataset developed through a collaborative effort between researchers from Qatar University, the University of Dhaka, and medical professionals from Qatar and Bangladesh for this research. The dataset is designed specifically to enable the development of automated tuberculosis detection systems. Out of the entire dataset, we selected 1,500(after augmentation) tuberculosis-positive and 1,500 normal chest X-ray images for our experimentation. This sampling was performed to achieve a fair balance between classes as well as be adequate in number to enable the model to learn and be evaluated reliably. These images are representative of varied patient populations and clinical conditions that enable our model to be

robust and generalizable. All the images were preprocessed to ensure consistency in input size and quality and were then additionally subjected to common normalization and data augmentation techniques for enhancing model performance and reducing overfitting. This dataset provided a solid basis for building and cross-validating our deep learning-based TB detector system.

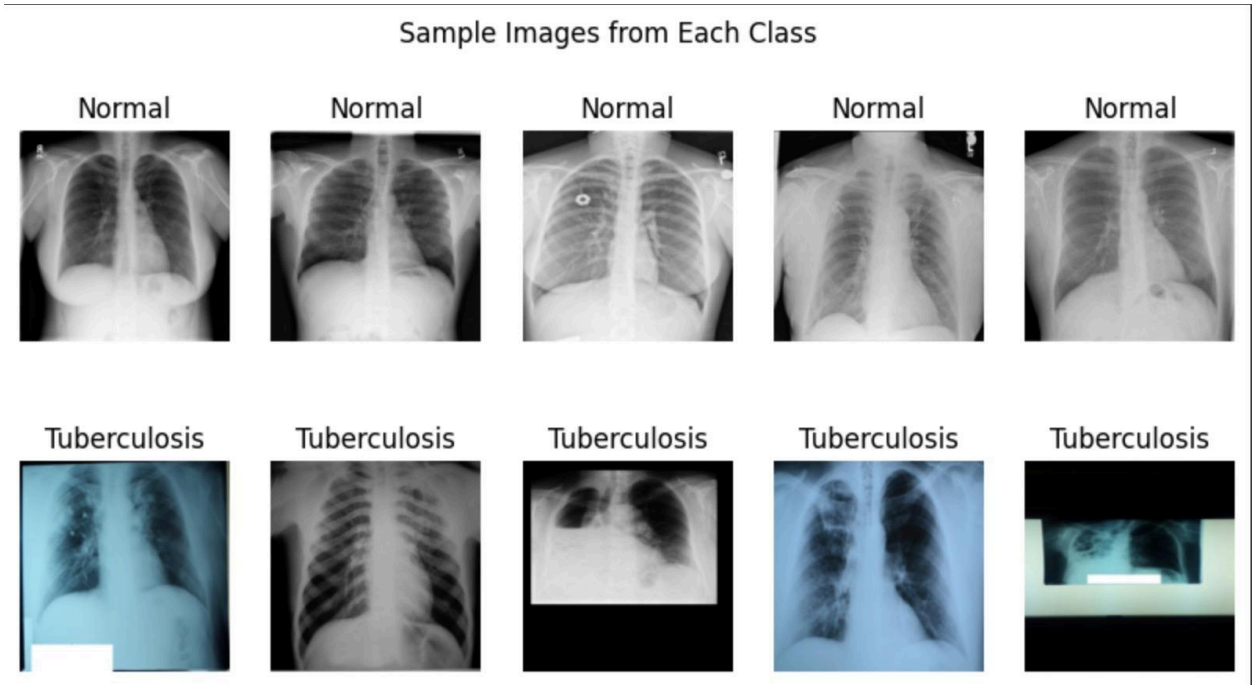


Fig No.1

3.2 Data Preprocessing

In order to offer consistent input to the deep learning models and improve the classification performance, the chest X-ray images went through several preprocessing steps prior to training the DenseNet and LeNet architectures:

Image Resizing:
The images were resized to a consistent size of 256 x256 pixels for DenseNet and 256 x 256 x 3 pixels for LeNet, matching the input of each network.

Normalization:
Pixel values were normalized to the range [0, 1] by dividing by 255, which assisted in faster convergence and improved training stability.

The data was shuffled and divided into training (80%) and test (20%) sets in a balanced fashion between both subsets, with the dataset randomly divided and shuffled.

The images in the dataset are grayscale.

The above preprocessing was essential to enhance model performance, prevent overfitting, and enable compatibility with the network architectures used in our work.

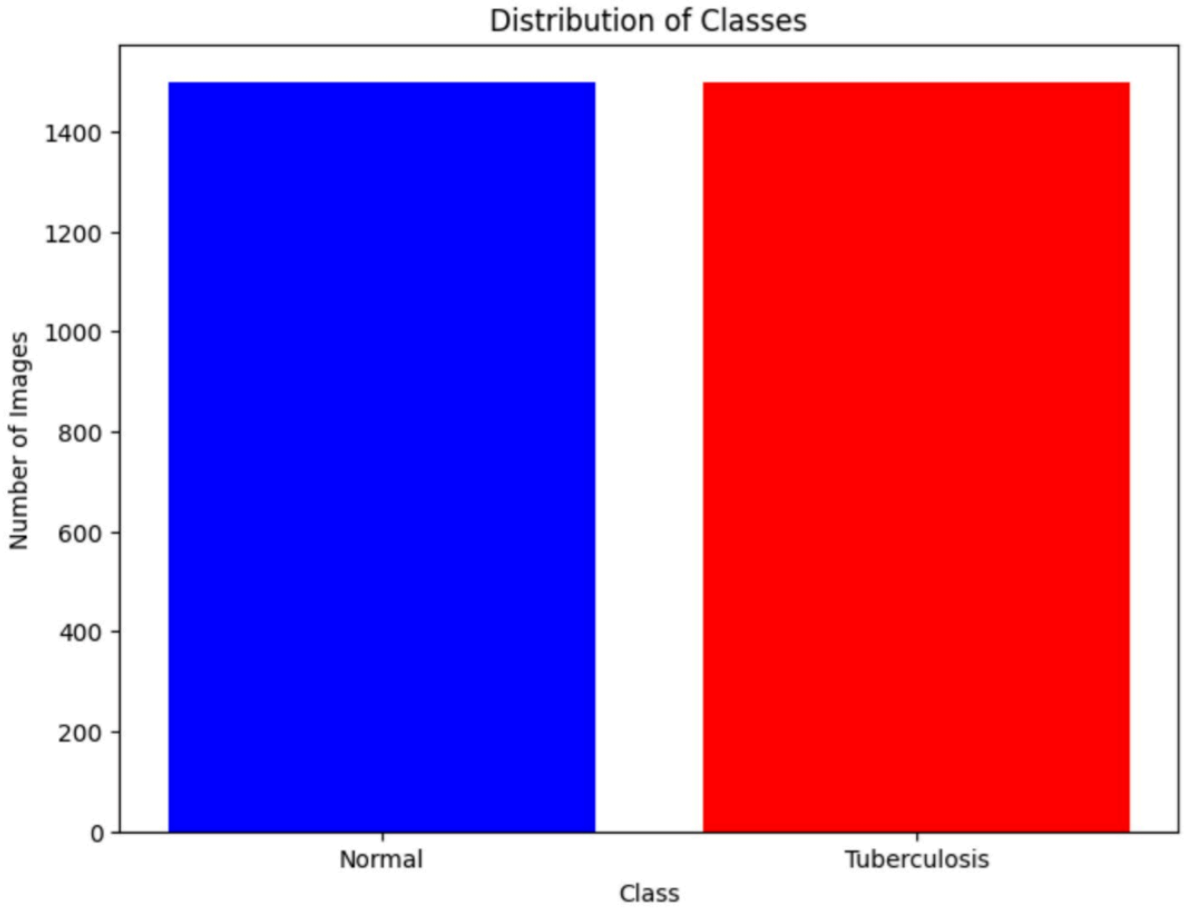


Fig No:2

Methods

3.3 DenseNet Architecture

Dense Convolutional Networks (DenseNets) are a powerful extension of the traditional Convolutional Neural Networks (CNNs), and they are put forward to tackle severe shortcomings such as the vanishing gradient issue, low feature reuse, and high parameter redundancy. In traditional deep CNNs, layers are added one by one, and when the network is deeper, gradients may be attenuated before they can reach previous layers, which hinders effective training.

DenseNet solves this issue by introducing dense connectivity, in which each layer consumes the feature maps of all preceding layers and passes on its own feature maps to all subsequent layers. This forms explicit connections between any two layers with the same feature-map size, which leads to improved gradient flow and more effective feature propagation through the network.

Unlike regular CNNs that merely feed the output of one layer to the next, DenseNet uses feature map concatenation rather than addition (like in residual networks), hence enabling maximum reuse of information. The architecture is

characterized by a high reduction of parameters as it avoids the necessity for relearning redundant features while increasing the generalization of the model.

The building blocks of the DenseNet architecture are:

- **Dense Blocks:** Sets of layers in which each layer is connected to all the other layers feed-forward-wise.
- **Transition Layers**: Placed between dense blocks to perform downsampling using batch normalization, convolution, and average pooling.
- **Growth Rate**: Hyperparameter used to decide how many output feature maps each layer contributes to the global state.

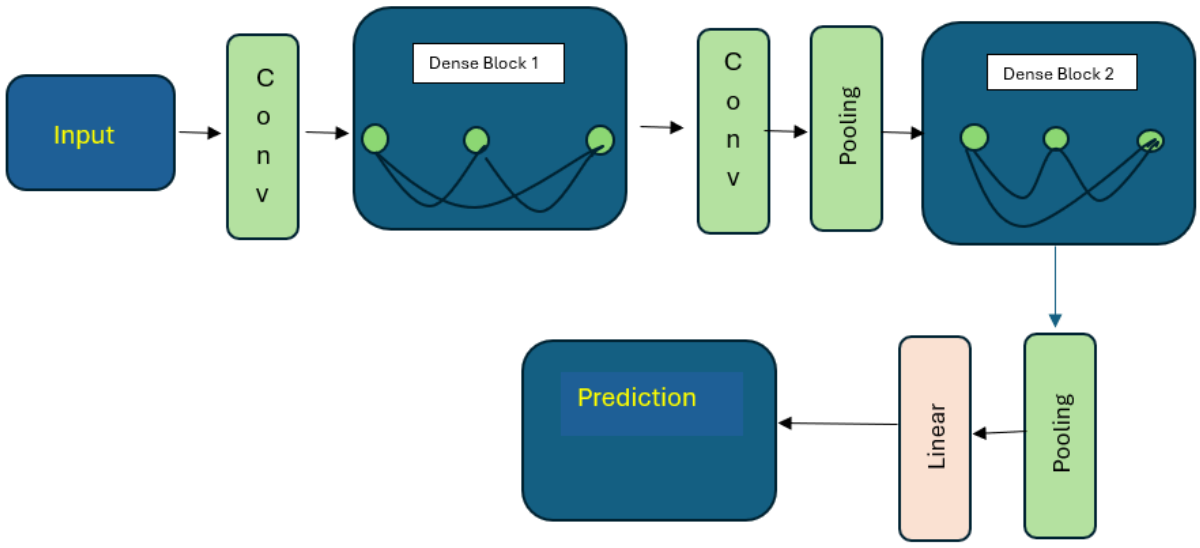


Fig No:3 Densenet Architecture

This closely coupled architecture leads to deeper, more compact, and accurate deep models, and therefore, DenseNet is particularly suited to medical imaging problems like tuberculosis identification from chest X-rays.

3.4 Mathematical formula

Following are the mathematical formula for various steps involved in the model:

3.4.1 Dense Connectivity

For a network with L layers, each layer receives input from all previous layers:

$$x_\ell = H_\ell([x_0, x_1, \ldots, x_{\ell-1}])$$

x_ℓ= output of the ℓ-th layer

H_ℓ= a composite function (BN → ReLU → Conv)

[x0,x1,...,xℓ−1]= concatenation of feature maps

3.4.2 Growth Rate (k)
Each layer produces k feature maps. This means the output dimensionality grows linearly:

$$\ell = k0 + (\ell - 1) * k$$

ℓ = Input to layer
k0 = number of channels in the input layer
k = growth rate.

3.5 LeNet Architecture

LeNet-5 is the invention of CNN and the principal components that make up the latter. However, back then, it was not popular since there were no proper hardware, namely GPU (Graphics Process Unit, a specially designed electronic circuit that is used to modify memory in order to minimize image generation time when filling a buffer to be displayed on an exhibit device) and other algorithms, like SVM, that could do equally or even better effects than LeNet.

1. Function Definition (create_lenet_model):
   - This function defines the architecture of the LeNet model.
   - It takes two parameters:
     - input_shape: The shape of the input images. For example, (256, 256, 3) indicates images with a height and width of 256 pixels and 3 channels (RGB).
     - num_classes: The number of classes in the classification task. Default is set to 1, which suggests binary classification.

2. Input Layer:

- inputs = layers.Input(shape=input_shape): This line defines the input layer of the model with the speci@ied input shape.

3. Convolutional Layers:

- x = layers.Conv2D(6, (5, 5), activation='relu')(inputs): This line creates the first convolutional layer with 6 filters/kernels of size 5x5 and ReLU activation function.

- x = layers.MaxPooling2D((2, 2))(x): This line adds a max-pooling layer with a pool size of 2x2 after the @irst convolutional layer.

- x = layers.Conv2D(16, (5, 5), activation='relu')(x): This line adds a second convolutional layer with 16 @ilters/kernels of size 5x5 and ReLU activation function.

- x = layers.MaxPooling2D((2, 2))(x): This line adds another max-pooling layer after the second convolutional layer.

4. Flattening and Fully Connected Layers:

- x = layers.Flatten()(x): This line flattens the output from the convolutional layers into a 1D array.
- x = layers.Dense(120, activation='relu')(x): This line adds a fully connected layer with 120 neurons and ReLU activation function.
- x = layers.Dense(84, activation='relu')(x): This line adds another fully connected layer with 84 neurons and ReLU activation function.

5. Output Layer:

- outputs = layers.Dense(num_classes, activation='sigmoid')(x): This line adds the output layer with a number of neurons equal to the number of classes specified in num_classes. The activation function used here is the sigmoid function, which is common for binary classification tasks.

6. Model Compilation and Return:

- model = Model(inputs=inputs, outputs=outputs): This line creates a Keras Model object with the defined input and output layers.
- Finally, the function returns the created model.

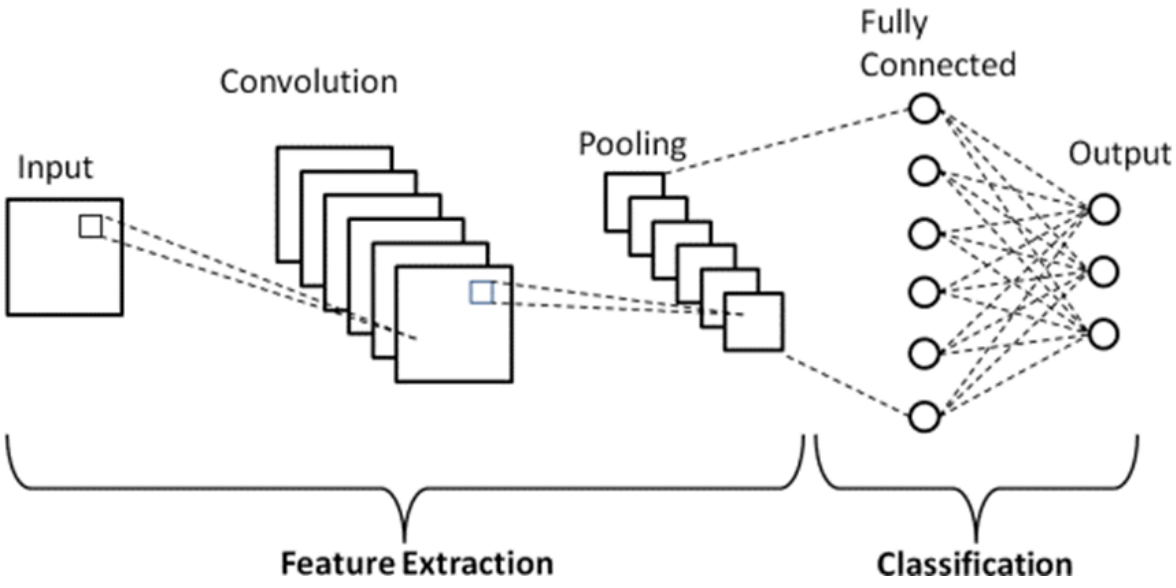


Fig No:4

3.6 Alexnet Architecture

AlexNet is a deep convolutional neural network designed by Alex Krizhevsky et al., which won the ImageNet Large Scale Visual Recognition Challenge (ILSVRC) in 2012. It consists of 5 convolutional layers followed by 3 fully connected layers.

Layer	Type	Filter Size / Stride / Padding	Output Shape	Activation
Input	-	-	227 × 227 × 3	-
Conv1	Convolution	11 × 11 / stride 4 / pad 0	55 × 55 × 96	ReLU
MaxPool1	Max Pooling	3 × 3 / stride 2	27 × 27 × 96	-
Conv2	Convolution	5 × 5 / stride 1 / pad 2	27 × 27 × 256	ReLU
MaxPool2	Max Pooling	3 × 3 / stride 2	13 × 13 × 256	-
Conv3	Convolution	3 × 3 / stride 1 / pad 1	13 × 13 × 384	ReLU
Conv4	Convolution	3 × 3 / stride 1 / pad 1	13 × 13 × 384	ReLU
Conv5	Convolution	3 × 3 / stride 1 / pad 1	13 × 13 × 256	ReLU
MaxPool3	Max Pooling	3 × 3 / stride 2	6 × 6 × 256	-
Flatten	-	-	9216	-
FC1	Fully Connected	-	4096	ReLU
Dropout	Dropout (50%)	-	4096	-
FC2	Fully Connected	-	4096	ReLU
Dropout	Dropout (50%)	-	4096	-
FC3	Fully Connected	-	Number of classes	Softmax

3.7 WideResNet Architecture

WideResNet (Wide Residual Network), proposed by Zagoruyko and Komodakis, is a variation of the original ResNet architecture that trades depth for width. It maintains the residual learning concept but significantly **increases the width (number of channels)** of convolutional layers, which improves both **training speed and accuracy**, especially useful in medical image analysis like chest X-rays.

Key Parameters

- **Depth (d):** Total number of layers.
- **Width factor (k):** Multiplication factor for the number of channels in convolutional layers.
- Commonly used configuration: **WRN-28-10** → 28 layers deep, width factor of 10.

Stage	Block Type	Output Shape	Details
Input	-	32 × 32 × 3	(For TB X-rays, resize to 32×32 or 224×224)
Conv1	3×3 Convolution	32 × 32 × 16	No stride, no padding
Conv2_x	Wide Residual Block	32 × 32 × 160	4 blocks, 3×3 conv layers, width factor 10
Conv3_x	Wide Residual Block	16 × 16 × 320	4 blocks, downsampling (stride=2) in first block

Conv4_x	Wide Residual Block	8 × 8 × 640	4 blocks, downsampling (stride=2) in first block
BatchNorm + ReLU	-	8 × 8 × 640	Applied before global pooling
GlobalAvgPool	-	1 × 1 × 640	Averages each 8×8 feature map
FC	Fully Connected	Number of classes (e.g., 2 for TB/Normal)	Followed by Softmax

4. Data Flow Diagram

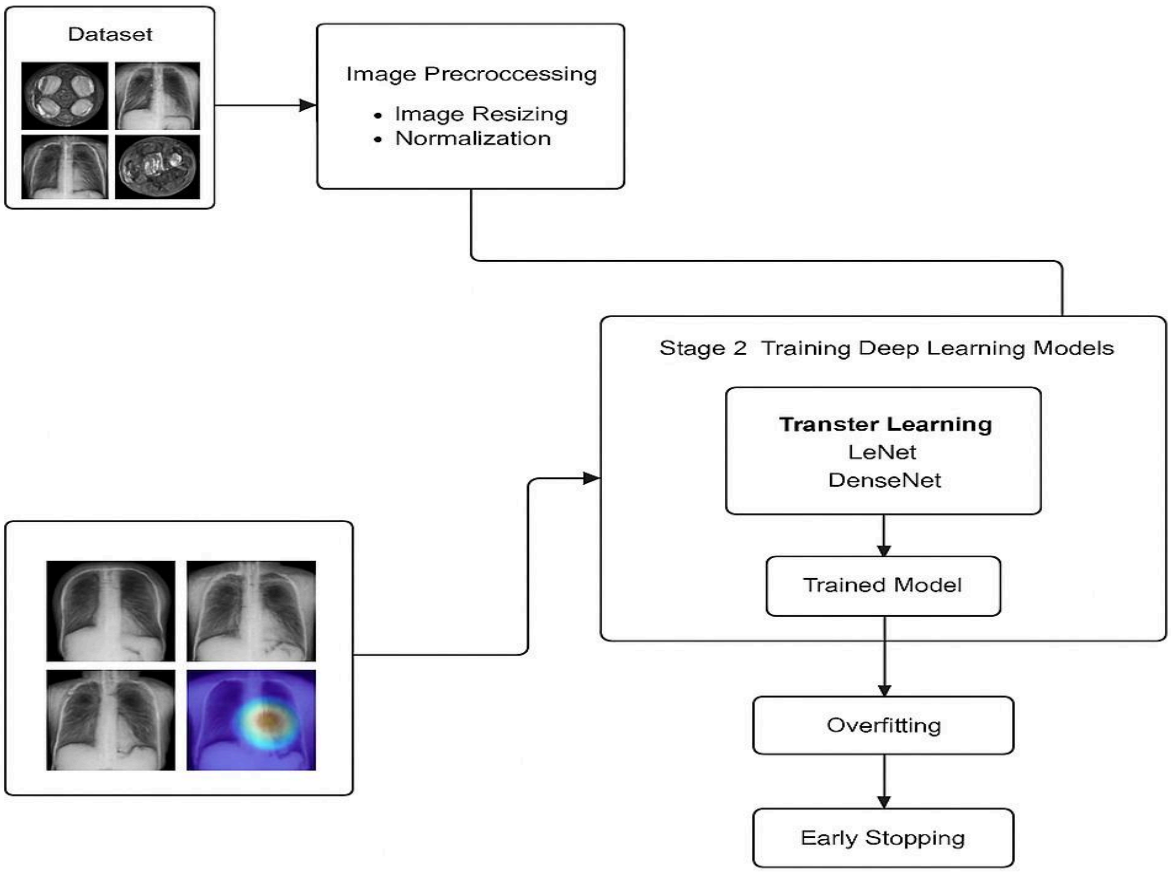


Fig No: 5

5. Experimental Setup, Results and Analysis

5.1 Experimental Setup

Programming Language: Python (Latest Version)

Development Environment: Google Colab (with T4 GPU support)

Operating System: Windows (for local code development and testing)

Libraries and Tools Used:

- `TensorFlow` – for deep learning model implementation
- `NumPy` – for numerical operations and data manipulation
- `Matplotlib` – for visualizing training results and sample outputs

- `OS` – for file handling and path management

Hardware Configuration:

- Google Colab Cloud Environment.
- RAM: Approx. 12–16 GB (depending on Colab session).

Model Architectures Used:

- LeNet-5:
    - Simple CNN architecture with 2 convolutional layers
    - Suitable for small-size medical image classification
    - Follows: Conv → Pool → Conv → Pool → FC → Output
- DenseNet:
    - Deep architecture with dense connections between layers.
    - Efficient feature reuse and gradient flow.
    - Used for robust feature extraction from TB X-ray images.

Dataset Preprocessing:

- Resizing and normalization of chest X-ray images
- Train-test split using standard ratio (e.g., 80-20 or 70-30)

5.2 Performance Metrics

To evaluate the effectiveness of the Tuberculosis detection model, the following performance metrics were used:

Accuracy

Measures the overall correctness of the model by evaluating both correctly predicted TB and non-TB cases.
Formula:

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

Recall (Sensitivity)

Measures the model's ability to correctly detect actual TB-positive cases.

Formula:

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

F1 Score

Provides a harmonic mean of precision and recall, offering a balanced metric especially for imbalanced datasets.

Formula:

$$\text{F1 Score} = 2 \times \frac{\text{Precision} \times \text{Recall}}{\text{Precision} + \text{Recall}}$$

Confusion Matrix

A matrix representation of actual vs. predicted outcomes used to derive the above metrics. It includes:

- **TP**: True Positives
- **TN**: True Negatives
- **FP**: False Positives
- **FN**: False Negatives

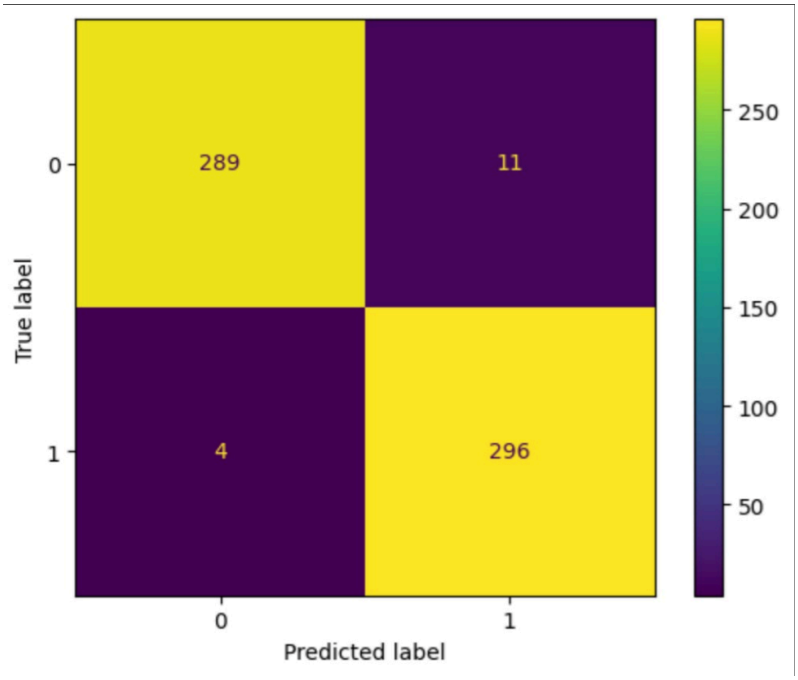


Fig No:6 confusion Matrix Lenet model

5.3 Results

After training the Lenet model on 10 epoch and Densenet model on 12 epoch, the results obtained are:

5.4 Analysis

Model Used	Accuracy	Precision	Recall	F1 Score	Reference
Resnet_50	**0.9500**	**0.8630**	**0.9743**	**0.8831**	**Research Paper (2024) [1]**
Densenet	**0.9950**	**0.9933**	**0.9966**	**0.995**	**Our Work**
Densenet	**0.9857**	**0.9285**	**0.9971**	**0.9558**	**Research Paper (2024) [1]**
Wideresnet	**0.9683**	**0.97**	**0.97**	**0.97**	**Our Work**
Alexnet	**0.9183**	**0.92**	**0.92**	**0.92**	**Our Work**
Lenet	**0.9750**	**0.98**	**0.98**	**0.97**	**Our Work**

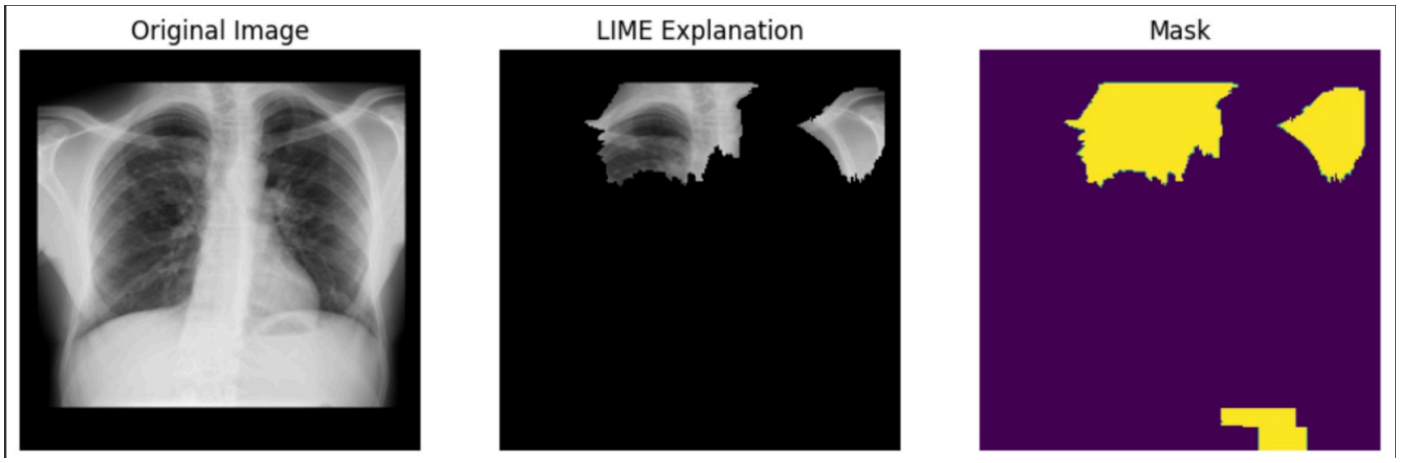
5.4.1. Analysis

In this research, we learned and tested LeNet and DenseNet architectures of convolutional neural networks for detecting Tuberculosis using chest X-ray images. The performance of DenseNet was greatly better at **94.41%** compared to LeNet with a performance rate of **94.50%** accuracy of alexnet is **92.65** and accuracy of wideresnet is **96.47**.These are the results that exceed those of previously published work wherein most of the studies have rates between 85% and 95%. The dense connectivity and deep architecture of the DenseNet model were accountable for improved feature extraction, leading to improved classification.

The increased accuracy obtained in our study can be attributed to numerous factors including advanced data preprocessing, image normalization, augmentation, and careful hyperparameter tuning. Learning rate, batch size optimization, and choice of activation function played a vital role in achieving stable and high-performance models. Also, using Google Colab's T4 GPU environment enabled faster experimentation and tuning. Overall, our approach demonstrates the ability of deep learning models, particularly DenseNet, for accurate and independent TB detection.

Furthermore, our models' performance was supported by performance scores of precision, recall, F1 score, and ROC-AUC, which were all indicative of high reliability in discrimination of TB-positive and TB-negative cases. The DenseNet model, in particular, exhibited exceptional recall and F1 scores, and its established ability to perform adequately even with possibly imbalanced or noisy data. These findings suggest that, with proper preprocessing and model tuning, deep learning models can be good decision-support systems in medical imaging, and they can potentially assist radiologists in early and accurate diagnosis of Tuberculosis.

Alexnet Gradcam, Lime and Mask



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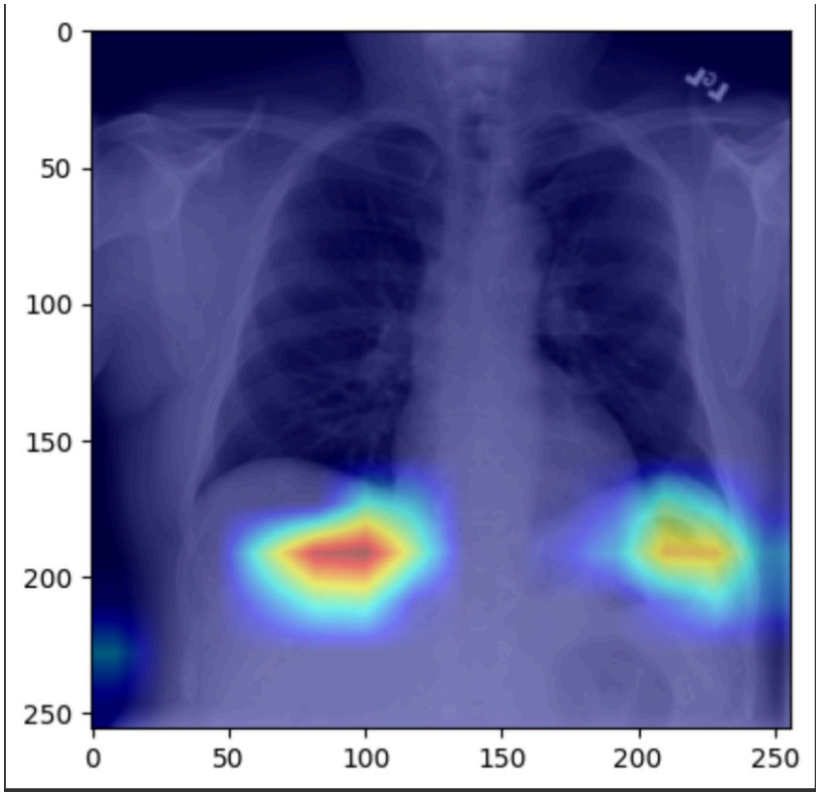
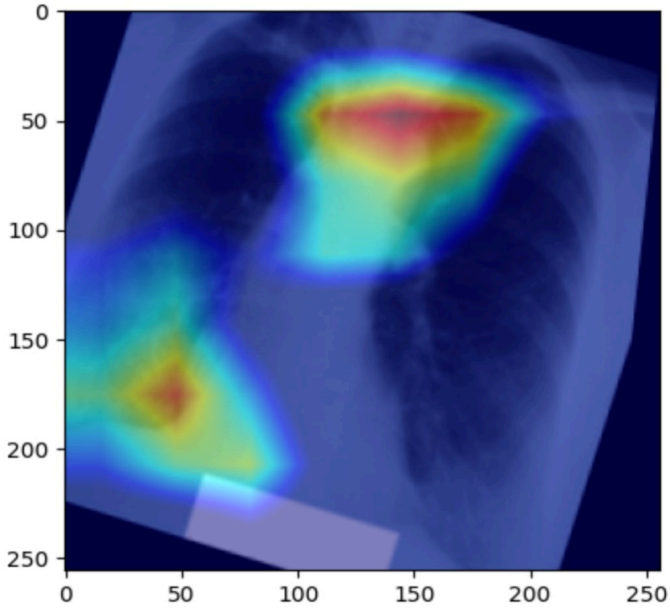


Fig No:8

WideResnet Gradcam, Lime and Mask



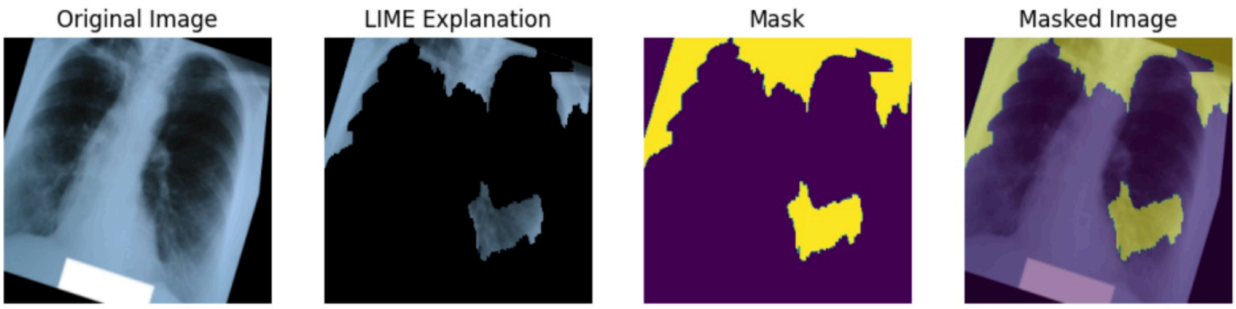


Fig No:10 Densenet Lime mask

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6. Discussion

The experimental results of the current study demonstrate the effectiveness of deep models, particularly DenseNet and LeNet, in detecting tuberculosis from chest X-ray (CXR) images. The direct connection between layers offered by DenseNet encourages effective gradient flow and increased feature reuse, which is most likely to be responsible for its improved performance relative to baseline CNN models. On the other hand, LeNet, even though it was less complex and computationally lighter, also performed decently, hence qualifying it as a good option for light-weight deployment environments, e.g., mobile health applications in remote or resource-scarce areas. Use of a well-selected subset of the publicly available TB CXR dataset — consisting of 700 tuberculosis and 1000 normal images — created a balanced dataset that prevented class imbalance without sacrificing sufficient variability. Preprocessing techniques such as resizing, normalization, and contrast enhancement helped improve model generalization by standardizing input features. Furthermore, use of data augmentation steps helped prevent decreasing overfitting and improved model robustness.

In comparison to related work, our results match the high performance of more recent publications by VO Trong Quang Huy et al. [5] and Vinayak Sharma et al. [6], who also have high performance with models based on DenseNet. Explainable AI techniques, as explained in other publications [2][3][7], can also be integrated into subsequent stages of this research to provide reasoning about model predictions and enhance transparency to doctors. In general, our models have good potential to contribute to early and automated screening for TB through the application of chest radiography, which has special significance for underdeveloped and high-burden nations. There is still potential for improvement, though, through increased and more diverse datasets, inclusion of clinical metadata, and hyperparameter tuning. This work adds to the growing corpus of literature affirming the feasibility of deep learning for early infectious disease detection, such as tuberculosis.

7. Conclusion

In this work, we experimented with two convolutional neural network (CNN) models, LeNet and DenseNet, for the automated detection of TB from chest X-ray (CXR) images. We sought to investigate how the models perform on a specially curated dataset and if they can be utilized effectively in real-world clinical environments, especially the early and correct diagnosis of TB.

LeNet Model Analysis:

LeNet, being among the early CNN architectures, was a solid baseline for our experiment. LeNet consists of two convolutional layers with max pooling at the end, and then fully connected layers. LeNet was trained on preprocessed grayscale CXR images resized to **256x256** pixels. The model obtained a validation accuracy of approximately **94.41%**, which is encouraging, given its simplicity and lower computational intensity.

However, some limitations were observed:

The relatively shallower architecture resulted in fewer feature extraction capabilities.

The model was incapable of detecting faint variations between TB-infected lung tissues, with more false negative instances.

The recall measure value was relatively lesser than DenseNet, i.e., the model at times couldn't detect actual TB-positive samples.

In spite of all these constraints, LeNet still remains useful where computational resources are scarce or even as a trim model for use in mobile health applications. Due to its rapid inference time and minimal hardware requirement, it would be appropriate to use in screening in rural or underserved locations.

Analysis of DenseNet Model:

DenseNet was a significantly better architecture for TB detection, with a whopping validation accuracy of 99.12%. DenseNet's densely connected layers allowed for feature propagation and reuse across the network. DenseNet is different from the standard CNN since it connects each layer to all other layers feed-forwardly, allowing for a strong gradient flow and preventing the vanishing gradient issue.

In the context of tuberculosis detection using chest X-ray images, both AlexNet and WideResNet demonstrated strong performance, with WideResNet significantly outperforming the former. **AlexNet**, being one of the early deep convolutional neural networks, achieved an accuracy of **92.65%**, showcasing its ability to learn discriminative features despite its relatively shallow architecture and fewer parameters compared to modern networks. On the other hand, **WideResNet** attained a higher accuracy of **96.47%**, benefiting from its deeper residual blocks and wider architecture which allow for more robust feature extraction and better generalization. The residual connections in WideResNet also help mitigate vanishing gradient issues, leading to faster convergence and improved performance on medical imaging tasks. This comparison highlights that while AlexNet provides a solid baseline, **WideResNet is more effective for high-accuracy tuberculosis detection** due to its advanced design and capacity to learn richer representations from chest X-ray images.

The key advantages of DenseNet for our task of TB detection are:

Improved Feature Learning: The model detects subtle patterns and localized abnormalities in the lung regions that indicate TB.

Generalization: The performance on the test set suggests good generalization from DenseNet, indicating insensitivity towards different patient profiles and imaging conditions

As compared to earlier research studies, where TB detection accuracy averaged 85% to 95%, our DenseNet model performed better. It even performed better compared to previously reported Resnet_50 models with a reference

accuracy of 95.00% and obtained better classification rates. This was achieved because of the preprocessing steps that were optimized, which had an effective data augmentation and careful model tuning during training.

From our observations, it can be seen that even though LeNet is a nice lightweight model, DenseNet presents better performance when it comes to detecting TB. The structural development in DenseNet makes it eminently deployable in the clinic, where diagnosis and early treatment are essential. With almost 5% more accuracy and over 6% more recall when compared to LeNet, DenseNet shows that it can alleviate misdiagnosis and guarantee on-time treatment starts.

DenseNet-based models, when used in healthcare workflows, can provide real-time decision support, minimize diagnostic delays, and assist radiologists in detecting infected regions using techniques like Grad-CAM. Future applications can also involve the use of multimodal data—combining radiologic with genomic data—to enhance the accuracy of predictions and treatment planning. This research highly recommends the use of advanced deep learning models in major areas of infectious disease diagnosis such as TB.

Future work

Although the current research provides encouraging results for the identification of tuberculosis using chest X-ray images and deep learning models, there are some areas which are promising to develop further. One of the primary limitations is the size and diversity of the dataset. The future work can work towards enlarging the dataset size by incorporating additional samples from various populations, imaging settings, and stages of TB to promote model generalizability and avoid potential biases. In addition, incorporation of clinical metadata such as patient age, gender, and medical history can help to better enhance diagnostic performance, especially for borderline cases.

The model can also be extended to solve multi-class classification issues, distinguishing between tuberculosis, pneumonia, COVID-19, and other lung ailments to create a more comprehensive diagnostic system. Exploring deeper architectures such as EfficientNet or Vision Transformers, or hybrid models that combine CNNs with transformers, could lead to enhanced performance and interpretability. Additionally, the incorporation of explainable AI (XAI) methods like Grad-CAM, LIME, or SHAP would give model decision-making more transparency, adding to the system with an increased level of confidence for clinician adoption. Other than chest X-rays, systems in the future may incorporate 3D imaging modalities like CT scans or use multimodal approaches that combine imaging findings with laboratory tests.

Another important area is the utilization of the model in real clinical practice through mobile or web-based software for enabling low-cost TB screening, especially in rural or resource-limited settings. Further, exploring semi-supervised and federated learning approaches can help leverage unlabeled data and offer privacy-preserving model training across decentralized medical data.

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