A HYBRID MODEL FOR CLASSIFICATION OF TUBERCULOSIS CHEST X-RAYS IMAGES

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ABSTRACT

Tuberculosis (TB), a grave infectious disease affecting millions globally, is often diagnosed using chest X-rays. For accurate diagnosis, especially for detecting early stage, medical practitioners require the assistance of advanced technologies. In contrast to existing models, which focus largely on TB detection in the images, the proposed work aims to classify the images affecting TB such that an appropriate method can be chosen for accurate chest TB detection in chest X-ray images. Thus, we aim to combine the powerful features of the VGG16 architecture with a convolutional neural network (CNN) for classification purposes. Drawing inspiration from VGG16, known for its effective method of capturing essential image information, we aim to modify VGG16 for feature extraction to identify signs of tuberculosis (TB) in images. For the classification task, we employ a CNN to categorize images impacted by TB. Our proposed technique is evaluated on a standard dataset, demonstrating its superiority over current leading methods in accuracy, recall, and precision.

Keywords: Tuberculosis; Bacterium; VGG-16 Model; Deep-Learning; Convolutional Neural Network; X-ray.

1.0. INTRODUCTION

As noted from recent work on topics related to health, the importance of early diagnosis and detection of symptoms is vital to control outbreaks and disasters caused by infectious diseases [1-2]. One such disease is Tuberculosis (TB), which remains a significant global health challenge, ranking among the top ten causes of death worldwide [3]. It is especially prevalent in low and middle-income countries, where conditions like poverty, overcrowding, and inadequate healthcare access amplify its effects. TB is caused by the bacterium Mycobacterium tuberculosis, which primarily attacks the lungs but can also affect other organs, making its diagnosis and treatment particularly difficult. [3] One of the cornerstones of TB diagnosis is the use of chest X-rays. These imaging studies provide a crucial visual assessment of the lungs, allowing radiologists to detect characteristic abnormalities associated with TB, including cavities, nodules, and patterns of infiltration. However, the interpretation of chest X-rays is far from straightforward. It demands not only specialized training and expertise but also relies heavily on subjective assessments, introducing a significant degree of variability into the diagnostic process. However, there are numerous methods developed in the past for TB detection and classification identification [4]. Most methods focus on detecting a vital region which indicates TB symptoms in the images for classification. Therefore, these methods are sensitive to clutter and background noise and hence the performance of the method is ineffective when the input data background TB and degrades normal images. In addition, the vital region in the TB images is not noticeable, and the state-of-the-art method may not perform well.

Therefore, detecting TB accurately is complex and challenging. It is evident from sample images shown in Fig. 1(a) and (b), where it is not so easy for eyes to identify the images in (a) are normal and images in (b) are TB images. It is further validated from the results of the existing methods [5, 6] which misclassify normal images as TB images and vice versa as shown in Fig. 1. To reduce the complexity of TB detection, it is necessary to classify the images affected by TB from normal images (TB free) such that one can choose the best state-of-the-art method for TB detection even if the vital region is not noticeable [7, 8]. This idea helps us to use available resources effectively rather than developing a new method. Thus, this work focuses on developing a new method for classification of TB images.

Inspired by the VGG16, which is simple, efficient and extracts effective features for classification [9], we adapt the same for feature extraction to classify the TB images from normal images in this work. Since VGG16 extracts distinct features which represent TB and normal images, we propose a simple convolutional neural network for classification of TB images. Therefore, the key contributions to the proposed work are as follows:

- Adapting the VGG16 for distinct feature extraction to classify the TB images from normal images.
- Proposing CNN for successful classification of TB images from normal images
- Fusing two simple models in a novel way to achieve the best classification results.

(a) Normal images

(b) Tuberculosis Images

Fig. 1. Sample normal and Tuberculosis (TB) images. Proposed method classifies successfully both normal and TB images while the existing methods [5, 6] misclassifies.

The structure of this paper is as follows: Section 2 reviews related work, highlighting the advancements and limitations of existing TB diagnostic methods. Section 3 describes the proposed model, including its architecture and the reasoning behind its design. Section 4 outlines the experimental setup, data processing, and results, showcasing the model's performance. Finally, Section 5 discusses the implications of the findings and proposes directions for future research.

2.0. RELATED WORKS

As mentioned in the introduction section, there are numerous methods for TB image classification, detection, and identification in literature [10]. To review the recent methods, we tabulate the analysis of the existing methods to make readers easy read. The quest to enhance Tuberculosis (TB) diagnosis through advanced technology has seen significant strides in recent years. This section critically analyzes seminal articles from 2021 to 2023, focusing on innovations in TB detection using chest X-rays, and employs a tabular format in Table 1 to list their methodologies, results, and limitations.

Table 1**:** Critical analysis of existing methods on TB detection

Year	Study Focus	Models/Techniques Used	Outcome	Limitations
2021[11]	CNN application in TB detection	Various CNN architectures (ResNet, InceptionV3)	High accuracies (85%-95%), effective pattern recognition in X-rays	Limited datasets, questions on generalizability
2022[12]	Hybrid models and dataset diversity	CNNs combined with SVMs, Random Forest	Improved specificity and sensitivity, accuracies up to 97%	Computational inefficiency, overfitting issues
2023[13]	Efficient models and explainable AI	Lightweight models, AI transparency focus	Point-of-care diagnostics potential, user-friendly AI solutions	Real-world applicability, long-term reliability concerns

Table 1 shows that a dynamic and evolving field, marked by significant technological advancements and a continual push towards more accurate, efficient, and user-friendly TB diagnostic tools. Despite advancements in accuracy and model complexity, challenges persist in areas such as dataset diversity, model interpretability, and real-world applicability. Future research is poised to address these challenges, further cementing the role of AI in revolutionizing TB diagnostics.

Similarly, Table 2 summarizes recent studies on tuberculosis (TB) detection methodologies and their corresponding accuracies, showcasing a range of approaches such as deep learning models, ensemble techniques, microscopy analysis, and optical sensors.

Table 2**:** Summarizing the outcome of the existing TB detection methods

Methods	Dataset Used	Accuracy	Remarks
Tasci et al. (2021) [9]	Montgomery dataset, Shenzhen dataset	Montgomery: 97.500%, Shenzhen: 97.699%	Ensemble CNN model for TB detection.
Ayaz et al. (2021) [10]	Montgomery dataset, Shenzhen dataset	97%	Combines features using Ensemble Learning for TB detection.
Ibrahim, et. Al. (2021) [11]	Tuberculosis microscopy images	98.15%	Analyzing tuberculosis using microscopy.
Gelaw et al. (2021) [12]	Merged various public datasets	97.72%	AI and imaging for TB detection.
Gröschel et. al (2021) [13]	Ground truth dataset of 20,408 isolates	77.6% and 75.4%	GenTB app for antibiotic resistance prediction.
Ullah et al. (2022) [14]	Tested 40 TB patients	95%	Optical sensor using Raman spectroscopy for TB detection.
Ramachandran, et. al (2022) [15]	Data from 368 HIV-infected Ugandan adults	88.9%	mNGS with MLC for TBM diagnosis.
Kuang, et. al (2022) [16]	Dataset of 10,575 MTB isolates	93.8%	In silico AMR predictions for MTB.
Gite et al. (2023) [17]	Not specified	98%	U-Net++ for lung segmentation in TB detection.
Park et. Al. (2023) [18]	Chest X-ray images from 3314 patients	85% for MTB-LD and 0.78% for	Distinguishing NTM-LD and MTB-LD in X-rays.
Rahman et. al (2024) [19]	40,000 CXR images; 3037 CXR images for drug-resistant TB	79.59% for three-class classification	Deep learning framework for TB classification.

The recent studies in tuberculosis (TB) detection have explored various methods, leveraging different datasets and technologies with a focus on enhancing accuracy and efficiency. Methods range from advanced convolutional neural networks (CNNs) and ensemble learning models using standard datasets like Montgomery and Shenzhen to innovative uses of AI in microscopy and imaging [20].

Recently, there are methods developed for focusing on improving early diagnosis. For instance, the approach [21] combines the DenseNet201, which is used for feature extraction and the XGBoost, which is used for classification. Another approach [22] employs the MobileNet transfer learning model, which is computationally lightweight, achieving a high accuracy. Similarly, the model [23] uses a VGG19-based transfer learning technique with hyperparameter tuning for classification of TB and normal images. Furthermore, an ensemble-based machine-learning approach integrating various classifiers has been proposed for demonstrating a high accuracy for TB detection in the images.

Despite these advancements, several limitations persist. Notably, the reliance on specific datasets may hinder the generalizability of these models across different populations [24]. The performance of these methods also varies widely, with some specialized approaches like the GenTB app and three-class classification for drug-resistant TB showing lower accuracy and specificity, underscoring challenges in broader applicability and effectiveness. Making the issues as foundation the proposed method is keen to resolve the same [25]. Dhruti et al. [26] proposed a method for TB detection and severity prediction using deep learning model. The approach uses the combination of VGG-16, DenseNet-121, ResNet-50 and AlexNet. However, it is not clear whether this method is robust to noise and degraded images. Genitha et al. [27] developed a model for TB detection and classification based on deep learning. The approach uses preprocessing and feature extraction and finally, CNN for detection. The method addresses classification of normal and TB images, but the scope is limited to particular dataset and simple images. Liu et al. [28] focuses on exploring computer aided tuberculosis diagnosis using deep learning for improving diagnosis. The main aim of the work is to detect the region in the image but not classification of normal and TB images. Hossain et al. [29] developed a method based on convolutional neural network for identifying tuberculosis using images. This approach comprises DenseNet-121 and ResNet-50 for TB detection. Perez-Siguas et al. [30] focused on early detection of tuberculosis. The method uses traditional preprocessing steps for enhancing the fine details in the images followed by feature extraction and classifier for detection. It is noted from the above review that the primary objective of the methods is to detect TB but not classification of normal and TB images.

In summary, most existing methods focus on detection by extracting cues in the images and from therefore, these methods perform well when the images contain noticeable cues. In other words, if the image does not provide sufficient region which indicates TB, the methods do not work well because the features extracted from TB images share with the features extracted from normal images. This makes TB detection challenging and complex. This observation motivated us to propose a method for classification of images affected by TB from normal images, such that the complexity of the TB detection is reduced, and hence overall performance of TB detection improves.

3.0. PROPOSED METHODOLOGY

The methodology employed in this research is a carefully crafted combination of scientific processes and techniques aimed at creating an advanced, reliable, and efficient deep learning model for detecting Tuberculosis (TB) from chest X-ray images. This section details the complete process for classifying TB images versus normal images. Figure 2 illustrates the architectural diagram of the proposed model. In Fig. 2, the input begins from the directory and proceeds through preprocessing steps such as resizing, augmentation, normalization, and rescaling. Finally, the feature analysis is deployed, and then it goes to feature selection. Once the feature is selected, the proposed work uses a pre-trained model of VGG-16 where it goes through several convolution layers for feature extraction and once it is done it goes to CNN layers where the convolution blocks extract the feature and finally the classifier along with the softmax activation segregates it into output which is either Normal or TB.

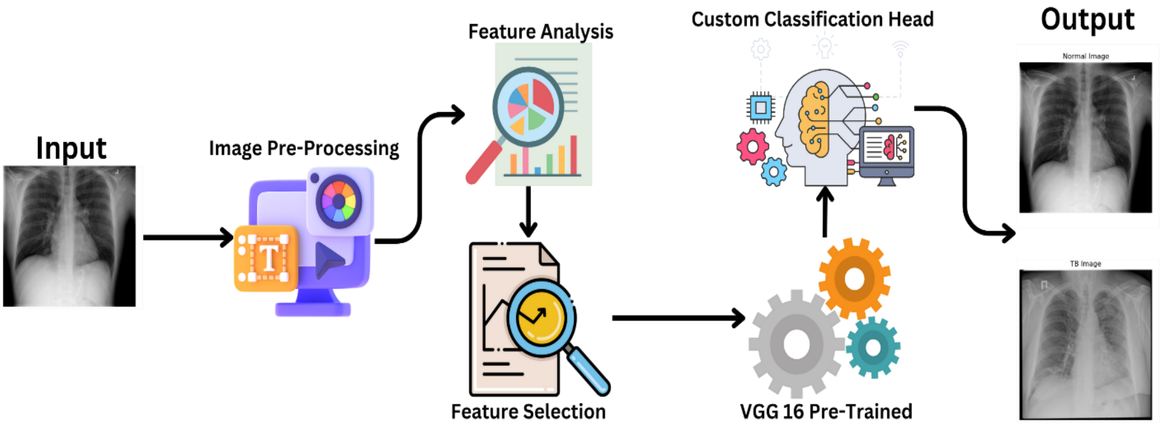


Fig. 2. Block diagram of the proposed work

3.1. Adapted VGG16 for Feature Extraction

As discussed earlier, the motivation to adapt the VGG16 architecture is due to its proven efficacy in image classification and recognition. Its design is characterized by its simplicity and depth, which are key to capturing the intricate patterns in chest X-rays for TB detection [31]. There are other well-known architectures, such as ResNet, Inception, and AlexNet. ResNet, known for solving vanishing gradient problems, was a strong contender. However, its complex residual connections make it less straightforward than VGG16. Inception models, with their parallel convolutional pathways, offer great performance but at the cost of increased model complexity. AlexNet, while historically significant, lacks the depth and sophistication of VGG16. VGG16's uniform architecture, consisting of repeated blocks of convolutional and max-pooling layers, simplifies the feature extraction process. This uniformity allows for a deep network that can learn a wide variety of features without the architectural complexities of other models. The VGG16 model architecture is modified to suit TB detection from chest X-rays. Here's a detailed analysis of each layer type.

The VGG16 architecture, developed by the Visual Geometry Group (VGG) at the University of Oxford, comprises a total of 16 layers, including 13 convolutional layers and 3 fully connected layers, as depicted in Fig. 3. The convolutional layers feature a consistent kernel size of 3×3 with a stride of 1, enabling the network to capture detailed spatial hierarchies in input images. These layers are interspersed with max-pooling layers that use a 2×2 pooling window to reduce spatial dimensions, thus managing computational load and preventing overfitting. Each convolutional layer is followed by a Rectified Linear Unit (ReLU) activation function, which introduces non-linearity and allows the model to learn complex patterns.

In this study, VGG16 is adapted by excluding the top classification layer (using include_top=False), converting the model into a powerful feature extractor. This modification utilizes the pre-trained weights from the ImageNet dataset, which includes a diverse range of image features, thereby improving the model's generalization to chest X-ray images. The architecture begins with the VGG16 base, followed by a Flatten layer that converts the 3D feature maps into 1D feature vectors. This is succeeded by a Dense layer with a sigmoid activation function, tailored for binary classification tasks. The resulting model effectively distinguishes between normal and tuberculosis-affected X-ray images, leveraging deep feature representations learned from the extensive ImageNet corpus, thus ensuring robust performance and enhanced diagnostic accuracy in medical image analysis. Figure 3 illustrates the adapted VGG16 architecture for this problem.

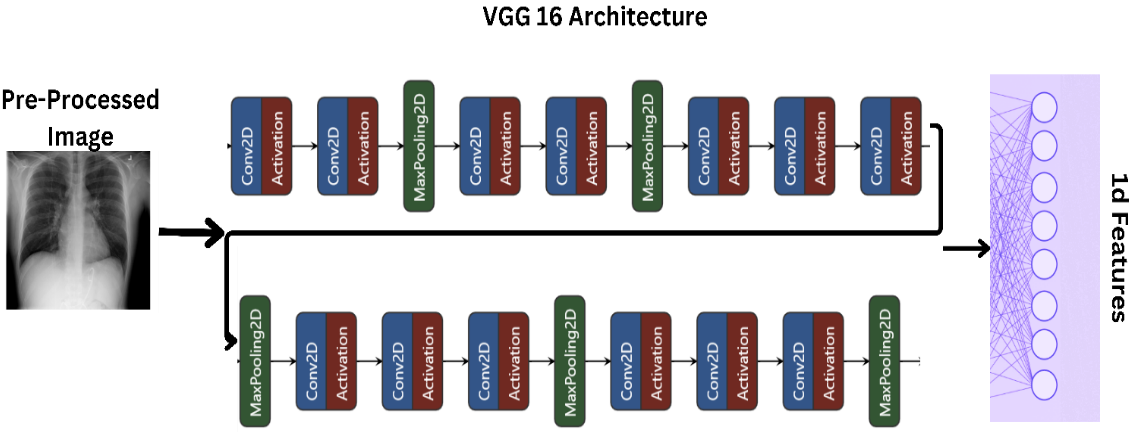


Fig. 3. Adapted VGG16 for feature extraction.

Convolutional Layers: These layers are the core building blocks of the model. They utilize filters to execute convolution operations, capturing the spatial and temporal dependencies within an image. In our model, these layers are designed to detect various features from simple edges to complex patterns indicative of TB as shown in Equation (1).

$$\text{Output} = \text{ReLU}\big(\text{Conv}(\text{Input})\big) \tag{1}$$

where **Conv** represents the convolution operation and **ReLU** is the activation function.

Pooling Layers: After the convolutional layers, pooling layers, particularly MaxPooling, are employed to decrease the spatial dimensions of the convolved features. This downsampling not only reduces the computational resources needed for data processing but also helps in controlling overfitting, as illustrated in Equation (2).

$$\text{Pooled Output} = \text{MaxPool}(\text{Input}) \tag{2}$$

Fully Connected Layers: Following multiple convolutional and pooling layers, the neural network's high-level reasoning is carried out via fully connected layers. In our model, these layers are customized to classify the features into TB and non-TB categories, as shown in Equation (3).

$$\text{Output} = \text{Activation}(W \cdot \text{Input} + b) \tag{3}$$

Final Layer: The final fully connected layer employs a sigmoid activation function to produce a probability value between 0 and 1, representing the likelihood of TB presence. In our model, we utilize the Rectified Linear Unit (ReLU) activation function. ReLU is favored because it introduces non-linearity, enabling the model to capture complex patterns. Moreover, it helps alleviate the vanishing gradient problem, thus aiding in the training of deep networks such as ours.

Regularization Techniques: To prevent overfitting, dropout layers are strategically included. Dropout randomly turns off a fraction of neurons during training, which helps in making the model robust by preventing it from being overly reliant on any one feature. The model is compiled using the Adam optimizer, renowned for its effectiveness in managing large datasets and high-dimensional spaces. For our binary classification problem (TB or no TB), we employ the binary cross-entropy loss function, which is suitable. To optimize training, techniques such as Learning Rate Scheduling (to dynamically adjust the learning rate) and Data Shuffling (to prevent model bias due to data order) are implemented. The corresponding loss function is presented in Equation (4).

$$\text{Loss} = -\frac{1}{N}\sum_{i=1}^{N}[y_i \log(p_i) + (1 - y_i)\log(1 - p_i)] \tag{4}$$

Training Process: The model is trained with a batch size of 32 images, balancing the need for computational efficiency and model performance. The number of epochs is set to 50, determined as optimal through experimentation. Early stopping is implemented to terminate training if the validation loss does not improve, preventing overfitting.

3.2. Proposed CNN for Classification of normal and TB images

The Convolutional Neural Network (CNN) architecture utilized in this study is fundamental for robustly analyzing and categorizing medical images, particularly chest X-rays. CNNs are tailored to process grid-like data, such as images, by employing key architectural concepts including local receptive fields, shared weights, and pooling operations.

The complete architecture is shown in Fig. 4. The architecture comprises various layers: Convolutional Layers, pivotal for detecting local patterns and features; Activation Functions like the Rectified Linear Unit (ReLU) introducing non-linearity for capturing complex image representations; Pooling Layers, reducing spatial dimensions and computational complexity; and Fully Connected Layers, performing high-level reasoning based on extracted features [32]. Towards classification, a final output layer with a sigmoid activation function is employed, facilitating binary classification probabilities for distinguishing between normal and tuberculosis classes. The hierarchical design of CNNs efficiently captures and learns from visual data's hierarchical nature, making them ideal for tasks like medical image analysis. Leveraging CNN depth and feature extraction capabilities, this study aims for high accuracy in distinguishing between normal and tuberculosis-affected chest X-ray images. Figure 4 shows the CNN Architecture adapted for the problem.

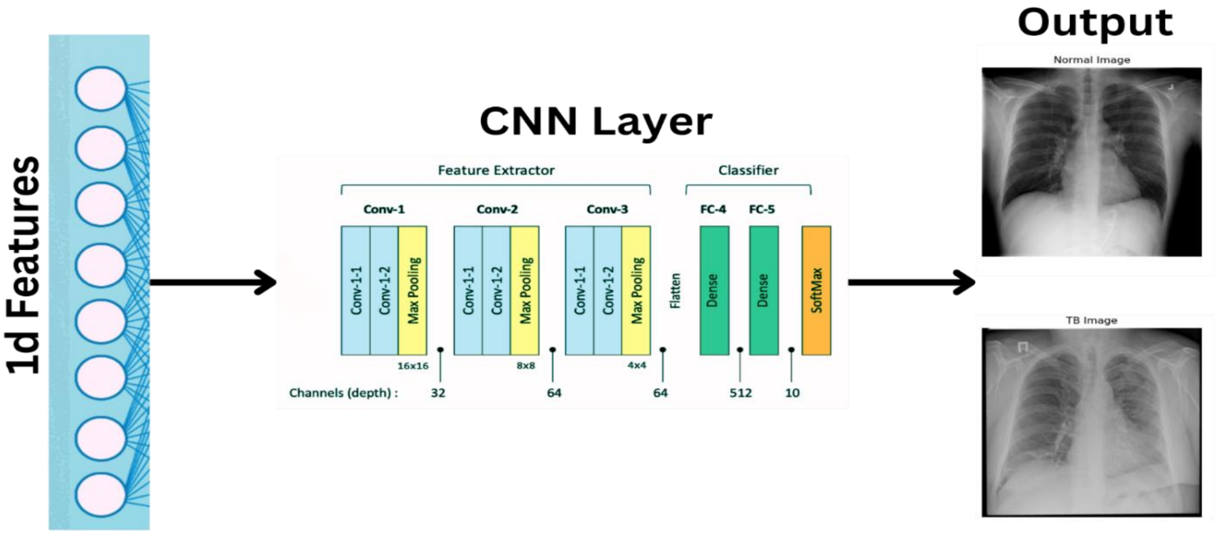
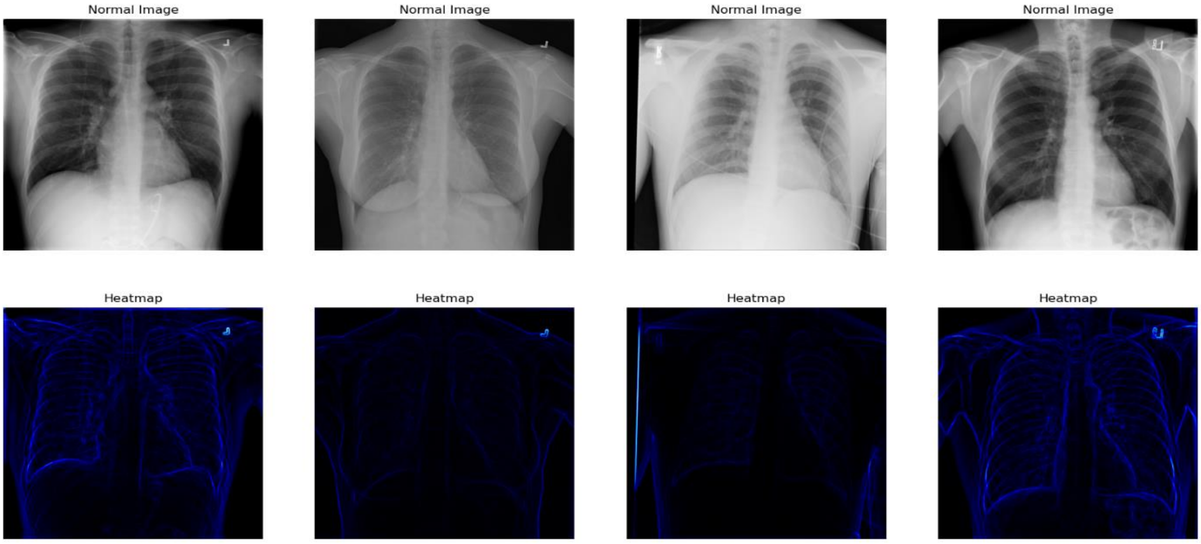
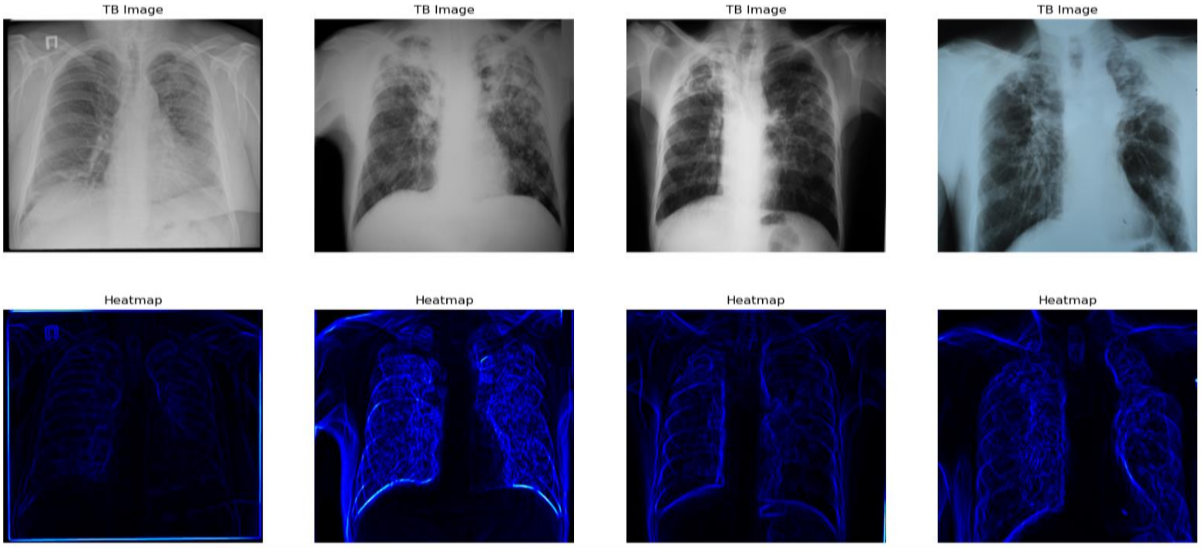


Fig. 4. Proposed CNN for classification of normal and TB images



(a) Normal images and respective heatmaps



(b) Tuberculosis Images and respective heat maps.

Fig. 5. Heatmaps of respective normal and TB images show that the proposed features are elegant to classify normal and TB images. Inconsistent structure with more brightness for TB while regular structure with low brightness for normal images.

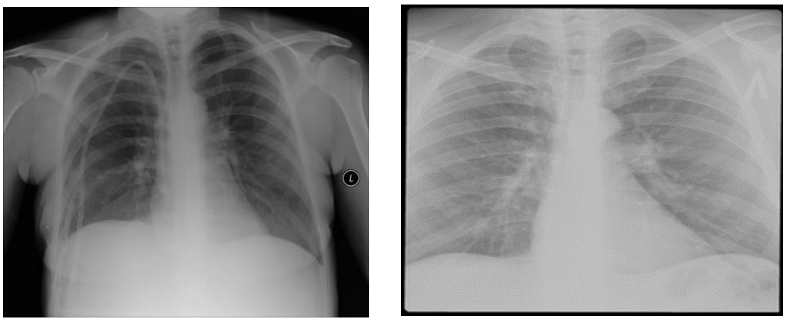
The efficacy of the proposed TB and normal image classification is demonstrated in Fig. 5. The TB images exhibit higher opacity and brighter regions, particularly highlighting cavities, compared to the heatmaps of normal images. This observation suggests that the combination of VGG16 and CNN effectively extracts distinctive features for the classification of TB and normal images.

4.0. EXPERIMENTAL RESULTS

During the experimentation phase, a thorough assessment of the model's performance was conducted using a range of metrics, including accuracy, recall, and precision. To evaluate both the proposed and existing methods, this study utilizes a standard dataset for experimentation.

4.1. Dataset and Evaluation

Comprising 4200 chest X-ray images, it is equally divided into two subsets: 3,500 images of healthy (normal) lungs and 700 images exhibiting TB symptoms. The selection criteria for these images were stringent, ensuring high-quality and clinically relevant data [33]. **Normal Images:** These were carefully selected to represent a range of healthy lung conditions, sourced from various health institutions and public databases. The inclusion criteria ensured a representation of different lung conditions that appear normal but vary subtly in terms of lung size, shape, and other minor variations not indicative of TB. **TB Images:** These images were specifically chosen to cover a wide spectrum of TB manifestations, including both early and advanced stages of the disease. The diversity in this subset is crucial to train the model to recognize various forms and severities of TB manifestations. Fig. 6 shows the normal and TB condition image.



Normal image TB image

Fig. 6. Sample normal and Tuberculosis images.

Accuracy: This is the most intuitive performance measure. It is essential to evaluate how often the model is correct as defined in Equation (5).

$$\text{Accuracy} = \frac{\text{True Positives (TP)} + \text{True Negatives (TN)}}{\text{Total Number of Cases}} \tag{5}$$

Recall: Crucial for medical diagnostics, sensitivity measures the model's ability to correctly identify positive TB cases. High sensitivity reduces the risk of false negatives, which is vital in ensuring patients receive timely treatment. It is calculated using Equation (6).

$$\text{Recall} = \frac{\text{True Positives (TP)}}{\text{True Positives (TP)} + \text{False Negatives (FN)}} \tag{6}$$

Precision: Precision is important in medical contexts to ensure that the predicted positive cases are truly positive, minimizing the risk of misdiagnosis. It is calculated using Equation (7).

$$\text{Precision} = \frac{\text{True Positives (TP)}}{\text{True Positives (TP)} + \text{False Positives (FP)}} \tag{7}$$

4.2. Ablation Study

As outlined in the Proposed Methodology section, the adaptation of VGG16 and the introduction of CNN are key components aimed at achieving the best results for classifying normal and TB images. To demonstrate the contribution and efficacy of this combined approach, we conducted a comparison of the performance between the proposed fused model and baseline architectures. The results, including accuracy, recall, and precision, are presented in Table 3. It is evident from the table that the proposed combination of VGG16 and CNN outperforms all baseline architectures across all metrics. Models such as Squeezenet (Resnet-based) and Densenet 121 exhibited lower accuracy rates. These models likely faced challenges in adequately extracting critical features or lacked the necessary depth to identify subtle tuberculosis indicators in the X-ray images. Conversely, more advanced architectures like the Vision Transformers Based Model, Modified CNN, Inception V3, and Xception demonstrated higher performance, indicating their enhanced capability in feature extraction and classification tasks. Notably, the proposed model, which integrates VGG-16 with a Custom CNN, achieved superior results compared to all the baseline architectures. This remarkable performance can be attributed to the robust feature extraction provided by the VGG-16 architecture and the additional refinement capabilities of the Custom CNN, which together facilitate the effective capture of complex patterns and anomalies indicative of tuberculosis. Therefore, one can infer that the proposed combination is better than existing baseline models for classification of normal and TB images.

Table 3: Assessing the contribution of the proposed combination with the baseline models for classification of normal and TB images.

#	Technique	Accuracy	Precision	Recall
(i)	Squeezenet (Resnet based Model)	0.72	0.88	0.52
(ii)	Vision Transformers Based Model	0.93	0.86	0.95
(iii)	Densenet 121	0.72	0.52	0.52
(iv)	Modified CNN	0.96	0.94	0.95
(v)	Inception V3	0.97	0.98	0.90

(vi)	Xception	0.94	0.95	0.82
(vii)	Proposed Model (VGG-16 with Custom CNN)	0.98	0.98	0.94

While several models were evaluated for tuberculosis detection in chest X-rays, such as Squeezenet, Vision Transformers Based Model, Densenet 121, Modified CNN, Inception V3, and Xception. The performance of these models is inferior to the proposed model. The reason for poor results of the existing models is that these models lack robustness and generalization for handling complex TB images.

4.3. Experiments on Classification

The quantitative results of the proposed and existing methods on the standard dataset are presented in Table 4, showcasing impressive performance in both normal and TB image classification compared to the performance of the existing models. It is observed from Table 4 that the proposed model, employing VGG-16 with CNN as an extractor, attains the highest accuracy for both classification of normal and TB images. The hybrid framework with CNN and classifiers [25] may not fully optimize performance due to potential limitations in capturing complex features necessary for accurate TB identification. Similarly, while transfer learning with MobileNet and hyperparameter tuning approaches are effective, they might not have fully exploited the rich feature representations required for optimal performance [31-32]. Additionally, methods combining HOG and LBP with several classifiers may not capture as diverse and complex features as CNN-based approaches like VGG-16 [33]. The proposed model's superior performance likely stems from the effectiveness of VGG-16 as a feature extractor, coupled with the robustness of CNN-based approaches for image classification tasks.

Table 4. Performance of the proposed and existing methods on TB image classification

Methods	Normal Class			TB Class		
	Accuracy	Precision	Recall	Accuracy	Precision	Recall
Hybrid framework with CNN and Classifiers [21].	0.965	0.960	0.982	0.970	0.970	0.874
MobileNet transfer learning model [22]	0.970	0.965	0.990	0.972	0.970	0.852
Transfer learning and hyperparameter tuning [23]	0.968	0.960	0.985	0.970	0.965	0.881
HOG And LBP fused with several classifiers [34]	0.970	0.965	0.988	0.972	0.975	0.912
Proposed Model (VGG-16 with CNN as Extractor)	**0.982**	**0.984**	**0.992**	**0.983**	**0.98**	**0.94**

Fig. 7 illustrate an instance of misclassification of normal and TB images by the proposed model. The reason for misclassification is due to the presence of subtle anomalies present in the normal X-ray image, which mimicked characteristics typically associated with TB-related abnormalities. These anomalies, while innocuous in nature, posed challenges for the model in accurately discerning between TB and normal cases. Furthermore, misclassification highlights the inherent variability and complexity of chest X-ray images, where nuanced features can sometimes blur the lines between pathological and non-pathological conditions. However, despite this instance of misclassification, it's crucial to acknowledge the overall robustness and effectiveness of our proposed model, as evidenced by its high accuracy and performance metrics. This shows that there is a scope for the improvement of the proposed work. One possible solution to these challenges is to explore an end-to-end model by unifying enhanced models and language models. This will be our future work.

Furthermore, as discussed in the methods [35, 36], sometimes, if the model works like black box, it is not so easy to analyze the outcome of the machine learning model and it may lead to confusion. One possible reason is unfair and biased training, labeling the samples and the process of machine learning. This work uses standard dataset and labels for evaluation. In addition, we follow the same instructions mentioned in the original work to calculate the classification rate. Therefore, it is necessary to verify and cross check the whole process of labeling and training to ensure fair and unbiased results. Henc, it is important especially for medical applications, like disease identification and classification. Thus, motivated by the work [35, 36], we will explore Explainable Artificial Intelligence (XAI) in the near future.

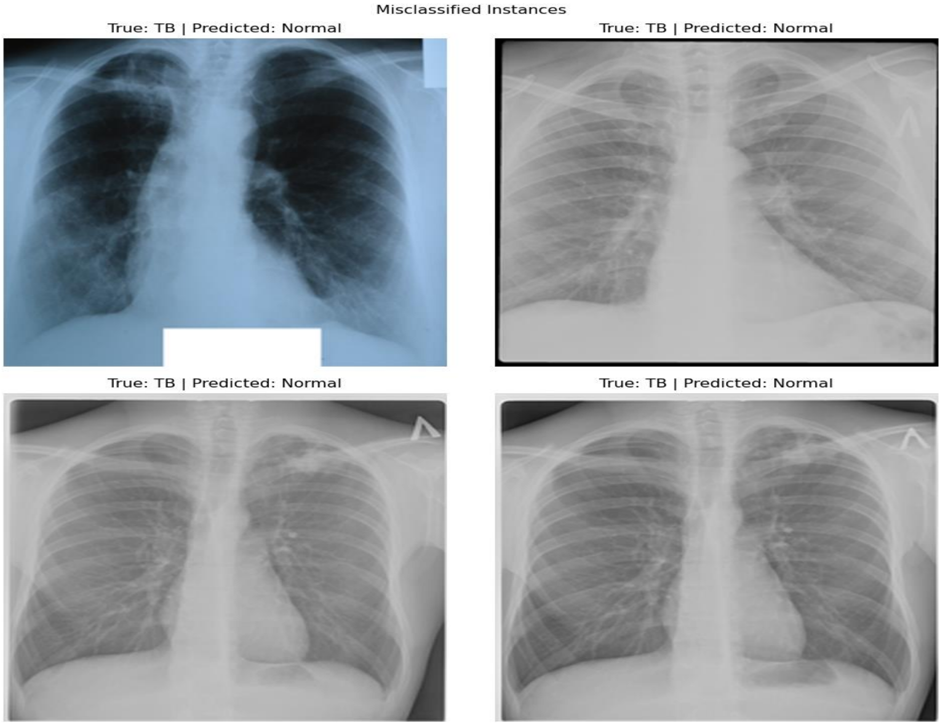


Fig. 7. Unsuccessful classification of the proposed method

5.0. CONCLUSION AND FUTURE WORK

In this work, we have proposed a new combination for classification of normal and TB images such that the performance of TB detection methods improves. Most existing methods do not consider mixed input of normal, and the images affected by TB for detection. Therefore, the existing model does not work well when normal images are supplied with a detection method. To overcome this limitation, this work focused on classification of TB and normal images. Inspired by the effective feature extraction by VGG16 and classification by CNN, we adapted VGG16 and proposed CNN for classification in this work. The experiments on ablation study, classification and comparative study with state-of-the-art methods show that the proposed method is outstanding. However, as discussed in the experimental section, the proposed method does not perform well when the normal and TB images share common characteristics. Therefore, this can be solved by developing a unified model with the combination of an enhancement model with a language model, which is our future work.

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