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Accurate and Robust Tuberculosis Detection Using Transferred Deep Learning Model

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KEYWORDS
Tuberculosis Detection,
Transfer Learning,
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VGG-19,
Deep Learning,
Medical Image Processing.

ABSTRACT

Tuberculosis (TB) is an infectious illness that is extremely dangerous to people's health. Early detection can help with therapy and reduce disease spread. Automatic TB detection is essential when there is a lack of diagnostic resources and a requirement for rapid detection. Automatic TB detection is a computer-based diagnostic system that may generate a rapid and precise diagnostic report as an output with less error than a human diagnosis report. This will give the ability to produce more effective mass screening with less resources. The major goal of this research paper is to create an effective computer-aided detection system that will help clinicians make more informed Tuberculosis diagnoses. The paper adopts a deep learning model to detect Tuberculosis infection. To lessen the need for data and hyperparameter adjustment, transfer learning was used. The transfer learning model was VGG-19, and a total of 4200 images were used to evaluate the model's performance. The test results show an accuracy 99.444%, which is achieved, and the recall is 97.143%. This suggests that the proposed model is accurate and robust and can be adopted as a means for TB detection in the future through real-time implementation.

الكلمات المفتاحية
اكتشاف مرض السل, التعلم بالنقل, الشبكات العصبية الالتفافية, معماريةVGG-19, التعلم العميق, معالجة الصور الطبية.

الملخص

يُعدّ مرض السل من الأمراض المعدية شديدة الخطورة على صحة الإنسان، حيث إن الكشف المبكر عنه يساعد في تحسين العلاج والحد من انتشار المرض. يُعتبر الكشف التلقائي عن السل أمرًا بالغ الأهمية في الحالات التي تشهد نقصًا في الموارد التشخيصية والحاجة إلى سرعة الكشف. يعتمد الكشف التلقائي على أنظمة تشخيصية حاسوبية قادرة على إنتاج تقارير تشخيصية دقيقة وسريعة مع معدل خطأ أقل مقارنةً بالتشخيص البشري، مما يتيح إمكانية إجراء فحوصات جماعية أكثر فعالية باستخدام موارد أقل. الهدف الرئيس من هذه الدراسة هو تطوير نظام فعال للكشف بمساعدة الحاسوب يساعد الأطباء على اتخاذ قرارات أكثر دقة في تشخيص مرض السل. اعتمد البحث على نموذج التعلم العميق للكشف عن عدوى السل، ولتقليل الحاجة إلى البيانات وضبط المعاملات الفائقة تم استخدام تقنية التعلم بالنقل .النموذج المستخدم هو VGG-19، حيث تم تقييم أدائه باستخدام 4200 صورة. أظهرت نتائج الاختبار تحقيق دقة بلغت 99.444% واستدعاء بنسبة97.143% ، مما يشير إلى أن النموذج المقترح يتميز بالموثوقية والدقة، ويمكن اعتماده كوسيلة للكشف عن مرض السل مستقبلًا عبر تطبيقات آنية في المجال الطبي.

1. INTRODUCTION

According to the World Health Organization's (WHO) annual report 2020, ten million people have been diagnosed with pulmonary tuberculosis (TB). The expected number of cases in 2019 is concentrated in South-East Asia (44%), Africa (25%), and the Western Pacific (18%). Cases occurred in lower proportions in the Eastern Mediterranean (8.2 %), the Americas (2.9 %), and Europe (2.5%) [1]. The majority of sick individuals came from low-income and impoverished areas with limited access to healthcare [2]. (Fig. 1) depicts the global yearly number of TB fatalities.

Tuberculosis is a contagious disease caused by the bacteria Mycobacterium tuberculosis. It is the leading infectious disease-related cause of death. Fortunately, antimicrobial medications are effective in treating this bacterial infectious disease. Tuberculosis can be cured if diagnosed early and treated appropriately [3].

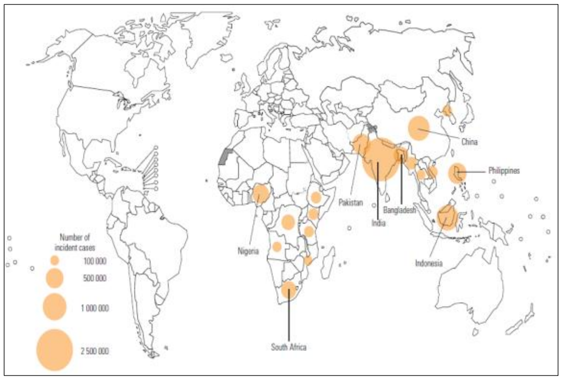


Fig. 1. Estimated number of TB deaths worldwide for the period 2000–2019 [1]

TB screening is the process of identifying apparently healthy individuals with probable active tuberculosis in the system by the use of tests, examinations, or other processes that should be applied to risky groups. The most effective form of tuberculosis screening is symptom inquiry and chest imaging (CXR) [4]. However, chest radiographs need to be examined by trained physicians with adequate clinical practice for the identification of tuberculosis. This process is time-consuming and costly, especially in developing countries. It is worth mentioning here that subjective discrepancies in radiographic illness diagnosis are unavoidable. Moreover, chest images CXR of TB are sometimes misclassified as other illnesses because of the similarity with other radiologic patterns of illness. This will lead to incorrect patient illness diagnosis, which will lead to wrong treatment medicine and worsen their health. In low-resource nations, especially in rural regions, there is also a scarcity of qualified radiologists. Therefore, an automatic BT diagnosis is essential to avoid such a problem that relies on computer-aided diagnostic tools. The outcome can play an essential role in mass screening for pulmonary tuberculosis [3,5].

Recently, Artificial Intelligence (AI) has become one of the major players in many applications and developments in our daily lives. It has been at the forefront of approaches used to enhance products and services. AI and Deep Learning applications in healthcare are increasing, and numerous approaches have been applied to aid physicians in their everyday responsibilities [6,7]. The use of AI technology in medical diagnostics has expanded significantly over the last decade, and deep learning neural networks are increasingly being utilized to analyze medical pictures [8]. Transferred deep learning for automatic Tuberculosis (TB) detection is a powerful technique that involves taking a pre-trained neural network model (originally trained on a massive general-purpose image dataset like ImageNet) and adapting (*transferring*) its knowledge to the specific task of identifying TB manifestations in medical images, primarily chest X-rays (CXRs). This approach addresses the major challenge of limited medical data by leveraging pre-learned features, leading to faster development and highly accurate, scalable diagnostic tools.

Tuberculosis remains a global health crisis, especially in low-resource regions. Key challenges include:

- Shortage of Skilled Radiologists: There is a critical lack of experts to interpret chest X-rays, which are a primary screening tool for TB.
- Human Error and Fatigue: Manual interpretation is subjective and can lead to diagnostic delays or errors.
- High Workload and Cost: Screening large populations is time-consuming and expensive.

An automated, accurate, and fast detection system can act as a decision-support tool, prioritizing cases for expert review and expanding screening coverage. Thus, the purpose of this endeavor is to develop an expert system that may be deployed to help the community in impoverished countries. A feasible method is presented for detecting tuberculosis from CXR pictures by leveraging the potential of deep transfer learning.

The paper is structured as follows: Section 2 presents important related works to find out research conducted in this era and to identify the research gap. Section 3 aims to show how the AI is achieved via convolutional neural networks CNNs. Thus, the section presents a brief description of CNNs as well as transfer learning concepts and the architecture of VGG19. Section 4 introduced the dataset used by the CNNs adopted in the research experiments, and presents the results of the required analysis observed from those results. Finally, the conclusion of the paper is presented in Section 5.

2. RELATED WORKS

The number of TB detection approaches based on AI techniques is reviewed in this section. Radiological patterns are commonly utilized to diagnose tuberculosis.

Duong et al. [7] proposed a TB detection model. With this model, the authors used three recent deep neural networks, DNNs, for classification engines. These engines are modified Efficient Net, modified original Vision Transformer, and modified Hybrid Efficient Net with vision transformer. They found that the accuracy of the TB detection can reached 97.72%. Rahman et al. [9] proposed a model to detect TB from chest X-ray images. A pre-trained network to extract features and an eXtreme Gradient Boosting (XGBoost) model have been used to distinguish between tuberculosis and normal patients.

The effectiveness of deep learning for identifying tuberculosis was investigated by Ho et al. [2]. On the dataset, many preprocessing approaches, tSNE visualization, and data augmentation are initially used. The X-ray images are then classified as having pulmonary TB symptoms or as healthy using three distinct pre-trained DCNNs, namely ResNet152, Inception-ResNet, and DenseNet121 models.

Pasa et al. [10] reported an automated diagnosis using a deep CNN with a shortcut link to locate TB. Kotie et al. [11] developed a customized CNN to identify tuberculosis (TB) from chest X-ray datasets representing diverse populations. To enhance generalization, they employed regularization techniques, batch normalization, dropout, and hyperparameter optimization. Nevertheless, all pre-trained CNN models consistently outperformed a custom architecture that relied on random weight initialization. To further refine the input data, they applied a U-Net-based segmentation approach to remove irrelevant regions from the chest X-rays. This segmentation was evaluated on an independent dataset, achieving good results, demonstrating strong generalizability and segmentation performance. Imam et al. [12] proposed a modified Inception convolutional neural network for TB recognition from X-Ray images. Gozes and Greenspan [13] used DenseNet-121 to build a model for tuberculosis detection using a small-scale dataset.

Authors in [14] proposed a method that implements segmentation and classification models to detect TB in CXR images. The UNet segmentation model is used to segment CXR images and select the region of interest. Thereafter, the Xception DL classification model is used to classify the lung sections into TB and normal classes. They used the

NIAID TB portal program dataset, sourced from the National Institute of Allergy and Infectious Diseases, contains a total of 1,400 images, divided equally into 700 images of TB-infected individuals and 700 control images. The study recorded a classification accuracy of 99.29%, accompanied by an AUC of 0.999. Their approach is significantly more cost-efficient when compared to conventional diagnostic techniques. Biochemical tests and analyses typically necessitate costly chemicals and equipment, along with highly skilled personnel, such as radiologists.

Authors in [15] presented a comprehensive evaluation of several CNN architectures—VGG16, VGG19, ResNet50, ResNet101, ResNet152, and Inception-ResNet-V2—in classifying CXR images as either TB-positive or TB-negative.

They showed that the VGG16 architecture consistently outperformed the other models across all the evaluation metrics.

Authors in [16] presented a DL technique based on a combined Data efficient image transformer and the Residual Network-16 (ResNet-16) model for effective TB diagnosis from X-ray images. The TBX11K dataset was utilized for this investigation. The dataset has three categories—Healthy, Sick but non-TB, and TB. Relying on only healthy X-rays as the negative category in clinical settings where there are many unwell but non-TB samples can cause considerable false positives in the model prediction, hence the adoption of the sick but non-TB class. The dataset was divided into training, validation, and testing sets for the experiment. The self-attention mechanism within the transformer part of the proposed model learns crucial information and constructs the relationship between image tokens. The ResNet-16 part uses depth-wise convolution to gather local representations and reduce computing costs while increasing the diagnosing accuracy. The global average pooling is applied to the feature maps at the final convolution layer to generate heatmaps based on the class activation map to show exactly where the prediction happened. The suggested model obtained TB diagnostic accuracy, sensitivity, specificity, and precision rates of 99.38%, 99.49%, 99.26%, and 99.24%, respectively. Additionally, it is lightweight (6.9M) and detects more quickly (4.79ms) than the other comparative cutting-edge versions.

Hansun et al [17] showed the high potential of both ML and DL for TB detection using CXR. Data volume and quality were the main concerns of this review, where most of the included studies used relatively small data sets. Therefore, proper data curation and augmentation, transfer learning, and multimodal approaches could be considered in future studies.

The research mentioned in [18] showed the important trade-offs that exist among model complexity, training duration, and performance. Models with greater numbers of parameters, like ResNet152 and Inception-ResNet-V2, needed extended training periods and increased computational power without delivering proportional enhancements in classification performance across all evaluation metrics. This finding underscores the importance of thoughtfully choosing the model architecture.

Chiu-Fan Chen et al [19] developed a free and open AI system that works well for identifying common TB characteristics on CXR. The accuracy is respectable and can be comparable to that of clinical specialists. They recommended a predictive value > 0.9 for a high likelihood of tuberculosis. Abnormal patterns are preferred, and TB may be taken into consideration when the predictive value is between 0.5 and 0.9. TB is improbable if the predictive value is less than 0.4. They suggested that more investigation and validation on a broader scale are needed to assess the algorithm's generalizability and compare its effectiveness across various populations.

Ajay Tiwari and Alok Katiyar [20] proposed a hybrid deep learning model for chest X-Ray image segmentation and classification aimed at diagnosing tuberculosis (HDL-ISCTB) has been proposed. The HDL-ISCTB model utilizes Otsu’s thresholding technique, which effectively segments the lung regions from the input images. This method successfully differentiates the lung areas from the background, thereby reducing computational complexity and minimizing potential noise. Furthermore, the segmented lung regions are subsequently processed through the CNN-LSTM architecture for classification purposes. The CNN-LSTM model capitalizes on the robust feature extraction capabilities of convolutional neural networks (CNNs) and the temporal dependencies captured by long short-term memory (LSTM) networks to derive strong representations from sequential chest X-Ray image data. A comprehensive series of experiments has been conducted to evaluate the performance of the proposed approach in relation to contemporary methods.

3. PROPOSED CNNs STRUCTURE AND TRANSFER LEARNING

Convolutional, pooling, and fully connected layers make up a comprehensive CNN architecture. The convolutional layers, which are the foundation of CNN, operate throughout the dataset to uncover common patterns buried within the local areas of the input picture [20]. Pooling layers, which are usually put after the convolutional layers, allow for non-linear down-sampling [21]. They separate the convolutional layer output into discontinuous sections and provide a single summary for each region to highlight the convolutional properties. One or more fully connected layers are often inserted at the very end of a CNN model before obtaining the classification result [22].

An automated, accurate, and fast detection system can act as a decision-support tool, prioritizing cases for expert review and expanding screening coverage. Traditional deep learning requires enormous datasets (millions of images) to train a model from scratch. This is often impractical in medicine. Training from first principles before they even look at a human body. This is slow and data-intensive. Transfer Learning is a brilliant biologist (the pre-trained model), and giving them a specialized, intensive course in radiology (fine-tuning on chest X-rays) [23]. They already understand patterns, edges, and shapes; they just need to learn how this applies to medical images.

The primary premise of transfer learning is that it is a process that retains previously acquired information to be applied to a connected task, with the goal of utilizing prior learning to more effectively create correct models for new specialized tasks. Creating and training a model from the start presents a number of difficulties: 1) the requirement for a huge dataset, 2) the use of costly hardware such as graphics processing units, and 3) more time is required, which could take weeks or longer [24]. Hence, employing a pre-trained model with internal parameters and well-trained feature extractors can typically increase the model's overall performance when solving identical issues on a smaller dataset.

The Process of how Transfer Learning is applied to TB detection is a typical pipeline that involves several key steps:

Step 1: Select a Pre-trained Model. Here, the researchers choose a state-of-the-art model architecture that has been pre-trained on a large dataset like ImageNet. Common choices include:

- VGGNet: Known for its simplicity and depth.
- ResNet: Uses "skip connections" to solve the vanishing gradient problem, allowing for very deep networks (e.g., ResNet50, ResNet101).
- DenseNet: Connects each layer to every other layer, promoting feature reuse. Often a top performer in medical imaging tasks.
- EfficientNet: Provides excellent accuracy and efficiency by scaling the model in a principled way.

These models have already learned to recognize universal low-level features (edges, corners, textures) and high-level features (shapes, patterns) from natural images.

Step 2: Prepare the Medical Dataset. Here, the dataset of chest X-rays is curated and preprocessed. This involves:

- Collection: Sourcing images from public datasets (e.g., NIH ChestX-ray14, Belarus Tuberculosis Portal, Shenzhen Hospital Dataset).
- Annotation: Each image is labeled by experts as "TB-positive" or "TB-negative" (and sometimes with more granular labels like severity or lesion location).
- Preprocessing: Standardizing image sizes, enhancing contrast, and normalizing pixel values to match the input requirements of the pre-trained model.

Step 3: Modify the Model Architecture. Here, the original pre-trained model is modified for the new task:

- Remove the Top Layer: The final classification layer (originally designed to classify, say, 1000 categories of cats, cars, etc.) is removed.
- Add New Layers: A new, randomly initialized set of layers is added on top. This typically includes:
- A Global Average Pooling layer to reduce dimensionality.
- One or more Fully Connected (Dense) layers.
- A final classification layer with a sigmoid activation (for binary classification: TB vs. No-TB) or softmax activation (for multiple classes).

Step 4: Train (Fine-tune) the Model. In this step, the core of transfer learning is achieved. There are two main strategies:

- Feature Extractor: Freeze the weights of all the pre-trained layers so they are not updated during training. The model uses them as a fixed feature extractor, and only the newly added top layers are trained. This is faster and requires less data.
- Fine-Tuning: Unfreeze some or all of the pre-trained layers and continue training with a very low learning rate. This allows the model to adapt its pre-learned features specifically to the nuances of chest X-rays. This is more computationally expensive but often leads to higher performance.

The model is trained on the TB CXR dataset, learning to associate the features from the pre-trained network with the presence of TB. The research study adopted the VGG19 in the usage of CNNs for TB detection. VGG19 is an advanced CNN with pre-trained layers. It has been widely used for understanding what defines an image in terms of shape, color, and structure that can be related to the images of Tuberculosis infectious illness. This is because the VGG19 is very deep and has been trained on millions of diverse images with complex classification tasks. It can perform a classification task of identifying images with and without trees. The VGG19 network design was suggested by Simonyan and Zisserman [25] with a structure model as shown in (Fig. 2).

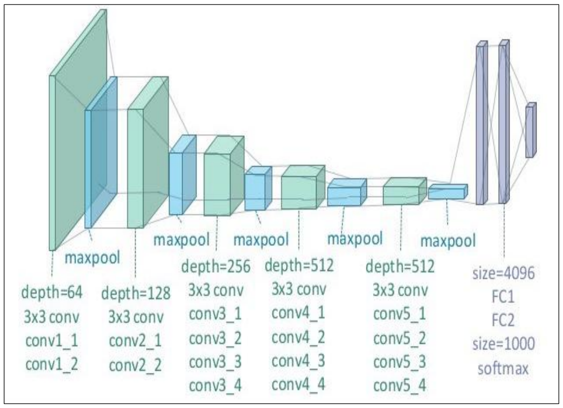


Fig. 2. VGG19 architecture.

The VGG19 network model consists of five convolutional layers, five max-pooling layers, and three fully connected layers. Convolution blocks 1 and 2 in the VGG19 model have two 3*3 convolution layers each. On the other hand, convolution blocks 3, 4, and 5 have four 3*3 convolution layers each [25].

4. SYSTEM SIMULATION AND EVALUATION

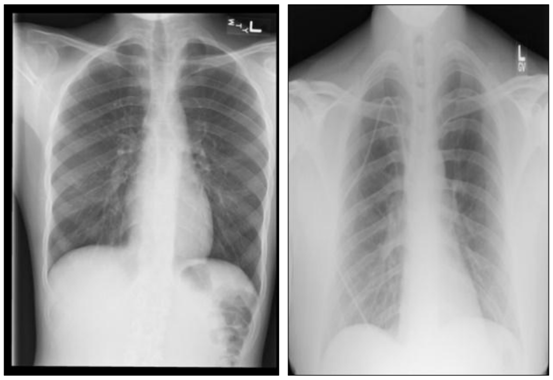
A. Dataset Generation Used in the Study

A Chest X-ray database for Tuberculosis (TB) detection was used by a team of researchers from the University of Dhaka and Qatar University in Doha, as well as medical physicians from Hamad Medical Corporation. They have collaborated to construct a dataset that can be adopted in TB detection [25,26]. In their dataset structure investigation, 700 tuberculosis cases and 3,500 normal cases were used. These cases have been summarized in Table 1.

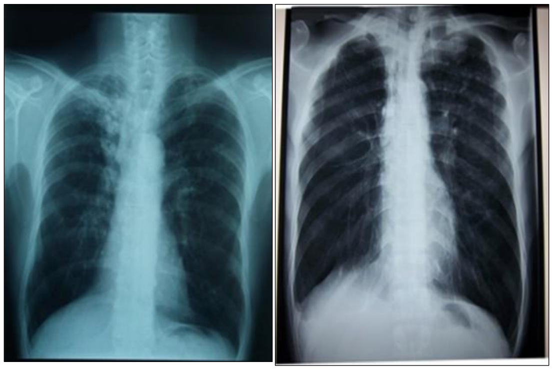
In this study, 70% of the total data was utilized for training, whereas 30% was used for testing. (Fig. 3) displays a few normal samples as well as tuberculosis case images.

Table 1. The Dataset Split.

Data Description	Tuberculosis	Normal
Training 70%	490	2450
Testing 30%	210	1050
Overall	700	3500



Normal (A and B)



Tuberculosis (C and D)

Fig. 3. Various normal and tuberculosis case images

B. System Implementation and Evaluation

(Fig. 4) illustrates the proposed model adopted in the TB detection using the CNN. This figure clarifies how to transfer the knowledge from the original model of VGG-19 and use it with a new dataset to detect tuberculosis and take advantage of the original CNN.

The proposed model has been simulated in PC with the following hardware and software specifications;

- Hardware: Intel Core i5, Intel Core i5 CPU operating at a frequency of 2.20 GHz with 8 GB RAM, and a GPU of Nvidia GeForce GTX 1050. The hardware includes also the memory of 200 GB SSD memory and a 500 GB hard drive storage.
- Software specification: Windows 10 operating system and simulated with Python 3.8 programming language.

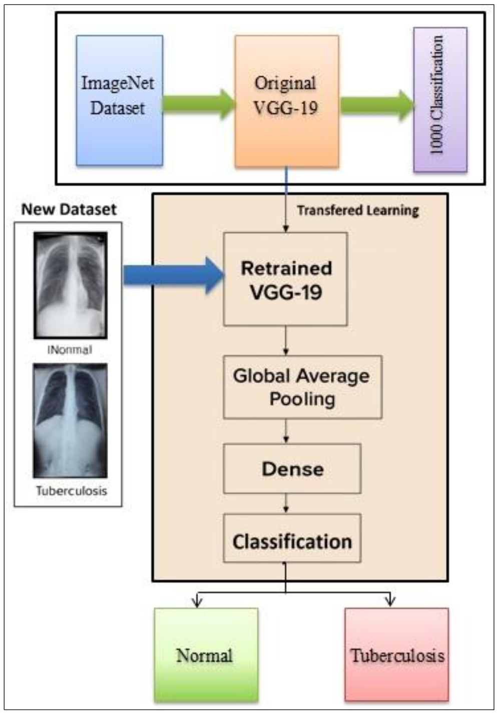


Fig. 4. The proposed model.

To evaluate the system, the following parameters were used to assess performance; True positive (TP) cases are those that have been properly predicted to have tuberculosis. False positive (FP) refers to normal instances that the created framework wrongly classifies as tuberculosis (TB). True negative (TN) instances are those that were accurately anticipated to be normal. False negative (FN) refers to TB cases that have been misclassified as normal. The five metrics used to evaluate models are accuracy, precision, Recall, and F1-score [9]. These metrics can be calculated using the following equations.

$$Accuracy = \frac{TP+TN}{TP+TN+FP+FN} \quad (1)$$

$$Precision = \frac{TP}{TP+FP} \quad (2)$$

$$Recall = \frac{TP}{TP+FN} \quad (3)$$

$$F1\ Score = \frac{2*TP}{2*TP+FP+FN} \quad (4)$$

The results of the proposed model are summarized in Table 2.

Table 2. Proposed Model Results.

Accuracy	Precision	Recall	F1 score
99.444%	99.512%	97.143%	98.313%

Additionally, the confusion matrix was computed, as shown in Fig. 5. As demonstrated by the results, the proposed model correctly classified 1260 instances with only 7 missing instances.

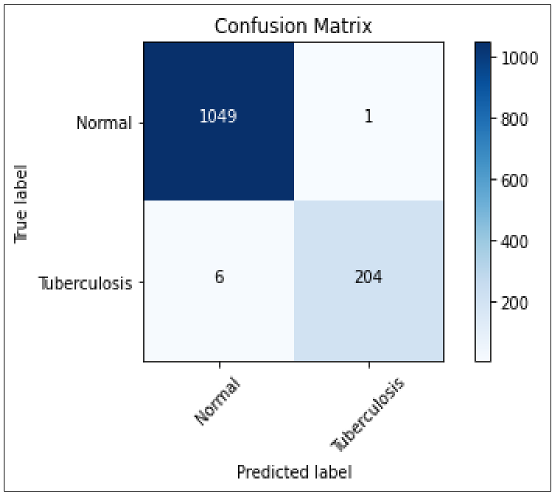


Fig. 5. Confusion matrix

The training and validation classification accuracy and error (model loss) curves are plotted as shown in Fig. 6 and Fig. 7. These two figures show the graphical performance evaluation of the proposed model.

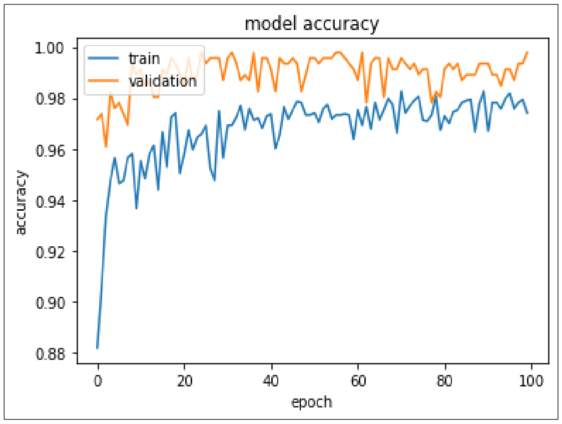


Fig. 6. Model Accuracy

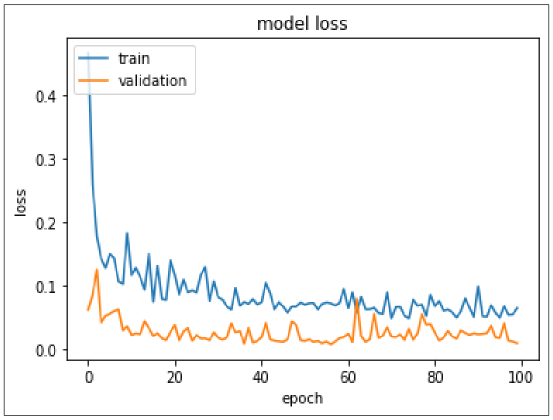


Fig. 7. Model Loss

Finally, the proposed system achieves the following:

- High accuracy with relatively small medical datasets (thousands instead of millions of images).
- Reduced training time and cost. Training from scratch is computationally prohibitive. Transfer learning drastically reduces the time and resources needed.
- These models consistently achieve performance metrics (Accuracy, Sensitivity, Specificity, AUC) that are comparable to or even exceed those of human experts.
- Once developed, the model can be deployed on mobile devices or in cloud-based systems to screen patients in remote areas.

5. CONCLUSION

This paper proposes a practical method for detecting tuberculosis in chest X-ray pictures. The suggested model is based on a pre-trained network's transfer learning approach. VGG-19 model was the pre-trained network employed in this investigation. The transfer of deep learning models represents a paradigm shift in medical image analysis. For tuberculosis detection, it offers a practical and highly effective path toward developing automated tools that can alleviate the burden on healthcare systems, reduce diagnostic delays, and ultimately contribute to the global fight against TB. It is not about replacing radiologists but empowering them with a powerful, scalable assistant. The VGG-19's regular layers were utilized, with the last layer changed to create two outputs instead of one thousand. The suggested model has higher accuracy, recall, and F1 score, according to the data. Because this article has already worked with a pre-trained model, the quantity of data necessary to train the model is small compared to creating a CNN from scratch.

This work shows that transfer learning with VGG-19 may be used to diagnose tuberculosis from chest X-ray pictures with great recall and accuracy. But there are some limitations to be aware of. The model may be affected by the dataset's class imbalance, which has fewer TB-positive patients than normal instances. Additionally, the evaluation was restricted to a single dataset without external validation. The suggested approach emphasizes how transfer learning might help automated tuberculosis screening, especially in environments with limited resources. To improve generalizability, clinical application, and overcome existing limitations, future studies should test various architectures, extend datasets, and conduct cross-population validation. AI-based diagnostic systems can develop into reliable instruments that support radiologists and enhance global TB detection efforts by resolving these issues.

Conflict of interest

The author declares that there is no conflict of interest regarding the publication of this research.

Consent for publications

The author confirms that consent for publication has been obtained. All data, images, and materials used in this study were collected and processed in accordance with ethical standards, and permission for publication has been granted by the relevant parties.

Availability of data and material

The datasets used and analyzed during the current study are available from the corresponding author upon reasonable request. All materials and methods applied in this research are described in detail within the paper to ensure reproducibility.

Authors' contributions

The author proposed, implemented, and evaluated the model of TB detection. The author also wrote the manuscript according to the journal specification template.

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