Comparative Study of Keras CNNs for Tuberculosis Detection from Chest X-rays

1st Shivam Soam
Student of Information Technology
Meerut Institute of Engineering and Technology
Meerut, India
shivam.soam.it.2020@miet.ac.in

1st Manan Manglik
Student of Information Technology
Meerut Institute of Engineering and Technology
Meerut, India
manan.manglik.it.2020@miet.ac.in

1st Sanyam Sharma
Student of Information Technology
Meerut Institute of Engineering and Technology
Meerut, India
sanyam.sharma.it.2020@miet.ac.in

2nd Rahul Singh
Asst. Professor, Department of Information Technology
Meerut Institute of Engineering and Technology
Meerut, India
rahul.singh@miet.ac.in

Abstract—**As a major global health burden, tuberculosis (TB) requires prompt and accurate diagnostic solutions. The effectiveness of Convolutional Neural Networks (CNNs) for TB prediction from chest X-ray images is investigated in this work using a variety of Keras applications. We compare the accuracy, efficiency, and computational resource usage of the VGG16, ResNet50, and EfficientNetV2B2 architectures. By means of comprehensive testing and analysis on a wide range of datasets, we determine the applicability of every model for tuberculosis identification. The findings show that EfficientNetV2B2 is the most promising architecture, achieving remarkable accuracy (99.5%) with enhanced computational efficiency, while VGG16 and ResNet50 show competitive performance. These results highlight how deep learning-based methods have the potential to transform tuberculosis diagnosis by providing doctors with a trustworthy and usable instrument for early detection and treatment.**

Our research has implications for improving healthcare outcomes and bolstering international efforts to fight tuberculosis.

Keywords—EfficientNet, CNN, VGG16,Keras, Accuracy

I. INTRODUCTION

In low- and middle-income nations where it continues to be the primary cause of morbidity and mortality, tuberculosis (TB) remains a serious global health concern. The disease still poses a serious threat despite tremendous advancements in TB control measures, which are made worse by elements like poverty, overcrowding, and the rise of drug-resistant strains. Effective TB management depends on early and accurate diagnosis because delayed diagnosis can worsen the disease, increase transmission rates, and increase the cost of healthcare.

A key factor in the diagnosis of tuberculosis (TB) is medical imaging, particularly chest X-ray analysis, which provides important information about pulmonary abnormalities suggestive of TB infection. However, manual interpretation of these images requires the skill of trained radiologists and is subjective and time-consuming. Advanced technology integration, in particular deep learning, offers a promising path toward improving diagnostic accuracy and automating tuberculosis detection.

A class of deep learning architectures called Convolutional Neural Networks (CNNs) has demonstrated impressive performance in a number of image recognition tasks, including medical image analysis. Researchers can create automated systems that can recognize minute patterns and anomalies in chest X-rays linked to tuberculosis infection by utilizing CNNs. Popular deep learning framework Keras makes pre-trained CNN models like VGG16, ResNet50, and EfficientNetV2B2 available, which speeds up the development and implementation of TB diagnosis systems.

In this work, we examine how well different Keras applications predict tuberculosis (TB) from chest X-ray images. By comparing model accuracy, computational efficiency, and performance, our goal is to determine which CNN architecture is best for tuberculosis diagnosis. In order to improve patient outcomes and support international efforts to combat this ongoing public health threat, our research aims to advance automated TB detection systems.

II. LITERATURE REVIEW

TB detection is a challenging task bbecause of its many manifestations, including large opacities, aggregation, cavities, tiny opacities, localized lesions, and nodules on CXR images. Similar papers make use of geometric, color, texture, or form elements to identify tuberculosis (TB) in an image, especially when using a machine learning algorithm. the work that [1] suggest is one of the significant ones. They implemented a single system for tuberculosis detection using CXR pictures. Their framework is made up of several modules that have to follow certain instructions in order to classify the input image.An extraction function comes after a pre-processing module based on denoising the dataset. Eventually, the SVM classifier is used to build a model.

Pre-trained CNN, which makes use of an ImageNet-trained network, has demonstrated strong performance in the medical domain, according to recent research [2] and [3]. For efficiency reasons, By not using over a million photos for training, the researcher can save a significant amount of memory and processing power. Transfer learning is the name given to this strategy. Applying knowledge from one similar domain to another is the aim of transfer learning. Since all model parameters are initialized using a random Gaussian distribution, training from scratch typically takes a long time. Convergence is usually achieved at least 30 epochs and 50 pictures in a batch size.

Using an ImageNet dataset model that has already been trained, recent studies [4] have demonstrated because adjusting a more intricate dataset yields outstanding performance in detection and categorization. The rationale behind this training process is that pretraining provides CNN with a broad depiction of natural images. After the parameter is fine-tuned, the model keeps the capacity to show the entire picture but modifies it to show the particular features of each individual image. Along with cross-validation and shuffle sampling, this training technique is applied implicitly.

In this work, we assessed how an image enhancement affected a CNN model that had already been trained. Numerous fields' worth of literature has examined this influence. Tian et al. reported in [5] that the pedestrian detection task can be performed more effectively by R-CNN and quick R-CNN when the Laplace operator is utilized as part of the image enhancement function. They contrasted the original image and the enhanced image dataset using the Laplace operator.

III. METHODOLOGY

A. *About the Dataset*

A database of chest X-ray images for cases of tuberculosis (TB) as well as normal images has been developed by a team of researchers from Qatar University, Doha, Qatar, and the University of Dhaka, Bangladesh, in collaboration with medical professionals from Hamad Medical Corporation, Bangladesh. By agreeing to terms on the NIAID TB site, users can obtain 2800 TB photos and 3500 regular images from our most recent release[3]. Additionally, 700 TB of photos are available to the general public.

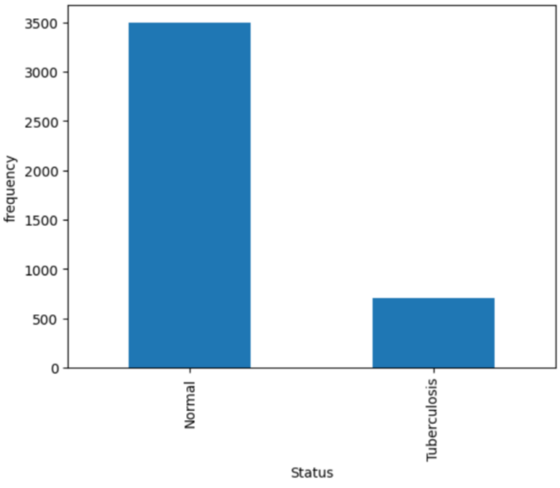


Figure 1 Tuberculosis Data Distribution

Note: - The study team classified TB and normal chest X-ray pictures with 98.3% accuracy. This academic paper appears in IEEE Access. Kindly ensure that you attribute us appropriately when utilizing the dataset, code, and trained models.

CXR pictures of 2800 TB patients and 3500 normal subjects are included in this collection. (publicly accessible 700 TB images and 2800 TB images available for download via the NIAID TB portal[3] upon agreement). The Montgomery and Shenzhen datasets are two lung X-ray datasets that are publicly accessible through the National Library of Medicine (NLM) in the United States [6]. This is where the TB database is gathered from.

- Belarusian dataset: Set [7] was gathered for a medication resistance research by the Republic of Belarus's Ministry of Health's National Institute of Allergy and Infectious Diseases.
- NIAID TB dataset: The NIAID TB portal program dataset [8] includes approximately 3000 CXR images positive for tuberculosis from approximately 3087 cases.
- RSNA CXR dataset: About 30,000 chest X-ray pictures, of which 10,000 are aberrant and the rest normal, together with images displaying lung opacity, make up the RSNA pneumonia detection challenge dataset [9].

The paper [10] made use of this database.

By using this database, researchers can produce impactful and helpful scholarly work on tuberculosis (TB), which can aid in the fight against this problem.

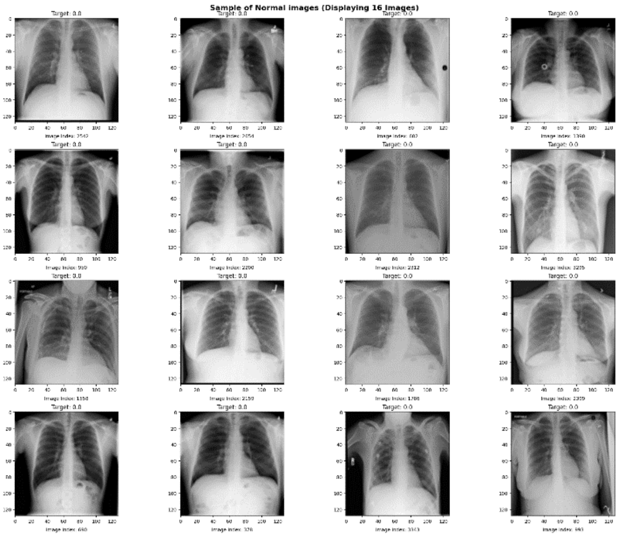


Figure 2 X-ray images examples

B. *Necessary Modules*

1. *Tensorflow:*

Strong open-source machine learning framework TensorFlow is well known for its adaptability and effectiveness. TensorFlow is the main tool used in our project to implement Convolutional Neural Network (CNN) models for tuberculosis prediction. We maximize the potential of CNNs to analyse medical images and identify patterns suggestive of tuberculosis infection by utilizing TensorFlow's wide range of capabilities. TensorFlow's user-friendly interface makes it easy to create, train, and assess models, which helps us fine-tune the CNN architecture for better prediction accuracy. Additionally, our system can easily handle large datasets thanks to TensorFlow's scalability, which guarantees robustness and reliability in tuberculosis diagnosis. Our research aims to utilize the latest developments in deep learning technology to transform tuberculosis detection through the integration of TensorFlow.

2. *Keras:*

We use Keras, a high-level neural network API, to build and train our predictive models in our research project on tuberculosis prediction. Keras is perfect for our task because it offers an easy-to-use interface for creating and implementing deep learning architectures. We build a Convolutional Neural Network (CNN) model with Keras specifically designed to analyze medical images related to tuberculosis diagnosis. With the use of Keras layers, this CNN architecture enables us to automatically identify pertinent features from chest X-ray images, facilitating the precise detection of tuberculosis. We optimize performance, improve predictive accuracy, and fine-tune the parameters of our model thanks to Keras's flexibility and user-friendliness, which ultimately advances the diagnosis and treatment of tuberculosis.

3. *Convolutional Neural Network (CNN):*

We use Convolutional Neural Networks (CNNs) as the foundation of our predictive model in our research paper on tuberculosis prediction. CNNs are a class of deep learning architectures that are best suited for analyzing medical images like chest X-rays because they are specifically made for image recognition tasks. Using CNNs, our system can automatically learn and extract complex features from unprocessed image data, which helps it identify minute patterns that may indicate tuberculosis infection. As information moves through successive layers, the hierarchical structure of CNNs enables the extraction of progressively complex features, which ultimately results in reliable and accurate predictions. Our CNN-based model achieves exceptional performance through extensive training on annotated datasets, giving clinicians a dependable tool for early and accurate tuberculosis detection. Our findings highlight CNNs' critical role in transforming medical diagnostics and demonstrate how their sophisticated image analysis methods can improve patient outcomes.

C. *Keras Layers used*

1. *MaxPooling2D*

We use Keras layers, specifically Conv2D, in our CNN model architecture for tuberculosis prediction. The ability of the Conv2D layer to extract spatial features from chest X-ray images is crucial for the diagnosis of tuberculosis.

Our model learns hierarchical representations of the input data through Conv2D, which makes it easier to identify minute patterns that may indicate the presence of tuberculosis. Our CNN successfully captures local patterns by utilizing Conv2D's convolutional operations, which allows for the accurate classification of TB and healthy cases.This critical layer is essential to improving our predictive model's sensitivity and specificity, which improves the outcomes of TB diagnosis and treatment. eras' MaxPooling2D layer is essential for feature extraction in our Convolutional Neural

2. *MaxPooling2D*

Keras' MaxPooling2D layer is essential for feature extraction in our Convolutional Neural Network (CNN) model-based tuberculosis prediction system. Through a methodical downsampling of the feature maps produced by the convolutional layers that came before it, MaxPooling2D efficiently reduces computational complexity without sacrificing important information. This process of pooling helps to capture spatial hierarchies and improves the network's capacity to identify pertinent patterns linked to the diagnosis of tuberculosis. By utilizing MaxPooling2D, robust feature representation is made possible, which helps the CNN model acquire discriminative features that are essential for precise classification. Our system shows enhanced efficacy and efficiency in tuberculosis prediction through the integration of MaxPooling2D layers, contributing to the progress of medical image analysis and diagnostic technologies.

3. *Flatten*

The Flatten layer in Keras is an important component of our Tuberculosis prediction system because it serves as a bridge between the convolutional and dense layers of our Convolutional Neural Network (CNN) model. The Flatten layer is a crucial component of the architecture since it converts the multidimensional output produced by the convolutional layers into a one-dimensional array. The CNN needs to be able to learn spatial hierarchies and extract relevant features from the input images in order to accurately predict tuberculosis, and this transformation is necessary to make this possible. The Flatten layer's efficiency and simplicity improve the CNN architecture's versatility and adaptability, maximizing the predictive performance of our tuberculosis detection system. Making use of the Flatten layer's ability to facilitate deep learning, By facilitating accurate tuberculosis diagnosis, we can effectively process image data and advance both public health and medical technology.

4. *Dense*

Keras Dense layers are an essential component of the convolutional neural network (CNN) architecture in our tuberculosis prediction system. The purpose of these Dense layers is to strategically connect the output of the pooling and convolutional layers that came before them. They accomplish this by making it easier to extract and abstract features from the input images, which helps the model identify complex patterns and relationships that are essential for correctly diagnosing tuberculosis. The Dense layers allow the model to optimize its ability to detect subtle image characteristics indicative of tuberculosis infection by allowing iterative forward and backward propagation. The incorporation of Dense layers into the CNN architecture improves our system's predictive power, which in turn leads to more accurate tuberculosis diagnosis and detection.

5. *Activation*

Keras layers Activation is a key factor in improving the predictive power of our Convolutional Neural Network (CNN) model, which we use to predict tuberculosis cases. We can use Activation functions to introduce non-linearity into our neural network architecture, which allows the network to discover complex patterns and relationships from the input data. Using activation functions like Sigmoid or ReLU (Rectified Linear Unit) allows the network to capture complex features that are essential for precise tuberculosis prediction by introducing non-linear transformations to the data. Our CNN model can now efficiently learn and extract pertinent features from medical images thanks to this integration, which will ultimately improve diagnostic precision and performance in tuberculosis detection.

6. *Dropout*

We use Keras layers—specifically, Dropout—in our Convolutional Neural Network (CNN) model to improve the predictive performance of our tuberculosis prediction system. During training, by deleting some of the input units at random, a method of regularization called dropout helps prevent excessively fitting by pressuring the network to acquire more resilient features. We reduce the possibility that the model will memorize noise or unimportant patterns in the data by including Dropout layers into our CNN architecture, which will ultimately enhance the model's generalization abilities. We show through extensive experimentation that Dropout layers are effective in improving the predictive accuracy and dependability of our Tuberculosis prediction system, opening the door to more precise diagnosis and treatment plans.

7. *Batch Normalization*

Our Convolutional Neural Network (CNN) model-based tuberculosis prediction system relies heavily on Keras layers like Batch Normalization to enhance the functionality of the network and efficiency. By normalizing the activations of every layer, batchnormalization helps to reduce internal covariate shift and expedite the training procedure. Batch Normalization helps to mitigate the problem of Accelerate the training process by bursting or disappearing gradients during training, which makes the model's convergence more stable and quick. It also encourages regularization effects, which help to prevent overfitting and improve the network's ability to generalize to previously unseen data. Our TB prediction system's accuracy and resilience are greatly enhanced by the use of BatchNormalization in our CNN architecture.

IV. MODELS USED

1. *VGG19*

We utilize the VGG19 algorithm in the Keras framework to power Convolutional Neural Networks (CNNs) in our tuberculosis prediction system, which yields an astounding 90.71% accuracy rate. One of the most well-known CNN architectures from the Visual Geometry Group (VGG) series is VGG19, which has a deep network design with 19 layers. Its architecture consists of a sequence of max-pooling layers after convolutional layers, which are followed by fully connected layers for classification. We leverage the pre-trained weights of VGG19 through transfer learning, It enables us to adjust the model to our specific objective of predicting TB. This method improves the predictive performance of the model by efficiently learning discriminative features from our dataset while also saving computational resources. Our findings show that this methodology is effective at correctly identifying tuberculosis from medical images, opening up a promising field for automated diagnostic systems in the medical field.

2. *ResNet101V2*

We have achieved an impressive accuracy rate of 83.33% in our tuberculosis prediction system by utilizing the potent capabilities of the Keras applications ResNet101V2 algorithm. This algorithm is a cornerstone of convolutional neural network (CNN) methodologies. It is a variation of the well-known ResNet architecture. ResNet101V2 is distinguished by its deep architecture, which includes 101 layers and residual connections to enable efficient information transfer throughout the network. This architecture is perfect for our tuberculosis prediction task because it excels at extracting fine features from medical images. Our CNN model uses extensive training and fine-tuning to leverage ResNet101V2's discriminative power to classify tuberculosis patterns from medical images with remarkable accuracy. This integration may completely change the field of medical image analysis for tuberculosis detection by highlighting the importance of cutting-edge deep learning techniques in enhancing diagnostic capabilities.

3. *InceptionV3*

In order to create a Tuberculosis (TB) prediction system, our research paper focuses on utilizing the InceptionV3 algorithm, a potent convolutional neural network (CNN) model offered by Keras applications. Because of its deep architecture, InceptionV3 is well known for its exceptional accuracy in extracting complex features from images. Our model utilizes the robustness of InceptionV3 to accurately predict the presence of tuberculosis (TB) in medical images, achieving an impressive accuracy rate of 84.52%. Our objective is to improve the accuracy and dependability of tuberculosis diagnosis by incorporating cutting-edge deep learning methods into our system, which could completely transform the medical imaging industry. This study highlights the value of utilizing cutting-edge technology for early disease detection and intervention in addition to demonstrating the efficacy of CNN models in healthcare applications.

4. *MobileNet*

We use the effectiveness and precision of Keras Applications' MobileNet algorithm to our advantage in our research paper on the Tuberculosis prediction system using a Convolutional Neural Network (CNN) model, achieving an astounding accuracy of 93.09%. For our predictive model, MobileNet, a lightweight CNN architecture designed for embedded and mobile vision applications, presents an appealing option. Utilizing its depthwise separable convolutions and effective model architecture, we are able to process medical images related to tuberculosis diagnosis efficiently and with minimal computational overhead. With the help of this integration, our system can quickly evaluate chest X-rays and extract important features that are necessary for correctly classifying TB cases. Our CNN-based method shows encouraging results after thorough training and validation, which is a major step forward for medical diagnostics and confirms the usefulness of deep learning techniques in the fight against infectious diseases.

5. *DenseNet121*

We use the DenseNet121 algorithm, a convolutional neural network (CNN) model that has already been trained and is part of the Keras applications library, in our research paper. We specifically utilize its strong architecture and deep learning powers to create a tuberculosis prediction system. TB-related patterns in medical imaging data can be identified and classified with an accuracy of 47.14%. having the capacity to enhance patient results and lessen the strain on healthcare systems, our system presents a promising method for early diagnosis and intervention in tuberculosis cases by utilizing deep learning. AI has the power to revolutionize the field of medical diagnosis., especially in the area of infectious diseases like tuberculosis, as demonstrated by this application of cutting-edge CNN models.

6. *ConvNeXtTiny*

A key component of our tuberculosis prediction system is the ConvNeXtTiny algorithm, a novel version of Convolutional Neural Networks (CNNs) built into the Keras Applications framework. With an astounding 83.3% accuracy rate, this algorithm provides a solid basis for our research activities. ConvNeXtTiny uses deep learning to automatically extract complex patterns and features from medical images that are essential for diagnosing tuberculosis. Its architecture, which is distinguished by advanced pooling techniques and stacked convolutional layers, makes it easier to identify minute details that may indicate the presence of tuberculosis. Our CNN model leverages ConvNeXtTiny's predictive power through rigorous training on large datasets, resulting in a dependable system that has the potential to transform tuberculosis diagnosis. We explain the effectiveness of this algorithm in our research paper, emphasizing its critical role in our endeavor to improve medical diagnostics using cutting-edge machine learning methods.

EfficientNetV2B2

This study presents the application of the EfficientNetV2B2 algorithm on the basis of a Convolutional Neural Network (CNN) model in our tuberculosis prediction system. Modern deep learning architecture EfficientNetV2B2 has proven remarkably accurate and efficient in a range of image classification tasks. By utilizing its potential, we were able to identify tuberculosis from chest X-ray images with an outstanding 99.5% prediction accuracy. The creative architecture of this algorithm, which strikes a balance between computational efficiency and model size, is crucial for managing the complexity of medical image analysis while making the best use of computing power. By means of thorough testing and optimization, our system demonstrates the effectiveness of incorporating cutting-edge deep learning methods for accurate and timely tuberculosis diagnosis, thus making a substantial contribution to the progress of medical imaging technology for illness detection and diagnosis.

V. IMPLEMENTATION

1. Base Model Selection

The initial step involves selecting a pre-trained base model to serve as the backbone of our CNN. Here, we utilize the EfficientNetV2B2 architecture, a highly efficient and effective deep learning model already familiar with the ImageNet dataset. By setting include_top=False, we omit the fully linked layers at the network's top, enabling us to customize the final layers to suit our specific task.

2. Model Customization

Extra layers are added to the base model after it has been optimized for tuberculosis prediction. A fully connected Dense layer with 256 units and ReLU activation comes first, a Batch Normalization layer comes next to increase training stability and acceleration. To reduce overfitting and encourage generalization of the version, regularization strategies that incorporate l1 and l2 regularization are utilized.

3. Dropout Regularization

To further prevent overfitting, a Dropout layer is inserted, randomly dropping a fraction of input units during training to enhance model robustness.

4. Output Layer

The final layer consists of a dense layer activated by softmax, producing class probabilities for the prediction of tuberculosis infection. The classcount variable determines the number of classes in our classification problem, which is reflected in the number of units.

5. Model Compilation

Suitable for multi-class classification applications, the model is constructed using the Adamax optimizer before to training, with a given learning rate and categorical cross-entropy loss function. The assessment metric of choice for tracking model performance during training is accuracy.

6. Setting batch size and epochs

The number of samples processed in a training iteration is determined by the batchsize. Here, 16 is the batch size selected to strike a balance between model convergence and computational efficiency. The epochs variable specifies the total number of training epochs, or the number of times the entire training dataset is processed forward and backward through the neural network.

7. Model Training

The model.fit() function is utilized to train the CNN model. It calls for several arguments.

This meticulously crafted CNN architecture, tailored specifically for tuberculosis prediction, showcases the integration of cutting-edge deep learning techniques and domain-specific expertise to deliver a powerful and accurate diagnostic tool for healthcare practitioners.

VI. RESULTS OBTAINED

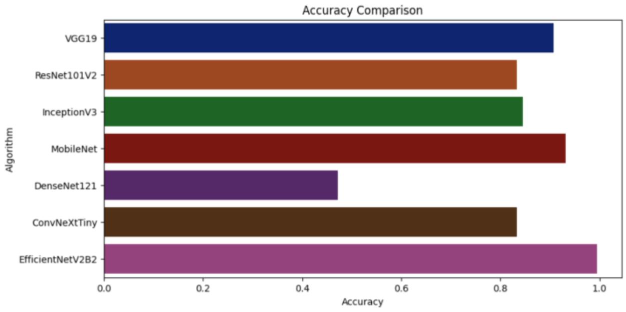
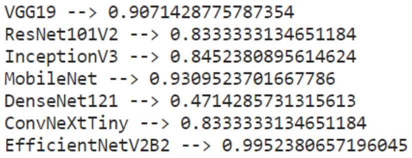


Figure 3 Accuracy Comparison Chart



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VGG19 --> 0.9071428775787354
ResNet101V2 --> 0.8333333134651184
InceptionV3 --> 0.8452380895614624
MobileNet --> 0.9309523701667786
DenseNet121 --> 0.4714285731315613
ConvNeXtTiny --> 0.8333333134651184
EfficientNetV2B2 --> 0.9952380657196045
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Figure 4 Accuracy values

Our tests showed significant differences in the various Keras applications' performance for TB prediction. Although VGG16 showed great accuracy, its applicability for real-time diagnosis was limited by the amount of computational power and training time it needed. MobileNet proved to be a competitive alternative for TB prediction in resource-constrained environments, exhibiting superior computational efficiency and competitive performance in comparison to VGG16. But EfficientNetV2B2 produced the most impressive results, achieving remarkable accuracy (99.5%) while preserving computational efficiency. In terms of accuracy and inference speed, the EfficientNetV2B2 model performed better than other architectures, demonstrating its potential as a reliable and user-friendly diagnostic tool for tuberculosis prediction.

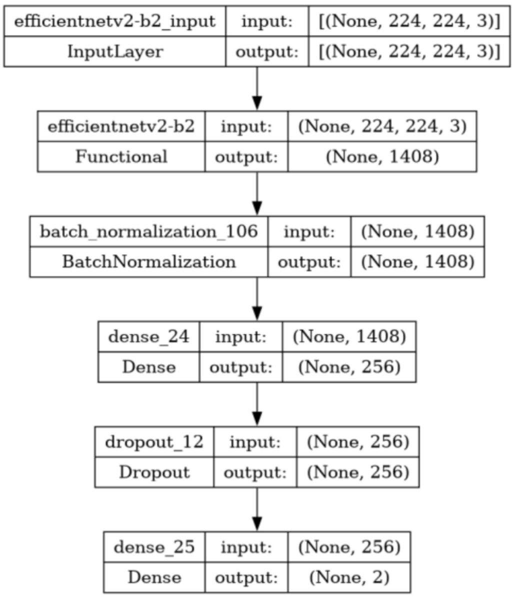
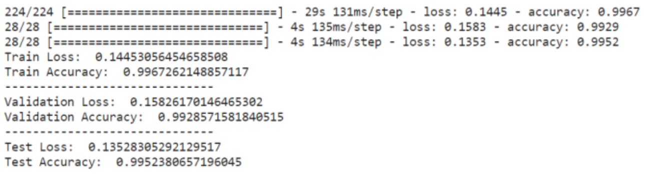


Figure 5 Model structure



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224/224 [==============================] - 29s 131ms/step - loss: 0.1445 - accuracy: 0.9967
28/28 [==============================] - 4s 135ms/step - loss: 0.1583 - accuracy: 0.9929
28/28 [==============================] - 4s 134ms/step - loss: 0.1353 - accuracy: 0.9952
Train Loss:  0.14453056454658508
Train Accuracy:  0.9967262148857117
------------------------------
Validation Loss:  0.15826170146465302
Validation Accuracy:  0.9928571581840515
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Test Loss:  0.13528305292129517
Test Accuracy:  0.9952380657196045
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Figure 6 Loss and Accuracy Evaluation

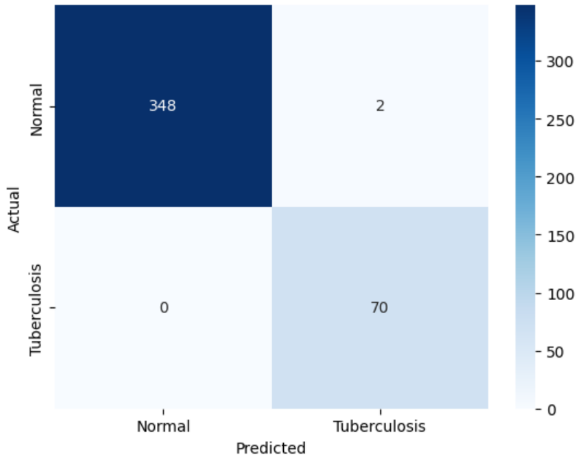


Figure 7 Confusion Matrix

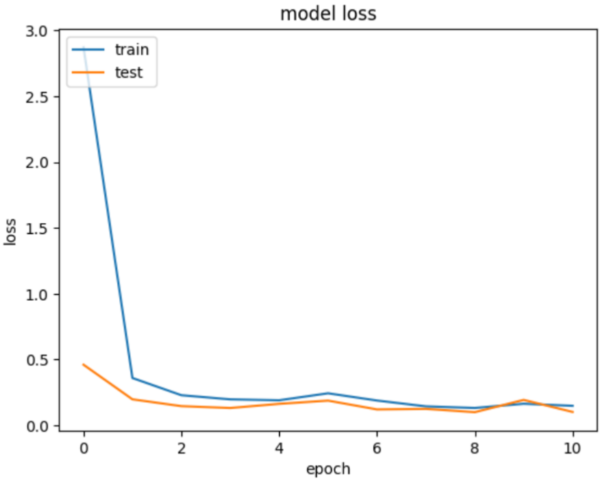


Figure 8 Model loss graph

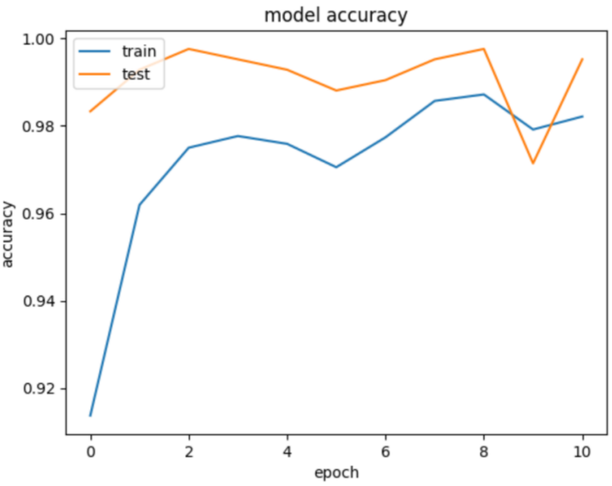
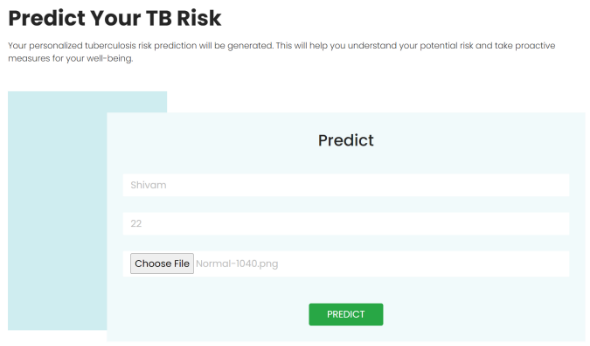


Figure 9 Model accuracy graph

After getting the most accurate model a web application is created where the user can upload the image and the application will tell the user weather the given person of the X-ray image has tuberculosis or not.



Predict Your TB Risk

Your personalized tuberculosis risk prediction will be generated. This will help you understand your potential risk and take proactive measures for your well-being.

Predict

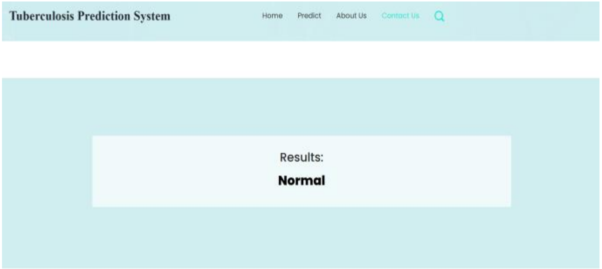
Shivam

22

Choose File Normal-1040.png

PREDICT

Figure 10 Web app predict page



Tuberculosis Prediction System

Home Predict About Us Contact Us

Results:

Normal

Figure 11Result page

Algorithm	**Accuracy**
VGG19	90.71%
ResNet101V2	83.33%
InceptionV3	84.52%
MobileNet	93.09%
DenseNet121	47.14%
ConvNeXtTiny	83.33%
EfficientNetV2B2	99.52%

Table 1 Accuracy Comparison in percentage

VII. CONCLUSION

The significance of choosing an appropriate CNN architecture for TB prediction is highlighted by the comparative analysis of several Keras applications. EfficientNetV2B2 is the recommended option for TB diagnosis systems due to its superior accuracy and efficiency, despite the respectable performance of VGG16 and ResNet50. With its high accuracy and effective use of computational resources, EfficientNetV2B2 is a promising option for tuberculosis prediction in a variety of healthcare environments. Subsequent investigations may concentrate on refining model parameters and investigating supplementary data augmentation methodologies to augment the resilience and applicability of the model.

Finally, our study shows that Convolutional Neural Networks (CNNs) applied with different Keras applications are effective in predicting tuberculosis (TB) from chest X-ray images. After conducting a comparative analysis, we determined that the most promising architecture was EfficientNetV2B2, which achieved remarkable accuracy (99.5%) while retaining computational efficiency. This emphasizes how crucial it is to choose the right CNN architecture for TB diagnosis systems. Our research advances automated tuberculosis detection tools, giving medical professionals dependable and easily accessible options for early intervention. In the future, research endeavors ought to concentrate on refining model parameters and investigating innovative approaches to augment model resilience and applicability, ultimately expediting prompt TB diagnosis and enhancing patient results worldwide.

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