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A Semantic Segmentation-Based Adaptive Convolution Neural Network Model for Tuberculosis Detection and Diagnosis



Abstract: -Objective: Tuberculosis (TB) continues to be a major cause of death from infectious diseases globally. Tuberculosis (TB) is a treatable condition with antibiotics, yet it is often misdiagnosed or left untreated, particularly in rural and resource-constrained regions. While chest X-rays are a key tool in TB diagnosis, their effectiveness is hindered by the variability in radiological presentations and the lack of trained radiologists in high-prevalence areas. Deep learning-based imaging techniques offer a promising approach to computer-aided diagnosis (CAD) for tuberculosis (TB), enabling precise and timely detection while alleviating the burden on healthcare professionals. This study aims to enhance tuberculosis detection in chest X-ray images by developing deep learning models. We leverage the Res-UNet architecture for image segmentation and introduce a novel deep learning network for classification, targeting improved accuracy and precision in diagnostic performance.

Methods: A Res-UNet segmentation model was trained using 704 chest X-ray images sourced from the Montgomery County and Shenzhen Hospital datasets. Following training, the model was applied to segment lung regions in 1,400 chest X-ray scans, encompassing both tuberculosis cases and normal controls, obtained from the National Institute of Allergy and Infectious Diseases (NIAID) TB Portal program dataset. The segmented lung regions were subsequently classified as either tuberculosis or normal using a deep learning model. This integrated approach of segmentation and classification aims to enhance the accuracy and precision of TB detection in chest X-ray images. Classification of segmented images was done using customized CNN and visualization was done using Grad-CAM.

Results: Res-UNet model demonstrated excellent performance for segmentation, achieving an accuracy of 98.17%, recall of 98.39%, precision of 97.45%, F1-score of 97.97%, Dice coefficient of 96.33%, and Jaccard index of 96.05%. Similarly, the classification model exhibited outstanding results, with a classification accuracy of 99.42%, precision of 99.00%, recall of 99.29%, F1-score of 99.29%, and an AUC of 99.9%.

Conclusion: The findings demonstrate the efficiency of our system in diagnosing tuberculosis from chest X-rays, potentially surpassing clinician-level precision. This underscores its effectiveness as a diagnostic tool, particularly in resource-limited settings with restricted access to radiological expertise. Additionally, the modified Res-UNet model demonstrated superior performance compared to the standard U-Net, highlighting its potential for achieving greater diagnostic accuracy.

Keywords: Tuberculosis, artificial intelligence, deep learning, chest X-ray segmentation, chest X-ray classification

I. INTRODUCTION

Tuberculosis (TB), caused by the bacterium *Mycobacterium tuberculosis*, is a highly infectious disease that primarily targets the lungs but can also affect other organs such as the kidneys, spine, and brain. The disease spreads through airborne particles expelled when an infected person coughs, sneezes, or talks, contributing to its high transmissibility. This study presents a novel approach to improving TB detection by leveraging chest X-ray image datasets. The proposed method, TbCNN-net, integrates semantic segmentation with an adaptive convolutional neural network (CNN) architecture to enhance diagnostic precision. In 2024 India TB report by Ministry of health and Welfare has reported, estimated TB cases of 27.8 lakhs with 25.5 lakh in 2024, increased cases from 24.2 lakh cases in 2023. There are various factors of risk of TB like undernourishment, diabetes, use of alcohol, HIV and smoking etc Ahmed et.al introduced Tb U-net with attention mechanism for efficient segmentation of lungs. They also proposed a densenet-169 CNN for accurate classification of TB, Covid and pneumonia disease's [1]. Saad I. Nafisah proposed Tb detection by using 9 different CNN models with u-net segmentation and efficientB3 achieved higher accuracy with 99.1% with ROC of 99.9%, recall of 98.8%, precision of 98.8%, f1_score of 98.8% [2]. Also it involved different visualization techniques like grad CAM and t-sne. [3] Vinayak Sharma et.al proposed an UNet model for segmentation with accuracy of 96.35%, jaccard index of 90.38%, dice coefficient of 94.88% and classification model of Xception with accuracy of 99.29%, precision of

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99.30%, recall of 99.29%, also they used Grad-CAM for showing the heatmap pattern. [4] developed a framework with nine different CNN models among which CheXNet was best performing model with accuracy of 96.47%, sensitivity of 98.56%, precision of 98.57%, f1_score of 98.56%. [5] train x-ray using unet model on TBX11 CXR dataset. Shallow models like VGG16, VGG-19 were used for classification with staple consensus region of interest for region localization on Montgomery Tb and Shenzhen tb datasets. [6] This study trained and evaluated ten different deep convolutional neural networks (CNNs) for distinguishing tuberculosis (TB) cases from normal cases. The models included ResNet50, ResNet101, ResNet152, InceptionV3, VGG16, VGG19, DenseNet121, DenseNet169, DenseNet201, and MobileNet. The approach presented here leverages histogram-matched chest X-ray (CXR) images, eliminating the need for object segmentation of regions of interest. This approach enhances the accuracy and detection performance of CNN models for TB identification by incorporating histogram matching with chest X-ray images (CXR). [7] proposed Res-UNet++ outperformed U-Net and ResNet architectures, achieving superior evaluation metrics, including a validation Dice coefficient of 96.36%, validation mean IoU of 94.17%, and validation binary accuracy of 98.07%. [8] A novel algorithm has been developed to refine segmented masks, enhancing final accuracy, alongside an efficient fuzzy inference system for more weighted activity assessment. [9] gives comparison between unet, unet++, transunet+. [10] Convnet achieved sensitivity 87.0%, f1-score of 87.0%, 88.0% precision. [11] The algorithm achieved outstanding performance in detecting pulmonary tuberculosis (PTB), with an area under the receiver operating characteristic curve (AUC) of 0.878 and a 95% confidence interval (CI) ranging from 0.854 to 0.900 in the NTUH-20 dataset. [12] Swin Resunet3 was used for segmentation of images and Multi-scale Attention-based Densenet with Extreme Learning Machine model was used for classification of tuberculosis [13] An attention block integrating VGG16 and VGG19 architectures is employed for classifying TB chest X-rays. In their study, [14] A deep learning model was proposed for tuberculosis diagnosis, incorporating deep learning features alongside Gabor and Canny edge detection in one approach, and excluding these techniques in another, achieving accuracies of 95.7% and 97.9%, respectively. [15] Truong-Minh Le et al used 5 pretrained models VGG16, EfficientB7, MobileNetV3, DenseNet121, RegNetY040 for classification of tuberculosis among which MobilenetV3 showed best performance with accuracy of 98.35%, f1_score of 98.32% on TB chest X-ray, Montgomery accuracy of 77.81% and f1_score of 78.92%, on Shenzhen dataset accuracy of 67.19%, f1_score of 74.86%, on India Chest X-ray with accuracy of 86.25%, f1_score of 83.75%

II. MATERIALS AND METHODS

A. Datasets and Preprocessing-

For the segmentation task, we utilized the Montgomery County and Shenzhen Hospital datasets, both obtained from the publicly available "Chest X-ray Masks and Labels" dataset on Kaggle. The combined dataset comprised 704 chest X-ray (CXR) images, each paired with corresponding segmentation masks. The data was split into 494 images (70%) for training, 140 images (20%) for validation, and 70 images (10%) for testing. To ensure a robust evaluation, we implemented a five-fold cross-validation strategy, allowing each image to be used at least once for both training and testing. For the classification task, we used the "National Institute of Allergy and Infectious Diseases (NIAID) TB Portal Program" dataset, which is part of the "Tuberculosis Chest X-ray Images" dataset on Kaggle. This dataset included 700 CXR images of tuberculosis (TB) patients and 3,500 control images. For our experiment, we selected 700 TB images and 700 control images, which were divided into 1,120 images (80%) for training, 140 images (10%) for validation, and 140 images (10%) for testing.

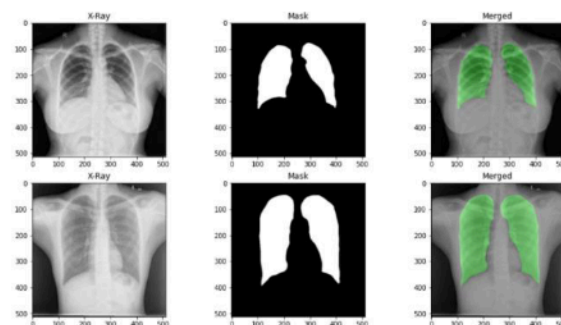


Fig. 1. Sample images from datasets

Before being input into the model, the images were normalized by scaling the pixel values to a $[0, 1]$ range, achieved by dividing each pixel by 255. This normalization process ensures uniformity across the dataset, optimizing the model's training performance.

B Methods

Figure 2 outlines the methodology employed in this study. We began by selecting a well-established chest X-ray (CXR) dataset that included both the images and their Figure 2 illustrates the methodology used in this study. We started by selecting a well-established chest X-ray (CXR) dataset, which included both the images and their corresponding segmentation masks for training the segmentation model. Next, we modified and optimized the model to improve its performance. The process began with the selection of a well-established chest X-ray (CXR) dataset, which included both images and their corresponding segmentation masks, for training the segmentation model. The U-Net architecture, a popular model for segmentation tasks, was modified and optimized to align with the study's objectives. The performance of the trained segmentation model was assessed using metrics such as accuracy, Dice coefficient, Jaccard index, and area under the curve (AUC). The model was then applied to CXR datasets containing both tuberculosis (TB) and normal cases to segment the lung regions while excluding background information. Following segmentation, a deep learning convolutional neural network (CNN) was developed and fine-tuned to classify the segmented lung images. The classification model's performance was evaluated using various metrics, including accuracy, precision, recall, F1-score, AUC, and receiver operating characteristic (ROC) curves.

UnetModel(Segmentation Model)

The U-Net model is a widely recognized and highly effective architecture for image segmentation, particularly in medical applications such as segmenting organs, tissues, or lesions in medical scans like CT, MRI, and CXR. It was originally designed for **bio-medical image segmentation**, but has since become widely adopted for various segmentation tasks. Originally developed by Olaf Ronneberger in 2015, U-Net has become one of the most popular and effective models for segmentation tasks in medical imaging, especially for analyzing radiological images.

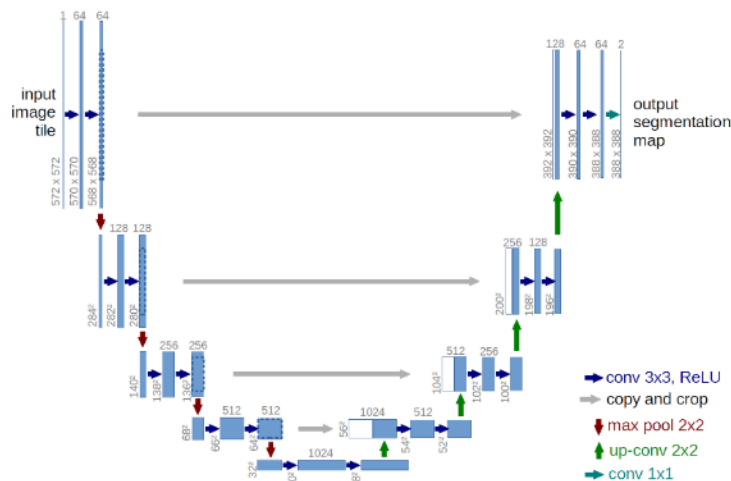
**Fig. 2. Architecture of U-Net**

Fig.2 illustrates the U-Net architecture, which comprises two main components: the encoder and the decoder. The encoder employs a sequence of convolutional layers combined with Relu activation and max-pooling operations. Conversely, the decoder reconstructs segmented images using up-convolution layers, depth concatenation, softmax activation, and max pooling. The process starts with a 224×224 pixel input image, which is processed by the encoder to extract features represented as numerical values between 0 and 255. These values are normalized to a scale of 0 to 1. As the image progresses through the encoder, its dimensions decrease after each max pooling operation. A bridge channel links the encoder and decoder, facilitating the transfer of extracted features. The decoder reconstructs the image by interpreting these numerical values, assigning pixel

values below 0.5 to 0 and those equal to or greater than 0.5 to 1. Skip connections between the encoder and decoder enable the direct transfer of image features, ensuring minimal information loss during neural node processing. The decoder's final output comprises binary images with pixel values of 0 (black) and 1 (white), producing black-and-white masks that emphasize regions of interest, such as the lung area in chest X-rays. The U-Net model was trained for 50 epochs per fold, using a learning rate of 0.001 and a dropout rate of 0.25. The batch size was set to four images per batch for both training and validation. The cross-entropy loss function, LCE, is expressed as

$$LCE = y_i \cdot \log(a_i) + (1 - y_i) \cdot \log(1 - a_i) \quad (1)$$

i represents the index of the sample (e.g., image).

y_i is the ground truth label, with $y_i=1$ for the positive class

and $1-y_i=0$ for the negative class.

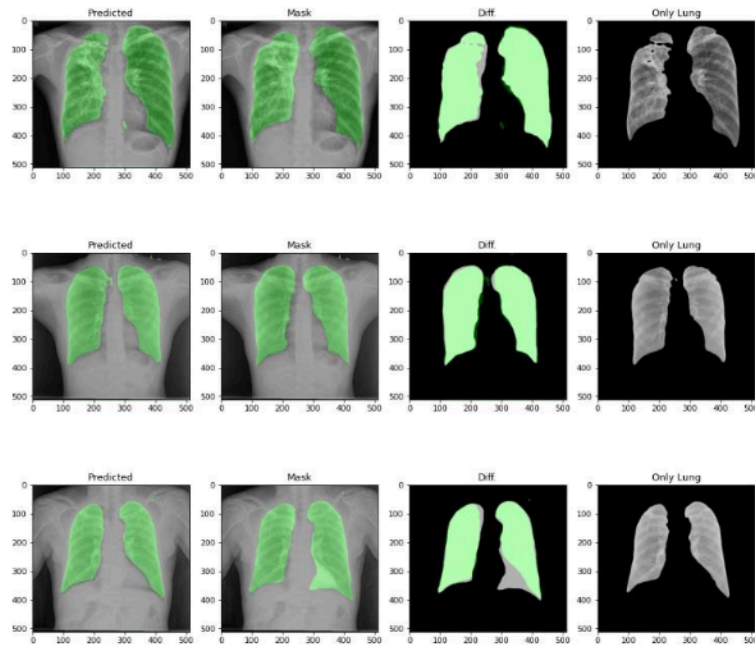


Fig. 3. Segmentation of chest X-ray using UNet

Modified U-Net Model

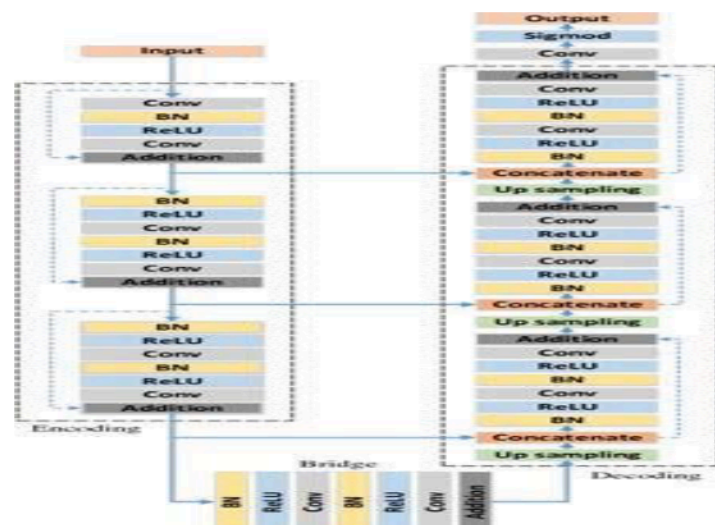


Fig. 4. Architecture of Res-UNet

For lung image segmentation, the researcher adopted a deep learning approach using U-Net with residual connections. U-Net, developed by Olaf Ronneberger et al. for biomedical image segmentation, can be further optimized by replacing standard convolutional units with residual units. This Figure 4 shows below architecture of residual U-net Network.U-Net (ResU-Net), which combines the advantages of both U-Net and residual neural networks to achieve better segmentation. results.The ResU-Net architecture is designed to simplify network training while preserving information flow through its skip connections in residual units, preventing degradation. It consists of three key components: **encoding**, **bridge**, and **decoding**.

- **Encoding:** The input image is transformed into a dense representation, capturing essential features.

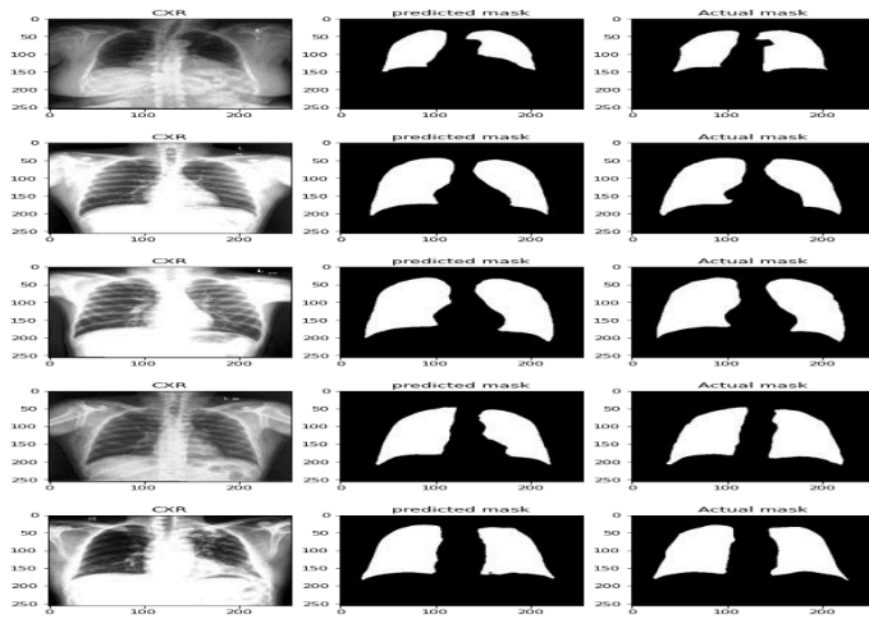


Fig.5 .Predicted and actual mask using Res-Unet

Classification Model

The classification model employs a convolutional neural network (CNN) architecture specifically designed for image classification. It processes input images through multiple convolutional layers that extract hierarchical features, with each layer followed by max pooling. The convolutional layers detect localized patterns and features, while max pooling reduces spatial dimensions, enhancing computational efficiency and feature abstraction. The features extracted by these layers are then flattened into vector representations and passed through multiple fully connected (dense) layers to complete the final classification. These dense layers enable the model to capture complex.

The equation for dense layer is given below-

$$y = \sigma(Wx + b) \quad (2)$$

x: The input vector or tensor. W: The weight matrix.

b: The bias vector.

σ : The activation function applied element-wise.

y: The output of the dense (fully connected) layer.

The output layer employs the sigmoid activation function (as shown in Equation 3) to estimate the probability of the input image belonging to a specific class.

$$\sigma(x) = 1 / (1 + e^{-x}) \quad (3)$$

Hybrid Model

The Hybrid Model enables the simultaneous segmentation and classification of input images by leveraging the strengths of both approaches. First, the segmentation model identifies and generates masks that highlight specific regions or objects within the image. The segmentation masks are subsequently input into the classification model, which conducts binary classification using the segmented regions. This approach allows the model to integrate global context with localized details, improving its capability to identify the presence or absence of specific features in the image. The model employs the binary cross-entropy loss function and the Adam optimizer to ensure efficient learning across both segmentation and classification tasks. The accuracy metric further highlights the model's effectiveness in executing both tasks with precision. This hybrid approach provides a flexible and reliable solution for complex image analysis, particularly in scenarios requiring continuous segmentation and classification.

TBNet-CNN Model

The proposed TBNet-CNN model integrates a segmentation model and a classification model into a single hybrid architecture, as illustrated in Figure 6. The process for developing and training this hybrid model using Tensorflow and Keras is detailed in Algorithm 1. The segmentation component is initially defined, consisting of convolutional layers for feature extraction and up sampling layers to generate segmentation masks. Next, the classification model is defined, incorporating convolutional and dense layers specifically designed for image classification tasks. These two components are then integrated to form the hybrid model. The model is trained using labelled data, with training data used for model construction and validation data for performance monitoring.

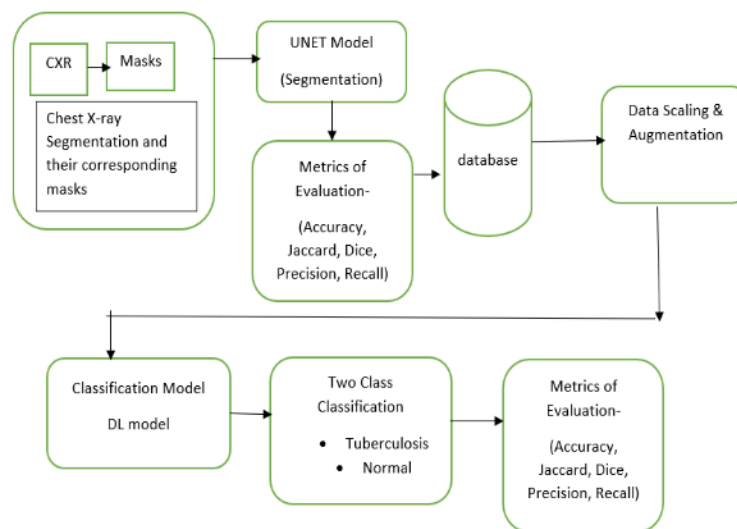


Fig.6. TBNet -CNN Model

Input: Input shape = (256, 256, 3)

1. Define the Segmentation Model

1. **Initialize Input Layer:**
inputs \leftarrow Input(input_shape)
2. **First Convolutional Layer:**
convolution1 \leftarrow Conv2D(32, (3, 3), activation='relu', padding='same')(inputs)
3. **Max Pooling Layer:**
pool1 \leftarrow MaxPooling2D(pool_size=(2, 2))(convolution1)
4. **Upsampling Layer:**
up1 \leftarrow UpSampling2D(size=(2, 2))(pool1)
5. **Final Convolutional Layer for Mask Generation:**
decoded \leftarrow Conv2D(3, (3, 3), activation='sigmoid', padding='same')(up1)

6. Define Segmentation Model:

```
segmentation_model ← Model(inputs, decoded, name='segmentation_model')
```

2. Define the Classification Model**1. Initialize Input Layer:**

```
inputs ← Input(input_shape)
```

2. First Convolutional Layer:

```
convolution1 ← Conv2D(16, (3, 3), activation='relu')(inputs)
```

3. Max Pooling Layer:

```
pool1 ← MaxPooling2D(pool_size=(2, 2))(convolution1)
```

4. Second Convolutional Layer:

```
convolution2 ← Conv2D(32, (3, 3), activation='relu')(pool1)
```

5. Max Pooling Layer:

```
pool2 ← MaxPooling2D(pool_size=(2, 2))(convolution2)
```

6. Third Convolutional Layer:

```
convolution3 ← Conv2D(64, (3, 3), activation='relu')(pool2)
```

7. Max Pooling Layer:

```
pool3 ← MaxPooling2D(pool_size=(2, 2))(convolution3)
```

8. Fourth Convolutional Layer:

```
convolution4 ← Conv2D(64, (3, 3), activation='relu')(pool3)
```

9. Max Pooling Layer:

```
pool4 ← MaxPooling2D(pool_size=(2, 2))(convolution4)
```

10. Fifth Convolutional Layer:

```
convolution5 ← Conv2D(64, (3, 3), activation='relu')(pool4)
```

11. Max Pooling Layer:

```
pool5 ← MaxPooling2D(pool_size=(2, 2))(convolution5)
```

12. Flatten the Output:

```
flatten ← Flatten()(pool5)
```

13. First Dense Layer:

```
dense1 ← Dense(256, activation='relu')(flatten)
```

14. Final Output Layer (Sigmoid):

```
output ← Dense(1, activation='sigmoid')(dense1)
```

3. Combine the Segmentation and Classification Models**1. Initialize Input Tensor:**

```
input_tensor ← Input(input_shape)
```

2. Apply Segmentation Model:

```
segmentation_output ← segmentation_model(input_tensor)
```

3. Apply Classification Model:

```
classification_output ← classification_model(segmentation_output)
```

4. Create Hybrid Model:

```
hybrid_model ← Model(inputs=input_tensor, outputs=classification_output, name='hybrid_model')
```

4. Compile and Train the Hybrid Model

1. **Compile the Hybrid Model:**
`hybrid_model.compile(optimizer='adam', loss='binary_crossentropy',
metrics=['accuracy','dice_coeff','jaccard_index'])`
2. **Define Log Directory for TensorBoard:**
`logdir = 'logs'`
3. **Train the Model:**
`hist ← hybrid_model.fit(train, epochs=25, validation_data=val, callbacks=[tensorboard_callback])`

C.Pseudo-code for Tuberculosis Detection System

The pseudocode in the proposed model section outlines the system's workflow, including input processing, segmentation, classification, and the final output. The process begins with an input image of size $(256 \times 256 \times 3)$, which is first processed by the segmentation model. This involves encoding the image using Conv2D and MaxPooling2D layers, followed by decoding with Upsampling2D and Conv2D layers to generate the segmented output. The segmented images are then passed to the classification model for further analysis. During classification, the images are processed through several Conv2D and MaxPooling2D layers, followed by a Flatten layer and two Dense layers to produce the final classification. This hybrid approach seamlessly integrates segmentation and classification, offering a robust solution.

1.Specify the input image shape:

Set the input shape to $256 \times 256 \times 256$ (height, width, and RGB channels).

2.Construct the segmentation model:

- a. **Input Layer:** Establish the input layer for the model.
- b. **Encoder:** Employ a series of Conv2D and MaxPooling2D layers to extract hierarchical features.
- c. **Decoder:** Use UpSampling2D and Conv2D layers to recover spatial dimensions and refine the segmented output.
- d. **Output Layer:** Use a sigmoid activation function for pixel-wise binary classification.

3.Build the Classification Model:

- a. **Input Layer:** Define the input layer for the classification model.
- b. **Convolution Layers:** Use a sequence of Conv2D and MaxPooling2D layers to extract important features.
- c. **Flatten Layer:** Flatten the feature maps into a 1D vector.
- d. **Dense Layer:** Use fully connected layers with Relu activation for complex feature interactions.
- e. **Output Layer:** Use a sigmoid activation function for binary classification

4.Integrate the Models:

- a. Use the output from the segmentation model as input for the classification model.
- b. Define the hybrid model by combining the segmentation and classification components into a unified framework.

5.Compile and Summarize the Hybrid Model: Compile the hybrid model with a suitable optimizer and loss function, and generate a summary of its architecture.

3.RESULTS

This section offers a detailed overview of the evaluation metrics employed to measure the performance of the TBNNet-CNN model. These metrics are crucial for determining how effectively the model identifies patterns and makes predictions, serving as key indicators of its overall performance. Accuracy is a key metric for classification models, representing the ratio of correctly predicted instances to the total number of instances, providing an overall assessment of prediction reliability. Recall measures the model's ability to accurately identify positive instances, which is especially important when detecting all positive cases is critical. The F1-

score, which combines precision and recall into their harmonic mean, provides a balanced evaluation of the model's performance, especially when both metrics are equally important or when dealing with imbalanced classes. Additionally, the confusion matrix offers a comprehensive breakdown of the model's predictions compared to the actual ground truth labels, consisting of four key elements: false positives (FP), false negatives (FN), true positives (TP), and true negatives (TN). This enables a deeper analysis of the model's predictive accuracy and error patterns. The equations for $f1_score$, recall, precision is given below-

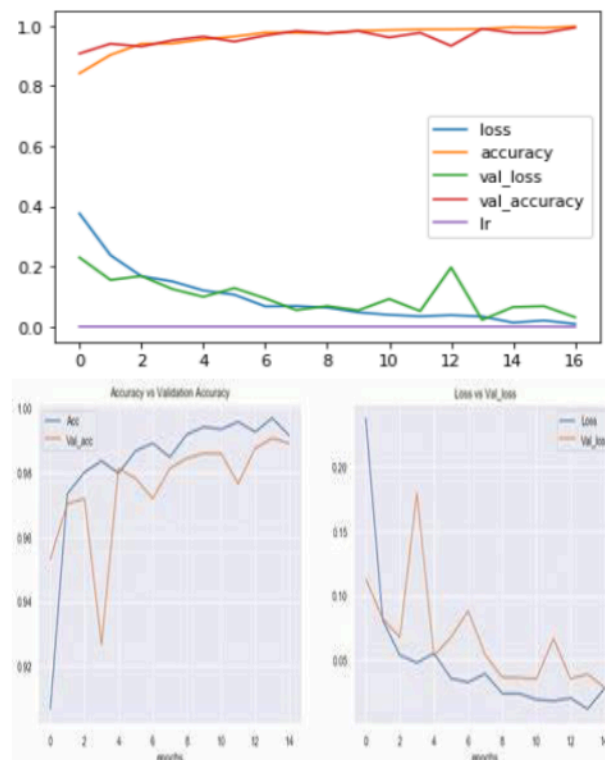
$$f1_score = 2 * (Precision * Recall) / (Precision + Recall) \quad (4)$$

$$Recall = True\ Positive / (True\ Positive + False\ Negative) \quad (5)$$

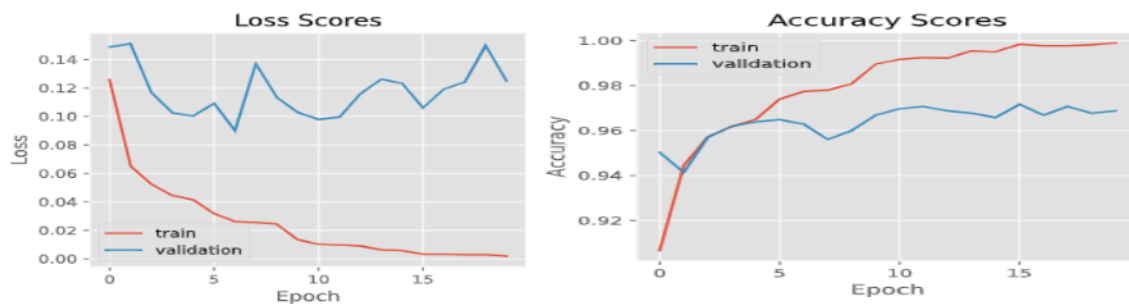
$$Precision = True\ Positive / (True\ Positive + False\ Positive) \quad (6)$$

$$Accuracy = True\ Positive + True\ Negative / (True\ Positive + True\ Negative + False\ Positive + False\ Negative) \quad (7)$$

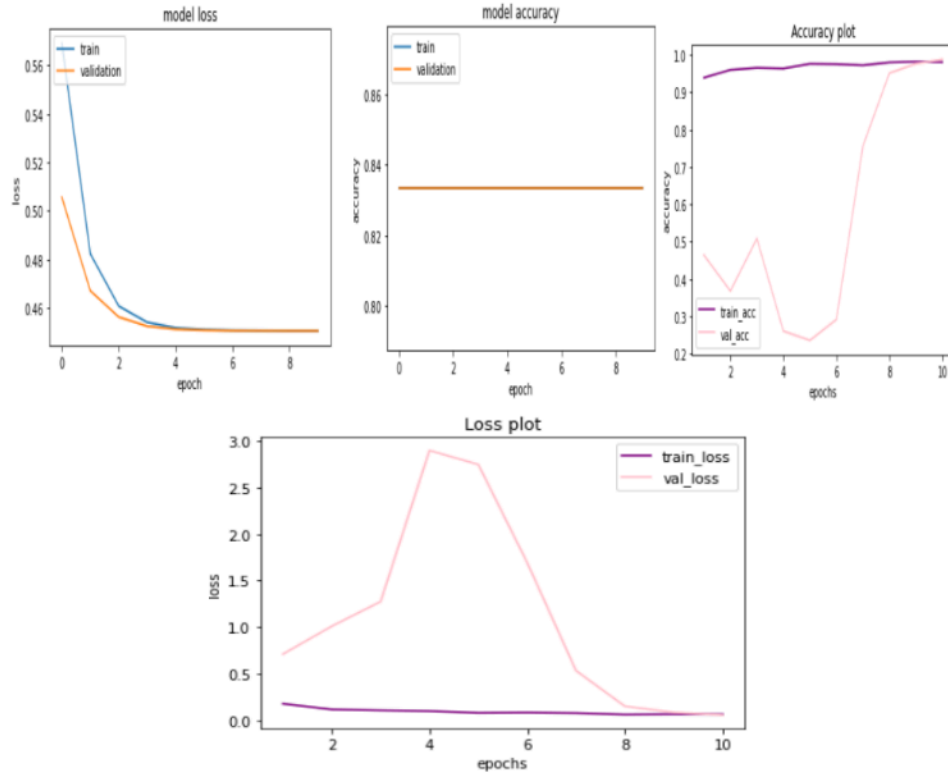
Loss curves and accuracy curves are shown for pre-trained and TBCNN-net model below figure-



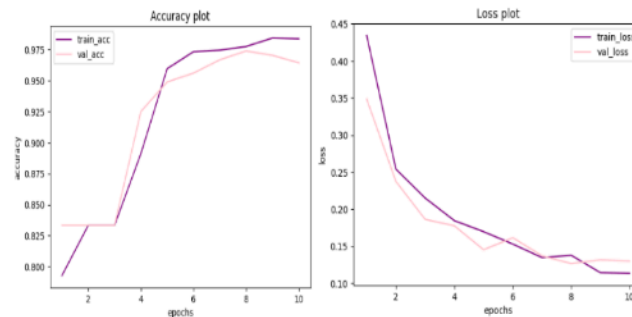
(a) Loss and accuracy curves for TBCNN-net (b) Loss and accuracy curves for VGG16



(c). Loss and accuracy curves for DenseNet121



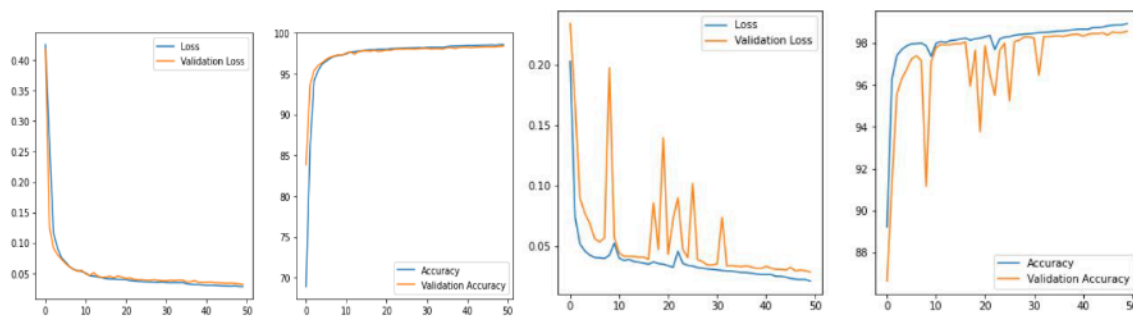
(d).Loss and accuracy curves for VGG19(e).Loss and accuracy for ResNet50



(f) Loss and Accuracy for Xception

Fig. 7. Loss and Accuracy curve of different CNN models

Tb-CNN net accuracy seemed to be higher as compared to other pre-trained model's and loss is also low as compared to other models. Unet and Res-Unet loss and accuracy curves are shown below-



(a)(b)

Fig. 8. Loss and Accuracy Curves of U-Net and ResUNet

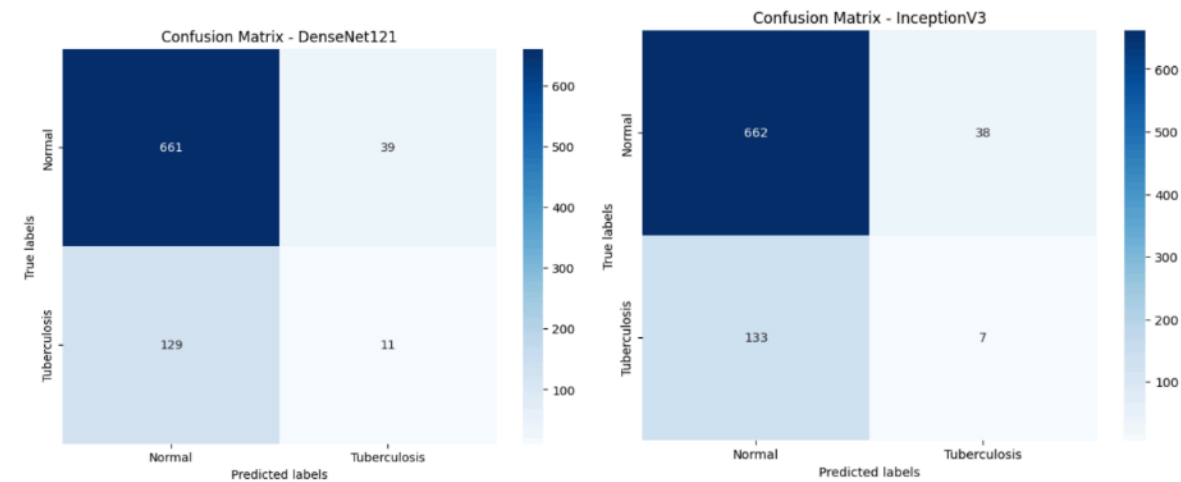
From above figure we can find out that Res-Unet performs better as compared to Unet

Table 1.ResUnet and Unet model performance metrics

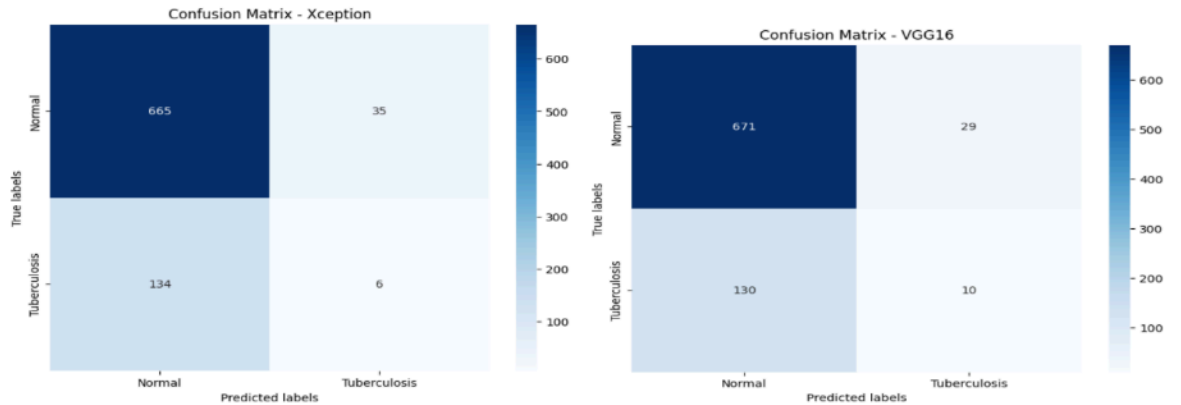
Model Name	Accuracy	Recall	f1_score	Precision	Dice_coeff
U-Net	97.77	98.08	97.8	97.52	96.53
Res-Unet	98.17	98.39	91.97	98.39	96.33

4.DISCUSSION

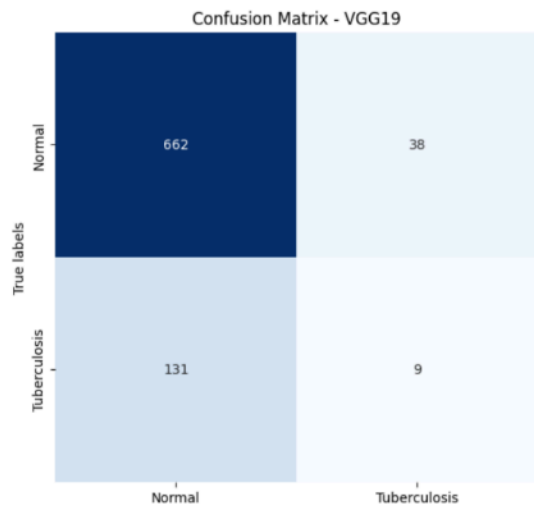
Confusion matrix for TBCNN-net and other pre-trained models are shown below-



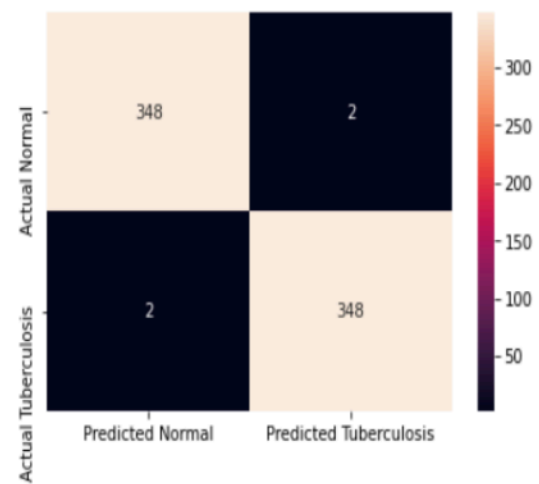
(a).Confusion Matrix of DenseNet121(b).Confusion matrix of InceptionV3



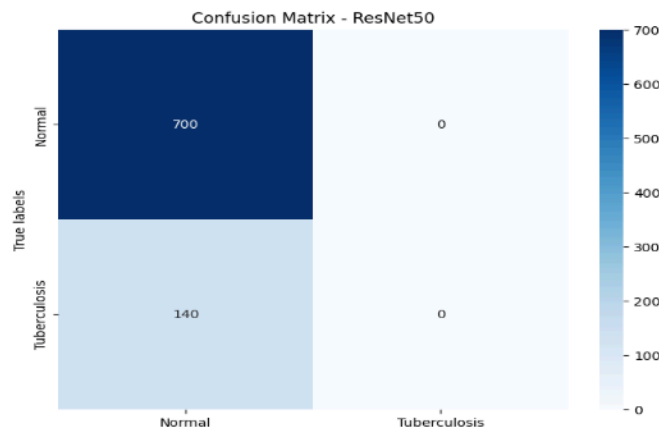
(c).Confusion matrix of Xception(d). Confusion matrix of VGG16



(e). Confusion Matrix of VGG19



(f). Confusion Matrix of TBCNN-net



(g). Confusion Matrix of ResNet50

Fig.9. Confusion Matrix of all pre-trained and TBCNN-net model

As compared to other pre-trained models TBCNN-net performed with predicted tuberculosis and actual tuberculosis as 348 cases next DenseNet121 with 11, VGG16 10 cases, VGG19 with 9, InceptionV3 with 7, Xception with 6 cases. Accuracy table is shown below TBCNN-net highest accuracy

Table 2. Metrics of Performance between TBCNN-net and other pre-trained models

Model Name	Accuracy	Precision	Recall	f1_score
VGG16	81.35	55	52	50
VGG19	80.59	51	51	49
DenseNet121	80.24	53	51	50
Xception	79.65	49	50	48
InceptionV3	79.17	49	50	48
ResNet50	83.35	42	50	45
TBCNN-net	99.42	99.00	99.29	99.29

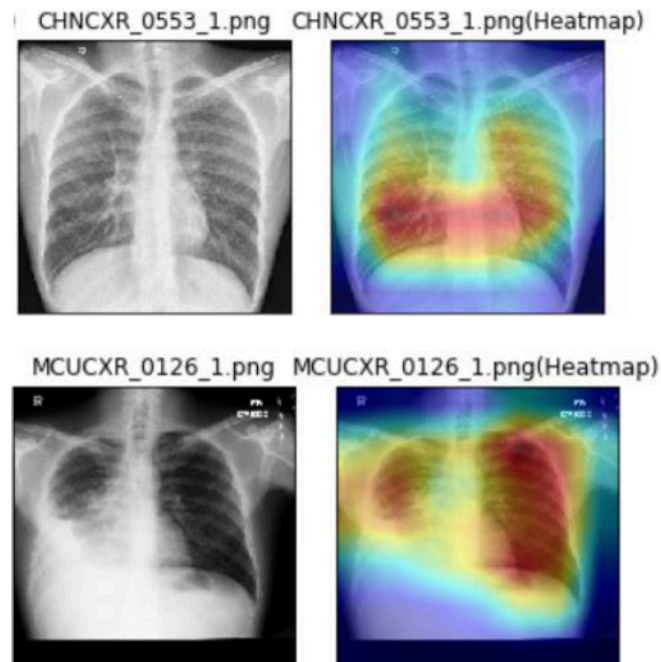


Fig.10. Heatmap for segmented images using gradCAM

5.CONCLUSION

This study introduces a novel deep learning-based CNN model, TBCNN-net, designed to detect tuberculosis (TB) from X-ray images. The model employs a two-stage architecture, combining a segmentation module with a classification module to enhance prediction accuracy. Comprehensive evaluations highlight the system's reliability and practicality, outperforming previous methods in terms of accuracy of 99.42% and recall of 99.29%. Additionally, its superior jaccard index of 96.05% and dice coefficient of 96.33% values further validate its performance using residual U-net architecture. When tested on unseen images, TBCNN-net demonstrated robustness and strong generalization across diverse datasets, maintaining high accuracy. Future research will focus on integrating multimodal data, including genetic information and clinical metadata, to create more advanced diagnostic tools and deepen insights into TB detection. values further validate its performance.

CONFLICT OF INTEREST

The authors report no conflict of interest

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