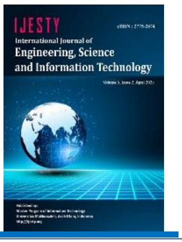
International Journal of Engineering, Science and Information Technology
Volume 5 No. 2 (2025) pp. 379-385
ISSN 2775-2674 (online)
Website: http://ijesty.org/index.php/ijesty
DOI: https://doi.org/10.52088/ijesty.v5i2.853
Research Paper, Short Communication, Review, Technical Paper



Detection of Tuberculosis Disease in Lung X-ray Images Using the DenseNet121 Method

Madyono[1]*, Anisah Nabilah[2]

[1]Department of Electronics, Politeknik Elektronika Negeri Surabaya, Surabaya, Indonesia
[2]Department of Informatics, Faculty of Computer Science, Universitas PGRI Jombang, Indonesia

**Corresponding author Email: madyono@pens.ac.id*

The manuscript was received on 20 July 2024, revised on 2 November 2024, and accepted on 5 March 2025, date of publication 10 April 2025

Abstract

Tuberculosis (TB) is a lung infection caused by Mycobacterium tuberculosis and can be detected through chest X-ray imaging. In this study, tuberculosis disease detection was carried out using the DenseNet121 method, a deep-learning architecture proven effective in medical image classification tasks. This study used a dataset of 4,200 lung X-ray images classified as positive or negative for TB. The DenseNet121 model was trained with this data to identify patterns in the X-ray images indicating tuberculosis infection. The results of the model evaluation showed high performance with a precision value of 0.91, a recall of 0.90, and an f1-score of 0.89. In addition, the model achieved an overall accuracy of 90.4%. The results of this study indicate that the DenseNet121 method can be a reliable tool in detecting tuberculosis from chest X-ray images so that it can assist medical personnel in the diagnosis process more quickly and accurately.

Keywords: *Tuberculosis, Lung X-ray, Deep Learning, DenseNet121, Disease Detection*.

1. Introduction

Tuberculosis (TB) is a lung infection caused by Mycobacterium tuberculosis [1][2]. This disease is still a global health problem with high morbidity and mortality rates, especially in developing countries. According to the WHO report, in 2020, there were around 10 million new cases of TB worldwide, with a death toll reaching 1.5 million people [3]. Early and accurate diagnosis is key in preventing and controlling this disease's spread.

Chest X-ray imaging is one of the methods often used in the diagnosis of TB because it is fast and relatively inexpensive compared to laboratory-based methods, such as sputum microscopic tests or polymerase chain reaction (PCR) [4][5]. However, radiologists' manual interpretation of X-ray images can cause subjectivity and take a long time [6]. Therefore, an automated method is needed to increase the accuracy and efficiency of detecting TB from X-ray images.

In recent years, artificial intelligence and deep learning have shown great potential in medical image analysis [7]. One branch of artificial intelligence is Computer Vision. Computer Vision is the science that studies how a computer can recognize an object [8]. One of the problems that can be solved from this branch of science is detecting objects and image classification. Object detection is one of the topics in artificial intelligence that continues to be studied and developed rapidly in the current era. Object detection is a technology related to computers that recognizes an object in a digital image, which can be a colour or object. One of the popular deep learning architectures in medical image classification is the Convolution Neural Network (CNN) [9][10]. This Deep Learning method is widely used to solve object detection and classification problems in images [11][12][13]. With the era of technology increasingly developing, in 2016 the DenseNet121 model appeared [14], having 8 million parameters. This model extensively utilizes the functions in each layer from the initial layer to the final layer [15], which has feature extraction and gradient propagation advantages and is more efficient than conventional models [16].

This study aims to detect tuberculosis from lung X-ray images using the DenseNet121 method [17] [18]. This training was carried out with numerous datasets, namely 4,200 lung X-ray datasets. Normalization and dataset augmentation were carried out for the training process to produce a high level of accuracy so that the training results produced were more optimal. With the results obtained, this study is expected to contribute to helping medical personnel detect tuberculosis more quickly and accurately, thereby increasing efficiency in diagnosing and treating patients.

2. Research Methods

The research was conducted using the DenseNet121 model. The research flow carried out was dataset collection, preprocessing, training, testing, and evaluation.

2.1. Dataset Collection

In this study, the lung X-ray image dataset was obtained online through the Kaggle platform, which provides various datasets for research purposes in machine learning and deep learning. The total dataset used in this study consists of 4,200 lung X-ray images, which are categorized as follows:

1. Three thousand five hundred images are standard lung X-ray images (non-TB).
2. Seven hundred images are lung X-ray images infected with tuberculosis (TB).

From the distribution of the data obtained, it can be seen that there is an imbalance (imbalanced data), where the number of standard lung images is much greater than the number of lung images infected with TB. This imbalance can impact model performance, especially regarding the model's ability to recognize minority classes (TB) well. Figure 1 shows several standard lung X-ray images and those affected by TB.

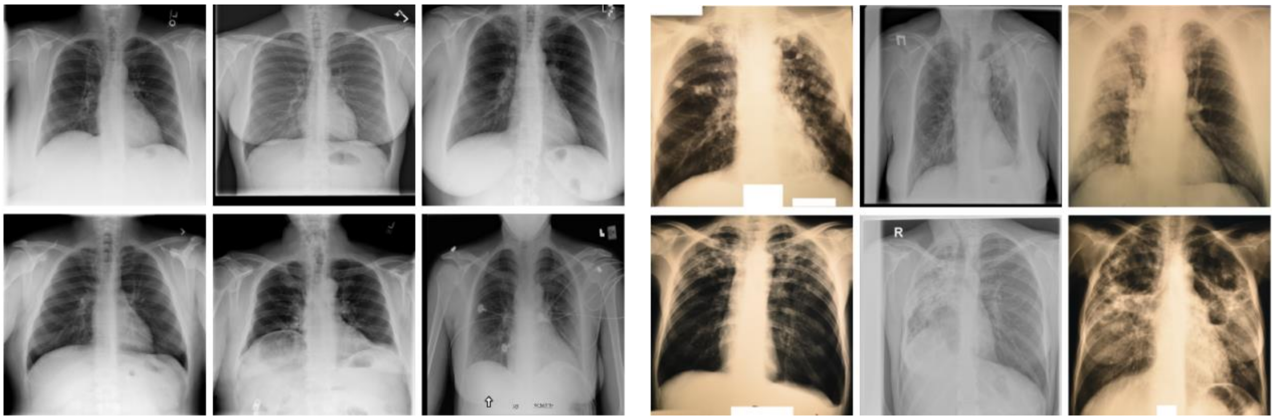

(a) (b)

Fig 1. Figure (a) Normal Lung X-Ray, and figure (b) Lung X-Ray affected by TB disease.

2.2. Balancing Data and Preprocessing

A data balancing process is carried out through data normalization and augmentation techniques to overcome data imbalance. Several data augmentation methods used in this study include:

1. Rotation - Rotate the image within a specific angle range to increase data variation.
2. Zoom - Enlarge or reduce the image so the model can recognize patterns from various scales.
3. Width Shift & Height Shift - Shift the image horizontally and vertically to increase the model's resilience to differences in object positions in the image.
4. Grey -Scale - Make data have a colour level of 0 to 255, which makes it easier to detect objects during training

In addition to augmentation, image normalization is carried out to ensure each image has a uniform colour scale. The model can more easily recognize patterns without being disturbed by differences in lighting or contrast. Figure 2 shows the results of the data preprocessing that has been carried out.

Fig 2. Lung X-ray image, the result of preprocessing using rotation and zoom techniques

By applying these data balancing and preprocessing techniques, the DenseNet121 model can learn better from a more representative dataset, improve its performance in detecting TB from lung X-ray images, and reduce bias due to unbalanced data distribution..

2.3. Training Dataset

In this study, the model training process was carried out by dividing the dataset into three main parts:

1. 80% for the training set (3,360 images) – Used to train the model to recognize patterns in lung X-ray images.
2. 10% for the validation set (420 images) – Used to evaluate model performance during training and prevent overfitting.
3. 10% for the test set (420 images) – Used to test model performance on previously unseen data.

This dataset separation was done randomly to ensure that each subset's distribution between standard and TB-infected X-ray images remained proportional. The model used in this study is DenseNet121, a deep-learning architecture proven effective in medical image classification. Transfer learning is applied to improve training efficiency by utilizing pre-trained model weights from the ImageNet dataset. The main steps in implementing transfer learning with DenseNet121 are as follows:

2.3.1. Data Preprocessing

All images are converted into a format that matches the DenseNet121 input (resolution 224x224 pixels). Normalize pixel values into the range [0,1] to accelerate model convergence. Data augmentation is performed to increase dataset diversity through rotation, zoom, width shift, and height shift.

2.3.2. Model Architecture Modification

Using the DenseNet121 model with initial weights from ImageNet. The fully connected layer at the end of the model is replaced with a custom layer for two-class classification (Normal and TBC). The Softmax activation function in the output layer is used to determine the probability of each class. Figure 3 is a diagram of the DenseNet121 architecture.

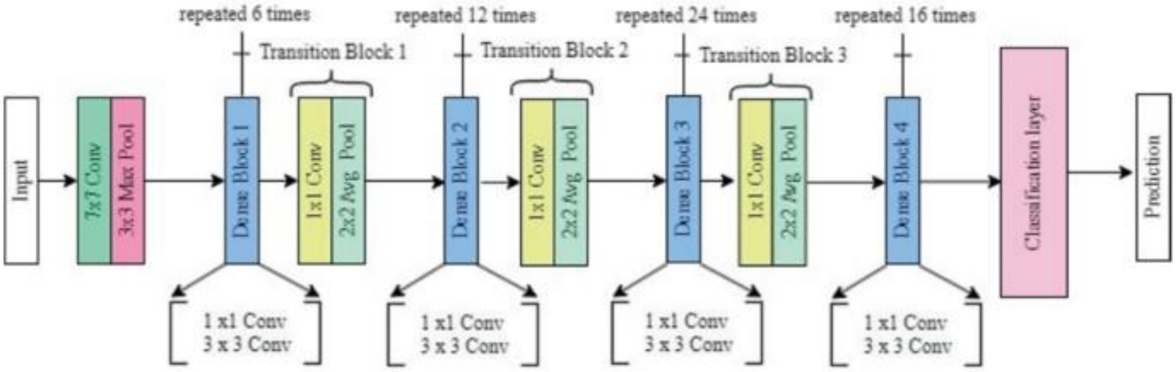


Fig 3. Arsitecture DenseNet121[19][20].

To illustrate how it works, the first dense block will be connected to the next dense block until it reaches the last dense block, then the output of the previous dense block uses the output of the first dense block, an illustration of how the dense block works is presented in Figure 4.

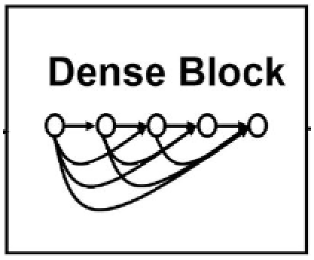


Fig 4. Dense Block Illustration

1. Model Compilation

We use the optimization method for data compilation, an essential process for optimizing input weights by comparing predictions and loss functions. The optimizations used are as follows:

a. Optimizer: Adam's learning rate was adjusted to achieve optimal convergence.
b. Loss function: Binary Crossentropy for binary classification.
c. Metrics: Accuracy, Precision, Recall, and F1-score to evaluate model performance.

2. Model Evaluation

Model evaluation is done by calculating several main metrics: Precision, Recall, F1-score, and Accuracy. These metrics measure how well the model classifies lung X-ray images as Normal or TB-infected.

Precision measures how many optimistic predictions are correct compared to the total positive predictions made by the model.

$$\text{Precision} = \frac{TP}{TP + FP} \quad \text{……(1)}$$

Where:
TP (True Positive): The number of TB cases that are detected as TB.
FP (False Positive): The number of standard cases incorrectly classified as TB.

High precision means the model rarely gives false optimistic predictions (minimal false positives).

3. Recall (Sensitivity or True Positive Rate)
Recall measures how many positive cases were successfully detected from the total number of existing positive cases.

$$\text{Recall} = \frac{TP}{TP + FN} \quad \text{……(2)}$$

Where:
FN (False Negative): The number of TB cases incorrectly classified as usual.

High recall means the model rarely misses positive cases (minimal false negatives), crucial in diagnosing diseases such as TB.

4. F1-score
The F1-score is the harmonic mean between Precision and Recall, used to balance the two.

$$\text{F1-score} = 2 \times \frac{\text{Precision} \times \text{Recall}}{\text{Precision} + \text{Recall}} \quad \text{……(3)}$$

A high F1 score indicates a balance between precision and sensitivity (recall).

5. Accuracy
Accuracy measures the percentage of correct predictions compared to the total test data.

$$\text{Akurasi} = \frac{TP + TN}{TP + TN + FP + FN} \quad \text{……(4)}$$

Where:
TN (True Negative): The number of standard cases classified as usual.
Accuracy provides a general idea of model performance. Still, it can be misleading if the dataset is imbalanced (e.g., if the data is primarily standard cases, the model can get high accuracy by simply always predicting normal).

5. Final Weight Loss
During training, the model uses a loss function to measure the difference between the prediction and the actual label. The model will adjust its weights based on this loss value to make it more accurate in prediction. In this study, Binary Crossentropy Loss was used because the problem faced was binary classification (Normal vs. TBC).

Binary Crossentropy Loss Formula

$$\mathcal{L} = -\frac{1}{N} \sum_{i=1}^{N} \left[y_i \log(\hat{y}_i) + (1 - y_i) \log(1 - \hat{y}_i) \right] \quad \text{……(5)}$$

Where :

N = Number of Samples in Dataset

y_i = Actual Label (0 for normal 1 for TB)

$y^{\wedge}_i$ = Model prediction probability for positive class (TBC)

This loss is calculated for each batch during training. Final Weight Loss is the final loss value after training is complete, which shows how well the model can predict labels while minimizing errors.
With the combination of metric evaluation and final loss, the model can be further optimized to improve its accuracy in detecting TB from lung X-ray images.

3. Result and Discussion

Training conducted on Lung X-ray data aimed at detecting TB disease was conducted using the DenseNet121 module, where several parameter settings exist to maximize the training process results. The optimizer used is Adam, and the epoch used is 10. A convolution matrix is used for evaluation; this evaluation helps determine the model's performance when faced with testing data. Figure 5 is the confusion matrix of the model when trained with DenseNet121.

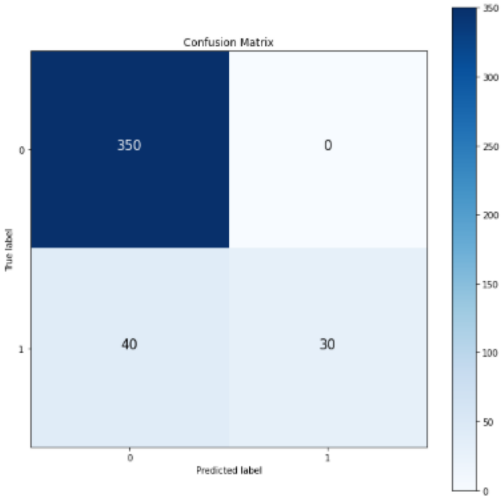
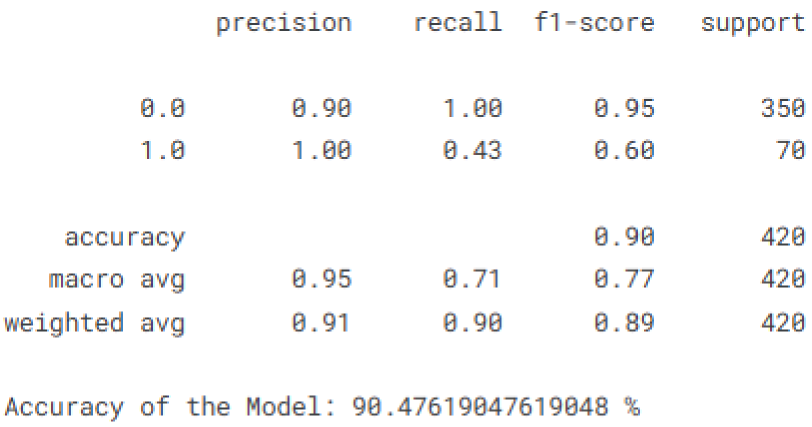


Fig 5. Confusion Matrix DenseNet121

Looking at the confusion matrix table, the True Positive (TP), True Negative (TN), False Positive (FP), and False Negative (FN) values are obtained. These values can be calculated to determine the accuracy, recall, precision, and F1 score values. In Figure 6, the results of the DenseNet121 model evaluation

.



```
              precision    recall  f1-score   support

         0.0       0.90      1.00      0.95       350
         1.0       1.00      0.43      0.60        70

    accuracy                           0.90       420
   macro avg       0.95      0.71      0.77       420
weighted avg       0.91      0.90      0.89       420

Accuracy of the Model: 90.47619047619048 %
```

Fig 6. DenseNet121 Model Evaluation Results

Looking at the evaluation results of the Lung X-ray data training, it produces a precision value of 0.91, a recall of 0.90, and an f1-score of 0.89; these values indicate the level of prediction accuracy, minimal detection and data classification errors, data balance, and most importantly the level of performance of data classification accuracy between regular lung X-Rays and lungs affected by TB disease of 90.4%.

In addition to looking at the curve of the level of data prediction accuracy, Figure 7 is a picture of the ROC AUC graph.

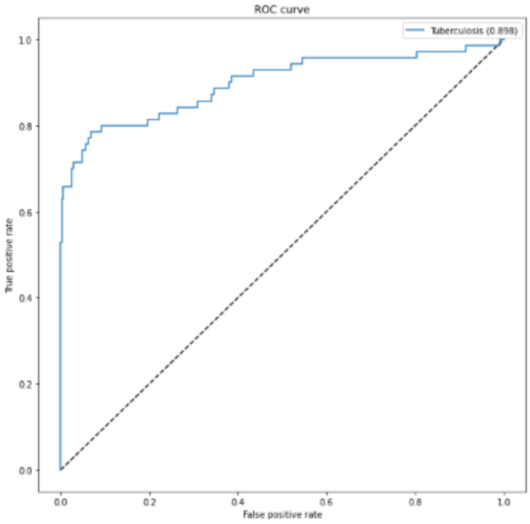


Fig 7. ROU AUC DenseNet121 graph

Looking at the ROU AUC curve of the training evaluation results with the DenseNet121 model, the data that was successfully detected correctly with two classifications, namely standard and tuberculosis, the data curve looks up; it can be said that the AUC has good performance.

The evaluation was conducted to understand how the convolutional neural network is driven to make classification decisions using the Grad CAM evaluation method. This evaluation method aims to determine the part of the image that has directed the convolutional neural network to its final decision. This method creates a heat map representing the activation class in the image received as input. Then, each activation class is associated with a specific output class. Figure 8 shows the results of the Grad CAM evaluation of the Lung X-ray image in the tuberculosis classification.

Fig 8. Grad CAM Evaluation

The Grad CAM Evaluation image can detect the location of TB disease detection on the lung X-ray image; when TB disease is detected, there is a heat map on the left side of the lungs.

4. Conclusion

The results of the research that has been done to detect TB disease in X-ray images of the lungs using the DenseNet121 model When evaluated using the confusion matrix, it produces a precision value of 0.91, recall of 0.90, and f1-score of 0.89, indicating that detection is done well. So, it can be concluded that the detection of TB disease with modern Confusion Neural Network (CNN) analysis using the DenseNet121 model was successful, with an average prediction accuracy of 0.91 and perfect accuracy.

References

[1] Abdullahi Ibrahim et al., "Automated detection of Mycobacterium tuberculosis using transfer learning", The Journal of Infection in Developing Countries, vol. 15, pp. 678-686, May 2021.

[2] Global Tuberculosis Report 2018. Licence: CC BY-NC-SA 3.0 IGO, 2018, [online] Available: https://creativecommons.org/licenses/by-nc-sa/3.0/igo, ISBN 978-92-4-156564-6.

[3] World Health Organization. (2021). Global tuberculosis report 2021. World Health Organization.

[4] Lakhani, P., & Sundaram, B. (2017). Deep learning at chest radiography: Automated classification of pulmonary tuberculosis using convolutional neural networks. Radiology, 284(2), 574-582.

[5] L. Racic, T. Popovic, S. Cakic and S. Sandi, "Pneumonia Detection Using Deep Learning Based on Convolutional Neural Network", 2021 25th International Conference on Information Technology (IT), 2021.

[6] Rajpurkar, P., Irvin, J., Zhu, K., Yang, B., Mehta, H., Duan, T., ... & Ng, A. Y. (2017). CheXNet: Radiologist-level pneumonia detection on chest x-rays with deep learning. arXiv preprint arXiv:1711.05225..

[7] Litjens, G., Kooi, T., Bejnordi, B. E., Setio, A. A. A., Ciompi, F., Ghafoorian, M., ... & van der Laak, J. A. (2017). A survey on deep learning in medical image analysis. Medical image analysis, 42, 60-88.

[8] C. Vogler and D. Metaxas, "Parallel hidden markov models for american sign language recognition", Computer Vision 1999. The Proceedings of the Seventh IEEE International Conference on, vol. 1, pp. 116-122, 1999..

[9] Vikas Mittal and R. K. Sharma, "Machine learning approach for classification of Parkinson disease using acoustic features", J. Reliab. Intell. Environ., vol. 7, no. 3, pp. 233-239, 2021.

[10] Lavanya Madhuri Bollipo and K. V Kadambari, "Fast and robust supervised machine learning approach for classification and prediction of Parkinson’s disease onset", Comput. methods Biomech. Biomed. Eng. Imaging Vis., vol. 9, no. 6, pp. 690-706, 2021.

[11] Lecun et al, "Gradient based learning applied to document recognition", Proceedings of IEEE, no.86 November, pp.2278-2324, 1998

[12] Mehera Binte Mizan, Md Al Mehedi Hasan and Syed Rahat Hassan, "A comparative study of tuberculosis detection using deep convolutional neural network", 2020 2nd International Conference on Advanced Information and Communication Technology (ICAICT), pp. 157-161, 2020.

[13] Mohammed Salih Ahmed, Atta Rahman, Faris AlGhamdi, Saleh AlDakheel, Hammam Hakami, Ali AlJumah, et al., "Joint diagnosis of pneumonia covid-19 and tuberculosis from chest x-ray images: A deep learning approach", Diagnostics, vol. 13, no. 15, pp. 2562, 2023.

[14] Lili Li, Shujuan Zhang and Bin Wang, "Plant disease detection and classification by deep learning-a review", IEEE Access, vol. 9, no. 2021, pp. 56683-56698.

[15] Krizhevsky, Alex, Ilya Sutskever, dan Geoffrey E. Hinton, "Imagenet classification with deep convolutional neural networks.", Communications of the ACM 60.6 84-90, 2017.

[16] Huang, G., Liu, Z., Van Der Maaten, L., & Weinberger, K. Q. (2017). Densely connected convolutional networks. Proceedings of the IEEE conference on computer vision and pattern recognition, 4700-4708.
[17] B. Ananthakrishnan, A. Shaik, S. Kumar, S. O. Narendran, K. Mattu and M. S. Kavitha, "Automated detection and classification of oral squamous cell carcinoma using deep neural networks", Diagn, vol. 13, no. 5, pp. 918, 2023.
[18] K. Shaheed, Q. Abbas, A. Hussain and I. Qureshi, "Optimized Xception Learning Model and XgBoost Classifier for Detection of Multiclass Chest Disease from X-ray Images", Diagnostics, vol. 13, pp. 2583, 2023.
[19] S. M. Fati, E. M. Senan and Y. Javed, "Early Diagnosis of Oral Squamous Cell Carcinoma Based on Histopathological Images Using Deep and Hybrid Learning Approaches", Diagn, vol. 12, pp. 1899, 2022.
[20] Dinesh Jackson Samuel and Rajesh Kanna Baskaran, Design to automate the detection and counting of Tuberculosis(TB) bacilli, pp. 11432, May 2021, [online] Available: https://doi.org/10.48550/arXiv.2105.11432.