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Convolutional Neural Network Architecture Densenet121 to Identify Tuberculosis

Fajri Nugraha[1], S. Sumijan[2,✉], Rini Sovia[3]
[1,2,3] Master of Informatics Engineering, Faculty of Computer Science, Universitas Putra Indonesia YPTK, Padang, 25221, Indonesia
fajrinugraha@uinib.ac.id

Abstract

Smoking habits and the normalization of smoking activities are often a problem in many developing countries in the world. Cigarette smoke can cause many health problems that increase the risk of developing diseases and worsen the condition of people with the disease, one of which is Tuberculosis (TB). In Indonesia, based on the WHO Global TB Report 2024, Indonesia ranks second in the world in TB cases, it is estimated that there are more than 1,000,000 new cases every year, this disease is a very serious health problem and has obstacles in the identification process. This research aims to develop a TB disease identification system using Deep Learning. The methods used in this study are Convolutional Neural Network (CNN) and Densenet121 architecture. Convolutional Neural Network (CNN) was chosen for its ability to perform X-ray image analysis for visual validation, while Densenet121 was chosen because of its flexible architecture that can be applied to a wide range of *computer vision* applications, including image classification, object identification, and semantic segmentation. The research stage includes data collection, then preprocessing the image, namely resize, normalization, and conversion to arrays, then building a Convolutional Neural Network model with the selected architecture, then model training, model performance evaluation using accuracy and AUC metrics and ending with testing and validation by experts. The dataset used in this study is X-Ray data of tuberculosis patients taken from *Kaggle* to build a Deep Learning model that is able to identify TB through 100 chest X-ray image datasets. The results of the study show that the CNN model is able to identify tuberculosis with an accuracy rate of up to 90%, so it can help speed up early diagnosis or screening so that patients can continue to receive treatment and treatment. Therefore, the application of deep learning with the Convolutional Neural Network (CNN) method and DenseNet121 architecture based on X-Ray image data is an effective approach in the early detection of tuberculosis and seeks to make an important contribution to the control of lung diseases related to exposure to cigarette smoke in Indonesia.

Keywords: Cigarette Smoke, TB, Deep Learning, CNN, Densenet121.

1. Introduction

Tuberculosis (TB) is an infectious disease caused by Mycobacterium tuberculosis, which can attack the lungs and other organs outside the lungs [1]. The disease remains a major global health problem and is among the top 10 causes of death worldwide [2]. Based on the Global Tuberculosis Report 2023 released by the World Health Organization (WHO), in 2022 there were around 10.6 million new cases of TB globally, with 1.3 million deaths in patients without HIV and 167 thousand deaths in patients with HIV [3].

Indonesia is one of the countries with the highest burden of TB in the world, ranked second after India with an estimated 969 thousand new cases in 2022, equivalent to 10% of the global total [4]. The 2018 Basic Health Research Report (Riskesdas) shows that the prevalence of tuberculosis in Indonesia is 759 per 100 thousand population [5]. This high number confirms that tuberculosis is still a public health challenge in Indonesia.

Early diagnosis of tuberculosis is key to breaking the chain of transmission and reducing mortality [6]. The gold standard method for TB diagnosis is microscopic examination and molecular-based tests, such as GeneXpert MTB/RIF, but these methods require time, cost, and trained human resources [7]. Meanwhile, thoracic imaging (X-ray) is a rapid screening method that is relatively inexpensive and widely available in healthcare facilities [8]. However, the interpretation of X-ray images is highly dependent on the expertise of the radiologist, and factors such as image quality or reader fatigue can degrade the accuracy of the diagnosis [9], [10].

The development of Artificial Intelligence (AI) technology, especially deep learning, offers potential solutions to improve the detection of tuberculosis based on medical images [11]. Convolutional Neural Networks (CNNs) have been used extensively in

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medical image processing due to their ability to extract complex and relevant visual features [12], [13]. A number of studies have shown that CNN is able to detect lung abnormalities such as tuberculosis with a level of accuracy equal to or even surpass that of radiologists [14].

One effective CNN architecture is DenseNet121, which connects each layer to all subsequent layers via dense connections, thus maximizing feature reuse and reducing the problem of gradient loss [15]. DenseNet121 has been used in a wide range of medical image classification studies, including the detection of pneumonia, COVID-19, and tuberculosis, with high accuracy results [16], [17].

Nonetheless, most CNN-based TB detection studies use international public datasets, which may not fully represent patient characteristics and image quality in Indonesia [18]. Differences in imaging tools, patient conditions, and disease distribution can affect model performance if applied to local populations [19]. Therefore, research is needed that develops and tests DenseNet121-based CNN models on datasets that have value and are relevant to this study.[4]

This study aims to develop a DenseNet121-based TB detection system with a transfer learning approach, using a processed and optimized chest X-ray image dataset. This model is expected to be able to provide fast, accurate detection results, and can be used as a screening tool in health facilities with limited resources.

Based on the previous explanation, it is hoped that the model built using CNN with the Densenet121 architecture can help carry out a faster, more accurate, tested and precise TB identification process, thereby increasing the effectiveness of medical interventions and the quality of life of patients.

2. Method

This section systematically explains the methods used in the research, the Tuberculosis (TB) identification process in this study is carried out by utilizing the *Convolutional Neural Network (CNN)* method and *DenseNet121 architecture through a* transfer learning *approach*. The research flow consists of five main stages: data collection, image preprocessing, model development, training and validation, and evaluation of results. All stages are run using the Python programming language, TensorFlow and Keras libraries, and the Google Colab computing environment, the research framework is described in Figure 2.1 as follows:

Figure 1. Research Framework

2.1. Datasets and Data Collection Processes

The dataset used was in the form of chest X-ray images of patients diagnosed with tuberculosis and patients with normal lungs. Data is obtained from the Kaggle platform for academic research purposes. The dataset has a JPEG image format with varying resolutions. All data were then categorized into two classes, namely tuberculosis as X-ray images of patients who have been validated to have Tuberculosis and Normal class, which is X-ray images of patients without indications of pulmonary abnormalities. The dataset is organized in a separate directory per class and is labeled according to the classification. The dataset sharing ratio is 80% of the training data and 20% of the test data.

2.2. Data Preprocessing

This stage aims to improve image quality and ensure input consistency before being fed into the CNN model. The preprocessing process resizes, which is to change the size of the entire dataset to 224×224 pixels to match the input of the DenseNet121 architecture, then normalize with the pixel value of each image normalized to the range of 0–1 by dividing each pixel by 255, thus accelerating convergence during training, then the normalized image is converted into a NumPy array so that it can be processed by TensorFlow and Keras, and finally data augmentation to reduce the risk of overfitting and improve generalization.

2.3. Building the CNN Model

The DenseNet121 architecture was chosen because of its ability to connect each layer with all previous layers so as to optimize gradient flow and efficiency of the parameters and models used are pre-trained on the ImageNet dataset. The step is to load the Pre-trained DenseNet121 without the final classification layer, then

freeze the initial layer to maintain the pre-trained weight, then add the Classification Layer with GlobalAveragePooling2D Dense(256, activation='relu') Dense(2, activation='softmax') to predict TB and Normal classes. The model was compiled using Loss Function (categorical crossentropy), Optimizer: Adam (learning rate = 0.0001), Evaluation Metrics: accuracy, precision, recall, F1-score

2.4. Training Model

The training process was carried out for 20 *epoches* with an *early stopping* mechanism to prevent overfitting. Validation is carried out at each epoch using validation data.

2.5. Model Performance Evaluation

Model evaluation is carried out on test data that has never been used in training. Evaluation metrics include, Accuracy, Precision, Recall, F1-score, ROC Curve and AUC to measure the sensitivity and specificity of the model. In addition to quantitative evaluation, visual analysis was carried out using Grad-CAM to identify the areas of imagery that the model focused on in decision-making. The results of future predictions can be compared with the diagnosis of a pulmonologist as an external validation to assess clinical suitability.

3. Results and Discussion

Based on the explanation of the Research Method, the purpose of this study is to build a model that is able to recognize the pattern of lung X-ray images to distinguish between TB and normal conditions. The training process was carried out using the transfer learning method with the DenseNet121 architecture, which utilizes the initial weight of the training on the dataset to accelerate convergence and improve accuracy, visualization of image samples from the images was also carried out to provide an overview of the training data used, providing a visual representation of the general differences between TB and Normal images, although visually these differences may be difficult to recognize especially people common. Based on this visualization, it can be seen that the TB class image generally has areas with different densities in the lungs, while the Normal class shows a relatively uniform lung pattern. This information is an important input for the DenseNet121 model training process to distinguish the two classes, here is an example of the image that will be used in the research as shown in Figure 3.1 below:

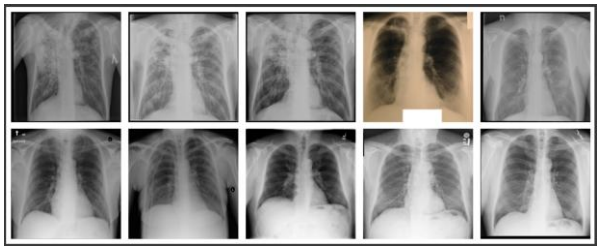

Figure 2. Example of an Image Dataset

We will start from the *pre-processing* stage, the purpose of this process is to ensure the quality and consistency of inputs. All images from the TBC and Normal classes are loaded, resized to 224×224 pixels according to the needs of *the DenseNet121* architecture, then normalized to the range of 0–1 so that the training process is more stable and quickly converges. Each image is labeled and converted to *a one-hot encoding format* before being divided into training data (80%) and test data (20%). This process ensures that the model receives input with a uniform format and optimal label representation for the classification of the two classes, Figure 3.2 below is an example of the pre-processing results.

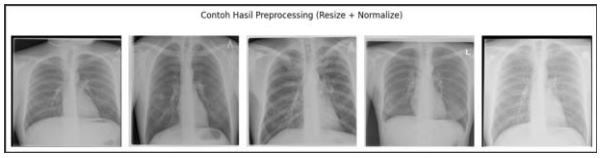

Figure 3.2 Pre-processing results

The model was developed using the DenseNet121 *pre-trained* on ImageNet, with the initial layer frozen to maintain the initial weight, and custom classification layers in the form of *GlobalAveragePooling2D*, *Dense(256, ReLU),* and *Dense(2, Softmax)* added. The optimizer used is Adam (*learning rate* 0.0001) with a categorical crossentropy loss function and evaluation metrics in the form of accuracy, precision, *recall*, and F1-score.

The training was conducted over 20 epochs and to prevent overfitting and maintain the generalization of the model, an EarlyStopping mechanism was used which would stop the training when there was no increase in the validation loss value in several consecutive epochs. The training data was enriched through image augmentation using rotation, shift, magnification, shear, and horizontal reversal techniques, so that the model could be more adaptive to variations in the position and orientation of the X-ray image. After the training process is completed, the model is evaluated using test data that is separate from the training data, which is 20% of the given dataset, the evaluation is carried out with various metrics such as accuracy, precision, recall, and F1-score with the following formula:

$$Accuracy = \frac{TP + TN}{TP + TN + FP + FN} \times 100\%$$

$$Precision = \frac{TP}{TP + FP} \times 100\%$$

$$Recall = \frac{TP}{FP + FN} \times 100\%$$

$$F1 - Score = \frac{2\ x\ Precision\ x\ Recall}{Precision + Recall} \times 100\%$$

The results of the evaluation showed an accuracy of 93%, with details as shown in table 1 as follows:

Table 1. Evaluation Results

Class	Accuracy	Recall	F1 Score	Support
TBC	0.95	0.95	0.95	19
Normal	0.91	0.91	0.91	11
Accuracy			0.93	30
Macro Avg	0.93	0.93	0.93	30
Weighted Avg	0.93	0.93	0.93	30

The results of the model evaluation for the TB class also showed an accuracy of 95%, indicating that most of the model's predictions for the TB class were correct, with a few *false* positives. A 95% recall indicates the model is capable of catching the majority of TB cases, although there are still some *false negatives*. An F1-score of 95% indicates a good balance between precision and recall. The results of the model evaluation for the normal class also showed a Precision of 91%, indicating that there are still some normal images that are misclassified as TB (*false positive*). However, the recall, which is also 91%, shows the model's ability to recognize most normal cases well. The F1-score of 91% confirms that although the precision is lower than that of the TBC class, the overall performance is still good, here is an example of a visualization of the correct and false identification results for each class shown in Figure 3.3, 3.4 and Figure 3.5.

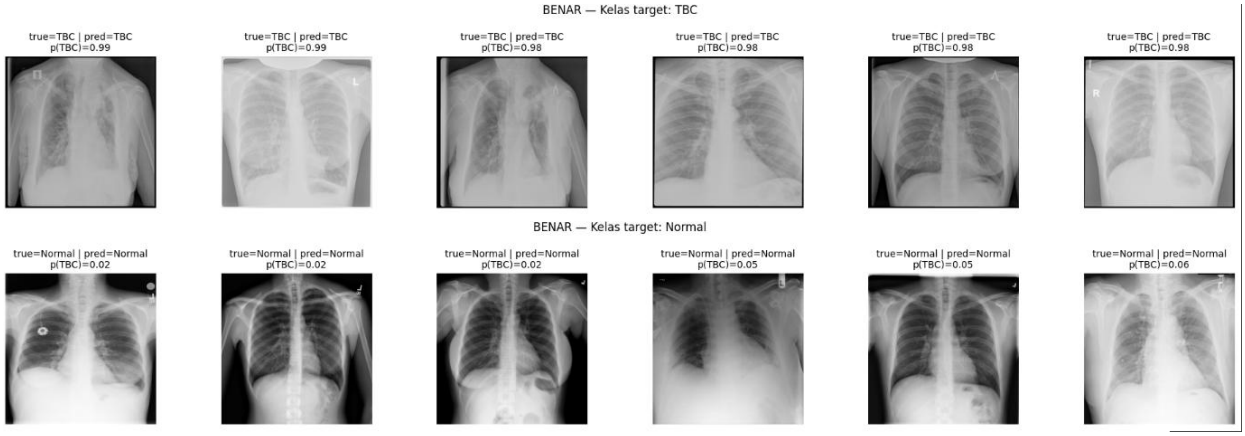

Figure 3.3 Visualization of Evaluation Results

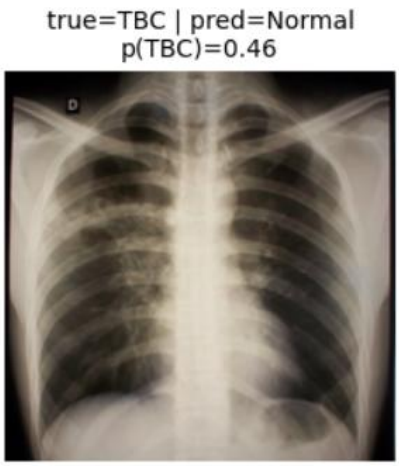

Figure 3.4 TB Error predicted as Normal

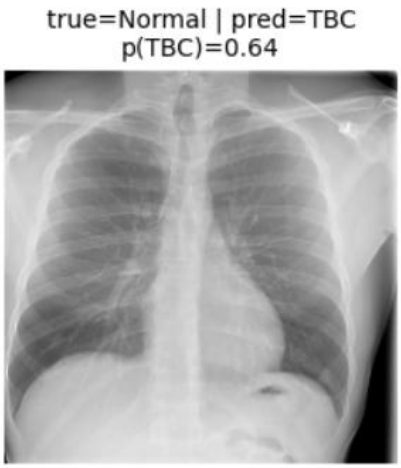

Figure 3.5 Normal Error is predicted as TB

Based on the results of Table 3.1 above, the model achieved an overall accuracy of 93% in the test data. This value shows that 9 out of 10 test images can be correctly identified by the constructed model, the accuracy obtained indicates that the transfer learning approach with the DenseNet121 architecture is able to capture visual patterns that are relevant in distinguishing the lung condition of TB-infected lungs from normal lungs.

Based on the information in the table, it was found that *the macro average* in the model was quite high, namely 89% to 93%, showing a fairly balanced average performance in both classes, without bias in one particular class, while *the weighted average* reached 93% which is identical to the accuracy indicating a fairly balanced distribution of test data so that it does not cause a large bias in the calculation.

This study also visualized the activation of the model using Grad-CAM. Grad-CAM is used to interpret the areas of the image that the model focuses on when performing the classification Figure 3.6 shows the results of the visualization of Gradient-weighted Class Activation Mapping (Grad-CAM) for five random samples of test data, consisting of X-ray images of patients with TB and Normal ground truth, as well as the predictions generated by the model.

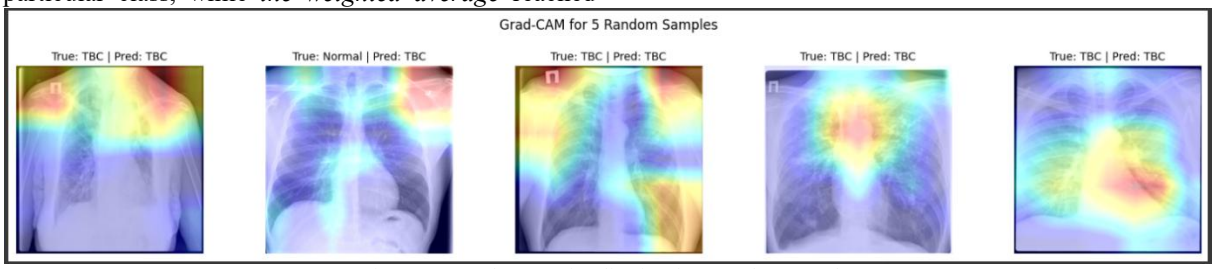

Figure 3.6 Grad-CAM visualization for 5 random samples

It is seen that in most of the images, the areas with red and yellow colors show the highest contribution rate to the model's prediction, followed by green and blue which indicate a lower contribution rate. In TB samples that are correctly predicted to be TB above, the highlighted areas tend to be in the upper and middle lungs, which is clinically relevant because TB infection often affects these parts. Normal samples with predictive results of TB still highlighted the lung area, although there were no visually obvious abnormalities to the casual observer. This can indicate the presence of false positives that may be caused by texture patterns or image artifacts that resemble the signs of tuberculosis in the training data.

Overall, this Grad-CAM visualization shows that the CNN model with the DenseNet121 architecture has a relatively precise focus on the lung area in making the prediction, not on the area outside the target organ. This supports the interpretation that the model leverages clinically relevant visual features, thereby increasing user confidence in the predicted results. However, the existence of false positive cases confirms the importance of further clinical validation before the model is implemented in a real medical environment.

4.Conclusion

This study developed a Tuberculosis (TB) detection model based on Convolutional Neural Network (CNN) with DenseNet121 architecture using a transfer learning approach. The model was trained using a chest X-ray imagery dataset obtained from Kaggle for TB and Normal patients who have gone through a pre-processing process including resize, normalization, conversion to array, and augmentation to improve generalization.

The test results showed that the model was able to achieve an accuracy of 93%, precision and recall of 95% in the TBC class, and precision and recall of 91% in the Normal class. The F1-score for both classes is in the range of 91–95%, which indicates a balanced performance between sensitivity and specificity. Grad-CAM visualizations show that the model consistently focuses attention on areas of the lungs, particularly the upper and middle areas that are clinically relevant to TB indications.

These findings prove that DenseNet121 is able to recognize significant visual patterns on X-ray images to distinguish TB-infected lungs from normal lungs. The application of this model has the potential to help the initial screening process quickly and accurately, so that it can support medical decision-making, especially in health facilities with limited resources.

However, false positives were still found indicating the need for further clinical validation and the possibility of adding training data from local sources to improve accuracy in real conditions. Further research is suggested to expand the number of datasets, combine images from various hospital sources, and explore the integration of this model with disease identification decision support systems so that it can be implemented effectively in health services.

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Biographies of Authors

Fajri Nugraha, S.Kom was born in Padang Panjang, West Sumatra, on October 28, 1996. He completed his Bachelor's degree (S1) in Computer Information Systems at STMIK Indonesia Padang, West Sumatra, and graduated with a Bachelor of Computer Science (S.Kom) with 3.57 GPA in 2018. Currently, he is pursuing a Master's program in Informatics Engineering (M.Kom) at Universitas Putra Indonesia YPTK Padang, which began in early 2024. In his professional career, he serves as an IT Support at Padang State University (Universitas Negeri Padang) from 2018 until 2019 and now as a Network Administrator at Islamic State University Imam Bonjol Padang (UIN Imam Bonjol Padang), where he is responsible to make sure network availability for the universities.

Dr. Ir. Sumijan, M.Sc was born in Nganjuk on May 7, 1966. He received the Bachelor Degree in Informatics Management in 1991 from Universitas Putra Indonesia YPTK, Master of Information Technology in 1998 from University Technology Malaysia (UTM). He completed Doctorate of Information Technology as Medical Image Expertise from Gunadarma University in December 2015 He is member of ACM (23145751). Scopus Id is 57194787076. Email: soe@upiyptk.org

Dr. Rini Sovia, S.Kom., M.Kom was born in Solok, April 5, 1976. Lecturer at Universitas Putra Indonesia YPTK Padang. He completed his education in informatics management in 1999 and his master's degree in informatics engineering in 2006. He is currently earning a doctorate in information technology in 2023. His areas of expertise include artificial intelligence (AI), expert systems (ES), data mining (DM), decision support systems (DSS), and databases. He can be reached at email: rini_sovia@upiyptk.ac.id