JURTEKSI (Jurnal Teknologi dan Sistem Informasi) ISSN 2407-1811 (Print)
Vol. XII No 3, June 2026, hlm. 523 – 530 ISSN 2550-0201 (Online)
DOI: http://dx.doi.org/ 10.33330/jurteksi.v12i3.4371
Available online at http://jurnal.stmikroyal.ac.id/index.php/jurteksi

COMPARISON OF RESNET-50 AND DENSENET-121 CNNARCHITECTURES FOR MALARIA IMAGE CLASSIFICATION

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Abstract: Malaria remains a major global health problem, particularly in tropical countries such as Indonesia. Accurate early diagnosis is essential for reducing malaria-related morbidity and mortality. Conventional microscopic examination is time-consuming, highly dependent on expert personnel, and prone to human error. This study compares the performance of two Convolutional Neural Network (CNN) architectures, ResNet-50 and DenseNet-121, for malaria image classification. The Cell Images for Malaria dataset provided by the National Institutes of Health (NIH) through Kaggle was used, consisting of 27,558 microscopic blood cell images categorized into Parasitized and Uninfected classes. The dataset was divided into 80% training data and 20% testing data. Image preprocessing included resizing to 224 × 224 pixels, normalization, labeling, and data augmentation using RandomFlip, RandomRotation, RandomZoom, and RandomContrast. Experimental results showed that the ResNet-50 model trained for 100 epochs achieved the highest performance, with an accuracy of 95.54% and precision, recall, and F1-score of 0.96. The confusion matrix indicated 5,272 correctly classified images out of 5,510 testing samples. These findings demonstrate that ResNet-50 outperformed DenseNet-121 and has strong potential for supporting accurate, reliable, and efficient computer-aided malaria diagnosis based on microscopic blood smear images.

Keywords: computer-aided diagnosis; convolutional neural network (CNN); densenet-121; early detection; image classification; malaria; microscopic blood smear images; resnet-50;

Abstrak : Malaria masih menjadi masalah kesehatan global yang serius, terutama di negara tropis seperti Indonesia. Diagnosis dini yang akurat sangat penting untuk menurunkan angka morbiditas dan mortalitas. Metode konvensional berupa pemeriksaan mikroskopis memiliki keterbatasan karena memerlukan waktu yang relatif lama, bergantung pada tenaga ahli, dan berpotensi menimbulkan kesalahan manusia. Penelitian ini bertujuan membandingkan kinerja arsitektur Convolutional Neural Network (CNN) yaitu ResNet-50 dan DenseNet-121 dalam klasifikasi citra malaria. Dataset yang digunakan berasal dari Cell Images for Malaria yang disediakan oleh National Institutes of Health (NIH) melalui platform Kaggle, terdiri dari 27.558 citra dengan pembagian 80% data latih, 20% data validasi. Tahap praproses meliputi cleaning, resizing citra menjadi 224×224 piksel, normalisasi, labeling, serta data augmentasi menggunakan RandomFlip, RandomRotation, RandomZoom, dan RandomContrast. Hasil pengujian menunjukkan bahwa model ResNet-50 pada epoch 100 memperoleh akurasi sebesar 95,54% dengan nilai precision, recall, dan F1-score masing-masing sebesar 0,96. Confusion matrix menunjukkan jumlah prediksi benar sebanyak 5.272 dari total 5.510 data uji. Hasil ini menunjukkan bahwa arsitektur CNN mampu mengklasifikasikan citra malaria dengan tingkat akurasi yang tinggi dan memiliki kemampuan generalisasi yang baik terhadap data baru. Penelitian ini memberikan kontribusi dalam evaluasi performa arsitektur CNN untuk mendukung pengembangan sistem diagnosis malaria berbasis citra mikroskopis yang lebih cepat dan akurat.

Kata kunci: convolutional neural network (CNN); citra mikroskopis hapusan darah; densenet-121; diagnosis berbantuan komputer; deteksi dini; klasifikasi citra; malaria; resnet-50

INTRODUCTION

Malaria remains a major global health problem, particularly in tropical countries such as Indonesia. The disease is caused by Plasmodium parasites transmitted through the bites of infected Anopheles mosquitoes [1]. Early detection and accurate diagnosis are essential to reducing malaria-related morbidity and mortality. However, conventional diagnostic methods, such as microscopic examination, have several limitations, including dependence on experienced personnel, time-consuming procedures, and susceptibility to human error [2].

Recent studies have increasingly applied deep learning techniques to automate malaria diagnosis through the analysis of microscopic blood smear images. Convolutional Neural Networks (CNNs) have demonstrated remarkable capability in automatically extracting image features, resulting in high classification performance. Nevertheless, several studies have reported that the generalization capability of CNN models remains a challenge, particularly when evaluated on different datasets. Therefore, selecting a CNN architecture that provides an appropriate balance between classification accuracy, model stability, and generalization capability has become an important aspect in developing artificial intelligence-based malaria diagnosis systems [3]. CNN has been widely adopted for medical image analysis and has proven effective in classifying microscopic malaria blood smear images [4].

Numerous studies have demonstra ted the effectiveness of CNN-based approaches for malaria detection. Pratiwi et al [5] eported that a CNN model achieved a validation accuracy of 95.83% using the RMSProp optimizer. Similarly, Jameela et al. [6] showed that deep learning combined with transfer learning significantly improved malaria detection performance from microscopic blood smear images. The use of pre-trained models enabled more effective training, particularly when the available training data were limited, resulting in better classification performance than conventional approaches. In addition, Sari et al. [7] chieved an AUC-ROC value of 0.986 with an overall accuracy of 95.5%, demonstrating the effectiveness of CNN models in malaria image classification.

The development of more advanced CNN architectures has further improved classification performance. Purnomo et al. [8] reported that EfficientNetV2S achieved an accuracy of 94% with precision, recall, and F1-score values of 96%, although the model exhibited a risk of overfitting due to limited training data. Hemachandran et al. [9] demonstrated that ResNet-50 outperformed conventional CNN and MobileNetV2 by achieving the highest validation accuracy of 96.70%. Likewise, Muhandisin and Azhar [10] successfully improved the performance of ResNet-50 to an accuracy of 98% through transfer learning and fine-tuning techniques.

Despite these promising results, previous studies have reported inconsistent findings regarding the comparative performance of ResNet-50 and DenseNet-121. Kareem et al. [11] found that DenseNet outperformed ResNet-50 in a federated learning environment, achieving an accuracy of 92.13% and an F1-score of 89.11%. In contrast, Laghari et al. [12]

demonstrated that transfer learning with several pre-trained CNN architectures produced competitive malaria classification performance, with ResNet-50 being one of the most effective models based on accuracy, precision, recall, and F1-score. These inconsistent findings indicate that the superiority of one architecture over another has not yet been conclusively established.

Based on the literature review, no consensus has been reached regarding the most effective CNN architecture for malaria image classification. Furtherm ore, most previous studies focused on evaluating a single model or comparing different models under different datasets, experimental settings, and training confi gurations, making objective comparisons difficult. Consequently, there is a need for a direct comparison of ResNet-50 and DenseNet-121 using the same dataset, preprocessing procedures, and training configuration.

This study compares the performance of ResNet-50 and DenseNet-121 for microscopic malaria blood smear image classification. These architectures were selected because they employ fundamentally different feature-learning strategies. ResNet-50 utilizes residual connections to overcome the vanishing gradient problem in deep neural networks, whereas DenseNet-121 employs dense connectivity that facilitates efficient feature reuse and strengthens information flow across network layers. The novelty of this study lies in the direct comparison of both architectures under identical experimental conditions, including the same malaria dataset, preprocessing pipeline, and training parameters, thereby providing a more objective evaluation of their classification performance.

The findings of this study are expected to provide valuable insights into the selection of an effective CNN architecture for malaria image classification and to support the development of faster, more accurate, and more reliable artificial intelligence-based malaria diagnosis systems.

METHOD

This study employed a deep learning approach based on Convolu tional Neural Network (CNN) architec tures for malaria image classification. The dataset used was the Cell Images for Malaria dataset provided by the National Institutes of Health (NIH) and publicly available through the Kaggle platform. The dataset consists of 27,558 red blood cell images categorized into two classes: Parasitized and Uninfected. To preserve the class distribution in each subset, the dataset was divided using a stratified sampling strategy into 80% training data and 20% testing data.

The research workflow is illustra ted in Figure X. The study began with the collection of the malaria image dataset, followed by splitting the dataset into training and testing sets. Subsequ ently, a preprocessing stage was perform ed, including image resizing to 224 × 224 pixels and pixel value normalization to the range of [0,1]. Data augmentation techniques were also applied to increase the diversity of the training samples and reduce the risk of overfitting. The augme ntation process included RandomFlip, RandomRotation, RandomZoom, and RandomContrast.

Two pre-trained CNN architec

tures, ResNet-50 and DenseNet-121, were employed in this study. Both models were initialized with weights pre-trained on the ImageNet dataset. ResNet-50 utilizes a residual learning mechanism that enables the training of very deep neural networks by alleviating the vanishing gradient problem. In contrast, DenseNet-121 adopts a dense connectivity mechanism in which each layer receives feature information from all preceding layers, thereby improving feature reuse and enhancing feature propagation throughout the network.

Both architectures were implemented using the transfer learning approach. The original classification layer of each pre-trained model was replaced with a fully connected layer consisting of two output neurons, representing the Parasitized and Uninfected classes. A Softmax activation function was applied to the output layer to generate the probability distribution for each class.

The models were trained using the Adam optimizer with an initial learning rate of 0.0001 and a batch size of 32. Training was conducted using 10, 50, and 100 epochs to evaluate the effect of the number of training iterations on model performance. In addition, an Early Stopping callback was employed to prevent overfitting by monitoring the validation loss during the training process.

Model performance was evaluated using four standard classification metrics: accuracy, precision, recall, and F1-score, which were calculated based on the values of True Positive (TP), True Negative (TN), False Positive (FP), and False Negative (FN). The evaluation metrics are defined as follows:

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

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

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

$$F1-Score = \frac{\mathrm{2x\ (Precision+Recall)}}{\mathrm{Precision+Recall}} \quad (4)$$

In addition to these evaluation metrics, a confusion matrix was used to analyze the distribution of correct and incorrect predictions for each class. Finally, the performance of ResNet-50 and DenseNet-121 was compared to determine the most effective architecture for malaria image classification.

RESULT AND DISCUSSION

Resnet-50

Training of the ResNet-50 model under 10, 50, and 100 epochs showed a similar learning pattern. The model rapidly achieved validation accuracy of approximately 94–95% within the first 10 epochs. Increasing the number of epochs improved the training accuracy to over 99%; however, the validation accuracy remained relatively unchanged, indicating mild overfitting. The ReduceLROnPlateau callback successfully stabilized the optimization process, while EarlyStopping prevented unnecessary training after convergence. The best testing accuracy of 95.54% was obtained at 100 epochs, although the improvement over 50 epochs was marginal.

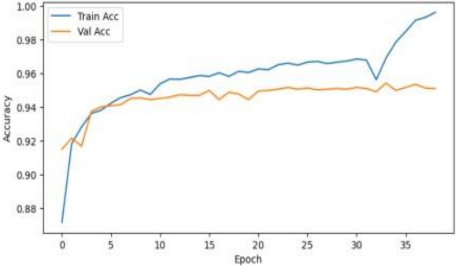

Image 1. Resnet-50 Epoch 100

The experimental results indicate that the ResNet-50 architecture achieved optimal performance during the early stages of training. At 10 epochs, the model had already attained stable validation accuracy of approximately 94%–95% due to the effectiveness of transfer learning, although further training gradually introduced signs of slight overfitting. When trained for 50 epochs, the training accuracy increased to over 97%, while the validation accuracy remained around 95%, resulting in a testing accuracy of 95.5%, which was consistent with the validation performance. At 100 epochs, although the training accuracy exceeded 99% following the fine-tuning process, the validation accuracy remained unchanged at approximately 95%, indicating a more pronounced degree of overfitting. Overall, the ResNet-50 model achieved its optimal performance within 10–50 epochs, and extending the training to 100 epochs did not produce a significant improvement in the model's generalization capability but instead increased the tendency toward overfitting. The performance comparison of the ResNet-50 model across the three epoch configurations is presented in Table 1.

Table 1. Resnet-50

Epoch	**Precision**	**Recall**	**F1-Score**	**Accuracy**
10	0.95	0.95	0.95	0.95
50	0.96	0.96	0.96	0.96
100	0.96	0.96	0.96	0.96

Densenet-121

The DenseNet-121 architecture consists of approximately 7.3 million parameters, including about 262 thousand trainable parameters, while the remaining parameters are inherited from the pre-trained ImageNet weights through transfer learning. The model processes 224 × 224 × 3 input images using convolution, batch normalization, ReLU activation, max pooling, and densely connected blocks that promote feature reuse and reduce the vanishing gradient problem. The extracted features are then passed through a Global Average Pooling layer, a Dense layer with 256 neurons, a Dropout layer, and a Softmax output layer for binary classification of Parasitized and Uninfected images. Training the DenseNet-121 model with 10, 50, and 100 epochs demonstrated stable learning performance. At 10 epochs, the model achieved a training accuracy of 93.82% and a validation accuracy of 93.94%, indicating rapid convergence without noticeable overfitting. Extending the training to 50 epochs further improved the training accuracy to approximately 95.6%, while the validation accuracy remained stable between 94% and 94.7%. The ReduceLROnPlateau callback optimized the learning process by gradually decreasing the learning rate, whereas EarlyStopping automatically terminated training at epoch 37 after the validation loss ceased to improve.

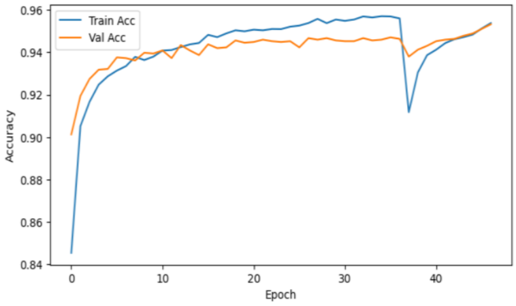

Image 2. Densenet-121 Epoch 100

When trained for 100 epochs, the training accuracy exceeded 99% following the fine-tuning stage; however, the validation accuracy remained around 95%, indicating mild overfitting. The final testing accuracy reached 95.54%, demonstrating that DenseNet-121 maintained good generalization performance despite the additional training epochs. Overall, the experimental results indicate that DenseNet-121 achieved its optimal performance within 10–50 epochs, while extending the training to 100 epochs provided minimal improvement in classification performance and mainly increased the tendency toward overfitting. The comparative performance of DenseNet-121 across different epoch settings is presented in Table 2.

Table 2. Model Densenet-121

Epoch	Precision	Recall	F1-Score	Accuracy
10	0.9478	0.9486	0.9473	0.9479
50	0.9521	0.9518	0.9524	0.9521
100	0.9540	0.9537	0.9542	0.9539

Comparison Of Model Perfomance

This study compared the performance of two CNN architectures, ResNet-50 and DenseNet-121, for classifying malaria cell images into two categories: Parasitized and Uninfected. Model performance was evaluated using accuracy, precision, recall, F1-score, and the confusion matrix. The experimental results indicate that both architectures achieved high classification performance. As shown in Figure 7, ResNet-50 consistently outperformed DenseNet-121, achieving an accuracy of 96% across the 10-, 50-, and 100-epoch training configurations, whereas DenseNet-121 maintained a stable accuracy of 95%. These findings suggest that both models converged during the early stages of training, as increasing the number of training epochs did not lead to further improvements in classification performance. Overall, ResNet-50 demonstrated superior classification accuracy, while DenseNet-121 remained a reliable alternative due to its stable and consistent performance.

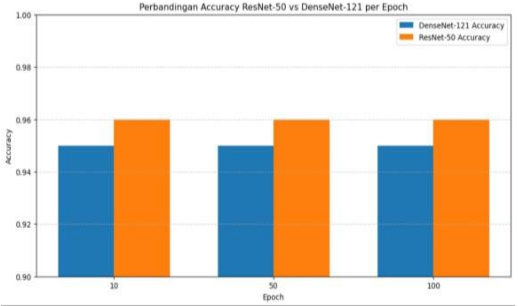

Image 3. Comparasion Of Model

CONCLUSION

This study demonstrates that the ResNet-50 architecture outperformed DenseNet-121 in the classification of malaria cell images. In addition to achieving higher classification accuracy, ResNet-50 exhibited more stable performance across all epoch configurations. These findings indicate that the residual connection mechanism employed by ResNet-50 enhances the learning process, enabling the model to achieve better generalization capability on malaria cell images than DenseNet-121 under the experimental conditions of this study.

From a practical perspective, the findings suggest that the ResNet-50 model has the potential to support microscopy-based malaria diagnosis by providing faster and more consistent image classification. The proposed model can serve as a decision-support tool for medical professionals during the initial screening process, thereby improving the efficiency of identifying malaria-infected blood cells. However, the model is not intended to replace clinical diagnosis but rather to complement existing diagnostic procedures by improving the accuracy and efficiency of malaria screening.

Despite these promising results, this study has several limitations. First, the experiments were conducted using only a single public dataset containing two classes (Parasitized and Uninfected), limiting the model's ability to classify different Plasmodium species and parasite developmental stages. Second, the study compared only two CNN architectures and did not evaluate more recent deep learning models or perform comprehensive hyperparameter optimiza tion.Future research is recommended to employ larger and more diverse datasets covering multiple Plasmodium species and parasite developmental stages. In addition, future studies should compare ResNet-50 and DenseNet-121 with more advanced deep learning architectures, such as EfficientNet, Vision Transformer (ViT), and ConvNeXt, while incorporating comprehensive hyperpara meter optimization to further improve classification performance and model generalization. Furthermore, evaluating the proposed models using external datas ets from different healthcare institutions would provide a more comprehensive assessment of their robustness and applica bility in real-world clinical settin gs.ResNet-50 dengan arsitektur CNN modern

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