



ResNet101 Model Performance Enhancement in Classifying Rice Diseases with Leaf Images

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Abstract

Indonesia is the fourth biggest rice producer in Asia with its production accounting for 35.4 million metric tons yearly. This figure can increase unless rice crop failure is resolved. Identifying rice diseases, however, may serve as an approach to minimizing the risk of crop failure. The classification to detect rice diseases was previously researched using ResNet101 method with 100% accuracy. Despite this perfect accuracy, this approach does not come without an issue, where the prediction is not yet optimal for each label and loss results which are regarded as too high due to overfitting. Departing from this issue, this research aims to improve the model by reducing the layer complexity of the model and comparing two layers structures of the model, two different data, and the ResNet101 model. The performance resulting from the model could be enhanced with the structuring of simple architectural layers. Despite the small quantity of dataset, the model performance can yield 100% accuracy in the classification of rice diseases with a loss value of 2.91%. The model performance in this research experienced a 2.7% increase at the loss value and it could accurately classify the type of rice diseases according to leaf images on each label. The problem solved by this research is that ResNet101 is able to classify rice disease accurately even with a small amount of data by utilizing the appropriate layer arrangement with data requirements. In addition, the overfitting that occurred in previous research can also be resolved properly. This matter proves that the correlation between the layers of the model with the amount of data is very influential.

Keywords: enhancement; performance; classification; disease; rice; resnet101

1. Introduction

The Indonesian economy heavily relies on agricultural sectors. In Indonesia and some other Asian countries, rice has been the main staple food. This condition has encouraged Indonesia to keep rice production stable. With the innovation in computer science, combined with agricultural sectors, Indonesia is expected to resolve rice disease issues [1]. Rice diseases threaten the sustainability of rice production as the main contributor to the staple food in Indonesia. Leaf blight, brown spot, and leaf smut are some of the diseases attacking rice plants, [2] and they require different treatments. Crop failure may hamper if treatments are delayed, causing the falling production of rice plants.

The identification of rice diseases can be performed by utilizing computer technology, specifically Artificial Intelligence (AI). The image-based introductory method can resolve this problem. Artificial Intelligence keeps growing in line with the application of Machine Learning. Deep Learning with algorithms works more like a human brain by utilizing an artificial neural

network [16]. Deep Learning is deemed to be excellent over Machine Learning [3]. Convolution Neural Network (CNN) is an excellent algorithm of Deep Learning applied compared to Machine Learning [4]-[7]. One of the architectural models of the method of CNN is Residual Network (ResNet) [8]. There are several ResNet existing in the method of CNN, consisting of ResNet-50, ResNet-101, ResNet-152, and many more [9].

Several studies have also proven the excellence of this architecture of CNN as reported in the research [10] on the classification of diseases attacking wheat leaves. The best scenario discussed in the research was related to the 80:20 ratio, with the data consisting of 232 training data and 59 test data by using the architecture of ResNet 152V2. The accuracy level reached 98%. The classification of rice diseases was once studied by employing the CNN method as in research [11].

The research classified three types of diseases attacking rice leaves, including Bacterial Leaf Blight, Brown Spot, and Leaf Smut. This classification used K-Means

based on centroid feeding to perform segmentation, followed by the omission of the green pixel on the data and other augmentation processes. By applying the algorithm Support Vector Machine (SVM) in the classification process, the research reached 93.33% and 73.33% accuracy for training data and validation data respectively.

Another relevant study proved the excellence of ResNet as in the research [12] on the excellence of ResNet101 in classifying rice diseases according to the images of leaves. The test results show that ResNet101 is capable of giving 100% accuracy according to validation data with the loss value representing 5.61% in 120 datasets. This accuracy was obtained from the application of Fully Connected Layer.

Dense Layer 512 was put as the first layer with the activation of 'relu', added with BatchNormalization layer and two Dropout layers as much as 0.7 and 0.7 respectively, while the second layer was composed of Dense Layer 64 with 'relu' as the activation, which was further added with BatchNormalization layer and two Dropout layers as much as 0.3 and 0.3 respectively. The layer was ended with Dense Layer with the output consisting of three classes by using the activation of 'softmax'.

High accuracy does not guarantee accurate classification in each label as in research [12]. This research carries shortcomings in terms of the classification of each image, which may be due to overfitting. Overfitting could result from irrelevant, too accurate or too complex training data, leading to unexpected results when new data were input [13][14].

The study [15] asserts that the more features a model has, the more complex the model will be created, allowing for overfitting because the maximum accuracy is reached during the training data process, but during the testing, the accuracy is relatively lower than the accuracy of the training.

This research aims to resolve the existing shortcomings in research [12] by lowering the loss value, reducing overfitting, and performing accurate classification according to limited data as done in research [12]. This can be performed by changing the layer structure in the model and replacing compiling types in the model. Lowering the learning rate value was also performed in this research to improve the model performance.

As reported in research [17], the use of a reduced learning rate will give more details of the model in the evaluation of the outcomes of the process of training data. The use of more data was also applied in this research. This application was intended to investigate the worthiness of the model made in research [12] and this research to apply more numbers of data

2. Research Methods

The stages of this research are presented in Figure 1. This research began with the collection of two different data, followed by data split into training and validation data in data preprocessing. Data augmentation was performed to maximize the information in the data before processing. This condition resulted in new data and could equalize models so that they could recognize data of all kinds [5]. Following the data augmentation, the model was trained and ended with model evaluation.

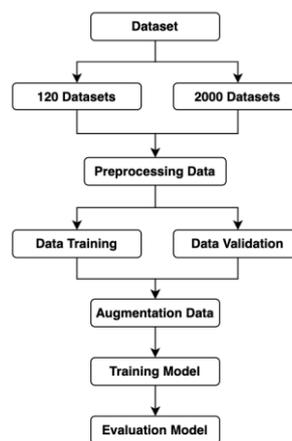


Figure 1. Research Method

2.1 Dataset

Manuscripts Dataset used in this research consisted of two different kinds of datasets. Dataset A was divided into three classes of disease on rice leaves. The class consisted of Bacterial leaf blight, brown spot, and leaf smut with each class of the data representing 40 datasets. The quantity of dataset A is presented in Figure 2 and Figure 3, as one of the samples of each class, while dataset B consists of four classes with the data in each class representing 500 datasets. The class of rice leaves in Data B consisted of BrownSpot, Healthy, Hispa, and LeafBlast. The quantity of the data used in dataset B is presented in Figure 4 and Figure 5, representing one of the samples in each class. These two datasets were obtained from an open repository site, Kaggle, with the title Rice Leafs, and UCI Machine Learning Repository with the title Rice Leaf Diseases Dataset.

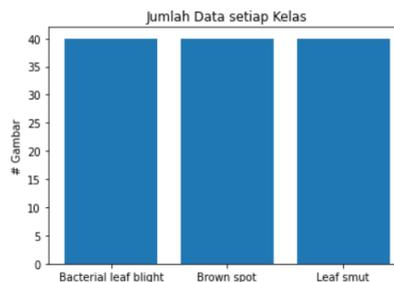


Figure 2. Characteristic Dataset A



Figure 3. Sample Dataset A

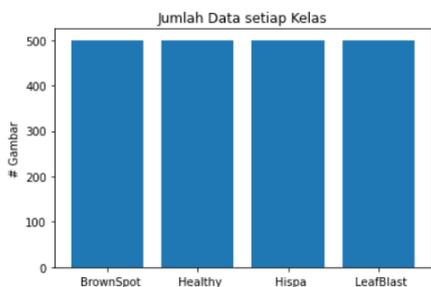


Figure 4. Characteristic Dataset B



Figure 5. Sample Dataset B

2.2 Architectural Model

The Pre-trained model in transfer learning is referred to as ResNet101 as applied in this research. This model involves the addition of three new architectural layers to the Fully Connected Layer. Combined layer structure of ResNet101 and Fully Connected Layer is presented in Figure 6, while the additional layer applied in the model is presented in Table 1. This additional layer consisted of three layers. The first layer involved Dense Layer 128 with 'relu' activation, added with BatchNormalization layer and one Dropout layer of 0.3. The second layer used was Dense Layer 32 and Dropout layer of 0.1. The last layer used was the Dense Layer with the output consisting of three classes with 'softmax' activation.

The simple application of layers in the dataset of small quantities can reduce the likelihood of overfitting so that the model can perform accurate classification [13]-[15]. The use of BatchNormalization was also used in the model to obtain a maximum training model capable of minimizing overfitting [18]. To prevent overfitting, dropout and adam optimizer were used, so that accuracy yielded by the model could be increased [5].

The function of loss in the model evaluation in this research used mean absolute error [19]. A learning rate of 0.0001 was used in the compiling model with the hope that the model could perform a more detailed evaluation in the process of data training [17].

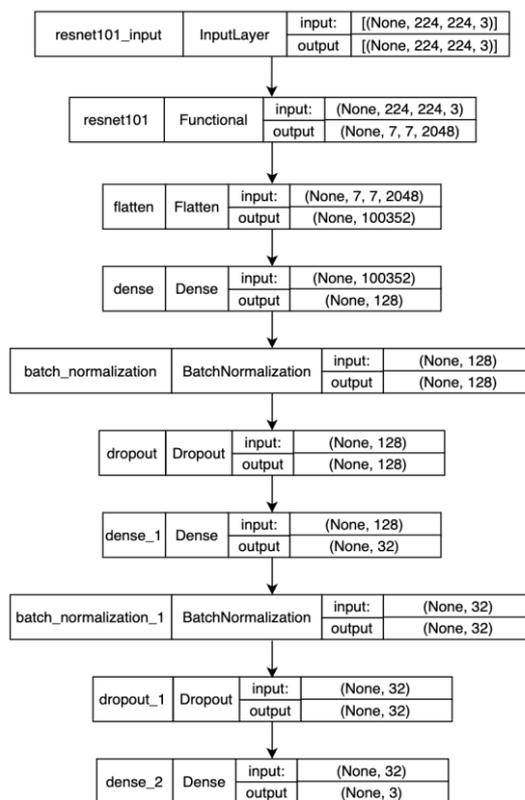


Figure 6. ResNet101 Architectural Model

Table 1. The Architecture of Model Additional Layer

Layer	Output Shape	Param
resnet101 (Functional)	(None,7,7, 2048)	42658176
flatten (Flatten)	(None, 100352)	-
dense (Dense)	(None, 128)	12845184
batch_normalization (BatchNormalization)	(None, 128)	512
dropout (Dropout)	(None, 128)	-
dense_1 (Dense)	(None, 32)	4128
batch_normalization (BatchNormalization)	(None, 32)	128
dropout_1 (Dropout)	(None, 32)	-
dense_2 (Dense)	(None, 3)	99
Total params: 55,508,227		
Trainable params: 12,849,731		
Non-trainable params: 42,658,496		

2.3. Data Augmentation

Data augmentation aims to give a variety of images, making the model recognize data unconditionally and improve the accuracy of the model [5],[20]. Preprocessing_function became the parameter in this research. This function was obtained from the library available in Tensorflow with the rotation range of 0.3, zoom of 0.4, and horizontal_flip with the True value.

2.4 Testing Scenario

This research employed two datasets and different classes. For an experiment, 120 data were used with the total data for each class accounting for 40 data. Each

class consisted of Bacterial leaf blight, Brown spot, and Leaf smut. The second experiment used 2000 data comprising 500 data for each class. The classes in the second experiment included BrownSpot, Healthy, and LeafBlast. This experiment was conducted to compare the worthiness of the layer structures between this research and research [12].

Data splitting in this research used a 9:1 ratio, consisting of 90% training data and 10% validation data. This data splitting was intended to balance this research and the previous research [12] by using the same validation data. The results of the data splitting in the first experiment are presented in Table 2 and the second experiment can be seen in Table 3.

Table 2. Data Splitting of the First Experiment

Data	Quantity
Training Data	108
Validation Data	12

Table 3. Data Splitting of the Second Experiment

Data	Quantity
Training Data	1800
Validation Data	200

Callback and Early Stopping are the two models functioning to detect the training process when it is in progress. The application of Callback and Early Stopping controls the value of vall-loss by using the learning rate determined. These two methods can also solve overfitting in the model [21],[22]. Considering this definition, this research employed the function of Callback. However, the functions were different, where the first Callback was intended to control the value of vall-loss during the data training process (epoch) by utilizing Early Stopping. The second Callback saved every complete model iteration if the accuracy increased.

3. Results and Discussions

The stages of the research results in clarifying the diseases identified on rice leaves are discussed in this section. The first stage involved data splitting after the data were collected as described earlier. Following the split of the data into training and validation data, data augmentation was performed for the two data. This augmentation process consisted of: rotation_range = 30, zoom_range = 0,4, horizontal_flip = True, batch_size = 64, class_mode = categorical, color_mode = rgb, shuffle = True and target_size = 224 x 224. The next stage was the making of the first Callback by using EarlyStopping to control the value of vall-loss when the epoch was in progress. The second Callback aimed to save every complete model iteration if the model accuracy increased.

The graphs showing accuracies for the first experiment with different layer structures and with 120 datasets are

presented in Table 4, while the second experiment is shown in Table 5 with different layers using 2000 datasets. This graph resulted from a complete iteration process up to the 100th epoch. Axis X on the graph shows the quantity of the iteration process of a model, while axis Y shows the level of accuracy with a value range of 0 to 1. The results described in the graphs show that the layers used in this research with 120 datasets gave a better result compared to that of the previous research. The accuracy reached 100%, where the overfitting was resolved.

Table 4. Comparisons of Accuracy in Dataset A

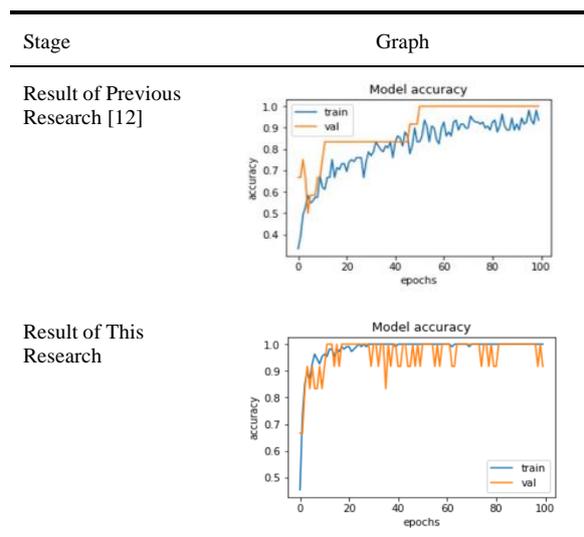
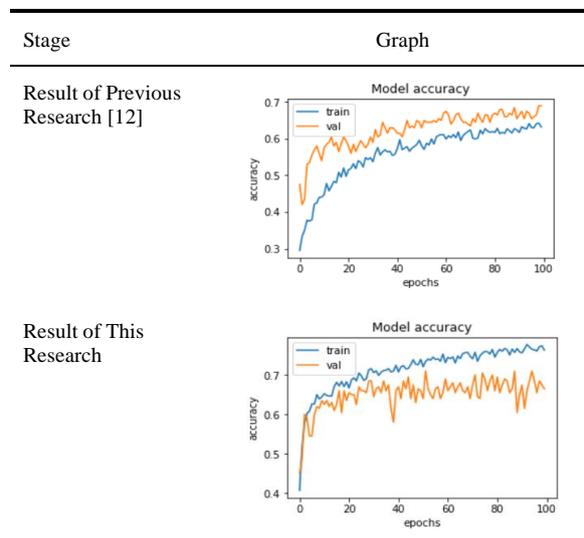


Table 5. Comparisons of Accuracy in Dataset B



The graphs showing the loss for the first experiment with the comparisons of different layer structures and 120 datasets are presented in Table 6, while the graphs of the second experiment are in Table 7 with different layer structures and 2000 datasets. The X axis in the graphs shows the process of model iteration taking place in 100 epochs. Axis Y represents the loss value with the top limit of 2.5 and the smallest target loss of

0. The loss graphs prove that the application of simple layers with 120 datasets as performed in this research could also give a better result. The smallest loss value was obtained from the iteration with 100 epochs, accounting for 2.91%. This proves that there was a reduction of loss from 5.61% to 2.91% (with a 2.7% increase in model performance).

Table 6. Comparisons of Loss Graphs in Dataset A

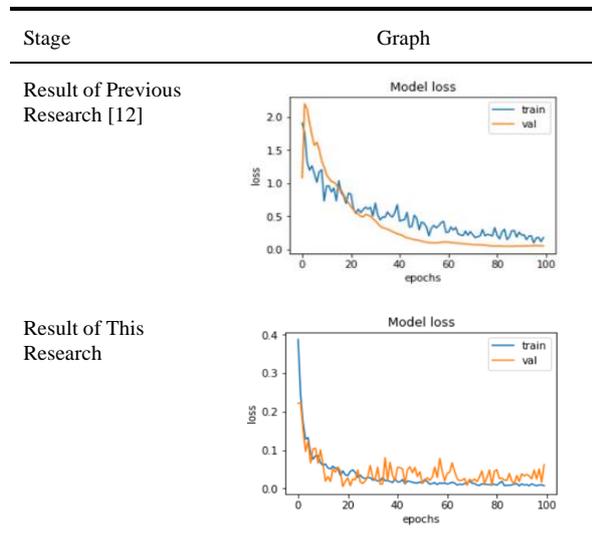
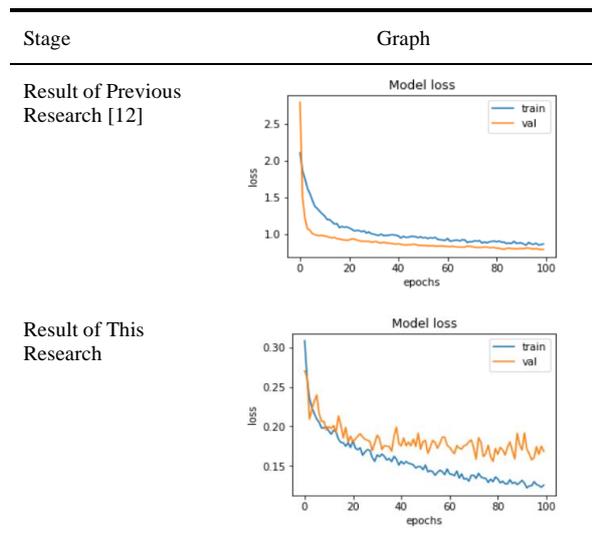


Table 7. Comparisons of Loss Graphs in Dataset B



The next stage of this research was an evaluation of the models. This stage used a confusion matrix table to measure the results of the model performance to find out the level of accuracy in correctly predicting or making errors in the prediction according to the total of existing data [23]. The results derived from the confusion matrix of the first experiment in comparing the layers of the models were different from those of the previous research, as shown in Table 8 with 120 datasets. These results consisted of three classes, including Bacterial leaf blight, Brown spot, and leaf smut. The second experiment with different layers in

the models and 2000 datasets can be seen in Table 9. The confusion matrix of the two layers in 120 datasets gave the same result of 1.00. This result can be seen from the value of the best val_accuracy when the iteration model process was in progress. If the accuracy is close to 1 or has the value of 1, the model performs well; if the accuracy is close to 0, this model indicates poor performance [24].

Table 8. Comparisons of Confusion Matrix in Dataset A

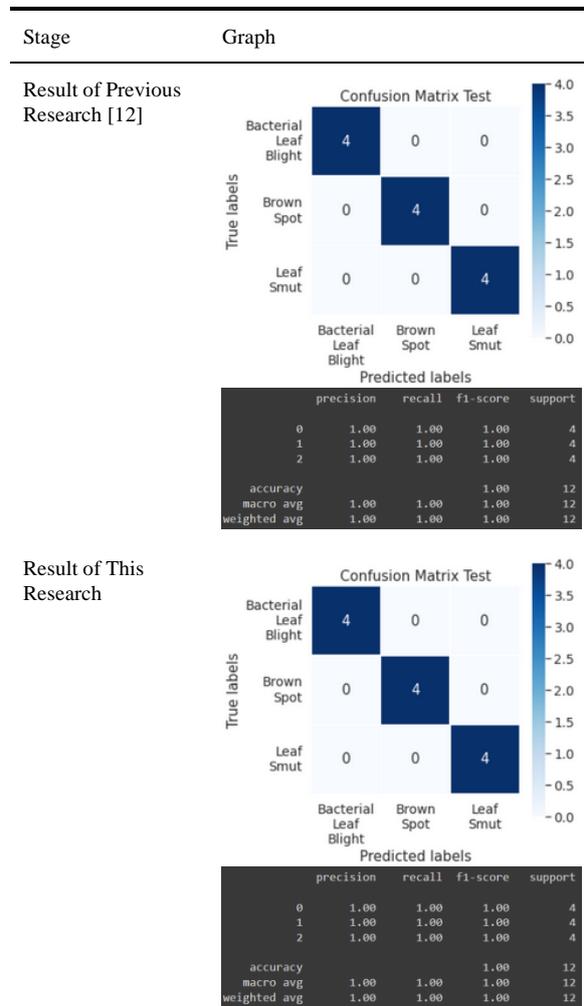
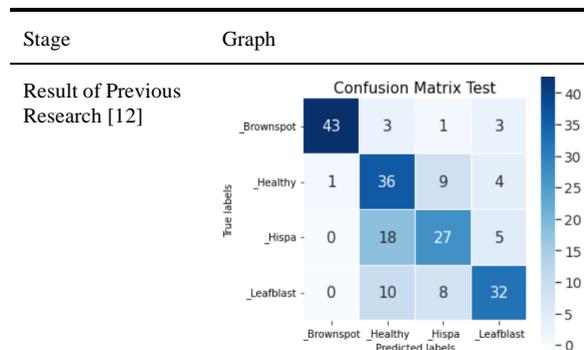


Table 9. Comparisons of Confusion Matrix in Dataset B



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This research ended by performing a prediction of each data in the experiment. Figure 7 shows the prediction results of each data in research [12] using 120 data, while Figure 8 represents the application of layers in the previous research [12] with 2000 datasets. The results of the prediction as given in this research with 120 datasets are presented in Figure 9, while those with 2000 datasets are shown in Figure 10. The best result was apparent in the model with 120 data. The use of 120 data with simple model layers and changing compile model could give accurate classification results for each data although this accuracy of each data did not reach 100%.

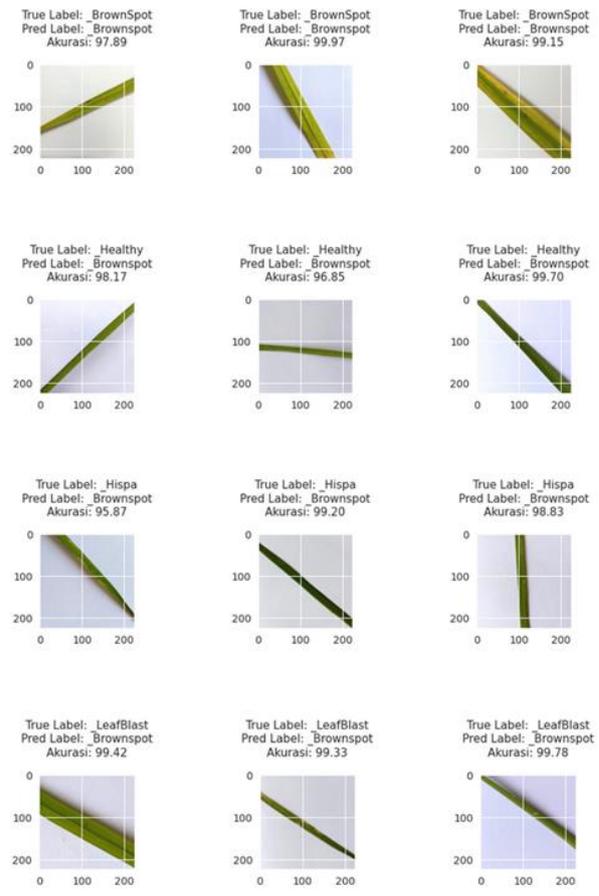


Figure 8. Prediction Results using [12] Data B

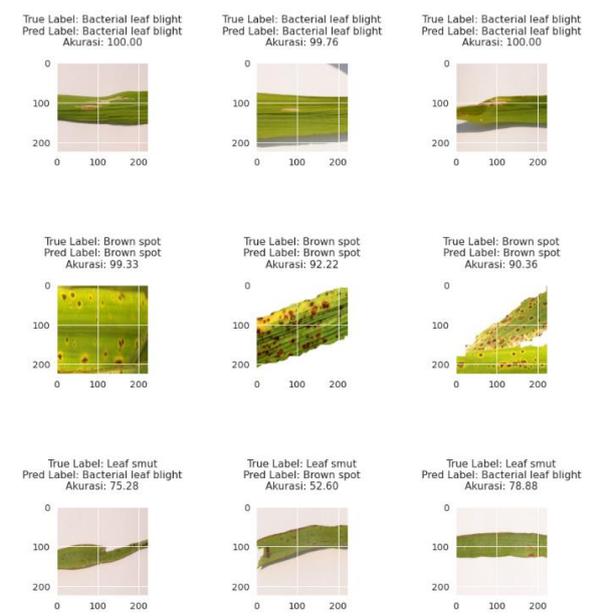


Figure 7. Prediction Results [12] using Data A

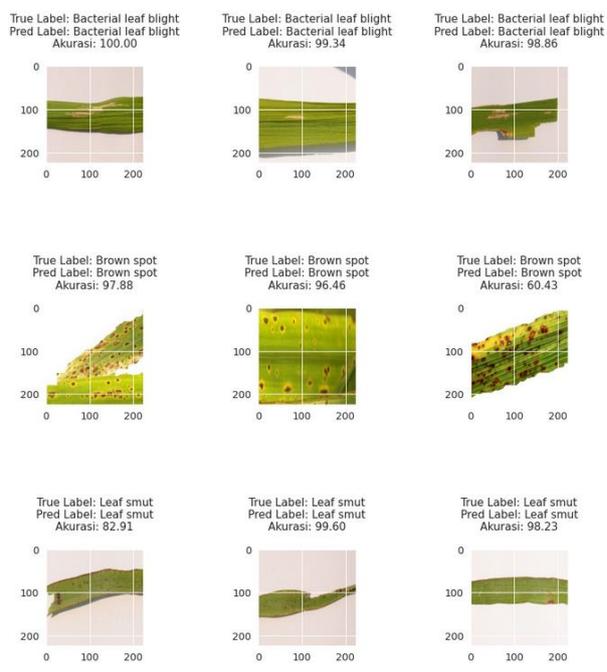


Figure 9. Results of this Research using Data A

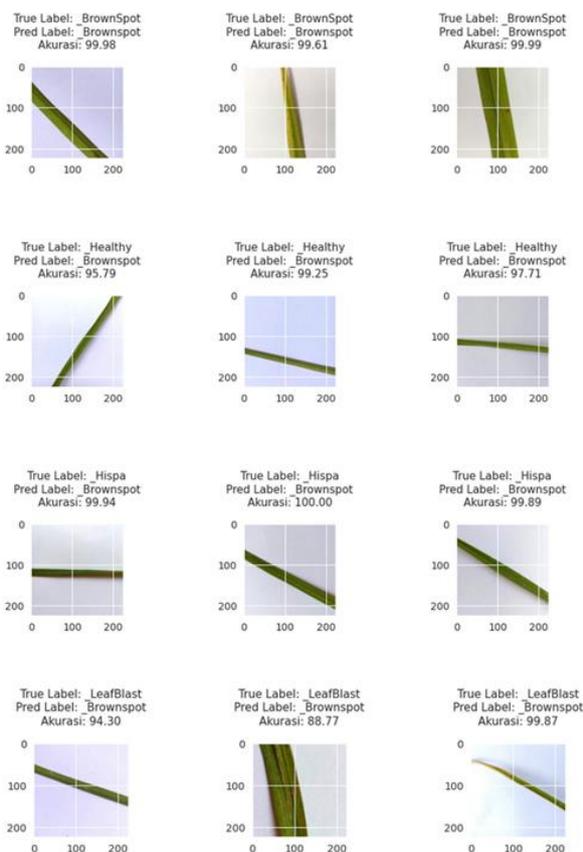


Figure 10. Results of this Research using Data B

4. Conclusion

The use of a simple layer as in ResNet101 to classify the diseases in rice according to leaf images with few datasets can improve the quality of the performance of the model. With the simpler suggestion of the architecture of a fully connected layer, the same accuracy of 100% can be given but with a lower loss of 2.91%. Moreover, the model can also perform accurate classification in each existing data using leaf images. This improvement was obtained from the application of additional architecture to the ResNet101 layer, consisting of Dense Layer 128 with 'relu' activation, added with BatchNormalization layer and one Dropout layer of 0.3 for the first layer of the added model. The second layer used Dense Layer 32 with 'relu' activation, added with BatchNormalization layer and Dropout layer of 0.1. The layer was ended with Dense Layer with the output consisting of three classes with 'softmax' activation. Application of architectural models can improve performance models being 2.7% of val-loss if compared with previous research [12]. This can be proven from the loss graph in Table 6. Problems that were resolved with this research ResNet101 is capable of classifying rice diseases accurately despite the amount of data slightly by utilizing the arrangement of layers according to data requirements. Plus,

overfitting in previous studies is well resolved. Comparison of Table 4 and Table 6 shows the overfitting that occurred between studies this with previous research [12] can be resolved well. In addition to handling overfitting, this study also adds predictions that each data based on its label that is not done research [12] with the aim to provide the quality of the model that is able to predict every data accurately. Predictive results of each data based on the label gives good predictive results appropriate. This proves that the correlation between the arrangement of the layers of the ResNet101 model with the amount of data is very influential. Research conducted in the future is expected to give a more accurate classification of each data, and the use of more data is also expected to give the prediction of each data with high accuracy in the ResNet101 model.

References

- [1] Klasifikasi Penyakit Tanaman Padi Menggunakan Model Deep Learning Efficientnet B3 dengan Transfer Learning," *J. Ilm. SINUS*, vol. 19, no. 1, p. 75, 2021, doi: 10.30646/sinus.v19i1.526.
- [2] R. A. Saputra, S. Wasiyanti, A. Supriyatna, and D. F. Saefudin, "Penerapan Algoritma Convolutional Neural Network Dan Arsitektur MobileNet Pada Aplikasi Deteksi Penyakit Daun Padi," *Swabumi*, vol. 9, no. 2, pp. 184–188, 2021, doi: 10.31294/swabumi.v9i2.11678.
- [3] M. Z. Alom *et al.*, "A state-of-the-art survey on deep learning theory and architectures," *Electron.*, vol. 8, no. 3, 2019, doi: 10.3390/electronics8030292.
- [4] W. jie Liang, H. Zhang, G. feng Zhang, and H. xin Cao, "Rice Blast Disease Recognition Using a Deep Convolutional Neural Network," *Sci. Rep.*, vol. 9, no. 1, pp. 1–10, 2019, doi: 10.1038/s41598-019-38966-0.
- [5] C. R. Rahman *et al.*, "Identification and recognition of rice diseases and pests using convolutional neural networks," *Biosyst. Eng.*, vol. 194, pp. 112–120, 2020, doi: 10.1016/j.biosystemseng.2020.03.020.
- [6] M. A. Islam, N. Rahman Shuvo, M. Shamsojjaman, S. Hasan, S. Hossain, and T. Khatun, "An Automated Convolutional Neural Network Based Approach for Paddy Leaf Disease Detection," *Int. J. Adv. Comput. Sci. Appl.*, vol. 12, no. 1, pp. 280–288, 2021, doi: 10.14569/IJACSA.2021.0120134.
- [7] J. Chen, J. Chen, D. Zhang, Y. Sun, and Y. A. Nanehkar, "Using deep transfer learning for image-based plant disease identification," *Comput. Electron. Agric.*, vol. 173, no. November 2019, p. 105393, 2020, doi: 10.1016/j.compag.2020.105393.
- [8] K. S. Wibawa, P. Studi, T. Informasi, F. Teknik, U. Udayana, and B. Jimbaran, "Segmentasi Buah Apel Menggunakan Framework YOLACT Arsitektur Resnet-101," vol. 1, no. 2, 2020.
- [9] Y. Ibrahim *et al.*, "Soft Error Resilience of Deep Residual Networks for Object Recognition," *IEEE Access*, vol. 8, pp. 19490–19503, 2020, doi: 10.1109/ACCESS.2020.2968129.
- [10] A. Ridhovan and A. Suharto, "Penerapan Metode Residual Network (Resnet) Dalam Klasifikasi Penyakit Pada Daun Gandum," *JUPI (Jurnal Ilm. Penelit. dan Pembelajaran Inform.)*, vol. 7, no. 1, pp. 58–65, 2022, doi: 10.29100/jupi.v7i1.2410.
- [11] H. B. Prajapati, J. P. Shah, and V. K. Dabhi, "Detection and classification of rice plant diseases," *Intell. Decis. Technol.*, vol. 11, no. 3, pp. 357–373, 2017, doi: 10.3233/IDT-170301.
- [12] Ulfah Nur Oktaviana, Ricky Hendrawan, Alfian Dwi Khoiril Annas, and Galih Wasis Wicaksono, "Klasifikasi Penyakit Padi berdasarkan Citra Daun Menggunakan Model Terlatih

- Resnet101,” *J. RESTI (Rekayasa Sist. dan Teknol. Informasi)*, vol. 5, no. 6, pp. 1216–1222, 2021, doi: 10.29207/resti.v5i6.3607.
- [13] R. F. Finazis and T. Soehartanto, “Pemodelan Polishing Unit Berbasis Jaringan Syaraf Tiruan di PT Saka Indonesia Pangkah Limited,” *J. Tek. ITS*, vol. 8, no. 2, pp. 194–199, 2020, doi: 10.12962/j23373539.v8i2.47237.
- [14] A. Septadaya, C. Dewi, and B. Rahayudi, “Implementasi Extreme Learning Machine dan Fast Independent Component Analysis untuk Klasifikasi Aritmia Berdasarkan Rekaman Elektrokardiogram,” vol. 3, no. 5, pp. 5007–5016, 2019.
- [15] I. Terapan, U. Telkom, T. Elektro, and U. Telkom, “Analisis Fitur Domain Waktu ECG Heart Rate Variability Berdasarkan Gain Informasi,” vol. 10, no. 2, 2022.
- [16] H. Hendriyana and Yazid Hilman Maulana, “Identification of Types of Wood using Convolutional Neural Network with Mobilenet Architecture,” *J. RESTI (Rekayasa Sist. dan Teknol. Informasi)*, vol. 4, no. 1, pp. 70–76, 2020, doi: 10.29207/resti.v4i1.1445.
- [17] N. U. R. Ibrahim, S. S. A. Idah, B. Hidayat, and S. Darana, “Klasifikasi Grade Telur Ayam Negeri secara non- Invasive menggunakan Convolutional Neural Network,” vol. 10, no. 2, pp. 297–308, 2022.
- [18] K. Thenmozhi and U. Srinivasulu Reddy, “Crop pest classification based on deep convolutional neural network and transfer learning,” *Comput. Electron. Agric.*, vol. 164, no. July, p. 104906, 2019, doi: 10.1016/j.compag.2019.104906.
- [19] M. Susanty, ; Raka, and S. Wardana, “PETIR: Jurnal Pengkajian dan Penerapan Teknik Informatika Prediksi Tekanan Pori Berdasarkan Data Logging Sumur Menggunakan Deep Neural Network,” vol. 14, no. 1, pp. 81–89, 2021, [Online]. Available: <https://doi.org/10.33322/petir.v14i1.964>.
- [20] R. Jain, P. Nagrath, G. Kataria, V. Sirish Kaushik, and D. Jude Hemanth, “Pneumonia detection in chest X-ray images using convolutional neural networks and transfer learning,” *Meas. J. Int. Meas. Confed.*, vol. 165, p. 108046, 2020, doi: 10.1016/j.measurement.2020.108046.
- [21] A. Chakraborty, D. Kumer, and K. Deeba, “Plant Leaf Disease Recognition Using Fastai Image Classification,” *Proc. - 5th Int. Conf. Comput. Methodol. Commun. ICCMC 2021*, no. Iccmc, pp. 1624–1630, 2021, doi: 10.1109/ICCMC51019.2021.9418042.
- [22] L. W. Liu, S. H. Hsieh, S. J. Lin, Y. M. Wang, and W. S. Lin, “Rice blast (*Magnaporthe oryzae*) occurrence prediction and the key factor sensitivity analysis by machine learning,” *Agronomy*, vol. 11, no. 4, pp. 1–15, 2021, doi: 10.3390/agronomy11040771.
- [23] M. Koklu, I. Cinar, and Y. S. Taspinar, “Classification of rice varieties with deep learning methods,” *Comput. Electron. Agric.*, vol. 187, no. November 2020, p. 106285, 2021, doi: 10.1016/j.compag.2021.106285.
- [24] S. Ramesh and D. Vydeki, “Application of machine learning in detection of blast disease in south indian rice crops,” *J. Phytol.*, vol. 11, pp. 31–37, 2019, doi: 10.25081/jp.2019