



Disease Detection on Rice Leaves through Deep Learning with InceptionV3 Method

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Abstract

The rate of growth in the agricultural sector in Indonesia puts demands on people who work as farmers to maintain and improve the quality of agriculture. Rice, which is one of the basic needs of the community, is currently the most in demand. Therefore, the need for rice continues to increase from year to year with the increase in the population of Indonesia. To maintain the quality and quantity of rice, it is necessary to monitor continuously which for developing countries, there are limited tools and costs to develop technology to deal with problems of maintaining rice quality, especially diseases in rice. Rice disease is influenced by various factors, some of which are season, weather, temperature, media, availability of water sources, and others. The purpose of this research is to prevent diseases in rice from spreading and spreading by making disease detectors in rice through a deep learning approach using the InceptionV3 method. There are 4 classes of rice diseases diagnosed, namely bacterial blight, blast, brown spot, and tungro. The total loaded dataset is 5932 images used in this study. The InceptionV3 model used can learn hidden patterns in the image thanks to the CNN transfer learning method technology with an accuracy of 97.47%. The results show that InceptionV3 can be one of the choices of various existing CNN methods because of its accuracy.

Keywords: rice leaves disease; deep learning; transfer learning; CNN; inceptionv3

1. Introduction

Indonesia's economy continues to grow from year to year for the better. This was particularly evident in 2018, especially in the agricultural sector. As of 2018, agricultural growth in Indonesia exceeded 9%. These are some very positive numbers. The government even claimed that the growth rate of Indonesia's agricultural sector was the highest in the last 10 years. This has brought Indonesia's agricultural industry to the attention of the international community. Of course, this shows that Indonesia is increasingly competitive in the international arena.

As a tropical archipelago with average land conditions in Indonesia that are fertile, not a few people work as farmers and the like. Or in other words, the agricultural system in Indonesia is a source of livelihood for the Indonesian people. Quoted from the website of the Ministry of Agriculture, rice has a high historical value and has long been the main staple food for Indonesia. Actually in Indonesia the source of carbohydrates is not only rice but also several plants, such as corn, sago, palm, cassava, cassava, or taro. However, rice remains the most popular and in high demand in Indonesia. A

food diversification program to reduce rice consumption was developed in the 1980s. But it has not shown satisfactory results, because rice is indeed very important for the lives of Indonesian people [1].

The demand for rice increases from year to year, along with the increase in population. Rice growth and development are influenced by temperature, water availability, proper rooting media, nutrient retention, erosion risk, and flooding [2]. In 2019, national rice production was 31.31 million tons, a 7.75% decrease compared to 2018 [3]. According to BPS [4], rice production in 2019 was still a surplus of 1.53 million tons. East Java Province is one of the national rice suppliers with a rice field area planted with rice in 2017 of 2,136,412.0 hectares [4]. The districts in East Java with the largest area of rice fields planted with rice are Jember District (161,640.3 hectares), and Banyuwangi District (120,430.3 hectares). In addition to the two districts located in the horseshoe area, Bondowoso District has high potential as a source of national rice supply. Based on data from BPS in 2018, starting in 2013 the area of land planted with rice increased from year to year. In 2013, the area of land planted with rice in Bondowoso Regency amounted to 57,727 hectares,

in 2014 it was 56,600 hectares, in 2015 it was 68,609 hectares, in 2016 it was 72,104.2 hectares, and in 2017 it increased to 79,018.4 hectares. The land expansion is supported by government programs through the utilization of dry land under stands and unproductive land into dry rice fields [5].

It is important to pay attention to the quality and quantity of rice, which is the staple food of the Indonesian people. Everything that affects the quality and quantity of rice production will certainly affect the mass population. Therefore, continuous monitoring of all factors that can cause a decline in rice quality is essential for proper mitigation [6]. One of the crucial factors in maintaining rice quality and quantity is rice diseases. Without timely monitoring and intervention, diseases can greatly reduce the quality of rice and can be a huge loss to farmers. The "deadly" diseases in question include Bacterial blight, Blast disease, Brown Spot disease, and Tungro disease. Bacterial blight caused by the bacterium *Xanthomonas oryzae* pv. *oryzae* (Xoo) is one of the most dangerous diseases that can reduce rice production by about 15-80%, depending on which stadia the rice plant is attacked [7]. The characteristics of the disease symptoms that appear are the color of the leaves becomes pale gray, then as time increases the plant becomes dry and the leaf blade folds along the mother leaf bone (Figure 2. (a)). The presence of Bacterial blight in the vegetative phase is called crackle, while in the generative phase it is called blight [8]. Then for Blast disease caused by the fungus *Magnaporthe grisea* Hebert, symptoms begin with the appearance of spots that are shaped like a rhombus with a pointed tip of brown color which over time develops to a larger size and is brown at the edges while in the middle is gray-white (Figure 2. (b)) [8]. Furthermore, brown spot disease is caused by the pathogens *Cercospora oryzae* and *Bipolaris oryzae*. These pathogens can cause rice leaves to wither and then dry prematurely, accompanied by symptoms of typical brown spots circled by yellowish color, variable size (spots) spread throughout the leaves (Figure 2. (c)). Severely infested rice can significantly reduce the number of tillers and grains and reduce their quality and weight [9]. Finally, Tungro disease is caused by RTBV (*Rice Tungro Bacilliform Virus*) and RTSV (*Rice Tungro Spherical Virus*) viruses where both types of viruses are transmitted by green leafhoppers (*Nephotetic virescens*) in a semi-persistent manner [10]. Symptoms of Tungro disease in rice are discoloration of leaves to yellow, reduced tillers, plant size does not grow as usual (stunted), delayed panicle emergence, and brownish grain (Figure 2. (d)) [11]. In relation to these problems, automatic detection of rice diseases is an interesting context in the field of agriculture and informatics.

Deep learning is one of the ways that can be used to detect diseases in rice plants in the field of informatics.

It is a combination of machine learning methods that mainly focus on automatic feature extraction and classification from images, which when widely found applications are commands for object (image) detection [12]. Machine Learning and deep learning have become mature disciplines in applying artificial intelligence to mine, analyze, and recognize patterns from data. The reclamation of advances in the field is for the benefit of clinically assisted decision-making with computer systems where it is increasingly becoming non-trivial, since the existence of data [12]. Deep learning often refers to a procedure where a convolutional neural network (CNN) is used for automated bulk feature extraction, which is achieved by a process called convolution where the layers process non-linear information [13].

Research related to the classification of rice plant diseases through deep learning has been developed with various models and results obtained. Deep learning approaches for image classification using algorithmic models such as Support Vector Machine (SVM), K-Nearest Neighbors (K-NN), Decision Tree, and Random Forest have been trained and produced accuracies of (respectively) 93.76%, 68.95%, 90%, and 96.83% [14] using the same dataset [15] as the research to be conducted in this paper. According to the study, the proposed deep learning is based on an approach where hyper-parameters can be optimized using nature-inspired optimization algorithms. Then, the study proposed a CNN model that produces higher performance and is adapted for plant disease classification when compared to other image classification techniques [14] which is 99.58%.

Previous research also used the architecture of MobileNet, NasNet, and SqueezeNet models to identify and recognize diseases in rice plants which gave quite good accuracy results, namely 93%. However, with parameter tuning, the accuracy can be increased by approximately 3%, to 96%. In addition, the augmentation process on the dataset also supports the accuracy of the model [16]. The Support Vector Machine (SVM) technique was also used for multi-class classification to identify three types of rice diseases (Bacterial leaf blight, Brown spot, and Leaf smut). Images of infected rice plants were captured using digital cameras from rice fields and obtained accuracy results of 93.33% on training data and 73.33% on test data [17]. The testing process of the test data was carried out randomly, this test for the classification of Brown spot and Bacterial leaf disease got the highest accuracy on the EfficientnetB3 architecture which was 79.53% at the 350th epoch, compared to the MobilenetV3 architecture which obtained a lower accuracy of 54.32% at the 300th epoch. Increasing epochs has been done but results in decreasing accuracy, indicating that the architecture experiences overfitting when epochs increase more than 350 for

EfficientnetB3 and more than 300 for MobilenetV3 [18].

Another study proposed a deep CNN method for rice blast disease recognition using a data set of 5812 which was divided equally between infected and uninfected rice plants. The methods used were CNN for feature extraction and SVM for classification, resulting in an average accuracy of 95.83% for a binary classification [19]. Relevant research using color features for rice plant diseases analyzed 14 color spaces and extracted 4 color features from each channel for a total of 172 features. The dataset used consisted of 619 images with 4 classes namely rice blast, bacterial leaf blight, healthy leaves, and sheath blight, using 7 different classifications to test the research, namely Logistic Regression, Random Forest, Decision Tree, Naïve Bayes, K-NN, SVM, and Discriminant Classifier (DC). The highest accuracy was obtained from using SVM, with an average accuracy of 94.65% [20]. Related research also proposes testing several deep learning methods including VGG16, VGG16 (with first three blocks of frozen) VGG19, ResNet, Xception, and CNN which they refer to as (5-layer convolutional) using a rice disease dataset of 4 classes with a total of 1600 images. Data pre-processing has also been tried so that this step requires data cleaning, data transformation, and data reduction (data compression) before input and processing. The highest accuracy results were obtained from the CNN (5-layer convolutional) method of 78.2% [21].

In essence, the main objective of this research is to prevent rice diseases from spreading. On the other hand, this research is also conducted to test and print the state-of-the-art (the level of performance currently achievable by a method) of a transfer learning method, which is basically a CNN that has been trained by a large number of image datasets and proposed by the scientific community. The idea of testing the case of disease detection in rice using a dataset sourced from Mendeley data [15] was processed and used to train and test the proposed InceptionV3 model. With transfer learning, the retention of knowledge extracted from a case task is key to performing other case tasks. This is likely to be an unlimited alternative choice and can be re-investigated in the future regarding its novelty and contribution to performance improvement. This research is expected to create a model with more than 95% accuracy.

This paper is organized into 4 sections. Section 1 is an explanation of the condition of agriculture in Indonesia, a brief review of data on rice production on related research, a review of related literature, the reason for the research, and the objectives of the research. Section 2 is a presentation of the proposed method, Section 3 is the results and discussion of the research obtained, and Section 4 contains the conclusions of the research.

2. Research Methods

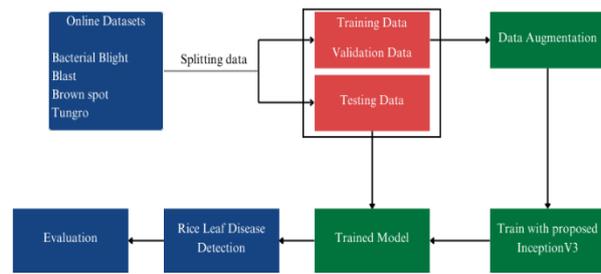


Figure 1. Research flow in block diagram form

Figure 1 shows the flow and implementation of the proposed InceptionV3 method. Based on the figure, there are 7 stages carried out in this research, namely providing datasets, splitting datasets (training data, validation data, and test data), data augmentation, training the proposed model, trained model, detection or prediction of rice plant diseases (using test data), and model evaluation.

In the first stage of the deep learning process, dataset provisioning is performed. This research uses datasets sourced from Mendeley data [15]. Mendeley data is a platform owned by Mendeley that was created to enable public and private sharing of data to fellow authors, researchers, and colleagues. In this research, the image dataset of rice disease [15] is needed which is public and consists of 4 classes in the Mendeley data platform for the object of research. In the second stage, a splitting process was carried out on the dataset which was divided into training data, validation data, and test data groups of 80:10:10. The training data and validation data will be used for the training process of the proposed model. Before going through model training, training data and validation data will go through a data augmentation process. As for the test data, it will be incorporated into the trained model to test the model's ability to detect rice disease classes and to evaluate the model. In the third stage, data augmentation is performed so that the model can better recognize image data objects so as to produce high accuracy. In the fourth stage, the results of the data augmentation process are used for training the proposed model. In the fifth stage, the trained model will use test data for testing and evaluation. In the sixth stage, the rice disease detection testing process is carried out using the classification report. In the last stage, model evaluation is conducted to determine the performance of the model using the confusion matrix and accuracy, precision, and f1-score calculation methods.

2.1. Dataset

In order to achieve the objectives of this research, the source dataset that has been accessed from Mendeley data [15] which contains 5932 images of rice divided into 4 disease classes. Among them are Bacterial blight, Blast, Brown spot, and Tungro. The dataset is divided

into 80:10:10 where 80% of the total image or 4746 images are used for training, 10% or 593 images are used for validation, and 10% or 593 images are used for testing. The rice dataset samples from each class are shown in Figure 2.

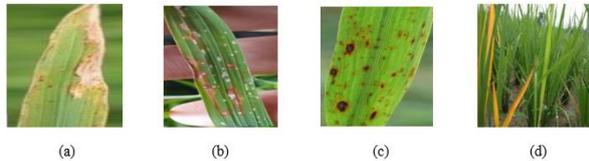


Figure 2. Sample image from the rice image dataset: (a) *Bacterial blight*, (b) *Blast*, (c) *Brown spot*, (d) *Tungro*

In the data augmentation part, which in this research uses ImageDataGenerator, which is a Keras class in the TensorFlow library used for augmentation, the rice image is rescaled to a size of 300 x 300 pixels. This pixel size is the fixed size of the source dataset. The reason it does not require rescaling is because the pixel size is good enough to run deep learning for satisfactory results. The larger the image resolution, the more features that can be captured by CNN. Considering the GPU used is NVIDIA GeForce GTX 1650. The next augmentation settings use batch_size = 128, rescale = 1/255, horizontal_flip = True, zoom_range = 0.2, and shear_range = 0.2. It is also worth noting that CNNs are able to ignore slight positional variations. As such, CNN searches for patterns not only for a specific position of the image but also searches for patterns that are moving.

2.2. InceptionV3 Method

InceptionV3 is one of the transfer learning methods with CNN and is one of the modified versions of the Inception family. Of course, the modification is based on the first version of the Inception model, which was developed by a Google research team in 2015 with the aim of improving visual performance and image understanding in computer vision tasks [22]. One of the key features of InceptionV3 is the use of the Inception module. The Inception module allows the network to extract features with varying receptive field sizes [23]. This module uses convolution operations with kernels of various sizes in parallel and then combines the results. In this way, InceptionV3 can efficiently extract information from images in different scales and levels of detail [23]. In addition, InceptionV3 also introduces the "Factorization into smaller convolutions" technique which breaks the convolution operation into several smaller convolution operations. This helps reduce the number of parameters that need to be calculated and speeds up the training and inference process [23]. It is evident from some of the improvements made, such as in LabelSmoothing and to spread the label information at the bottom of the network there is the use of auxiliary classification. Of course, also for the side-head layer, batch normalization was used.

The intention of the Inception model is that feature extraction and transfer learning can be achieved through 1x1 convolution, 3x3 convolution, 5x5 convolution, pooling, and so on [24]. This concept can obtain the best feature extraction method through training, or in another sense, giving input to several of these feature extraction methods simultaneously, and then merging. The comparison between InceptionV3 and the first version of Inception is mainly to replace the 5x5 convolution with the stacking of two 3x3 convolutions [25]. InceptionV3 is prioritized for image analysis and object detection. InceptionV3 has advantages in image recognition performance on various computer vision tasks, such as image classification and object detection [23]. Its ability to extract features with various scales and levels of detail and the use of optimization techniques make it one of the popular architectures in the world of image processing and pattern recognition. An illustrative concept of the InceptionV3 canonical [26] has been presented in Figure 3.

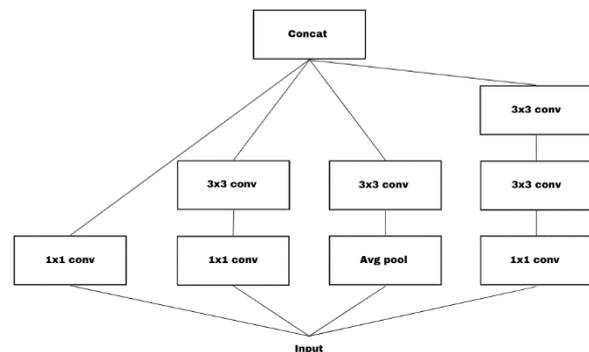


Figure 3. InceptionV3 module canonical illustration concept

In the InceptionV3 research model, freeze the base-layer in InceptionV3 so that it is not retrained by using the command include_top = false and for weights = 'imagenet', then adding the layer to be trained just above or after the base-layer is required. For the optimization algorithm, the adam stochastic gradient descent optimizer was chosen, and the activation used ReLU-activation and softmax. Then for back propagation, it was decided to use learning rate = 0.001 in the InceptionV3 model. The following is a picture of the InceptionV3 model architecture presented in Figure 4.

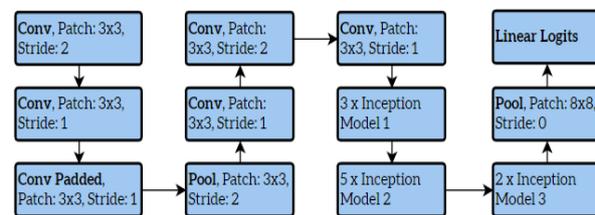


Figure 4. Presentation of the research model of transfer learning InceptionV3

Figure 4 is a description of the basic architecture of the InceptionV3 model based on transfer learning CNN

used as a research paper. It has proposed an initial model that combines several different sizes of convolutional filters into a new filter. This kind of design reduces the number of parameters to be trained and reduces computational complexity [27].

Regarding the fully connected layer, it was decided to use the layer arrangement presented in Table 1.

Table 1. Fully connected layer arrangement in the research model

Layer	Type	Output Shape
global_average_pooling2d	GlobalAveragePooling2D	(None, 2048)
dense	Dense	(None, 1024)
batch_normalization_94	BatchNormalization	(None, 1024)
dense_1	Dense	(None, 512)
batch_normalization_95	BatchNormalization	(None, 512)
dense_2	Dense	(None, 256)
batch_normalization_96	BatchNormalization	(None, 256)
dense_3	Dense	(None, 128)
dense_4	Dense	(None, 4)

Based on Table 1, after the training process in the InceptionV3 base model architecture is passed, then the concat results or output of the InceptionV3 model enter the fully connected layer stage, where there are pooling layers, dense layers, and batch normalization. The function of the pooling layer is to reduce the spatial dimension of the feature representation generated by the previous layer, then the features are connected by the dense layer globally to produce the final prediction. batch normalization is intended to increase the speed, stability of the training model, and normalize the input of each layer in the CNN so that it is easier to manage. In Table 1 the dense layer and batch normalization layer are repeated several times which in this research is intended to increase the accuracy of the prediction results.

2.3. Performance Evaluation

Regarding the measurement of the performance and quality of classification performance with CNN, the calculation methods used are accuracy, precision, recall, and f1-score by using test data as model testing after completing the training process on the model, and then describing it through the confusion matrix presented in Figure 5. The following are the formulas of these performance measurements from (1) to (4) and an example of the confusion matrix in Figure 5.

$$Accuracy = \frac{(TP)}{Total\ Dataset} \quad (1)$$

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

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

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

TP, FP, and FN, TP (True Positive) is the amount of actual data that is positive and correctly predicted as positive, in which case the model can classify a disease in rice correctly. FP (False Positive) is the amount of actual data that is negative but predicted as positive, which in this case the model predicts a disease in rice whose actual data does not match what is predicted. Likewise, FN (False Negative) is the amount of actual data that is positive but predicted as negative, in which case the model predicts a disease in rice whose actual data does not match what is predicted.

		Confusion Matrix			
		Bacterialblight	Blast	Brownspot	Tungro
True Labels	Bacterialblight	TP	FN	FP	FN
	Blast	FP	TP	FN	FN
	Brownspot	FN	FN	TP	FP
	Tungro	FN	FP	FN	TP
		Predicted Labels			

Figure 5. Confusion matrix of order 4x4 with representation of the classification process results (TP, FP, and FN)

3. Results and Discussions

This research uses an image dataset of 4 types of rice plant disease classes that have been divided by a ratio of 80% training data, 10% validation data, and 10% test data. The nature of the disease is relatively difficult to know the type for laymen in the field of botanical science because of its similar characteristics. Therefore, in this research it was decided to use deep learning with the InceptionV3 transfer learning method so that the model can recognize the type of rice plant disease optimally. The results and discussion have been presented in the following session.

3.1. Trained Model

The performance generated from the InceptionV3 model is surprising, here are the records of training accuracy, data loss, validation accuracy, and validation loss by the InceptionV3 model presented in Table 2.

Table 2. InceptionV3 model training's record results using rice dataset for 34 epochs

Epochs	Accuracy	Loss	Validation accuracy	Validation loss
1	0.9818	0.0583	0.8417	0.4633
2	0.9883	0.0338	0.9570	0.1278
3	0.9867	0.0355	0.9589	0.1345
4	0.9887	0.0334	0.8808	0.5226
5	0.9889	0.0320	0.9843	0.0596

Epochs	Accuracy	Loss	Validation accuracy	Validation loss
6	0.9983	0.0075	0.9921	0.0102
7	0.9980	0.0071	1.0000	0.0040
8	0.9945	0.0213	0.9589	0.1385
9	0.9772	0.0607	0.9433	0.1687
10	0.9900	0.0301	0.9882	0.0384
11	0.9939	0.0193	0.9628	0.0855
12	0.9887	0.0370	0.9316	0.2598
13	0.9963	0.0129	0.9882	0.0224
14	0.9971	0.0075	0.9843	0.0375
15	0.9965	0.0092	0.9902	0.0350
16	0.9974	0.0098	0.9882	0.0168
17	0.9982	0.0044	1.0000	0.0020
18	0.9982	0.0075	1.0000	0.0058
19	0.9811	0.0809	0.9433	0.1690
20	0.9902	0.0314	0.9589	0.1154
21	0.9880	0.0318	0.9882	0.0364
22	0.9978	0.0078	0.9960	0.0122
23	0.9930	0.0282	0.9687	0.1245
24	0.9854	0.0472	0.9472	0.2192
25	0.9937	0.0194	0.9921	0.0364
26	0.9989	0.0057	0.9980	0.0120
27	0.9987	0.0055	0.9941	0.0114
28	0.9974	0.0065	0.9980	0.0057
29	0.9969	0.0135	0.9941	0.0080
30	0.9976	0.0072	0.9960	0.0080
31	0.9967	0.0115	0.9824	0.0408
32	0.9941	0.0166	0.9804	0.0583
33	0.9889	0.0368	0.9921	0.0156
34	0.9967	0.0068	0.9980	0.0061

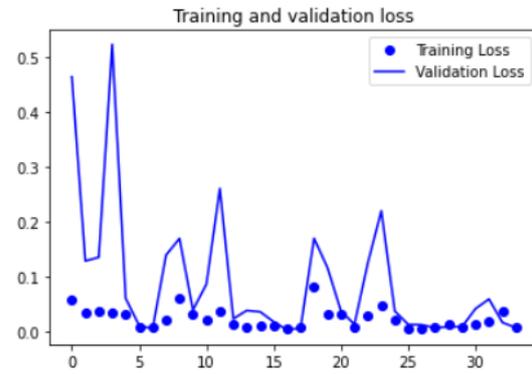


Figure 7. InceptionV3 model training result (loss record)

Figure 7 shows the training and validation loss graphs for the trained model. This graph is a representation based on the training's record table in Table 2 in the loss and validation loss columns. Regarding the loss graph (Figure 7), it shows similar "characteristics" to the accuracy graph. The difference is that this time the decrease in validation loss displayed by the graph is really significant. Namely at the 4th, 12th, and 24th epochs. This is certainly reasonable considering that the validation data provided is only 10% of the entire dataset.

Seen in Table 2, the best model fit occurs at the 26th epochs. This means that the model can predict rice diseases with almost 100% accuracy. The training's record uses plotting from the 'matplotlib.pyplot' library with graphical displays presented in Figure 6 and Figure 7.

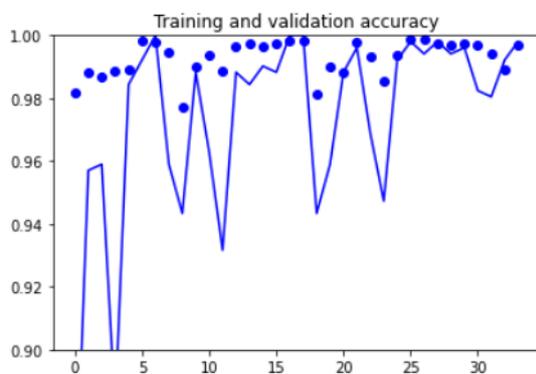


Figure 6. InceptionV3 model training result (accuracy record)

Figure 6 shows the training and validation accuracy graphs for the trained model. This graph is a representation based on the training's record table in Table 2 in the accuracy and validation accuracy columns. As seen in the accuracy graph (Figure 6), there is a slow increase in accuracy at the 1st to 6th epochs and then there is also a very small or insignificant decrease in accuracy of 0.02%. While in validation accuracy, the graph seems to drop significantly, but when looking back at Table 2, the resulting validation accuracy is also stable.

3.2. Classification Report and Evaluation

To get the TP, FN, and FP values that will be calculated for the classification report, it is necessary to use a confusion matrix to provide an overview of the extent to which the classification model is able to classify data into the correct class and is able to identify prediction errors made by the model. Figure 8 shows the results of the confusion matrix using the test data used in this study.

		Predicted Labels			
		Bacterialblight	Blast	Brownspot	Tungro
True Labels	Bacterialblight	138	4	6	0
	Blast	2	145	1	1
	Brownspot	0	1	147	0
Tungro	0	0	0	148	

Figure 8. Confusion matrix results using test data

Classification reports are created with the aim of helping to illustrate the extent to which the proposed model can predict different classes of data, as well as helping to identify classes that may have performance issues. This is an important tool in the effort to optimize and improve the performance of deep learning classification models. Evaluation is also done based on

the confusion matrix which is then calculated and represented through the reports in Table 3 and Table 4.

Table 3. Classification report of the InceptionV3 model using test data

Label	Precision	Recall	F1-Score	Support (data test)
Bacterial blight	0.99	0.93	0.96	148
Blast	0.97	0.97	0.97	149
Brownspot	0.95	0.99	0.97	148
Tungro	0.99	1.00	1.00	148

Table 3 shows the results of the classification report using test data, where all performance values illustrate excellent results. The calculation of each value in the precision, recall, and f1-score columns is based on the formula described in the research method. Precision is the proportion of true positive predictions compared to total positive predictions. Recall is the proportion of true positive predictions compared to the total true positive actual data. F1-score is the harmonic mean of precision and recall. The sophistication of the proposed InceptionV3 model with data augmentation and simple fully connected layer arrangement in this study can result in excellent overall performance. Table 4 shows the overall performance evaluation of the proposed model.

Table 4. Evaluation calculation results of the InceptionV3 model using test data

Accuracy	Precision	F1-Score
0.9747	0.9750	0.9746

4. Conclusion

In fact, InceptionV3 is very effective to be the choice of various CNN transfer learning – based models. An analysis of the effectiveness of InceptionV3 has been presented in this paper. The results are satisfactory and show its effectiveness for the case at hand. Although the number of images from the dataset used is relatively small. It is certainly surprising that only freezing the base-layer so that it is not retrained, then with relatively "simple" data augmentation settings, and not adding many dense-layer parameters close to the output which aims to allow more information extraction from the final convolution layer, resulted in an excellent average accuracy of 97.47%. The benefit of this research is that diseases in rice can be detected easily and efficiently using the attached image dataset. It is possible that the model will be deployed through website applications and mobile applications and patented. As a result, it does not require much cost, can be used by anyone, improves the quality of rice farming, and can help welfare for developing countries. In the future, the model will be retrained to improve accuracy. In this project for future work, hyperparameters such as the number of epochs, batch size, dense-layer parameters, etc. can be reset for more accurate and satisfactory

results. The choice of model optimizer can also affect the performance of the model.

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