Detection of Rice Plant Diseases using Convolutional Neural Network

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Abstract. Agricultural sector is the main sector that plays an important role in the national economy, from absorbing labours to playing as a contributor for foreign exchange. Indonesia is an agrarian country whose livelihood of the majority population is farming. Rice is one of the cultivation plants that becomes the staple food of most population. Thus, rice availability and its quality are factors that must be put in high consideration, either for national consumption or for export quality. This study aims to detect diseases in rice plants (by observing the leaves) that may cause a decrease in rice production or may result in bad quality rice using an artificial intelligent approach. The method used in this research is Convolutional Neural Network (CNN). This CNN is the result of the development of multilayer perception (MLP) which is used to manage two-dimensional data. The input from CNN is in the form of 2-dimensional data which is then propagated on a network with parameters at different weights and linear operations. CNN is one method of deep learning. The CNN method has many types of layers, namely the convolution layer, the subsampling / pooling layer, and the fully connected layer. This study uses different CNN architectures to find the best accuracy value. This study used four types of leaf diseases in rice plants with each type of disease consisting of 2,239 training image data and 168 image data. This research has succeeded in detecting diseases in leaf images automatically with the best training accuracy obtained at 91%.

Keywords: Convolutional Neural Network, plant disease detection, multilayer perceptron, agriculture, rice disease

1. Introduction
Rice plants (Oryza sativa L.), is an important food crop that has become a staple food for more than half of the world's population. In Indonesia, rice plants are rice-producing food crops which play an essential role in Indonesia's economic life [1] whose average rice consumption is around 90.10 kg/person/year [2]. According to [3], the total area of rice fields in Indonesia in 2015 reached 8,087,393 hectares.

Rice plants may also be infected with diseases, caused by weather, soil environment problem, viruses, fungal, or other types of animals, such as rats, grasshoppers, leafhoppers, and stinky bugs (walang sangit) [4]. Those diseases can threaten the sustainability of rice stock availability and may disrupt food security and national economic growth. The accuracy of the diagnosis of rice diseases is one of the key factors to determine the best effort to treat rice disease.
Convolutional Neural Network (CNN) is a deep learning method with neural networks approach that are commonly used to analyse visual imagery [5]. It is basically a neural network applied with a convolution operation instead of a matrix multiplication. A CNN has multiple layers consisting input layer, a series of hidden layers, and an output layer. The hidden layers consist of pooling layers, fully-connected layers, and normalization layers. There is no “one best CNN architecture fit for all” and achieving the best accuracy result takes several experiments which may involve applying different order of hidden layers, specific for each case. Figure 1 shows a typical CNN architecture with multiple layers.

Figure 1. A typical CNN architecture (source: https://upload.wikimedia.org/wikipedia/commons/6/63/Typical_cnn.png)

Some CNN applications are in image recognition [6] [7], recommender system [8], and natural language processing [9]. CNN is one method of deep learning that has a special layer which allows it to conduct feature extraction and direct extraction training from raw input data [10]. In agricultural sector, CNN has been extensively used to identify and classify diseases, such as in [11], [12] and [13], while in [14] was used to detect defect in mangosteen fruit. Some research by [15] and [16] achieved prominent results with high accuracy above 93% on detecting rice diseases.

This research investigates rice plant diseases from 2,239 leaf images from publicly available image dataset to determine a class among four types of diseases using a Convolutional Neural Network.

2. Materials and Methods

Dataset used in this research were collected from [17] with a total of 2,239 leaf images. The images were split into training and testing data of 2,071 and 168, respectively. We limit the number of disease classes to four most common cases, which are: Leaf Blast, Brown spot, Bacterial Leaf Blight, and Tungro. The training size for each class category are 515, 513, 528, and 515, respectively. The CNN architecture is described in Figure 2. There are 2 (two) convolutional layers with ReLU, 2 (two) subsampling (pooling) layers, and 4 (four) fully connected layers. The first convolutional layer has 128 filters and a 3x3 receptive field. The first subsampling layer has a 2x2 receptive field having the same number of filters as that of the previous layer. The second convolutional layer also has the same setting as the first one (128 filters an 3x3 receptive field), as well as the second subsampling layer having the same setting as that of the first one. Last, the first fully connected layer has 16 nodes while the second one has 4 nodes, matching the number of output classes.
Pre-processing steps include conversion to grayscale and resizing to 50x50 pixels, which then were stored in an array. The training images were supplied to the network structure in Figure 2 and once a model is generated, it will be used to predict and evaluate the test data.

3. Results and Discussion

The whole experiment was implemented in Python using TensorFlow Keras library. Stored data in array were loaded into the convolution network and layers were added one by one. The activation function used in each convolution layer was ReLU while the fully connected layer used Softmax function. The final model was then compiled using the following parameters setting:

loss=sparse_categorical_crossentropy, optimizer=adam, metrics=accuracy

and fitted using the following settings:

batch_size=32, epoch=10, validation_split=0.1.

The value of validation_split=0.1 means that of those data in training set, as much as 10% would be used as validation data so that training accuracy can be calculated afterwards. In this research with 2,071 total training data, it is 1,863 data for training and 208 samples for validation.

We experimented on six different sizes of models while maintaining fixed values for number of epochs, batch size, and validation split. For each model, its training accuracy and training loss values were noted as listed in Table 1.

| Model Name | Convolution 1 size | Convolution 2 size | Fully-connected size | Training Accuracy | Training Loss |
|------------|--------------------|--------------------|----------------------|-------------------|---------------|
| asa7       | 256                | 256                | 256                  | 93.05%            | 0.2264        |
| asa8       | 128                | 128                | 16                   | 93.60%            | 0.198         |
| asa9       | 256                | 256                | 16                   | 91.40%            | 0.238         |
| asa10      | 128                | 128                | 128                  | 87.40%            | 0.329         |
| asa11      | 64                 | 64                 | 64                   | 91.50%            | 0.23          |
| asa12      | 64                 | 64                 | 16                   | 91.50%            | 0.249         |
| **Average** | **91.41%**       |                    |                      | **0.25**          |               |

Training process was performed in 10 epochs on 1,863 data. In Table 1, we used three different sizes of convolution layers: 64, 128, and 256 nodes, while the fully connected layers only varied in between 16 and the size of the respective convolution layers. The highest accuracy of training data was 93.6% and
the lowest loss value was 0.198, both were from model asa8. Figure 3a described the plot of model accuracy, while 3b showed the plot of model loss from model asa8.

Figure 3. Plots of (a) Model Accuracy and (b) Model Loss of Training and Validation Data

Table 2. Confusion Matrix

| Real    | Prediction | blast | blight | brownspot | tungro | total |
|---------|------------|-------|--------|-----------|--------|-------|
| blast   |            | 16    | 0      | 25        | 3      | 44    |
| blight  |            | 4     | 7      | 31        | 5      | 47    |
| brownspot |          | 1     | 0      | 30        | 1      | 32    |
| tungro  |            | 0     | 0      | 12        | 33     | 45    |
| Precision |          | 0.761905 | 1      | 0.306122  | 0.785714 |
| Recall  |            | 0.363636 | 0.148936 | 0.9375    | 0.733333 |
| F-Measure |          | 0.492308 | 0.259259 | 0.461538  | 0.758621 |
| Accuracy |            |        |        |           |        | **0.511904762** |

As can be seen from table 2, the system performed the best in predicting tungro disease and the worst in blight disease, showed by the harmonic average (F-Measure) values of 0.758621 and 0.259259, respectively. The system’s accuracy was 0.512 or 51.2% which was twice as better as random guessing. The low accuracy was caused by the high number of wrong prediction of blight disease, which was mistakenly predicted as brownspot disease. However, the system was very good in recalling brownspot disease and was quite good at predicting tungro disease which indicated that it has successfully learn the two types of diseases.

According to [18], a deep neural network seems to perform better than shallow ones since it can generate better generalization. A systematic and heuristic approach was also suggested in [19] to get a near-optimal solution using genetic algorithm approach. As also noted in [20], controlled and systematic experiments accompanied by a good intuition may also help to get the best number of layers and nodes in a neural network. Making use of an automated search to test a number of different network
configuration was also one of the suggested approach, although there is a challenging effort in terms of time and resource when coping with large models or datasets.

This experiment’s result might be escalated by experimenting on more varieties of CNN architecture, i.e. the number of hidden layers and nodes in each layer.

4. Conclusion

A Convolutional Neural Network architecture has been proposed to predict diseases in rice among four types of diseases: blast, blight, brownspot, and tungro. The best model generated by the system has 128:128:16:4 layer configuration and it has 91.41% training accuracy and an average of 51.2% testing accuracy.

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