IJIREEICE

ISSN (Online) 2321-2004
ISSN (Print) 2321-5526

International Journal of Innovative Research in
Electrical, Electronics, Instrumentation and Control Engineering

Vol. 9, Issue 5, May 2021

DOI 10.17148/IJIREEICE.2021.9505

Rice Leaf Disease Classification using Deep Learning

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Abstract: Rice has become one of the most important crops in Asian countries, so the detection of disease in rice crops is a must to increase production. These diseases are mainly caused by bacteria, viruses, and fungi. We classified mainly three types of diseases such as brown spot, hispa, and leaf blast. In this study, we used Convolutional Neural Network to detect and classify the leaf disease in paddy crop. A CNN is a deep learning algorithm that takes an input image, allots values to various aspects that are present in the image, and differentiates from one another. Here AlexNet and LeNet algorithms are used to train and test the sample images of diseased as well as healthy rice crops. This model shows an accuracy of 97% which is quite high when compared to the existing model. In the existing model, the diseased parts of crops are detected using the pattern recognition method, in which some of the affected portions are left out where the leaf patterns are either unclear or not present. The proposed method examines the image row by column so that no affected spots are left out.

Keywords- RiceLeaf Diseases, AlexNet, LeNet, Convolution Neural Network, Disease detection, Disease classification.

I INTRODUCTION

In India rice plays a major role in the food department. Rice comprises nearly 42% of food grains production all over the country. It is the major crop in southern India and some other parts of the world. Hence it is necessary to have a sustainable balance in rice production. Cultivating rice crops is the livelihood for the majority of people in many countries. Hence the government of India has also implemented various policies for farmers to improve the production of rice. They have provided various subsidies like electricity, fertilizer, hybrid seeds, farming tools. The cost of electricity has been reduced for those who cultivate crops. Even though the area of cultivation for rice has been increased from 50 to 59%, a vast area of cultivation is affected by uneven rainfall. In some places, the rainfall is less which leads to drought and scarcity. In other cases, there is heavy rainfall which leads to the drowning of crops. There are also some other factors like soil fertility, labor wages, and other input supplies. Of all these constraints one major issue that can be resolved is discussed here, that is the diseases that affect the crop. These diseases are mainly caused by bacteria, fungi, and viruses.

In this paper, three diseases are mainly classified, brown spot, hispa, and leaf blast. [Figure 1a] Brown spot is a fungal disease caused by *Cochliobolus miyabeanus*, which is also called *Helminthosporium* leaf spot. The spots are smaller on young leaves when compared to the older ones and vary in size and shape from tiny dark spots to large circular spots in which tiny spots are dark-reddish brown and large spots have a dark brown margin and a light reddish-brown or gray center with a gold halo. [Figure 1b] Hispa is a common disease found in Southeast Asia, caused by a beetle of kind *Dicladispa armigera* that is commonly known as an invasive pest. The beetle scrapes out the upper surface of the leaf blade leaving only the lower epidermis as white streaks appear parallel to the midrib and translucent white patches near leaf veins. [Figure 1c] Leaf blast is a fungal disease caused by *Magnaporthe grisea* in which white to gray- green lesions or spots, with dark green borders, appears at the initial stage and elliptical or spindle-shaped and whitish to grey centers with red to brownish border in older lesions. In the process of classifying disease,the image of a diseased or healthy leaf is augmented and uploaded in the model which passes through a series of layer in which the images gets evaluated based on certain features and the result is displayed in a web framework.

(a) (b) (c)

Figure 1.Three classes of rice leaf diseases. (a) Leaf blast (b) Hispa (c) Brownspot

II LITERATURE SURVEY

Bhagyashri *et al*, [2017] present that the automatic rice disease detection system using different types of features like area, GLCM, and color moment. For the selection of the extracted features, a genetic algorithm is used resulting in low dimensionality and computational complexity. The segmentation provides higher accuracy with less computational time using the k-means clustering algorithm

Harshad Kumar *et al*, [2016] uses a machine learning technique to identify the diseased rice leaf using the concept of image processing. It predicts various rice leaf diseases by comparing various segmentation techniques. This obtained the accuracy of 80%, 60%, 65% for rice blast, rice sheath blight, and brown spot.

Karen Simnoyan *et al*, [2013] proposed the effect of depth on the accuracy in large-scale image recognition settings. This literature mainly focused on the improvement of prior-art configurations using convolution filters by increasing depth

Nuttakarn Kitpo *et al*, [2018] found that using drones for field surveying in large-scale areas helped users save time and money time-consumption, and it also facilitated real-time data collection, with the acquired images being used later on the server given for analysis. They also created a rice disease detection system based on the HSV color.

Syeda Airas Burhan *et al*, [2020] tells that the application of Deep Learning Techniques for pest and disease detection in rice crops will be a revolutionary idea. Deep learning techniques can improve the image processing part of this project by more efficient leaf segmentation and background removal. The objective of image processing should clean the images and enhance the area of interest for better feature extraction. Incorporating other significant factors such as weather conditions, rice varieties, soil conditions, and moisture levels into the model's training can further improve the efficiency and reliability of this approach.

Xuexue Zhang *et al*, [2019] concludes according to the study, the degree of fragmentation and spatial complexity of rice patches are negatively correlated links to rice sheath blight disease incidence and progression. The rice-growing regions Sheath blight thrives in areas with high connectivity and low fragmentation.

III MATERIALS AND METHODS

In this section the process of classifying disease using AlexNet is explained. This model propose how to detect rice leaf disease using AlexNet and LeNet algorithm of convolutional neural network to attain the classification on test dataset based on training dataset.

1. IMAGE DATASET

The dataset for this model is comprised of three types of diseases in rice leaves and some of the healthy leaves. As mentioned earlier, the three types of disease are brown spot, hispa and, leaf blast. The dataset for these three classes and the healthy class were collected from kaggle .The datasets are classified into two categories as training set and testing set. The training set comprises of 170 images belonging to all four classes. The testing set comprises of 90 images in all four classes. For every class a random number of images are collected. Table I represents the datasets collected in every class. The sample of collected dataset is shown in Figure 2.

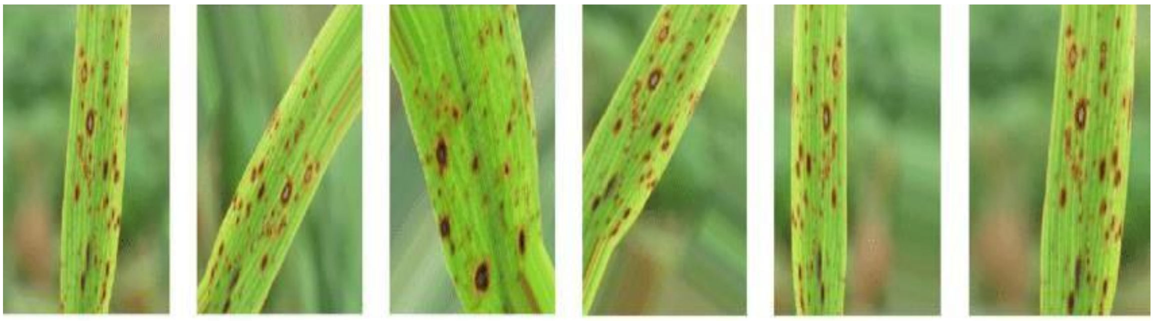
Table I. Datasets collected in every class of disease

Classes	No. of images	No. of training images	No. of testing images
Brown Spot	55	30	25
Hispa	85	55	30
Leaf blast	40	25	15
Healthy	80	60	20

Figure 2.Sample of collected dataset

2. PREPROCESSING DATA

In the preprocessing part the collected datasets of diseased and healthy leaves are sampled and divided among the training and testing sets. A large amount of data is required to make the model more robust. The training set undergoes an augmentation process which includes flipping of the image horizontally or vertically, zooming of image and dimension changes as well. As a first step of preprocessing the null values are cleared followed by removing the duplicate values and then the features are aggregated. The dimensions of the image are reduced. The main purpose of preprocessing is to encode the data such that the machine can understand. Hence the samples that are present in training set are trained and evaluated in the validation set. When the results of validation set is satisfying the process can be pursued for making predictions on the uploaded test data. Figure 3 shows the augmentation process of given data.



(a) (b) (c) (d) (e) (f)

Figure 3. Augmented image of brownspot diseased leaf (a) input image (b) rotated image (c) zoomed image (d) dimension changed image (e) mirror flipped image (f) scaled image

3. MODEL ARCHITCTURE

In this model two algorithm are used to improve the accuracy rate, one is the AlexNet architecture and the other is LeNet algorithm. These algorithm are used to train the samples and classify the data. The flow of process is explained with the help of block diagram in the Figure 4.

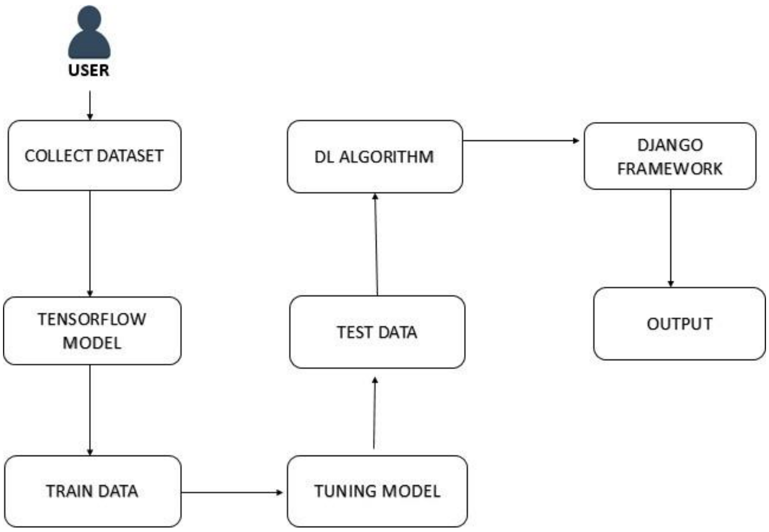


Figure 4. Block diagram of proposed model

3.1 AlexNet MODEL

There are several types of convolutional neural network architecture available in deep learning. ImageNet is a kind of CNN architecture of large visual database which is used for image recognition process in the software world.

AlexNet is a significant architecture of convolutional neural network which exceeds all the earlier models by providing better performance and reduction in error. It is similar to the architecture of LeNet and ImageNet but differs in the intensity, and number of filters present in each layers. The AlexNet comprises of five convolutional layer, three max pooling layers, 2 fully connected dense layer and one softmax layer. Every convolutional and dense layer is followed by a ReLU nonlinear activation function. Figure 5 represents the architecture of AlexNet algorithm.

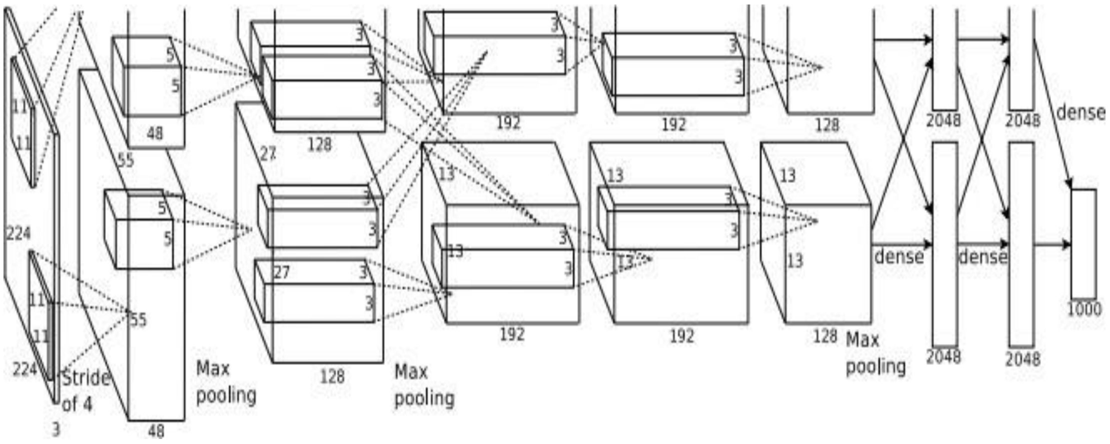
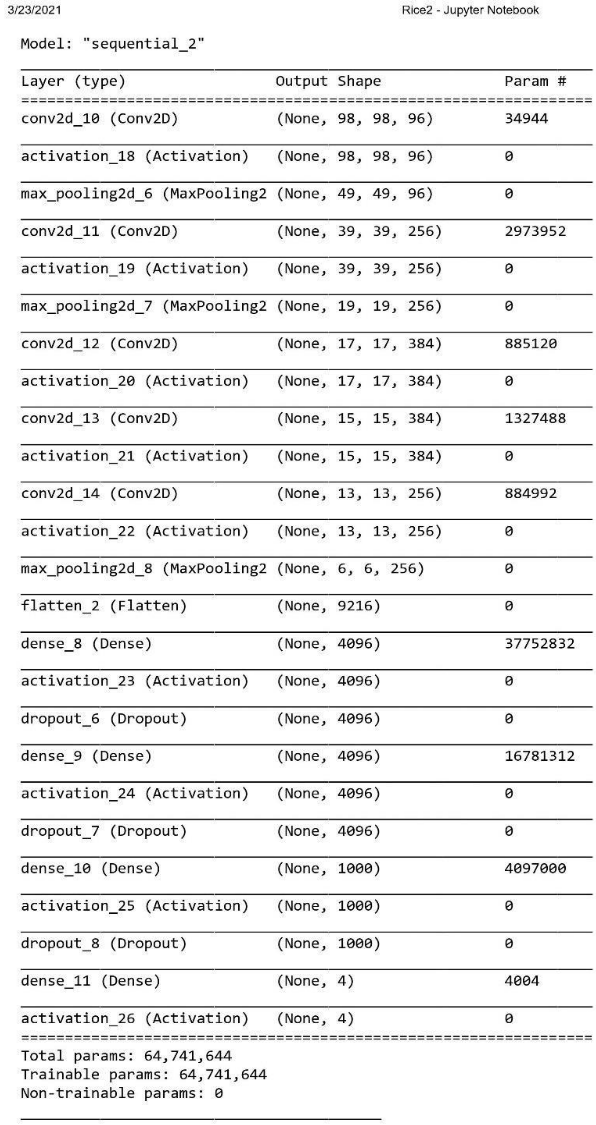


Figure 5. AlexNet Architecture

The input image for AlexNet model is given in the form of a RGB image of size 256x256. This image is fed into the first layer of AlexNet model that is the input layer. In this layer the high level features are extracted. The image from the input layer is passed on to the next layer of architecture which is the convolutional layer. The major task of convolution layer is to identify the low level conjunction of features from the previous input layer. These low level features are extracted with the help of kernels present in the convolutional layer. Multiple number of kernels are present in every convolutional layers which extract different features from the image. There are 96, 256 and, 384 kernels present in Conv1, Conv2, Conv3 layers. The convolutional layer is followed by max pooling layer. Here the down sampling process is done on the width and height of the image, keeping the depth same. This layer also reduces the computational complexity that is the power required to process through reduction of dimension and some more features are extracted here. Thus the process goes on for next convolution and max pooling layers in the same way. Three max pooling layers are present in AlexNet architecture. The resultant output of final max pooling layer is fed to the fully connected dense layer. The flattening process is done here by converting the data into a one dimensional vector. Three fully connected dense layers are present in AlexNet. Followed by the dense layer is the softmax layer which is the output layer. The softmax activation function is applied to data from dense layer which performs normalization and provides a probability distribution among four classes of leaves. ReLU nonlinear activation function at each convolution layer is used here, so that the detailed information are represented and transferred to following layers of model. Using this activation function the neural network can train the data faster when compared to sigmoid or tanh functions. The extracted features are summarized and used to classify the disease in softmax layer. The images in training set are passed through the layers number of times to reduce the rate of error and increase the accuracy. Passing the data number of times to get better accuracy is called epochs. Table II shows the effect of layers on rice leaf disease classification.

Table II. AlexNet architecture on rice leaf disease classification



3/23/2021 Rice2 - Jupyter Notebook

```
Model: "sequential_2"
_________________________________________________________________
Layer (type)                 Output Shape              Param #
=================================================================
conv2d_10 (Conv2D)           (None, 98, 98, 96)        34944
_________________________________________________________________
activation_18 (Activation)   (None, 98, 98, 96)        0
_________________________________________________________________
max_pooling2d_6 (MaxPooling2 (None, 49, 49, 96)        0
_________________________________________________________________
conv2d_11 (Conv2D)           (None, 39, 39, 256)       2973952
_________________________________________________________________
activation_19 (Activation)   (None, 39, 39, 256)       0
_________________________________________________________________
max_pooling2d_7 (MaxPooling2 (None, 19, 19, 256)       0
_________________________________________________________________
conv2d_12 (Conv2D)           (None, 17, 17, 384)       885120
_________________________________________________________________
activation_20 (Activation)   (None, 17, 17, 384)       0
_________________________________________________________________
conv2d_13 (Conv2D)           (None, 15, 15, 384)       1327488
_________________________________________________________________
activation_21 (Activation)   (None, 15, 15, 384)       0
_________________________________________________________________
conv2d_14 (Conv2D)           (None, 13, 13, 256)       884992
_________________________________________________________________
activation_22 (Activation)   (None, 13, 13, 256)       0
_________________________________________________________________
max_pooling2d_8 (MaxPooling2 (None, 6, 6, 256)         0
_________________________________________________________________
flatten_2 (Flatten)          (None, 9216)              0
_________________________________________________________________
dense_8 (Dense)              (None, 4096)              37752832
_________________________________________________________________
activation_23 (Activation)   (None, 4096)              0
_________________________________________________________________
dropout_6 (Dropout)          (None, 4096)              0
_________________________________________________________________
dense_9 (Dense)              (None, 4096)              16781312
_________________________________________________________________
activation_24 (Activation)   (None, 4096)              0
_________________________________________________________________
dropout_7 (Dropout)          (None, 4096)              0
_________________________________________________________________
dense_10 (Dense)             (None, 1000)              4097000
_________________________________________________________________
activation_25 (Activation)   (None, 1000)              0
_________________________________________________________________
dropout_8 (Dropout)          (None, 1000)              0
_________________________________________________________________
dense_11 (Dense)             (None, 4)                 4004
_________________________________________________________________
activation_26 (Activation)   (None, 4)                 0
=================================================================
Total params: 64,741,644
Trainable params: 64,741,644
Non-trainable params: 0
_________________________________________
```

3.2 OPTIMIZATION

3.2.1 Adam Optimizer

Adam is an optimization algorithm which has a capability of adaptive learning. This technique is specially designed for deep neural network. It provides huge performance gain in terms of training speed and also calculates a performance rate for every individual parameters. In this work the compilation and optimization process are done using Adam optimizer.

3.2.2 RMSprop Optimizer

The RMSprop optimizer is same as gradient descent algorithm that differs only in the way how gradients are calculated. This optimizer restricts the oscillation in vertical direction so that the process proceeds deeper in horizontal direction increasing the rate of learning.

IV FINDINGS AND ANALYSIS

This section describes the findings and analysis of the proposed model.

4.1 ENVIRONMENT

This experiment is done in APU Quad Core A6 processor with 4GB RAM and Intel HD Graphics. This work is done in python environment in jupyter notebook with keras and tensorflow packages under windows 10 operating system

4.2 PARAMETERS

Adam optimizer is used for optimization of loss function. Categorical cross entropy is the loss function used here for training the model. The batch size is 32 which is a default value and 50 epochs are given to get better accuracy. The learning rate is 0.001.

4.3 PERFORMANCE ANALYSIS

The performance of this model is measured using various metrics such as accuracy, loss, precision, recall and specificity. These metrics are evaluated using True Positive, True Negative, False Positive, False Negative values. Also graphical representation are made for loss and accuracy for better understanding of performance. The calculation of these metrics are given below.

4.3.1 Accuracy: It is a measure of how accurate the model can identify the diseased or healthy condition. The value of accuracy can be found with the help of sensitivity and specificity scores.

$$\text{Accuracy} = \frac{\text{Number of correct prediction}}{\text{Total number of prediction}}$$

$$= \frac{TP+TN}{TP+TN+FP+FN}$$

From Figure 6. It is clear that the accuracy is increased considerably for both validation and training set. The graph is plot for accuracy against epochs. It can be observed that the accuracy rate for both testing and training set are almost similar at epochs ranging somewhere around 20 to 30. The accuracy rate increases considerably for training set as the number of epochs increases. It is noted that the accuracy range is similar and constant after 50 epochs, hence the epochs is set default at 50 and the batch size is set default at 32.

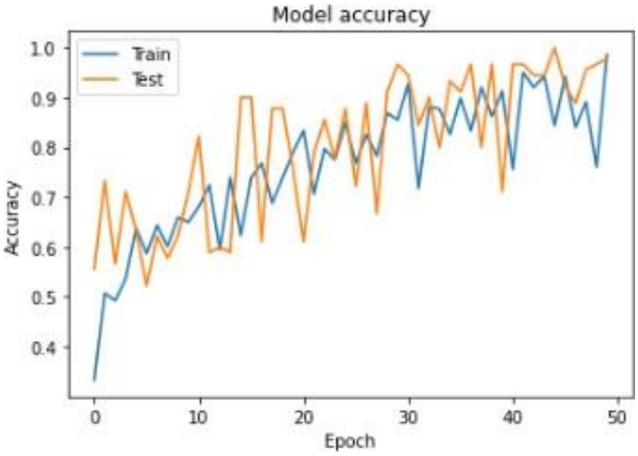


Figure 6. Accuracy rate of training and validation set

4.3.2 Loss: It is a scalar value that must be reduced while training a dataset of the model. When the loss value decreases regularly it is known that the model executes the result properly.

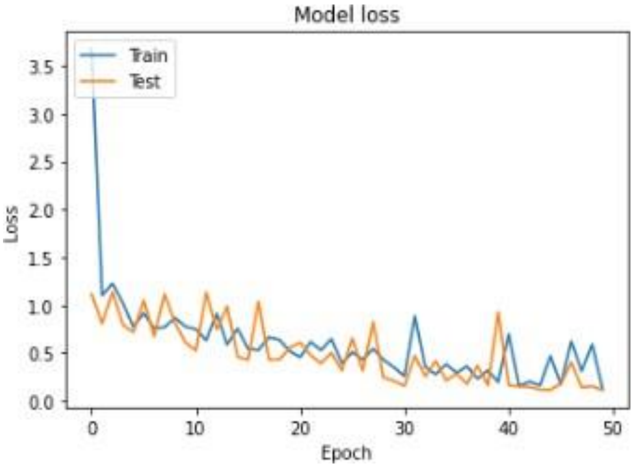


Figure 7. Loss rate of training and validation set

From Figure 7. It is clear that the loss rate reduces considerably for both training and validation set. The graph is plotted with loss against epoch. The loss value for training set decreases regularly and it remains almost same for epochs ranging from 20-40.

4.3.3 Sensitivity: Sensitivity is also denoted as recall value. It is the ratio of true positives that are correctly recognized by a diagnostic test. It defines how well the test is at detecting a disease. The value of sensitivity represents the probability of a test that identifies the leaf that do have disease. If the false positive value is very much less, then it is known that the numerical value of sensitivity is higher. Thus the leaf is tested to be diseased. The sensitivity value is calculated as follows,

$$\text{Sensitivity} = \frac{\text{Number of True positive}}{\text{Number of all positive}} = \frac{\text{TP}}{\text{TP+FN}}$$

4.3.4 Specificity: It determines how likely a crop without any disease affected can be ruled out. Specificity is a ratio of true negatives that are correctly identified by a diagnostic test. It put forward how well a test is correctly identifying a normal crop. The value of specificity can be calculated as follows,

$$\text{Specificity} = \frac{\text{Number of True negative}}{\text{Number of all negative}}$$

$$= \frac{TN}{TN+FP}$$

4.3.5 Confusion Matrix: It is also known as the error matrix, which is used to describe the performance of a model that are easily understandable. This matrix comprises of values like True positive, True negative, False positive and, False negative of this model is shown in Table III, that are described below,

True positive: Condition which is predicted true and it is affected True negative: Condition which is predicted false and it is not affected False positive: Condition which is predicted true but not affected False negative: Condition which is predicted false but affected

Table III. Confusion matrix

n = 360	Predicted: NO	Predicted: YES	
Actual: NO	TN = 268	FP = 2	270
Actual: YES	FN = 3	TP = 87	90
	271	89	

4.3.6 AUC: The Area Under Curve is one of the most important analysis for checking a model’s performance. It is a performance measurement curve for classifying problems at various threshold values. It depicts how well the model is capable of classifying different classes. When the value of AUC is higher it denotes that the model predicts the binary values better. The graphical representation of AUC is shown in Figure 8.

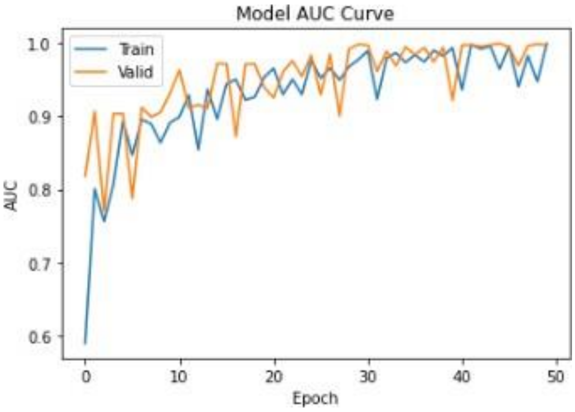


Figure 8. AUC rate for training and validation set

DOI 10.17148/IJIREEICE.2021.9505

This model shows high rate of value for all the metrics which indicates the better performance. The value of accuracy, loss, sensitivity, specificity, precision, F1 score and confusion matrix for this work are mentioned in Table IV.

Table IV. Value of performance metrics of this model

ATTRIBUTES	VALUE
Accuracy	97.77
Loss	11
Sensitivity	97.75
Specificity	99.25
Precision	97.75
F1 score	97.75
Confusion Matrix	[[87.0 , 2.0] , [3.0 , 268.0]]

V RECOMMENDATIONS

In this model the output is displayed using Django framework which can be developed in future as a mobile or web application. This work can be optimized and can be implemented in Artificial intelligence environment. To ponder different deep neural networks and make the most profound gaining knowledge of calculation and to enhance the grouping precision by improving the coherence and robustness of the rice ailment analyses framework.

VI CONCLUSION

This model uses convolutional neural network to detect and classify three types of diseases present in rice leaf. The performance of this model is enhanced by increasing number of epochs. This model shows an accuracy of 97.77% which is pretty good when compared previous works. The value of other metrics are also satisfactory. If the model is provided with large data, this approach gives specific and brief results for leaf sickness prediction. This model is effective with high reliability and robustness on different datasets. This model provides better results in real time application.

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