

## TRANSFER LEARNING APPROACH FOR PLANT DISEASE DIAGNOSIS IN PADDY CROPS WITH SMALL DATASET AND COMPLEX IMAGE BACKGROUND

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### **Abstract:**

Rice is one of the important and preferable grains among agricultural crops but it is susceptible to various viral, bacterial and fungal diseases. Various Deep CNN model has been implemented to diagnose such diseases. But many times, the lack of plant leaf picture datasets that can portray the wide range of symptoms and circumstances of features observed in reality is the main problem in using Deep CNN to automatically identify crop diseases. In this paper, we have discussed about a proposed transfer learning model which can deal these issues effectively. Transfer learning model learns the significant features so deeply and nicely that it gives promising result even for unprocessed input data.

### **1. Introduction**

To overcome the issue related to large dataset availability, we apply transfer learning approach and to provide varieties in visual appearance of symptom, we apply image augmentation techniques. These both approaches are applied to build effective disease classification model for Rice crop using InceptionV3 CNN architecture.

By the way, many automatic and computerized methods have been developed to diagnose paddy diseases. But most of them are unable to give effective results for small dataset with complex background images. Sometimes it is very difficult to get a large image data set available to provide learning to a deep learning model. Even if a large dataset is available, the deep learning model memorizes the image features due to the lack of variety in the visual appearance of the disease symptoms. These issues cause problem of overfitting. Therefore, there is always search for the techniques, which reduce the problem of overfitting even with small dataset in hand.

The motive of this paper is to develop a model, which can obtain discriminating features automatically from the leaf images with complex background from small rice leaf dataset, to develop a transfer learning model, which can recognize and classify the 5 types of deadly rice diseases with higher accuracy and to analyze the classification result. The paper is organized into

5 sections. Section 2 presents some related works are discussed. Section 3 discusses methods and materials used in “Transfer Learning Approach for Plant Disease Diagnosis in Paddy Crops with Small Dataset and Complex Image Background”. Section 4 discusses experimental results and discussions of the proposed model. Section 5 concludes the paper.

## 2. Related Methods

Shrivastava et al. (2019) [1] used TL approach in their study. In their research, they looked at 3 different kinds of paddy leaf infections. Pre-trained CNN model was utilized as features extractor using transfer learning (TL) approach. SVM was used as classifier. The suggested TL approach was found to be 91.37 percent accurate.

Pre-trained Deep CNN models were employed by Hassan et al. (2021) [2] to recognize diseases in plants. They have used the transfer learning (TL) approach to propose a method to recognize the diseases. Pre-trained CNN-based TL models were trained and verified using 53,407 leaf pictures from the PlantVillage database. They used 4 different pre-trained CNN architecture namely InceptionResnetV2, MobileNetV2, InceptionV3, and EfficientNetB0 to develop transfer learning models. EfficientNetB0 beat the other three models, with excellent accuracy of 99.56 percent.

Patil et al. (2021) [3] suggested a deep CNN-based crop disease identification and crop recommender system. For the disease identification system, they have developed 2 models, the first one was a simple deep convolution model and the other was a pre-trained VGG-16-based transfer learning model. A Content-based filtering approach was used to recommend suitable crops. In performance assessment, the VGG-16-based model was found more accurate than simple CNN with a validation accuracy of 97.53 percent.

To diagnose leaves infection in paddy crops, Acharya et al. (2020) [4] used five pre-trained convolution neural networks “ResNet, GoogLeNet, ResNeXt, Wide ResNet, and ShuffleNet” to implement ensemble learning. They acquired images of 3 kinds of leaves. These 3 types of leaves represented 3 types of diseases; 'Brown-spot, BLB, and Blast'. The proposed method has a 95.54 percent accuracy rate.

From the discussion of above transfer learning methods, it is clear that TL models gives higher accuracy.

## 3. Methods and Materials

To diagnose paddy plant illnesses and improve classification, we used the transfer learning strategy with pre-trained DCNN architecture. In this section, we present cutting -edge methods and materials utilized for our study.

### 3.1 Base Methods

In this section, we have discussed about basic components of CNN. Further, structure of InceptionV3 model is discussed. InceptionV3 is a pre-trained CNN model that acts as backbones of the proposed work.

### 3.1.1 CNN

In the last few decades, CNN has proved to be a breakthrough in the domain pattern recognition and computer vision. Nowadays Deep learning, particularly CNN is becoming very popular among researchers because of its accurate classification and effective Learning ability. CNN is a feed-forward NN that is widely used in image recognition. CNN has several hidden layers that have the potential to extract the relevant discriminating features even from complex problems.

The beauty of CNN is that it works well for a very large number of labelled images and effectively processes each and every portion in the images to extract the characterizing features. A typical CNN contains several hidden layers, an input layer, and output layer. CNN accepts the input data especially images as a multidimensional array. Hidden layers contain multiple basic blocks consisting of convolution and pooling layers. These blocks are connected in a sequential manner one after another. The architecture of CNN always performs two types of basic operations namely convolution and pooling operations.

1. Convolution layer (CL): Convolution operation plays an important role to extract feature maps from input image samples. The convolution operation is used to convolved one feature matrix with many different sized filter matrices to get many feature maps (feature matrices). Convolution operation is shown in Figure 1 with help of an example.

2. Batch Normalization Layer (BNL): BNL is used to normalise the input channel by re-centering and re-scaling across a particular mini-batch size. Re-centering and re-scaling are performed by computing means and standard deviation across a mini-batch size.

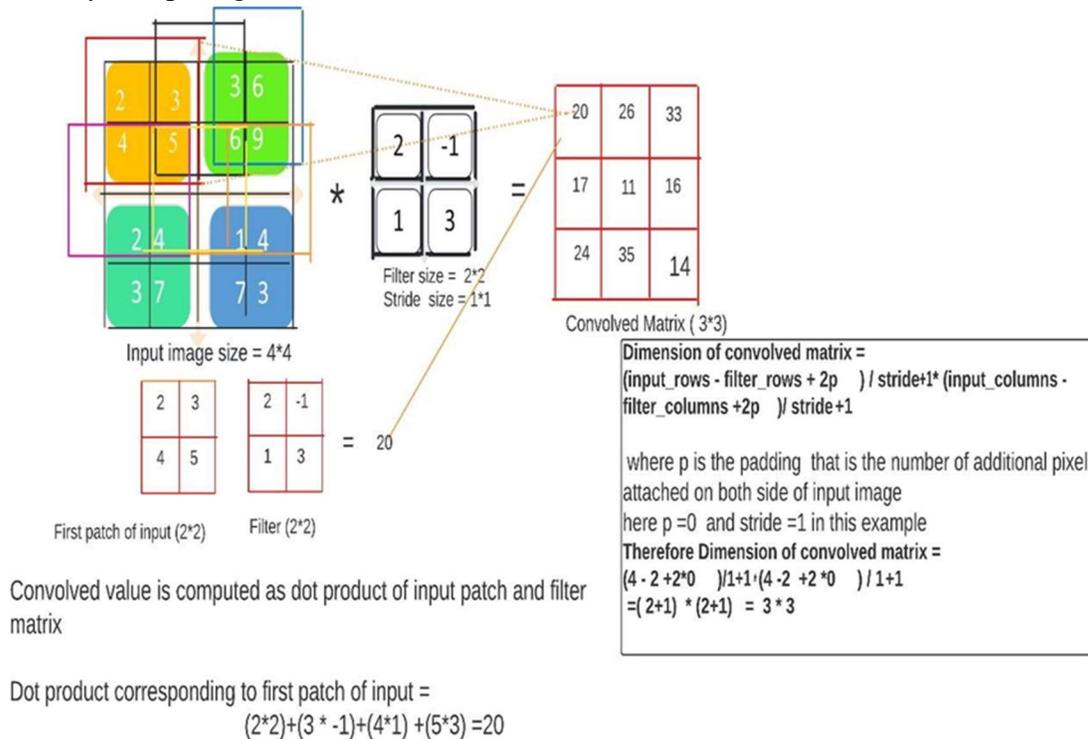


Figure 1. Convolution Operation

The BNL assists in accelerating the learning process while simultaneously ensuring network regularisation to avoid overfitting. Batch normalization operation can be applied before or after activation layer. Batch\_Norm operation uses batch\_wise mean and variance of input samples. Batch wise mean is calculated by using Eq. (1). Batch wise variance is calculated by using Eq. (2). Batch normalization computation is shown in Eq. (3).

$$mean = \frac{1}{n} \sum_{j=1}^n z_j^{(i)} \quad (1)$$

$$variance = \frac{1}{n} \sum_{j=1}^n (z_j^{(i)} - mean)^2 \quad (2)$$

$$Batch_{Norm} = \frac{Z^{(i)} - mean}{\sqrt{variance + \epsilon}} \quad (3)$$

Where mean, variance and Batch\_Norm are the dimension wise computation along a mini-batch. These computations are performed for all input dimensions. Here, n is the size of mini-batch, Z is the d-dimensional input data,  $z_j(i)$  is the value of i-th dimension in j-th input data along a mini-batch,  $Z(i)$  is the value of i-th dimension of an input.

3. Relu Layers (RL): After the Convolution, the ReLU layer is utilized to convert all negative values of the convolved feature maps to zero. ReLU is recommended as an activation function because of its ability to quickly converge. ReLU operation is shown in figure 2.

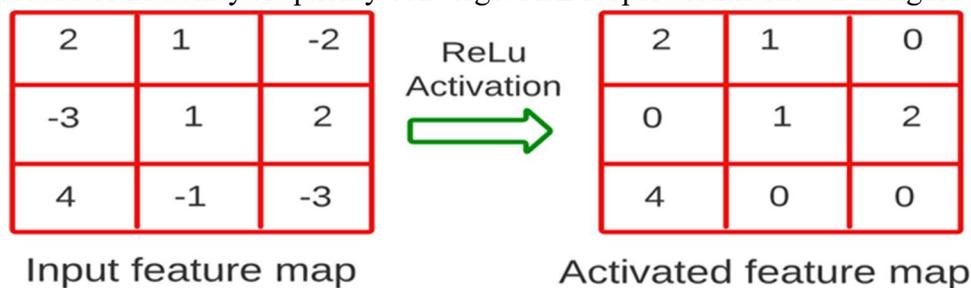


Figure 2 Relu Activation

#### 4. Pooling Layers (PL):

A Pooling Layer is usually applied after a ReLU Layer. This layer's major goal is to lower the dimension of the convolved feature map in order to decrease the computational complexity. Generally, pooling means a small area, therefore a small area is taken of the input matrix and the average value is computed for all cells present in that area in case of average pooling. In the case

of max pooling, the greatest value is selected among all cells present in that small chosen pool(area). when pooling is performed on an image, only summarised value (average or max) is taken over all of the present values. Max pooling operation is shown in figure 3.



Figure 3 Max Pooling operation

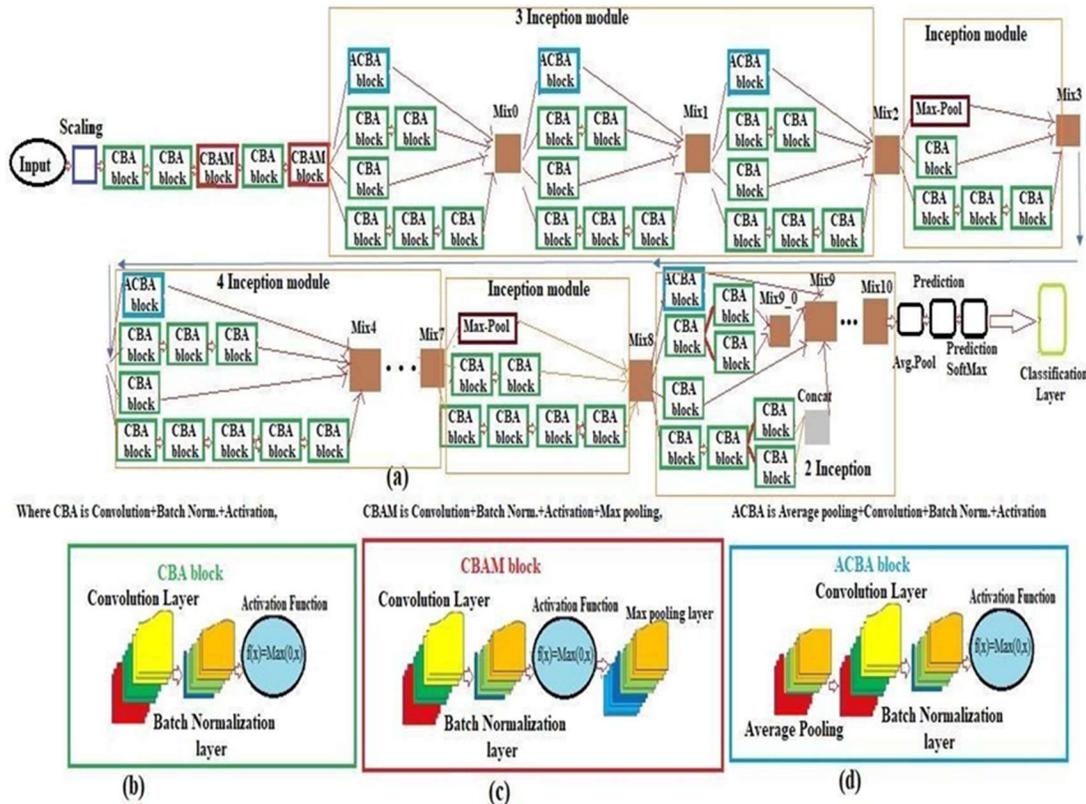
## 5. Fully connected layers (FC)

The CNN's last layer is made up of FC layers (flatten layers) along with a Softmax layer that assign the input picture into any one of the pre-defined categories. A FC is a feed-forward NN that is employed to complete the classification operation. For each labeled category, SoftMax activation produces probability.

### 3.1.2 InceptionV3

The easiest technique to enhance the capabilities of DNN is to raise the breadth and depth of the networks. However, as the breadth and depth of the network grow, it includes more parameters and consumes more computational resources. To address these issues, Szegedy et al. (2016) [5] first incorporated the Inception module into the GoogLeNet architecture, and it won the ImageNet ILSVRC challenge competition with an outstanding performance.

The design of InceptionV3 is divided into two parts: the first is a deep convolutional structure with numerous inception modules to retrieve essential features, and the second is an FC network with SoftMax function at the end to implement classification. The primary objective of this method was to increase efficiency and construct a deeper network to detect complicated attributes from input photos. In the inception modules, CLs with variable kernel sizes (1\*1, 1\*3, 3\*1, 3\*3) are executed in parallel, and the outputs are merged before being transmitted to the next layer. Figure 4 depicts the architecture of InceptionV3.



**Figure 4 InceptionV3 architecture**

We updated the native InceptionV3 architecture's last three layers (out of 316 layers) to transfer the learned weights of the pre-trained model to our model dealing with our particular dataset. During fine-tuning, the starting layers of the native InceptionV3 model are locked, and only the last three layers are customized to meet our requirements. Figure 10 depicts the customization of layers.

### 3.2 Proposed Work

This section covers the complete process of developing a disease classification and diagnostic model. Figure 5 depicts the flow diagram of the proposed system.

#### 3.2.1 Image samples collection

We used the rice diseased dataset [6] to get 2,550 photo of rice leaves in 5 categories to provide learning to suggested approach. Each kind of disease consists of 510 image samples. Figure 6 shows 5 disease categories on the x-axis and respective image sample counts on the y-axis. Infection symptoms, causing organism and sample images of all 5 diseases are shown in Figure 7.

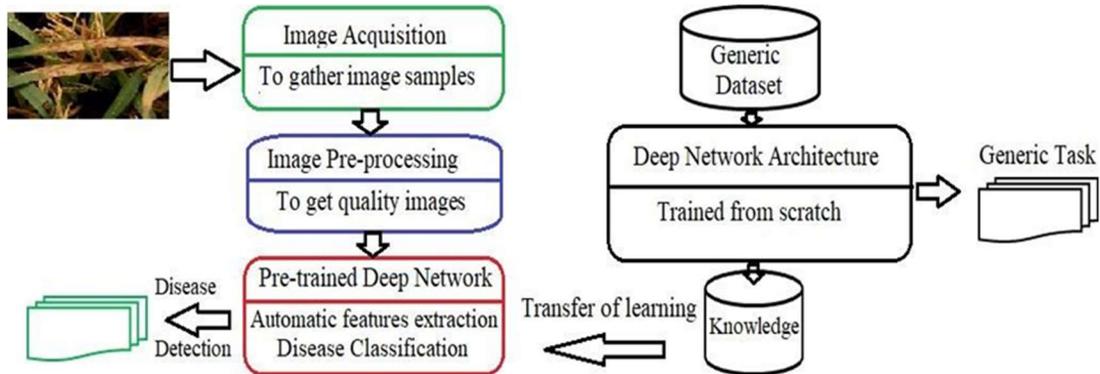


Figure 5 Flow diagram of Suggested method

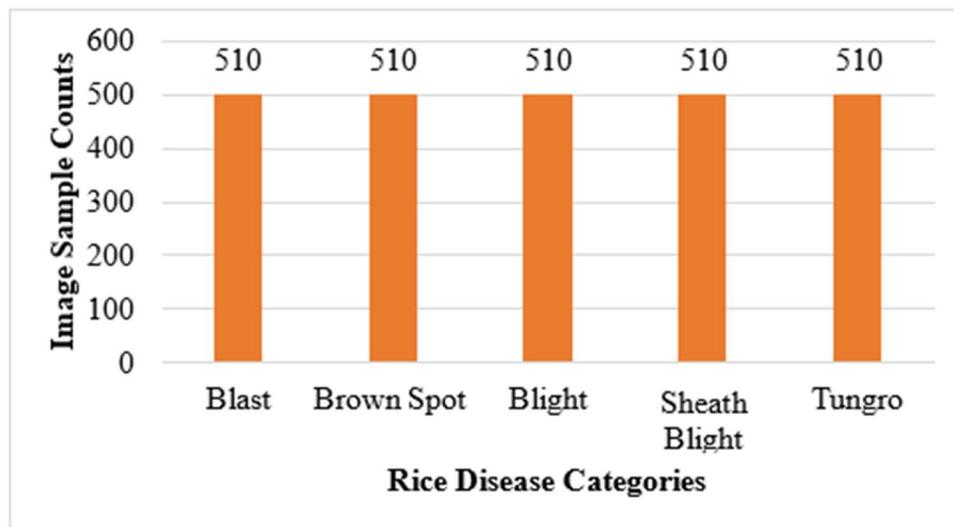


Figure 6 Description of Data set

### 3.2.2 Pre-processing of images

Pre-processing is a crucial step in DIP to produce high-quality photos that meet our needs. Resizing, Contrast stretching, and augmentation are the 3 main preprocessing methods employed in this study. The resizing method is used to create a resized picture with the required input size of 227\*227 for InceptionV3.

Disease	Symptoms	Causing Pathogen	Sample Image
<b>Brown Spot</b>	The disease manifests itself as circular to oval spots with dark brown spots	Caused by pathogen; Drechslera oryzae	
<b>Blast</b>	Oval or spindle-shaped lesions with an ashy greyish centre and a brown border are common.	Caused by fungus; Pyricularia oryzae	
<b>Blight</b>	Symptoms include elongated sores on the leaf tip that are a few inches long. initially white color that turns to yellow	Caused by bacterium; Xanthomonas oryzae	
<b>Sheath Blight</b>	Grayish-green-colored lesions are appeared on the leaf sheath. Adjacent infected regions frequently converge, damaging the stem and forcing it to fall and die.	Caused by fungus; Rhizoctonia solani	
<b>Tungro</b>	Symptoms include empty or partially filled seeds, discolored lesions, slower development, and fewer tillers.	Mixture of two viruses (RTBV and RTSV)	

Figure 7 Description of dataset's diseases

Contrast stretching operation is applied after resizing the input images. Conversion of RGB photographs to a format that includes luminance information is the first step required to apply the contrast stretching. As a consequence, we transformed resized sample to L\*a\*b\* format. The contrast is adjusted using the luminosity element L\*. The luminance is adjusted to vary the pixel intensity while keeping the original colour. The global contrast enhancement of the L component is calculated using Eq.4.

$$L_{new}(x, y) = \frac{L(x, y) - L_{Low}}{L_{High} - L_{Low}} \times 100 \quad (4)$$

Here,  $L(x, y)$  is the new contrast increased luminosity of the pixel  $(x, y)$ ,  $L(x, y)$  is the old luminosity value,  $L_{High}$  is the highest luminosity level of the input sample, and  $L_{Low}$  is lowest Luminosity level of the input sample.

After the contrast has been adjusted, the image is converted back to RGB format. Transformation of input image to contrast stretched image is shown in figure 8.

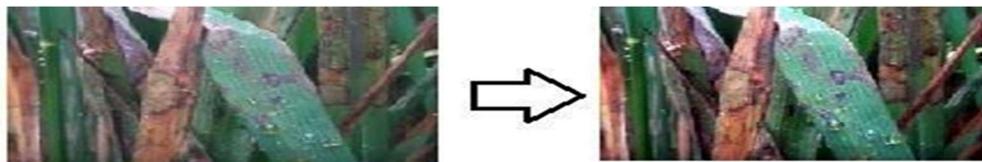


Figure 8 Transformation of input image to contrast stretched image

The augmentation method is used to increase the visual diversity of input samples. In this study, the augmentation process includes operations such as reflection, translation, and scaling. Augmented image samples are shown in Figure 9. Here, reflection operation randomly reflects the training samples along the y-axis. Translation operation randomly translate the training samples up to 30 pixels vertically and horizontally. Similarly scaling operation scale the training samples 10% vertically and horizontally. Data augmentation prevents the network from being overfit and remembering the exact characteristics of the training pictures.



Figure 9 Augmented Image Samples

### 3.2.3 Building of suggested model using Transfer Learning (TL)

TL as discussed in Lumini (2019) [7] is a novel learning methodology in which a DCNN model pre-trained on huge dataset is utilized to build a model for another task with specific dataset. In the simple learning process (without TL), the starting weights of the DL model are initialized with random values. Whereas, in transfer learning, the starting weights of the DL model are initialized with the pre-trained model's learned parameters (weights and biases). Thus, transfer learning model utilized learned knowledge of pretrained model to capture the varieties of most significant features from present dataset. In this study, we look into using a InceptionV3 pre-trained on a massive ImageNet [8] database, which is then deployed to the Rice diseased dataset [6]. The basic steps of the TL methodology are given below.

1. Selection of pre-trained DCNN model as foundation:

A InceptionV3 pre-trained DCNN is selected as the base model, and the learned parameters (Biases and weights) of InceptionV3 pre-trained on ImageNet are utilized to assign the initial parameters of the suggested model.

2. Changes to the base model:

Parameters of the initial 313 layers of the base model have been locked. In order to obtain a new customized model that fits on our task, the structure of the rest 3 final layers is changed. Figure 10 depicts the changes in the last 3 layers of native InceptionV3 model.

3. Apply finetuning to the customized model: To lower the loss function.

5 categories of leaf pictures from the Rice diseased database are utilized to finetune the customized model.

Layer Number	Native Layers	Modified layers
314	Predictions (1000 fully connected layers)	Predictions (5 fully connected layers)
315	Prediction SoftMax (with activation 1x1x1000)	Prediction SoftMax (with activation 1x1x5)
316	Classification Layer (1000 classes)	Classification Layer (5 disease classes)

Figure 10 Changes in Native InceptionV3 model

### 3.2.4 Disease Diagnosis and Classification

Three layers of InceptionV3 have been changed to work with the samples we have collected from rice diseased database. In customized InceptionV3 model, the final 1000 FC layers are replaced with 5 FC layers. The SoftMax layer with activation 1\*1\*1000 has been changed with SoftMax layer with activation 1\*1\*5. SoftMax activation function is used to determine the classwise probability for the input sample. This probability is used to assess which output class is appropriate for a given input image. finally, classification layer with 1000 classes is changed to the classification layer with 5 classes.

## 4. Implementation and Results

The experimental setting and assessment of performance of the recommended model are shown in this section. This section discusses the disease wise number of samples used to train and test the model, the training-validation process as well as the result analysis.

### 4.1 Experimental Setting

The database of leaf images of rice plant is acquired from the rice diseased dataset. There are five kinds of diseased leaves in this dataset. The dataset is divided into 70:30 partitions, with 70% of the samples acting as training samples and 30% serving as validation samples.

To conduct the experiment, we used the ESBS, DSBS, and Healthy leaves classes as input data. These 3 categories were created using the Brown spot class partitioning approach applied to the paddy leaf samples database [9]. Figure 11 depicts the procedure for creating a new data collection for the model's learning. 3008 photographs of ESBS class, 986 photographs of DSBS class, and 4000 photographs of healthy class make up the new dataset for model's learning. The same has been elaborated in literature using TL approach [13].

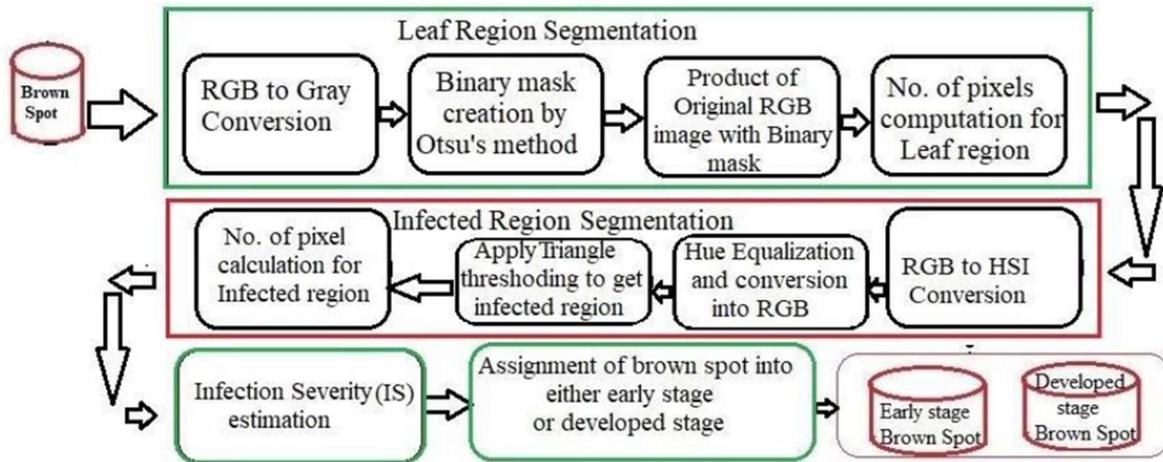


Figure 11 Estimation of Severity of Infection (IS) and Partition of collected Brown spot dataset

Infection severity (IS) =  $N1 / N2$  is used to calculate severity where  $N1$  is pixel counts in infected area and  $N2$  is pixel counts in entire Leaf area. Calculating the white pixels count in the binary mask formed by otsu's approach yields the total pixels count in the entire leaf area ( $N2$ ). Eq. 5 is utilized to compute the pixels count in the diseased area ( $N1$ ) using the binary picture.

$$(N1) = N_{tb} - N_{ob} \quad (5)$$

Where  $N_{tb}$  denotes the black pixels count in a picture generated by triangle thresholding and  $N_{ob}$  is the black pixels count in a binary mask created by Otsu's approach. After the computation of IS for the supplied brown spot leaf picture, it is classified into one of the two categories: ESBS and DSBS. We've set the severity threshold at 0.01 to classify the brown spot illness into one of the two categories (ESBS and DSBS). The following rule is used to categorize the input sample:

For the input brown spot picture  
 if (IS ≤ 0.01)  
 then keep input picture in ESBS class.  
 Otherwise, keep input picture in the DSBS class

Brown spot detection at initial stage means ability to recognize the tiny spots in sample leaf picture (tiny infected areas). Therefore, we attempt to maintain the severity threshold as low as possible for brown spot identification at initial stage. We conducted multiple tests with different alternative criteria less than 1% and found that nearly all photos of acquired brown spot dataset were classified as developed stage brown spot in these circumstances. As a result, we decided on a severity threshold of 1%. Table 1 depicts the summary of the obtained dataset and the division of Rice leaf classes into training and testing samples.

Table 1. Division of dataset into Training and Testing samples

Disease categories	Training sample counts	Validation Sample counts
Blast	357	153
Brown Spot	357	153
Blight	357	153
Sheath Blight	357	153
Tungro	357	153

#### 4.2 Training-validation process

This experiment was conducted by providing pre-processed data samples to the suggested deep CNN model. The proposed model's classification performance was examined on the training and validation dataset (shown in table 1). Six epochs were employed, each with 178 iterations. A total of 1,068 iterations were performed to observe the results of the recommended technique. The validation frequency was set to 178 iterations, while the global learning rate was set at 0.0003.

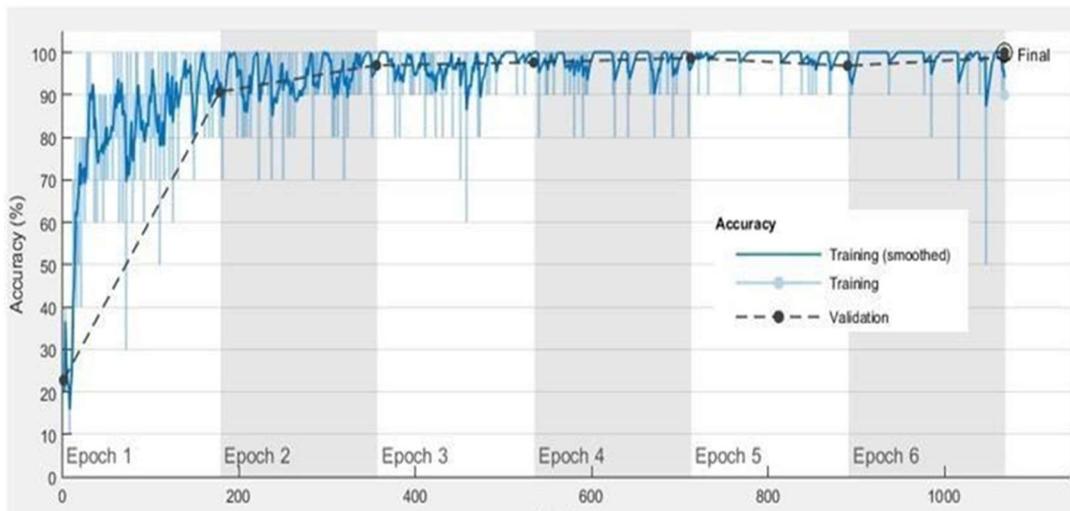


Figure 12 Training and Validation Processes of Inception V3

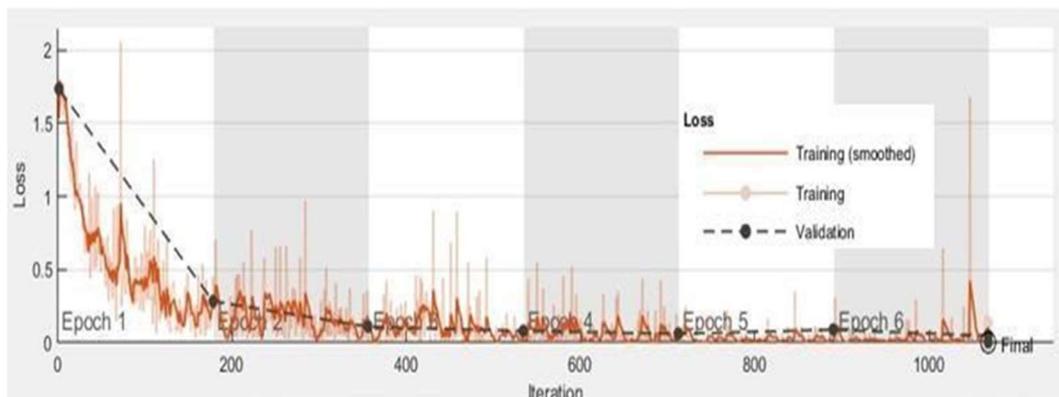


Figure 13 Training and validation loss rate of InceptionV3

The validation frequency was set to 178 iterations, while the global learning rate was set at 0.0003. We increased the FC layer's 'BiasLearnRateFactor' and 'WeightLearnRateFactor' values to enable quicker learning in the changed layers than in the fixed layers.

Figure 12 depicts the training and validation process. Figure 12 shows how the model's accuracy changes as the number of epochs in the training-validation process increase. Figure 13 shows how the loss fluctuates as epochs grow. Loss interprets model goodness for validation and training datasets. A better model is one with a lower loss. A confusion matrix is used to demonstrate the model's performance.

#### 4.3 Results and Discussion

A confusion matrix is used to demonstrate the model's performance. Figure 14 shows the recommended model's correct and incorrect classifications using a confusion matrix. In this confusion matrix, the predicted disease is represented on the y axis, while the actual disease is shown on the x-axis. The confusion matrix (Figure 14) illustrates the class wise true as well as false classifications done by the suggested model. Class wise precision is shown in the rightmost column and class wise recall is depicted in the bottom row. The Overall validation accuracy of suggested system is depicted in lowermost cell of rightmost column.

The developed model learned the discriminating characteristics of images in such a good manner that the precisions of all 5 classes are recorded 100% and recall of all 5 classes are recorded 100%. Wrong classification is reduced to zero in all the 5 classes. The Overall validation accuracy of suggested system is obtained as 100 %.

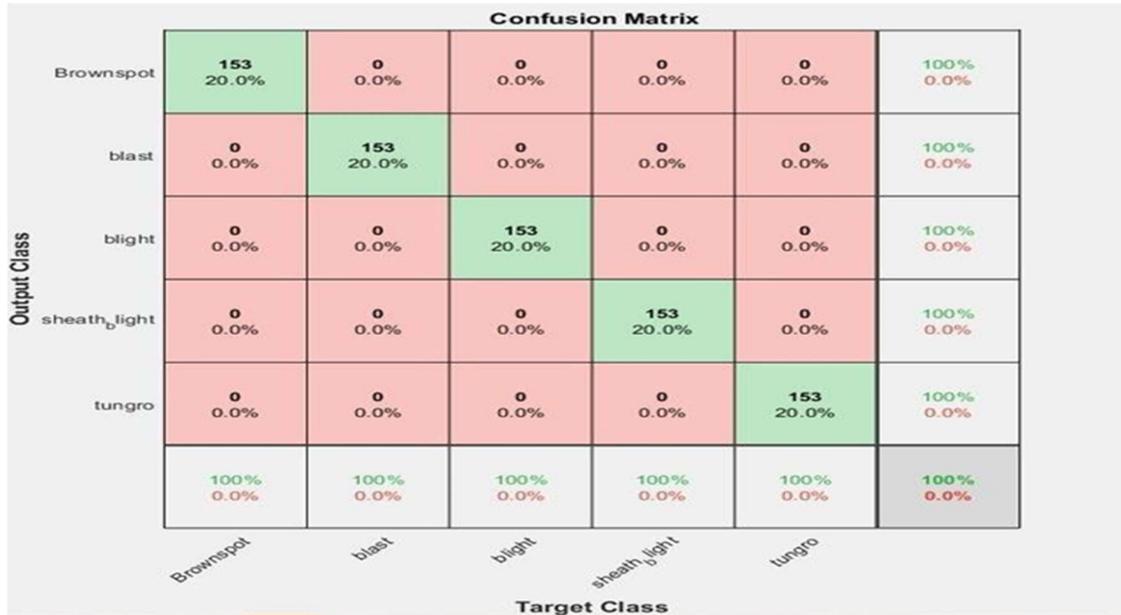


Figure 14 Classification results of suggested model using Confusion matrix

From the result analysis, it is clear that transfer learning (TL) is able to recognize and classify the diseases with excellent accuracy even with a small dataset and complex background images. Here, the contrast stretching process played a crucial role to enhance the visual appearance of input images. Contrast stretched images are very useful in the extraction of correct and significant features. Further, to achieve variety in visual appearance, an image augmentation process was used. The image augmentation process stops the model to memorize the training features and helps to generalize the learning. Thus, image augmentation reduces the chance of overfitting.

#### 4.4 Results comparison of proposed approach with the existing methods

We compared the findings of our proposed model to those of the other relevant existing approaches.

**Table 2 Comparative analysis of accuracies of proposed model with existing models**

Authors	Methods	Plant	Overall Accuracy
Islam et al.,2021[74]	“VGG-19, ResNet-101, Inception-Resnet-V2, and Xception”	Paddy	92.68%

Hassan et al.,2021[108]	MobileNetV2, Inception-ResnetV2, InceptionV3, and EfficientNetB0	14 different plant species	99.56%
Patil et al.,2021[109]	VGG16	-----	97.53%
Acharya et al.,2020[110]	Wide ResNet, ResNet, GoogLeNet, ShuffleNet,and ResNeXt	Paddy	95.54%
Proposed approach	InceptionV3	Paddy	100%

All of the approaches compared here used photos of plant leaf samples to detect plant diseases. For illness detection, all the techniques in this comparison utilized the transfer learning approach. We have compared works of Islam et al. (2021) [10] (“VGG-19, ResNet-101, Inception-Resnet-V2, and Xception”), Hassan et al. (2021) [2] (MobileNetV2, Inception-ResnetV2, InceptionV3, and EfficientNetB0), Patil et al. (2021) [3] (VGG16), and Acharya et al. (2020) [4] (Wide ResNet, ResNet, GoogLeNet, ShuffleNet, and ResNeXt). Our approach performed better than that of compared method with an accuracy of 100%. This comparison is shown in table 5.2.

## 5. Conclusion

The suggested approach is capable of handling data sets consisting of images with complex background and also capable of automatically extracting the features from the input samples. The suggested system's strength is its capacity to detect paddy infection with 100% accuracy even with small dataset in hand.

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