Rice Leaf Disease Classification Using CNN

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Abstract

Rice is amongst the majorly cultivated crops in India and its leaf diseases can have a substantial impact on output and quality. The most important component is identifying rice leaf diseases, which have a direct impact on the economy and food security. Brown spot, Leaf Blast, Hispa are the most frequently occurring rice leaf diseases. To resolve this issue, we have studied various machine learning and deep learning approaches for detecting the diseases on their leaves by calculating their accuracy, recall, and precision to measure the performance. This study helps the farmers by detecting the diseases in rice leaves in order to get a healthy crop yield. The deep learning models perform well when compared with the machine learning methods.

Keywords: rice leaf diseases; deep learning; Convolutional neural networks; machine learning; transfer learning

INTRODUCTION

India is a land of Agriculture as it plays an essential role in our country because a lot of the people are dedicated to the agricultural industry. Crop production is amongst the major factors which are affecting domestic market conditions in our country. Agricultural firms began to search for new high-yield, cost-effective inventions as a consequence of expanding population, variable weather conditions, and political unpredictability. The health of the plant/crop is critical for achieving food security and sustainability in agriculture. However, the plants can quickly become infected with illnesses, which can cause major social and economic problems, due to a variety of factors. Crop diseases can affect its growth and development, and also crop yield and quality, and are one of the most common reasons for productivity loss. To avoid soil pollution, the illness should be detected and certain pesticides should be used from their beginning stage.

There are a variety of methods for detecting plant diseases in their early stages. The traditional method of plant disease detection is naked eye monitoring, which is ineffective and inaccurate for large crops.The major goal of this paper is to research and diagnose rice leaf illnesses in advance, as well as to identify the disease's name so that appropriate precautions can be followed. Rice is a standout amongst the most vital food plantations .in our country, as well as one of the crops having a variety of purposes and high nutritional worth, with a production volume of 104.80 million tons coming from various Indian states. Because our country is the largest producer of rice at the second position in the world, the country's rice-growing region is constantly expanding. It contains a high amount of carbohydrates and protein, as well as a significant amount of dietary fiber and minerals. Plant illnesses are caused by pathogens, fungus, bacteria, viruses, and other microbes in the majority of cases. Rice leaves are sensitive to diseases that are caused by fungus, viruses, and the varied field environment makes it simple for pathogens to infect the leaves.

Brown Spot Healthy Rice Leaf

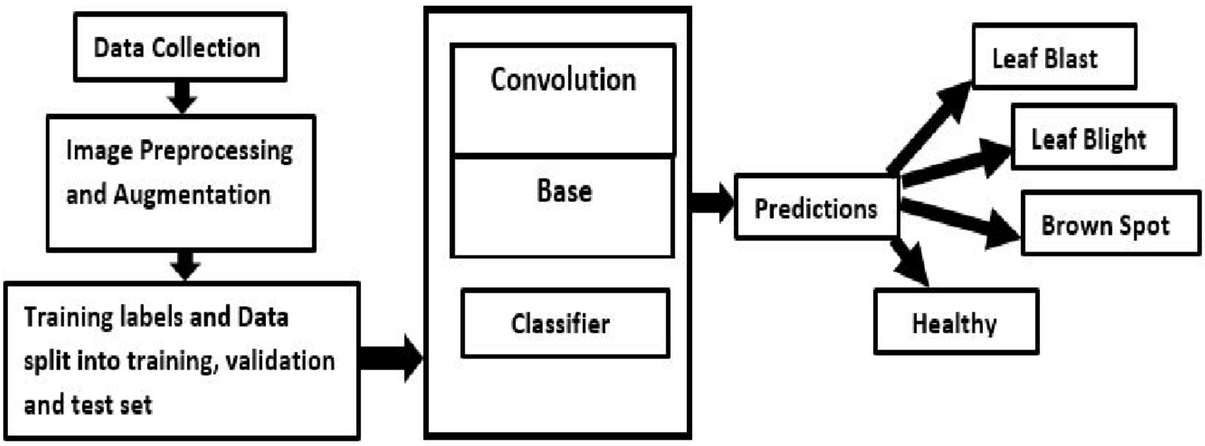
Hispa Leaf Blast

Types of Rice Leaf Dieases

Climate changes will create an ideal environment for those pathogens to thrive. The growth of crops is hampered in their initial stages due to fungi-caused illnesses. If illness strikes while the crop is still growing, it might reduce the crop's yield. Manually determining the presence of illnesses in large agriculture regions is quite challenging. Diseases, particularly in rice plants, have become a problem since farmers are unable to identify leaf disease with the naked eye, and they must consult the expert in order to discover that specific disease, which takes more time and requires much expense. The most frequently occurring diseases in rice leaf are Brown spot, Hispa, LeafBlast, Healthy.

Thus, disease detection in leaves is an important topic that provides many benefits in monitoring large fields of crops. Rice leaf disease can affect yield and quality by damaging the green layer from the leaves. The way to control these rice diseases is to rapidly and precisely detect the disease type and then implement appropriate corrective actions in a timely manner[8]. Using digital image processing techniques and deep learning networks, the detection of disease is efficient, consumes less time, and is accurate. Advances in Computer vision offer an opportunity to extend and increase plant protection.

The content of the paper is organized in the following manner: In Section 2, we'll go through a few previous kinds of research that have been done using image processing techniques, ML methods, and DL models for recognizing diseases in the leaves of rice plants. Section 3 is about the different deep learning methods studied for rice leaf disease detection, and the final section concludes the experimental results and future scope.



. Overview of Proposed Method

In this paper we are working on an automated system to detect the fungal disease of rice plants which is a major cause for a loss of a rice plant. This type of disease may occur and spread due to climate change and moisture on the leaves. The first step is acquiring the image. The act of obtaining a picture from a source is known as image acquisition. The input can be taken from different resources especially hardware such as sensors or cameras etc. This is a crucial step in the entire process because processing is impossible without an image. This step is always the initial phase in the process. The second step is dataset collection. The dataset in our method consists of a number of images of the four diseases of rice leaf which we are predicting. We train the dataset using a wide variety ofimages to get better accuracy. The next step is preprocessing of data. Collected data should be preprocessed involving data cleaning and removing all the inconsistencies from the data. We do this process to obtain a clean dataset for achieving better accuracy. Then we perform feature extraction which involves extraction of only those features which are important and which are most required. Then we use various DL methods which we are employing in our method and train and test the dataset accordingly. Finally, the images are classified according to their respective diseases. In our method, we have tested four diseases that affect the rice plant.

Literature Survey

(HaixiaQiet al.,2021) this paper dealt with the automatic identification of groundnut leaf diseases using the stack ensemble technique. The proposed research was conducted on diseased groundnut leaves to identify four groundnut leaf diseases, in this study, they merged deep learning models with traditional machine learning approaches. Deep layer networks, such as ResNet50 and DenseNet121, performed the best when it came to dataset prediction. The maximum accuracy for data augmentation was 97.59 percent.ResNet50 had the best identification performance when integrated with the LR model.

(GowriShankaret al.,2020) in this paper, they discussed the automatic identification of groundnut leaf diseases. A DL model was employed to increase the network's speed and accuracy in finding and classifying different disease-infected patches on groundnut leaves. To grow the efficiency of previous algorithms, they replaced the typical SVM classifier with KNN for distinguishing four different pathologies (Leaf Blight, Leaf Spot, Stem Rot, and Bud Necrosis).

(Ramakrishna et al.,2015) this paper discusses one of the most common illnesses that affect ground leaves in its early stages. The suggested scheme incorporates four leading phases for the detection and categorization of groundnut leaf disease. The initial process is to do a color renovation on the images that will be used as input. The plane separation would be the next step. The extraction of features is the next phase. The backpropagation algorithm is employed to detect the leaf disease as a last step.

(NilamBhiseet al.,2020) In the suggested research, disease detection is carried out in two stages. The type of crop and the type of the disease are determined in the first step using a CNN. Tensorflow lite is used to categorize the uploaded picture numerical value to the dataset values, and Keras frameworks are used to classify the dataset values. In terms of disease diagnosis performance, the findings show that the Mobile Net Model outperforms other models.

(Salini et al.,2021) The focus of this research is to reduce pesticide use in agriculture while making better quality and quantity of output. For feature extraction, they use image processing techniques, and for classification, they use SVM. To improve performance and provide a better outcome, the model was combined with data augmentation. This research aims to detect three major rice plant diseases: Bacterial Leaf Blight, Brown Spot, and Leaf Blight. The input to this model is the full image for processing, and the output will be the disease that has affected the plant, as well as the model's accuracy.

(Mahalakshmi et al.,2021) To identify the existence of disease as well as to detect specific types of disease, the author extracted color and texture features of corn leaves then the collected features are categorized using Binary SVM and multi-class SVM. The proposed system's accuracy is 85 percent, which is its best performance.

(Saleem et al.,2019) this paper reviewed the detection of several plant diseases and their classification by deep learning. Alternative deep AEES 2022 IOP Conf. Series: Earth and Environmental Science 1032 (2022) 012017 IOP Publishing do learning models and machine learning methods for visualizing plant diseases are examined in this study with the conclusion that deep learning models are more accurate than conventional machine learning techniques. (Shruthi et al.,2019) , ML techniques were used to describe the steps involved in the detection of general plant disease. They have used a CNN to detect the diseases with high accuracy.

(Yang Lu et al.,2018) this article mainly focuses on the identification of diseases on rice crops. To detect diseases in the rice crop, it employs deep Convolutional neural networks.. One of the backdrops of this study is that they used less data for training.

(Azathet al.,2021) this research paper presents the work on the cotton leaf for the detection of diseases and pest diagnosis using image processing and Deep Learning.

Research Methodology:

Research methodology for developing a rice leaf disease detection system using Convolutional Neural Networks (CNN) involves a systematic approach to collect data, preprocess it, design and train the CNN model, and evaluate its performance. Below is a step-by-step research methodology for such a project:

Problem Definition:

Define the specific objectives of your research, such as the types of rice leaf diseases to be detected and the scope of the project.

Data Collection:

Collect a large and diverse dataset of rice leaf images. This dataset should contain healthy leaves and leaves affected by various diseases.

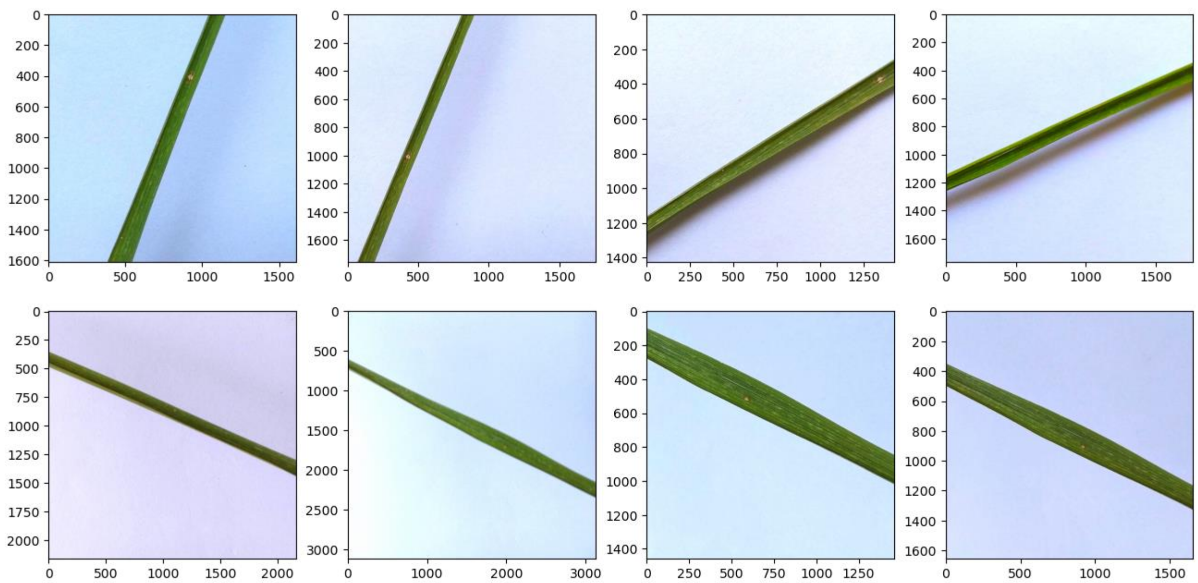
Label the dataset with appropriate disease classes.

Data Preprocessing:

Perform data augmentation to increase the diversity of the dataset. Techniques may include rotation, flipping, scaling, and adding noise.

Split the dataset into training, validation, and test sets.

Normalize the pixel values of the images.



Model Architecture:

Choose a CNN architecture suitable for image classification. Popular choices include VGG, ResNet, Inception, or custom architectures.

Modify the chosen architecture if necessary to match the specific requirements of the problem.

Model Training:

Use the training dataset to train the CNN model. This involves feeding the model with the labeled images and optimizing the model's weights.

Experiment with different hyperparameters such as learning rate, batch size, and the number of epochs.

Model Evaluation:

Evaluate the model's performance using the validation dataset. Common evaluation metrics include accuracy, precision, recall, F1-score, and confusion matrices.

Monitor the model's performance during training to detect overfitting and fine-tune hyperparameters as needed.

Model Optimization:

Fine-tune the model based on the validation results.

Implement techniques like dropout and batch normalization to improve generalization.

Testing:

Evaluate the model's performance on the test dataset, which it has never seen during training.

Report the results, including accuracy and any relevant metrics.

Visualization:

Visualize the learned features using techniques like activation maps or t-SNE to understand what the model is focusing on during classification.

Error Analysis:

Analyze the misclassified images to identify common patterns or challenges faced by the model.

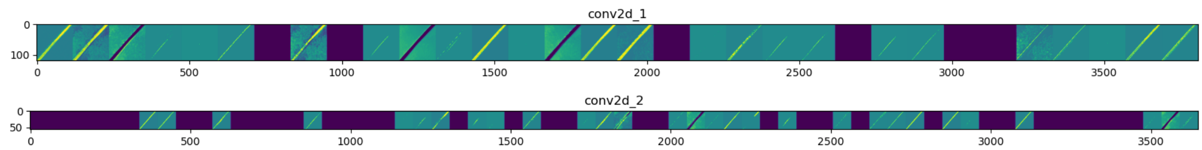
CNN-Based Rice Leaf Disease Recognition Model

We propose a custom CNN-based model for recognizing rice leaf diseases. The model is designed with a depth of 10 layers. These are input layer, convolution layer 1 (Conv1), max pooling layer (Pooling1), convolution layer 2 (Conv2), max pooling layer 2 (Polling2), convolution layer 3 (Conv3), max pooling layer 3 (Pooling3), two dense layers (Dense1 and Dense2) and an output (softmax) layer 3 for an input image of size w × h.

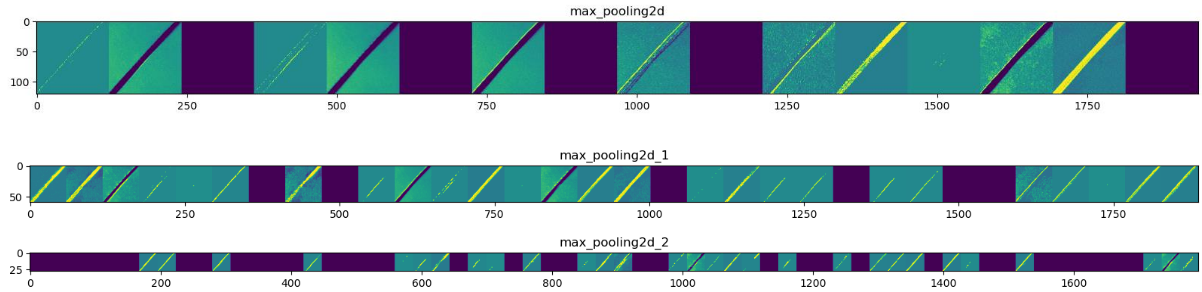
Input Layer: The input layer of our model is fed by an RGB image of size w0 × h0, where w0 is the width and h0 is the height of the image, respectively

Convolution Layer(s). A convolution layer’s primary task is to identify local conjunctions of features from the previous layer and map their presence to a feature map. In our model, we use three convolution layers, including several filters to get the output feature maps. Thus, these maps save the information where the feature takes place in the image and how well it assembles to the filter. Therefore, each filter is trained spatial regarding the position in the volume it is applied to, and each filter detects certain features from the rice leaf disease image. In this layer, the following equation computes the output feature maps.

```
Model: "Conv2D_Model"
_________________________________________________________________
 Layer (type)                Output Shape              Param #
=================================================================
 conv2d (Conv2D)             (None, 242, 242, 16)      448

 max_pooling2d (MaxPooling2  (None, 121, 121, 16)      0
 D)

 conv2d_1 (Conv2D)           (None, 119, 119, 32)      4640

 max_pooling2d_1 (MaxPoolin  (None, 59, 59, 32)        0
 g2D)

 conv2d_2 (Conv2D)           (None, 57, 57, 64)        18496

 max_pooling2d_2 (MaxPoolin  (None, 28, 28, 64)        0
 g2D)

 flatten (Flatten)           (None, 50176)             0

 dense (Dense)               (None, 128)               6422656

 dropout (Dropout)           (None, 128)               0

...
Total params: 6480292 (24.72 MB)
Trainable params: 6480292 (24.72 MB)
Non-trainable params: 0 (0.00 Byte)
```



Pooling Layer(s). In our model, pooling plays a vital role by reducing variance and computation complexity, resulting in fewer parameters to learn. It performs a down-sampling operation along with the spatial dimensions and reduces the dimensions of the feature map. Furthermore, it summarizes the feature that appears in a portion of the feature map generated by the convolution layer. Therefore, the rest of the operations are performed on summarized features that make the model more robust to variations in the location of the rice leaf disease images' features. In our model, we use 3 pooling layers, namely Pooling1, Pooling2 and Pooling3. Table 2 illustrates the model parameters of these pooling layers for an RGB image of size 256 × 256 and 2 × 2 pool.



Dense Layer(s). The output of the final max Pooling layer is flattened into a one-dimensional vector to fed into a fully connected dense layer. This layer produces a one-dimensional vector M of size 64 which is fed into second fully connected dense layer to produce a one-dimensional vector
M

of size 5.

Output (Softmax) Layer. The output layer applies the softmax activation function which exponentially normalizes the dense layer(s) output
M

and produces a distribution of probabilities across the five different rice leaf disease classes. The softmax function in our model relies upon the following formula

Feature Map:

A feature map is a 2D array that represents the output of applying a convolutional filter to a specific region of input data, such as an image.

Each element in the feature map corresponds to a weighted sum of the values in the input region, capturing specific features or patterns.

Feature maps are essential in CNNs for detecting various features, from edges and textures in the early layers to complex shapes and object parts in deeper layers.

They play a crucial role in the network's ability to recognize and extract meaningful information from the input data.

Effect of Epochs:

"epochs" refer to a fundamental training parameter that plays a crucial role in the process of optimizing the network's ability to recognize patterns in the data. An epoch represents a single pass through the entire training dataset during the training phase of a neural network. In other words, it involves presenting each training sample to the network once and adjusting the model's internal parameters, such as weights and biases, based on the computed errors. Training a CNN typically requires multiple epochs, during which the network refines its feature detection and classification abilities through a process called backpropagation. By iterating through the dataset over several epochs, the model gradually improves its performance and generalization. The number of epochs is a hyperparameter that data scientists and machine learning practitioners must carefully tune, as using too few may result in underfitting, while using too many may lead to overfitting, where the model performs well on the training data but poorly on unseen data. Striking the right balance in terms of the number of epochs is essential to ensure the CNN's optimal performance.

```
Epoch 1/10
41/41 [==============================] - 328s 8s/step - loss: 1.1924 - accuracy: 0.4821 - val_loss: 2.0428 - val_accuracy: 0.1875
Epoch 2/10
41/41 [==============================] - 296s 7s/step - loss: 1.0720 - accuracy: 0.5748 - val_loss: 1.8263 - val_accuracy: 0.2937
Epoch 3/10
41/41 [==============================] - 296s 7s/step - loss: 1.1167 - accuracy: 0.5385 - val_loss: 1.4390 - val_accuracy: 0.1875
Epoch 4/10
41/41 [==============================] - 381s 9s/step - loss: 1.0552 - accuracy: 0.5840 - val_loss: 1.9590 - val_accuracy: 0.1766
Epoch 5/10
41/41 [==============================] - 472s 12s/step - loss: 0.9821 - accuracy: 0.6149 - val_loss: 2.1686 - val_accuracy: 0.142
Epoch 6/10
41/41 [==============================] - 478s 12s/step - loss: 0.9969 - accuracy: 0.6053 - val_loss: 2.2199 - val_accuracy: 0.118
Epoch 7/10
41/41 [==============================] - 469s 11s/step - loss: 0.9932 - accuracy: 0.5992 - val_loss: 2.0264 - val_accuracy: 0.164
Epoch 8/10
41/41 [==============================] - 475s 12s/step - loss: 0.9720 - accuracy: 0.6134 - val_loss: 1.9389 - val_accuracy: 0.123
Epoch 9/10
41/41 [==============================] - 460s 11s/step - loss: 0.9580 - accuracy: 0.6168 - val_loss: 2.2272 - val_accuracy: 0.146
Epoch 10/10
41/41 [==============================] - 301s 7s/step - loss: 0.9645 - accuracy: 0.6088 - val_loss: 2.0772 - val_accuracy: 0.2000
```

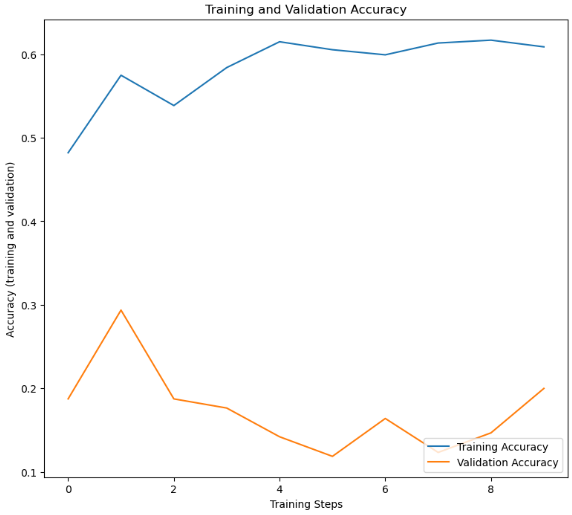
Training the Model and Classification of Rice Leaf Diseases

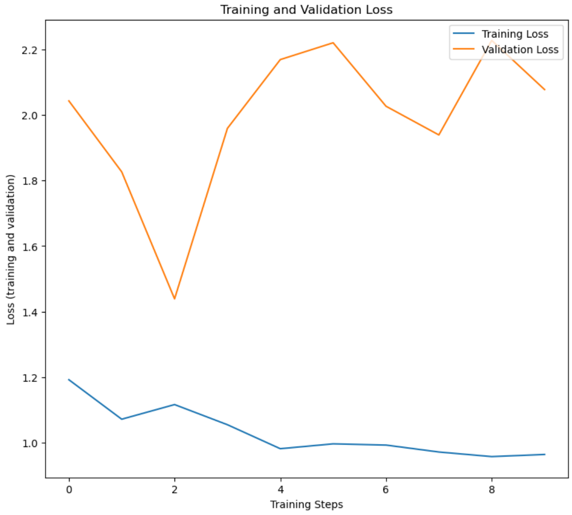
In our CNN-based rice leaf disease recognition model, deep features of rice leaf diseases are extracted by our custom CNN-based model. Activations in each layer of our CNN-based model transform the detailed information in the input rice leaf disease image into a more abstract representation as the image passes through the deeper layers of the model and summarize the important features of it. The visual representations of a sample rice leaf image in each of the convolution and pooling layers of our model are illustrated Deeper and more accurate (summarised) information is then used as feature and classified using softmax layer of our model. To train our model, we pass the images in batches to learn and optimize the network parameters in the convolution, pooling and dense layers to summarize the features into a 1×64 vector. These features are then passed into another dense layer to produce a 1×5 vector. This vector is finally then passed into the softmax layer to classify a rice leaf disease image into its corresponding class. We pass the training images a number of times called epochs and validate the model and the corresponding parameters through the set of validation images. We use "Categorical Cross-Entropy" as the loss function for our model. Our model can also be extended to adapt into the binary classification task by having two class of training images and restricting the output of the softmax layer into two labels.

Performance Analysis:

To further evaluate the performance of our model, we also consider the metrics such as accuracy, precision, recall and F1 score of each rice leaf disease class and Our CNN-based model achieves accuracy, precision, recall and F1 score 97.82%, 94.8%, 95% and 94.6%, respectively, on average, which is superior to the average performance achieved by the state-of-the-art models.

We are considering the training and validation accuracy of our model. And the below graph shows the best fitted graph of our model and other performance also we are considering in our model





Conclusion and Future Work:

In this paper, we have proposed a custom CNN-based model that can classify five common rice leaf diseases commonly found in Bangladesh. Our model is trained to recognize the rice leaf diseases in different image backgrounds and capture conditions. Our model achieves 97.82% accuracy on independent test images. Moreover, our model is effective with respect to memory storage due to its reduced number of network parameters. Despite having better accuracy, we aim to improve the reliability and robustness of our model on different datasets from other regions. We will work on classifying rice leaf disease images when complex backgrounds are present and have varied illumination condition. Also, as classification accuracy is an incomplete description of most real-world tasks [4,8], we will concentrate on interpretable CNN-based models to present features in understandable terms for which diseases will be classified.

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