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A HYBRID APPROACH FOR PLANT DISEASE IDENTIFICATION

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Abstract:

Early detection of plant diseases prevents their negative effects on the crops. Several learning models are available in the literature to identify plant diseases. However, deep learning models require much more parameters and, thus, take more time and are difficult to implement on small devices. This paper presents a new deep learning model based on the initialization process and residual connections using depth separation to reduce the number of parameters. The proposed model was trained and tested on three different plant disease datasets. The efficiency of the rice crop data is 99.39%, that of the bacterial crop is 99.66%, and that of the cassava data is 76.59%. Compared with the deepest learning model in the state, the application model is more accurate due to fewer parameters.

Keywords: Deep learning , Plant Disease Identification, CNN

Introduction:

Mostly, plant diseases are caused by bacteria and fungi, which negatively affect crop yield and quality. One of the greatest challenges to plant protection is timely and early detection of disease symptoms P.K. Sethi et al.(2020). In developing countries, detecting diseases on large farms by specialists and agronomists is the main method, which is time-consuming and expensive. With the smart tools to detect the disease, it proves to be an easy and efficient way to determine the disease and decrease the overall costs V. Singh and AK Misra (2017). In recent times, deep learning has been gaining popularity in the field of agriculture for plant detection S.H. Lee et al. (2017), fruit discovery G. Farjon (2019) disease identification S.P. Mohanty et al. (2016), J. Chen et al. (2020) , K. P. Ferentinos et al. (2018) Plant. reconnaissance , pest detection, etc. The CNN-based model is so popular because it simply and easily extracts the required features from the dataset.

Many popular deep learning models have been developed for plant disease identification, such as AlexNet V. Hoang Trong et al. (2020) Google Net , VGG Net , ResNet, DenseNet.
C. Szeged et al. (2012) K. Simonyan and A. Zisserman (2014), K. He X (2015) , G. Huang (2016) In that respect, there is a large number of possible constraints that depend on the depth and number of filters used in the model. Deep learning models generally require fewer parameters. So, computational cost, with regard to deep learning models, is quite high. It will be difficult to use small equipment with limited resources K. Zhang et al. (2019)

Recently, researchers have implemented deep learning using high-performance hardware along with GPUs and servers. It will not be possible to use complex devices with a GPU in agriculture due to their high costs. The results are smaller applications with lower power consumption and better computing speed.

Considering the above, we developed a new deep learning model to identify diseases in plants. This work presents a new CNN architecture based on Inception and ResNet to identify fewer common diseases. Inception's architecture uses multiple factors to achieve better features; Convolution with different filters. We use residual connections to solve the vanishing gradient problem. We use the difference between the variables of the connection model, which reduces the size and computational complexity without affecting performance. The model was trained on three different data sets, and performance was evaluated.

2. Related Work:

Recent studies on plant disease identification using deep learning models have been reviewed and discussed herein. Mohanty et al. (2019) identified 26 diseases of 14 different plant species using AlexNet and GoogleNet. They use transfer learning and learning through art to train the model. With the use of GoogleNet, they managed to attain a high accuracy of 99.34%. Ferentinos (2020) applied five different deep learning algorithms, including VGG, AlexNet, AlexNet OWT Bn, over feat, and GoogleNet, to the identification of 58 leaf diseases. Geetha Ramani and Pandian used a nine-layer deep CNN to identify plant diseases with 96.46% accuracy. Inspired by Alex Net and Google Net architectures, Liu et al. (2017) developed a model that identified four different diseases in orange juice with 97.62% accuracy by replacing the full algorithm of AlexNet with the baseline algorithm. Four different deep learning algorithms used by Ahmad et al.: VGG16, VGG19, ResNet, and InceptionV3. Explain some of the diseases that affect tomato crops. They tune the network parameters to achieve the best results. The best outcome was achieved using InceptionV3, with a good 99.60% and 93.70% testing and snapshot respectively. Rangarajan and Purushothaman (2021) first employed the VGG16 model to identify different strains. VGG16 is used for feature extraction. They applied several SVM units for classification. They used three different color image models—RBR, YCbCr, and HSV—to check the performance of the model. They recorded the highest accuracy of 99.4% by using the RGB images.

3. Materials and Methods:

A. Convolutional neural network

A convolutional neural network (CNN) is a neural network that is suitable for many computer tasks such as recognition and classification. The advantage of CNN is that it learns and extracts features from training images; on the other hand, traditional methods require the manual extraction of features from images. A CNN contains many different layers: layers, layers, and layers. The main and important process within a CNN is the convolution operation that removes features from the input image. The convolutional layer consists of a small set of numbers called kernels, which are used to process them to create an output called the feature map. Different convolutional kernels are used to extract different types of features. There are usually several convolutional layers, depending on the size of the input image. After the convolution layer, pooling is done, which is responsible for reducing the remaining part of the convolutional feature map. The pooling layer performs subsampling operations on feature maps; this ultimately helps reduce the computational complexity required to process the data. There are many types of job pooling, such as maximum pooling, minimum pooling, average pooling. The last output map of the convolution or pooling operation is converted into a vector where each input is connected to each output by a weight. This layer is also called a dense layer. It can have one or more fully connected layers, and the last fully connected layer has the same number of outputs as the number of groups.

Residual Network

Convolutional neural network can achieve high performance in task classification. As network depth increases, performance gradually saturates and degrades rapidly.

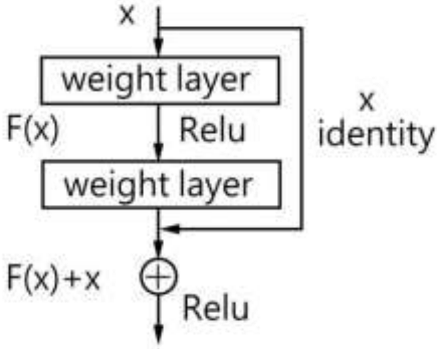


Fig 3.1. Basic block diagram of residual network.

A convolutional neural network (CNN) is a type of neural network that is useful in many domains. The problem was brought to light by He et al. in 2015, and they introduced a deep learning system called ResNet, where deep learning is possible by providing connections between network parts and solving the problem of gradient loss that usually arises when increasing the depth of the network. Figure 1 illustrates a block diagram of the ResNet model. In deep learning, we can easily train a large network using the connections between the network parts, thus using the connections between network parts to solve the problem of gradient loss that usually arises when increasing the depth of the network. ResNet offers a cross-connection called "identity mapping," which combines the output of the previous layer with the output of the next layer. It does not create a limit for self-reporting, and so ResNet can be able to train deep networks with lower latency than other networks, such as VGG. In our work, we propose a hybrid CNN model that uses the initial architecture of both smooth convolution and deep discrete convolution. In the proposed model, the 3x3 convolution of the Inception A block is replaced by 3x3 depth-separable convolution (3x3 depth convolution and 1x1 point-wise convolution), and the 5x5 convolution is replaced with two. The 3x3 cross-sectional area. The 7 × 7 convolution used in Inception B is replaced with 7 × 7 depth-separable convolution (7 × 7 depth convolution and 1 × 1 pointwise convolution). The 3x3 layers of Reducer A are replaced by 1x1 layers, followed by 3x3 depth separation convolutions. In Reducer B, we replace the 3x3 and 7x7 convolutions with 1x1 convolutional layers and 3x3 depth-separated convolutional layers. Figure 2 and 3 show the parameter comparison between the original start-A block and the modified start-A block with depth separation convolutions. It can be seen from Figure 2 and 3 that fewer parameters are required in the modified start-A block than in the original start-A block. Figure 5 shows the CNN architecture to identify plant diseases. Models include convolutional layers, batch normalization, and smoothing layers; starting blocks have individual convolutional layers in depth, followed by pooling layers and entire layers. In this architecture, we replace standard convolutions with depth separation convolutions. We utilize 1 standard convolution, 3 deep discrete convolution layers, 2 maximum pooling layers, and 1 global average pooling operation. We apply a convolution layer after each block, followed by batch normalization and smoothing. The function to use is Relu. Batch normalization and activation functionality improve performance and speed up the process. After global mean pooling, we use dropout, which reduces the risk of model overfitting. While the requirement in our proposed model is 428x100, the number of parameters in the inception V3 model is 23,851,784, which is more than the recommended model. It was found that the proposed model uses 70% less than the first V3 architecture.

4.RESULTS AND DISCUSSION

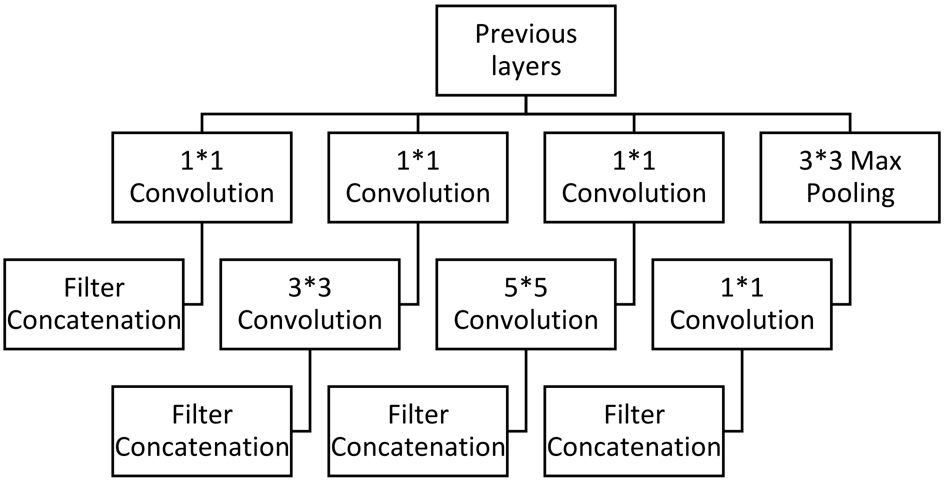


Fig 4.1. Inception architecture of (a) Original inception-A block

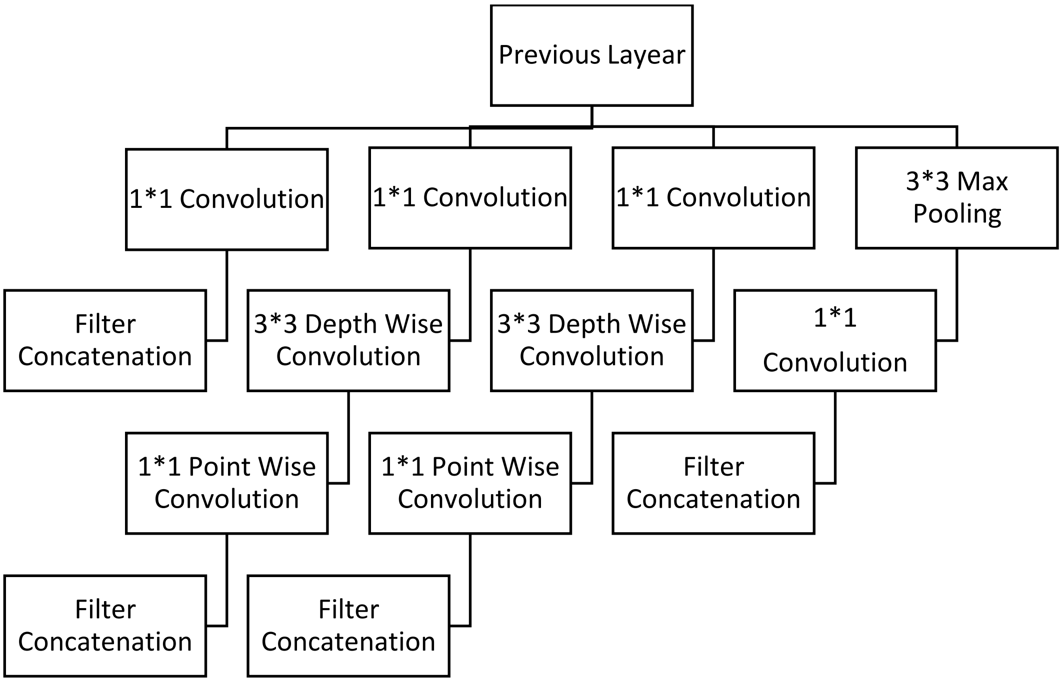


Fig 4.1. Inception architecture of (b) Modified inception-A block

4.2 EXPERIMENTAL RESULT

To evaluate the performance of the model, we consider different statistics such as number of parameters,
accuracy, precision, recall, f1 score, and express it as
precision =TP + TN/TP + FP +TN + FN (3)
Sensitivity=TP/TP + FP (4) Recall=TP/TP + FN (5) f 1 − Score=2 × Precision × Recall/Precision + Recall (6)
Where TP = true positive, TN = true negative, FP = False Positive, FN = False Negative.

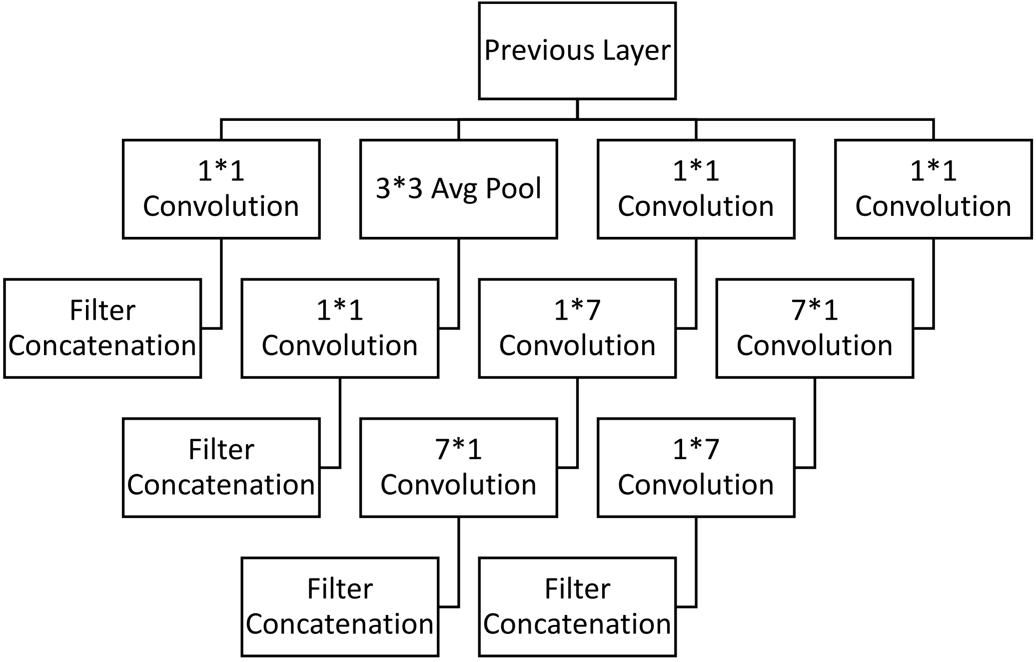
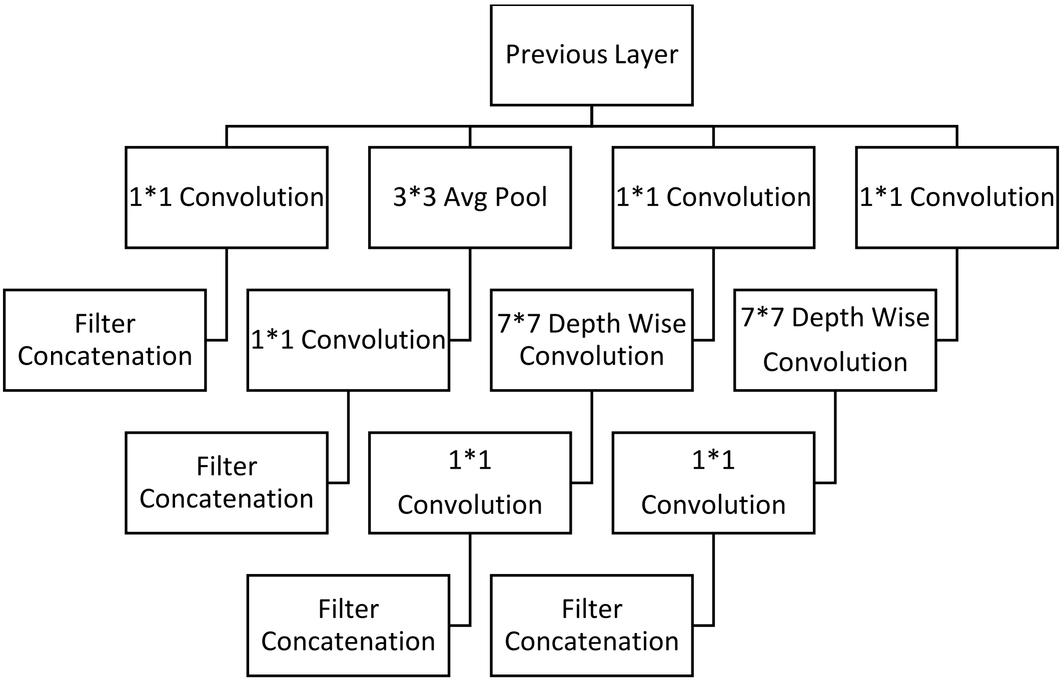


Fig 4.2 Inception architecture of (a) Original inception-B block



(b) Modified inception-B block

After several training cycles, the model achieved maximum training and loss of 99.81% and 0.0015, respectively, on the PlantVillage dataset (potato, corn, tomato), and the accuracy and loss were 99.39% and 0.0549, respectively. On rice data, the model achieved the highest learning rate of 99.94%, a learning loss of 0.0030, a validation accuracy of 99.66%, and a validation loss of 0.0041. To evaluate the power of our model, we considered data of casava plants where images were taken in field conditions. And the background image is complicated.

5. Output and Conclusion

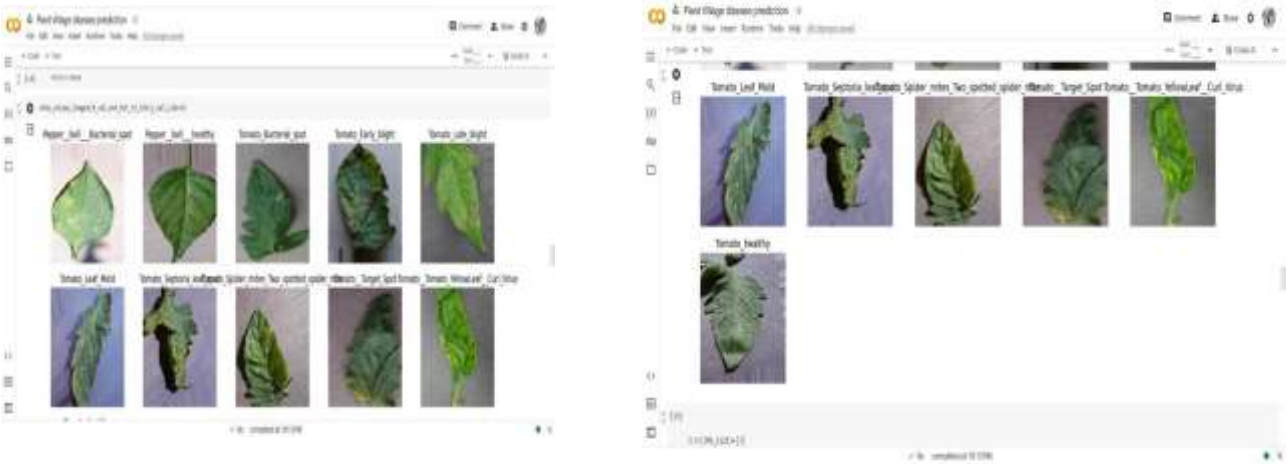


Fig 5.1 Plant Village Dataset Outputs

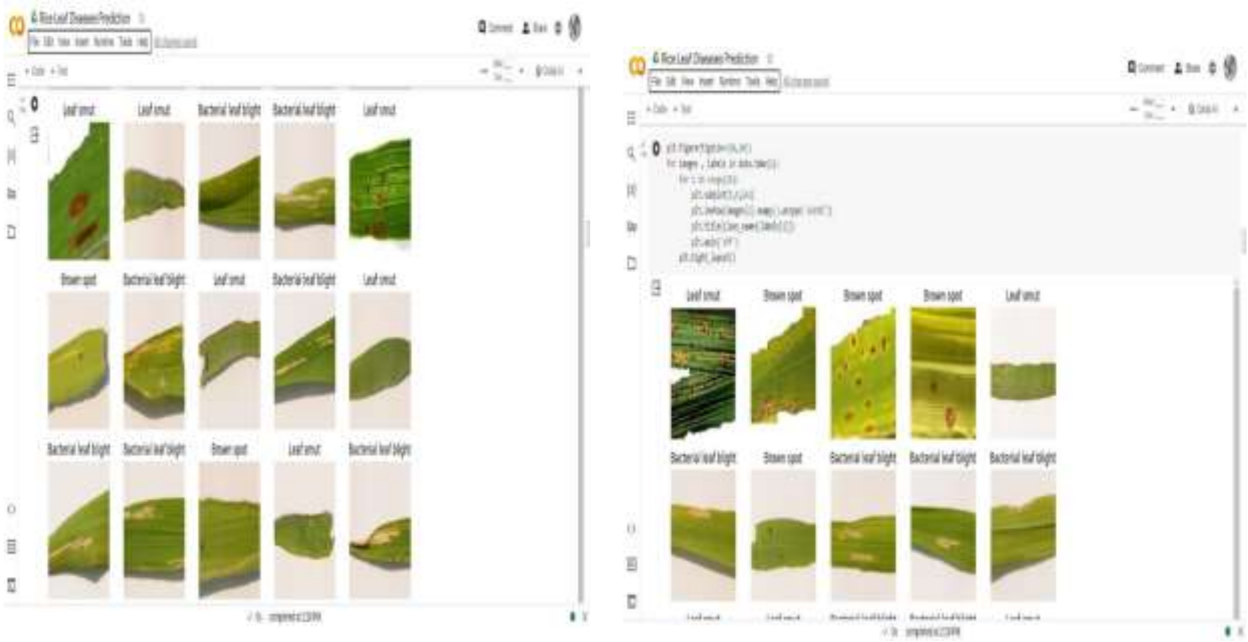


Fig 5.2 Rice Disease Dataset Outputs

And a picture has many leaves. The training and validation accuracy of the plant datasets was lower compared to the PlantVillage and Rice plant datasets. The training and validation accuracy 98.17% and 76.59% respectively. Due to the disparity of the data, the quality of cassava data is lower than that of weed and rice data, and the images in the data contain images with difficult backgrounds.We split the dataset into 80%-20% training and validation sets, train the model for up to 50 epochs and evaluate the performance of the training set and validation set.

FIG 5.3**.** Sample images of Plantvillage dataset, rice and cassava plant dataset.

Cassava Dataset Outputs:

index	filename	label	prediction
0	kaggle/input/cassava-disease-classification/test/cbb/train-cbb-447.jpg	cbb	cbsd
1	kaggle/input/cassava-disease-classification/test/cbb/train-cbb-213.jpg	cbb	cgm
2	kaggle/input/cassava-disease-classification/test/cbb/train-cbb-194.jpg	cbb	cbb
3	kaggle/input/cassava-disease-classification/test/cbb/train-cbb-172.jpg	cbb	cbsd
4	kaggle/input/cassava-disease-classification/test/cbb/train-cbb-186.jpg	cbb	cmd

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```
train=train.assign(prediction=result)
train.head()
```

```
soltest=pd.DataFrame()
soltest=soltest.assign(filename=id)
soltest.head()
```

5.2 Comparison with Existing Literature

The performance comparison of our proposed CNN model is performed against other deep learning models in the literature. Shown below are the performance comparisons with some deep learning models. As can be seen from the figure, the proposed CNN model outperforms other deep learning models. We can also see that the proposed model should have fewer gaps than other deep learning models. Since the model uses fewer parameters, it takes less time to train the model than other deep learning models. It can be observed in the figure that the model was used on images taken under a controlled environment in the plant village dataset. In this study, we used three different datasets, namely images of wheat seeds captured in the field and the background images. The dataset Cassava contains an image of crops with multiple leaves in a single image. Our proposed CNN model has advantages in terms of performance, size, and learning time.

5.3 Conclusion

Deep learning is an effective and recent technology in pattern recognition and is used to detect the occurrence of diseases in plants. In this paper, we propose a new CNN model based on threshold and residual connections, which is effective in classification and performs accurately in the identification of diseases. We also reduce the computational cost by reducing the number of variables by 70% through the use of variable of the variable in the design. Therefore, the network's training takes less time than the CNN model. Results from the experiments indicate that the proposed model has better performance. We tested our three different contract data to evaluate the performance of the model. The testing accuracy of the models of Plant Village, Rice, and Cassava datasets is 99.39%, 99.66%, and 76.59%, respectively.

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