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**Identification of Plant Diseases using Convolutional Neural Network** 

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#### I. Introduction

Deep learning model such as AlexNet, VGG, ResNet, Inception, DenseNet requires large parameter to train the model. Implement these models in agriculture field requires high powered devices which may not be feasible in agriculture domain. In this point of view a shallow CNN network and hybrid CNN model is proposed which uses very much less parameter as compared with the different well known DL models. In one approach, identification of the plant diseases using shallow VGG network is proposed which uses only seven layers of VGG19 model. In another approach, a CNN which uses inception layer with residual connection is build. The number of parameters used in this model is much less as compared with several models.

### plant disease identification system II.



Figure.1 Overall flow diagram of plant disease identification system.

In recent times, several popular deep learning models such as AlexNet, VGGNet, ResNet, Inception, DenseNet, Xception, etc., have been used in the identification of plant dis- eases. Among this model, VGG is a relatively simple network developed by Simonyan and Zisserman [1]. VGG network consists of several convolution layer and pooling layer with different numbers of filter. VGGNet has two models VGG16 and VGG19. VGG16 consists of 16 convolutions and pooling layer with fully connected layer. VGG19 consist of 19 convolutions and pooling layer with fully connected layer. The number of parameters generated in the VGG network is 140 million. The VGG network is pretrained on a large dataset (ImageNet) with 1000 categories

In this work, we have used shallow VGG model which takes nine layers of the VGG19 model that includes 7 convolution layer and 2 max-pooling layer. The input size used in our implemented model is  $256 \times 256 \times 3$  and after performing the convolution and pooling operation the output size is  $64 \times 64 \times 256$ . Instead of a fully connected layer, we have used global average pooling layer which reduces the number of parameters and dropout layer. The dropout layer plays an important role in reducing the overfitting problem of the network. After extracting the features using Shallow VGG, we have classified them using Random forest and Xgboost classifier. The parameter generated in our implemented model is 1.73 million which is much lesser in comparision with the original VGG19 model. Tables 4.1 and 4.2 show the parametergenerated on VGG19 and shallow VGG model respectively.



Figure 2. Basic VGG19 architecture with transfer learning process.

The input size used in our model is  $256 \times 256 \times 3$ . The convolution layers of the network extract the features and pooling layers are used to reduce the dimension of the features. Instead of using a fully connected layer on top, we have used global average pooling. Global average pooling has an advantage over a fully connected layer is that it is more familiar to the convolution structure. Another advantage is that overfitting

can be avoided in the global average pooling layer since there is no parameter to optimize [164]. The model first extracts the features by  $3 \times 3$  convolution with 64 filters. Next,  $2\times 2$  max-pooling is used which reduces the feature dimension and computation. Next  $3 \times 3$  convolution is used with 128 filter to extract the features. The second  $2 \times 2$  max-pooling layer further reduces the feature dimension. The third block of convolutional layer uses  $3 \times 3$  convolution and 256 filter.

At last global average pooling layer is used and it generates 256 neurons which is used for classification. Later, dropout is used to reduce over-fitting and also to improve the generalization of the model. After that classification of the diseased leaves are performed using Random Forest and Xgboost classifier. Figure 4.3 shows the proposed model used in the identification of plant diseases.



Figure.2 VGG19 model

## **Dataset Used**

Corn dataset consist of 4188 images of 4 different categories(Blight, Common rust, healthy, Gray leaf spot). Potato disease consist of early blight, late blight and healthy images. Tomato disease include bacterial spot, early blight, healthy and late blight images. Moreover some field conditioned images captured under non uniform illumination, field background condition image taken by smart phone from shillong, India region is also used to train the network and to evaluate the performances. The images are resized to 256×256 pixel to fit in the model. Table 4.3 summarizes thedataset used along with the number of images in actual dataset and images captured in field condition.

Result analysis and comparison

Accuracy =  $\frac{TP + TN}{TP + FP + TN + FN}$ Precision =  $\frac{TP}{TP + FP}$ Recall =  $\frac{TP}{TP + FP}$ Specificity =  $\frac{TN}{TN + FP}$  $\frac{2 \times \text{precision} \times \text{recall}}{\text{precision} + \text{recall}}$ 



The accuracy obtained in shallow VGG with Xgboost is 0.9447, 0.9874, 0.9391 in corn, potato, and tomato, respectively. The values obtained in all indices using Shallow VGG with Xgboost is far better than the shallow VGG with RF and VGG19 model. Moreover, the number of the parameters is also important which determines the computational cost of the model. From Table 4.4, it can be see that the number of parameter used in our implemented shallow VGG model is much less as compared with the original VGG19 model. Our implemented Shallow VGG network uses only 8% of the total parameter as compared to the VGG19 model.

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