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Leaf Disease Classification in Bell Pepper Plant using VGGNet

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Abstract

In the era of artificial intelligence, deep learning, and computer vision play a vital role in leaf-based disease identification and categorization. Leaf diseases are the most dangerous calamity that has direct detrimental effects on farmers' lives, and consequently on gross yield production and the world economy. Nutritious food for all is a great challenge faced by the farmer and agricultural research community. Bell peppers can be categorized as fruit or vegetable that is universally available and full of various nutrients like carbs, vitamins, and fat. Leaves of bell pepper plants infected by bacterial spot diseases affect their yield significantly. The aim of this study is to classify bacterial spots and healthy images of bell peppers' leaf images taken from the PlantVillage dataset using CNN-based pre-trained architecture. Two CNN architectures, i.e., VGG16 and VGG19 are applied through transfer learning in the binary classification of leaf-based disease. A total of 2475 images are used for training, validation, and testing purposes, with 1478 healthy images and 997 images with bacterial disease spots. Although both VGG16 and VGG19 achieved good performances, VGG16 architecture performs slightly better than VGG19.

Keywords: Bell Peppers' leaf disease, Deep Learning, Convolutional Neural Network, Bacterial spot, Leaf disease classification

1. Introduction

The disease not only affects the leaves of the plants, but also affects crops, fruits, stems, and roots. Diseases are directly related to the productive outcomes of farmers, and therefore to the total agricultural production and world economy. Leaf disease deteriorates the quantity and quality of yields which leads to scarcity and insecurity of food worldwide [1]. Around 16% of crop yields are damaged and hence wastage globally because of plant disease, is the vital reason for food scarcity and price hikes [2]. Currently, in lower and most middle lower-income countries, poor people fight for food as the world population is increasing day by day. The

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Food and Agriculture (FAO) organization assists in providing food and nutrition security for the people by taking different protective measures. According to the report prepared by FAO, the population worldwide will hit 9.1 billion by 2050, and a 70% increase in production is required to ensure a safe and secure food supply for this huge population worldwide [3]. Moreover, the presence of disease in the plant may have an adverse effect on the total amount of yield production and the grade of the yields. Behind plant disease, there are various factors involved, which can be categorized into two groups: abiotic factors and biotic factors. Biotic factors are responsible for biotic diseases whereas abiotic diseases occur due to abiotic factors [4]. The types of factors are summarized in Table 1.

Table 1. Types of factors responsible for crop and leaf disease [4]

Abiotic factors	Biotic factors
▪ Environmental factors - Pollution ▪ Nutrition ▪ Weather condition - Water - Temperature	▪ Virus ▪ Bacteria ▪ Weeds ▪ Pests

Recently deep learning and the convolutional neural network have demonstrated their superiority in leaf and crop disease detection and classification. Diseases are very common in plants farm and their proper management is crucial for sustainable agriculture. Delayed identification and misdiagnosis of leaf disease are always harmful to the agricultural farm as those may decrease yield production. Early detection and accurate diagnosis of a plant disease play a crucial role in healthy yield production. Manual disease identification using the traditional way is a very difficult task as it needs a lot of labor, expert scientists, machinery, and time [5]. In most agricultural farming, plant, and leaf disease identification is monitored by farmers which takes much time and often leads to misdiagnosis because farmers are not very skilled at identifying all diseases with bare eyes. Sometimes various diseases exhibit the same symptoms, for which disease categorization becomes difficult; therefore, the accepted treatment methods become unable to work against the disease. In addition to those problems, the manual system is erroneous [6]. In contrast, deep learning and computer vision-based approaches minimize the problems with the traditional system. Computer-assisted automatic disease diagnostic systems can diagnose diseases accurately and within a short time. Additionally, the automatic system requires less amount of human expertise, and saves time.

The rest of this paper is arranged as follows: section 2 briefly describes the literature review. The overall methodology is explained in section 3. The result and discussion are presented in section 4 followed by conclusion in section 5.

2. Literature review

Various research works have been conducted worldwide on potato leaf disease classification and detection over the last decades. Very recently, there is a significant advancement in automatic potato leaf disease identification using deep learning and CNN-based approaches. However, there is scope for better analysis, and hence, it is considered an attractive research area among scientists and the research community [7]. All the methods studied in the literature review are summarized below.

Very recently a significant number of CNN architectures have emerged rapidly, and their performances are overwhelming in various research fields. Different prize-winning ALexNet, VGGNet, ZFNet, ResNet, DEnseNet, EfficientNet, and MobileNet are noteworthy, and those models have demonstrated in various image and video processing areas with satisfaction [8]. In [9], the authors used the Local Binary Pattern (LBP), VGG16, and combined both LBP and VGG16 features as feature extractors and Random Forest as a classifier. The combined LBP and VGG16 features showed an accuracy of 99.75% in comparison with others. Several pre-trained CNN models have been applied via transfer learning for the binary classification of leaf disease in bell peppers [10]. VGG16, VGG19, ResNet50, ResNet101, ResNet152, InceptionResNetV2, and DenseNet121 architectures were applied on public dataset, and DenseNet121 achieved 96.87% accuracy at testing. In [11], three CNN models, i.e., InceptionV3, ResNet50, and VGG16 were implemented for bacterial spot detection in bell pepper plants using the PlantVillage dataset. The VGG16 model exhibited an accuracy of 99.72% and the AUC value was 0.998. A capsule network [12] was proposed for bacterial leaf spot classification where the pooling layer is eliminated from the model to overcome the weakness. The proposed CapsNet scored an accuracy of 95.76%, a sensitivity of 96.37%, and a specificity of 97.49%.

A lightweight neural network-based approach was proposed in [13]. Various CNN pre-trained models were used to classify potato leaf disease classification in a website and achieved top-1 accuracy of over 93%. In [14], a custom lightweight architecture, called MobOca_Net which is modified from MobileNetV2 was proposed using the attention method and attained better results in potation leaf disease identification. The proposed model exhibited 97.73% accuracy on the public dataset. Deep EfficientNet [15] models were used via transfer learning (all layers trainable) to classify plant leaf disease and then the performance comparison was studied. A total of 55,448 images of the original and 61,486 images of the augmented form of the PlantVillege dataset were used for training the models. B4 and B5 models of the EfficientNet outperformed others in terms of accuracy and precision. In [16], the performance of machine learning and deep learning models for disease detection were evaluated in citrus plants. In machine learning, RF, SVM, and SGD were used and Inception-v3, VGG-16, and VGG-19 were applied in deep learning. The VGG16 of deep learning showed the best classification accuracy of 89.5% and the RF of machine learning showed the least classification accuracy of 76.8%.

3. Methodology

Deep learning-based pre-trained CNN architecture is used to classify leaf disease in bell pepper plants in this study. Few active steps are needed to classify bacterial spot leaves in bell peppers. The steps involved are shown as a block diagram of the overall methodology in figure 1.

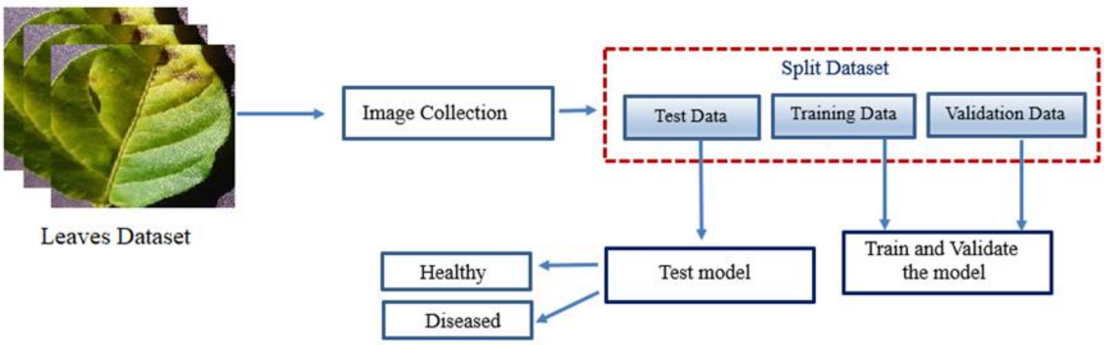


Figure 1. Block diagram of the overall methodology

3.1 Dataset Collection

The leaf images of bell peppers are collected from the PlantVillage dataset [17][18]. This bell pepper leaf dataset contains 2,475 images in total where 997 images are bacterial spots diseased, and 1478 images are healthy. The original raw images are used without any image preprocessing tasks. The disease has been identified and confirmed by expert plant pathologists. The sample images from the healthy and diseased classes are shown in Figure 2

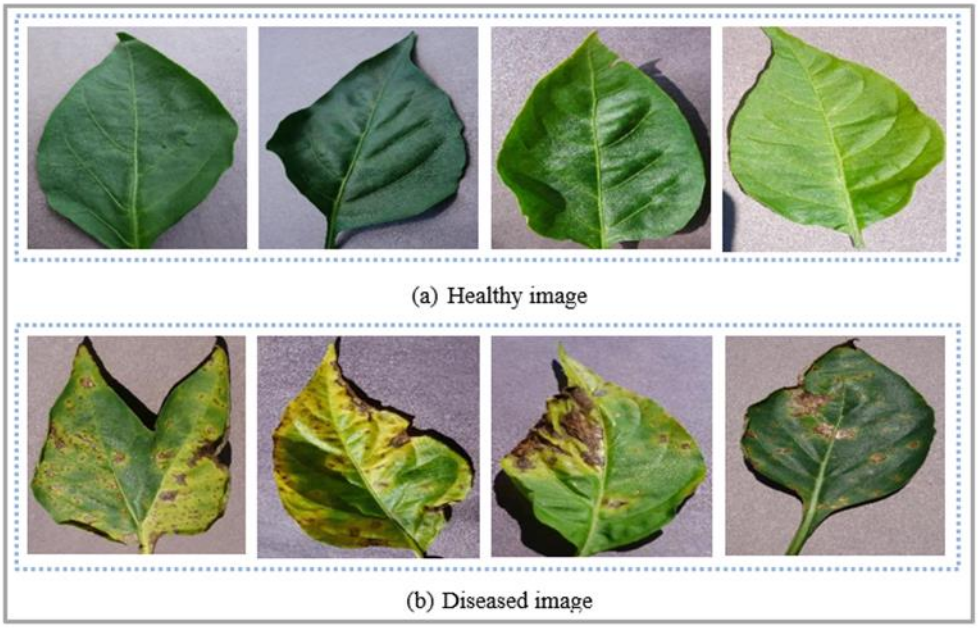


Figure 2. Sample images of bell peppers from the PlantVillage dataset. 2(a) shows the healthy leaf image and 2(b) shows the bacterial spots diseased image

3.2 Details about training, validation, and testing

The pre-trained CNN model VGGNet [19] i.e., VGG16 and VGG19 models are applied via transfer learning for leaf disease classification in bell peppers. As the name implies, VGG16 and VGG19 models have 16 and 19 layers, respectively. The size of VGG16 and VGG19 models is 528MB and 549MB, respectively. The general structure of VGG16 and VGG19 architectures is described in Figure 3. VGGNet is a computationally expensive network because it has been designed with a lot of parameters, i.e., VGG16 and VGG19 architectures consists of 138.4 million and 143.7 million parameters, respectively [20], hence usually requires more time to train the model.

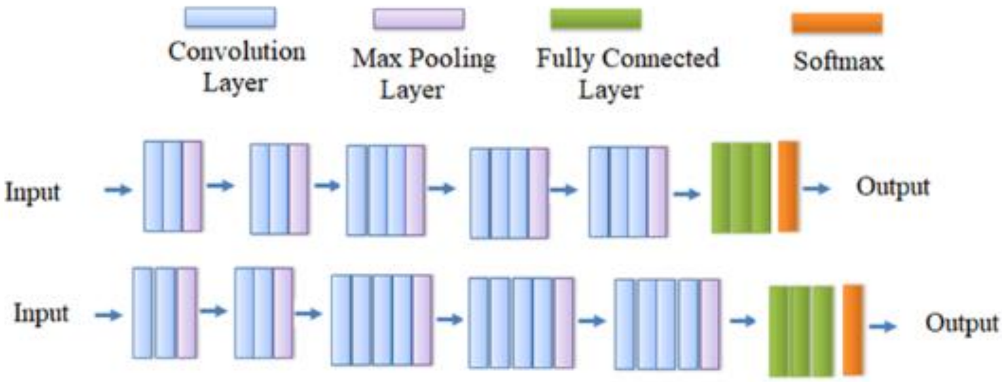


Figure 3. General structure of VGG16 and VGG19 architectures

Before feeding the images into models, the datasets are divided into the train, validation, and test sets. After splitting, the training, validation, and testing sets contains 2004, 223, and 248 images, respectively. The Sklearn train_test_split function is used to divide the dataset into training, validation, and testing datasets. Both models are trained and validated using training and validation sets at each epoch of a total of 50 epochs where the Adam optimizer is used throughout the training period. Adam [21] optimizer is treated as the default optimizer in deep learning methods because of its unique features and benefits. Adam is an extension of stochastic gradient descent that updates the learning rate and weights while training the model. This optimizer is simple to implement, is computationally efficient, requires less memory, and is suitable for large problems in terms of parameters and/or data. For loss calculation, 'sparse_categorical_crossentrophy' is used as it is faster because it uses numerical encoding, and the 'accuracy' metric is added to track accuracy at the validation level. The sigmoid activation function is used as a classifier at the classification stage which uses the real value as input and output ranging from 0 to 1. This function is used for multiclass classification and is often used in CNN where the output is predicted as a probability.

3.3 Platform and Framework

For this study, Anaconda is used with Python default version 3.9 in a Windows environment. Spyder is a free Integrated Development Environment (IDE) included in Anaconda and used as a development environment. This experimental work was performed on a computer with Windows 10, SSD 1T, 16 GB RAM, and NVIDIA GEFORCE RTX 2080 with 16 GB Memory.

4. Results and Discussion

The pre-trained models VGG16 and VGG19 are trained using the training images of the bell pepper plants collected from the Plant Village dataset. The number of epochs was set to 50 with batch size 32 in the training process. The performance of the models is evaluated using the test image set at the time of the testing period. To compute the precision, recall, and f1-score of the models, sklearn.metrics.classification_report is used. To evaluate the accuracy of the models, sklearn.metrics.confusion_matrix is used. The classification report of the VGG16 and VGG19 models is depicted in Figure 4

```
Accuracy: 0.97
Precision: 0.99
Recall: 0.93
F1_score: 0.96
              precision    recall  f1-score   support

           0       0.95      0.99      0.97       145
           1       0.99      0.93      0.96       103

    accuracy                           0.97       248
   macro avg       0.97      0.96      0.97       248
weighted avg       0.97      0.97      0.97       248
```

(a)

```
Accuracy: 0.96
Precision: 0.99
Recall: 0.91
F1_score: 0.95
              precision    recall  f1-score   support

           0       0.94      0.99      0.97       145
           1       0.99      0.91      0.95       103

    accuracy                           0.96       248
   macro avg       0.97      0.95      0.96       248
weighted avg       0.96      0.96      0.96       248
```

(b)

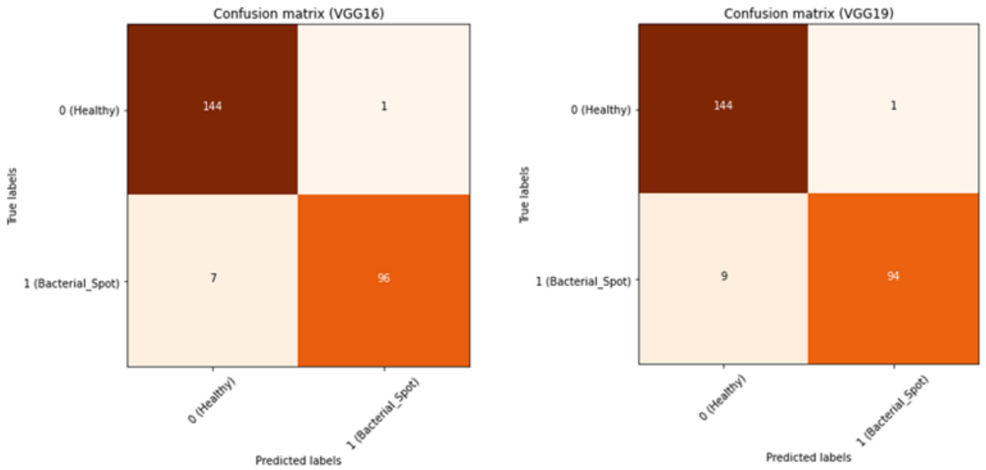
Figure 4. Classification Report. 4 (a) shows the report of VGG16 architecture, and 4 (b) shows the report of VGG19 architecture.

An optimized performance has been shown by both models in the evaluation. The VGG16 architecture via transfer learning achieved the best accuracy 97% compared to the VGG19 model which achieved 96%. The detailed result for both models is shown in Table 2.

Table 2. Results of VGG16 and VGG19 models on the test dataset

Model	Accuracy	Precision	Recall	F1 score
VGG16	97%	99%	93%	96%
VGG19	96%	99%	91%	95%

The confusion matrix result for both models is shown in Figure 5. VGG16 architecture exhibits slightly higher performance than the VGG19 model. However, both VGG16 and VGG19 models demonstrate the same result in the case of the healthy class where all the healthy images are predicted correctly except one. In the healthy class (class 0), both models made the wrong prediction in one sample out of 145 samples, so the precision value is 99% for both models. For the bacterial spot (class 1), the VGG16 model made the wrong prediction in 7 samples out of 103 samples and the VGG19 model made the wrong prediction in 9 samples out of 103 samples, so the recall value is 93% by VGG16 and 91% by VGG19 model.



(a) (b)

Figure 5. Result from the confusion matrix. 5(a) shows the result of VGG16 architecture, and 5(b) shows the result of VGG19 architecture.

Among the 103 diseased images, 96 and 94 images are identified correctly identified by VGG16 and VGG19 models respectively. Therefore, the VGG16 model shows slightly better results than the VGG19 model in the case of the diseased class.

5. Conclusion

Nowadays, it is very significant to detect and classify leaf-based plant diseases because the overall quality and productivity of yields depend on this. Since the analog system has a few unavoidable drawbacks, it would be very helpful if this system could be a deep learning-based automatic system. In this study, transfer learning-based VGGNet is applied to classify leaf-based disease classification in bell pepper plants. However, the limitation of having a free dataset is that only have two classes in the PlantVillage dataset such as diseased (bacterial spots) class and healthy class are available. The VGG16 and VGG19 models show 97% and 96% classification accuracy respectively. This work can help farmers and the research community in early disease identification and classification.

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