Identification of Bacterial Leaf Blight and Powdery Mildew Diseases Based on a Combination of Histogram of Oriented Gradient and Local Binary Pattern Features

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Abstract. Quantity and quality of agricultural products are significantly reduced by diseases. Identification and classification of these plant diseases using plant leaf images is one of the important agricultural areas of research for which machine-learning models can be employed. The Powdery Mildew and Bacterial Leaf Blight diseases are two common diseases that can have a severe effect on crop production. To minimize the loss incurred by Powdery Mildew and Bacterial Leaf Blight diseases and to ensure more accurate automatic detection of these pathogens, this paper proposes an approach for identifying these diseases, based on a combination of Histogram of Oriented Gradient (HOG) and Local Binary Pattern (LBP) features (HOG + LBP) using Naïve Bayes (NB) Classifier. The NB classifier was also trained with only the HOG features and also trained with only the LBP features. However the NB classifier trained with the HOG + LBP features obtained a higher performance accuracy of 95.45% as compared to NB classifier trained with only HOG features and NB classifier trained only with LBP features with accuracy of 90.91% and 86.36 % respectively.

Keywords: Plant Disease, Bacterial Leaf Blight, Powdery Mildew, Plant Disease Detection.

1 Introduction

Detection and classification of plant diseases is one of the most important trending topics in agricultural literature [1]. Identification and classification of plant diseases has drawn increasing attention given the significance of automating this process in

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many agricultural crops such as strawberry, rice, cucumber, tomatoes, potatoes, corn, soya beans, yam, vegetables etc.

Digital image processing and examination is a significant technology generally used to monitor, recognize, and analyze these diseases that influence plant development [2]. Through the improvement of computer handling capabilities and the ongoing growth of digital image acquisition systems, digital image processing and examination technology have become an imperative method for plant disease discovery and recognition [2,3].

In every aspect of human life, agriculture plays a crucial role, such as clothing, food, medicines, and jobs [4]. Rural people in Nigeria rely on crop production as their main source of revenue, and a large part of Nigeria's economy also depends on agricultural products. The revenue and satisfaction from agricultural commodities relies on the quality and quantity of the harvest. Diseases have been described as one of the key factors for the deterioration of the quality and quantity of agricultural products which can contribute to food insecurity and reduction in the farmer sales revenue and thus affect the country's GDP [5]. Since these plant diseases are inevitable, the identification and recognition of these plant diseases is imperative for better production. And one of the best ways to identify a plant infected by a disease is by testing its leaf condition [6].

This paper is centered on recognizing two regular plant diseases which are the Bacterial Leaf Blight (BLB) and the Powdery Mildew (PM) disease. PM is brought about by pathogens producing specificity parasitic on the surface of plants which develop pathogenic fungi with white powder disease signs [2]. Powdery mildew can affect many different plants, like vegetable, fruit, and agronomic crops, as well as ornamental woody and herbaceous. In commercial and residential plantings, this common and widespread disease may occur [7]. Powdery mildew can damage fruit production, flowering, plant strength, and yields. It has been recognized that this disease causes a yield reduction of up to 40% - 80% and this makes its identification important [8].

Rice is one of Nigeria's main food crops and BLB infection is a typical rice disease in Nigeria caused by Xanthomonas oryzae pv. oryzae [9] . It is a vascular ailment that causes a systemic infection along the veins that produces tannish-grey to white lesions. Side effects are seen at the tillering stage and the illness rate increases with plant development, peaking at the flowering stage [10]. Rice yield loss can be as high as 50% when the crop is seriously infected with this disease [10,11]. The intensity and effect of the harm caused by this disease has prompted the creation of strategies for detecting, controlling and managing this disease, in order to minimize crop loss and avoid a widespread outbreak.

The seriousness of the harm caused by BLB and PM disease has made it early discovery significant, so as to control and deal with their widespread. Despite, years of plant disease identification and classification research, the identification accuracy has not been satisfactory especially for diseases like bacteria leaf blight and powdery mildew with an accuracy below 92%. Also most researches on powdery mildew diseases focuses on a single crop type while powdery mildew affect many types of crops.

Several efforts have been made to overcome this limitations by implementing various working machine learning algorithms. However, these methods has not produced considerable achievement as evident in numerous research such as Prajapati, Shah and Dabhi [12], Maniyath et al. [13] and Mahmud, Chang and Esau [14]. This is due to the fact that the amount of dataset used for experimentation is quite small or due to the fact that the feature vectors extracted are not sufficient enough to describe the diseases efficiently.

Based on this identified limitations, this study considers detection of powdery mildew disease for various crop types for improved robustness of the proposed system. The LBP and HOG as texture descriptors and gradient descriptor respectively are combined together to create a more robust feature vector that describes the diseases efficiently for improved detection rate. This study's principal contributions are as follows:

1. Fusion of HOG and LBP features for improved disease identification using Naïve Bayes Classifier.
2. Comparative experimentation of different feature descriptors used for plant disease classification.
3. Presentation of a method for detecting BLB and PM diseases.

2 Related Work

Food is an essential survival requirement for humans. And as the global population rises daily, it has become imperative to grow enough crops to feed the growing population. Nevertheless, these crops are threatened by various diseases, which cause serious harm to the crop quantity and quality. Because plant disease is inevitable, disease detection plays a crucial role in the domain of agriculture [15].

Maniyath et al. [13] conducted crop diseases detection by leveraging on HOG to accomplish feature extraction, and these extracted features were feed to a random forest classifier to categorize the images into disease or healthy images. The proposed system was trained using pictures of papaya leaves. Nevertheless the model performance accuracy of 70% was low as compared to related works with 96.6% accuracy[16] and 85% accuracy [4]. It is suggested that by training with an increased number of images the accuracy of the system could be improved.

Prajapati, Shah and Dabhi [12] suggested a system for the identification and classification of rice plant disease based on the segmentation and Support Vector Machine (SVM).The three rice diseases that have been identified are bacterial leaf blight, brown spot, and leaf smut. This study attained a training accuracy of 93.33 % while achieving a test accuracy of 73.3%. However the size of dataset used was small with a total of 120 images, 40 images for each identified diseases. This shows that the model accuracy could be improved by increasing the dataset size.

Mahmud, Chang and Esau [14] used Color Co-occurrence Matrix (CCM) which is an image processing based texture analysis technique with SVM and K-Nearest Neighbor (KNN) classifier to discover PM disease of strawberry plant. The experimental result indicated that SVM could effectively detect PM disease of strawberry with an accuracy of 95.5% as compared to KNN which obtained an accuracy of 89.78%. But conducting classification with SVM was found to have some limitation on the speed of training and testing. The model, however, focused on detecting only powdery mildew without considering other common diseases that could affect strawberry plants.

Durga and Anuradha [4] have proposed the identification of 4 common maize and tomato diseases, namely tomato mosaic virus, common rust , northern blight, and bacterial spot, using SVM and Artificial Neural Network (ANN). 200 tomatoes and maize leaf images were used, 160 of the images were used for training whereas 40 images were used for testing. HOG feature descriptor was used for extraction of features. SVM achieved an accuracy of 60-70% for tomato crops and 70-75% for maize crops while ANN achieved an accuracy of 80-85% for tomato crops and 55-65% for maize crops. It can be seen from the obtained results that more improved algorithms, such as deep neural networks, are recommended to improve the detection rate of maize crops diseases.

Al-qarallah et al. [1] proposed an image processing method for detection of cucumber powdery mildew infection. In this work several classifiers have been tested on the extracted features, and these classifiers are Random Forest (RF), SVM, Instance Based k-nearest neighbor (IBk), and Multilayer Perceptron (MLP). Results obtained suggested that IBk and RF performed better than MLP and SVM. Nevertheless, this study did not discuss the feature extraction process used or explain how the extracted features were obtained or what features were used for classification, such as textural, color or shape features [17].

3 Methodology

This section describes the techniques used to attain this study's objective. Figure 1 describes the techniques used, such as image acquisition, color segmentation, preprocessing of images, extraction of features, normalization of features, combination of features and classification of diseases. These steps are discussed below.

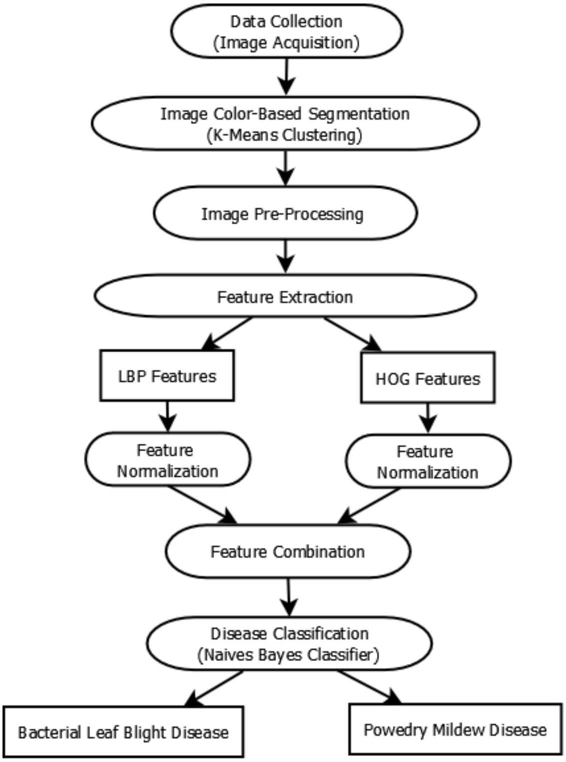

Fig. 1. Proposed System

3.1 Data Collection (Image Acquisition)

Appropriate datasets are needed at all phases of object recognition study, starting with the training phase to testing the efficiency of the recognition algorithms. The leaf image datasets were collected from UCI repository and the Embrapa Repositório Digipathos plant database. A total of 200 images were collected which consist of 106 leaf images infected with powdery mildew disease and 94 leaf images infected with bacterial leaf blight.

Fig. 2. Rice leaf infected with Bacterial Leaf Blight Disease

Fig. 3. Cucumber Leaf Infected with Powdery Mildew Disease

Figure 2 shows a rice leaf infected with bacterial leaf blight disease and Figure 3 shows a cucumber leaf infected with powdery mildew disease.

3.2 Image Color-Based Segmentation (K-Means Clustering)

Image segmentation is a process of splitting a digital image into multiple distinctive regions, containing each pixel having similar traits [18]. K-means algorithm was used for clustering the existing spectral groupings embedded in the datasets. The goal of color-based segmentation is to separate colors using the L*a*b * color space and K-means clustering in an automated manner. The method of segmentation is summarized as follows:

1. Read image, and convert image from color space RGB to color space L*a*b *. The color space L*a*b * helps one to calculate the subtle variations in colour. The L*a*b* space consists of ‘L*' layer of luminosity, 'a*' layer of chromaticity showing where color falls across the red-green axis, and 'b*' layer of chromaticity indicating where color occurs along the blue-yellow axis. All of the color information is in the 'a*' and 'b*' layers [19].
2. Categorize the colors in 'a*b*' space via K-means clustering.
3. Tag every pixel in the Image using the results from K-means.
4. Generate images that segment the image by color.
5. Segment the disease into a separate image
6. Eradicate noise from separated disease image, mask original image with separated disease image and store the image.

Fig. 4. Powdery Mildew infected leaf

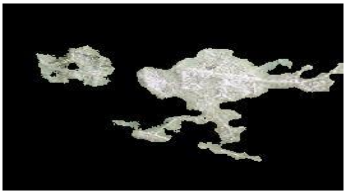

Fig. 5. K-means clustering color-based segmented image for Powdery Mildew

Fig. 6. Bacterial Leaf Blight Infected Leaf

Fig. 7. K-means clustering color-based segmented image for Bacterial Leaf Blight

Figure 4 shows the original leaf image infected with powdery mildew while figure 5 demonstrates a segmented PM disease after the color segmentation was done using k-means clustering. Figure 6 shows the original image of the leaf infected with BLB disease while Figure 7 shows the segmented BLB disease after the color segmentation was done using k-means clustering.

3.3 Image Pre-Processing

The following image pre-processing procedures were used: The image of the segmented disease was translated to gray scale format after which the gray scale image was enhanced using the histogram equalization technique [20]. The improved gray scale image was transformed to binary form, holes of the objects were filled and unwanted noise were eliminated in order to make the image better, clearer and easier to interpret.

3.4 Feature Extraction

Feature extraction is performed on the pre-processed images for both PM and BLB images. Two feature extraction techniques were used to extract the disease features and these techniques are:

- **Local Binary Pattern (LBP):** LBP was selected for feature retrieval, as it has demonstrated to extract relatively high quality features that improves the efficiency of classification [21]. LBP is a type of gray level that supports the local contrast function of an image within the reach of the texture function. LBP is an effective image texture identifier that thresholds the neighboring pixels based on the value of the present pixels. Given a neighborhood of S sampling points on an R radius circle. And a pixel given at (x_p, y_p). LBP can be stated as presented in Equation 1 below:

$$\mathrm{LBP}_{S,R(x_p,y_p)} = \sum_{S=0}^{S-1} C(i_S - i_P)2^S \tag{1}$$

  Where i_S and i_p are, individually, gray-level values of the focal pixel and P surrounding pixels in the circle neighborhood with R radius, and function c(x) is defined in equation 2 as:

$$c(x) = \begin{cases} 1 & \text{if } x \geq 0 \\ 0 & \text{if } x < 0 \end{cases} \tag{2}$$

- **Histogram of Oriented Gradient (HOG):** HOG is a feature descriptor centered on the gradient approximation used in computer vision and image processing for object recognition purposes. HOG descriptor technique counts gradient orientation incidents in located portions of an image detection window [22]. HOG has been used for extraction of features, as it demonstrates invariance to geometric and photometric changes [22]. The HOG features can be created as follows: firstly the image is preprocessed and resized, then the gradient in the x and y direction for every pixel in the image is calculated, after which the magnitude and orientation is calculated using the formulas in equation 3 and equation 4 respectively.

$$\text{Total Gradient Magnitude} = \sqrt{(G_x)^2 + (G_y)^2} \tag{3}$$

  Where G_y is the gradient in the y direction, and G_x is the gradient in the x direction.

$$\text{Orientation} = tan\,(\theta) = G_y/G_x \tag{4}$$

  The value of the angle (θ) is presented in equation 5

$$\theta = atan\,(G_y/G_x) \tag{5}$$

3.5 Feature Normalization

After Extracting the HOG and LBP features from the disease images, the LBP and the HOG features were normalized using Z-Score. This was done in order to scale the features within a specific range as the HOG and LBP features can greatly be of different scale which can have a great effect on the ability of the classifier to learn. Therefore normalization was done to ensure feature values of both HOG and LBP weights on the same scale. Z-Score is a statistical calculation of a score's correlation to the mean in a group of scores [23]. Z-Score can be determined using the formula in Equation 6.

$$Z_{score}(i) = \frac{x_i - \mu}{s} \tag{6}$$

Where s= standard deviation, μ = distribution mean and x_i = each object in the distribution. The standard deviation can be determined using the formula in Equation 7:

$$s = \sqrt{\frac{1}{n-1}\sum_{i=1}^{n}(x_i - \mu)^2} \tag{7}$$

3.6 Feature Combination

In this step the normalized HOG and LBP features were concatenated to form new features. HOG consists of 10 features as only the features of the ten (10) strongest points in the disease images were extracted and the LBP consist of 59 features. The 10 HOG features and 59 LBP features were concatenated to form new dataset consisting of 69 features. And this 69 features were used to train and test the Naïve Bayes classifier.

3.7 Disease Classification

The concatenated features were feed to a Naïve Bayes (NB) classifier to perform classification task. NB model is a family of simple probabilistic classifier based on the implementation of the Bayes theorem with clear assumptions of independence between the features. NB classifiers are vastly scalable, and allow a number of linear parameters in the number of learning problem features. Naïve Bayes (NB) classifier classifies the leaf images into two categories which are BLB or PM diseases.

3.8 Performance Metrics

The five performance metric used to evaluate the proposed method is discussed below and shown in Equation 8, 9, 10 and 11 respectively.

1. **Accuracy:** Accuracy is measured in terms of the rate of correct classifications. That is the number of accurate predictions made divided by the total number of predictions made. The exact formula is illustrated in Equation 5 below:

$$\text{Accuracy} = \frac{\text{True Positive} + \text{True negative}}{\text{True Positive} + \text{True negative} + \text{False Positive} + \text{False negative}} \tag{8}$$

2. **F-Score:** is a proportion of the validity of the test. This is the weighted harmonic mean of a test precision and recall. The formula for F-score is given in Equation 6 below:

$$\text{F} - \text{Score} = 2 * \frac{\text{precision} * \text{recall}}{\text{precision} + \text{recall}} \tag{9}$$

3. **Recall:** it is also known as sensitivity and it is a statistic that calculates the amount of accurate positive predictions that could have been made from all positive predictions. Recall is determined based on the formula in Equation 7.

$$\text{Recall} = \frac{True\ Positives}{True\ Positives + False\ Negatives} \tag{10}$$

4. **Precision:** is a measure which calculates the amount of positive predictions which are correct. It is defined as the number of true positives divided by the total amount of true positives and false positives. Precision is determined according to the formula in Equation 8.

$$\text{Precision} = \frac{True\ Positives}{True\ Positives + False\ Positives} \tag{11}$$

5. **Area under the Curve (AUC):** the Area under ROC Curve is used to rate the performance of a model for classification. This measures all of the entire 2-dimensional field below the ROC curve. AUC provides an aggregate output metric over all possible classification thresholds.

4 Result and Discussion

To evaluate this proposed system the examples were randomly selected and split into training and testing dataset. The dataset was split into training and testing based on a ratio of 75% for training and 25% for testing. In this study BLB and PM plant diseases were identified using three algorithms which are:

1. Feature extraction using HOG algorithm and classification using NB based on HOG Features.
2. Feature extraction using LBP algorithm and classification using NB based on LBP Features.
3. Merging HOG and LBP features to generate new features and classification using NB based on concatenated features.

Table 1 presents results obtained after running the three algorithms described above.

Table 1. Performance of Proposed Algorithm (Combined HOG and LBP Features) as compared to use of LBP Features only and HOG Features Only

Algorithm	Accuracy (%)	Precision (%)	Recall (%)	F-Score (%)	AUC
HOG + NB	90.91	100	77.78	87.50	0.9813
LBP +NB	86.36	87.50	77.78	82.35	0.9938
HOG + LBP + NB (Proposed system)	95.45	100	88.89	94.12	0.9948

From Table 1 it can be seen on the accuracy column that the proposed method (HOG + LBP +NB) performs better with an accuracy of 95.45% as compared to HOG + NB with an accuracy of 90.91% and LBP +NB with an accuracy of 86.36%. From the Precision column it can be seen that LBP + NB has a lower precision of 87.50% as compared to HOG +NB and HOG + LBP +NB with a precision of 100%.

Under the Recall column HOG + LBP +NB is able to achieve a true positive rate of 88.89% which is higher than the true positive rate of 77.78% achieved by HOG +NB and LBP +NB. Based on the F-Score of 94.12% achieved by HOG + LBP +NB is can be seen that HOG + LBP +NB performs better than HOG +NB and LBP +NB with and F-Score of 87.50% and 82.35% respectively. Also by comparing the values of the AUC for each algorithm it can be seen that HOG + LBP +NB has a higher value of 0.9948 as compared to HOG +NB and LBP +NB with values of 0.9813 and 0.9938 respectively.

Table 2. Confusion Matrix for LBP + NB

n = 50	Actual Positive (1)	Actual Negative (0)	
Predicted Positive (1)	16 (32%)	5 (10%)	**21**
Predicted Negative (0)	2 (4%)	27 (54%)	**29**
	18	**32**	

Table 3. Confusion Matrix for HOG + NB

n = 50	Actual Positive (1)	Actual Negative (0)	
Predicted Positive (1)	16 (32%)	4 (8%)	**20**
Predicted Negative (0)	0 (0%)	30 (60%)	**30**
	16	**34**	

Table 4. Confusion Matrix for HOG + LBP + NB

n = 50	Actual Positive (1)	Actual Negative (0)	
Predicted Positive (1)	18 (36%)	2 (4%)	**20**
Predicted Negative (0)	0 (0%)	30 (60%)	**30**
	18	**32**	

Table 2 presents the confusion matrix for LBP + NB model with 21 predicted positives and 29 predicated negatives whereas the actual positive is 18 examples and the actual negative is 32 examples.

Table 3 presents the confusion matrix for HOG + NB model with 20 predicted positives and 30 predicated negatives whereas the actual positive is 16 examples and the actual negative is 34 examples.

Table 4 presents the confusion matrix for HOG + LBP + NB model with 20 predicted positives and 30 predicated negatives whereas the actual positive is 18 examples and the actual negative is 32 examples.

With the proposed system (HOG + LBP + NB) achieving a higher Accuracy, Precision, Recall and AUC as compared to HOG + NB and LBP + NB, it can be deduced that bacterial leaf blight and powdery mildew plant disease can effectively be detection using the proposed system.

Table 5. Comparison of Proposed System with Existing Methods

Algorithm	**Accuracy (%)**
SVM (trained with color, texture and shape feature)[12]	88.57%
Color Co-occurrence Matrices + SVM [14]	91.86%
HOG + Random forest [13]	70.14%
HOG + LBP + NB (Proposed System)	**95.45%**

From the accuracy results in Table 5 it can be seen that the proposed system produced 95.45% accuracy which is the highest accuracy when compared to existing works such as Maniyath et al. [13] with 70.14% accuracy, Prajapati, Shah and Dabhi [12] with 88.57% accuracy and Mahmud, Chang and Esau [14] with 91.86% accuracy. This shows that the proposed system can detects plant diseases effectively.

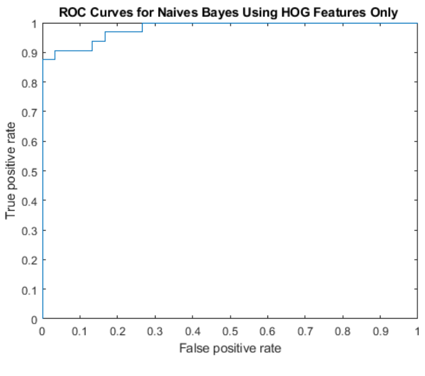

Fig. 8. ROC Curve for NB Classifier using HOG features only

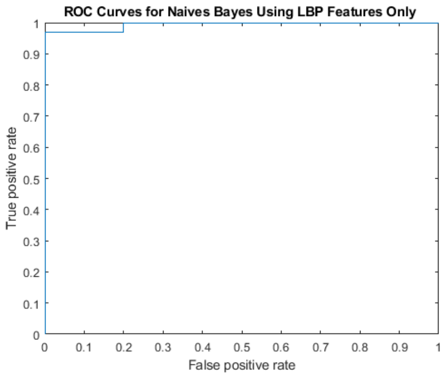

Fig. 9. ROC Curve for NB Classifier Using LBP Features only

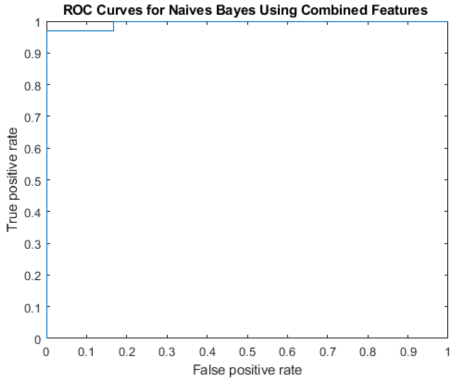

Fig. 10. ROC Curve for NB Classifier using combined LBP and HOG features

Figure 8 shows the ROC curve of Naive Bayes (NB) classifier trained using only HOG extracted Features for bacterial leaf blight and powdery mildew plant disease identification. Figure 9 shows the ROC curve of Naive Bayes (NB) classifier trained using only LBP extracted Features for bacterial leaf blight and powdery mildew plant disease detection and Figure 10 shows the ROC curve of Naive Bayes (NB) classifier trained using the concatenated HOG + LBP extracted Features for bacterial leaf blight and powdery mildew plant disease identification.

5 Conclusion

In this paper, we were able to detect BLB and PM disease effectively as compared to existing researches on disease identification due to the combination of features extracted using two powerful feature extractors namely LBP and HOG. From this study it can be established that feeding a Naïve Bayes classifier with concatenated feature vectors (HOG +LBP) can improve the classification accuracy as compared to use of features extracted using a single feature extractor. In conclusion a system was developed which can perform BLB and PM disease detection based on LBP + HOG + NB algorithm.

6 Future Work

In this study only two common plant diseases were identified, hence for future work more common diseases such as anthracnose, leaf smut, brown spot etc. can be added for identification in order to improve the system robustness. Two feature extractors were used and combined in this work, for future work other feature extractors can also be used and combined. The combined feature vectors were only feed to the NB classifier without testing its effect on the result of other classifiers. Hence it is recommended that the combined features be feed to other classifiers in order to obtain various classification results. This study was limited to just two plant diseases. For further work more plant diseases can be incorporated to improve model robustness.

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