

# Multiclass Plant Leaf Disease Prediction Using Fuzzy Multimodal Feature Extraction

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## Abstract

Delayed identification of crop diseases, which significantly impact agricultural yields, remains a critical challenge. Crop diseases are a major factor contributing to reducing productivity. Since leaves are the mirrors of crop health, by investigating the leaves, a prediction of crop health can be made. This study aims to predict crop disease in the vegetative growth phase with greater efficiency. The two most prominent features, color and texture of the leaves, are extracted with different techniques, followed by fuzzification of these features. Two machine learning models, the bootstrap model and the multi-class support vector machine (MSVM), are employed for disease prediction. The findings show that for multi-class disease prediction, the bootstrap model with histogram and modified co-occurrence matrix features obtains a superior average accuracy of 98.07%, while the MSVM with fuzzy features delivers an average accuracy of 80.11% in the potato crop with early blight disease.

**Keywords:** modified co-occurrence matrix (MCCM), fuzzy hue saturation value (HSV), local binary pattern (LBP), multi-class support vector machine (MSVM)

## 1. Introduction

Crop diseases and pests pose a significant threat to global agricultural production and food security. The detrimental impact on crop yields is increasing, leading to substantial losses. Alterations in plant morphology not only detrimentally impact crop growth but also result in a significant decline in both quality and yield. In severe instances, entire harvests may be lost [1].

Crop diseases are significant biological calamities that badly impact agricultural productivity and the safety of the ecosystem. Accurate detection and identification of disease types are crucial for minimizing damage [2]. Thus, precise crop disease diagnosis remains a critical challenge. Leaves are the most exposed constituent of a plant. Some insects may attack leaves or may face unfavorable weather conditions during the plant's growth period, leading to severe disease.

Commonly, the hue saturation intensity (HSI) and hue saturation value (HSV) color models are widely employed for color feature extraction, while the local binary pattern (LBP) is commonly utilized for texture feature extraction. In the proposed work, a novel approach is introduced that leverages fuzzy HSV for color feature extraction and fuzzy LBP for texture feature extraction. Additionally, a second feature extraction technique based on a histogram and a modified co-occurrence matrix (MCCM) is utilized to capture both color and texture features.

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The extracted fuzzy HSV and fuzzy LBP features are fed into a multi-class support vector machine (MSVM) for classification, while the histogram and MCCM features are used to train a bootstrap model. The primary objective of this study is to compare fuzzy HSV and fuzzy LBP with histogram and MCCM across various performance parameters, to evaluate their effectiveness in classification tasks.

### 1.1. Background

The primary method for predicting crop diseases is manual leaf observation in the field. However, this manual observation requires expertise and much experience in agriculture. This is a time-consuming process and can cover only a limited field area. The solution to every contemporary problem can be found in the technology that evolves every day. Hence, the above problem can be conquered by technology. Advancing technology offers a solution to this challenge, as the agricultural industry increasingly benefits from innovations in disease management and control.

High-resolution images of agricultural fields are captured by remote sensing technologies, including satellites, drones, and airborne sensors. These images are then analyzed using image processing techniques to identify and monitor disease patterns across vast areas, thereby facilitating early detection and intervention [3].

Machine learning and artificial intelligence (AI) play a key role in analyzing large datasets, including images, environmental data, and disease records. These technologies detect disease patterns, predict outbreaks, and recommend optimal management strategies [4]. Through continuous learning and improvement, AI and machine learning contribute to more efficient and sustainable crop production.

Precise diagnosis in plant disease identification systems can be problematic, as disease symptoms may appear visually identical across different conditions. Therefore, it is essential to extract features that can effectively capture the visual aspects of a leaf image to provide the most relevant description of the disease class. Feature extraction reduces the data dimensionality by grouping relevant information into manageable subsets. Further, data reduction accelerates the learning process and minimizes the computational demands placed on the machine learning model [5]. The feature extraction phase plays a vital role in precisely classifying different diseases by distinguishing infections from similar ones, based on specific symptoms or visible lesions. However, some plant leaf images exhibit nearly identical spots, posing classification challenges for such systems. Nevertheless, by employing a suitable and effective feature extraction approach, it is possible to address the issue of similar lesion visibility and achieve a satisfactory resolution. Notably, color, texture, and shape are crucial features that play a key role in the prediction of plant diseases.

### 1.2. Existing Models Literature Survey

Li et al. [6] presented an innovative approach for feature extraction in hyperspectral image analysis called spectral-Gabor space discriminant analysis (SGDA). The authors showed that hyperspectral images are high-dimensional data, making preprocessing essential before extracting spatial features. In this study, principal component analysis (PCA) was employed to extract the desired principal components. The extracted principal components are then fed to derive Gabor spatial features, which effectively capture low-level spatial structures of various orientations and scales. To improve the representation of the hyperspectral data, the original spectral features are combined with the extracted Gabor spatial features, resulting in fused features. In the suggested SGDA method, a p-factor  $\alpha$  was introduced to regulate the relative contributions of spectral and Gabor spatial information.

Hegde et al. [7] explored two approaches for feature extraction in the categorization of white blood cells (WBCs): the run-of-the-mill image processing approach and the use of a convolutional neural network (CNN) as a feature generator. The classification of WBCs was conducted in two steps. Initially, WBCs are categorized as normal or abnormal, followed by the division of normal WBCs into five variants: lymphocyte, monocyte, neutrophil, eosinophil, and basophil. For feature extraction,

they employed state-of-the-art image processing techniques to capture shape, texture, and color features. In particular, the authors use the LBP representation of grayscale images to effectively capture local textures.

Additionally, the authors explored the suitability of features obtained from different layers of a pre-trained CNN, specifically AlexNet, using the “CNN as a feature generator” method. The results from both feature extraction methods are compared. The predictor's performance is evaluated using the extracted features. Remarkably, comparable accuracy using both the existing approach and the “CNN as a feature generator” approach was achieved. However, the classifier demonstrated slightly better performance when utilizing the features from the fully connected layer 8 (fc8) of AlexNet for the classification of WBCs. Overall, an accuracy of 99.7% in differentiating between usual and unusual WBCs and an average accuracy of 98.9% in classifying normal WBCs into their respective types was achieved. Consequently, the authors quote that training at CNN requires a large dataset and significant computing resources compared to the well-known image processing approach.

## 2. Literature Review

Ahmad et al. [8] proposed a novel approach aimed at automating the identification of plant diseases through a series of sequential steps, including pre-processing, segmentation of the diseased leaf area, feature calculation using the gray-level co-occurrence matrix (GLCM), feature filtration, and categorization. In the study, the authors computed six color features and twenty-two texture features. To perform the classification of plant diseases, support vector machines (SVM) in a one-vs-one configuration were utilized. The proposed model for disease identification achieved an impressive accuracy of 98.79% with a standard deviation of 0.57 through ten-fold cross-validation. When tested on a self-created dataset, the accuracy for disease identification is 82.47%, while the accuracy for differentiating between healthy and diseased samples is 91.40%. These reported performance measures either surpass or are on par with existing approaches and are particularly superior to feature-based methods. Consequently, the authors demonstrated that their method is the most suitable approach for automating leaf-based plant disease identification.

Nagi et al. [9] developed a model for identifying plant leaf diseases using fuzzy feature extraction and the probabilistic neural network (PNN). The proposed method consisted of two main sections. Firstly, the features (color and texture) were obtained from the leaf images using a fuzzy variant of the gray-level co-occurrence matrix and a color histogram. Secondly, the PNN was employed for classification. To evaluate the effectiveness of the proposed method, leaf images of maize, grapevine, and tomato were obtained from the PlantVillage database. The model achieved an impressive recognition accuracy of 95.68%. Furthermore, it outperformed other commonly used classifiers such as SVM, decision tree (DT), and random forest (RF) in terms of accuracy. Overall, the combination of fuzzy feature extraction and the PNN classification approach has been proven to be highly effective for plant leaf disease recognition. Finally, the authors concluded that the results obtained surpass those of other classifiers, validating the applicability of this method.

In a study, Basavaiah et al. [10] proposed a methodology for detecting and classifying four major diseases of tomato plants: Septoria spot, bacterial spot, yellow curl, and mosaic virus. Multiple feature extraction methods were employed to capture distinctive characteristics of these diseases. Subsequently, the DT classifier and RF classifier were utilized for disease classification. The classification results demonstrated an accuracy of 90% for the DT classifier and 94% for the RF classifier. The authors noted that the random forest classifier exhibited higher accuracy compared to the decision tree classifier. This finding highlighted the superiority of the RF classifier in this context. The method proposed in this study offered several advantages. Firstly, it significantly reduced computational time, making it more efficient than other commonly used techniques.

Through a rigorous literature review, several areas for improvement are identified:

- (1) The robustness of the system in the presence of noise and artifacts commonly found in imaging, such as motion artifacts or variations in imaging conditions, needs further evaluation. Enhancing the method's robustness is crucial for ensuring reliable disease prediction.

- (2) Training CNN and other deep learning models require large datasets and substantial computational resources, which limits their accessibility and practicality, especially in resource-constrained environments.
- (3) Research into more efficient algorithms or models that can achieve high accuracy with fewer resources and smaller datasets is needed.
- (4) Further research should focus on how to effectively integrate multimodal features to improve the accuracy and reliability of disease prediction models.
- (5) A lack of standardized evaluation metrics for comparing the performance of different feature extraction and classification methods.

The purpose of this study is to present multimodal feature extraction techniques that effectively capture essential features and introduce a unique integration of machine learning models with the extracted features. The study also explores the fusion of fuzzy features with a multiclass disease prediction model, such as multiclass SVM.

### 3. Proposed Methodology

The present work is structured as a dataset collection followed by preprocessing, feature extraction, training of the machine learning model, testing of the trained model, and disease prediction. For data collection, a real-life dataset of potato crop leaves is used, which is taken from Kaggle.

#### 3.1. Data collection

The dataset used in the present work is adopted from Kaggle.com [11]. The dataset consists of 1500 images of potato plant leaves. The data is distributed into three directories: train, test, and validation. Within each directory, data is categorized into three different classes: potato leaf with early blight, potato leaf with late blight, and healthy leaf. The training set contains 300 images per class, while the test set and validation set contain 100 images corresponding to each class of potato images. The sample of the early blight is shown in Fig. 1. The characteristic symptoms of the early blight include small, dry, papery spots that turn dark brown to black and become oval or angular. The spots can grow up to 12 mm in diameter and are usually confined to the main veins of the leaflets.



Fig. 1 Potato leaf with early blight

This section considers samples of two well-known diseases affecting potato crops. In case of late blight, dark, water-soaked lesions appear on the leaves, often starting at the tips or margins and spreading toward the center. The lesions are not confined by the leaf veins, and they may have a yellow edge. The primary difference between early blight and late blight is that early blight first infects the oldest leaves, causing brown areas with concentric rings, while late blight causes watery blisters on leaves, brown or black lesions on the lower leaves, and leaf rotting. A sample of a leaf infected with late blight disease and a sample of a healthy potato leaf are shown in Fig. 2 and Fig. 3, respectively.



Fig. 2 Potato leaf with late blight



Fig. 3 Healthy Potato leaf

### 3.2. Pre-processing of the image

Preprocessing an image involves making it more suitable for further analysis. This process includes filtering noise and isolating the actual leaf from the background. For image processing, a modified grab-cut method has been utilized. The method is explained as follows.

#### 3.2.1. Grab-cut method

Grab-cut utilizes graph cuts as the foundation for its image segmentation approach. By employing a Gaussian mixture model (GMM), the algorithm approximates the color distribution for both the desired object and the background [12]. In the grabcut, an initial rectangle is provided, where everything outside the rectangle is designated as a definite background. Conversely, the region inside the rectangle is considered unknown. Any additional user input indicating foreground and background is regarded as hard labeling, meaning these designations remain unchanged throughout the process. After receiving user input, the system performs an initial labeling process based on the provided data, assigning pixels as either foreground or background (hard labeling).

#### 3.2.2. Application of Gaussian Mixture Model

A Gaussian mixture model (GMM) is employed to create models for the foreground and background components [13]. By leveraging the provided data, the GMM learns and generates new pixel distributions. This process involves assigning labels to the unknown pixels, classifying them as either probable foreground or probable background based on their color statistics and their relationship with other hard-labeled pixels [14]. Subsequently, a graph is constructed using this pixel distribution. Each pixel serves as a node in the graph, along with two additional nodes: the source node and the sink node. The foreground pixels are connected to the source node, while the background pixels are connected to the sink node [15].

Once the graph is constructed, a min-cut algorithm is applied to divide it into two distinct components: the source nodes and the sink nodes. This separation is achieved by minimizing a cost function, which is determined by the sum of edge weights that are cut. Subsequently, the pixels connected to the source node are classified as foreground, while those connected to the sink node are classified as background. This iterative process continues until the classification reaches a state of convergence, ensuring refined segmentation results [16].

### 3.3. Feature extraction

Feature extraction in image processing refers to the process of identifying and capturing distinctive and meaningful characteristics or patterns from an image. It involves transforming raw image data into a compact representation that retains relevant information for further analysis or classification tasks.

In the process of feature extraction, specific algorithms or techniques are applied to extract relevant visual cues or attributes from the image. These cues can be derived from various levels of abstraction, ranging from low-level features like

color, texture, and shape, to higher-level features such as edges, corners, or even semantic concepts [17]. In this study, feature extraction is performed on the color and texture features of the potato plant leaves. The MCCM, histogram, fuzzy HSV, and fuzzy LBP methods are used for feature extraction.

### 3.3.1. Histogram

Histogram feature extraction is a fundamental technique in image processing that provides a compact yet informative representation of image content, making it useful for a wide range of applications [18]. Histogram feature extraction from a leaf image involves quantifying the distribution of pixel intensities within the image. This process involves grayscale conversion, histogram calculation, normalization, and feature representation.

### 3.3.2. Modified co-occurrence matrix (MCCM) features

To enhance the effectiveness of feature extraction from images, a novel method called MCCM is introduced. The color co-occurrence matrix (CCM) utilizes features like energy, entropy, inverse difference, and contrast [19]. Instead of employing all the traditional CCM features, some negative and low-value features have been omitted. Employing MCCM improves the model's learning outcomes compared to utilizing the complete set of CCM features [20]. In the equations below,  $IDM$  represents the inverse difference moment,  $IR(i, j)$  denotes the selected image region co-occurrence matrix, and  $i$  and  $j$  represent the intensity of pixels in the image.

### 3.3.3. Fuzzy HSV feature extraction

The fuzzy HSV method for leaf image feature extraction incorporates fuzzy logic principles into the HSV color space to extract features from leaf images [21]. Incorporating "fuzzy" into the task implies a representation wherein color categories lack precise delineation, exhibiting a degree of ambiguity or uncertainty [22]. Fuzzy logic facilitates the modeling of imprecision and uncertainty, offering a valuable framework for tasks involving color perception and classification, especially in scenarios where colors exhibit nuanced variations in shades or tones.

$$Energy = \sum_{i, j} IR(i, j)^2 \quad (1)$$

$$Entropy = -\sum_{i, j} IR(i, j) \log(IR(i, j)) \quad (2)$$

$$IDM = \sum_{i, j} (1 / (1 + |i - j|)) IR(i, j) \quad (3)$$

$$Contrast = \sum_{i, j} (i - j)^2 (IR(i, j)) \quad (4)$$

### 3.3.4. Fuzzy LBP feature extraction

The LBP technique is a statistical method in image processing, offering a means to extract potent features from images. Its widespread adoption in computer vision applications underscores its efficacy, making it a cornerstone in visual computing [23]. Fuzzy LBP incorporates fuzzy set theory to handle imprecise or uncertain pixel intensity values. Instead of strictly binary decisions, fuzzy logic allows for gradual transitions between foreground and background intensities. The computation of membership function values of neighboring pixels concerning a center pixel, considering their intensity differences and fuzziness, is given in Eq. (5). If  $I_c$  represents the intensity value of the center pixel and  $I_n$  denotes the intensity values of its neighbors, then the fuzzy LBP formula for a center pixel with  $N$  neighbors is expressed as:

$$LBP_{PR}^{FUZ}(I_c) = \sum_{n=0}^{N-1} \mu(I_n - I_c) 2^n \quad (5)$$

where  $P$  represents the number of sampling points around the center.  $R$  denotes the radius of the circular sampling region.  $\mu(I_n - I_c)$  is the membership function indicating the degree of membership of the neighboring pixel intensity to the foreground or background.

### 3.4. Model learning

This phase of machine learning involves the training of two multiclass models. The first model, which uses MCCM and histogram features as the training input, is a bootstrap model, while the second model, which uses fuzzy LBP and fuzzy HSV as the training features, is a multiclass SVM model.

#### 3.4.1. Bootstrap sampling

Bootstrap learning, commonly referred to as bootstrap aggregating or bagging, represents a machine learning ensemble technique designed to enhance model stability and accuracy by mitigating variance and overfitting. It involves training multiple models utilizing subsets of the initial dataset and combining their predictions to yield a conclusive decision [24]. Below is an outline of how the bootstrap learning model operates:

Bootstrap Sampling: Given an original dataset  $D$  of size  $N$ , bootstrap sampling involves selecting  $N$  samples randomly with replacement from  $D$  to create a sample  $D_i$ . This process is repeated to create multiple bootstrap samples.

$$D_i = \text{BootstrapSample}(D) \tag{6}$$

Furthermore, the process includes model training and model aggregation. In model training, corresponding to each bootstrap sample  $D_i$ , a base learning algorithm, such as a decision tree or neural network, is trained independently to create a base model  $M_i$ . In the model aggregation phase, the predictions of all base models are combined to make a final prediction. The aggregation method varies depending on the problem, with averaging for regression and voting for classification. If  $y_1, y_2, y_3, y_4, \dots, y_k$  represent different bootstrap samples, then the equations are

$$M_i = \text{TrainModel}(D_i) \tag{7}$$

$$Y = \text{AggrePredicn}(y_1, y_2, y_3, \dots, y_k) \tag{8}$$

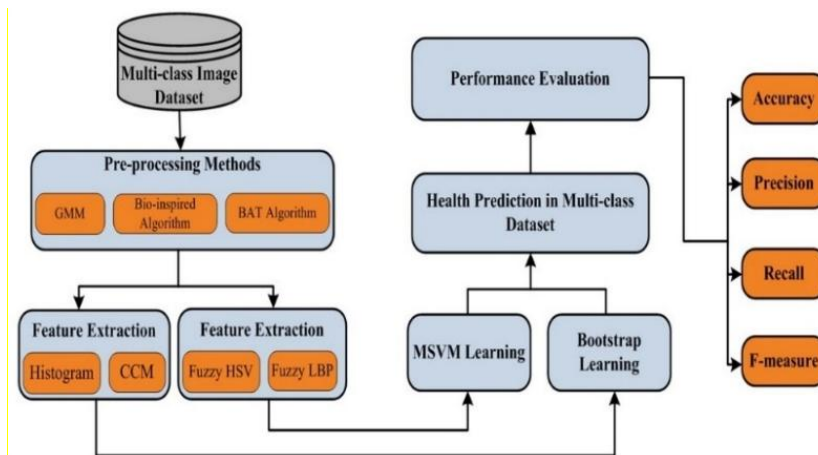


Fig. 4 Architectural design of the disease prediction model

Fig. 4 depicts the complete architecture of the proposed work. The block diagram illustrates the overall workflow, including the distinct phases of the multi-class disease prediction process. The first phase involves pre-processing the dataset using the three algorithms shown in the block diagram. The second phase covers feature extraction using the techniques

highlighted in the diagram. Phase three incorporates the training of the bootstrap and MSVM models for disease prediction, and finally, the two models are compared based on the four parameters shown at the leaves of the architectural diagram.

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Algorithm 1 Health prediction using bootstrap learning

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**Input:** Potato image dataset, which contains a set of healthy and diseased leaf images.

**Output:** Prediction accuracy using the bootstrap model.

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**Method:**

step 1. Apply the Bat algorithm and GMM for preprocessing and leaf region selection of the input image.

step 2. Apply the histogram method and MCCM method for color and texture features, respectively.

step 3. Normalize the features obtained from the above methods.

step 4. Apply the bootstrap learning model to get prediction accuracy.

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### 3.4.2. MSVM learning

The MSVM formulation aims to find optimal hyperplanes that best separate data points into  $k$  classes using the one-vs-all strategy [25]. A training dataset  $\{(x_1, y_1), (x_2, y_2), \dots, (x_n, y_n)\}$  where  $x_i$  is the feature vector and  $y_i$  is the class label with  $y_i \in \{1, 2, \dots, k\}$  for  $k$  classes. The optimization function for the problem is

$$\min_{w_j, b_j} \frac{1}{2} \|w_j\|^2 + C \sum_{i=1}^n \max(0, 1 - y_{ij}(w_j x_i + b_j)) \quad (9)$$

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Algorithm 2 Health prediction using MSVM

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**Input:** Potato image dataset, which contains a set of healthy and diseased leaf images.

**Output:** Prediction accuracy using the MSVM model.

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**Method:**

step 1. Extract fuzzy HSV features from the input image.

step 2. Extract fuzzy LBP features from the input image.

step 3. Normalize the features obtained from the above methods.

step 4. Apply the MSVM learning model to obtain prediction accuracy.

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## 4. Result and Discussion

The disease prediction results of the bootstrap model and multiclass SVM learning model have been presented in this section. The BAT-based crop leaf disease prediction bootstrap model (BCDPBM) [24] uses a novel approach of the BAT algorithm for preprocessing of the image, and the feature extraction is done using a unique combination of histogram feature and MCCM feature. The prediction of multi-class leaf disease is also performed using multi-class SVM with fuzzy HSV and fuzzy LBP feature extraction techniques. It is found that the Bootstrap model, along with the MCCM features, outperformed the MSVM model with fuzzy features. The bootstrap model gives an average accuracy of 98.07% as compared to the average accuracy of 80.11% exhibited by MSVM in multi-class disease prediction. Table 1 shows the accuracy of the BCDPBM model along with multi-class SVM. The table highlights significant differences in the performance of the BCDPBM model and MSVM model across varying numbers of test images, the result shows that BCDPBM encounters a very low error rate of 0.51 % as compared to the 21.63 % error rate of MSVM. Fig. 5 graphs the accuracy comparison of the two models along with the error rate.

Table 1 Accuracy and error rate of multiclass plant leaf disease prediction in the BCDPBM and MSVM models

Testing images	BCDPBM		MSVM	
	Accuracy %	Error %	Accuracy %	Error %
75	97.3	2.7	82.67	17.33
150	95.12	4.88	80.92	19.08
225	99.12	0.88	79.82	20.18
300	99.34	0.66	78.81	21.19
400	99.49	0.51	78.37	21.63

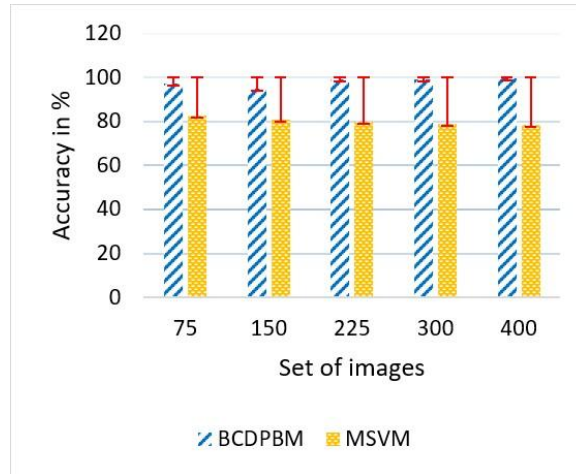


Fig. 5 Accuracy and error rate of multiclass plant leaf disease prediction in the BCDPBM and MSVM models

Table 2 shows the precision value comparison between the BCDPBM model and the Multi-class SVM model for different datasets. The results indicate that the BCDPBM model achieves a precision value of “1” for all datasets, surpassing the multi-class SVM model, which displays precision values of 0.84, 0.80, and 0.83 for datasets of sizes 225, 300, and 400, respectively.

Table 2 Precision values for plant leaf disease prediction using BCDPBM and Multiclass SVM models for distinct size datasets

Testing images	BCDPBM	MSVM
75	1	1
150	1	1
225	1	0.8491
300	1	0.8052
400	1	0.83

Table 3 presents the recall values in the case of different numbers of images shown by the two models discussed above. Table 4 shows the F-measure values exhibited by the BCDPBM and Multiclass SVM models. The results show that the BCDPBM model gives an average F-measure value of 0.99 as compared to the F-measure value of 0.84 given by multi-class SVM.

Table 3 Recall the value of Plant leaf Disease Prediction in BCDPBM and a Multiclass SVM model for distinct-sized datasets

Testing images	BCDPBM	MSVM
75	0.96	0.8
150	0.9804	0.7632
225	0.9867	0.7895
300	0.9901	0.8158
400	0.9924	0.83

Table 4 F-measure of plant leaf disease prediction in BCDPBM and a multiclass SVM model for distinct-sized datasets

Testing images	BCDPBM	MSVM
75	0.9796	0.8889
150	0.9901	0.8529
225	0.9933	0.8182
300	0.995	0.8105
400	0.9962	0.83

The accuracy of binary class disease prediction is shown in Table 5. If the number of images is increased for the testing, the accuracy is also proportionally increased in the case of BCDPBM, while the multiclass SVM shows a random accuracy value. The first model shows the highest accuracy of 99.74 %, whereas the second model depicts the highest accuracy of 94.67 %. The graphical representation of the accuracy comparison of the two models mentioned in Table 5 is presented in Fig. 6.

A comprehensive comparison of the BCDPBM and MSVM models with the existing models is presented in Table 6. Models like Fine-tuned DenseNet, Fine-tuned MobileNet based on optimal mobile network-based convolutional neural network (OMNCNN), and crop leaf health prediction model (CLHPM) have been added to the comparison table. The BCDPBM and MSVM models with proposed features show noteworthy contributions.

Table 5 Accuracy of binary class plant leaf disease prediction in BCDPBM and the MSVM model across different dataset sizes

Testing images	BCDPBM	MSVM
75	98.65	94.67
150	99.34	93.42
225	99.56	91.23
300	99.67	90.4
400	99.74	91.35

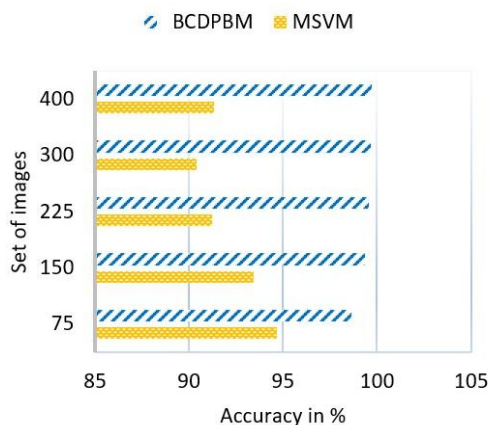


Fig. 6 Accuracy of binary class plant leaf disease prediction in the BCDPBM and MSVM models

Table 6 Comparison of MSVM and BCDPBM models with the existing models

Dataset	Model	Accuracy in %	References
Kaggle dataset	CLHPM	99.23	[20]
PlantVillage dataset	Fine-tuned DenseNet	98.17	[26]
PlantVillage dataset	Fine-tuned MobileNet based with OMNCNN	98.7	[27]
Kaggle dataset	MSVM	92.21	Proposed
Kaggle dataset	BCDPBM	99.39	Proposed

Table 7 additionally compares the accuracy performance of MSVM and BCDPBM across different dataset sizes for three types of conditions: healthy leaf, leaf with early blight, and leaf with late blight. The table shows accuracy in each disease category. The MSVM model shows variability in performance, particularly for Early Blight, whereas BCDPBM demonstrates consistent and superior accuracy across all classes and dataset sizes.

Table 7 Accuracy in each disease category by BCDPBM and MSVM model

Testing images	BCDPBM			MSVM		
	Healthy Leaf	Early Blight	Late Blight	Healthy Leaf	Early Blight	Late Blight
75	88	96	64	96	96.5	99.90
150	91.83	93.87	57.14	98	98.40	99.96
225	86.48	94.66	59.21	98.64	98.64	99.50
300	96	79	61.38	99	99.20	99.98
400	88.40	81.67	62.04	99.25	99.23	99.92

## 5. Conclusions and Future Scope

This research presents a novel approach to crop disease prediction by leveraging leaf features and machine learning techniques. The present work contributes to advancing the field of agricultural disease prediction by introducing fuzzy HSV and fuzzy LBP methods for color and texture feature extraction, respectively, along with instance histogram and modified co-occurrence matrix (MCCM) techniques. Through comparative analysis, the effectiveness of the bootstrap model utilizing MCCM features is demonstrated. The work is concluded as follows

- (1) An impressive average accuracy of 98.07% for multiclass classification and an average accuracy of 99.39% for binary classification is achieved.
- (2) Significant differences in precision, recall, and F-measure are also found in the experiments.
- (3) Overall, the bootstrap model with MCCM and histogram feature extraction methods give better results as compared to the MSVM model with fuzzy HSV and fuzzy LBP feature extraction methods.

Future research could focus on enhancing the robustness and scalability of the bootstrap model, potentially incorporating additional features or refining existing ones to achieve even higher accuracies. Real-time on-field images can also be considered for experimentation to get area-specific disease predictions in crops.

## Conflicts of Interest

The authors declare no conflict of interest.

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