BAT Algorithm-Based Multi-Class Crop Leaf Disease Prediction Bootstrap Model

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Abstract

In the task of identification of infected agriculture plants, the leaf-based disease identification technique is especially effective in better understand crop disease among various techniques to detect infection. Recognition of an infected leaf image from healthy images gets encumbered when the model is required to detect the type of leaf disease. This paper presents a BAT-based crop disease prediction bootstrap model (BCDPBM) that identifies the health of the leaf and performs disease prediction. The BAT algorithm in the proposed model increases the capability of the Gaussian mixture model for foreground region detection. Furthermore, in the work, the co-occurrence matrix feature and histogram feature are extracted for the training of the bootstrap model. Hence, leaf foreground detection by the BAT algorithm with the Gaussian mixture improves the feature extraction quality for bootstrap learning. The proposed model utilizes a dataset of real leaf images for conducting experiments. The results of the model are compared with different existing models across various parameters. The results show the prediction accuracy enhancement of multiclass leaf disease using the BCDPBM model.

Keywords: image processing, leaf disease prediction, co-occurrence matrix (CCM), machine learning

1. Introduction

The cruciality of the agricultural sector is multi-nationally recognized considering the amount of labor required and the input cost. To satisfy both the quality and quantity of production, numerous agricultural processes and components have become automated over time. Technically, agricultural production must be grown utilizing an efficient approach [1] due to accumulative demand in the agricultural business. Crops are any plant or cluster of plants that are farmed and harvested commercially or for subsistence purposes. Given the fundamental survival need, a sufficient supply of food must be guaranteed [1]. However, plant diseases have typically been one of the most significant challenges posing a danger to the safety and sufficient availability of food for humans. The gap between the survival and destruction of crops in farmlands impacted by these plant diseases can be severe if their early diagnosis and efficient control are not prioritized [2].

Phytopathology specializes in the myriad of plant diseases that affect plant life [3]. Pests, contagious diseases, and natural disasters are only a few of the variables that might stunt plant development. Disrupting the food chain, as a consequence of pathogenesis on plants, can be zoogenic or anthropogenic, which incurs underproduction and environmental instability. If the pathogens are abundantly generated and diffused, a devastating consequence would reflect on the agricultural sector across the country.

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To identify plant diseases, visual examination and automatic plant disease detection systems are two main methods. Many models were developed to learn and classify images like convolutional neural networks (CNN) [4] and were used to find infected leaf images [5]. Meanwhile, a few flaws exist in the current automatic plant disease detection system. To maintain stability in the automatic system, the following challenges must be conquered.

(1) The unpredictable conditions during picture capture may contribute extra features, perplexing users for illness identification.

(2) Complicated background features in digital photos impede the segmentation procedure to pinpoint the infected area (region of interest).

(3) Differentiation between the sick and healthy images is a wearisome task.

The research gap identified is as follows:

(1) It is found in Pratap and Kumar [6] and Fuentes et al. [7] that scarce work has been done on image background removal. This restriction reduces the feature learning capability of mathematical models.

(2) Most of the models presented in Pratap and Kumar [6], Fuentes et al. [7], and Mousavi and Farahani [8] work for special types of leaves and their relevant diseases.

(3) Some of the work extracts complex features like biorthogonal wavelets [9], which eventually consumes a longer time for classification.

The primary objectives of this work are as follows:

(1) To propose a bootstrap learning algorithm for predicting multiclass plant diseases.

(2) To remove the need for a specific background of the input image.

(3) To train a model that automatically identifies the health of the image.

The remaining sections of the article are structured as shown below: In Section 2, the related work is presented, and the methodology is discussed in detail in Section 3. Subsequently, Section 4 illustrates several experiments that are conducted. Finally, the conclusions are presented in Section 5.

2. Related Work

Pratap and Kumar [6] proposed a model that was trained to recognize leaf diseases. This study illustrated the utilization of deep learning architectures for leaf disease diagnosis and purposively underlines the potential of EfficientNetB4 as a formidable tool. Authors optimized EfficientNetB4 as EfficientLeafNetB4 and found that it outperformed ResNet-50, DenseNet-121, MobileNet-V2, and VGG-16 in detecting diseases in chili leaves.

Mousavi and Farahani [8] developed an automatic diagnosis approach called advanced VGG16. The system comprised a quadcopter to photograph, a central computer to analyze images, and a hexacopter to spray pesticides based on the kind of illness uncovered by the computer and the affected area as recorded by the quadcopter. The suggested method relied on the deep learning technique of accelerated R-CNN, which was based on enhanced VGG16. In addition, the suggested technique was used to evaluate alternative networks for disease detection in grapevine gardens, such as VGG16, GoogLeNet, AlexNet, and ResNet50.

Mazumder et al. [9] provided a novel approach to disease detection in prime corn leaves using the biorthogonal wavelet transform (BWT). To extract the damaged part of the corn leaf from the input image, the biorthogonal wavelet decomposition and pixel-by-pixel morphological operation were employed. By exploring the discriminating power of the bior3.3, bior3.5, and bior3.7 biorthogonal wavelet filters, the authors suggested a unique technique. Specifically, the technique extracts color, and channel-wise wavelet entropy characteristics using 2-dimensional BWT at several levels for feature extraction.

Liu et al. [10] created pictures of four distinct grape leaf diseases to be used in preparing an identification model. The research offered a novel model termed LeafGAN based on generative adversarial networks (GANs). Grape leaf disease images are first generated using a generator model with degressive channels; then, using their excellent feature extraction capability on grape leaf lesions, images of real and fake diseases are differentiated. The dense connectivity strategy is used for the work. Subsequently, the instance normalization is fused into an efficient discriminator. To stabilize the training process, the deep regret gradient penalty technique is implemented.

Bhuyan and Huque [11] examined smart farming that predicted crop illnesses and created an effective classification model for plant disease detection based on monitoring sophisticated agricultural fields using top-tier sensors. Fuentes et al. [7] proposed the integration of deep feature extractors such as VGG net and residual network (ResNet) with these meta-architectures to enhance detection performance. By leveraging powerful feature representations learned from large-scale image datasets, these feature extractors contribute to improving the discriminative power of the detection models.

Madhurya and Jubilson [12] devised an optimized framework based on YOLOv7, termed YR2S, for disease detection in leaves. Leveraging pre-processing and hybrid optimization techniques, the proposed framework incorporates PCFAN for feature map generation and ShuffleNet with enhanced rat swarm optimizer (ERSO) for classification optimization. Through FCN-RFO, the framework facilitates the segmentation of disease-prone areas, contributing to effective disease detection in plants. Shovon et al. [13] introduced the PlantDet model, leveraging architectures like InceptionResNetV2, EfficientNetV2L, and Xception to address issues of underfitting and enhancing robustness. Through techniques such as pre-processing, data augmentation, and incorporating various architectural components such as global average pooling layer and dropout mechanisms, the PlantDet model exhibits improved performance and robustness, particularly in scenarios with limited data and diverse backgrounds.
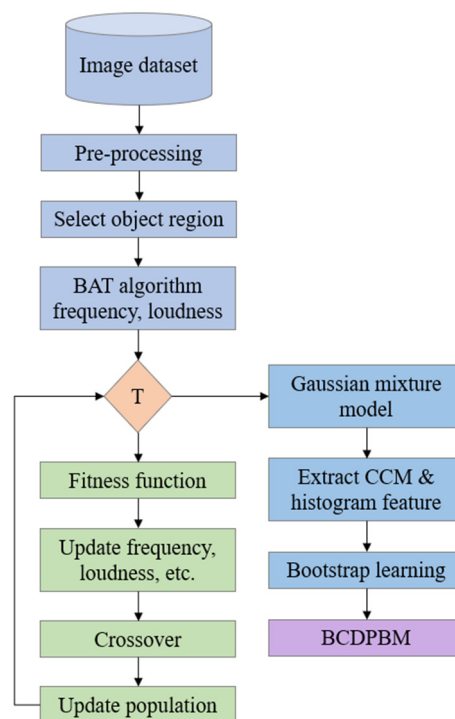
3. Proposed Methodology

Fig. 1 Block diagram of BCDPBM

In this section, the proposed BAT-based crop disease prediction bootstrap model (BCDPBM) is rather comprehensive, and a schematic is depicted in Fig. 1. In the work a novel approach has been employed to make use of the BAT algorithm with Gaussian mixture model (GMM) for background detection that forms a unique combination for the preprocessing of the leaf

image. The unprecedented collaboration of modified co-occurrence matrix (MCCM) and histogram features is particularly pivotal in the bootstrap learning in the proposed model. A visual representation of the model's logic is provided in Fig. 1 by outlining its constituent parts. The entire process has been segmented into feature extraction and mathematical model training.

3.1. Pre-processing

To moderate the noise level of the model and the running cost, the input picture dataset is preprocessed. During preprocessing, a square matrix representing the picture is created [14]. The outcome of preprocessing is delineated by the notation processed leaf image (PLI). The leaf image dataset (LID) is preprocessed and stored in PLI as shown in the equation. In addition, from the image's backdrop, the present work recognizes the area that contains the leaf [15-16]. Since the input is an RGB picture, the selected region is converted to hue saturation value (HSV) and grayscale.

$$PLI \leftarrow PreProcess(LID) \tag{1}$$

3.2. Leaf region selection

The leaf region is captured for the identification of the leaf health. To enhance the process of this captivation of the desired leaf area BAT algorithm is utilized. The BAT algorithm chooses the leaf region corresponding to the BAT agent with the highest fitness value as the final selection. The steps involved in this process are briefed below.

3.2.1. BAT algorithm

Motivation for the BAT algorithm originates from bat colonies that use echolocation to predate. The process and characteristics of bat echolocation are illustrated in Ghanem et al. [17]. Bats use echolocation to gauge distance and to unveil the differences between barriers and prey. Bats use a combination of random factors, including their flight speed v_i, frequency f_{min}, location x_i, wavelength λ, and volume A_0, to locate prey. These factors could be performed per se, based on the proximity of a possible blockage, i.e., concretely, in the exact rate of pulse emission, r ranges in [0,1], and pulse discharge frequency. The presumption relies on the range of audibility spanning between the extremes of a positive high A_0 and a constant low A_{min}. Bats are first defined by their positions (xt_i), emission pulse rates (rt_i), velocities (vt_i), decibel levels (At_i), and frequencies (ft_i). At instant t in the search area, the foreground and background halves of this algorithm are handled independently. Therefore, the algorithm generates potential pixel sets in each location, evaluates the fitness of each set, and then adjusts the pixel values by the fitness value [16].

3.2.2. BAT population

During this process, it is considered that bats are present based on the pixel values in the area [17]. Each bat represents a range of values from 0 to b, and there are c potential values for the cluster centers. If there are m bats in a population, the population matrix will include $m \times c$ rows and columns. In a BAT population, the pixel value is picked at random among those that are accessible in the region R.

$$BPb \leftarrow GeneratePopulation(m, b, R) \tag{2}$$

3.2.3. Initialize parameters

Each bat differs from frequency f, loudness l, pulse rate r, velocity v, position x, and sensing wave λ. Hence, this needs to be initialized to start the algorithm. Once the algorithm starts, parameter values are modified. While initializing these parameters, it is essential to consider the characteristics of the leaf images, such as size, complexity, texture, and color distribution.

3.2.4. Fitness value

The fitness of each bat Bb is calculated. The lowest Euclidean distance between each pixel in the area and the bat pixel set is used to compile this evaluation. Therefore, the bat with the lowest fitness value is the optimal option in the cluster. The goal is to iteratively improve the solutions over time, ultimately converging towards an optimal or near-optimal solution that maximizes the fitness value.

3.2.5. Update parameters

The echolocation technique used by tiny bats serves as an inspiration for the BAT algorithm. In a 2-dimensional search or solution space, each bat has a velocity v and a position x at time t [18]. There is a current optimal bat, denoted by b^*. Thus, the three laws may be expressed in terms of accelerating velocity (v) and acceleration (f) as the following equations:

$$f_i = f_{min} + \left(f_{max} - f_{min} \right) \beta \tag{3}$$

$$v_i^t = v_i^{t-1} - 1 + x_i^{t-1} - 1 - x_i \times f_i \tag{4}$$

$$x_i^t = x_i^{t-1} - 1 + v_i^t \tag{5}$$

where $\beta \in [0,1]$ is a random vector drawn from a uniform distribution.

The loudness and pulse emission rates are regulated by the following equations:

$$l_i^{t+1} = \alpha l_i^t \tag{6}$$

and

$$r_i^{t+1} = r_i^t \left[1 - e^{-\mu t} \right] \tag{7}$$

where $0 < \alpha < 1$ and $\mu > 0$ are constants. In essence, here α functions as the cooling factor of a cooling schedule in simulated annealing.

3.2.6. Crossover

At this point, the BAT algorithm performs a crossover operation that is optimal for the present population based on the minimal value of the fitness vector f [16]. The best b^* bat pixel set's values are therefore replicated across the population. In genetic algorithms, this process of copying characteristics from one organism to another is known as a crossover.

3.2.7. Population updating

At this point in the BAT algorithm, the fitness levels of the offspring are compared to those of its parents. If the offspring's fitness is lower, it will be replaced by a new bat, while the parents stay on. If the iterations have reached the maximum number after the population's most recent update, the algorithm will progress to determine its fitness value.

3.2.8. Gaussian mixture model (GMM)

Nurhadiyatna et al. [19] and Bariko et al. [20] proposed a flexible, modifiable GMM to mitigate the impact of repeating tiny pixels in the image's foreground. The grab-cut method's foreground image area feature is applied to other input photos to locate the same region. By employing a GMM Model for leaf image analysis, effective segmentation of leaf regions from complex backgrounds and facilitation of various downstream tasks such as disease detection, and plant phenotyping are performed.

3.3. Feature extraction

This module briefs about the feature extraction techniques employed for property assessment of the images. It comprises sections of CCM feature extraction followed by histogram feature extraction. To show the comparison between healthy and diseased leaves, two sample images are juxtaposed in Fig. 2 corresponding to the healthy leaf, and early blight infection on the tomato plant leaves respectively.

Fig. 2 Healthy leaf and leaf with early blight

Fig. 3 depicts images corresponding to the bacterial spot and late blight infection on the tomato plant leaves respectively, while Fig. 4 gives a pictorial representation of the late mold, Septoria spot, and the spider mites respectively if surveying the surfaces from left to right.

Fig. 3 Leaf with bacterial spot and late blight infection

Fig. 4 Leaf with late mold, Septoria spot, and spider mites' symptoms

3.3.1. Modified co-occurrence matrix (MCCM)

Leaf texture features are crucial in the discerning of image health [21]. Image is transformed into RGB and HSV format where red, green, hue, and saturation matrix values are considered [15-16]. This paper extracts the MCCM feature from the image as shown in Fig. 4. Instead of using all CCM feature sets (energy, entropy, inverse difference, contrast) some of the negative and low values are abolished. This updated positive value set is a modified CCM model. It is perceived that the use of the MCCM presided over high learning of the model.

3.3.2. Histogram

Unhealthy plant leaves would temporally undergo discoloration from green to yellowish and brown. Thus, images could also be chromatically classified [16], and the foreground region of the grab-cut is used to extract the histogram feature value set. Extracting features from leaf images based on histograms offers a concise and informative depiction of image content.

3.4. Bootstrap learning

Bootstrap bagging, also known as "bootstrap aggregating," epitomizes a machine-learning ensemble technique designed to enhance the accuracy and robustness of predictive models [22]. To train the mathematical model extracted features are blended and normalized for the training. The MCCM gives 9 feature values, and the histogram provides 16 values. Consequently, the training vector consists of 25 different values. This method operates through a sequence of key steps:

3.4.1. Bootstrap sampling

Initially, random subsets of the training data are selected with replacements. These subsets mirror the original dataset's size precisely. The procedure, termed "bootstrap sampling," introduces a vital element of randomness and diversity into the training sets. Training by small bundles of datasets elevates the learning and accuracy of class detection in the Bootstrap model. Consequently, multiple models are generated, and each model has been trained on a distinct subset of the data. So cumulative decision by different models reduces the false prediction.

3.4.2. Prediction aggregation

As a decisive step, predictions are made by each of the base models for every data point in the test dataset. The ultimate prediction is typically derived from combining these individual predictions. The aim is to leverage the collective insights and strengths of the individual models to arrive at a more accurate and robust prediction.

Proposed BCDPBM algorithm
Input: LID // leaf image dataset
Output: BCDPBM // BAT-based crop disease prediction bootstrap model
1   **START**
2   Loop 1: n // n: number of images in ID
3   PLI ← Pre-process (LID) // Processed leaf image
4   Bbp ← Generate_population (m, b, R) // BAT population generated to optimize input image features.
5   Bbp ← Initialize_parameters (Bbp)
6   Loop 1:t
7   F ← Fitness (Bbp)
8   Bbp ← Update_parameter (F, Bbp)
9   Bbp ← Crossover (Bbp)
10   Bbp ← Update_population (Bbp)
11   End Loop
12   b^* ← Fitness (Bbp) // Cluster image for getting foreground.
13   CLR ← GMM (b^*, PLI) // Filter foreground and background.
14   C ← MCCM (CLR) // Extract the MCCM feature from the image.
15   H ← Histogram (CLR) // Extract histogram feature from the image.
16   C ← Normalize (C) // Normalize the features, as both features have different value ranges.
17   TF ← [C, H] // Training features TF are used after the normalization.
18   Do ← LID // Collect the desired class of the leaf training dataset.
19   End Loop
20   BCDPBM ← Bootstrap_learning (TF, Do) // Train the bootstrap model.
21   **END**

4. Result and Discussions

Core i7 CPU and 8 GB of RAM hardware configuration are employed for conducting the experiments, and MATLAB 2021 is used to create the suggested model. Actual crop leaf data is used in the experiments. The dataset [23] is concretely described in Table 1.

Table 1 Image dataset description

Feature	Description
Dimensions	256 × 256
Types of images	7
Crop	Tomato
Total images	2000

The proposed BCDPBM model is compared with existing models such as MobilenetV2 [24-25], support vector machine (SVM), and CNN [4]. Table 2 shows that the prediction accuracy of the diverse types of diseases in all sets of testing images is above 98.6% accuracy. This is achieved using a bootstrap learning model with MCCM and histogram features. It is observed that the genetic algorithm has enhanced the learning of the model as well.

Table 2 Multiclass image detection of BCDPBM

Testing images	Accuracy (%)	Error
75	97.3333	0.026667
150	98.6667	0.013333
225	99.1111	0.008889
300	99.3333	0.006667
400	99.5	0.005

Table 3 shows that the prediction precision value of the healthy class of images is "1" in all the testing images. Furthermore, it is revealed that the average recall value is 0.9818, also with an increase in the number of testing images recalled, and other parameter values are elevated. As a result, it evinces the improvements in performance using the BAT algorithm in the proposed model. The reduction of features by BAT optimization increases the training of the bootstrap model.

Table 3 Multiclass image prediction BCDPBM model evaluation parameter values

Testing images	Precision	Recall	F-measure	Accuracy
75	1	0.96	0.979592	98.6486
150	1	0.98	0.989899	99.3289
225	1	0.986667	0.993289	99.5536
300	1	0.99	0.994975	99.6656
400	1	0.9925	0.99620	99.75

Table 4 shows the comparison in the accuracy of different models of leaf disease prediction. It reveals that the BCDPBM has increased the prediction accuracy by 3.43% as compared to the MobileNetV2 model. Further use of the MCCM feature with histogram has enhanced the learning and prediction accuracy.

Table 4 Accuracy value of tomato healthy leaf prediction

Leaf types	MobileNetV2	SVM	CNN	BCDPBM
Early blight + healthy	94.19	92.50	94.80	98.36
Bacterial spot + healthy	96.51	92.65	96.55	98.82
Late blight + healthy	93.02	93.05	96.30	98.36
Late mold + healthy	95.35	92.50	94.50	98.33
Septoria spot + healthy	96.51	94.35	97.50	98.63
Spider mites + healthy	98.84	92.80	97.20	98.97

Recall values of comparing plant disease models are shown in Table 5. It is observed that the bootstrap model performs well in different sets of testing images. BCDPBM shows a recall value of 0.96 with early blight and healthy leaf types while presenting a recall value of 0.98 with spider mites and healthy leaf types.

Table 5 Recall-value of tomato healthy leaf prediction

Leaf types	MobileNetV2	SVM	CNN	BCDPBM
Early blight + healthy	0.8837	94	94	0.96
Bacterial spot + healthy	0.9302	95.10	94.55	0.973
Late blight + healthy	0.8605	94.55	94.25	0.9796
Late mold + healthy	0.907	94	95.00	0.9792
Septoria spot + healthy	0.9302	94.35	94.05	0.9836
Spider mites + healthy	0.9767	94.15	94	0.9882

F-measure values of different plant images are illustrated in Table 6. It is noteworthy that the use of the BAT optimization algorithm for image feature dimension reduction has increased the correct nosological prediction. The current BCDPBM model has increased the f-measure value by 3.93% as compared to the MobileNetV2. Table 7 throws some light on the True Positive Rate (TPR) of different models.

Table 6 F-measure value for distinct size leaf class of tomato healthy leaf prediction

Leaf types	MobileNetV2	SVM	CNN	BCDPBM
Early blight + healthy	0.9383	92.5	94.5	0.9796
Bacterial spot + healthy	0.9639	92.00	94	0.9863
Late blight + healthy	0.925	92.50	95.15	0.9897
Late mold + healthy	0.9512	92.15	94.66	0.9895
Septoria spot + healthy	0.9639	92.77	94.90	0.9917
Spider mites + healthy	0.9882	92.95	94.67	0.9941

Table 7 TPR value of tomato healthy leaf prediction

Leaf sets	MobileNetV2	SVM	CNN	BCDPBM
50	0.92	0.9	0.93	0.96
100	0.9	0.86	0.94	0.973
200	0.9	0.9	0.93	0.9796
300	0.9067	0.86	0.96	0.9792
400	0.8713	0.88	0.95	0.9836
500	0.8968	0.85	0.96	0.9882

Table 8 shows that the current model BCDPBM has increased the two-class prediction accuracy compared to MobileNetV2, SVM, and CNN's well-known competing models discussed in Yamashita et al. [4], Ahmed et al. [24], and Nguyen et al. [25].

Table 8 Accuracy value for distinct size leaf classes of tomato healthy leaf prediction

Leaf sets	MobileNetV2	SVM	CNN	BCDPBM
50	96	95	98.9	100
100	95	96	98	98.99
200	95	95.5	97.8	99.4975
300	95.33	95.9	99.1	99.65
400	93.3	94	98.95	99.74
500	95.08	95.7	98.5	99.79

It is worth mentioning that testing leaf image count is directly proportional to the accuracy of the BCDPBM. Besides, the use of selected and concise 32 features has improved the correct healthy class prediction accuracy. The prediction accuracy of the BCDPBM model is improved by 4.66% compared to the MobileNetV2. Fig. 5 represents the graph of accuracy values obtained from different machine learning models tabulated in Table 8.

It is found that the use of a BAT algorithm with selected values for foreground detection mitigates the noisy data in the image. Moreover, the extraction of modified CCM features with histogram values for the training of the bootstrap model has increased the learning and disease detection accuracy of multiclass leaf diseases.
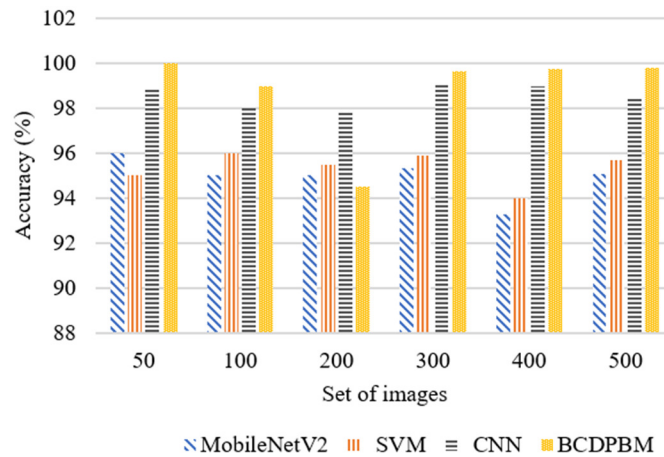
Fig. 5 Accuracy values obtained from different machine learning models

5. Conclusions and Future Scope of Work

There have been several efforts taken to guarantee the excellent quality of agricultural output as the agriculture business expands. Given that diseases and other abnormalities in plants and crops have a significant economic impact, several tools and methods have been created to withstand plant diseases. Significant economic losses are incurred owing to the agricultural output impacted by Phyto pathological factors. This paper has illustrated a disease prediction model that uses the BAT algorithm to identify the leaf region and further extracts content features for training. Histogram and CCM features are used in the present work for the training of the bootstrap model. Experiments are conducted on a real multiclass disease dataset. The result proves that the BCDPBM model has increased the comparing parameter values. It is observed that the multiclass disease prediction accuracy of the BCDPBM is 98.78%. which outperforms the competing models like SVM, CNN, and MobilnetV2 concerning accuracy. Moreover, it is noteworthy that the BCDPBM shows the f-measure value as 98.84 %, which surpasses the other competitive models. The major strength of the model is that it compatibly functions on all sets of different crops without any variation in the model. Another discovery is that the model can accurately predict leaf classes after being trained for different images. Nevertheless, the model has a limitation with the suitability of working on constant background images. Therefore, researchers can involve random background of leaf images in the dataset for training and testing post hoc or perform experiments for crop health prediction by plant stem.

Conflicts of Interest

The authors declare no conflict of interest.

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