



Identification and Classification of Plant Diseases through Image Processing and Different Hybrid Optimization Techniques

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Abstract

Crop disease diagnosis is of great significance to crop yield and agricultural production. Optimization algorithms have become the main research direction to solve the issues related to diagnosis of crop diseases. Crop diseases are a major threat to global vegetable supply security, and the latest technologies need to be applied to the agriculture field to control diseases. This paper provides methodology en route for identification and classification of plant leaf ailments. Image acquisition, image preprocessing, feature extraction, feature selection, and eventually classification of plant diseases are all steps in the methodology. The training of a deep convolutional neural network to extract the features from the source image. An optimal set of features is selected using Population-based incremental learning (PBIL) and are categorized into 20 various classes, containing together healthy and diseased categories. Presented method provides better classification accuracy.

Keywords: Population-based incremental learning, CNN, Image acquisition, Feature extraction

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1. Introduction

Plant diseases have a detrimental effect on agricultural production. Food insecurity will worsen if plant diseases are not identified in a timely manner. Plant diseases must be prevented and controlled effectively

on the basis of early detection, and they are a key factor in managing and making decisions regarding agricultural productivity. Identification of plant diseases has been a critical concern in recent years [1-2]. Plants with a disease typically have noticeable tinges



or lesions on their leaves, stems, flowers, or fruits. The majority of diseases and pest conditions exhibit a distinct visual pattern that can be utilized to specifically identify irregularities. Most disease signs may first develop on the leaves of plants, which are typically the main source for identifying plant illnesses [3]. On-site identification of diseases and pests of fruit trees is typically done by agricultural and forestry experts, or by farmers using their own knowledge. This approach is not only arbitrary, but also time-consuming, arduous, and ineffective. Farmers

with little experience could make mistakes and utilize medications carelessly when making identifications. Environmental contamination brought on by quality and output will result in avoidable financial losses. In order to overcome these difficulties, the application of image processing methods for plant disease recognition has emerged as a popular study area.

Fig. 1 illustrates the typical procedure for utilizing conventional image recognition processing technology to detect plant diseases.

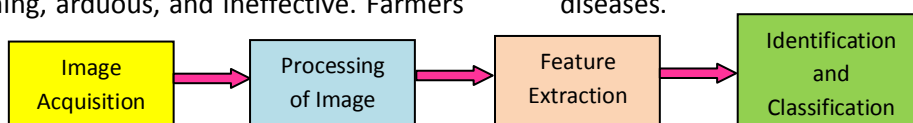


Fig. 1 Typical Image Recognition

To extract the colour and texture properties of apple spots, Dubey and Jalal [4] incorporated the global colour histogram (GCH), colour coherence vector (CCV), local binary pattern (LBP), and completed local binary pattern (CLBP). They utilized the K-means clustering approach to split the lesions regions. Moreover, three different apple illnesses are found and classification accuracy of 93%. Through the use of stepwise discriminant and Bayesian discriminant principal component analysis (PCA), Chai et al. [5] investigation of four tomato leaf diseases—early and late blight, leaf mildew, and leaf spot—extracted 18 distinguishing parameters, including colour, texture, and shape information of tomato leaf spot images. In order to extract the characteristic parameters and build the discriminant model, principal component analysis and fisher discriminant methods are utilized. The two techniques' respective accuracy rates are 94.71% and 98.32%. Li and He [6] chosen five different apple leaf illnesses to study: rust disease, yellow leaf disease, round spot disease, and speckled deciduous disease. By taking the apple leaf spot image's eight qualities, including its colour, texture, and shape. The disorders are categorised and

identified using the BP neural network model, and the average recognition accuracy was 92.6%. Guan et al. [7] approach of classifying and recognising three rice illnesses (blast, stripe blight, and bacterial leaf blight) had the best recognition accuracy of 97.2%. They collected 63 attributes from rice leaf disease spots, including their morphology, colour, and texture.

Tomatoes are a significant food crop in many parts of the world. With a per capita consumption of 20 kg, or 15% of all vegetable consumption, Europe uses 31 kg of tomatoes per person per year compared to North America's 42 kg [8]. Techniques for crop production and early identification of pests, bacteria, and viral illnesses must be developed in order to meet the demand for tomatoes on a global scale. In several studies, early disease detection and subsequent disease management have been used to increase tomato plant survival. Using a pre-trained CNN-based architecture called Residual Network, also known as ResNet, Manpreet et al. [9] classified seven tomato illnesses with an accuracy of 98.8%. There have been some papers published to summarize the research on agriculture (including the identification of plant diseases)



by DL [10-11], but they lacked some of the most recent advancements in visualization techniques used in conjunction with DL and altered the well-known DL models that are used to identify plant diseases.

The focus of the paper [12] was on imaging techniques, which are presented in a number of imaging techniques for plant disease detection. SVM, K-means, and KNN are the main strategies for classifying and treating plant diseases that have been reported. Many developed/modified DL architectures used to identify and categorize plant diseases are given in the article [13]. It gave a thorough description of how DL models are used to depict different plant diseases. However, there is no discussion of disease early detection or how to identify and categorize plant illnesses using small samples. The authors of the publication [14] provided a thorough analysis of recent research on plant disease recognition using IPTs from the standpoint of feature extraction based on manually built or deep learning techniques. Finally, it can be said that shallow classifiers trained using manually created features have been surpassed by deep learning algorithms. However, they lacked some of the most current advancements in visualization techniques, and there was no mention of early disease detection or how to identify and categorize plant illnesses based on small samples.

Because there are such wide differences in leaf size, shape, colour, and location, it is still difficult to localize and classify crop diseases in an efficient and effective manner. Additionally, the brightness changes that occur when taking images of the leaves make the detecting procedure more difficult. This study attempted to address the abovementioned issues by integrating a tailored CenterNet framework with DenseNet-77 at the key points computation level to calculate the deep key points of input samples and localization and classification of

different plant diseases. According to findings, the proposed method is resistant to alterations in shape, rotation, colour, brightness, contrast, lightning conditions, blurring, and large numbers of noisy input samples. Here are the principal benefits of the newly adopted framework: (i) While reducing the training and testing time, the customized CenterNet model with DenseNet77 for features computation improves the detection and classification accuracy of plant diseases, (ii) Due to the robustness of the CenterNet model, present method accurately localizes the damaged area of plant leaves, (iii) Due to the CenterNet model's ability to handle the over fitted model training data, our strategy improves the classification accuracy of plant leaf diseases, (iv) PBIL is used to pick the features and a deep neural network to extract the features. To train a classifier to categorize photos into their appropriate classes, the best set of features is used, (v) presented a smartphone-friendly method that is computationally ideal.

2. Methodology

The three studies in the paper—(i) a binary classification of healthy and unhealthy segmented leaves; and (ii) a five-class classification of healthy—are carried out using segmented leaf images. The optimal segmentation network for separating leaves from the background was investigated using several U-net segmentation model variations. The Score-Cam visualization technique, which has been proved to be extremely trustworthy in various applications, is used to further validate the segmented leaf pictures used in categorization. Efficient networks, which the authors have used with relative effectiveness in earlier publications, are used for the categorization.



2.1. Description of Dataset:

A total of 9250 photos from 20 different plant leaf classes have been examined. Each class is given a crop-disease pairing, and when the model has been trained, it attempts to predict the right pairing

using an image of the diseased plant leaf. All of the images are shrunk to 256× 256 pixels for our model's predictions to be accurate, and it was trained on these downsized images. The Plant Village dataset's coloured, resized photos have been used throughout the entire process.



Fig. 2 Sample Images from plant village dataset

2.2 Approach

The three components of our strategy are feature extraction, feature selection, and classification. When features need to be extracted from coloured raw photos, a deep neural network is quite helpful. In order to extract features from the input image, trained one such architecture, DenseNet77, using transfer learning. By removing DenseNet77's SoftMax layer and taking into account the output of 200 nodes, features are extracted. The PBIL feature selection algorithm is fed these 200 DenseNet77-extracted features as

input. In PBIL, each feature is represented with binary selection. As a result, it gives a sample space of 1 to 4200, from which we choose a population size of 150. The velocity and parameters are adjusted using the global and local best of each particle using the multi-objective fitness function. Set the velocity function's self-confidence range and swarm confidence range to each be 0.50. Following testing with various variables, these values are picked for the best outcomes. As a result, an ideal set of features are given to hybrid classifier. Entire process is shown in Fig. 3.

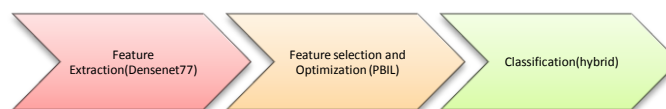


Fig. 3 Proposed method process flowchart

2.3 Feature Extraction

The features that are extracted have a significant impact on how well any detection or recognition system performs. For feature extraction, a deep neural network was trained. Transfer learning was performed since the dataset size was insufficient to train the neural network to the appropriate level from scratch. Transfer learning improves the training procedure by making certain adjustments to the current model. The SoftMax classifier used in the original

DenseNet77 model's classification function calculates the likelihood of each of the dataset's 1,500 classes. In Densenet77, there are three fully connected layers and five convolutional layers with SoftMax output and Max Pooling. On the basis of the output from the previous layer, the last fully connected layer makes predictions. The weights of the penultimate layer are reset in order to train the transfer learning model using the present dataset because it was trained using a different dataset. Lowered the number of classes from 1500 to 150, which is the ideal

number of features for the model, because DenseNet77 produces SoftMax output. These 150 classes' output was considered to be features.

2.4 Population Based Incremental Learning Algorithm

In the stage before, each image had 100 features retrieved using deep neural networks. More than 150 features can be extracted using deep learning techniques. It is required to employ an optimization strategy that can only describe the dominant or significant features because the previous stage requires a lot of processing. The best collection of characteristics is chosen using PBIL, one of these heuristic techniques. A revolutionary evolutionary method called population-based incremental learning (PBIL) combines competitive learning and the workings of the Genetic Algorithm. PBIL often uses binary coding, which causes coding redundancy and probability conflict and decreases the algorithm's effectiveness. The non-inferior solution set represents the best value in the evolution process, and it is used to update the value probability vector P_i of each gene location depending on the coded value on the corresponding gene position. The following updates are made to each P_i component:

$$P_{ik} = (1 - LP)P_{ik} + LP \left(\frac{n_k}{PI^*} \right), k = 1, 2, 3, \dots, d_i \quad (1)$$

Where LP is the learning probability, PI^* is the number of individuals in the current non-inferior solution set, and n_k represents the number of individuals in the sub-interval on the i^{th} gene position in PI^* individuals.

2.5 Feature Selection

The goal of PBIL is to find the extracted features that are most descriptively

subset. Each member of the population stands for a potential candidate for the answer. Evolution is driven by fitness function, which indicates the level of fitness anticipated in upcoming trials. The feature vector retrieved in this case has a length of 150, and the initial coding of each particle was created at random, yielding the binary alphabetic string $S = K_1K_2K_3K_4 \dots K_n$, $n = 1, 2, 3, \dots, q$. Each index in the binary string S indicates which feature should be chosen; a value of 1 designates the chosen feature, while a value of 0 indicates rejection. In the 2^q search space, the algorithm is utilised to look for the best solution. For instance, when PBIL is used to evaluate a 12 dimensional dataset ($n = 12$), $S = K_1K_2K_3K_4K_5K_6K_7K_8K_9K_{10}K_{11}K_{12}$, can choose any subset of features that is smaller than n . By setting bits 1, 4, 6, 7, 9 and 11, for example, PBIL can select a random collection of six features, $K_1K_4K_6K_7K_9K_{11}$. Based on the fitness value, it is determined for each particle how well the chosen feature subset maintains the highest level of accuracy in representing the original feature set. The parameters that the PBIL will iteratively evolve are represented by indices denoted by q in the particle. Every iteration, the fitness function K calculates the value of each particle's goodness or fitness. The fitness function, which assesses the quality of developed particles based on their capacity to maximise classification accuracy, is what propels this evolution. The fitness function, which trains the classifier with the features represented by the particle, is a m -fold cross validation function, where $m = 12$. The classifier's precision serves as a fitness metric and an evolutionary tool.

2.6 Classification

The image is finally categorised into numerous illness classes. The classifier is trained using the best set of features determined by PBIL from features extracted



by DenseNet77. Based on which hybrid technique is chosen for the classification of the images, the cross validation accuracy of a number of classifiers, including XGBoost, Support Vector Machine, Random Forest, and K-Nearest Neighbor (KNN), was evaluated.

3. Results and Discussion

This section presents a thorough analysis of the findings from numerous experiments to gauge the effectiveness of the proposed method's evaluation. In this part, there is also a description of the dataset that was used to assess performance. The Nvidia

GTX1070 GPU-based hardware used to run the Python implementation of the described framework. In the previously described method, transfer learning was utilised to fine-tune CenterNet on the Plant Village dataset for the classification and categorization of plant leaf diseases rather than training the model from scratch using the framework with pre-trained weights obtained from MS-COCO. The suggested method was evaluated using a variety of metrics, including Intersection over Union (IOU), accuracy, precision, recall, and mean average precision (mAP). The accuracy was calculated as follows:

$$Accuracy = \frac{T_p + T_n}{T_p + F_p + T_n + F_n} \quad (2)$$

Below expression illustrates the mAP computation, where q is the query or test picture and AP is the average precision of each class. Q represents the entire sample of test images.

$$mAP = \sum_{p=1}^R AP(t_p) / R \quad (3)$$

The IOU, precision, and recall are each represented by following expressions respectively.

$$IOU = \frac{T_p}{F_n + F_p + T_p} \times 2 \quad (4)$$

$$Precision = \frac{T_p}{F_p + T_p} \quad (5)$$

$$Recall = \frac{T_p}{F_n + T_p} \quad (6)$$

Trained the proposed model using roughly 350 images of each class with a 70%–30% train–cross validation split in order to evaluate the effectiveness of the suggested strategy on unobserved data and monitor overfitting in the approach. The testing dataset included 240 images, or 12 images for each of the 20 classes. 90 features are taken from the model after it had been trained on 20 classes. 35 ideal features are retrieved using PBIL, and these features are then used to train the classifier. With roughly 6475 images for training and 2775 images for cross-validation, the DenseNet77 model for feature extraction was trained for 20 classes. The split between cross validation and training was 30% to 70%. 9250 pictures in total are utilized to train the model.

The accuracy that was attained for the specified number of iterations is shown in Table I.

Table I DenseNet77 Training Accuracy

S.No	Epochs	Training accuracy
1	500	98.23
2	1000	98.23



For each image, 90 characteristics were retrieved. From the 90 features that the neural network extracted, an ideal feature subset is chosen using PBIL. The values of the parameters that PBIL demands are shown in Table II.

Table II Parameter setting of PBIL

S.No	Parameter	Value
1	Population size	100
2	Error	0.02

Table III indicates the performance of PBIL. The global best fitness value and global best parameter, which reflect the ideal feature subsequent to the global best fitness value, are specified by the 'gbest' fitness.

Table III PBIL results

S.No	Parameter	Value
1	Global best fitness	0.991
2	Iterations	98

To determine a technique's effectiveness, a variety of plant diseases must be accurately detected and classified. Therefore, experimentation is used to assess how well the proposed method works in identifying the class of each plant disease. The Plant Village dataset's are used to test images to apply the trained Custom CenterNet classifier to. Table IV shows how well the novel method performs in classifying plant diseases in terms of recall, precision, and F1-score.

Table IV Performance of the suggested method across classes

S.No.	Name of the Class	Precision	Recall	F1-Score	S.No.	Name of the Class	Precision	Recall	F1-Score
1	Apple_Healthy	1.000	1.000	1.000	11	Tomato_Healthy	1.000	1.000	1.000
2	Apple_Cedar_Rust	0.996	0.982	0.989	12	Tomato_Mosaic_Virus	0.9992	0.984	0.987
3	Apple_Black_Rot	0.993	0.995	0.994	13	Tomato_Septoria_Leaf_Spot	0.995	0.993	0.994
4	Apple_Scab	1.000	0.984	0.991	14	Tomato_Bacterial_Spot	0.995	0.979	0.986
5	Maize_Healthy	1.000	1.000	1.000	15	Corn_Healthy	1.000	1.000	1.000
6	Maize_Gray_Leaf_Spot	0.994	0.985	0.989	16	Corn_Gray_Leaf_Spot	1.000	0.978	0.982
7	Maize_Northern_Leaf_Blight	0.995	0.992	0.993	17	Corn_Common_Rust	0.999	0.997	0.998
8	Maize_Corn	0.998	0.989	0.993	18	Corn_Northern	0.987	0.985	0.989



	mmon_Rus t					thern_Lea f_Blight			
9	Strawberry _Healthy	1.000	1.000	1.000	19	Raspberry _Healthy	1.000	1.000	1.000
10	Strawberry _Leaf_Scorc h	0.998	0.997	0.998	20	Soybean_ Healthy	1.000	1.000	1.000

Table V, summarizes the cross validation findings for various classifiers that were graded on Accuracy, Precision, Recall, and F1-score. The cross validation of the classifiers XGBoost, SVM, Random Forest, and KNN is assessed.

Table V Cross-validation results of different Classifiers

S.NO	Classifier	Accuracy	Precision	Recall	F1-score
1	KNN	0.9857	0.9882	0.9742	0.9803
2	Random forest	0.9802	0.9774	0.9719	0.9739
3	SVM	0.9912	0.9886	0.9866	0.9872
4	XGboost	0.9886	0.9849	0.9823	0.9830
5	Proposed	0.9921	0.9897	0.9887	0.9894

The above results unambiguously demonstrate that the proposed technique beats the alternative approaches, which use highly deep architectures that are prone to an over-fitting issue. As opposed to competing methods, the proposed framework makes use of PBIL and DenseNet-77 for deep feature computing, which recovers more representative and trustworthy features from which Custom CenterNet derives a more potent representation of plant sick sections. Additionally, the approaches in the literature cost more to compute than proposed approach. So, proposed approach is superior in terms of effectiveness and efficiency for classifying plant diseases.

4. Conclusions

The method that is being used here presents a brand-new framework for the automatic identification and classification of plant diseases. In this research, a CenterNet customized with the DenseNet-77 as a basis

network has been proposed. More specifically, DenseNet-77 and PBIL to pull out the representative collection of features from the input sample is provided. The hybrid classifier is then trained using the computed key points to identify and categorize various plant diseases. The developed system can quickly find and categorize the twenty different crop diseases found in the dataset of Plant Village. Additionally, proposed system can reliably classify plant diseases even when there are a number of artefacts present. Experimental findings show that the proposed model works better than the most recent plant disease classification methodology currently in use. In quintessence, it is essential to create a smartphone application that is user-friendly for the general public and in particular for farmers, students, researchers, and enthusiasts in the disciplines of agriculture. The proposed model for disease detection could be incorporated into the application. More functionality, such as



optimal climate conditions, plant nutrients, and cures for plant illnesses, might be added to the scope to provide comprehensive knowledge on crops under one roof.

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