
Pattern Recognition Approach for Crop Disease Identification Using Leaf Texture and Color Feature Extraction

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ABSTRACT

Crop diseases reduce yield and quality, and visual inspection can be time-consuming and dependent on lighting conditions, leaf characteristics, and disease similarity. Traditional image-based recognition approaches can have redundant descriptors and confuse similar disease patterns based on visual appearance only. A novel Hybrid Color–Texture Optimization with Support Vector Machine (HCTO-SVM) pattern recognition approach is developed to identify crop diseases from complementary color and texture features. The leaf images are pre-processed and segmented; color features are extracted using the Hue, Saturation, and Value (HSV) color space, and texture features are extracted using the Gray-Level Co-occurrence Matrix (GLCM) and Local Binary Pattern (LBP). The complementary descriptors are fused, and Particle Swarm Optimization (PSO) is used for discriminative feature selection and to reduce redundancy. A Support Vector Machine (SVM) with a Radial Basis Function (RBF) kernel performs nonlinear pattern recognition for final crop disease identification. Evaluation on the Kaggle PlantVillage dataset shows 98.76% Macro-F1, 98.21% MCC, 98.14% Cohen's Kappa, and 98.63% Balanced Accuracy, demonstrating consistent recognition across the evaluated disease classes. A unified color–texture representation, optimized feature selection, and nonlinear recognition framework for robust crop disease recognition are presented. The strategy facilitates early screening, precision agriculture and scalable crop health monitoring.

Keywords: Crop Disease Identification; Pattern Recognition; HSV Color Features; GLCM Texture Analysis; Local Binary Pattern; Particle Swarm Optimization; Support Vector Machine.

1. Introduction

a. Agricultural Disease Recognition

Plant diseases substantially affect crop productivity and quality, creating a need for automated and reliable visual identification in precision agriculture. Recent publications have produced discriminative representations of plant images using deep learning and vision-transformer architectures. Transformer-based visual representation learning has been shown to enable automated plant disease detection with efficient Vision Transformer architectures [1]. The application of handcrafted visual descriptors for grape leaf disease diagnosis has been shown to be helpful when combined with automatic K-means segmentation, color representations, feature reduction, and machine learning [2]. Multitask learning has explored simultaneous disease localization and classification in vision-transformer learning [3]. Transfer

learning architectures have also been evaluated for cotton disease detection [4], and lightweight deep architectures have been developed for efficient tomato disease classification that account for limited time and computing resources [5].

b. Existing Method Limitations

Despite advances in automated crop disease recognition through deep learning, several challenges remain in real-world image-based pattern recognition. In general, deep architectures require heavy computational capacity and massive training sets, making them infeasible in low-resource agricultural settings. Learned representations can also make it obscure the contribution of specific visual characteristics to the discrimination of diseases. Deep learning models were explored for plant disease classification and detection of damage [6], and deep transfer learning was used for plant disease identification from images [7]. Further studies have been carried out on improved convolutional learning of diseased cotton leaves and plants [8]. In contrast, traditional feature-based ones are still interesting since they allow explicit representations of color, texture and spatial properties. GLCM, LBP, segmentation and SVM have proven to be useful for plant leaf disease classification [9] and hybrid multiclass SVM approaches have been attempted for the detection of diseases [10].

c. Color–Texture Feature Gap

Prior studies show that deep-learning and handcrafted-feature methods work well, but targeted fusion of complementary color and texture features with systematic feature optimization remains underexplored. Some traditional methods use single descriptors, static feature sets and/or segment-based representations, which may contain redundant information and/or less discriminative features. Recently, work on improving precision agriculture has focused on learning-based methods instead of compact color–texture pattern representations. In agricultural sensing, hybrid optimization with deep belief networks was analyzed [11], and the incorporation of GLCM and SIFT features with SVM for detecting diseases in tomatoes was studied [12]. SVM-based classification of various crop diseases has also been studied, such as kernel comparison methods [14]. The objective is to create a small, discriminative pattern recognition algorithm that leverages complementary leaf color and textural information while eliminating redundant features. Fusing HSV, GLCM, and LBP descriptors, combined with optimization and nonlinear classification, provides an interpretable, computation-efficient solution for automated crop disease identification.

The HCTO-SVM framework is developed to accomplish the following objectives:

- To construct a hybrid leaf representation by integrating HSV color, GLCM texture, and LBP texture features for discriminative crop disease characterization.
- To optimize the fused color – texture feature space using Particle Swarm Optimization (PSO) to remove redundant features and preserve disease-related patterns.
- To design an RBF-kernel Support Vector Machine (SVM) Classifier for Nonlinear pattern Recognition for accurate crop disease identification.
- To validate the proposed HCTO-SVM framework using Macro-F1, MCC, Cohen's Kappa, and Balanced Accuracy on the Kaggle Plant Village dataset.

The principal contribution is the HCTO-SVM framework, which uses HSV color, GLCM texture, and LBP texture descriptors, PSO-based feature optimization, and RBF-SVM for crop disease identification. The framework aims to minimize feature redundancy and improve discrimination between similar disease patterns. The rest of the paper is structured as follows: Section 2 discusses related work; Section 3 outlines the proposed methodology;

Section 4 presents the dataset, experimental configuration, results, and analysis. Last, Section 5 concludes the study and highlights potential future research directions.

2. Literature Survey

Nandhini et al. [15] propose MHGSO-DenseNet (Mutation-based Henry Gas Solubility Optimization–DenseNet-121), which is an optimized DenseNet-121 for plant disease identification. The method achieved 98.7% accuracy on 14 Plant Village classes and 98.81% on the field dataset. However, deep network computation is quite resource-intensive. Zhao et al. [16] added the residual layer and Inception layer into the structure and embedded an attention mechanism to the residual layer to obtain RIC-Net (Residual-Inception Convolutional Network). The network was able to have an overall accuracy of 99.55% for multiple crop diseases. But it requires computation of deep CNN and learned representations.

Quan et al. [17] presented a lightweight MS-Net (Multi-Scale Network) with skip connections, feature weighting based on optimization and plant-specific pretraining. It achieved 99.80% test accuracy on PlantVillage and 97.8% on complex-background images. However, performance can drop in uncontrolled field settings. Ullah et al. [18] presented DeepPlantNet (Deep Plant Network), which is a unique use of convolutional layers, fire modules, mixed convolutional filters, batch normalization, and Leaky-ReLu for disease classification. The results show that the model achieved 98.49% accuracy for eight classes and 99.85% for three classes. However, training requires significant computing power. Chen et al. [19] then proposed INC-VGGN (Inception-enhanced VGG Network), using transfer learning by combining the Inception module with VGG-based feature extraction to identify plant diseases. Although the framework showed good classification results, deep feature learning has high computational requirements and provides limited explicit feature interpretability. Too et al. [20] introduced FT-CNN (Fine-Tuned Convolutional Neural Network) and systematically compared VGG, Inception, ResNet, and DenseNet on PlantVillage. With the lowest parameter count, DenseNet-121 achieved the best test accuracy of 99.75%. However, the study focused on comparing architectures, not explicitly optimizing the color–texture feature.

Rehman et al. [21] presented a novel approach, WOA-DTL (Whale Optimization Algorithm – Deep Transfer Learning), that combines pretrained deep models with image augmentation, contrast enhancement, feature fusion, and whale optimization-based feature optimization. It had a 95.7% accuracy for the six citrus diseases. Because it is specialized for citrus, its crop use is therefore restricted. Alzoubi et al. [22] proposed an Enhanced PSO-SVM (Particle Swarm Optimization–Support Vector Machine) based fig leaf disease detecting system. They extracted disease-related visual characteristics using image-processing operations and optimized SVM classification parameters using PSO. Demonstrated good disease classification; however, it was designed for crops and will not easily transfer to other plant species. Araujo and Peixoto [23] proposed CM-LBP-BoVW-SVM (Color Moments–Local Binary Pattern–Bag of Visual Words–Support Vector Machine), integrating color, texture, and local visual characteristics before SVM classification of soybean diseases. The proposed method achieved better disease recognition, but manually designed descriptors are sensitive to feature quality and may contain redundant information. Fan et al. [24] proposed TL-HOG-CL (Transfer Learning–Histogram of Oriented Gradients–Centre Loss) to improve feature compactness and discrimination using transfer-learning features, HOG descriptors, and centre loss. On the three datasets, it achieved accuracies of 99.79%, 92.59%, and 97.12%. However, transfer learning comes at the cost of greater computational complexity. Previous work has shown the success of deep learning, transfer learning, handcrafted descriptors, and optimized classifiers in crop disease recognition. However, few studies have combined HSV color features, GLCM and LBP texture features, PSO-based feature optimization, and RBF-SVM-

based classification in a compact pattern recognition framework. Although deep models offer strong representations, they can be overly complex, while handcrafted methods may include redundant information. To address these limitations, we propose a unified, optimized color–texture representation that enables HCTO-SVM for crop disease identification.

3. Proposed Methodology

The proposed framework for crop disease identification, Hybrid Color–Texture Optimization with Support Vector Machine (HCTO-SVM), has four stages: image preprocessing, complementary color–texture feature extraction, feature optimization, nonlinear classification, and, lastly, disease assignment. It combines Hue, Saturation, and Value (HSV) color features with Gray-Level Co-occurrence Matrix (GLCM) and Local Binary Pattern (LBP) texture features. A kernel-based Support Vector Machine (SVM) with a Radial Basis Function (RBF) kernel then performs nonlinear classification to reduce feature redundancy and retain discriminative descriptors using Particle Swarm Optimization (PSO).

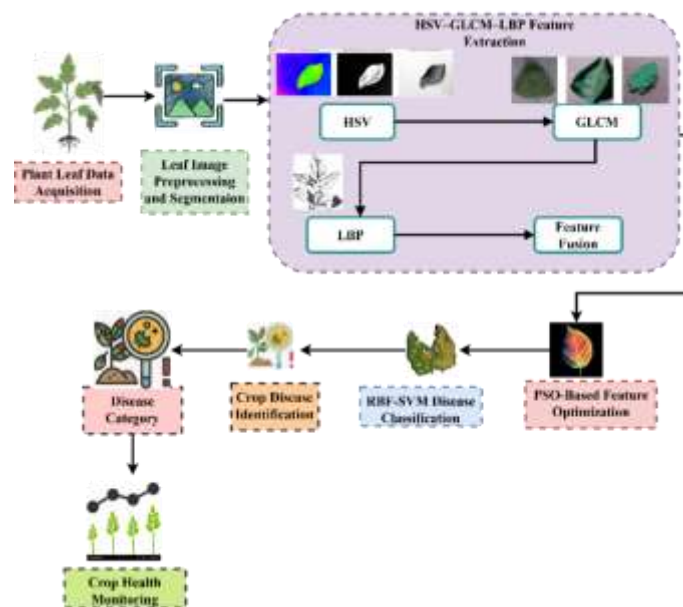


Figure 1: Overall architecture of the HCTO-SVM framework for crop disease identification

Fig. 1 depicts the general architecture of the proposed HCTO-SVM framework for crop disease identification. The pipeline starts with images captured by PlantVillage, which then undergo preprocessing, including image resizing, noise reduction, segmentation, and intensity normalization. The pipeline then extracts parallel HSV color features, GLCM texture features, and LBP texture features from the standardized images and fuses them. Next, PSO removes the redundant features and keeps the most discriminative descriptors. The optimized feature representation is fed to the RBF-SVM (classifier) for nonlinear disease pattern recognition. Finally, the trained classification algorithm assigns leaf images to the disease categories: healthy, fungal, bacterial, viral, and pest.

a. Data Acquisition and Preprocessing

The Kaggle PlantVillage dataset is acquired for automated crop disease identification and organized by disease category. The collected leaf images are cleaned to remove invalid or unusable samples and standardized through resizing, noise suppression, background segmentation, and intensity normalization. The preprocessing operation is formulated as

$$I_i^p = \mathcal{N} \left(\mathcal{S} \left(\mathcal{D} \left(\mathcal{R}(I_i) \right) \right) \right). \quad (1)$$

Where, in Equation(1), I_i denotes the acquired leaf image i , $\mathcal{R}(\cdot)$ represents image resizing, $\mathcal{D}(\cdot)$ denotes noise reduction, $\mathcal{S}(\cdot)$ represents leaf-region segmentation and background suppression, and $\mathcal{N}(\cdot)$ denotes intensity normalization. The processed image I_i^p provides a standardized leaf representation with reduced noise and irrelevant background information, thereby establishing a consistent input for subsequent color and texture feature extraction.

b. HSV–GLCM–LBP Feature Extraction

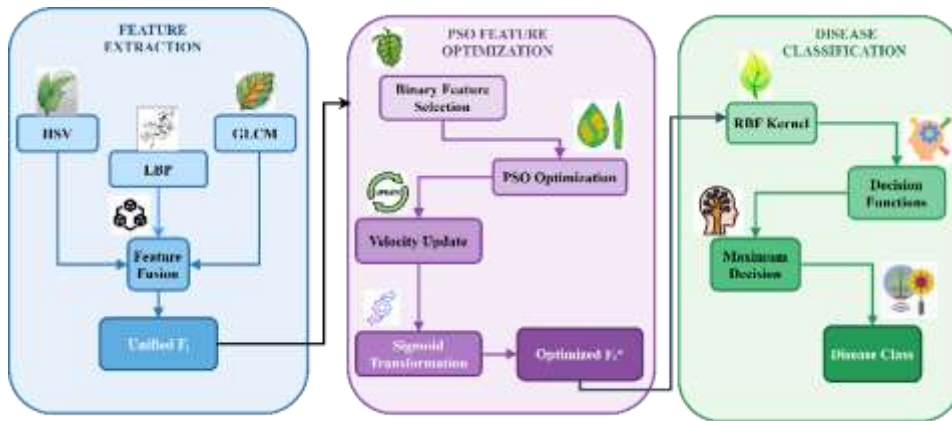


Figure. 2: HCTO-SVM workflow for crop disease identification.

Figure 2 depicts the HCTO-SVM workflow such as HSV – GLCM – LBP feature extraction, PSO based feature optimisation and RBF-SVM based classification. The features extracted are fused, optimised using binary selection and classified using RBF kernel decision functions to determine the final crop disease class. The preprocessed leaf image is transformed into the Hue, Saturation, and Value (HSV) color space to characterize disease-related variations in leaf color and intensity. The HSV representation is expressed as

$$H_i = \mathcal{T}_{HSV}(I_i^p) = [h_i, s_i, v_i]^T. \quad (2)$$

Where, in Equation(2), $\mathcal{T}_{HSV}(\cdot)$ denotes the HSV transformation, while h_i , s_i , and v_i represent the hue, saturation, and value components, respectively. The resulting descriptor H_i captures complementary chromatic characteristics that support the differentiation of healthy and diseased leaf regions. Texture information is extracted using the Gray-Level Co-occurrence Matrix (GLCM) to characterize spatial relationships between neighboring intensity levels. The normalized GLCM probability is defined as

$$P_i(a, b, | \delta \theta) = \frac{G_i(a, b, | \delta \theta)}{\sum_{a=0}^{L-1} \sum_{b=0}^{L-1} G_i(a, b, | \delta \theta) + \epsilon}. \quad (3)$$

Where, in Equation (3), $G_i(a, b, | \delta \theta)$ denotes the occurrence frequency of the gray-level pair (a, b) at distance δ and orientation θ , L represents the number of gray levels, and ϵ prevents numerical instability. The normalized matrix P_i characterizes spatial intensity relationships and provides texture information associated with disease-induced surface variations. LBP descriptors are additionally extracted to capture local intensity patterns and fine-grained surface irregularities. The complementary color and texture descriptors are subsequently integrated into a unified feature vector as

$$F_i = [\text{vec}(H_i)^T, \text{GLCM}_i^T, \text{LBP}_i^T]^T. \quad (4)$$

Where, in Equation(4), $\text{vec}(H_i)$ denotes the vectorized HSV representation, while GLCM_i and LBP_i represent the extracted GLCM and LBP descriptors. The fused vector F_i combines chromatic information, spatial texture relationships, and local texture patterns into a comprehensive representation for feature optimization.

c. PSO-Based Feature Optimization

The fused HSV–GLCM–LBP representation may contain redundant or weakly discriminative features. Particle Swarm Optimization (PSO) is therefore employed to identify a compact subset of informative descriptors. Each particle represents a binary feature-selection configuration formulated as

$$z_q^{(t)} = [z_{q1}^{(t)}, z_{q2}^{(t)}, \dots, z_{qd}^{(t)}], z_{qj}^{(t)} \in \{0, 1\}. \quad (5)$$

Where, in Equation(5), $z_q^{(t)}$ denotes the feature-selection vector of particle q at iteration t , and d represents the total number of fused features. A binary value of one retains the corresponding feature, whereas zero excludes it. This representation establishes candidate feature subsets for searching combinations that preserve disease-discriminative information while limiting redundant descriptors. The particle velocity is updated according to individual and collective search experiences as

$$v_q^{(t+1)} = \omega v_q^{(t)} + c_1 r_1 (p_q^{best} - z_q^{(t)}) + c_2 r_2 (g^{best} - z_q^{(t)}). \quad (6)$$

Where, in Equation(6), ω denotes the inertia coefficient, c_1 and c_2 represent the cognitive and social acceleration coefficients, r_1 and r_2 are random values, p_q^{best} represents the personal-best solution, and g^{best} denotes the global-best solution. The updated velocity $v_q^{(t+1)}$ guides each particle toward promising feature combinations by incorporating both its previous search direction and the best solutions identified by the particle and swarm. The updated velocity is converted into a binary feature-selection decision using a sigmoid transformation as

$$z_{qj}^{(t+1)} = \mathbb{I} \left[\frac{1}{1 + \exp(-v_{qj}^{(t+1)})} > \tau \right]. \quad (7)$$

Where, in Equation(7), $v_{qj}^{(t+1)}$ denotes the updated velocity of feature j , τ represents the selection threshold, and $\mathbb{I}[\cdot]$ denotes the indicator function. The resulting binary vector determines which descriptors are retained and which are discarded, producing an optimized feature representation with reduced redundancy and improved discriminative potential.

d. RBF-SVM Disease Classification

The optimized feature representation is fed into a Support Vector Machine (SVM) with a Radial Basis Function (RBF) kernel to model nonlinear relationships among disease patterns. The kernel similarity between two optimized feature vectors is defined as

$$K(F_i^*, F_j^*) = \exp \left(-\gamma \|F_i^* - F_j^*\|_2^2 \right). \quad (8)$$

Where, in Equation(8), F_i^* and F_j^* denote optimized feature vectors, γ controls the RBF kernel width, and $\|F_i^* - F_j^*\|_2^2$ represents the squared Euclidean distance between the feature vectors. The kernel transforms feature relationships into nonlinear similarity values, enabling separation of disease classes with overlapping color and texture characteristics. For multiclass disease recognition, the SVM generates class-specific decision functions using the optimized representation. The classification function is expressed as

$$f_c(F_i^*) = \sum_{j=1}^N \alpha_{jc} y_{jc} K(F_j^*, F_i^*) + b_c, \hat{y}_i = \arg \max_{c \in \{1, \dots, C\}} f_c(F_i^*). \quad (9)$$

Where, in Equation (9), N denotes the number of training samples, α_{jc} represents the learned SVM coefficients, y_{jc} denotes the corresponding class label, b_c is the class-specific bias, C represents the number of disease classes, and $\hat{y}_i$ denotes the predicted class. The class with the maximum decision value is selected as the disease category for the input leaf image.

e. Crop Disease Identification

The optimized feature representation is classified using the trained RBF-SVM model to generate the final disease category for each leaf image. The learned nonlinear decision boundaries distinguish disease-specific color and texture patterns and assign each input sample to its corresponding crop disease class. The complete identification process is expressed as

$$\hat{y}_i = \mathcal{SVM}_{RBF}(F_i^*) = \mathcal{SVM}_{RBF}\left(\mathcal{PSO}\left(\mathcal{F}_{HSV, GLCM, LBP}(\mathcal{P}(I_i))\right)\right). \quad (10)$$

Where, in Equation (10), I_i denotes the input leaf image, $\mathcal{P}(\cdot)$ represents preprocessing and segmentation, $\mathcal{F}_{HSV, GLCM, LBP}(\cdot)$ denotes hybrid HSV, GLCM, and LBP feature extraction, $\mathcal{PSO}(\cdot)$ represents feature optimization, F_i^* denotes the optimized feature representation, $\mathcal{SVM}_{RBF}(\cdot)$ represents the RBF-kernel SVM classifier, and $\hat{y}_i$ denotes the final identified crop disease class. The complete HCTO-SVM sequence therefore converts the input leaf image into an optimized color–texture representation and assigns it to the corresponding crop disease category.

Table I. Major Crop Disease Identification Classes with Color and Texture Characteristics

Detected Class	Crop	Color Characteristics	Texture Characteristics	Identification Type
Healthy Leaf	Multiple crops	Predominantly uniform green	Smooth and consistent surface	Healthy
Apple Scab	Apple	Brown or olive-colored lesions	Irregular and rough lesion patterns	Fungal
Corn Common Rust	Corn	Reddish-brown rust spots	Raised and scattered surface patterns	Fungal
Tomato Bacterial Spot	Tomato	Dark brown to black spots	Irregular localized spot texture	Bacterial
Tomato Yellow Leaf Curl Virus	Tomato	Yellowing and pale green regions	Wrinkled and distorted leaf texture	Viral
Tomato Spider Mites	Tomato	Yellow or bronzed discoloration	Fine stippling and irregular surface patterns	Pest

Table I presents representative crop disease classes along with their crop type, characteristic color patterns, and texture properties. These visual characteristics correspond to the HSV, GLCM, and LBP features HCTO-SVM uses to distinguish healthy, fungal, bacterial, viral, and pest-related conditions.

Algorithm 1: HCTO-SVM-Based Crop Disease Identification

Input: $D = \{(I_i, y_i)\}_{i=1}^N$

Output: $\{\hat{y}_i\}_{i=1}^N$

1. Initialize $N, Q, T, \omega, c_1, c_2, \tau$.
2. For $i = 1, \dots, N$ do

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3.    $I_i^p = \mathcal{N} \left( \mathcal{S} \left( \mathcal{D}(\mathcal{R}(I_i)) \right) \right)$ .
4.    $H_i = \mathcal{T}_{HSV}(I_i^p) = [h_i, s_i, v_i]^T$ .
5.    $P_i(a, b | \delta\theta) = \frac{G_i(a, b | \delta\theta)}{\sum_a \sum_b G_i(a, b | \delta\theta) + \epsilon}$ .
6.   Extract  $LBP_i$  and construct
      
$$F_i = [\text{vec}, (H_i)^T \text{GLCM}_i^T \text{LBP}_i^T]^T$$
.
7.   End For
8.   Initialize  $Q$  binary feature-selection vectors  $z_q^{(t)}$ .
9.   For  $q = 1, \dots, Q$  do
10.  Initialize  $p_q^{best}$ .
11.  End For
12.  While  $t < T$  do
13.  For  $q = 1, \dots, Q$  do
14.   $v_q^{(t+1)} = \omega v_q^{(t)} + c_1 r_1 (p_q^{best} - z_q^{(t)}) + c_2 r_2 (g^{best} - z_q^{(t)})$ .
15.  For  $j = 1, \dots, d$  do
16.   $z_{qj}^{(t+1)} = \mathbb{I} \left[ \frac{1}{1 + \exp(-v_{qj}^{(t+1)})} > \tau \right]$ .
17.  End For
18.  Evaluate fitness and update  $p_q^{best}$ .
19.  End For
20.  Update  $g^{best}$ .
21.   $t \leftarrow t + 1$ .
22.  End While
23.  For  $i = 1, \dots, N$  do
24.  Obtain optimized features  $F_i^*$  using  $g^{best}$ .
25.   $K(F_i^*, F_j^*) = \exp(-\gamma \|F_i^* - F_j^*\|_2^2)$ .
26.   $f_c(F_i^*) = \sum_{j=1}^N \alpha_{jc} y_{jc} K(F_j^*, F_i^*) + b_c$ .
27.   $\hat{y}_i = \arg \max_c f_c(F_i^*)$ .
28.  for  $i=1, \dots, N$  do
29.  Apply the complete HCTO-SVM identification sequence:
      
$$\hat{y}_i = \mathcal{SVM}_{RBF}(F_i^*) = \mathcal{SVM}_{RBF} \left( \mathcal{PSO} \left( \mathcal{F}_{HSV, GLCM, LBP}(\mathcal{P}(I_i)) \right) \right)$$

30.  End For
31.  Return  $\{\hat{y}_i\}_{i=1}^N$ .
    
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Algorithm 1 shows the HCTO-SVM scheme for crop disease identification, applying image preprocessing, HSV–GLCM–LBP feature extraction, PSO feature selection, RBF-SVM classification, and an optimized leaf image representation for disease prediction.

4. Results and Performance Analysis

a. Dataset Description & Experimental Setup

The experiments use the Kaggle PlantVillage labelled dataset[25], which consists of 15 plant disease classes and 21,639 leaf images. It contains healthy and diseased leaves from pepper, potato, and tomato crops, including bacterial, fungal, and viral diseases, pest damage, and target spots. Classes are Pepper Bacterial Spot, Pepper Healthy, Potato Early Blight, Potato Late Blight, Potato Healthy, Tomato Bacterial Spot, Tomato Early Blight, Tomato Late Blight,

Tomato Leaf Mold, Tomato Septoria Leaf Spot, Tomato Spider Mites, Tomato Target Spot, Tomato Yellow Leaf Curl Virus, Tomato Mosaic Virus and Tomato Healthy. Before HSV, GLCM and LBP feature extraction, images are processed.

The HCTO-SVM framework is implemented in Python 3.10 using OpenCV, NumPy, Pandas, and scikit-learn. The images are split into 70%, 15% and 15% training, validation and testing sets, respectively, using stratified sampling among the 15 disease classes. Image preprocessing includes resizing, normalization, noise reduction, and leaf segmentation. HSV descriptors are used to capture the color characteristics and GLCM and LBP for complementary texture characteristics. PSO is conducted in 50 iterations, and RIC-Net, MS-Net and INC-VGGN are trained in 50 epochs under the same data partition. An RBF-SVM is used to classify the optimized features, and Macro-F1, MCC, Cohen's Kappa, and Balanced Accuracy are used to evaluate the performance.

b. Disease Classification Consistency Analysis(DCCA)– Macro-F1 Score

Disease Classification Consistency (DCCA) evaluates the consistency of crop disease identification across variations in leaf color and texture. For each disease class c , precision and recall are first calculated as

$$P_c = \frac{TP_c}{TP_c + FP_c}, R_c = \frac{TP_c}{TP_c + FN_c}, F1_c = 2 \frac{P_c R_c}{P_c + R_c}. \quad 11(a)$$

The Macro-F1 score is obtained by averaging the F1-scores across all 15 classes:

$$\text{Macro-F1} = \frac{1}{C} \sum_{c=1}^C F1_c. \quad 11(b)$$

Where, in Equation 11(a-b), TP_c , FP_c , and FN_c denote the true-positive, false-positive, and false-negative predictions for class c , respectively, and $C = 15$ represents the total number of dataset classes. The high Macro-F1 value indicates consistent, balanced crop disease identification across all disease and healthy classes.

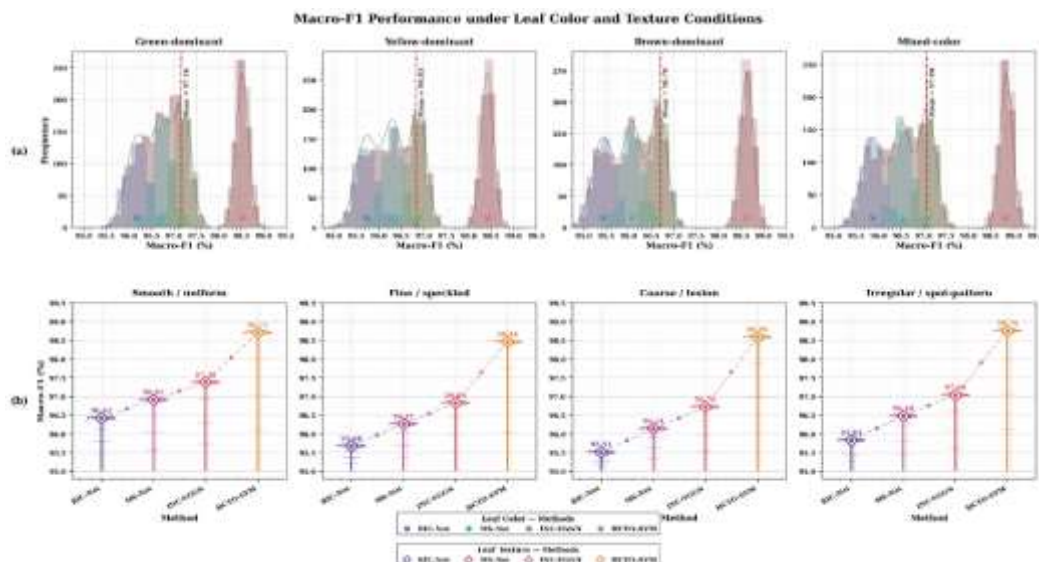


Figure 3: (a) Macro-F1 performance under different leaf color conditions. (b) Macro-F1 performance under different leaf texture conditions.

Figure 3(a) shows Macro-F1 in various leaf colour conditions. For disease identification, HCTO-SVM achieves high Macro-F1 (98.41–98.84%), indicating consistent and balanced disease identification despite variations in leaf colour. Macro-F1 in different leaf

texture conditions is provided in fig 3(b); HCTO-SVM achieves 98.46-98.76%, showing that it identifies disease across textures without significant disturbance.

c. Prediction Correlation Strength Analysis (PCSA) – Matthews Correlation Coefficient

Prediction Correlation Strength (PCSA) measures agreement between the real label and the predicted label during model training. MCC provides a correlation-based measure of prediction quality, with higher scores indicating greater agreement between predictions and label actualization. MCC is calculated by

$$MCC = \frac{TP \cdot TN - FP \cdot FN}{\sqrt{(TP+FP)(TP+FN)(TN+FP)(TN+FN)}}. \quad (12)$$

Where, in Equation (12), TP , TN , FP , and FN denote true-positive, true-negative, false-positive, and false-negative predictions, respectively.

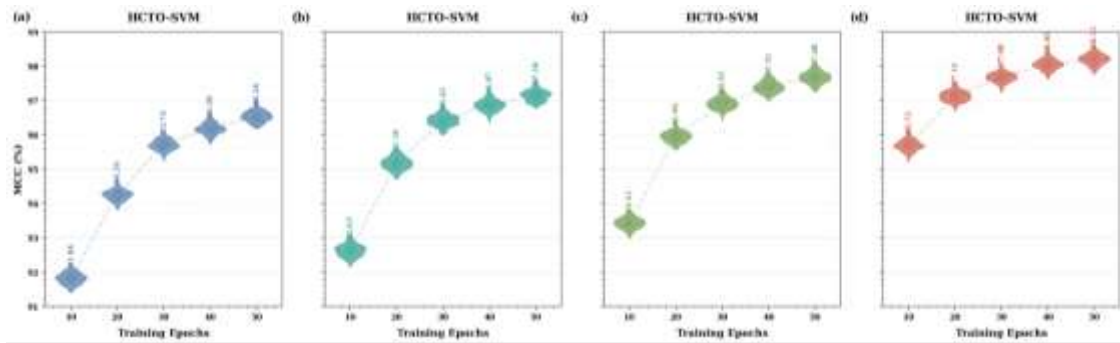


Figure 4: MCC performance across training epochs for RIC-Net, MS-Net, INC-VGGN, and HCTO-SVM.

Figure 4 shows Macro-F1 performance across 10–50 training epochs for RIC-Net, MS-Net, INC-VGGN, and HCTO-SVM, highlighting performance progression and convergence across different training stages.

d. Prediction Agreement Reliability (PAR) – Cohen’s Kappa

Prediction Agreement Reliability (PAR) measures the agreement between actual and predicted disease labels while accounting for chance agreement. Cohen’s Kappa is given by

$$\kappa = \frac{P_o - P_e}{1 - P_e}. \quad (13)$$

Where, in Equation (13), P_o represents the observed agreement between actual and predicted labels, and P_e denotes the agreement expected by chance. PSO iterations are used as the experimental condition because they directly control the optimization process for selecting discriminative features. Higher Cohen’s Kappa values indicate stronger prediction agreement.

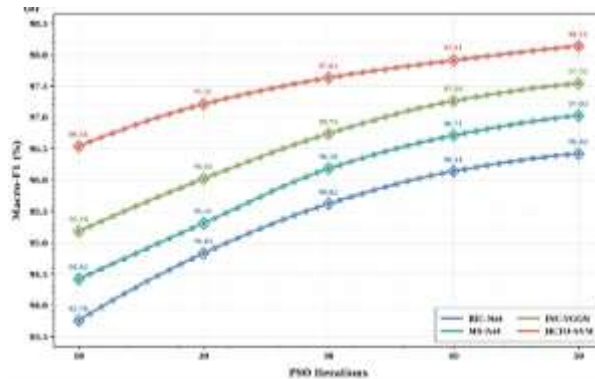


Figure 5: Cohen's Kappa across PSO Iterations

Figure 5 shows increasing Cohen's Kappa with progressive PSO iterations. HCTO-SVM reaches 98.14% at 50 iterations, indicating highly reliable agreement between predicted and actual labels after feature optimization.

e. Class-Balanced Accuracy (CBA) – Balanced Accuracy

Class-Balanced Accuracy (CBA) evaluates consistently the model identifies samples across different disease conditions. It gives equal importance to each condition, making it useful for examining recognition performance across diseases. For each disease condition, d , the class-wise recognition rate is expressed as:

$$BA_d = \frac{TP_d}{TP_d + FN_d}. \quad (14)$$

Where, in Equation (14), TP_d denotes the correctly identified samples for disease condition d , and FN_d denotes the samples of condition d incorrectly classified as another condition. Higher values indicate more consistent disease recognition. The reported overall HCTO-SVM Balanced Accuracy of **98.63%** indicates strong and balanced identification performance across the evaluated disease classes.

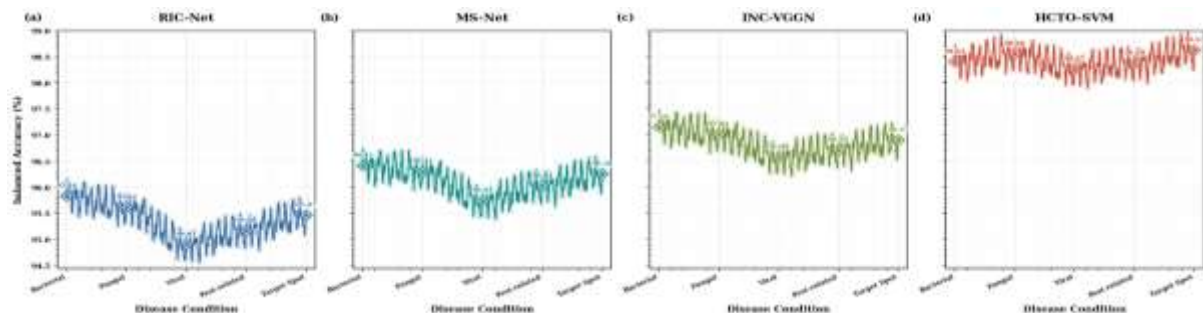


Figure 6: Disease-specific performance comparison of RIC-Net, MS-Net, INC-VGGN, and HCTO-SVM: (a) RIC-Net, (b) MS-Net, (c) INC-VGGN, and (d) HCTO-SVM.

Figure 6 shows consistently high Balanced Accuracy across the evaluated disease conditions. HCTO-SVM achieves 98.27–98.63%, indicating balanced recognition across different disease patterns.

f. Ablation Study

The ablation study analyzes the contribution of each major HCTO-SVM component. HSV provides colour information, while GLCM and LBP provide complementary texture information. PSO performs discriminative feature selection, and RBF-SVM performs the final non-linear classification. These are removed one at a time, and the other components are still in place. The full configuration has all 5 components.

Table II. Ablation Configurations of HCTO-SVM

Configuration	HSV	GLCM	LBP	PSO	RBF-SVM	Macro-F1 (%)	MCC (%)	Kappa (%)	Balanced Accuracy (%)
Without HSV	✗	✓	✓	✓	✓	95.84	94.96	94.71	95.62
Without GLCM	✓	✗	✓	✓	✓	96.31	95.48	95.27	96.14
Without LBP	✓	✓	✗	✓	✓	96.47	95.71	95.53	96.32

Without PSO	✓	✓	✓	✗	✓	97.18	96.63	96.47	97.24
Without RBF-SVM	✓	✓	✓	✓	✗	96.92	96.18	95.94	96.87
Complete HCTO-SVM	✓	✓	✓	✓	✓	98.76	98.21	98.14	98.63

Table II results show that removing individual components reduces performance compared with the complete HCTO-SVM framework. Removing HSV reduces color description, and omitting GLCM or LBP reduces texture description. Previously extracting PSO reduces performance as redundant features will be present in the fused representation. With the combined contribution of all integrated parts, the complete HCTO-SVM achieved a Macro-F1 score of 98.76%, an MCC score of 98.21%, a Cohen's Kappa score of 98.14%, and a Balanced Accuracy of 98.63%.

5. Conclusion

The HCTO-SVM framework combines HSV color content, GLCM and LBP-based texture features, feature optimization using PSO and disease classification using RBF-SVM. The complementarity of the two color–texture representation to capture both chromatic variation as well as disease related surface patterns and PSO to remove redundant features and preserve the discriminative information for classification. The RBF-SVM offers nonlinear decision boundaries to separate visually similar patterns of disease over the evaluated crop classes. Evaluation was performed on the Kaggle PlantVillage dataset, exhibiting a macro-F1, MCC, Cohen's Kappa and Balanced Accuracy of 98.76%, 98.21%, 98.14% and 98.63%, respectively, with consistent recognition of the evaluated disease classes. The results validate the potential of the optimized representation for automated, reliable crop disease identification and scalable monitoring of plant health. The framework needs further validation across a variety of imaging scenarios, including varying illumination, occlusion, complex backgrounds, and natural leaf variation. Future studies will include more diseases, optimise the computational process, and enable real-time deployment on a mobile (or edge)- based agricultural monitoring system.

REFERENCES

- [1]. Parez, S., Dilshad, N., Alghamdi, N. S., Alanazi, T. M., & Lee, J. W. (2023). Visual intelligence in precision agriculture: Exploring plant disease detection via efficient vision transformers. *Sensors*, 23(15), 6949.
- [2]. Javidan, S. M., Banakar, A., Vakilian, K. A., & Ampatzidis, Y. (2023). Diagnosis of grape leaf diseases using automatic K-means clustering and machine learning. *Smart Agricultural Technology*, 3, 100081.
- [3]. Hemalatha, S., & Jayachandran, J. J. B. (2024). A multitask learning-based vision transformer for plant disease localization and classification. *International Journal of Computational Intelligence Systems*, 17(1), 188.
- [4]. Johri, P., Kim, S., Dixit, K., Sharma, P., Kakkar, B., Kumar, Y., ... Ijaz, M. F. (2024). Advanced deep transfer learning techniques for efficient detection of cotton plant diseases. *Frontiers in Plant Science*, 15, 1441117.
- [5]. Ahmed, S., Hasan, M. B., Ahmed, T., Sony, M. R. K., & Kabir, M. H. (2022). Less is more: Lighter and faster deep neural architecture for tomato leaf disease classification. *IEEE Access*, 10, 68868–68884.
- [6]. Sai Reddy, B., & Neeraja, S. (2022). Plant leaf disease classification and damage detection system using deep learning models. *Multimedia Tools and Applications*, 81(17), 24021–24040.
- [7]. Chen, J., Chen, J., Zhang, D., Sun, Y., & Nanekaran, Y. A. (2020). Using deep transfer learning for image-based plant disease identification. *Computers and Electronics in Agriculture*, 173, 105393.

- [8]. Rai, C. K., & Pahuja, R. (2023). Classification of diseased cotton leaves and plants using improved deep convolutional neural network. *Multimedia Tools and Applications*, 82(16), 25307–25325.
- [9]. Jamjoom, M., Elhadad, A., Abulkasim, H., & Abbas, S. (2023). Plant leaf diseases classification using improved K-means clustering and SVM algorithm for segmentation. *Computers, Materials & Continua*, 76(1), 367–382.
- [10]. Sahu, S. K., & Pandey, M. (2023). An optimal hybrid multiclass SVM for plant leaf disease detection using spatial Fuzzy C-Means model. *Expert Systems with Applications*, 214, 118989.
- [11]. Rajalakshmi, S., Dhote, S. N., Baskar, S., Pethuraj, M. S., & Poornima, D. (2025). A hybrid optimization framework with deep belief networks for moisture and nutrient sensor-based agricultural insights. *Results in Engineering*, 107149.
- [12]. Khan, R., Ud Din, N., Zaman, A., & Huang, B. (2024). Automated tomato leaf disease detection using image processing: An SVM-based approach with GLCM and SIFT features. *Journal of Engineering*, 2024(1), 9918296.
- [13]. Ibrahim, S., Fuad, N. A. M., Ghani, N. A. M., Aminuddin, R., & Sunarko, B. (2025). Support Vector Machine (SVM) for tomato leaf disease detection. *AGRIVITA Journal of Agricultural Science*, 47(2), 338–353.
- [14]. Sridhar, P., & Angamuthu, P. (2025). Enhancing image based classification for crop disease detection using a multiclass SVM approach with kernel comparison. *Scientific Reports*, 15(1), 40055.
- [15]. Nandhini, S., & Ashokkumar, K. (2022). An automatic plant leaf disease identification using DenseNet-121 architecture with a mutation-based Henry gas solubility optimization algorithm. *Neural Computing and Applications*, 34(7), 5513–5534.
- [16]. Zhao, Y., Sun, C., Xu, X., & Chen, J. (2022). RIC-Net: A plant disease classification model based on the fusion of Inception and residual structure and embedded attention mechanism. *Computers and Electronics in Agriculture*, 193, 106644.
- [17]. Quan, S., Wang, J., Jia, Z., Yang, M., & Xu, Q. (2023). MS-Net: A novel lightweight and precise model for plant disease identification. *Frontiers in Plant Science*, 14, 1276728.
- [18]. Ullah, N., Khan, J. A., Almakdi, S., Alshehri, M. S., Al Qathrady, M., El-Rashidy, N., ... Ali, F. (2023). An effective approach for plant leaf diseases classification based on a novel DeepPlantNet deep learning model. *Frontiers in Plant Science*, 14, 1212747.
- [19]. Too, E. C., Yujian, L., Njuki, S., & Yingchun, L. (2019). A comparative study of fine-tuning deep learning models for plant disease identification. *Computers and Electronics in Agriculture*, 161, 272–279.
- [20]. Rehman, M. Z. U., Ahmed, F., Khan, M. A., Tariq, U., Jamal, S. S., Ahmad, J., & Hussain, I. (2022). Classification of citrus plant diseases using deep transfer learning. *Computers, Materials & Continua*, 70(1), 1401–1417.
- [21]. Alzoubi, S., Jawarneh, M., Bsoul, Q., Keshta, I., Soni, M., & Khan, M. A. (2023). An advanced approach for fig leaf disease detection and classification: Leveraging image processing and enhanced support vector machine methodology. *Open Life Sciences*, 18(1), 20220764.
- [22]. Araujo, J. M. M., & Peixoto, Z. M. A. (2019). A new proposal for automatic identification of multiple soybean diseases. *Computers and Electronics in Agriculture*, 167, 105060.
- [23]. Fan, X., Luo, P., Mu, Y., Zhou, R., Tjahjadi, T., & Ren, Y. (2022). Leaf image based plant disease identification using transfer learning and feature fusion. *Computers and Electronics in Agriculture*, 196, 106892.
- [24]. Kaggle. (n.d.). PlantVillage dataset [Data set].
<https://www.kaggle.com/datasets/abdallahalidev/plantvillage-dataset>