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An ROI-Guided Optimized Machine Learning Framework for Orange Disease Recognition with Feature Selection and Explainability

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ABSTRACT: Orange is one of the most economically significant citrus crops worldwide, which is essential for the global food distribution network and supports rural livelihoods. However, its high susceptibility to destructive diseases results in substantial yield losses and long-term economic damage. Despite recent advances in smart agriculture, early and precise disease diagnosis remains challenging due to visual resemblance among disease symptoms, high computational cost, and limited model interpretability. To overcome these difficulties, we introduce a novel lightweight and Region of Interest (ROI)-guided explainable machine learning framework to identify orange disease that integrates a strategic feature selection method with Adaptive Step-Controlled Gorilla Troops Optimizer (ASC-GTO). The proposed method starts with Contrast Limited Adaptive Histogram Equalization (CLAHE)-based image enhancement, followed by K-means clustering to accurately segment and separate the diseased part, which is labelled as ROI. To extract discriminative features from the ROI, Gray-Level Co-occurrence Matrix (GLCM)-based texture and color features are first extracted. Least Absolute Shrinkage and Selection Operator (LASSO) is then used for ranking the features and finding the most discriminative features for each class. Finally, the proposed feature selection method integrates the union and intersection of top features identified in the class-wise scenario using LASSO with globally dominant features found by feature ranking to get a compact and discriminative feature subset for better multi-class classification. Model hyperparameter optimization was performed using the proposed ASC-GTO. Experimental findings indicate that the proposed method outperforms existing techniques with an accuracy of 99.57% on the widely adopted orange disease dataset from Kaggle. Furthermore, it significantly reduces computational complexity, with reductions of 22.2%, 34.76%, and 7.5% in training time, model size, and inference time, respectively, compared to models trained on unprocessed raw input images. Model explainability is further analyzed using SHAP and LIME to identify the most influential features contributing to the prediction outcomes. Overall, the proposed method supports early disease intervention, precision agriculture, and sustainable farming.

KEYWORDS: Orange disease detection; explainable machine learning; ROI extraction; citrus disease; feature selection; plant disease detection; LASSO; SHAP; LIME; hyperparameter optimization; Gorilla Troops Optimizer

1 Introduction

The global citrus industry is a vital element of the agricultural economy, which plays a substantial role in food security, international trade, and rural livelihoods in over 140 countries. According to the United Nations' Food and Agriculture Organization (FAO)¹, citrus fruits are one of the most widely cultivated fruits in the world, with oranges contributing to the largest share of citrus production in the world. The global orange production has been consistently over 75 million metric tons per year in recent years, accounting for almost half of the global citrus production, and the key exporters are Brazil, China, India, the United States, and Spain [1,2]. These countries account for significant amounts of orange production, primarily for juice processing and export. Due to this high demand for fresh and processed products, oranges are a very important fruit crop economically around the world [3].

Despite their remarkable economic importance, orange crops are particularly vulnerable to harmful citrus diseases, including citrus greening and citrus canker. These diseases lead to significant yield reduction, deterioration of fruit quality and endanger overall productivity. Despite the recent advancements in smart agriculture technologies, the detection of diseases in many countries is still based on visual examination. This traditional approach is subjective, labour intensive, and requires expert skill [4]. It often finds infections only at later stages when the treatment options are limited, expensive, and less effective. This results in financial losses and the unnecessary use of pesticides, as well as possible food safety issues. These challenges raise the need for automated and reliable systems for early detection of diseases, which allows for quick intervention to mitigate financial losses, minimize pesticide misuse, and support sustainable practices in orange farming [5].

With the rise of Artificial Intelligence (AI) in the modern times, Machine Learning (ML) and Deep Learning (DL) have emerged as transformative technologies in smart automation and Data-driven Decision Making [6]. Owing to their capability in processing complex multi-dimensional data and extract hidden patterns, these techniques have gained a lot of importance across domains. They are particularly effective in agriculture where early detection is vital to prevent huge yield losses and sustainable crop production [7].

However, most of the prior studies are mainly based on deep learning frameworks, which are computationally intensive to deploy in real-world agricultural scenarios with limited resources. Although some studies have employed machine learning methods [8], they often suffer from limited model optimization, inadequate feature selection and high computational cost, making them less suitable for real-world deployment. Moreover, limited focus on model explainability decreases transparency and impedes trust in predictions [9]. Furthermore, the lack of validation and benchmarking adds to the lack of credibility and effectiveness of the existing solutions in practice. To address these limitations, this work proposes an optimized framework which is efficient, interpretable and has low computational complexity for accurate and reliable diagnosis of orange disease.

1.1 Challenges

While AI-driven methods have enhanced the ability to identify diseases in agriculture, there are several practical challenges with identifying orange disease:

- Symptoms of orange diseases are very similar in appearance, making accurate identification challenging.
- Full fruit images can include healthy skin areas, shadows, variations in illumination and background noise. In many cases, the disease-affected area occupies only a small portion of the image which reduces the visibility of disease-specific patterns.
- Complex deep learning models typically require large amounts of computational power for training and deployment, making them impractical in real-world agricultural applications.

¹[https://www.fao.org/markets-and-trade/commodities-overview/food-and-agriculture-market-analysis-\(FAMA\)/citrus/](https://www.fao.org/markets-and-trade/commodities-overview/food-and-agriculture-market-analysis-(FAMA)/citrus/).

- Extracted features can include redundant or less informative attributes, which can impact classification performance. Therefore, an appropriate feature selection approach should be employed to keep the most discriminative and relevant features.
- In order to improve trust and transparency in decision-making for agricultural disease diagnosis, model predictions must be interpretable.

1.2 Limitations of Prior Work

While smart agriculture has rapidly advanced, the current AI-based methods for orange disease classification have some drawbacks. The main research gaps are summarized as follows:

- Most existing studies mainly rely on deep learning models that are computationally expensive.
- Most of the available approaches are based on the complete image analysis with no proper segmentation of the affected regions. Therefore, irrelevant visual information like healthy peel regions, shadows, illumination changes, and background noise can be captured. In many cases, the disease-affected area occupies only a small portion of the image, reducing the visibility of disease-specific patterns.
- Several machine learning-based methods lack effective feature selection strategies. Thus, the model has redundant and less informative features, which may negatively impact classification performance.
- Prior studies often do not optimize model hyperparameters systematically. Therefore, suboptimal hyperparameters often get trapped in local optima, affecting the disease detection performance.
- Many previous works provide limited explainability for understanding disease prediction decisions.

1.3 Components of the Proposed Solution

In this study, we systematically overcome the shortcomings of existing methods. The salient contributions are outlined below:

- Proposed a hierarchical multi-class feature selection framework (HMSFO) which combines the union and intersection of class-wise top features learned using LASSO with globally dominant features identified through feature ranking. This approach provides the selection of highly discriminative features, which results in better classification accuracy.
- Introduced an effective preprocessing pipeline that enhances the contrast of the images and extracts the Region of Interest (ROI) that helps to improve the visual clarity and focus on the disease-relevant areas. This approach reduces the background noise, improves the model accuracy and decreases the computational complexity by removing irrelevant regions before training.
- Proposed a novel Adaptive Step-Controlled Gorilla Troops Optimizer (ASC-GTO) that adaptively adjusts the step sizes in order to solve the unstable convergence problem of classical GTO. It guarantees stable convergence and better optimization accuracy through large exploratory steps for the global search in early iterations and smaller steps for local search refinement in later stages.
- Performed model explainability using SHapley Additive exPlanations (SHAP) and Local Interpretable Model-agnostic Explanations (LIME) to identify the most important features impacting model predictions, which enhances transparency and reliability in the decision-making system.

2 Literature Review

Orange cultivation is greatly affected by diseases including greening, black spot and canker which results in poor fruit quality, low yield and heavy economic setbacks. With the recent developments in Machine Learning (ML) and Deep Learning (DL), automated image-based fruit disease detection systems have been

developed, which are more accurate and reliable than manual inspection. However, challenges remain in achieving optimal feature selection, effective model optimization and sufficient explainability.

2.1 Machine Learning Approaches

Early ML-based approaches demonstrated the feasibility of automated fruit disease detection by exploring classical machine learning techniques. Awate et al. [10] developed a fruit disease classification system using K-means segmentation and ANN-based classification with color, texture, morphology, and structural features. Benlachmi et al. [11] developed a fruit disease detection system using texture and color features with KNN, Decision Tree, and Random Forest classifiers, where Random Forest achieved the highest accuracy of 99%. Liu et al. [12] applied machine learning with rhizosphere and phyllosphere bacterial features to predict citrus HLB, although the approach depends on complex microbiome data and is unsuitable for real-time image-based detection.

2.2 Deep Learning Approaches

Numerous studies highlight the success of deep learning models for detecting orange diseases, with notable enhancements in accuracy and reliability. A CNN-based model proposed in study [13] achieved 97% accuracy using improved preprocessing and colour segmentation, however its performance might be restricted by using a small dataset. Similarly, the modified DenseNet-121 (DS-MENet) model proposed by Liu et al. [14] achieved an accuracy of 95.02% with a better robustness for noisy conditions. Dhiman et al. [15] introduced a hybrid model combining CNN and LSTM optimized for portable devices that reached an accuracy of 98.25%, emphasizing its potential in real-time use. The YOLO-Citrus model in literature [16] further improved the detection performance with a 96.6% mAP that offers a lightweight solution for complex orchard environments.

Other deep learning frameworks have also shown a good performance, with a two-stage detection-classification model in study [17] achieving 94.5% accuracy, and CNN-based models in [18,19] achieving 93.2% and 96.1% accuracy, respectively. Furthermore, Syed-Ab-Rahman et al. [20] achieved 94.37% detection accuracy and 95.8% precision on a two-stage deep CNN model, while performance may vary in real-world conditions. The enhanced MobileNetV3 model in the paper [21] achieved 98.85% accuracy whereas a multi-component CNN model in study [22] achieved 97.75% accuracy, showing further performance improvement with the combined inputs of features. Faisal et al. [23] used a Citrus Plant Dataset of healthy and diseased leaves to develop a CNN-based transfer learning framework, with EfficientNetB3 achieving 99.58% accuracy. Shastri et al. [24] explored an Enhanced-CNN (E-CNN) architecture to detect citrus fruit and leaf disease in a variety of benchmark datasets with a highest accuracy of 98%. Based on this progress, Sankaran et al. [25] proposed CitrusDiseaseNet, a multi-stage ensemble of CNNs and Vision Transformers along with handcrafted texture descriptors (LBP, GLCM) with PCA-reduced embeddings which showed more robust performance on orange and lemon datasets. Devora-Guadarrama et al. [26] have shown that lightweight CNNs, like EfficientNetB0 can reach 99.88% accuracy when identifying citrus canker and Huanglongbing and can be effective for deployment in practical scenario.

Qiu et al. [27] proposed a multimodal image-text model, where ShuffleNetV2 + TextCNN achieved 98.33% accuracy on mixed-background images. Yu et al. [28] reviewed non-destructive quality evaluation using computer vision and spectroscopy, highlighting the role of data fusion in grading, damage detection, and traceability. Kaur et al. [29] introduced the NL-FuRBE ensemble by combining VGG19, AlexNet, and Xception with image enhancement techniques, achieving 96.51% accuracy for citrus leaf disease detection.

2.3 Deep Learning Approaches with Explainable AI

Notwithstanding these impressive classification outcomes, the lack of interpretability in deep learning models remains a critical concern for real-world agricultural deployment. Irondi et al. [30] developed an explainable citrus quality assessment framework by integrating Vision Transformers with the lightweight large language model Phi-3-mini, achieving an accuracy of 98.29%. Srinivasan et al. [31] proposed DBA-ViNet, a dual-branch attention-guided network with Grad-CAM-based explainability for fruit disease classification, achieving 99.51% accuracy and outperforming several state-of-the-art deep learning models. Additional related studies are summarized in Table 1.

Table 1: Review of existing studies.

Ref	Year	Context	Proposed Approach	Limitation	Performance
Machine Learning Approaches					
[32]	2019	Fruit disease detection	Hybrid framework using K-Means segmentation with ANN and SVM classifiers	Relied on handcrafted phenotypic features	93.12%
[33]	2018	Orange disease detection and severity estimation	Computer vision framework using K-means clustering, multi-class SVM, and fuzzy logic for severity analysis	Focused only on orange fruits and surface-level defects	90%
Deep Learning Approaches					
[34]	2022	Citrus disease identification	Two-stage deep learning framework using optimized YOLOv4 and EfficientNet	Moderate accuracy with a relatively small dataset	89.00%
[35]	2024	Orange disease classification	MobileNetV2-based transfer learning model	Limited dataset size; prone to misclassification	95.00%
[36]	2025	Orange ripeness classification and black spot detection	Hybrid ViT-CapsNet model integrating global and spatial feature extraction	High model complexity + lack of explainability	96.12%
Deep Learning Approaches with Explainable AI					
[37]	2025	Orange diseases classification	Hybrid Res-Inception model with Grad-CAM, Score-CAM, and LIME	Moderate dataset size; high computational complexity	98.93%

(Continued)

Table 1 (continued)

Ref	Year	Context	Proposed Approach	Limitation	Performance
[38]	2022	Multispecies fruit disease detection	Multimodal deep learning framework integrating RGB, thermal, and hyperspectral images with CNN, YOLO, hybrid models, Grad-CAM, and SHAP for explainability	Increased model complexity and dependence on multimodal data acquisition	93.05%
[39]	2026	Citrus disease detection	CNN, ViT, and SVM ensemble with Grad-CAM, Grad-CAM++, and LIME for explainability	High computational complexity; requires large-scale data	99.00%

Despite progress, existing fruit disease detection studies often lack explainability, optimal feature selection, efficient hyperparameter tuning, and computational feasibility. To address these gaps, this study proposes an optimized, lightweight, and interpretable framework for reliable orange disease recognition.

3 Materials and Methods

In this study, an ROI-guided explainable machine learning framework is proposed to accurately and reliably identify the orange disease with low computational overhead. The methodology starts with a detailed preprocessing pipeline where all the input images are resized to keep uniformity. Contrast enhancement methods are applied to improve the visibility of disease patterns. Image segmentation is done using K-means clustering to divide each image into three parts: background, foreground and diseased regions. The defective part is extracted as the Region of Interest (ROI) as it contains the most relevant information for the detection of a disease. By keeping the focus on the ROI only, the proposed framework is able to effectively reduce the background noise, improve the quality of features and reduce the computational complexity by removing the irrelevant regions before training.

From the extracted ROI, two main categories of features are extracted—texture features and color features. In order to discover the most informative features, feature ranking is executed by the Least Absolute Shrinkage and Selection Operator (LASSO). In order to perform feature selection, we proposed a hierarchical multi-class feature selection framework (HMSFO) that combines class-wise LASSO rankings with global top-ranked features. This strategy guarantees the selection of highly discriminative features based on their class-specific and overall discriminative power.

To further improve the model performance, a novel Adaptive Step-Controlled Gorilla Troops Optimizer (ASC-GTO) is proposed. The proposed optimizer adjusts the step sizes in an adaptive way to overcome the unstable convergence behavior of the classical Gorilla Troops Optimizer (GTO). It uses larger exploratory steps in the early iterations to provide global search and smaller steps in the later iterations for refined local optimization which ensures stable convergence and better optimization accuracy.

Multiple baseline machine learning models, including Random Forest, XGBoost, Decision Tree, K-Nearest Neighbors (KNN) and Support Vector Classifier (SVC) are explored in this framework. In addition,

model explainability is performed using LIME and SHAP for increasing transparency and practical trustworthiness by finding the most influential features driving prediction outcomes. An outline of the proposed methodology is presented in Fig. 1.

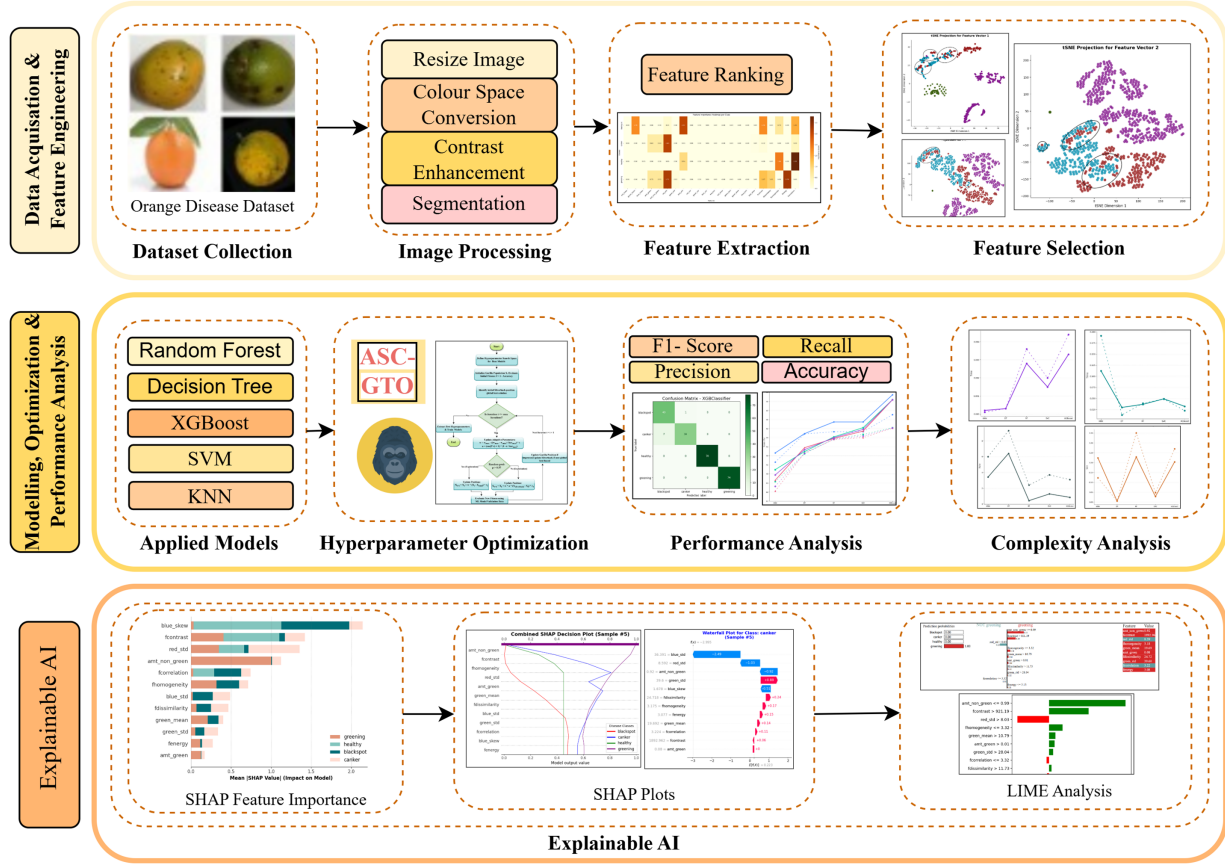
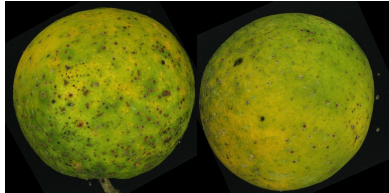


Figure 1: Overview of proposed methodology.

3.1 Dataset Description

This study uses the Orange Disease Dataset available on Kaggle. It includes images of four different classes: Greening, Canker, Blackspot and Healthy. There are 206 images of Blackspot, 201 images of Canker, 369 images of Greening and 388 images of Healthy samples. Examples of each category are displayed in Table 2.

Table 2: Description of representative orange diseases.

Class	Description	Visualization
Canker	A bacterial disease caused by <i>Xanthomonas citri</i> , and causing raised, rough, corky lesions on the surface of orange fruits. Spots typically have a brown center and yellow margins and can develop into scabby or cratered.	
Blackspot	A fungal disease caused by <i>Phyllosticta citricarpa</i> and characterized by dark sunken or hard spots on the peel of the fruit. Lesions can be like black specks, cracked spots or virulent blotches.	
Greening	A serious bacterial disease caused by <i>Candidatus Liberibacter</i> species that leads to small, misshapen and unevenly colored fruits. Affected oranges often remain partially green even when ripe.	
Healthy	Healthy orange fruits exhibit a smooth, firm and evenly colored peel (typically bright orange when ripe). The surface is free from lesions, discoloration, cracks or deformities.	

3.2 Image Preprocessing

All images are preprocessed before the feature extraction process to enhance image quality and normalize the input data. This involves resizing images to a common size, improving the contrast to reveal disease patterns, converting the color space to gain more discriminative color information, and finally segmentation to isolate the Region of Interest (ROI). ROI extraction helps reduce background noise, improve feature quality and enhance overall classification performance. The preprocessing pipeline is illustrated in Fig. 2.

The RGB images are first transformed to the CIE $L^*a^*b^*$ color space where the luminance component L^* is separated from the chromatic components a^* and b^* , which enhances the flexibility of the processing and the accuracy of the segmentation. Next, Contrast Limited Adaptive Histogram Equalization (CLAHE) is applied to the L^* channel to enhance image visibility while preserving color information and preventing over-enhancement. Finally, K-means clustering is performed on the a^* and b^* channels to segment the images into background, foreground, and defected regions, where the defected region is selected as the ROI for subsequent disease analysis.

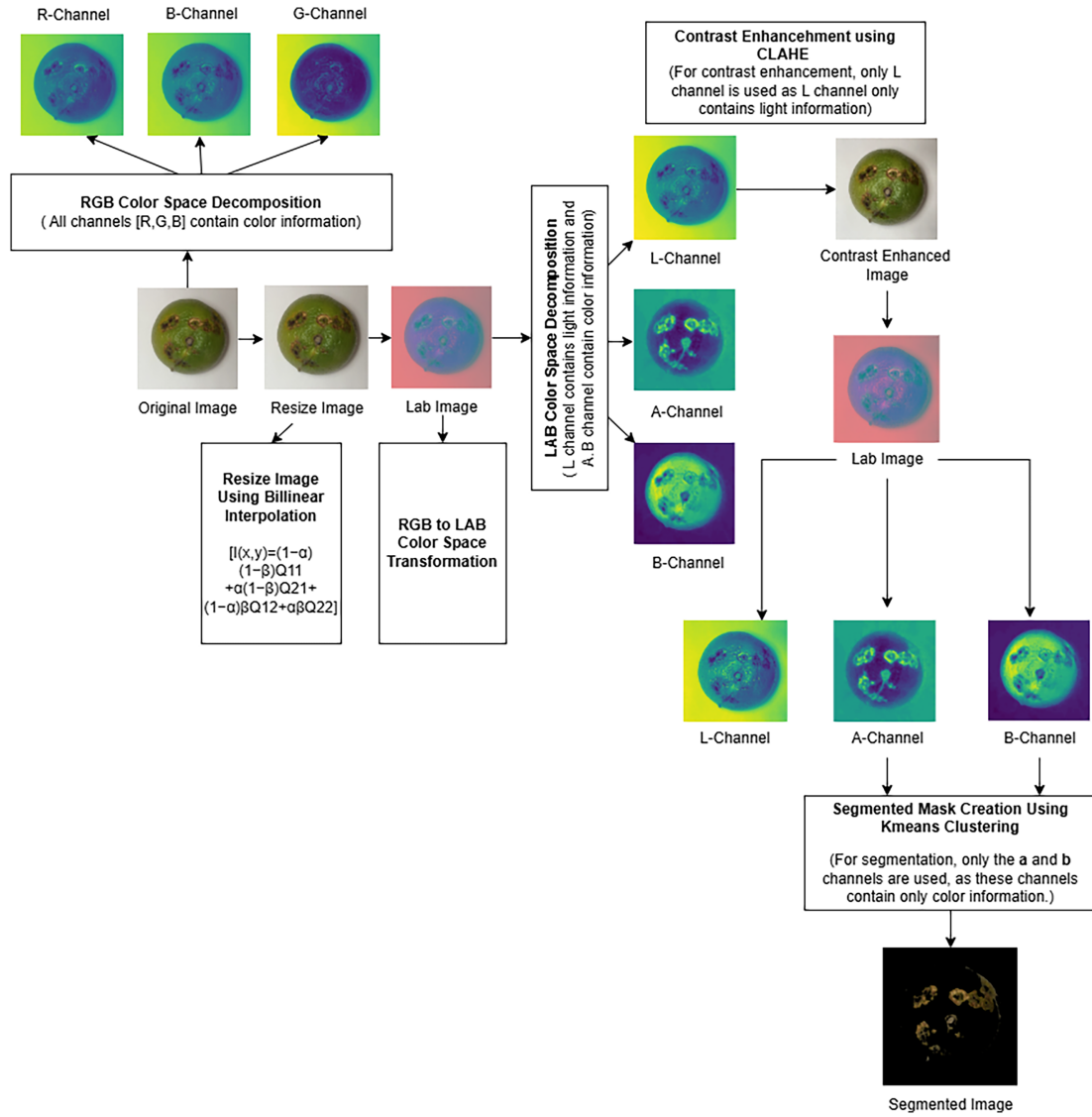


Figure 2: Data preprocessing.

3.3 Feature Engineering

Feature engineering significantly contributes to enhancing the predictive capabilities of ML classifiers by ensuring that they operate on the most relevant attributes. This step involves feature extraction, ranking and selection.

3.3.1 Feature Extraction

Feature extraction is one of the most crucial steps in the proposed framework. In this study, the ROIs extracted from the images during the preprocessing stage were considered to capture disease-specific information. Accordingly, a total of 22 texture- and color-based features were extracted.

3.3.2 Proposed Feature Selection Method (HMSFO)

We proposed a Hierarchical Multi-Class Sparse Feature Optimization (HMSFO) algorithm to select the most informative features from the dataset through a hierarchical and sparsity-driven approach. For

each class, a one-vs.-rest strategy is applied to convert the problem into binary classification and a sparse optimization model with L1 regularization is used to learn class-specific feature weights which ensures that only important features receive nonzero importance scores. These class-wise importance values are aggregated to compute global feature importance and all features are ranked accordingly. From this ranking, the top- k important features are selected for each class and combined to form a useful feature set while the remaining features are treated as non-useful. The top- k ($k = 7$) features for each class are selected using the correlation heatmap to form class-wise subsets. The union of these class-wise feature subsets retains features that are important for at least one class, while their intersection identifies features that remain consistently important across all classes. In parallel, a set of globally dominant features is picked by selecting the top- p ($p = 5$) features from global ranking. Finally, the optimized feature space is constructed by combining the union set, intersection set and uniquely selected global features resulting in compact, informative and balanced feature subset that captures class specific as well as global significant patterns for improved multi-class classification performance.

Unlike conventional LASSO-based feature selection, which typically relies on a single global sparse importance pattern, the proposed HMSFO employs LASSO as a base ranking mechanism within a hierarchical multi-class framework. Specifically, HMSFO performs class-wise one-vs.-rest feature ranking and integrates class-specific union features, commonly shared intersection features as well as globally dominant features to generate a compact, balanced and discriminative feature subset. Algorithm 1 illustrates the proposed framework for feature selection.

Algorithm 1: Hierarchical multi-class sparse feature optimization (HMSFO)

Input: Dataset $D = \{(x_i, y_i)\}_{i=1}^m$, feature set $F = \{f_1, f_2, \dots, f_n\}$, regularization parameter λ , Top- k , Top- p

Output: $F_{\text{ranked}}, \{F_c^{(k)}\}_{c=1}^C, F_U, F_\cap, F_\oplus, F^*$

1: $\tilde{X} \leftarrow \text{mean_imputation}(D)$

2: $Z \leftarrow \text{standardize}(\tilde{X})$

3: **for** $c = 1$ to C **do**

4: Construct binary labels $y^{(c)}$ (one-vs.-rest)

5: $w^{(c)*} \leftarrow \arg \min_{w^{(c)}} (L^{(c)}(w^{(c)}) + \lambda \|w^{(c)}\|_1)$

6: $I^{(c)} \leftarrow |w^{(c)*}|$

7: **end for**

8: **for** $j = 1$ to n **do**

9: $GI[j] \leftarrow \sum_{c=1}^C I_j^{(c)}$

10: **end for**

11: $F_{\text{ranked}} \leftarrow \text{argsort}(GI)$

▷ Descending order

12: **for** $c = 1$ to C **do**

13: $F_c^{(k)} \leftarrow \text{Top-}k \text{ features from } I^{(c)}$

14: **end for**

15: $F_U \leftarrow \bigcup_{c=1}^C F_c^{(k)}$

16: $F_\cap \leftarrow \bigcap_{c=1}^C F_c^{(k)}$

17: $F_{\text{global}}^{(p)} \leftarrow \text{Top-}p \text{ features from } F_{\text{ranked}}$

18: $F_\oplus \leftarrow F_{\text{global}}^{(p)} \triangle F_U$

19: $F^* \leftarrow F_U \cup F_\cap \cup F_\oplus$

20: **return** $F_{\text{ranked}}, \{F_c^{(k)}\}_{c=1}^C, F_U, F_\cap, F_\oplus, F^*$

Computational complexity analysis of HMSFO:

The proposed HMSFO selects the most useful features by using class-wise LASSO learning, global feature ranking, and final feature subset formation. Let m be the number of samples, n be the number of features, C be the number of classes and T_L be the number of LASSO iterations. The preprocessing step takes $O(mn)$ time, while class-wise LASSO optimization takes $O(CT_L mn)$ time. Feature ranking and selection require $O(Cn \log n)$ time. Therefore, the overall time complexity of HMSFO is $O(CT_L mn + Cn \log n)$. Since the LASSO step is the most time-consuming part, it mainly controls the total complexity. The space complexity is $O(mn + Cn)$, mainly for storing the feature data and class-wise feature weights. Overall, HMSFO adds only a one-time feature selection cost and helps reduce the final feature size before model training.

3.4 Proposed ASC-GTO Algorithm

To optimize model hyperparameters, we propose an Adaptive Step-Controlled Gorilla Troops Optimizer (ASC-GTO), which extends the classical GTO by introducing a dynamic step-size control mechanism. Classical GTO may suffer from unstable convergence and local optima entrapment due to the absence of explicit step-size regulation. ASC-GTO addresses this issue by balancing global exploration and local exploitation where larger steps are used in the early iterations to explore the search space, while smaller steps are applied in later iterations for fine local refinement. This adaptive strategy enables more stable and effective hyperparameter optimization for orange disease classification.

The classical GTO mainly operates through two phases:

- **Exploration:** Gorillas move toward randomly selected individuals to explore new regions and maintain population diversity.
- **Exploitation:** Gorillas move toward the Silverback, representing the best solution found so far, to refine the optimal solution.

Although classical GTO balances between global and local search, it does not directly control the size of the steps, which may lead to unstable convergence and ability to get trapped in local optima. To address this, we introduce a step controlled mechanism which incorporates adaptive control parameters in the position update process.

- **Adaptive Inertia Weight:** In order to dynamically regulate the magnitude of movement of each gorilla, an adaptive inertia weight w is introduced:

$$w = w_{\max} - \left(\frac{w_{\max} - w_{\min}}{iter_{\max}} \right) \times iter \quad (1)$$

here, $iter$ denotes the current iteration and $iter_{\max}$ is the maximum iteration count. The parameters $w_{\max}$ and $w_{\min}$ signifies the upper and lower limits of the inertia weight.

At the early stages of optimization, the weight of the inertia is large, which enables gorillas to move larger and cover a greater space. The weight of inertia decreases as the iterations advance and this helps to reduce the step size and create a finer local search. This is an adaptive mechanism that will allow a smooth transition between exploration and exploitation during the optimization process.

- **Adaptive Exploration Coefficient:** To supplement the inertia control, the exploration coefficient is redefined to add an iteration-dependent behavior. The coefficient a is given by:

$$a = (\cos(2r) + 1) \times \left(1 - \frac{iter}{iter_{\max}} \right) \quad (2)$$

where $r \in [0, 1]$ is a random variable.

The cosine term involves a regulated oscillatory motion, which provides variety to the search process. Meanwhile, the linearly diminishing factor slowly diminishes the strength of exploration over time. This leads to increased exploration in the initial stages and transition to exploitation as the process continues to bring about stable convergence to the optimal solution.

- **Modified Position Update Mechanism:** The adaptive inertia weight and exploration coefficient are added to the movement equations to improve the classical GTO position update. During the exploration phase ($p < 0.5$), the i -th gorilla's position is updated as:

$$X_i^{t+1} = X_i^t + w \cdot (X_i^t - X_{\text{rand}}) \cdot r_1 \quad (3)$$

where X_{rand} is a randomly chosen gorilla, and $r_1 \in [0, 1]$ is a random vector.

During the exploitation phase ($p \geq 0.5$), the update becomes:

$$X_i^{t+1} = X_i^t + w \cdot a \cdot (X_{\text{silverback}} - X_i^t) \cdot r_1 \quad (4)$$

where $X_{\text{silverback}}$ denotes the global best solution.

The proposed ASC-GTO modifies the search step size and direction of the search during the optimization process using the dynamic inertia weight w and the coefficient a that changes with the iteration. This dynamic control is useful to explore complex hyperparameter spaces in machine learning, exploring a wide variety of hyperparameter combinations initially and refining promising solutions subsequently. This transition maintains a constant convergence, prevents premature convergence and eventually enhances the performance of the models.

The integration step as shown in Fig. 3 integrates the ASC-GTO algorithm and five machine learning classifiers to produce an automatic feedback loop of determining the best model settings without human intervention. It uses the following steps: initialize a random sample of gorillas as hyperparameter combinations, compute their fitness with k -fold cross-validation, update their positions with respect to fitness, and choose the most successful parameters. Once the maximum number of iterations has been met, the most successful parameters are then utilized to train and test the final machine learning model to ensure it performs well on the unseen data.

Computational complexity analysis of ASC-GTO: Let N be the number of gorillas, D be the search-space dimension, T be the maximum number of iterations, K be the number of cross-validation folds, and $\Psi_{\text{model}}(m, q)$ be the training and validation cost of a classifier using m samples and q selected features. The population initialization requires $O(ND)$ time, and the position update in each iteration also requires $O(ND)$. The adaptive inertia weight and exploration coefficient require only constant-time operations. The main cost comes from fitness evaluation using K -fold cross-validation, which requires $O(NK\Psi_{\text{model}}(m, q))$ per iteration. Therefore, the overall time complexity of ASC-GTO is $O(TN(D + K\Psi_{\text{model}}(m, q)))$, and its space complexity is $O(ND)$. Since the adaptive step-control mechanism adds only constant-time calculations, ASC-GTO does not increase the asymptotic complexity compared with classical GTO, while improving convergence stability.

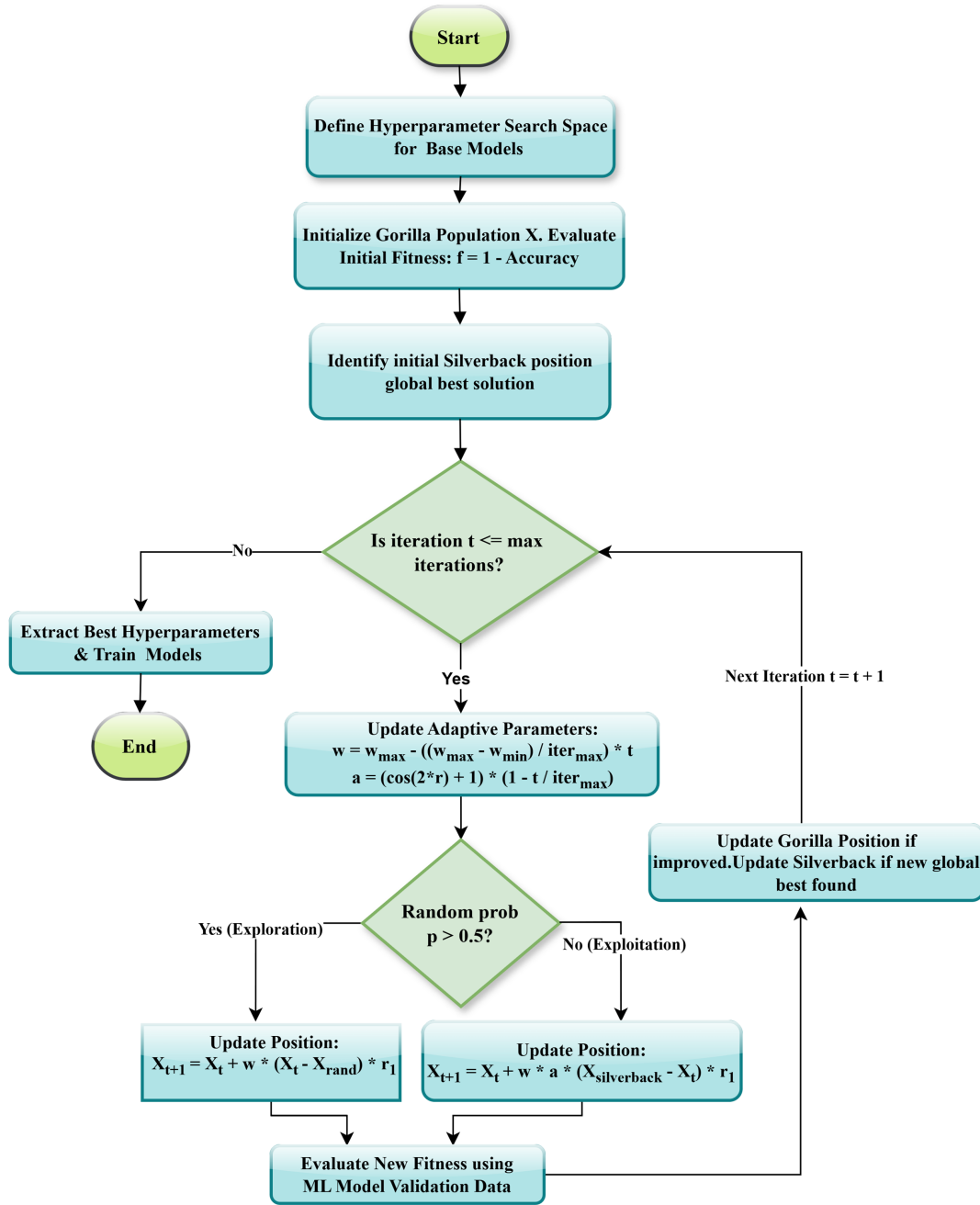


Figure 3: ASC-GTO integration with ML models.

4 Results

4.1 Comparison of Feature Vectors

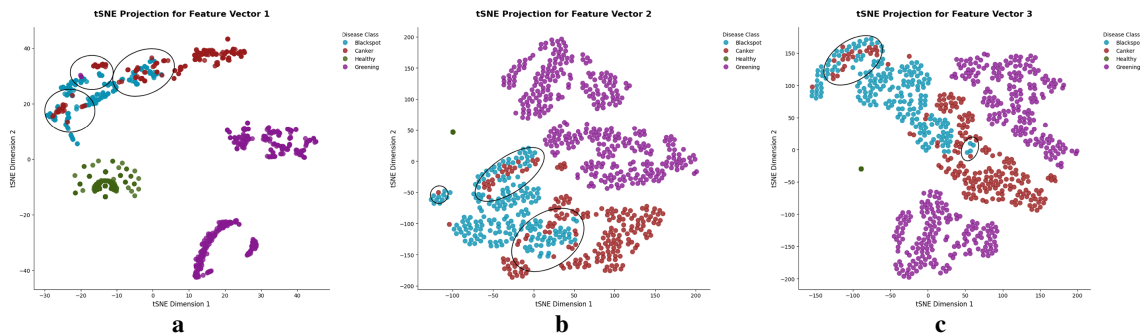
Table 3 compares the classification performance obtained using three feature vectors. Feature Vector 1 is constructed by randomly selecting ten features from the extracted feature set and is used as a baseline. Feature Vector 2 is generated by selecting the top 10 features according to LASSO-based feature ranking. In contrast, Feature Vector 3 represents the proposed HMSFO-based feature vector, which integrates class-wise discriminative features with globally dominant features to form a compact and informative feature subset.

Table 3: Performance comparison of classifiers using different feature vectors.

Feature Vector	Classifier	Accuracy (%)	Precision (%)	Recall (%)	F1-Score (%)
Feature Vector 1	Random Forest	94.02	92.30	92.28	92.29
	Decision Tree	93.16	90.85	90.24	90.54
	SVC	91.88	90.44	89.77	90.10
	KNN	91.88	89.72	88.96	89.34
	XGBoost	95.30	93.52	94.11	93.81
Feature Vector 2	Random Forest	94.87	93.07	92.68	92.88
	Decision Tree	94.44	92.46	92.89	92.67
	SVC	96.15	94.81	94.51	94.66
	KNN	91.88	90.13	88.96	89.54
	XGBoost	96.15	94.81	94.51	94.66
Feature Vector 3	Random Forest	99.57	99.40	99.39	99.40
	Decision Tree	93.59	90.97	91.13	91.05
	SVC	98.72	98.30	98.17	98.23
	KNN	96.58	96.02	95.12	95.57
	XGBoost	99.15	98.80	99.05	98.92

The results demonstrate that Feature Vector 3 consistently outperforms the other feature vectors across most classifiers and evaluation metrics. Random Forest achieves the highest accuracy of 99.57%, followed by XGBoost with 99.15% and SVC with 98.72%. Moderate performance is observed in Feature Vector 2, demonstrating the effectiveness of LASSO-based ranking compared to a random selection. However, the performance of Feature Vector 1 is quite inferior as there is no relevance-based feature selection. In general, the results verify that the proposed Feature Vector 3 using HMSFO is the most discriminative for accurate identification of orange disease.

It can also be seen in Fig. 4 that among the three feature vectors, Feature Vector 3 has the best discriminative power, where the overlap between the two classes, Blackspot and Canker, is minimal in the t-distributed Stochastic Neighbor Embedding (t-SNE) projection and the classes are clearly separated, which shows good representation of the features. Minimal overlap is crucial for accurate identification because it boosts the confidence of the model in distinguishing between similar patterns of the disease and minimizes the chances of misclassification. This improved separability indicates that Feature Vector 3 contains more distinguishing and class-specific features, making it the most suitable for accurate orange disease detection.

**Figure 4:** T-SNE visualization of the extracted feature vectors (a) Feature Vector 1 (b) Feature Vector 2 (c) Feature Vector 3.

4.2 Impact of Proposed ASC-GTO on Model Performance

Table 4 presents the class-wise performance of the models optimized with classical GTO, Particle Swarm Optimization (PSO) and ASC-GTO. The results show that ASC-GTO provides the best overall performance for the key classifiers, particularly Random Forest, SVC, and XGBoost. Notably, the accuracy of the Random Forest algorithm is enhanced from 95.73% using classical GTO and 97.65% using PSO to 99.57% using ASC-GTO. Similarly, XGBoost improves from 98.72% and 98.93% to 99.15%, while SVC improves from 95.73% and 97.22% to 98.72%.

Table 4: Class-wise performance analysis (%) for each model.

Model	Blackspot			Canker			Greening			Healthy			Accuracy
	P	R	F	P	R	F	P	R	F	P	R	F	
Hyperparameter Optimization using Classical GTO													
Random Forest	91.89	82.93	87.18	84.44	92.68	88.37	100.00	100.00	100.00	100.00	100.00	100.00	95.73
Decision Tree	82.98	95.12	88.64	86.84	80.49	83.54	100.00	95.95	97.93	100.00	100.00	100.00	94.44
SVC	80.39	100.00	89.13	100.00	82.93	90.67	100.00	95.95	97.93	100.00	100.00	100.00	95.73
KNN	73.58	95.12	82.98	89.66	63.41	74.29	98.65	98.65	98.65	100.00	100.00	100.00	92.31
XGBoost	95.24	97.56	96.39	97.50	95.12	96.30	100.00	100.00	100.00	100.00	100.00	100.00	98.72
Hyperparameter Optimization using PSO													
Random Forest	94.50	90.24	92.32	92.15	95.12	93.61	100.00	100.00	100.00	100.00	100.00	100.00	97.65
Decision Tree	82.95	89.00	85.86	84.00	81.50	82.73	100.00	97.30	98.63	100.00	100.00	100.00	94.02
SVC	86.50	100.00	92.76	100.00	87.80	93.50	100.00	100.00	100.00	100.00	100.00	100.00	97.22
KNN	79.00	97.56	87.30	95.00	71.95	81.88	98.66	100.00	99.32	100.00	100.00	100.00	94.49
XGBoost	95.28	98.50	96.86	98.50	95.12	96.78	100.00	100.00	100.00	100.00	100.00	100.00	98.93
Hyperparameter Optimization using Proposed ASC-GTO													
Random Forest	97.62	99.48	98.80	100.00	97.56	98.76	100.00	100.00	100.00	100.00	100.00	100.00	99.57
Decision Tree	82.93	82.93	82.93	80.95	82.93	81.93	100.00	98.65	99.32	100.00	100.00	100.00	93.59
SVC	93.18	100.00	96.47	100.00	92.68	92.20	100.00	100.00	100.00	100.00	100.00	100.00	98.72
KNN	85.42	100.00	92.14	100.00	80.49	89.19	98.67	100.00	99.33	100.00	100.00	100.00	96.68
XGBoost	95.35	100.00	97.62	100.00	95.12	97.50	100.00	100.00	100.00	100.00	100.00	100.00	99.15

The class-wise results indicate that ASC-GTO achieves higher precision, recall, and F1-scores for the visually similar Blackspot and Canker classes, where misclassifications are more likely to occur. The performance of Greening and Healthy classes is near perfect in most optimized models. While PSO is competitive in some classifiers, the proposed ASC-GTO gives the best overall accuracy with Random Forest (RF), which shows its effectiveness in hyperparameter optimization of orange disease classification.

4.3 Impact of ROI Extraction on Model Performance and Computational Complexity

Fig. 5 indicates that the extraction of ROI not only enhances the model performance in all the evaluation metrics but also reduces the computational complexity. ROI extraction focuses on the diseased part of the image and eliminates the irrelevant background information to improve the representation of the disease-specific features and reduce noise from healthy peel regions, shadows, and illumination changes. For this reason, all the classifiers perform better with accuracy improvements between about 2% and 3.5% as shown in Fig. 5a. The highest improvement is observed for the Decision Tree model, with an accuracy gain of 3.19%.

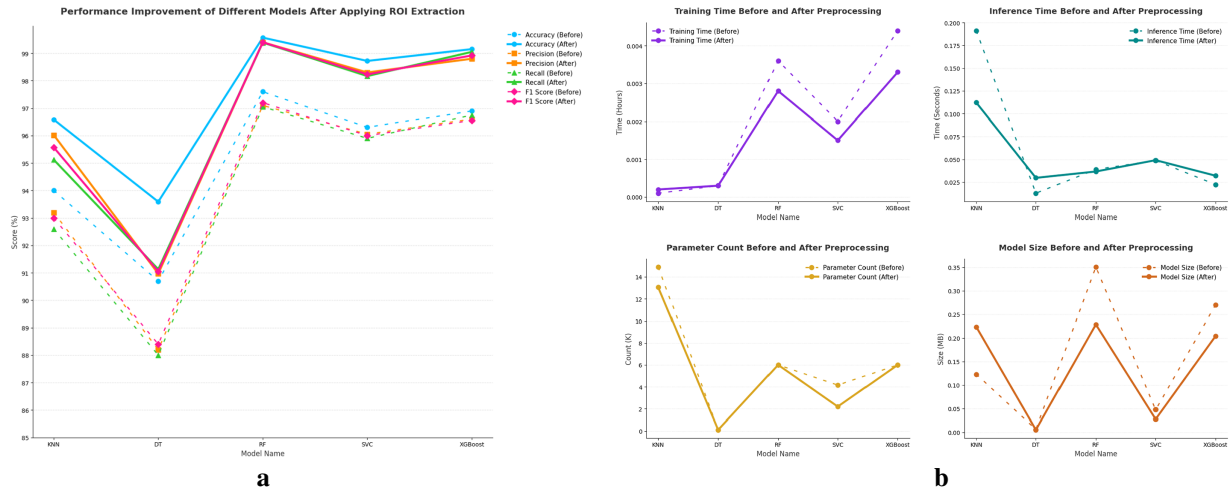


Figure 5: Improvement after ROI extraction: (a) performance gain and (b) computational complexity reduction.

Furthermore, Fig. 5b demonstrates that ROI extraction results in reduced computational complexity while improving predictive performance. Since the models are trained on a compact and disease-focused input region, feature dimensionality, memory usage, training time, inference time, model size, and parameter requirements are reduced. Notable reductions include model size decreases of 34.76% for Random Forest, 41.67% for SVC, and 24.44% for XGBoost, along with training time reductions of 22.22% for Random Forest and 25% for both SVC and XGBoost. Furthermore, ROI extraction reduced the average inference time by approximately 15.4%, highlighting its contribution to improving model efficiency. These results show that ROI extraction can improve classification accuracy while reducing computational complexity, making the model more suitable for lightweight deployment on resource-constrained devices such as smartphones and smart agriculture embedded systems.

4.4 Convergence Analysis of the Proposed ASC-GTO

The convergence behavior of the proposed ASC-GTO was compared with classical GTO, Bayesian Optimization, PSO and Grid Search over 20 iterations, as shown in Fig. 6. The outcomes show that ASC-GTO achieves faster and more stable convergence compared with the other methods. It quickly decreases the test error in the initial iterations and settles around the 7th iteration at a final error of 0.075. In contrast, classical GTO converges more slowly and stabilizes at a higher error of approximately 0.087, while PSO, Bayesian Optimization, and Grid Search also remain at comparatively higher final error levels.

This convergence analysis is a good indicator of the fact that the adaptive step-controlled mechanism improves the balance between global exploration and local exploitation. Overall, ASC-GTO demonstrates superior convergence stability and optimization accuracy which supports its effectiveness for reliable hyperparameter optimization in orange disease classification.

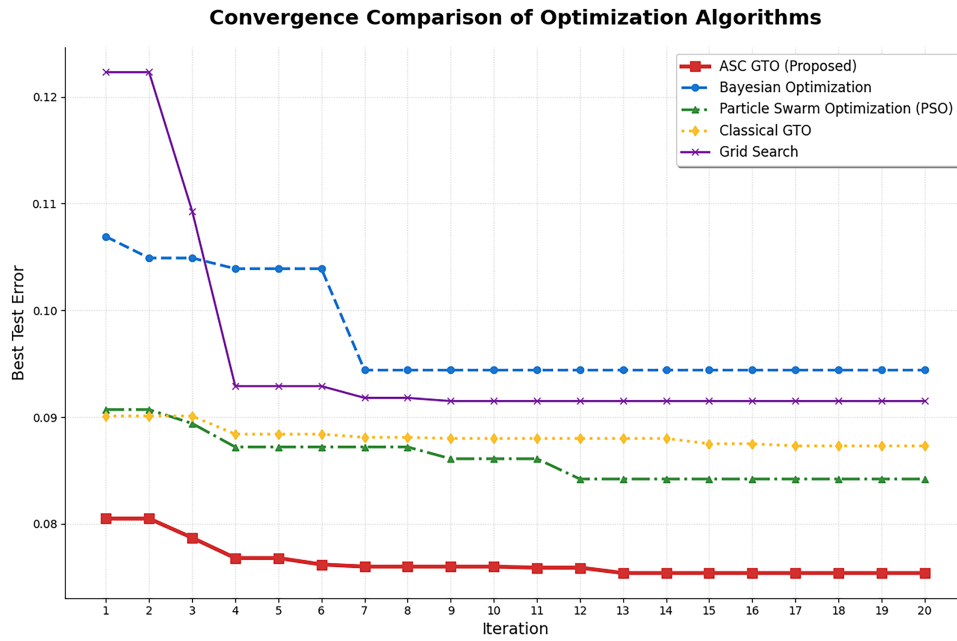


Figure 6: Convergence analysis of the proposed ASC-GTO.

4.5 K-Fold cross Validation

Stratified 5-fold cross-validation was performed to evaluate the reliability and generalizability of the proposed ASC-GTO optimized Random Forest model. The model obtained a mean accuracy of 98.2% with a low standard deviation of 0.011, as presented in Table 5, which represents the stable performance of the model over various data partitions and a minimal risk of overfitting. The obtained results validate the robustness of the proposed optimization and feature selection approach for the identification of the orange disease.

Table 5: Performance evaluation using 5-Fold cross-validation (ASC-GTO optimized random forest).

Fold	Precision	Recall	F1-Score	Accuracy
Fold 1	0.987	0.983	0.981	0.983
Fold 2	0.987	0.983	0.981	0.982
Fold 3	0.974	0.972	0.963	0.967
Fold 4	1.00	1.00	1.00	1.00
Fold 5	0.987	0.981	0.981	0.981
Mean	0.9870	0.9838	0.9812	0.9826
Standard Deviation	0.0092	0.0102	0.0131	0.0117

4.6 Error Analysis

The confusion matrices in Fig. 7 show that most misclassifications occur between blackspot and canker, mainly due to their visual similarity. Decision Tree exhibits the highest confusion, with 14 cross-class misclassifications, whereas KNN and SVM reduce this error. Random Forest and XGBoost achieve near-optimal performance, producing only one misclassification between blackspot and canker.

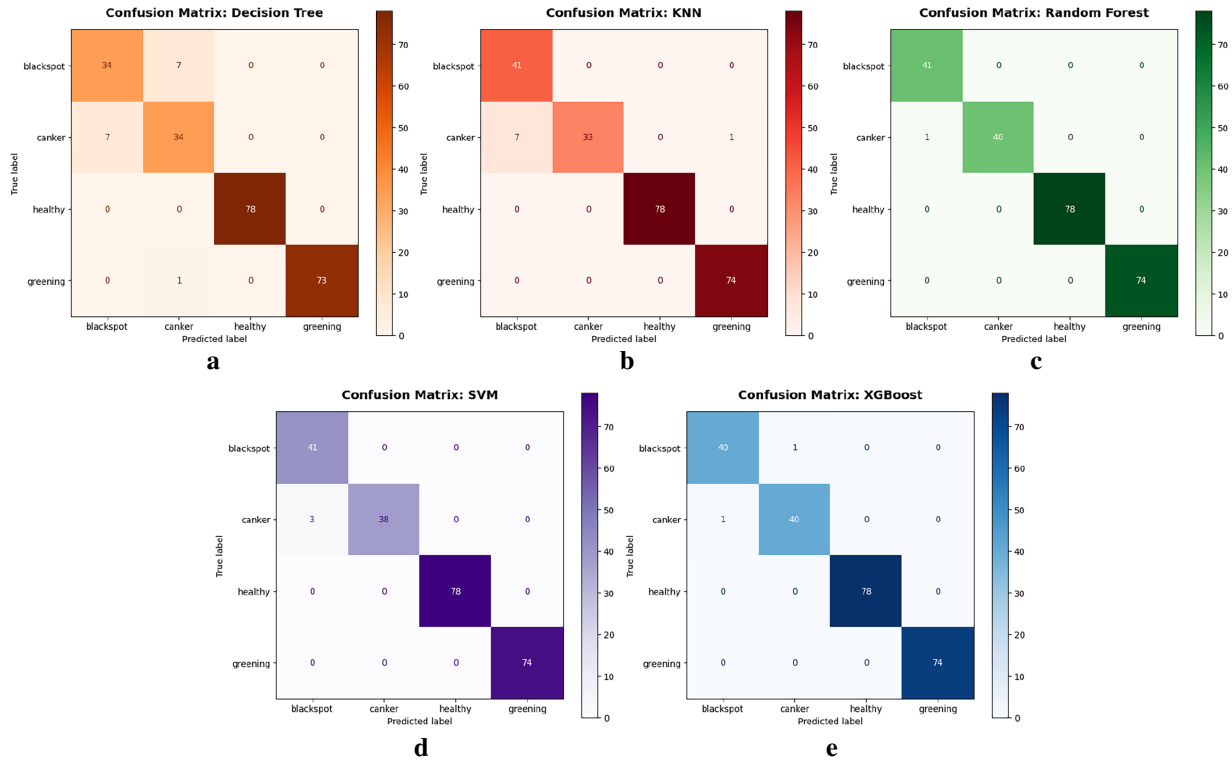


Figure 7: Confusion matrix for (a) Decision tree (b) KNN (c) Random forest (d) SVC (e) XGBoost.

Healthy and greening samples are classified with almost perfect accuracy across all models. Overall, the ASC-GTO-optimized Random Forest model provides the most reliable classification performance, with minimal inter-disease confusion.

4.7 Model Explainability

In smart and sustainable agriculture, model interpretability is crucial for trust and transparency. In this study, SHapley Additive exPlanations (SHAP) and Local Interpretable Model-agnostic Explanations (LIME) were employed to provide both global and local interpretability by identifying the most influential features contributing to each prediction.

4.7.1 Explainability Analysis Using SHAP

SHAP analysis was conducted to interpret the contribution of individual features to the proposed model's predictions. As shown in Fig. 8, color and texture features such as blue_std, green_std, blue_skew, homogeneity, red_std, green_mean, contrast, and dissimilarity show strong contributions.

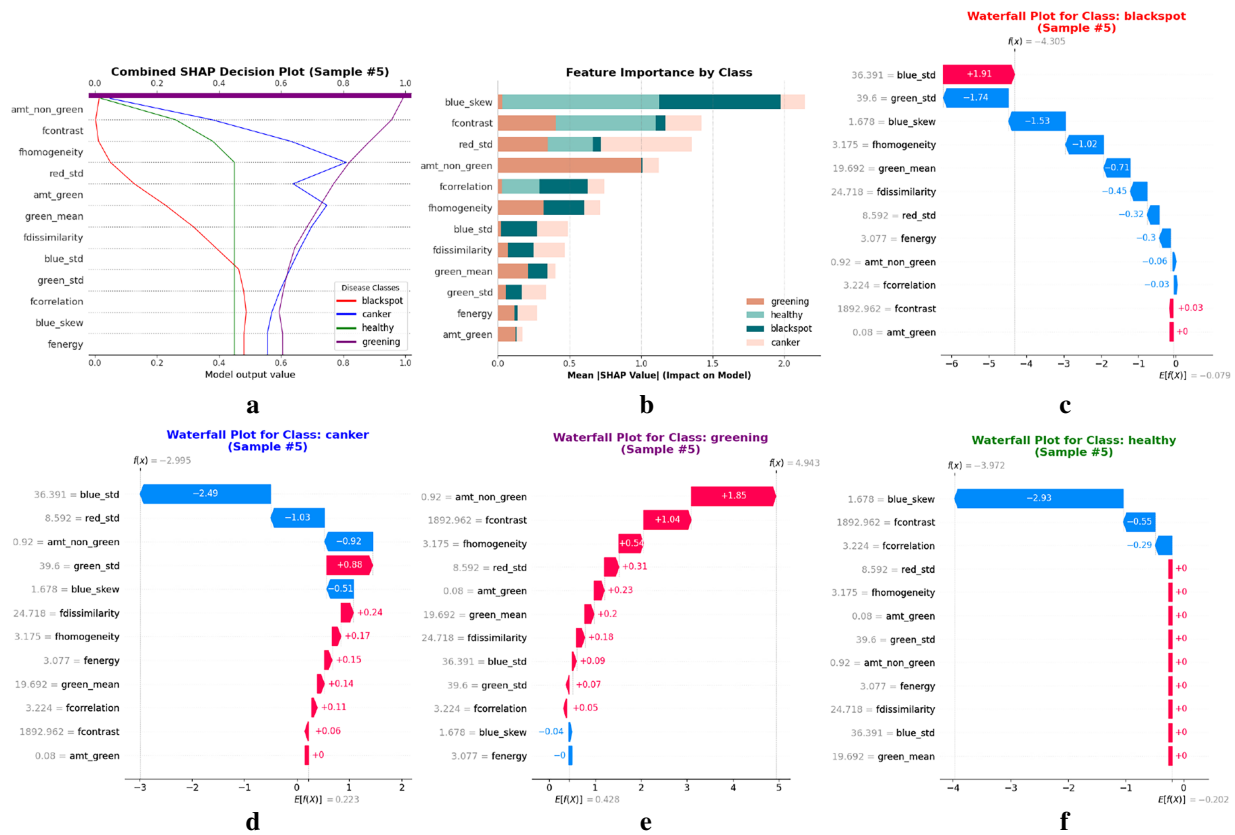


Figure 8: Explainability analysis using SHAP: (a) Combined SHAP decision plot (b) Feature importance by class (c) Waterfall plot for blackspot (d) Waterfall plot for canker (e) Waterfall plot for greening (f) Waterfall plot for healthy.

These findings are biologically meaningful because the target diseases are mainly identified through visible changes in peel color, lesion formation, and surface texture. Citrus black spot commonly produces dark spots or blotches on fruit, citrus canker is associated with raised brown lesions, yellow halos, and corky surfaces, while citrus greening often causes fruits to color unevenly and remain partially green². Therefore, the strong influence of color-channel statistics and texture features indicates that the model is capturing disease-relevant visual symptoms rather than arbitrary image patterns. For blackspot and canker, RGB color statistics and texture features reflect dark lesions, corky spots, irregular discoloration, and rough lesion boundaries. For greening, amt_non_green, contrast, and homogeneity are consistent with uneven color development and greenish appearance. Overall, SHAP confirms that the proposed model relies on biologically relevant color and texture characteristics extracted from ROI-segmented regions, thereby improving the interpretability of orange disease detection.

4.7.2 Explainability Analysis Using LIME

LIME analysis further supports the SHAP findings by providing instance-level interpretability. As shown in Fig. 9, the selected sample is predicted as greening with a probability of 1.00, while the probabilities for other classes are negligible.

²<https://www.aphis.usda.gov/plant-pests-diseases/citrus-diseases>.



Figure 9: Explainability analysis using LIME.

The local explanation shows that `amt_non_green`, `homogeneity`, `contrast`, `dissimilarity`, and `blue_skew` are the most influential features for the greening prediction. This pattern is biologically meaningful because citrus greening commonly causes poor and uneven fruit coloration, misshapen fruit and fruit that may remain partially green³. Therefore, the strong contribution of `amt_non_green` reflects abnormal greenish coloration, while `homogeneity`, `contrast`, and `dissimilarity` capture irregular color distribution and texture variation within the diseased ROI. Overall, the agreement between SHAP and LIME confirms that the model relies on disease-relevant color and texture features, improving its trustworthiness and interpretability.

4.8 Ablation Study

To assess the contribution of each major component, an ablation analysis was conducted using the component-wise experimental results. Three feature vectors were used to evaluate the effect of the proposed HMSFO feature selection strategy. As displayed in Table 3, Feature Vector 3 outperformed the other two with Random Forest obtaining the highest accuracy of 99.57%, justifying the effectiveness of the optimized feature representation.

Second, the impact of ASC-GTO was assessed by comparing it with classical GTO and PSO. The results in Table 4 indicate that ASC-GTO boosts the accuracy of the Random Forest classifier from 95.73% to 99.57%, highlighting its effectiveness in enhancing hyperparameter optimization and model stability.

Finally, the results for performance and computational complexity in Fig. 5 are used to assess the contribution of ROI extraction. The results indicate that the proposed ROI-based preprocessing method enhances the classification accuracy and decreases training time, inference time, model size, and overall computational cost. Overall, the ablation results confirm that HMSFO, ASC-GTO and ROI extraction each contribute to the accuracy, stability and efficiency of the proposed framework.

4.9 Comparison with Related Work

This research examines a range of methods previously proposed for early detection of orange disease. A systematic comparison with existing approaches is shown in Table 6, highlighting the strengths of our proposed model in terms of reliable recognition of diseases, improved interpretability and low computational overhead.

³<https://crec.ifas.ufl.edu/research/citrus-production/disease-identification/citrus-greening-huanglongbing/>.

Table 6: Comparison with existing studies.

Ref	Context	ROI Extraction	Feature Selection	Classifier	Accuracy (%)	XAI Used
[36]	Orange Ripeness classification and black spot detection	No	No	Hybrid ViT-CapsNet	96.12	No
[35]	Orange disease detection	No	No	MobileNetV2	95	No
[14]	Citrus fruit disease detection	No	Yes (MCF feature fusion)	DS-MENet	95.02	No
[13]	Orange disease detection	Yes (color segmentation)	No	CNN	97	No
[37]	Orange disease detection	No	No	Res-Inception	98.93	Yes
Proposed Framework	Orange disease detection	Yes (k-means clustering)	Yes (HMSFO)	Random Forest	99.57	Yes

5 Conclusion and Future Work

This study introduced a lightweight and explainable machine learning model for multi-class orange disease detection. The framework includes CLAHE-based image enhancement, ROI extraction using K-means, texture and color feature extraction, hierarchical feature selection using HMSFO, and adaptive hyperparameter optimization using ASC-GTO. The experimental results showed that the proposed method achieved a high accuracy of 99.57% and reduced the training time, inference time, parameter count, and model size compared with the raw-image-based models. Furthermore, SHAP and LIME analyses added value to the model's interpretability by highlighting the most important features contributing to the predictions. Overall, the proposed framework offers an accurate, efficient and interpretable solution for early orange disease diagnosis with a strong potential for future deployment in edge-based precision agriculture systems.

While CLAHE-based enhancement, ROI extraction, and 5-fold cross-validation were employed for enhancing robustness and generalizability, these steps cannot fully guarantee the performance under real-world conditions with occlusion, complex background, weather variation, and uncontrolled image acquisition. Future work will validate the proposed framework using larger, more diverse, and real-field agricultural datasets. Moreover, future work will explore deployment and benchmarking on edge/mobile devices to evaluate hardware-specific inference latency, memory usage, power consumption, and real-time performance.

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Availability of Data and Materials: The implementation code for the proposed model is publicly available at the following GitHub repository: [Data](#).

Ethics Approval: Not applicable.

Conflicts of Interest: The authors declare no conflicts of interest.

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