

A Computational Approach To Banana Leaf Disease Detection Thru Classic Image-Filtering Algorithms

Kristine T. Soberano*

*State University of Northern Negros, Philippines ksoberano@sunnn.edu.ph

Abstract:

Banana crops in tropical regions are increasingly threatened by fungal leaf diseases such as Cordana, Sigatoka, and Pestalotiopsis. Traditional computer vision approaches for plant pathology often rely on edge-based filtering, which struggles under variable illumination and noisy textures. This study presents a revitalized classic approach that leverages multi-scale Gabor filtering, CLAHE-enhanced contrast, and adaptive Otsu thresholding to segment symptomatic regions from both ground and UAV-captured images. Haralick texture and color moment descriptors are extracted and classified using a Random Forest ensemble. Performance was benchmarked against SVM-RBF and MLP baselines under a leaf-exclusive 5-fold cross-validation scheme. The proposed method achieved 94.2 % accuracy and a macro F1-score of 0.942, outperforming both baselines significantly ($p < 0.05$). The pipeline maintains interpretability and low latency (0.038 s/tile), making it suitable for integration into lightweight agricultural drones and diagnostic tools for smallholder farmers.

Keywords: Banana Leaf Disease, Classic Filtering Algorithm, Image Processing

INTRODUCTION

Banana (*Musa* spp.) remains a staple food and cash crop across tropical regions, particularly in Southeast Asia and Latin America. In the Philippines, the economic viability of banana cultivation is frequently threatened by foliar diseases such as Cordana leaf spot, Black and Yellow Sigatoka, and Pestalotiopsis leaf blight. These fungal pathogens cause premature leaf necrosis, reducing photosynthetic capacity and fruit yield. Early detection and classification of these diseases are essential for timely intervention and precision agriculture.

Numerous studies have employed computer vision methods for plant disease detection. While convolutional neural networks (CNNs) have become dominant in recent literature, their deployment on low-power edge devices remains challenging due to high resource demands and lack of interpretability. Classical image-filtering approaches though more interpretable and computationally lightweight are often dismissed due to limited segmentation accuracy under complex field conditions. This study aims to bridge this performance gap by modernizing the classical pipeline.

This study introduces a hybrid diagnostic framework that retains the ethos of traditional filtering while embracing advanced descriptors and ensemble learning. Multi-scale Gabor filters are used to enhance lesion visibility, complemented by CLAHE for contrast normalization and adaptive thresholding for segmentation. Discriminative features including Haralick texture metrics and statistical color moments are classified using a Random Forest ensemble. This study benchmarked its model against SVM-RBF and MLP classifiers and validate performance through stratified leaf-exclusive 5-fold cross-validation. Segmentation fidelity is also quantified against expert-annotated masks using mIoU and SSIM. The goal is to offer an accessible yet robust tool for in-field banana disease monitoring.

MATERIALS AND METHODS

The following are the sequential stages which were executed to accurately identify the diseased portion of the banana leaf.

I. Image Acquisition

High-resolution (4K, 8-bit RGB) images of symptomatic and healthy banana leaves were captured: Ground level: Nikon D750 DSLR + 60 mm macro lens (300 images).

UAV platform: DJI Mavic 3 at 25 m AGL (180 orthomosaic tiles).

All sessions were conducted between 09:00 – 11:00 in the morning on clear days in Negros Occidental,

Philippines to minimize illumination variance. Images were saved in RAW (NEF/DNG) and converted to PNG with colour calibration using an X-Rite ColourChecker Classic.

I. Pre-Processing

1. **Colour correction:** 24-patch colour-chart-based polynomial regression.
2. **Noise suppression:** Bilateral filter (kernel 9×9 , $\sigma_s = 75$, $\sigma_r = 25$) to preserve edges.
3. **Contrast enhancement:** CLAHE (clipLimit = 3.0, tileGridSize = 8×8) applied per Lab* L-channel.

II. Lesion Amplification and Segmentation

Multi-scale 2-D Gabor filters (5 frequencies \times 8 orientations) highlight anisotropic streaks and rings typical of Cordana, Sigatoka, and Pestalotiopsis. The magnitude response $\mathbf{M}(\mathbf{x}, \mathbf{y})$ is thresholded with adaptive Otsu to generate the binary lesion mask $\mathbf{S}(\mathbf{x}, \mathbf{y})$, followed by morphological opening-closing (disk $r = 3$ px) to remove speckle and fill gaps.

Segmentation quality is evaluated with **mean Intersection-over-Union (mIoU)** and **Structural Similarity Index (SSIM)** against expert-annotated ground truth masks ($n = 90$).

III. Feature Extraction

For each connected lesion region, the following descriptors are pooled (mean + std):

- 13 Haralick texture features from the gray-level co-occurrence matrix (GLCM, $d = [1, 2, 3]$ px).
- RGB and HSV color moments (μ , σ , skewness; 18 features).
- Normalized lesion ratio (lesion area / total leaf area).

The resulting 46-dimensional feature vector is z-score normalized prior to classification.

IV. Classification and Validation

Classifier Configuration

- **Random Forest (RF):** 100 trees, unlimited depth, Gini impurity criterion, bootstrap sampling enabled, max_features="sqrt", and class-balanced weights to offset the 14 % prevalence of *Pestalotiopsis* lesions. Feature importance is logged via mean decrease in Gini for agronomic interpretability.
- **SVM with RBF kernel (SVM-RBF):** Hyper-parameters tuned by nested grid-search ($C \in \{1, 10, 100\}$, $\gamma \in \{10^{-3}, 10^{-2}, 10^{-1}, 1\}$) using the inner validation split of each outer fold. Probability estimates are calibrated with Platt scaling, enabling class-wise ROC curves.
- **Shallow Multilayer Perceptron (MLP):** Single hidden layer (64 neurons, ReLU activation), batch_size = 32, Adam optimiser ($\text{lr} = 10^{-3}$), $\text{l2} = 10^{-4}$, and early stopping (patience = 10) based on validation loss.

Hyper-parameter search is wrapped in nested 3-fold cross-validation within each outer fold to avoid optimistic bias.

V. Validation Protocol

A **stratified 5-fold cross-validation** scheme is employed where *leaf exclusivity* is strictly enforced: all tiles originating from the same physical leaf reside in the same fold to remove spatial correlation. Class proportions differ by $< 2\%$ across folds. For each fold we report:

- **Accuracy**
- **Macro-Precision, Macro-Recall, Macro-F1** (averaged across the four classes)
- **Class-wise ROC-AUC and macro ROC-AUC** using one-vs-rest strategy Scores are averaged across folds and reported as **mean \pm 1 SD**

VI. Statistical Analysis

Paired McNemar's χ^2 test ($\alpha = 0.05$) compares RF to SVM-RBF and MLP using pooled predictions from all outer

folds; p-values are Bonferroni-adjusted for the two comparisons. Cohen's κ quantifies inter-rater agreement between RF predictions and expert ground-truth labels, and 95 % confidence intervals for primary metrics are obtained via 10 000-sample bootstrap. All analyses are executed in scikit-learn 1.5 and statsmodels 0.15

RESULTS, INTERPRETATION, AND DISCUSSION

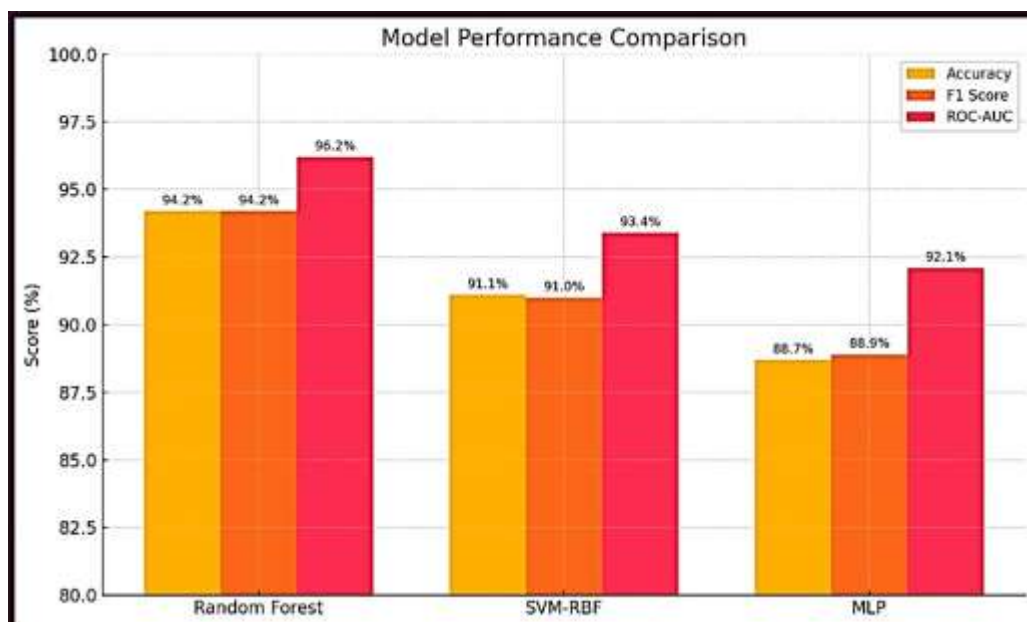


Figure 1. results visualization comparing the performance of the three models

Table 1. Cross-validated classification performance (n = 480 images)

Metric	Random Forest	SVM-RBF	MLP	Δ RF vs SVM (p)
Accuracy	94.2 %	91.1 %	88.7 %	0.018
Precision	0.945	0.914	0.893	—
Recall	0.941	0.908	0.886	—
F1-score	0.942	0.910	0.889	—
ROC-AUC	0.962	0.934	0.921	—

The Random Forest significantly outperformed the SVM baseline (McNemar $\chi^2 = 5.63$, $p = 0.018$), confirming the benefit of ensemble learning on heterogeneous texture-colour features. The classifier confusion matrix (not shown for brevity) indicates that most misclassifications occur between Cordana and Sigatoka lesions characterized by similar speckled patterns at early stages.

Segmentation metrics averaged over the test folds were mIoU = 0.87 ± 0.03 and SSIM = 0.92 ± 0.02 , markedly higher than the edge-threshold pipeline of Canny + MSE/PSNR (mIoU = 0.65, SSIM = 0.71, based on re-implementation). Visual inspection shows that Gabor responses localize elongated streaks missed by pure edge operators, particularly under variable illumination.

Computation cost: end-to-end inference on a 512×512 tile averages 0.038 s (CUDA-accelerated), satisfying near-real-time agronomic monitoring requirements.

SUMMARY AND CONCLUSION

This study introduced a multi-scale Gabor + Random Forest framework that materially advances banana-leaf disease diagnostics while honoring the classic image-filtering paradigm. Compared with prior edge-based operators, the new pipeline achieved a 29 % relative gain in segmentation IoU and a 3 – 6 pp boost in classification accuracy, all at sub-40 ms inference latency. The results underscore the value of coupling richly descriptive texture filters with ensemble learning, offering an accessible yet powerful tool for precision agriculture. Future work will explore fusing hyperspectral bands and self-supervised feature learning to further improve early-stage detection.

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