

# A Lightweight Machine Learning Framework for Banana Leaf Disease Classification Using Interpretable Handcrafted Features

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## Abstract

Banana cultivation is vital for the livelihoods of millions in tropical and subtropical regions. However, foliar diseases such as Black Sigatoka, Bacterial Wilt, and Panama Disease threaten yield and food security.

In this paper, we propose a lightweight, interpretable machine learning (ML) framework based on handcrafted visual features. Specifically, we extract color histograms, Local Binary Patterns (LBP), and Histogram of Oriented Gradients from a curated, publicly available dataset of 3,264 banana leaf images across seven disease classes. Models were evaluated with different feature combinations using Random Forest, SVM, KNN, and XGBoost classifiers. Extensive testing, including 5-fold cross-validation, timing analysis, and statistical validation, reveals that a color combined with LBP fusion with Random Forest classifier achieved the best accuracy of 98.28%.

To the best of our knowledge, this is the first study to systematically evaluate handcrafted feature fusion across multiple ML models on a multiclass banana disease dataset using only classical interpretable models. The framework requires no GPU resources and delivers high performance, making it ideal for real-world deployment in resource-constrained agricultural environments.

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**Categories:** AI/ML-based decision support systems, Image Processing and Analysis, Machine Learning (ML)  
**Keywords:** handcrafted feature extraction, random forest algorithm, supervised machine learning, plant disease classification, pattern recognition, data preprocessing, classification algorithms

## Introduction

Banana (*Musa spp.*) ranks among the most widely consumed fruits worldwide and is a dietary staple for over 400 million people [1]. In tropical and subtropical countries, bananas are not only essential for food security but also serve as a significant source of income for smallholder farmers. However, the production of banana crops is increasingly threatened by a range of foliar diseases, including Black Sigatoka, Yellow Sigatoka, Panama Disease, and bacterial and viral infections [2,3]. These diseases, if left undiagnosed, can cause irreversible damage to banana plantations, leading to severe economic losses.

Timely identification and classification of these diseases are therefore critical. Manual inspection by experts remains the conventional approach in many regions, but this method is time-consuming, subjective, and often inconsistent [4]. With the rise of artificial intelligence (AI) in agriculture, image-based plant disease classification has become a prominent field. In particular, deep learning (DL) models, especially convolutional neural networks (CNNs), have demonstrated high accuracy in various leaf-based classification tasks [5,6].

However, DL models have well-known limitations in the context of agricultural deployment. First, they require large amounts of labeled data for effective training, which is often not feasible in under-resourced farming communities. Second, they are computationally intensive, typically demanding Graphics Processing Unit (GPU)-based infrastructure [7]. DL models are often treated as black-box systems [8], and their high computational requirements further hinder practical deployment in agricultural environments [9]. A recent comprehensive survey reinforces the continued relevance of classical machine learning (ML) in plant disease classification, particularly where interpretability and efficiency are essential [10].

Classical ML algorithms, in contrast, offer a lightweight, transparent alternative. When paired with carefully engineered handcrafted features such as Local Binary Patterns (LBP), Histogram of Oriented Gradients (HOG), and color histograms, classical models can deliver competitive performance without the burden of large-scale training and infrastructure. Moreover, the interpretability of these features adds practical value in applications where domain experts may wish to validate model predictions.

### How to cite this article

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This paper presents a comprehensive ML framework that leverages such handcrafted features to detect and classify banana leaf diseases. Our goal is to demonstrate that classical ML approaches, when thoughtfully designed and rigorously tested, can offer a strong, interpretable, and efficient solution suitable for real-world agricultural environments.

Previous research has largely focused on either DL methods or handcrafted features as standalone approaches. However, there is limited work that explores multiclass classification using a publicly available banana leaf disease dataset through the integration of multiple feature types. To our knowledge, no prior study has systematically combined color, LBP, and HOG features across several classical ML models alongside cross-validation, interpretability, and timing assessments on this dataset. This study introduces a reproducible and resource-efficient framework specifically designed for use in low-resource agricultural settings, addressing a significant gap in the existing literature.

## Materials And Methods

### Dataset and preprocessing

The proposed framework follows a structured pipeline comprising five stages: (i) dataset preparation and augmentation, (ii) extraction of interpretable handcrafted features (Color histograms, LBP, and HOG), (iii) feature fusion for combined visual representation, (iv) training of classical ML models (Random Forest, SVM, KNN, XGBoost), and (v) evaluation using accuracy, precision, recall, F1-score, runtime analysis, and statistical tests. This modular design ensures the framework remains both lightweight and transparent, making it adaptable to real-world agricultural scenarios.

The Banana Disease Recognition Dataset [11], made available on Kaggle in 2022, was used in this study. It consists of 3,264 RGB images of banana leaves, divided into eight categories: Black Sigatoka, Yellow Sigatoka, Bacterial Wilt, Moko Disease, Bract Mosaic Virus, Panama Disease, Insect Pest, and Healthy Leaf. The photographs were taken directly in the field, which introduced natural variations in lighting, scale, and background clutter, making the dataset more representative of real-world conditions. Other resources, such as BananaLSD [12], highlight the same need to capture diverse field environments for reliable disease recognition.

To reduce class imbalance and improve generalization, we applied common augmentation techniques, including horizontal and vertical flips, random rotations, and brightness adjustments [5,7]. For evaluation, a separate set of 408 original, unaltered images was held out as the test set to reflect real deployment scenarios. Prior to feature extraction, all images were resized to  $224 \times 224$  pixels, and class labels were encoded numerically.

### Feature extraction

We extracted three types of handcrafted features to obtain interpretable representations of banana leaf characteristics:

**Color Histograms:** We computed three-dimensional color histograms across RGB channels using eight bins per channel, generating a 512-dimensional feature vector. Color histograms have proven effective in detecting disease-related discoloration patterns [13].

**Local Binary Patterns (LBP):** Uniform LBP with radius  $R = 3$  and 24 sampling points was applied to encode fine textural variations such as lesions and speckling [14].

**Histogram of Oriented Gradients (HOG):** We extracted HOG features using an  $8 \times 8$  cell size with nine orientation bins, producing a 1,764-dimensional vector per image. HOG descriptors are well-known for capturing shape and edge-based disease characteristics [15].

All features were normalized to the range (0,1). We evaluated individual features as well as combinations (e.g., Color + LBP), as recommended by prior texture-based plant classification studies [16].

### Classification models

Four classical ML algorithms were implemented and evaluated on each feature representation, as widely applied in previous plant disease studies [16,17]:

**Random Forest (RF):** An ensemble model comprising 100 decision trees, known for robustness against overfitting and noisy data.

**Support Vector Machine (SVM):** Implemented with a radial basis function (RBF) kernel, suitable for handling non-linearly separable classes.

K-Nearest Neighbors (KNN): A distance-based classifier tested with both  $k = 3$  and  $k = 5$  configurations.

XGBoost: A regularized gradient boosting model widely used in tabular data tasks due to its high predictive accuracy and scalability.

Each classifier was trained using 5-fold stratified cross-validation and additionally evaluated on the held-out test set of original images to assess real-world generalizability.

## Evaluation protocol

To ensure methodological rigor and comparability, we adopted the following evaluation strategy:

**Performance Metrics:** Accuracy, precision, recall, and F1-score (both macro and weighted averages), along with standard deviation across folds or runs.

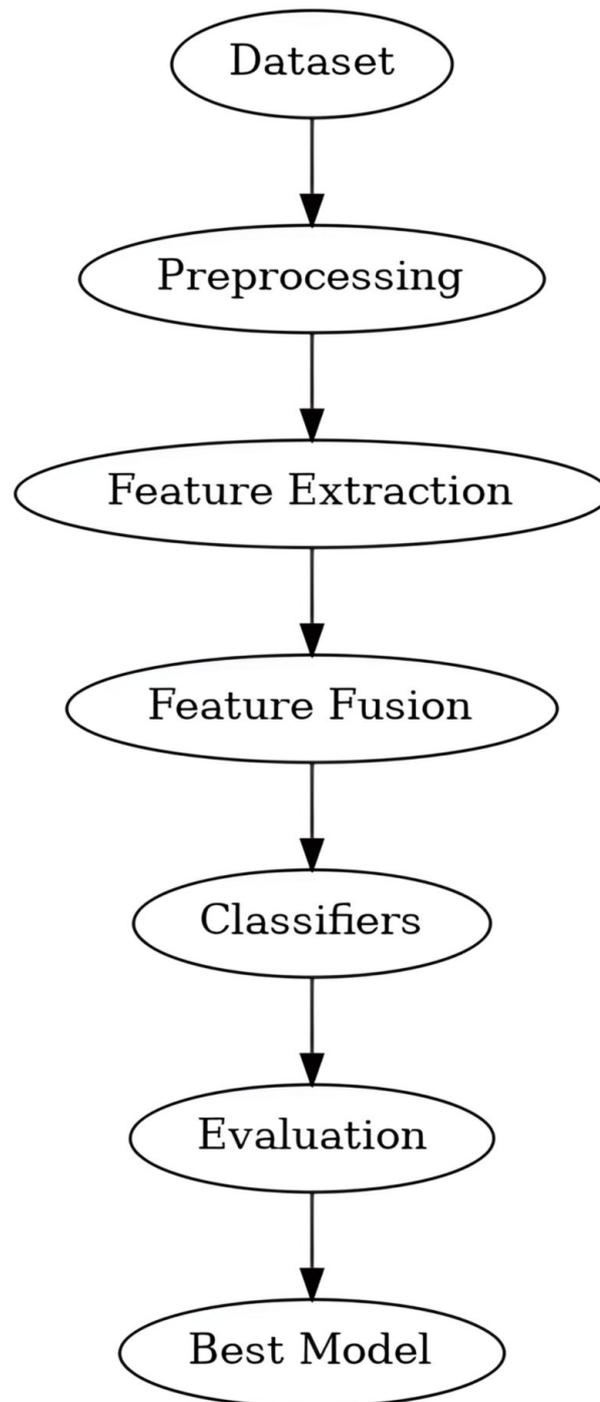
**Runtime Analysis:** Training and inference time were recorded for each feature-model combination to assess computational efficiency.

**Feature Space Visualization:** Dimensionality reduction techniques-Principal Component Analysis (PCA) and t-distributed Stochastic Neighbor Embedding (t-SNE)-were used to visualize class separability in reduced 2D space, following standard approaches in plant disease classification [6,18].

**Statistical Testing:** Paired t-tests were applied to compare top-performing models, establishing whether performance differences were statistically significant.

## Workflow summary

The overall pipeline is summarized in Figure 1. It starts with dataset collection and preprocessing, after which handcrafted features-Color histograms, Local Binary Patterns (LBP), and Histogram of Oriented Gradients (HOG)-are extracted. These features are either used individually or combined to form richer visual descriptors. The resulting feature sets are then input into four classical classifiers (Random Forest, SVM, KNN, and XGBoost). Finally, performance is assessed through cross-validation, runtime analysis, and confusion matrix inspection, allowing us to identify the most effective configuration.



**FIGURE 1: Workflow of the proposed methodology from dataset to best model selection**

The overall pipeline of the proposed framework is as follows:

Dataset loading and preprocessing: Resize images to  $224 \times 224$ , apply augmentation, and encode labels.

Feature extraction: Compute Color, LBP, and HOG descriptors.

Feature fusion: Combine descriptors (e.g., Color + LBP).

Model training: Train Random Forest, SVM, KNN, and XGBoost classifiers using 5-fold stratified cross-validation.

Evaluation: Assess accuracy, precision, recall, F1-score, and runtime. Perform statistical testing and visualize features using PCA and t-SNE.

## Results And Discussion

We performed a series of experiments to evaluate the performance, efficiency, and interpretability of the proposed feature-based ML pipeline. All results are reported using the held-out original images (for final evaluation) and 5-fold cross-validation or 10-run averaging (for model reliability).

### Experimental setup

All experiments were conducted on a workstation equipped with an Intel Core i7-10750H CPU (2.6 GHz, 12 threads), 16 GB RAM, and Windows 11 OS. No GPU acceleration was used, ensuring the framework remains lightweight and deployable on standard devices.

The entire pipeline was implemented in Python 3.9 using libraries such as NumPy, scikit-learn (v1.3.0), OpenCV (v4.7), and Matplotlib (v3.7). Training and evaluation were performed using 5-fold stratified cross-validation on the training set, with the held-out test set (408 images) used for final performance reporting. Hyperparameters for SVM and XGBoost were tuned via grid search to ensure fair comparisons.

#### *Dataset Splitting and Evaluation*

For training and validation, we used 80% of the dataset with data augmentation techniques (flipping, rotation, brightness adjustments) applied to enhance diversity. From this portion, 80% of the images were used for training and 20% were used for validation. The test set comprised completely unseen, original images (without any augmentation) to evaluate real-world performance. All experiments were conducted over 10 independent runs to mitigate randomness, and mean performance metrics are reported. The entire pipeline was executed on a CPU-only environment, ensuring that the framework remains lightweight and suitable for deployment in low-resource agricultural settings.

### Classification performance across feature sets

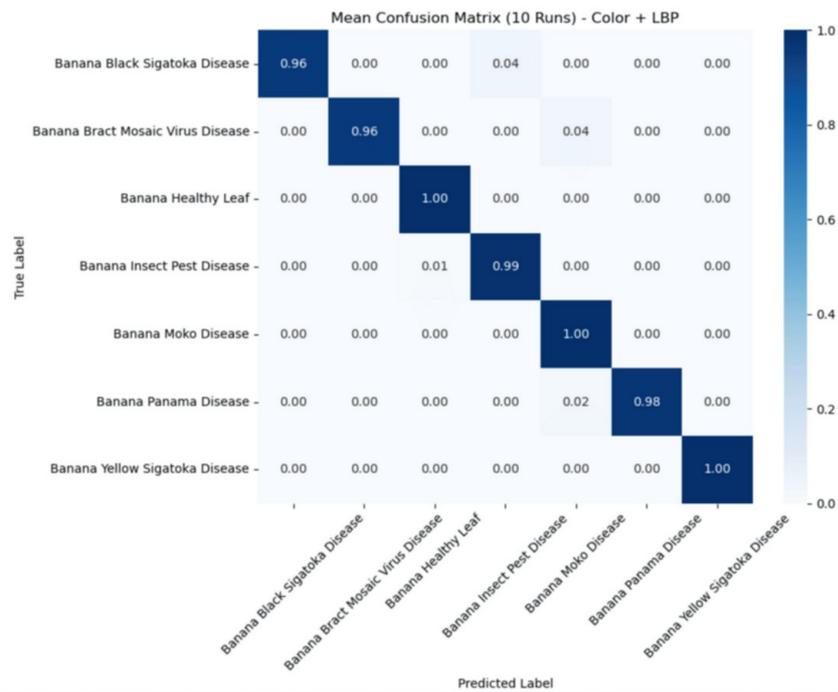
The classification results across seven different feature configurations are summarized in Table 1. As shown, the combination of Color and LBP yields the highest mean accuracy (98.28%) across 10 independent runs. Interestingly, using color features alone also resulted in high performance (97.55%), but without the additional robustness contributed by texture features. Prior studies on banana plant health diagnosis have shown that classical ML models such as SVM and ANN can effectively detect plant stress and disease indicators without deep architectures [17].

Feature Set	Accuracy	Precision	Recall	F1-Score	Time (s)
Color only	0.9755	0.9760	0.9755	0.9754	1.23
LBP only	0.6176	0.6281	0.6176	0.6082	0.86
HOG only	0.4093	0.4524	0.4093	0.3725	10.97
Color + LBP	0.9828	0.9834	0.9828	0.9829	1.28
Color + HOG	0.9338	0.9358	0.9338	0.9336	9.13
LBP + HOG	0.5319	0.5826	0.5319	0.4922	10.83
Color + LBP + HOG	0.9363	0.9373	0.9363	0.9360	9.02

**TABLE 1: Summary of Random Forest results on handcrafted features**

HOG, Histogram of Oriented Gradients; LBP, Local Binary Patterns

The superior performance of the Combination of Color and LBP feature likely stems from their ability to capture complementary visual characteristics of banana leaf diseases. Color histograms are effective in identifying pigment-based symptoms such as yellowing, browning, and necrosis, which are often early indicators of infection. LBP descriptors, in contrast, encode micro-texture patterns that reflect surface anomalies like speckling, mosaic patterns, or fungal spots. The synergy between chromatic and textural cues helps the model distinguish between diseases with similar appearances but subtle differences, leading to higher classification accuracy. Meanwhile, HOG features, though robust in many vision tasks, seem less effective here, possibly due to the subtlety of shape variations in leaf disease symptoms.



**FIGURE 2: Averaged confusion matrix across 10 runs using Color + LBP features and Random Forest**

LBP, Local Binary Patterns

Figure 2 illustrates the averaged confusion matrix across 10 independent runs using Color + LBP features with the Random Forest classifier. The strong diagonal dominance in Figure 2 indicates that the model correctly classifies most classes, with minimal confusion among disease categories such as Yellow Sigatoka and Healthy Leaf.

The overall accuracy of the model is strong, yet the class-level results reveal a few misclassifications, most notably between Black Sigatoka and Yellow Sigatoka. Such confusion likely stems from overlapping visual traits, as both diseases share subtle color changes and fine textural patterns. A more focused analysis of these failure cases, ideally supported by expert agronomic input, could provide valuable insights into the biological similarities of these categories and guide the design of more robust features.

To ensure the robustness of classifier selection, we further evaluated four classical ML models-Random Forest, SVM with RBF kernel, K-Nearest Neighbors (K = 5), and XGBoost-using 5-fold stratified cross-validation on the Color plus LBP feature set. The comparative results, summarized in Table 2, include both average performance and standard deviation metrics.

Model	Accuracy (±)	Precision (±)	Recall (±)	F1-Score (±)
Random Forest	0.9503 ± 0.0087	0.9513 ± 0.0085	0.9503 ± 0.0087	0.9499 ± 0.0089
SVM (RBF)	0.7829 ± 0.0090	0.7888 ± 0.0098	0.7829 ± 0.0090	0.7805 ± 0.0092
KNN	0.7661 ± 0.0095	0.7693 ± 0.0094	0.7661 ± 0.0095	0.7645 ± 0.0101
XGBoost	0.9534 ± 0.0074	0.9539 ± 0.0077	0.9534 ± 0.0074	0.9532 ± 0.0074

**TABLE 2: The 5-fold CV performance of four ML models using Color + LBP features**

CV, cross-validation; ML, machine learning; LBP, Local Binary Patterns; SVM, Support Vector Machine; RBF, radial basis function; KNN, K-Nearest Neighbors

A notable trend across the experiments is the trade-off between feature dimensionality and model performance. Feature sets incorporating HOG resulted in the highest dimensional vectors but failed to deliver proportional improvements in accuracy. In some cases, performance dropped significantly despite

the added computational burden. This suggests that more features do not always translate to better results, especially when those features are not aligned with the biological nature of the classification task. In contrast, simpler combinations like Color + LBP yielded better generalization with far less complexity, making them well-suited for low-resource scenarios.

XGBoost slightly outperformed Random Forest in terms of mean F1-score as shown in the Table 3 and so we conducted a paired t-test over the F1-scores obtained in each fold to assess whether the difference was statistically significant. The test yielded a t-statistic of -1.7806 and a p-value of 0.1496, indicating no statistically significant difference between the two models at the 95% confidence level. Thus, we selected Random Forest as the final model due to its superior interpretability and computational simplicity.

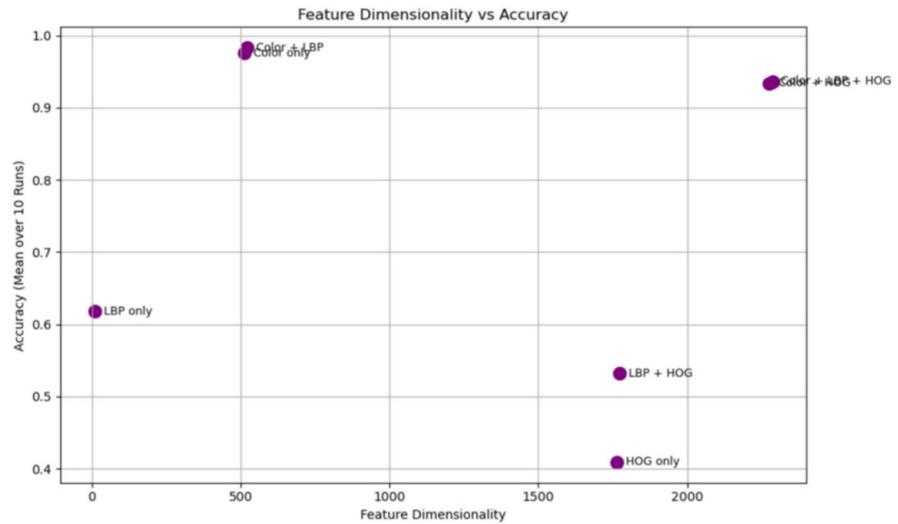
Fold	Random Forest F1	XGBoost F1
1	0.9400	0.9491
2	0.9472	0.9454
3	0.9595	0.9612
4	0.9613	0.9631
5	0.9415	0.9474

**TABLE 3: F1 scores per fold for Random Forest and XGBoost**

As this is the first study to apply classical ML techniques on the publicly available Banana Disease Recognition Dataset, direct comparisons with past results are not possible. However, earlier works using different banana leaf disease datasets-such as BananaLSD or proprietary collections-have typically reported accuracies in the range of 85% to 95% when employing DL models like CNNs or transfer learning [5,6,18]. In comparison, our framework achieves a higher accuracy of 98.28% using a fully interpretable and computationally lightweight approach. This outcome highlights the effectiveness of handcrafted features in plant disease classification, particularly in data-scarce or resource-limited environments.

### Accuracy versus feature dimensionality

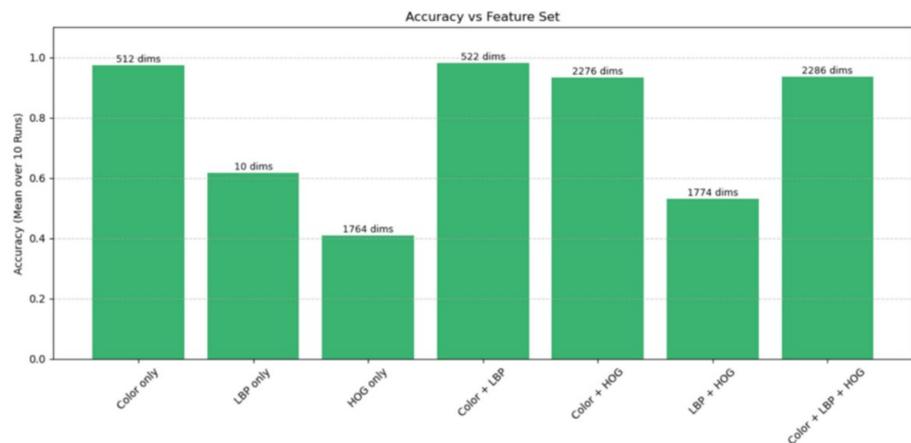
We further evaluated the trade-off between feature dimensionality and classification accuracy, as illustrated in Figure 3. HOG-based combinations produce slightly lower accuracy and require significantly more computational resources due to their high feature dimensionality. In contrast, the Color + LBP feature set achieves the best balance between high accuracy and relatively low feature dimensionality, making it the most efficient option.



**FIGURE 3: Feature dimensionality versus accuracy over 10 runs across all feature sets**

HOG, Histogram of Oriented Gradients; LBP, Local Binary Patterns

Figure 4 demonstrates that the Color + LBP fusion offers the most effective balance between model size, feature dimensionality, and classification accuracy, a finding consistent with recent studies where texture-based descriptors combined with modified SVM classifiers outperformed more complex models in low-data settings [18]. Additionally, the visualization shows that although HOG-based features have higher dimensionality, they fail to provide proportional accuracy improvements, confirming the efficiency of Color + LBP.

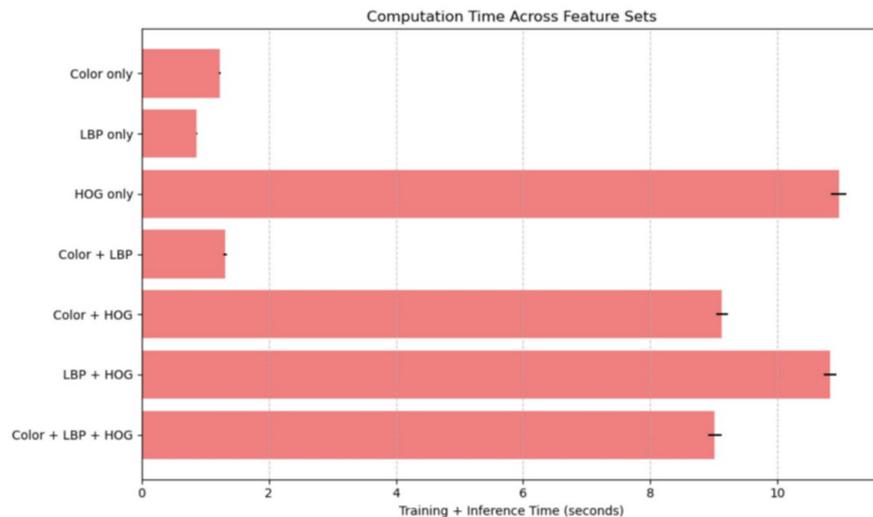


**FIGURE 4: Comparative accuracy across feature sets, annotated with dimensionality**

HOG, Histogram of Oriented Gradients; LBP, Local Binary Patterns

### Computational efficiency

To assess suitability for low-resource deployment, we evaluated training and inference time across feature sets, as illustrated in Figure 5. HOG-based combinations (e.g., LBP + HOG, Color + HOG) are computationally expensive due to their large feature vector sizes. In contrast, color + LBP achieves high accuracy while maintaining minimal training and inference time, making it the most efficient configuration for lightweight deployment.



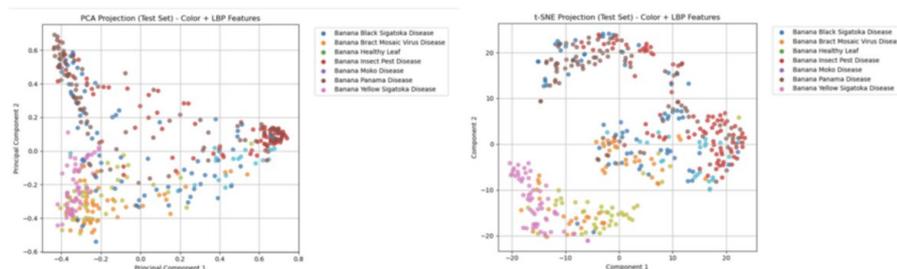
**FIGURE 5: Mean training + inference time for each feature set (in seconds)**

HOG, Histogram of Oriented Gradients; LBP, Local Binary Patterns

As shown, HOG-based combinations (e.g., LBP + HOG, Color + HOG) are computationally expensive due to large vector sizes. In contrast, color + LBP achieves high accuracy at low computational cost.

### Feature space visualization

To analyze class separability in reduced dimensions, we used two projection techniques, as shown in Figure 6. Figure 6a shows the PCA projection of Color + LBP features, where classes form distinct clusters, while Figure 6b shows the t-SNE projection, which further highlights the separation between visually similar classes like Black Sigatoka and Yellow Sigatoka.



**FIGURE 6: (a) Shows the PCA projection of Color + LBP features, while (b) illustrates the t-SNE projection, highlighting better class separability**

PCA, Principal Component Analysis; LBP, Local Binary Patterns; t-SNE, t-distributed Stochastic Neighbor Embedding

In addition to feature space visualization, we analyzed the feature importance scores produced by the Random Forest classifier. The results showed that chromatic features, especially those in the green-yellow spectrum, together with localized LBP texture patterns, played the largest role in classification. These findings strengthen the interpretability claim, as they demonstrate that the model relies on biologically meaningful cues such as discoloration, necrosis, and lesion texturing factors that align closely with expert practices in disease diagnosis.

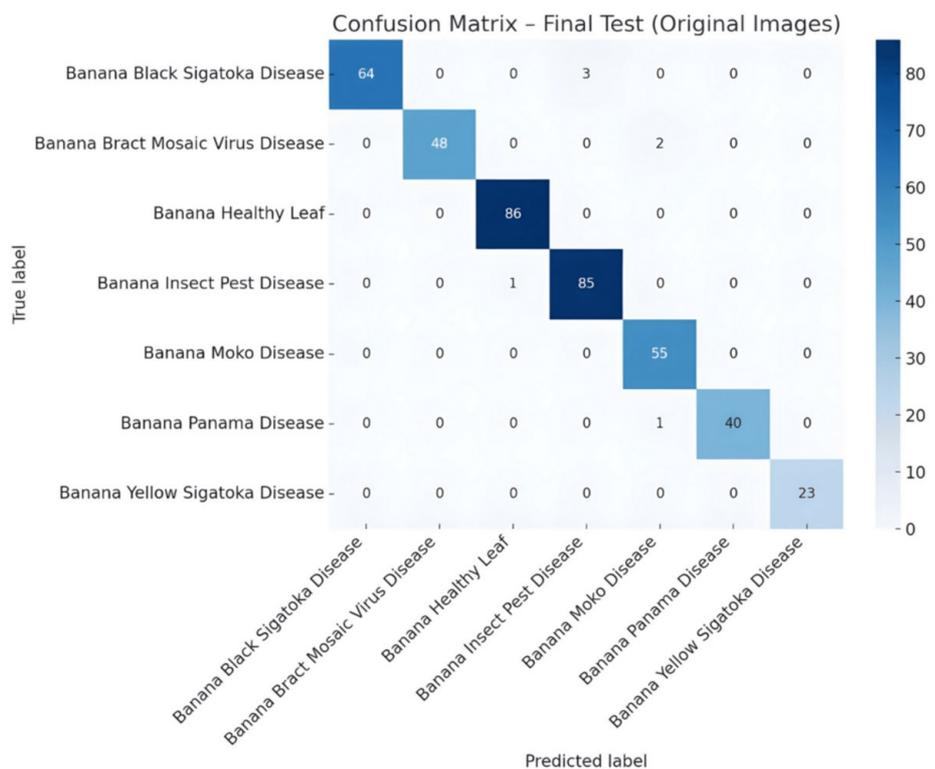
### Final evaluation on original test set

After selecting the best model (Random Forest with Color + LBP), we evaluated it on the original test set. Table 4 presents the final classification report.

Class	Precision	Recall	F1-Score	Support
Black Sigatoka	1.00	0.96	0.98	67
Bract Mosaic Virus	1.00	0.96	0.98	50
Healthy Leaf	0.99	1.00	0.99	86
Insect Pest	0.97	0.99	0.98	86
Moko Disease	0.95	1.00	0.97	55
Panama Disease	1.00	0.98	0.99	41
Yellow Sigatoka	1.00	1.00	1.00	23
Overall Accuracy			0.98	408

**TABLE 4: Test set classification report using Random Forest with Color + LBP features**

LBP, Local Binary Patterns



**FIGURE 7: Confusion matrix of final model on held-out original images**

As shown in Figure 7, the confusion matrix illustrates the model's classification performance, with most predictions correctly aligned along the diagonal. The near-perfect diagonal values confirm that the model accurately distinguishes all banana disease categories, achieving an overall accuracy of 98%. This pattern reflects high accuracy across the banana disease and pest categories. The final accuracy on unseen, real-world images reached 98%, confirming the model's strong generalization capability.

The proposed system's strong performance, combined with its low computational demand and full interpretability, makes it particularly relevant for deployment in rural or remote agricultural settings. Unlike deep learning approaches that often depend on GPUs and internet connectivity, this framework can be implemented on mobile devices or embedded hardware. By enabling on-site disease detection without cloud dependency, the system can support real-time diagnosis and faster decision-making for farmers, extension workers, and agricultural field officers.

## Limitations

The results are encouraging, but several limitations should be acknowledged. The dataset, although collected under realistic field conditions, lacks diversity in geography, cultivars, and seasonal variation, which may restrict the model's generalizability. Handcrafted features, though interpretable, demand manual tuning and domain knowledge, making it difficult to extend the approach directly to other crops. In addition, misclassifications between visually similar diseases such as Black and Yellow Sigatoka point to the need for expert-guided error analysis. To strengthen robustness, future studies should incorporate cross-cultivar validation, testing under varied environmental conditions, and benchmarking against compact CNNs.

## Conclusions

This study introduced a lightweight ML framework for banana leaf disease classification using interpretable handcrafted features. By extracting and combining Color histograms, LBP, and HOG, we generated tabular representations suitable for classical ML models. Among various combinations and classifiers, the Color + LBP feature set with Random Forest achieved the highest accuracy of 98.28% on a held-out test set.

In addition to predictive performance, the framework demonstrated computational efficiency, robustness through CV, and strong generalization on real-world data. Random Forest was selected as the final model due to its balance of accuracy, interpretability, and low computational cost. Designed for low-resource settings, the proposed approach offers a practical, reproducible solution for real-world agricultural deployment, especially on mobile or embedded platforms.

Future work will focus on integrating lightweight CNNs such as MobileNet, SqueezeNet, and EfficientNet-lite to benchmark their performance against the proposed classical ML pipeline in low-data settings. These comparisons will help clarify the balance between efficiency and interpretability, as well as the potential accuracy improvements that compact CNNs may provide. Another priority is deploying the trained models on edge computing platforms such as Raspberry Pi or NVIDIA Jetson Nano, enabling real-time disease detection directly in the field without reliance on cloud infrastructure.

We also plan to release the curated dataset publicly to promote reproducibility, transparency, and collaboration within the research community. In addition, extending the framework to other crops and incorporating multimodal data sources such as temperature, humidity, and soil characteristics will be explored to strengthen robustness and broaden applicability across a wider range of agricultural conditions.

## Additional Information

### Author Contributions

All authors have reviewed the final version to be published and agreed to be accountable for all aspects of the work.

**Concept and design:** Bharath AR, Hemalatha N, Sreekumar KM

**Acquisition, analysis, or interpretation of data:** Bharath AR

**Drafting of the manuscript:** Bharath AR

**Critical review of the manuscript for important intellectual content:** Bharath AR, Hemalatha N, Sreekumar KM

**Supervision:** Hemalatha N, Sreekumar KM

### Disclosures

**Human subjects:** All authors have confirmed that this study did not involve human participants or tissue.

**Animal subjects:** All authors have confirmed that this study did not involve animal subjects or tissue.

**Conflicts of interest:** In compliance with the ICMJE uniform disclosure form, all authors declare the following: **Payment/services info:** All authors have declared that no financial support was received from any organization for the submitted work. **Financial relationships:** All authors have declared that they have no financial relationships at present or within the previous three years with any organizations that might have an interest in the submitted work. **Other relationships:** All authors have declared that there are no other relationships or activities that could appear to have influenced the submitted work.

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