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Research Article

Optimized Machine Learning Framework for Detection of Banana Leaf Disease

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ABSTRACT

Introduction: Banana plants are prone to various diseases which significantly impact yield and agricultural productivity. Leaf diseases of banana such as Cordana and Sigatoka significantly affect global banana production, making early and accurate detection essential for crop health management. This research proposes an optimized approach based on machine learning for automatic detection and classification of banana leaf disease. The methodology includes image pre-processing, augmentation, RGB color to L*a*b*color space conversion, K-Means segmentation followed by thresholding. This is followed by feature extraction (GLCM, LBP, Hu moments, Color features), PCA-based dimensionality reduction, and finally classification using SVM, KNN, Random Forest, and Gradient Boosted Stacking Ensemble models. The results obtained demonstrate the efficacy of the features after Principal Component Analysis (PCA) reduction, with the Gradient Boosted Stacking Ensemble model achieving the highest accuracy among the different models. The best classification performance was obtained with the Gradient Boosted Stacking Ensemble which achieved an accuracy of 95.53%. The proposed model outperformed other individual models like Random Forest, KNN and SVM which achieved accuracies of 78.45%, 84.71% and 82.22% respectively. Further, performance evaluation using precision, recall, F1-score, ROC curves, AUC and confusion matrices validates the robustness of the proposed ensemble method in classifying healthy and diseased banana leaves. The framework thus developed provides a scalable and reliable solution for automated detection of banana leaf disease which will support early disease management strategies in precision agriculture.

Keywords: Segmentation, Local Binary Pattern, Machine Learning, Stacking Ensemble, Classification.

1. INTRODUCTION

The economy of an agricultural country depends mainly on the agricultural production. Agriculture plays a very important role in sustaining the economy of numerous developing countries, where a large part of the population relies on farming for their livelihood. Among the agricultural products, banana (Musa spp.) is one of the major fruit which is widely cultivated and consumed in a large scale all over the world due to its nutritional value and economic importance [1]. Bananas are cultivated worldwide in the tropical and subtropical regions in more than 130 countries [2]. It significantly contributes to rural development and income generation for farmers. However, banana productivity is frequently threatened by various biotic stresses, particularly fungal foliar diseases such as Cordana leaf spot and Sigatoka [3]. The leaf spot disease Cordana [4] caused by the fungus *Cordana musae*, manifests as brown elliptical lesions that lead to premature leaf necrosis, ultimately reducing photosynthesis and fruit yield. On the other hand, Sigatoka (caused by *Pseudocercospora musae* or *Pseudocercospora fijiensis*) progresses more aggressively, with yellow to dark necrotic streaks that severely damage foliage [5-7].

Timely and accurate disease identification is critical for managing these infections and ensuring optimal crop productivity. However, in most cases, farmers are not aware about disease infection and the level of severity of crop infection. They ultimately rely on advice from experts who are in agricultural research institutes and seek guidance from these advisory experts which are carried out manually. This task consumes a lot of time, requires a huge amount of labour, costlier to implement and are prone to faulty diagnosis. Due to advancements in the field of image processing and machine learning techniques, automated disease detection in leaves as well as plants have become popular in precision agriculture.

Early detection of diseases in crops and accurate disease classification is a major component of precision agriculture [8]. These systems offer scalable, consistent, and real-time monitoring solutions which subsequently helps in early diagnosis [9]. Image segmentation is considered as a crucial component in this whole process. The segmentation process isolates the diseased regions in the image for detailed analysis and extraction of features [10]. Several studies have investigated the use of machine learning techniques to estimate the incidence and severity of diseases in plants. The results obtained has demonstrated robust performance in practical scenarios [11].

This study introduces a hybrid classification framework which integrates transformation of color space from RGB to L*a*b*, K-means segmentation, feature extraction from texture, shape, and color descriptors followed by dimensionality reduction using Principal Component Analysis (PCA). The extracted features are then fed to machine learning classifiers, including SVM, KNN, Random Forest, and a Gradient Boosted Stacking Ensemble to evaluate the classification performance. This integrated methodology ensures that only the most informative and discriminative features are retained, improving both classification accuracy and computational efficiency.

The manuscript has been organized into the following sections: related works for banana disease detection has been summarized in Section 2. A detailed description of the proposed methodology that has been adopted in this study has been described in Section 3. Then, Section 4 presents a discussion on the experimental results along with the key findings of the results obtained. Lastly, Section 5 draws the conclusion and highlights future work that can be enhanced and incorporated with this study.

2. RELATED WORKS

Tuazon et al. [12] developed a portable system for the detection of Sigatoka disease on the leaves of banana. Banana leaf images captured by camera has been used for the research. Processing of these images were done through different methods such as stitching, equalization and then segmentation. This is followed by feature extraction and finally classification by SVM. The model thus designed could achieve an accuracy of 90% in classifying banana leaves as healthy and Sigatoka-infected.

Miguel Dita et al. [13] provided a comprehensive overview on the epidemiology of banana disease called Fusarium wilt in their study. The study further discussed several factors impacting disease intensity, along with the roles of the soil and plant microbiome in the progression of the disease. A review on the influence of biotic and abiotic factors on the level of disease intensity has been presented. The study discusses a framework of practices and their effects on the intensity of disease. These can eventually be used by researchers, organizations involved in plant protection, plant growers and extension workers.

Akshaya Aruraj et al. [14] employed classifiers such as SVM and KNN to detect banana plant diseases (Cordana leaf spot and Black Sigatoka). They utilized Local Binary Patterns (LBP) for texture feature extraction from enhanced images. Evaluated on the Plant Village dataset, their proposed methodology achieved classification accuracies of 89.1% and 90.9% in two different experiments using SVM.

W. Liao et al. [15] introduced an SVM-based machine learning method for early detection of banana disease using hyperspectral remote sensing images acquired from close-range. Using morphological openings and closings, their approach extracted spectral and spatial features from disease infected leaves of banana at the early stage and late developmental stages. Their approach could achieve an average accuracy of approximately 96% in the early stage, 90% for mid-stage, and 92% for late-stage detection using both spectral and morphological information.

Chaudhari & Patil et al. [16] designed an automated approach for identifying banana plant diseases. After resizing the images and L*a*b* color space transformation, their method involved using K-Means Clustering for extraction of texture features, shape and color features from the input images. This again is followed by classification using Support Vector Machine. The proposed work achieved an overall accuracy of 85% in identifying the four diseases: Banana Bacterial Wilt (BBW), Panama disease, Sigatoka and Cucumber Mosaic Virus (CMV).

Selvaraj et al. [17] employed UAV and multispectral (MS) satellite imagery for pixel-based classification of banana in field landscapes. High-resolution images which are UAV-RGB images has been used for object-based banana localization and subsequently the detection of banana disease. Following resizing and preprocessing, they utilized SVM and RF classification methods, achieving high accuracy with fewer errors in detecting banana plants and the major banana diseases. Specifically, their model accurately classified healthy banana and diseased banana plants (BBTD, BXW, healthy cluster of banana, and individual banana plants) with 99.4%, 92.8%, 93.3%, and 90.8% accuracy, respectively. The inherent resistance of SVM and RF to overfitting makes them suitable for complex datasets, although careful parameter tuning is crucial for optimal performance.

Zhang et al. [18] investigated methods for detecting Banana Fusarium Wilt (BFW) by identifying spectral features of infected canopies and developing optimal classification models for different infection stages. They employed supervised learning methods (LR, RF, SVM, BPNN) and the unsupervised approach (ISODATA, HA). Among the supervised approaches, Random Forest (RF) using five multispectral bands emerged as the model which is the most optimal. The model achieved a high overall accuracy of 97.28% with a faster runtime of 22 minutes. Among the unsupervised algorithms, Hotspot Analysis (HA) demonstrated consistently high and balanced overall accuracy exceeding 95%. The study recommended HA for BFW recognition, particularly in late stages of infection, while RF was suggested for early detection to attain slightly higher accuracy.

Bhuiyan et al. [19] designed BananaSqueezeNet, a computationally efficient model for detection of leaf diseases of banana: Cordana, Sigatoka and Pestalotiopsis. The model demonstrated exceptional performance in diagnosing these diseases from the leaf images of banana. The model achieved an accuracy of 96.25%, precision of 96.53%, specificity of 98.75%, recall of 96.25%, F1-score value of 96.17%, and MCC value of 95.13%. Beyond leaf diseases, the capability of BananaSqueezeNet extends to identifying banana fruit and stem diseases as well. Its compact design makes it suitable for resource-constrained devices, although this size reduction inherently leads to a trade-off with representational capacity, potentially impacting classification accuracy.

3. PROPOSED METHODOLOGY

Our proposed methodology for detection of banana leaf diseases consists of the following stages: (a) image acquisition (b) pre-processing of the image (c) segmentation using k-means (d) feature extraction (e) feature reduction and (f) disease classification. Fig. 1 presents the framework of the proposed methodology.

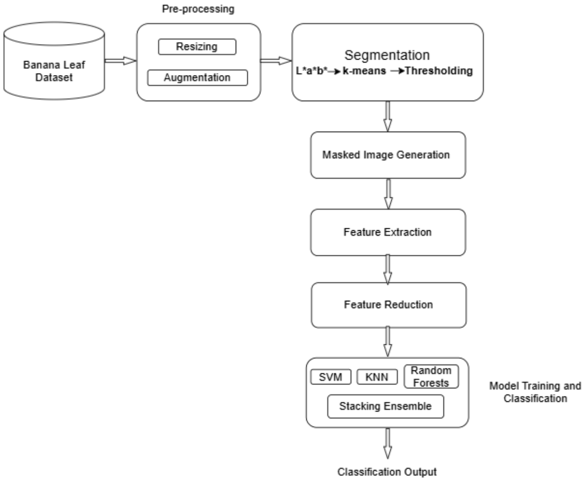


Fig.1: Framework of the proposed methodology

3.1 Dataset and Pre-processing

The experimental dataset that has been employed in our study has been acquired from the Banana Leaf Spot Diseases (BananaLSD) dataset. The dataset consists of labeled images of banana leaves categorized into three classes: Cordana, Healthy, and Sigatoka. For effective learning and to ensure consistency across all stages of the research, each image in the dataset has been resized to a standardized resolution of 256 × 256 pixels. The image resizing step is critical as it harmonizes the input dimensions across varying original image sizes thus ensuring compatibility with downstream processes such as segmentation followed by feature extraction and model training. The image resizing was performed using bilinear interpolation, which computes the pixel intensity at each target location (x,y) based on a weighted average of its nearest four pixels in the original image. The resized image $\boldsymbol{I'(x',y')}$ is calculated using equation (1).

$$I'(x',y') = \sum_{i=0}^{1}\sum_{j=0}^{1} w_{ij} \,.\, I(x_i,y_j) \tag{1}$$

where $I(x_i,y_j)$: original pixel values

w_{ij} : interpolation weights based on the distance from the original pixel location

(x',y') : co-ordinates in the resized image.

This pre-processing step is critical as it reduces the computational complexity and also ensures that the images conform to the input requirements of traditional machine learning models.

3.2 Data Augmentation

In machine learning framework, data augmentation serves as an essential step particularly in image-based classification tasks. Augmentation artificially increases the diversity and volume of training samples without actually collecting new data. This helps prevent overfitting, improves robustness, and enables the model to learn invariant features under transformations such as rotation, brightness, scale etc. Our original dataset (BananaLSD) exhibited a class imbalance across the three categories: Cordana, Healthy, and Sigatoka which could potentially bias the model during training. To mitigate this, a targeted augmentation factor was applied to each class. The final augmented dataset comprises 10,067 images, forming a balanced representation suitable for robust model training. Python libraries like OpenCV, PIL, or imgaug were used to apply different transformations probabilistically to each image.

3.3 L*a*b* Color space conversion and segmentation using K-Means Clustering

The image segmentation step is essential to enhance the isolation of disease-specific region. Each augmented image was first converted from RGB color to the L*a*b* color space. Among the three channels, the ‘a’ channel was extracted for further analysis, as it effectively highlights color shifts from healthy green areas to diseased red/brown patches. Following this, K-Means clustering (K=2) was applied on the extracted ‘a’ channel. The choice of K=2 reflects the binary nature of the problem, separating diseased regions from healthy background. To further refine the region of interest, Otsu’s thresholding was employed on the K-Means segmented output. This step binarized the clustered image, isolating the most relevant regions, typically corresponding to diseased areas. These thresholded binary masks were then multiplied with the original augmented RGB images, resulting in segmented images that preserved only the infected regions for subsequent feature extraction.

3.4 Multiplication with Augmented Images

To preserve structural details and color features present in the original leaf images, the thresholded binary masks were element-wise multiplied with the corresponding RGB augmented images. This step: (i) retained disease-relevant features (ii) masked out irrelevant background noise (iii) ensures that the final image reflected both color texture and spatial structure of the infected area. The resulting disease-isolated images served as the input for feature extraction, ensuring only the most relevant visual patterns are analyzed. Fig. 2 shows sample images of diseased leaves of Cordana and Sigatoka, thresholded image obtained after segmentation and the resulting multiplied images.

3.5 Feature Extraction

Following segmentation, discriminative features were extracted from the images obtained by multiplying the thresholded images with the augmented images highlighting disease-specific regions. To capture textural morphological, and color characteristics of banana leaf, a hybrid feature set was constructed comprising texture, shape and color descriptors. Computation of texture features were performed using: (a) Gray-Level Co-occurrence Matrix (GLCM) to measure the spatial relationships that exists between pixels (b) Local Binary Patterns (LBP) with parameters for capturing local textures and (c) Gabor filters for frequency and orientation-based texture analysis. Healthy and disease affected leaf areas exhibit variations in textures, and the GLCM enables the differentiation between these textures by analyzing the spatial relationships (adjacency) of gray levels.

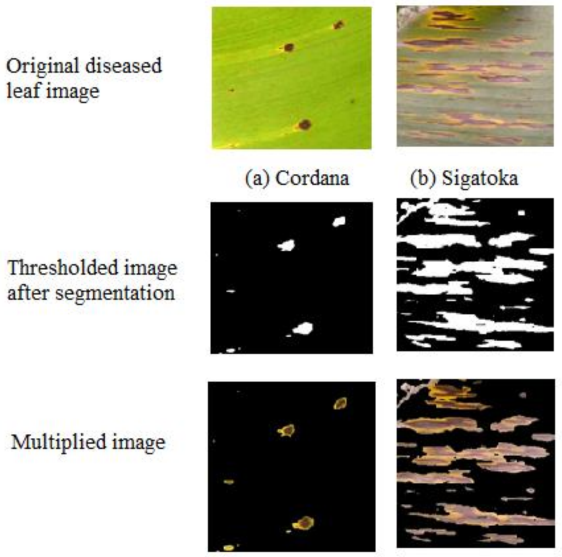


Fig. 2: Sample of diseased image and resulting multiplied image.

In our proposed method, for local binary pattern technique, comparison of the centre pixel and the adjacent pixels were done using equation (2) having results zero or 1.

$$LBP_P^R = \sum_{p=0}^{P-1} s(g_p - g_c).2^p \quad , \quad S(x) = \begin{cases} 1, & x \geq 0 \\ 0, & x < 0 \end{cases} \tag{2}$$

where P is the number of sampling points, R is the radius, g_c is the intensity of center pixel and g_p is the intensity of neighboring pixels, Shape features were derived from: Hu's Moments, applying logarithmic transformation to capture invariant shape properties, and Contour-based analysis, which quantifies the geometry of segmented regions. The first Hu moment is given by equation (3).

$$\phi_1 = \eta_{20} + \eta_{02} \tag{3}$$

where η_{pq} are normalized central moments of the binary contour image. Additionally, color features were derived by computing mean and standard deviation values from each RGB channel. Equation (4) provides the formula for calculating the mean, which is the sum of all elements divided by the number of elements.

$$\text{Mean, } \mu = \frac{1}{N} \sum_{i=1}^{N} x_i \tag{4}$$

where, x_i is the pixel intensity and N is the total number of pixels in the region. The square root of the variance called standard deviation is calculated using equation below. The standard deviation denoted by σ measures the spread of pixel intensities and is defined by equation (5).

$$\text{Standard Deviation, } \sigma = \sqrt{\frac{1}{N} \sum_{i=1}^{N} (x_i - \mu)^2} \tag{5}$$

3.6 Dimensionality Reduction using PCA

The high dimensionality of the extracted features posed challenges for computational efficiency and risked over-fitting. To address this, Principal Component Analysis (PCA) was applied, which resulted in a dimensionality reduction of the images to be used for training and testing the different machine learning models. The PCA reduced features preserved most of the relevant information while improving training speed and model generalization.

3.7 Model Training and Evaluation

The reduced features obtained after employing PCA reduction technique were then used to train and evaluate several traditional machine learning classifiers such as Support Vector Machine (SVM), K Nearest Neighbor (KNN), Random Forests (RF) and Stacking Ensemble (SVM+KNN+Random Forests).

The Support Vector Machine algorithm operates by finding a hyperplane that effectively categorizes data points within an N-dimensional space [20]. This objective makes SVM one of the most powerful methods available for handling both linear and nonlinear classification problems. For a linear SVM, the decision boundary is defined by equation (6).

$$f(x) = u^T x + b \tag{6}$$

where u is the input feature vector, and parameter b is the bias term. The predicted class is determined by the sign of *f(x)*. Here, x is classified as positive class if $f(x) > 0$ and a negative class if $f(x) < 0$.

K-Nearest Neighbors (KNN) classifies a new data point by identifying its K nearest neighbors in the dataset and assigning it to the class that is most prevalent among those K data points. KNN can also use metrics other than Euclidean distance, such as Manhattan distance or Mahalanobis distance [21]. Random Forest (RF) operates by integrating multiple decision trees through ensemble learning. Conceptually, each decision tree within the forest serves as an independent classifier, and consequently, an input sample passed through N trees will yield N individual classification predictions [22].

A stacking ensemble was constructed by combining the predictions of SVM, KNN, and Random Forest as base learners. A Gradient Boosting Classifier was used as the meta-learner to combine the base model predictions and make final predictions. The meta-learner in the stacking architecture aggregates their predictions to produce a more balanced, accurate output. This hybrid ensemble leverages: (a) the diversity of base models for capturing varied data aspects and (b) the boosting strategy in the final estimator to minimize prediction error iteratively. Stacking helps improve performance by combining strengths of different models. This approach reduces overfitting of individual models and improves generalization ultimately leading to more robust classification performance. The final ensemble prediction is defined by equation (7).

$$\hat{y} = \sum_{m=1}^{M} \alpha_m \, . \, h_m(x) \tag{7}$$

where $h_m(x)$: prediction from the m-th base model

α_m: weight assigned to that model

$\hat{y}$: final ensemble prediction.

The different steps for the algorithm of the gradient boosted stacking ensemble approach is as given below.

Algorithm: Gradient Boosted Stacking Ensemble

```
Input: Training dataset $TDS = \{( x_1, y_1),( x_2, y_2),.....,( x_n, y_n)\}$
Output: Trained ensemble classifier $E$

Step 1: Train base-level classifiers
  for c=1 to number of base classifiers $CL$ do
```

```
    Train base classifier $B_c$ on $TDS$
  end for

Step 2: Generate meta-level training data
  for i=1 to n do
    Use each $B_c$to predict $x_i$: , $p_i^1$, $p_i^2$ ….., $p_i^{CL}$

Form meta-instance $z_i$ = ($p_i^1$, $p_i^2$ ….., $p_i^{CL}$, $y_i$)
  end for

Construct meta-dataset  $TDS_{meta}$= { $z_1$, $z_2$,….., $z_n$}

Step 3: Train meta-classifier
  Train Gradient Boosted classifier $E$ on $TDS_{meta}$

Return: Final ensemble classifier $E$
```

4. RESULTS AND DISCUSSION

The calculation of the true positive (TP) value, true negative (TN) value, false positive (FP) and false negative (FN) values were done for each model. Here, the evaluation metrics has been calculated on the 80% training and 20% testing dataset since it represents a balanced trade-off between learning and testing. Each model was evaluated using: Recall, Precision, F1-Score, Accuracy, AUC (Area Under the Curve), ROC(Receiver Operating Characteristics) Curve Analysis and Confusion Matrix. Table I. presents the classification metrics such as precision, recall and F1-score of the different models SVM, KNN, Random Forests and Stacking Ensemble model in the three categories of banana leaf: Cordana, Healthy and Sigatoka.

Table I. EVALUATION REPORT

Model	Class	Precision	Recall	F1-Score
SVM	Cordana	0.76	0.87	0.81
	Healthy	0.92	0.90	0.91
	Sigatoka	0.80	0.70	0.74
KNN	Cordana	0.78	0.90	0.84
	Healthy	0.92	0.93	0.93
	Sigatoka	0.85	0.71	0.77
Random Forests	Cordana	0.74	0.85	0.79
	Healthy	0.86	0.91	0.88
	Sigatoka	0.75	0.59	0.66
Stacked Ensemble	Cordana	0.95	0.95	0.95
	Healthy	0.98	0.97	0.97
	Sigatoka	0.93	0.94	0.94

Precision was calculated as the ratio of number of true positives to the sum of true positives and false positives and is given by equation (8).

$$Precision = \frac{True\ Positive(TP)}{True\ Positive(TP) + False\ Positive(FP)} \tag{8}$$

Recall, as defined by Equation (9), is the ratio of true positives to the sum of true positives and false negatives

$$Recall = \frac{True\ Positive(TP)}{True\ Positive(TP) + False\ Negative(FN)} \tag{9}$$

F1-score was computed using equation (10).

$$F1 - Score = 2 * \frac{Precision * Recall}{Precision + Recall} \tag{10}$$

Overall accuracy represents the general classification performance of each model category and is calculated using Equation (11). The overall accuracy of SVM, KNN, Random Forests and Stacking Ensemble was 82.22%, 84.71%, 78.45% and 95.53% respectively.

$$Accuracy = \frac{TP + TN}{TP + TN + FP + FN} \tag{11}$$

The accuracy results for the different models SVM, KNN, Random Forests and Stacking Ensemble has been presented in the table shown below in Table II.

Table II. Accuracy results

Model	Accuracy (%)
SVM	82.22
KNN	84.71
Random Forests	78.45
Stacking Ensemble	95.53

To better understand the per-class performance of the classification models, bar charts were plotted showing Accuracy, Precision, Recall, and F1-score for each class, Cordana, Healthy, and Sigatoka across four models: SVM, KNN, Random Forest, and Stacking Ensemble in Fig. 3. These visualizations helped assess how well each model distinguishes between the three classes. Notably, the Stacking Ensemble consistently outperformed the individual models, showing higher and more balanced scores across all metrics and classes.

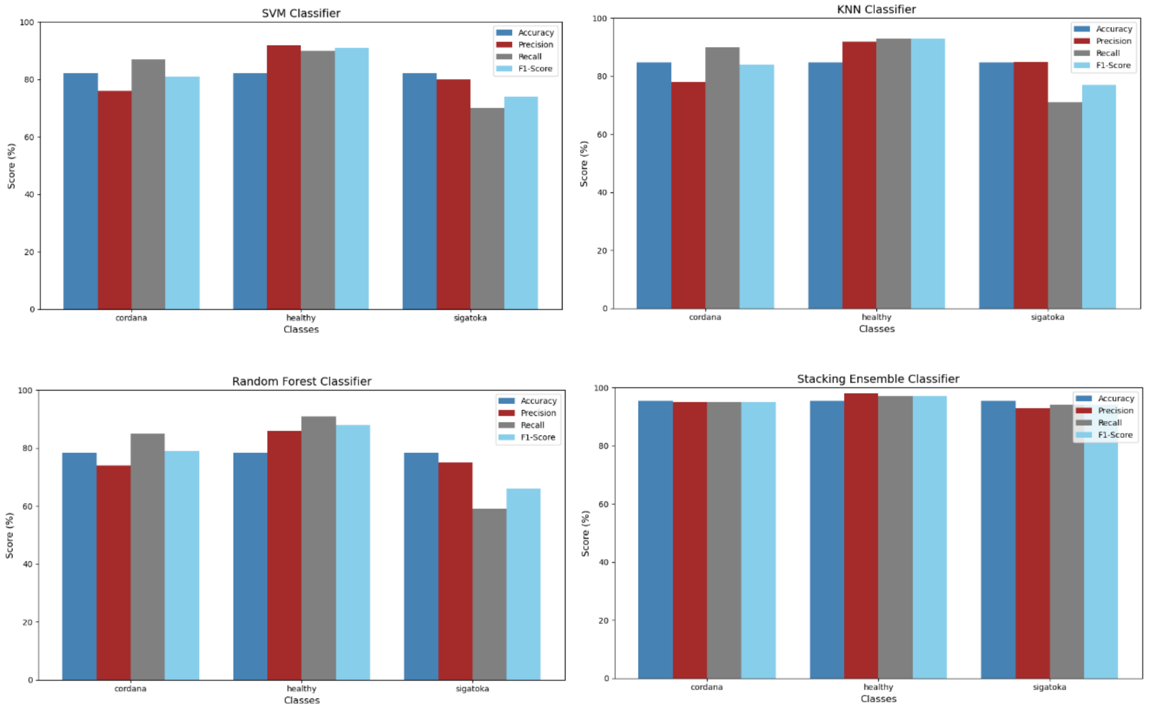
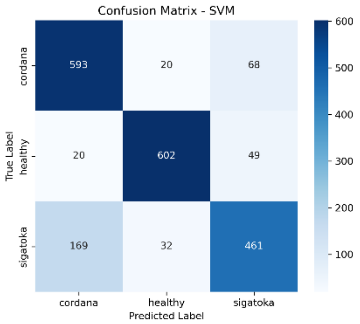


Fig.3: Graphical representation of evaluation metrics for the models.

Fig. 4 represents the Confusion Matrix and ROC Curve of SVM, KNN, Random Forests and Stacking Ensemble Classifiers. For evaluating the classification performance of the proposed models, Confusion matrices and Receiver Operating Characteristic (ROC) curves were analyzed. The confusion matrices reveal class-wise performance by showcasing true positive and misclassified samples for Cordana, Sigatoka, and Healthy leaf classes. Notably, the Stacking Ensemble model demonstrated the highest classification accuracy with minimal misclassification across all classes, especially for Healthy. The ROC curves further reinforced these findings, with Stacking Ensemble achieving near-perfect AUC scores (0.99 for Cordana and Sigatoka, 1.00 for Healthy), indicating excellent model discrimination capability. Comparatively, Random Forest and SVM also showed strong performance with AUC values ranging from 0.90–0.98, while KNN performed competitively with an overall average AUC around 0.96. The results obtained clearly indicates the efficacy of the proposed ensemble model in enhancing the classification among the different classes and accuracy in disease detection in banana leaves.

<table>
<tr><th>Model</th><th>Accuracy %</th><th>Confusion Matrix</th><th>ROC Curve</th></tr>
<tr><td>SVM</td><td>82.22</td><td>


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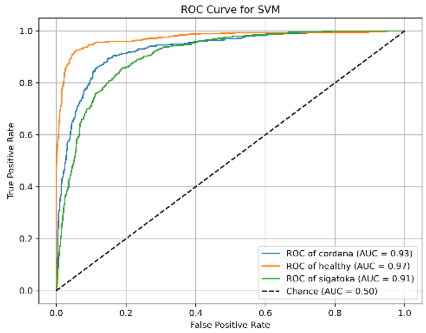
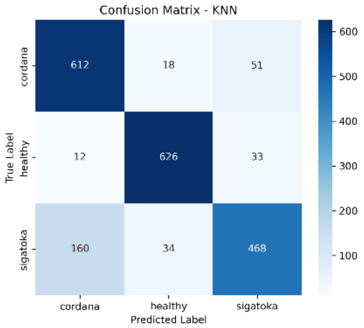


</td></tr>
<tr><td>KNN</td><td>84.71</td><td>


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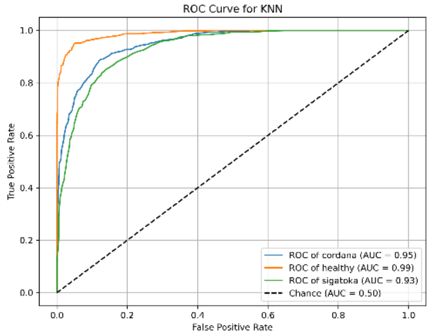
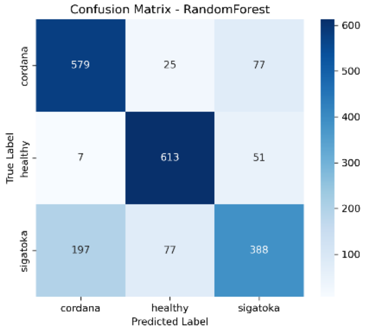


</td></tr>
<tr><td>Random Forests</td><td>78.45</td><td>


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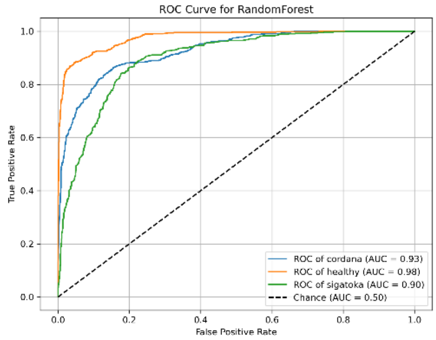

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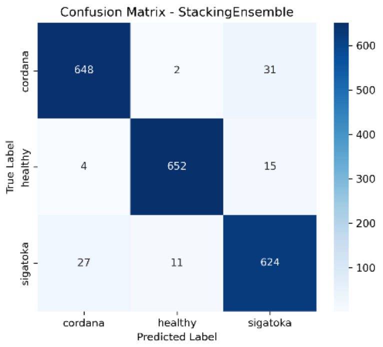
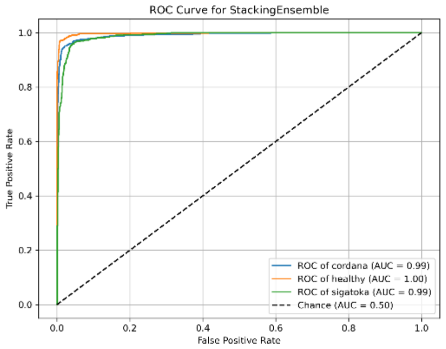
Stacking Ensemble	95.53		

Fig. 4: Confusion Matrix and ROC Curve of SVM, KNN, Random Forests and Stacking Ensemble.

Author	Diseases Detected	Algorithm used	Dataset	Performance
Aruraj et al. [14]	Black Sigatoka, Cordana	Texture features (LBP) + SVM/KNN	Plant Village dataset	89.1% and 90.9% accuracy.
Helmawati, N., & Utami, E. [23]	Sigatoka, Cordana, Pestalotiopsis	CNN	BananaLSD dataset	92.85% accuracy.
Vidhya, N. P., and R. Priya [24]	Leafspot, Sigatoka	KNN,SVM,Alexnet	Real-time dataset	Accuracy of 76.49% for KNN, 84.86% for SVM and 96.73% for Alexnet.
Rajalakshmi et al. [25]	Sigatoka, Cordana, Pestalotiopsis	Custom 8-layer CNN (8C-DCNN)	768 leaf images	98.92% average accuracy
Jiménez et al. [26]	Black Sigatoka, Cordana	ResNet-50, EfficientNet-B0, and VGG-19	900 leaf images (field, Ecuador)	88.90%, 88.33%, and 87.22% accuracy for ResNet50, EfficientNetB0, and VGG19 respectively.
Bhuiyan et al. [19]	Sigatoka, Cordana, Pestalotiopsis	BananaSqueezeNet	937 leaf images (BananaLSD)	96.25% accuracy

Cihan Unal [27]	Sigatoka, Cordana, Pestalotiopsis	DenseNet-201, EfficientNet-b0, and VGG16	BananaLSD Dataset	98.12%, 87.81%, 97.81%, accuracy for DenseNet-201, EfficientNet-b0, and VGG16 respectively
Ravi Kumar Tirandasu and Prasanth Yalla [28]	Sigatoka, Cordana, Pestalotiopsis	hybrid BAT + KNN	937 leaf images	95% accuracy
Rehman et al.[29]	Sigatoka, Cordana, Pestalotiopsis	VGG19 + Passive Aggressive Classifier	1600 images	Accuracy of 99.16% for RGB vision, 98.02% for night vision, 96.05% for infrared vision, and 96.10% for thermal vision
Thomas, D. and David, J.M. [30]	Sigatoka, Cordana, Pestalotiopsis	ACO + CNN	2825 images	98.64 % accuracy
Proposed Methodology	Sigatoka, Cordana	**SVM, KNN, Random Forest, Stacking Ensemble**	BananaLSD Dataset	95.53% for Stacking Ensemble

Table III: Comparison for studies of Sigatoka and Cordana banana leaf diseases.

Table III. presents a relative comparison of a selection of recent leaf-level studies on detection of Sigatoka and Cordana banana leaf diseases. The table highlights the methods adopted by different researchers, dataset used in their research, and the performances achieved. The comparative analysis in the table shows that deep learning models, especially custom CNNs and pre-trained architectures, have achieved higher accuracies in classifying banana leaf diseases like Sigatoka and Cordana. However, these models often suffer from certain limitations such as requirement of large datasets, high computational resources etc. In contrast, this study utilizes traditional machine learning classifiers such as SVM, KNN, Random Forest, and a Gradient Boosted Stacking Ensemble. These classifiers were trained on carefully extracted texture, shape, and color features from segmented banana leaf images. Our proposed approach, the stacking ensemble, achieved an accuracy of 95.53%, which is comparable to several deep learning approaches, while maintaining computational efficiency and model transparency.

5. CONCLUSION AND FUTURE WORK

This research presents a comprehensive traditional machine learning approach for the detection and classification of banana leaf diseases, specifically Sigatoka and Cordana. The methodology employed image segmentation techniques, texture, shape, and color features extraction, followed by feature reduction using Principal Component Analysis (PCA). The PCA reduced features are finally used for training and testing the machine learning models such as SVM, KNN, Random Forests and Gradient Boosted Stacking Ensemble. The Gradient Boosted Stacking Ensemble achieved an accuracy of 95.53% indicating a highly competitive performance compared to several deep learning models. Additionally, the model offers advantages such as interpretability, lower computational cost and ease of deployment. However, the performance of the model may be influenced by several factors such as variation in the image quality, lighting conditions and the generalization of features under diverse environments. To address these challenges, our future work will emphasize and focus on upgrading and expanding the dataset size with samples from real-world environments. With enhanced segmentation techniques and hybrid models integrating traditional and lightweight deep learning models, the performance can be further enhanced. . Furthermore, the development of a mobile or edge-based model will enable the farmers to detect the banana diseases in real time or on- field. This will help in timely intervention in banana farming which eventually will lead to an increase in agricultural productivity.

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