

# Optimization of Mango Leaf Disease Detection Using a Hybrid Machine Learning Approach

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**Abstract**—Mango cultivation is essential in northern Côte d'Ivoire, substantially contributing to the national economy. However, microbial diseases affecting mango leaves represent a significant challenge for farmers. Early detection of these diseases is crucial for effective crop management and plantation protection. Infrastructure constraints limit the ability to detect mango leaf diseases early. To deal with this challenge, a new approach based on artificial intelligence has been developed to detect and classify mango leaf diseases. The study is based on two methodological approaches. Firstly, we use machine learning algorithms, including Random Forests, Support Vector Machines (SVMs), and eXtreme Gradient Boosting (XGBoosting). In parallel, a second approach incorporates Convolutional Neural Networks (CNNs) to extract complex visual features from leaf images. These features are combined with the three machine learning algorithms mentioned above for classification. The results show that the second approach, which combines CNNs with machine learning algorithms, outperforms the first. In particular, the accuracy of the second approach, with CNNs combined with SVMs, stands out, achieving the highest accuracy scores. The performance of the VGG16-SVM, ResNet-SVM, and VGG19-SVM models are evaluated with high precision and accuracy scores, respectively. These results offer promising prospects for the practical application of these techniques in fields such as medical image classification, materials analysis, and other areas where spectroscopy is used as a classification tool.

**Keywords**—mango leaf, machine learning algorithm, deep learning, disease detection and classification, Convolutional Neural Network (CNN), feature extractor

## I. INTRODUCTION

Ensuring food security is a significant challenge, especially for developing countries. Agriculture plays a crucial role in economic development, guaranteeing the subsistence of populations and creating wealth [1, 2]. However, plant diseases threaten global food security, leading to significant yield losses and crop destruction. Early detection of plant diseases is imperative to enable growers to take corrective action and minimize losses. Traditional manual detection methods are often slow, inaccurate, and costly. Against a backdrop of climate change, the growing demand for agricultural experts such as pollinators, agronomists, and pathologists underlines the need for innovative solutions to guarantee food security. Automating the detection of plant diseases from their leaves represents a significant advance [3, 4]. Artificial Intelligence (AI) techniques have enabled the development of automated models offering accurate detection and identification of plant leaf diseases. Deep learning, a technical evolution of machine learning, has

emerged as a practical approach for processing large amounts of data and automatically learning the characteristics of the inputs. Our project focuses on detecting, identifying, and classifying mango leaf diseases.

In this study, we propose two distinct approaches. The first exploits machine learning algorithms to detect mango leaf diseases, capitalizing on their capabilities to achieve high disease detection and classification accuracy. Next, we evaluate the performance of combining Convolutional Neural Networks (CNNs) with machine learning algorithms, comparing them with existing approaches. This comparison highlights the superior efficiency of the CNN algorithm combined with the Support Vector Machine (SVM), outperforming the other approaches studied and those described in the literature. We use a database called MangoLeaf to evaluate and compare the performance of these different approaches. Methods for identifying diseases with more significant potential have interested many researchers.

Our research focuses on five primary areas. Following a literature review in Section II, which includes an in-depth analysis of existing work on the subject and a precise identification of gaps and unresolved issues, we present the material and methods in Section III. Section III presents the database used, the hardware configuration of the experiment, and a clear explanation of the methodological approach adopted. We then present the results and discuss the performance of our system in Section IV. Finally, we end the document with a conclusion in Section V.

## II. LITERATURE REVIEW

Plant diseases are a major threat to agricultural production. They affect the quality and quantity of agricultural production. These diseases sometimes affect the whole plant or, often, parts of it. Organs susceptible to disease include leaves, trunk, fruit, and flowers. Methods of identifying diseases with greater potential have interested many researchers. Nagaraju *et al.* [5] have developed a model based on Deep Learning techniques to detect lesion areas on mango leaves. They use features such as leaf color, venation, petiole condition, and tip shape to diagnose anthracnose disease. The results of their experiment can classify the level of anthracnose disease infection on mango leaves with an accuracy of at least 92%. However, this study was carried out on a small dataset of just 100 images, which may limit the generalizability of the results to other datasets. The study, therefore, considered only a few features for anthracnose detection. It is possible that other features, such as leaf texture,

could improve the accuracy of the model. Pramanik *et al.* [6] conducted a study based on transfer learning with the DenseNet-201, ResNet-50, ResNet-152V2, and Xception algorithms for the cost-effective classification of lemon leaf diseases. The results of their experiments gave an accuracy of 94.34%. However, this work did not evaluate the performance of the models on unsupervised data. This means we do not know how the models would perform on data not marked as having diseases.

To help the plant owner take effective corrective action, Mimi *et al.* [7] investigated computer vision techniques to help plant owners identify their plants automatically and conveniently. This research designs three machine learning systems based on CNNs from images captured by cell phones. Their approach gives a high accuracy of 97.35%, enabling end-users to monitor their plants. Nevertheless, the systems have been trained on images of plants taken under laboratory conditions. The systems may not be as accurate when identifying plants taken under natural conditions. Similarly, the systems were evaluated on a dataset of plants grown in gardens. The systems may not be as accurate when used to identify wild plants.

For intelligent diagnosis of plant diseases, Chakraborty *et al.* [8] have proposed a model based on the DenseNet-121 algorithm, which classifies leaf images from a dataset called "PlantDoc". The results of their experiments gave a classification accuracy of 92.5%. However, the model is not evaluated on an independent dataset. The PlantDoc dataset is used to both train and evaluate the model. This may bias the results, as the model may learn to remember specific images from the dataset and not be able to generalize to new images. The model is not compared with other state-of-the-art models. The article by Chakraborty *et al.* does not compare the DenseNet-121 model with other state-of-the-art models for leaf image classification.

Patil *et al.* [9] focused their study on four main diseases affecting rice cultivation to improve farmers' production. They proposed a method using an Artificial Neural Network (ANN) to detect, classify, and predict the occurrence of rice diseases according to various agrometeorological conditions. An accuracy rate of 92.15% in rice disease prediction was achieved in their experiment. However, their approach only considered four rice diseases. There are many other rice diseases, and the study did not evaluate the method's effectiveness in detecting and classifying these diseases. The study was carried out in a single region. The study's results may not apply to regions with different climatic and environmental conditions.

Mia *et al.* [10] presented the "Neural Network Set Model" for mango leaf disease detection, which helps to detect diseases optimally compared to manual practice. This technique provides for the recognition of mango leaf diseases, such as "Dag disease", "Golmachi", "Moricha disease", and "Shutimold", using machine learning by supervising the symptoms of different leaf types. Images of leaves contaminated by the disease are collected, and training data is generated using the classification technique. The submitted system can classify the analyzed diseases with an average accuracy of 80% and contribute to disease prevention and managing the infected plant with the necessary treatments, thus increasing mango production. However, the study only

considered four mango leaf diseases. There are many other mango leaf diseases, such as anthracnose, cercosporiosis, and rust. The study did not evaluate the model's effectiveness in detecting these diseases. The model may be less effective in detecting mango leaf diseases that are not included in the study.

Prakash *et al.* [11] presented a system that employs the BPNN technique for segmentation purposes. The classification process is carried out using the K-means clustering technique. The proposed backpropagation neural network model solves the difficulty of manual detection and identification of mango leaf disease. The proposed strategy is tested with different clusters and test datasets, creating a mango leaf disease control identification and prediction system with 94% accuracy. However, the dataset used in the study contains only 100 images of mango leaves, which may limit the model's accuracy. A larger dataset would enable the model to learn the different characteristics of mango leaves and could lead to higher classification accuracy. The study did not evaluate the model's effectiveness over a longer period. The model may be less effective at detecting mango leaf diseases over a longer period. For example, the model may be less effective at detecting mango leaf diseases that appear later in the growing season. The study did not evaluate the model's effectiveness in treating other types of mango leaf diseases.

### III. MATERIALS AND METHODS

#### A. Materials

The database used for our study is MangoLeafBD, a public database published by Sawkat Ali *et al.* on the Mendeley website. It can be accessed at <https://data.mendeley.com/datasets/hxsnvwt3r/1>

A set of images of mango leaves divided into eight categories. Each category represents a type of leaf disease: Anthracnose, Bacterial Canker, Cutting Weevil, Die Back, Gall Midge, Healthy, Powdery Mildew, and Sooty Mould.

Similarly, each disease category consists of 500 mango leaves. In summary, the MangoLeafBD database contains 4,000 images of mango leaves in JPG format. The experiments were carried out using the Python programming language (Anaconda Spyder) version 3.8 with the Tensorflow, Scikit-learn, and Keras libraries on a ThinkPad laptop equipped with an Intel(R) Core i5-10700 processor running at 2.90 GHz and 16 GB of RAM.

#### B. Learning Algorithms

The choice of the appropriate learning algorithm [12] is essential for the performance of a prediction model. In the present study, we used machine learning algorithms such as random forest, support vector machine, XGBoost, CNN's VGG16, VGG19, and ResNet50V2 algorithms. Each classification algorithm has advantages and disadvantages, and we have chosen to use them individually and in combination. When the data is insufficient, the training set can use bootstrapping to train various classifiers using the different classification algorithms. If the data is too large to train a single classifier, it can be partitioned according to sample size. The data can be partitioned into subsets with a single classifier for training.

1) *Random Forest (RF)*

The random forest is a supervised learning algorithm used for classification and regression. It combines several decision trees to give more accurate predictions. Random forest remains useful for datasets with categorical or continuous variables and can structure missing data. In the RF algorithm, the dataset is first randomly divided into two parts: in-bag data for training and out-of-bag data to measure the level of learning. 2/3 of the data set is for training data, and 1/3 is for validation data. Subsequently, numerous decision trees are randomly created using “seed samples” from the dataset. Randomly selected predictors at node points determine the branching of each tree. With random forests,  $B$  samples are drawn randomly from the training database with a discount  $z_i, i = 1, \dots, B$  (each sample having  $n$  points).  $B$  (each sample having  $n$  points). For each sample  $i$ , we build a CART tree  $G(x)$  using a slightly modified algorithm: we randomly draw a subset of the attributes ( $q$  among the  $p$  attributes) and choose the best cut from this subset each time a node is to be cut. Regression: aggregation by the mean Random forests improves bagging [13] for CART decision trees to make the trees used more independent (less correlated). They are simple to implement with few parameters but give good results, especially in high dimensions.

$$G(x) = \frac{1}{B} \sum_i^B G_i(x) \quad (1)$$

Ranking: aggregation by vote

$$G(x) = \text{vote Majority}(G_1(x), \dots, G_B(x)) \quad (2)$$

Trees are less correlated because they are learned on sets of attributes that generally overlap by  $q \ll p$  [14].

2) *Support Vector Machine (SVM)*

Support Vector Machine (SVM) remains one of the most popular supervised learning algorithms for classification and regression problems. However, it is mainly adopted for classification problems in machine learning. The algorithm aims to implement the best decision to dissociate the  $n$ -dimensional space into classes to place the future data point in the best category easily. It sets the choice on the extreme points/vectors that help create the hyperplane. These extreme cases are called support vectors. Consequently, the algorithm is called a Support Vector Machine. The SVM algorithm can be deployed for face detection, image classification, text categorization, and more. Classification of leaf images with the SVM model is essential to generating the ideal hyperplane as the decision surface with the highest margin for leaf disease interclasses. Due to inherent separation problems, we present the radial Basis Function Kernel (RBF) and its associated decision components for SVM classification. A nonlinear kernel improves overall SVM performance [14].

$$K(x, x_i) = \exp\left(-\frac{\gamma \|x - x_i\|^2}{2\sigma^2}\right) \quad (3)$$

The RBF kernel, defined by Eq. (3), requires only two variables ( $C$  and  $\gamma$ ) to operate. This makes it mathematically simpler and easier to manipulate than other kernels, which can often involve many parameters. The classification step uses training data to implement SVM with an RBF-based learning pool as the set learning procedure [15].

3) *XGBoost*

XGBoost is a machine-learning algorithm that is an improved model of the Gradient Boost algorithm. It solves common commercial problems using minimal resources [16]. XGBoost is an assembly of decision trees (weak learners) that predict residuals and correct errors in previous decision trees. The particularity of this algorithm lies in the decision tree used. XGBoost is a robust algorithm capable of solving a variety of machine-learning problems. It is known for its accuracy, speed, and flexibility. XGBoost has been successfully used in many fields, including finance, healthcare, marketing, and engineering.

4) *VGG16*

VGG is a convolutional neural network proposed by K. Simonyan and A. Zisserman of Oxford University. It gained notoriety by winning the ILSVRC (ImageNet Large Scale Visual Recognition) competition 2014. The model achieved an accuracy of 92.7% on ImageNet, which is one of the highest scores obtained. It advanced on previous models by proposing convolution kernels of smaller dimensions ( $3 \times 3$ ) in the convolution layers than before [17]. The model was trained over weeks using state-of-the-art graphics cards. VGG16 is a convolutional neural network model used for image recognition. It has only 16 layers composed of weights instead of relying on many hyperparameters. It is considered one of the most powerful vision model architectures. The following figure shows the original structure of this algorithm.

5) *VGG19*

The VGG19 is a deep-learning neural network with 19 connection layers, including 16 convolutions and three fully connected layers. Convolution layers extract features from input images, and fully connected layers classify leaf images according to these features [18, 19]. Also, max-pooling layers will reduce features and avoid over-fitting. It deploys an alternating structure of multiple convolution and non-linear activation layers, which is still more efficient than simple convolution. The layer structure extracts image features more effectively, uses Maxpooling for sub-sampling, and modifies the Linear Unit (ReLU) according to the user’s needs. The sub-sampling layer is mainly used to improve the anti-distortion capability of the image grating [20] while retaining the main characteristics of the sample and reducing the number of parameters. The expression of the subsampling layer is as follows in Eq. (4).

$$X_{P_j}^{(n)} = f(\tau_j^n \text{down}(X_j^{(n-1)}) + b_j^{(n)}) \quad (4)$$

Among them,  $\text{down}(X_j^{(n-1)})$  is the maximum sampling function,  $\tau_j^n$  is the coefficient corresponding to the  $j$ -th feature map of the  $n$ -th layer and the  $n$ -th layer, and  $f(\tau_j^n \text{down}(X_j^{(n-1)}) + b_j^{(n)})$  is the ReLU activation function [21].

6) *ResNet50V2*

ResNet-50 is a deep convolutional neural network trained on over a million image databases. This network can classify images into 1,000 objects, including keyboards, mice, pencils, etc. The network’s depth of 50 levels enables it to learn more complex features from images. The network has an input image of  $224 \times 224$  pixels. ResNet has several variants,

including ResNet-50, ResNet-101, and ResNet-152.

### C. Methods

The methodology used in this study is based on several well-defined steps, providing a solid and rigorous approach to achieving our objectives. We are investigating more advanced techniques for the detection of mango leaf diseases. Here is a breakdown of the process:

#### Step 1: Data pre-processing

The database images were organized and classified into eight folders corresponding to different types of mango leaf disease. Each image was resized to  $150 \times 150$  pixels. We also applied extraction techniques to target specific areas of the leaf in our images. After resizing, the training and test images were converted into arrays, and the values assigned to the pixels in these arrays were adjusted to the interval  $[0, 1]$ .

#### Step 2: Feature extraction

In this step, we use convolutional neural networks to extract features from the input data. This step enables us to highlight patterns and significant information in the data. Next, we divide the data into three sets to evaluate our model's effectiveness on separate datasets and ensure that it can be generalized to new data.

#### Step 3: Learning with cross-validation

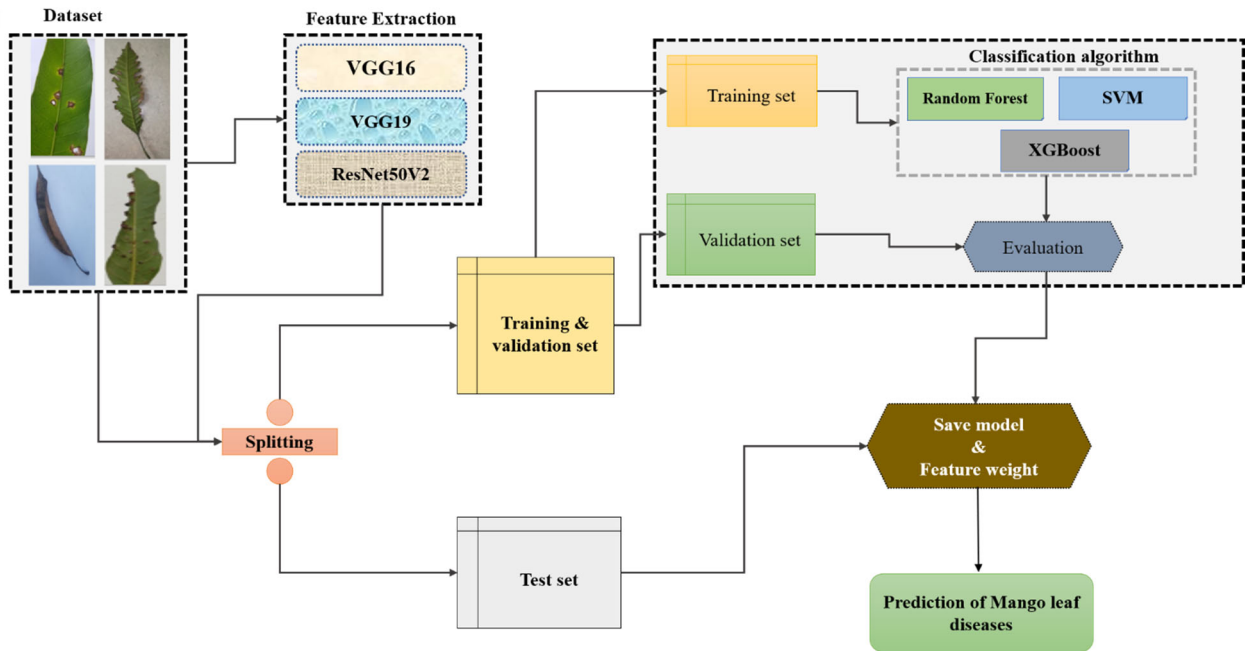


Fig. 1. Presentation of our method.

#### A. Evaluation Metrics

To validate the performance of the pre-trained models in our study, we will use the following metrics:

Accuracy is a performance metric that shows how well the system has classified the data into the correct category or class.

$$\text{Accuracy} = \frac{TP + TN}{TP + FP + TN + FN} \quad (5)$$

where, TP stands for True Positives. These are the individuals the test correctly identified as having the condition. TN, or True Negatives, represents the number of healthy people correctly identified as not having the condition by the test. FP (False Positives): indicates the number of healthy individuals incorrectly identified as positive. FN stands for False

Negatives. These are the sick people the test wrongly identified as healthy.

#### Step 4: Testing and evaluation

The test phase is essential to assess the quality of our model and detect disease. Each algorithm is trained on pre-processed data and extracted features; then, the model is evaluated on an independent test dataset. We use the test dataset, which is independent of the training and validation datasets, to evaluate the actual performance of our model. Following this well-structured methodology, we can conduct an in-depth study of mango leaf disease type detection, pre-processing the data, extracting relevant features, training our model with cross-validation, and rigorously evaluating its performance.

Model selection is made by comparing the cross-validation evaluation values for each model. The cross-validation used in this study implements stratified sampling or stratified k-folds cross-validation. This technique is applied so that the proportion between classes in each fold remains consistent with the original proportion of the dataset.

Fig. 1 describes all the steps involved in our method.

Negatives. These are the sick people the test wrongly identified as healthy.

Precision is the ratio of correctly positive images to the total number of true positive images.

$$\text{Precision} = \frac{TP}{TP + FP} \quad (6)$$

Recall is the ability of a classifier to determine actual positive results. The following formula defines it.

$$\text{Recall} = \frac{TP}{TP + FN} \quad (7)$$

The F1-score is the weighted average of precision and recall. This formula illustrates it.

$$\text{F1 - Score} = 2 \times \frac{\text{Precision} \times \text{Recall}}{\text{Precision} + \text{Recall}} \quad (8)$$

The Matthews Correlation Coefficient (MCC) defines the quality of machine learning classifications.

$$MCC = \frac{TP \times TN - FP \times FN}{\sqrt{(TP+FP)(TP+FN)(TN+FP)(TN+FN)}} \quad (9)$$

An estimator's mean squared error evaluates the average of the squared errors. The mean squared error is the average square difference between the estimated and true values.

$$MSE = \frac{1}{n} \sum_{i=1}^n (Y_i - \hat{Y}_i)^2 \quad (10)$$

where,  $n$  is the number of data points or number of observations.  $Y_i$  represents observed values.  $\hat{Y}_i$  represents predicted values.

#### IV. RESULTS AND DISCUSSIONS

The results of our study are divided into four distinct aspects. Firstly, we present the results of the mango leaf

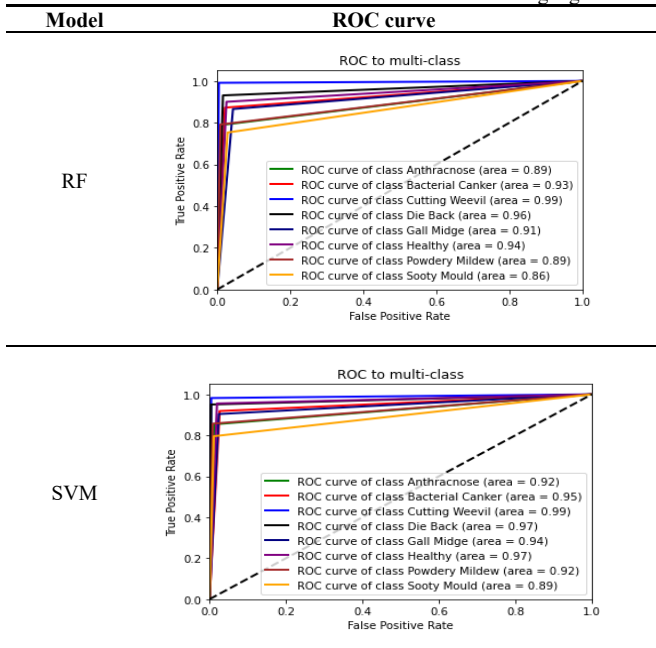
Table 1. Performance evaluation using machine learning algorithms exclusively

Models	Accuracy (%)	Precision (%)	F1-score (%)	Recall (%)	MCC (%)	MSE	Time (s)
Random Forest	87.15	86.72	86.25	86.25	84.33	1.47	0.71
SVM	87.56	88.47	88.00	88.0	86.33	1.00	8.11
XGBoost	90.71	90.56	90.24	90.25	88.88	0.93	24.06

The XGBoost model showed the highest performance of the three, with an accuracy of 90.71%, a precision of 90.56%, and an F1-score of 90.24%. XGBoost is our study's most accurate model for mango leaf disease classification. The SVM model also performs well, with an accuracy of 87.56% and an F1-score of 88.00%. It lies between Random Forest and XGBoost in terms of accuracy. Although less accurate than XGBoost and SVM, Random Forest remains a viable model with an accuracy of 87.15%. However, it has a much shorter execution time than XGBoost. It is important to note that XGBoost's execution time is significantly higher than that of the other model.

Table 2 shows the ROC curve for the Machine Learning algorithms Random Forest, Support Vector Machine, and XGBoost.

Table 2. Presentation of the ROC curve for Machine Learning algorithms



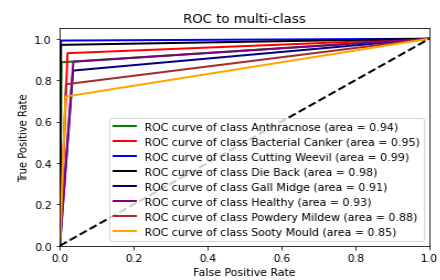
disease classification. We employed diverse Machine Learning algorithms, including Random Forest, SVM, and XGBoost.

In addition, we explored the use of feature extractors based on Convolutional Neural Networks (CNNs). We combined these feature extractors with the Machine above Learning algorithms to enrich our analysis. Specifically, we used the VGG16 model in conjunction with these algorithms. We also employed the VGG19 model to extract features and combined it with the same Machine Learning algorithms.

##### A. Case 1: Single Use of Machine Learning Algorithms

Table 1 shows the performance evaluation results using exclusively Machine Learning algorithms, namely Random Forest, SVM (Support Vector Machine), and XGBoost. These results are essential for understanding the effectiveness of each model in classifying mango leaf diseases.

XGBoost



The accuracy rate of detection and identification of the diseases related to our study by algorithms (Random Forest, SVM, and XGBoost) is as follows.

Table 3 shows the results of the precision rates for each disease from the Random Forest, SVM, and XGBoost algorithms.

Table 3. Accuracy rate of disease diagnosis by Machine Learning algorithms

Mango Leaf disease	RF Precision (%)	SVM Precision (%)	XGBoost Precision (%)
Anthracnose	89	92	94
bacterial canker	93	95%	95
Cutting weevil	99	99	99
Die Back	96	97	98
Gall Midge	91	94	91
Healthy	94	97	93
Powdery mildew	89	92	88
sooty mould	86	89	85

The disease detected with the highest accuracy was Cutting weevil, with 99% for all three algorithms, followed by Die Back, with 98% for XGBoost, 97% for SVM, and 96% for Random Forest. We note that sooty mould is the disease detected with a lower accuracy rate of 85% by the XGBoost.

Fig. 2 shows the performance histogram using exclusively Machine Learning algorithms.



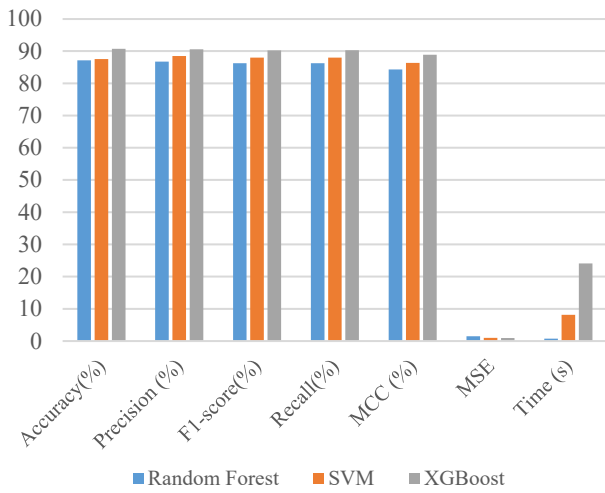


Fig. 2. Histogram of performance using exclusively machine learning algorithms.

Table 4. Performance evaluation using the VGG16 CNN extractor with Machine Learning algorithm

Models	Accuracy (%)	Precision (%)	F1-score (%)	Recall (%)	MCC (%)	MSE	Time (s)
VGG16-RF	91.56	89.73	89.33	89.5	88.07	1.39	0.68
VGG16-SVM	97.75	98.42	98.37	98.37	98.14	0.18	5.97
VGG16-XGBoost	94.31	93.09	92.95	93.00	92.01	0.71	3.31

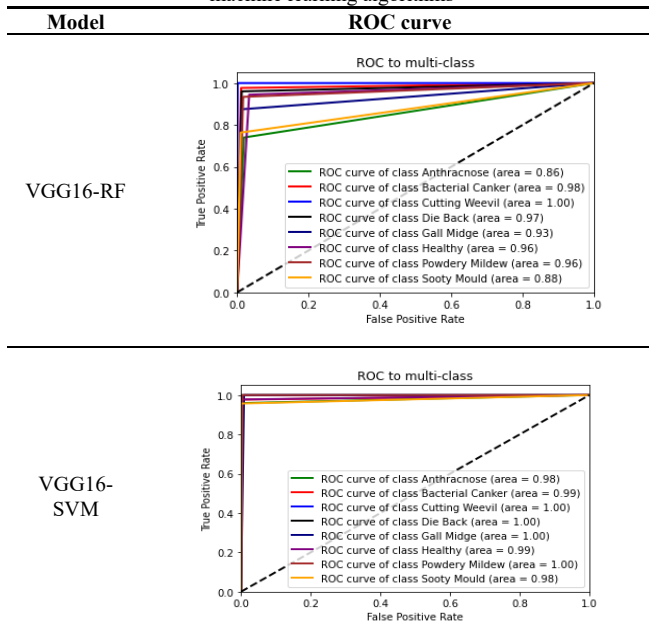
The VGG16-RF offers solid performance, albeit slightly less than other models. However, it offers a relatively short runtime.

It is essential to note that, as shown in Table 1, the use of the VGG16 feature extractor considerably improves performance compared to the exclusive use of Machine Learning algorithms.

The use of the VGG16 feature extractor combined with Machine Learning algorithms, in particular SVM, leads to remarkable performance in the classification of mango leaf diseases.

Table 5 shows the ROC curve for the VGG16 combination with the Machine Learning algorithms.

Table 5. Presentation of the ROC curve of the VGG16 algorithms with machine learning algorithms



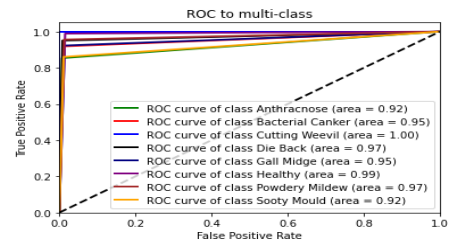
A. Case 2: Using VGG16 with Machine Learning Algorithms

Table 4 shows the results of the performance evaluation using the CNN-based feature extractor with VGG16 model coupled with Machine Learning algorithms. This evaluation is essential and helps us understand how using the VGG16 extractor improves the performance of classification algorithms compared to the exclusive use of these algorithms.

Using the VGG16 feature extractor with the SVM (VGG16-SVM) gives the best performance in terms of accuracy (97.75%), precision (98.42%), F1-score (98.37%), and MCC (98.14%). Combining the VGG16 feature extractor with the SVM effectively classifies mango leaf diseases.

The VGG16-XGBoost model also performs well, with an accuracy of 94.31% and an F1-score of 92.95%. Although this performance is lower than that of the VGG16-SVM, the execution time is shorter, which is an essential factor to consider.

VGG16-XGBoost



The accuracy rate of detection and identification of diseases related to our study with the combination of VGG16 associated with three machine learning algorithms (Random Forest, SVM, and XGBoost) is as follows.

Table 6 shows the results of the precision rates for each disease from the combined methods between VGG16 and the Random Forest, SVM, and XGBoost algorithms. The disease detected with the greatest accuracy was cup weevil, with 100% accuracy for all three methods, followed by dieback, with 100% accuracy for VGG16-SVM and 97% for the other two methods. Powdery mildew was detected 100% by VGG16-SVM and 97% and 96%, respectively, by VGG16-XGBoost and VGG16-RF. However, we note that VGG16-SVM is the method that detects at least 98% for anthracnose, sooty mould, 99% for health disease, bacterial canker and 100% for the rest of the diseases.

Table 6. Accuracy rate of disease diagnosis with VGG16 and the three Machine Learning algorithms

MangoLeaf disease	VGG16-RF Precision (%)	VGG16-SVM Precision (%)	VGG16-XGBoost Precision (%)
Anthracnose	86	98	92
bacterial canker	98	99	95
Cutting weevil	100	100	100
Die Back	97	100	97
Gall Midge	93	100	95
Healthy	96	99	99
Powdery mildew	96	100	97
sooty mould	88	98	92

Fig. 3 shows the performance histogram using the VGG16

feature extractor with Machine Learning algorithms.

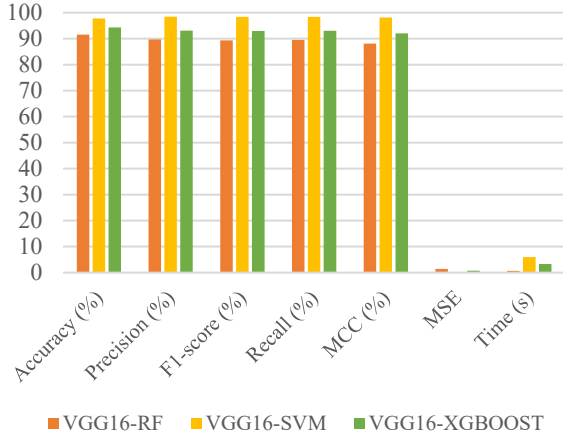


Fig. 3. Histogram of performance using the VGG16 feature extractor with machine learning algorithms.

A. Case 3: Using VGG19 with Machine Learning Algorithms

Table 7 shows the results of a performance evaluation using the CNN extractor of the VGG19 model coupled with Machine Learning algorithms. These results are essential for understanding how using the VGG19 extractor affects the performance of classification algorithms compared to the exclusive use of these algorithms. The VGG19-SVM (Support Vector Machine) model performed best in this context, with an accuracy of 97.12%, 97.51%, and an F1-score of 97.49%. These results indicate that combining the VGG19 extractor with the SVM is particularly effective for classifying mango leaf diseases. The VGG19-RF (Random Forest) model also performs well, with an accuracy of 91.65% and an F1-score of 90.39%. Its accuracy is high, though slightly lower than that of the VGG19-SVM. The VGG19-XGBoost model also performs well, with an accuracy of 93.56% and an F1-score of 93.35%. However, its execution time is significantly longer than that of the other models. The VGG19 feature extractor significantly improves performance compared to the exclusive use of Machine Learning algorithms, as shown in Table 1. It should be noted that using the VGG19 feature extractor combined with Machine Learning algorithms, particularly SVM, leads to outstanding performance in mango leaf disease classification.

Table 7. Performance evaluation using the VGG19 CNN extractor with machine learning algorithms

Models	Accuracy (%)	Precision (%)	F1-score (%)	Recall (%)	MCC (%)	MSE	Time (s)
VGG19-RF	91.65	90.68	90.39	90.50	89.18	1.03	0.56
VGG19-SVM	97.12	97.51	97.49	97.5	97.14	0.19	4.26
VGG19-XGBoost	93.56	93.49	93.35	93.37	92.44	0.81	28.47

Table 8 shows the ROC curve for the VGG19 combination with the Machine Learning algorithms.

Table 9 presents the precision rates for each disease from the combined methods between VGG19 and Random Forest, SVM, and XGBoost algorithms.

Table 8. Presentation of the ROC curve of the VGG19 algorithms with machine learning algorithms

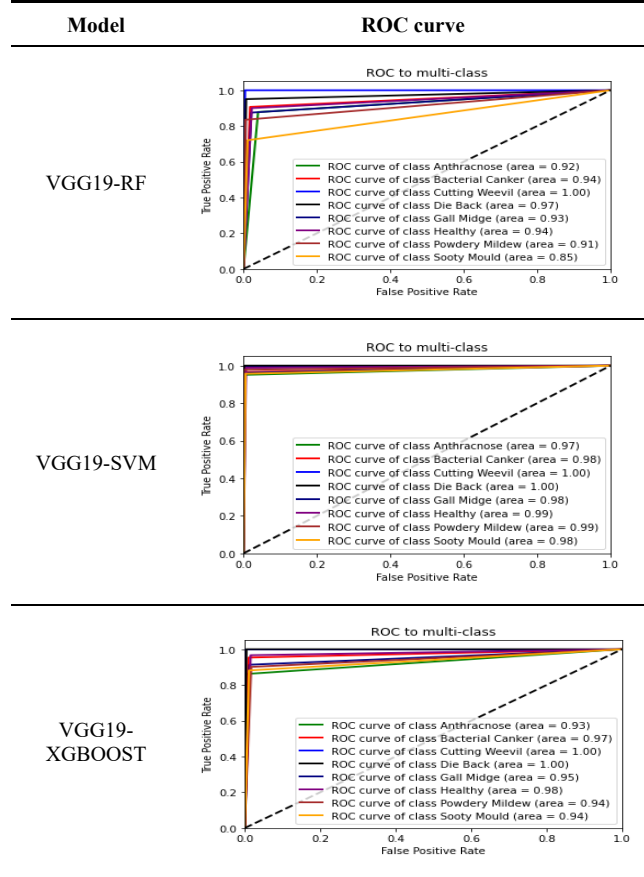


Table 9. Accuracy rate of disease diagnosis with the combination of VGG19 and the three Machine Learning algorithms

MangoLeaf disease	VGG19-RF Precision (%)	VGG19-SVM Precision (%)	VGG19-XGBoost Precision (%)
Anthracnose	92	97	93
bacterial canker	94	98	97
Cutting weevil	100	100	100
Die Back	97	100	100
Gall Midge	93	99	95
Healthy	94	99	98
Powdery mildew	91	99	94
sooty mould	85	98	94

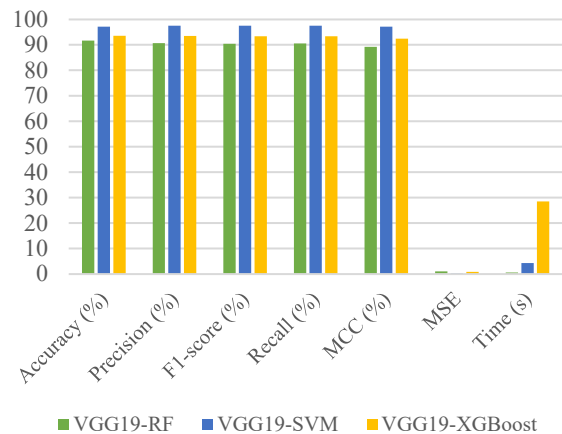


Fig. 4. Histogram of performance using the VGG19 feature extractor with machine learning algorithms.

The disease detected with the highest accuracy was cup weevil, with 100% accuracy for all three methods. It was followed by Die Back, with 100% accuracy for VGG19-SVM, VGG19-XGBoost, and 97% for VGG19-RF. The other diseases were also detected with reasonable accuracy.

However, sooty mould was detected with the lowest accuracy rate, at 85%.

Fig. 4 shows the performance histogram using the VGG19 feature extractor with Machine Learning algorithms.

**B. Case 4: Using ResNet50V2 with Machine Learning Algorithms**

Table 10 shows the performance evaluation results using the ResNet50V2 model feature extractor combined with Machine Learning algorithms.

Table 10. Performance evaluation using the ResNet50V2 feature extractor with Machine Learning algorithms

Models	Accuracy (%)	Precision (%)	F1-score (%)	Recall (%)	MCC (%)	MSE	Time (s)
ResNet50V2-RF	91.28	90.35	90.05	90.12	88.75	1.19	0.51
ResNet50V2-SVM	97.31	97.14	97.12	97.12	96.70	0.33	2.77
ResNet50V2-XGBoost	94.40	94.41	94.24	94.25	93.44	0.55	20.83

These results are essential for understanding how the use of the ResNet50V2 extractor affects the performance of classification algorithms compared to the exclusive use of these algorithms.

The ResNet50V2-SVM (Support Vector Machine) model performed best in this context, with an accuracy of 97.31%, a precision of 97.14%, and an F1-score of 97.12%. These results indicate that combining the ResNet50V2 extractor with the SVM is particularly effective for classifying mango leaf diseases.

The ResNet50V2-XGBoost model also performs well, with an accuracy of 94.40% and an F1-score of 94.24%. However, its execution time is significantly longer than that of the other models.

The ResNet50V2-RF (Random Forest) model shows solid performance, albeit slightly inferior to other models. It offers a relatively short execution time. The inclusion of the ResNet50V2's CNN extractor demonstrably enhanced performance compared to employing solely machine learning algorithms, as Table 1 illustrates. In conclusion, using the ResNet50V2 model's CNN extractor in combination with Machine Learning algorithms, particularly SVM leads to exceptional performance in classifying mango leaf diseases.

Table 11 shows the ROC curve for the ResNet50V2 combination with the Machine Learning algorithms.

Table 12 presents the results of the accuracy rates for each disease based on combined methods between ResNet50V2 and the Random Forest, SVM, and XGBoost algorithms. The disease detected with the highest accuracy is Cutting weevil with 100% for all three methods, followed by Die Back with 100% accuracy for Resnet50V2-SVM, ResNet50V2-XGBoost, and 97% for ResNet50V2-RF. The other diseases are also detected with an attractive accuracy rate. However, it is sooty mould that is detected with the lowest accuracy rate at 85% with ResNet50V2-RF. Overall, ResNet50V2-SVM was the best method for identifying diseases, with a minimum accuracy rate of 97% for Anthracnose, followed by 98% for sooty mould and Gall Midge, then 99% for Healthy and Powdery mildew, and finally 100% for Cutting weevil and Die Back.

Table 11 Presentation of the ROC curve of the ResNet50V2 algorithms with Machine Learning algorithms

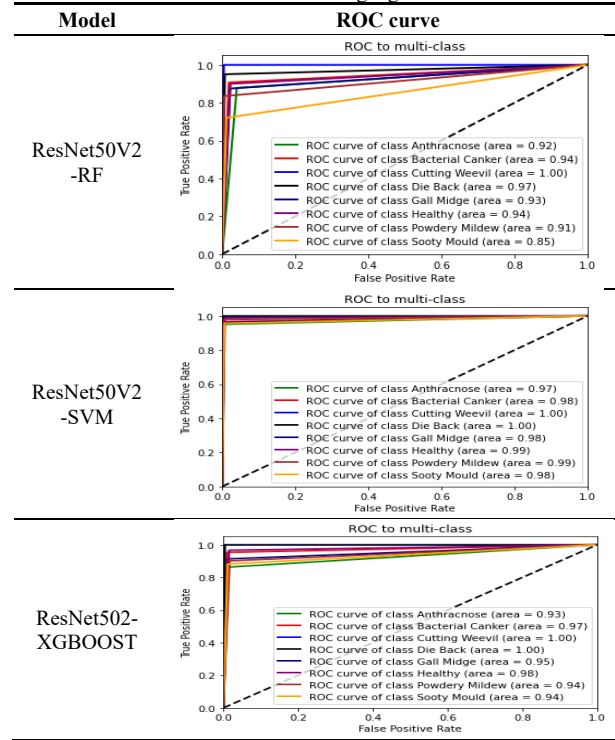


Table 12 Accuracy rate of disease diagnosis with ResNet50V2 combination and the three machine learning algorithms

MangoLeaf disease	ResNet50V2-RF Precision (%)	ResNet50V2-SVM Precision (%)	ResNet50V2-XGBoost Precision (%)
Anthracnose	92	97	93
bacterial canker	94	98	97
Cutting weevil	100	100	100
Die Back	97	100	100
Gall Midge	93	98	95
Healthy	94	99	98
Powdery mildew	91	99	94
sooty mould	85	98	94

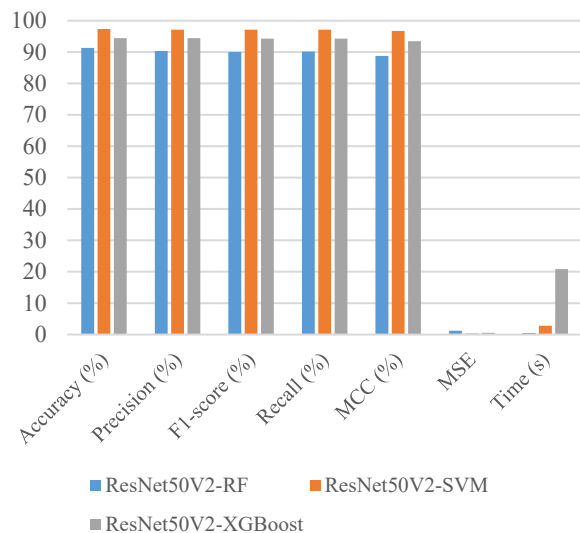


Fig. 5. Histogram of performance using the ResNet50V2 feature extractor with machine learning algorithms.

Fig. 5 shows the performance histogram using the ResNet50V2 feature extractor with Machine Learning algorithms.

**C. Comparison of the Various Methods**

Table 13 shows the results of different models regarding



accuracy and the corresponding execution times. These models have been evaluated for a classification task, and the results indicate their performance in terms of accuracy as well as the time required to run each model.

Table 13. Comparison table

Models	Accuracy (%)	Times (s)
XGBoost	90.71	24.0659
VGG16-SVM	97.75	5.97628
VGG19-SVM	97.12	4.26817
ResNet50V2-SVM	97.31	2.77105

In terms of accuracy, models based on knowledge transfer from convolution neural networks (VGG16, VGG19, and ResNet50V2) in combination with SVM achieve outstanding performance, with accuracies over 97%. This demonstrates that using these pre-trained models to extract features from input data is highly effective for classification.

The XGBoost model also performed well, with an accuracy of 90.71%. Although it is slightly lower in accuracy than models based on knowledge transfer, it remains a valid choice, especially if runtime is a critical factor.

The XGBoost model is the slowest in terms of execution time, taking around 24.066 s. However, models based on knowledge transfer require less time.

Among the knowledge transfer-based models, the ResNet50V2-SVM model is the fastest, requiring just 2.77105 s to execute.

Fig. 6 shows the performance histogram for comparing the different models in our study.

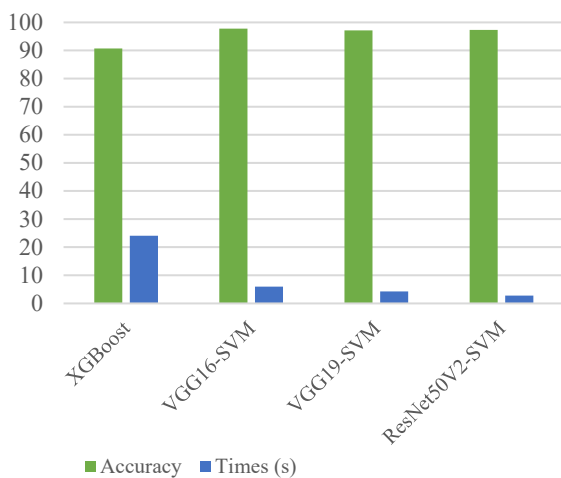


Fig. 6. Histogram of the comparative performance of the different models in our study.

## V. CONCLUSION

Although various automated or Computer vision-based tools are available to identify and classify diseases affecting mango leaves, this area of research still needs to be explored. This paper highlights a hybrid method coupling deep learning feature extractors and machine learning algorithms for mango leaf disease classification. Our study first used three machine learning algorithms, Random Forest, SVM, and XGBoost, to detect and identify mango leaf diseases. We then sought to optimize these results by combining feature extractors from algorithms such as VGG16, VGG19, and ResNet50V2. The results show that the hybrid methods used have significant potential for detecting mango diseases. The VGG16-SVM

model achieved 97.75% accuracy, underlining its potential for accurate disease detection. Sooty mould proved to be the most difficult disease to identify, with an accuracy of 85%. The other diseases, Cutting weevil, Die Back, Gall Midge, and Powdery mildew, were detected with 100% accuracy by most models. The VGG16-SVM model has demonstrated its ability to identify mango leaf diseases effectively. Our method has made a significant contribution to improving mango disease diagnosis and management, as well as to plant disease control and crop preservation.

## CONFLICT OF INTEREST

The authors declare no conflict of interest.

## AUTHOR CONTRIBUTIONS

Abou Bakary BALLO led the research by designing the models for data analysis. Abou Bakary BALLO wrote the manuscript with the support of Moustapha Diaby. Adama Coulibaly encouraged and supervised the work. The results were analyzed and discussed by all the authors. All authors had approved the final version.

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