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Research paper

Machine Learning-Driven Detection of Corn Leaf Diseases for Smart Agriculture

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ABSTRACT

In this study, the authors attempted to predict corn disease using machine learning (ML) algorithms. They attempted to predict the crop disease into four categories, such as healthy (class 1), Grey Leaf Spot (class 2), Common Rust (class 3), and Northern Leaf Blight (class 4), using bagging, boosting, random forest and ensemble algorithms. The entire database is split into a 70:30 ratio for training and testing the classifiers, respectively, and a 5-fold cross-validation has been done to evaluate the performance of the classifier. They used a handcrafted feature extraction method to extract the features from the leaf image, such as color, texture, vegetation indices, and morphological features and fed them into the machine learning algorithms for further classification. The ensemble learning technique combines different ML supervised algorithms and predicts the result by majority voting. The usage of the ensemble technique may overcome the different types of errors and focus on different data patterns as multiple ML techniques are used. The overall accuracy of Bagging, boosting, random forest, and ensemble algorithms is 84.6%, 86.9%, 89.6%, and 91.9%, respectively. Compared to the other methods, the ensemble algorithm exhibits more accuracy. The class-wise healthy, Grey Leaf Spot, Common Rust, and Northern Leaf Blight accuracy is 99.1%, 97.5%, 98.3%, and 98.3%, respectively, for the ensemble model. Though the ensemble techniques combine 3 different types of ML algorithms for prediction, the average time taken to predict the disease is about 6.89 ms. Thus, the authors suggest that the ensemble algorithm predicts crop disease better than individual ML techniques.

Keywords: Corn leaf, Disease prediction, Machine learning, Ensemble approach

Corn (maize), a most significant cereal crop in the world, is used as a primary source of nutrition, animal feed, and a vital component of many industrial goods. Its yield is essential for maintaining worldwide food security and bolstering agricultural industries, especially in emerging nations. However, several diseases, including common rust, grey leaf spot, northern corn leaf blight, southern corn leaf blight, and leaf spot diseases, can seriously harm corn farming, about 20% to 50 % (Hooker, 1985; Mueller *et al.,* 2016; Rossai *et al.,* 2022). If these illnesses are not detected and treated promptly, they drastically lower crop quality and yield.

Corn disease diagnosis has historically relied on inspections performed manually by farmers or agricultural specialists, which is laborious, subjective, and frequently unfeasible for large-scale cultivation. Additionally, the visual symptoms of many diseases may resemble one another, resulting in incorrect diagnosis and postponed treatment. In rural areas with restricted access to crop pathologists and sophisticated testing facilities, this problem is made even more difficult. An automated, precise, and effective disease detection system is therefore desperately needed to help farmers make timely decisions. The prediction of infection in plants is critically needed so that the farmers can medicate them promptly and precisely. The yield of corn gets reduced due to these corn foliar diseases. Common rust leaves reduced the yield by about 5 to 20 %, whereas due to grey leaf spot and northern corn leaf blight, the yield is reduced by about 40% and 50%, respectively (Hooker, 1985; Mueller *et al.,* 2016; Rossai *et al.,* 2022).

Intelligent farming systems now have more options due to recent advancements in computer vision and machine learning (ML). Due to its non-invasive aspect and capacity to evaluate intricate visual patterns, machine learning approaches for image-based illness detection have attracted a lot of attention. Machine learning algorithms can distinguish between healthy and unhealthy plants by extracting discriminative attributes from leaf images such as colour, texture, and structure. These methods allow for scalable,

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real-time illness monitoring and less reliance on expert knowledge. Recent research emphasises how data-driven approaches and AI-facilitated methods might improve agricultural decision-making (Paul *et al.,* 2026). In a similar vein, Paul *et al.,* (2025) study shows how well sophisticated deep learning frameworks function to provide reliable detection of plant disease in real-world applications. These advancements show an increasing tendency toward intelligent technology for applications in agriculture that are precise, scalable, and transportable.

Machine learning classifiers like Support Vector Machines, Random Forest, k-Nearest Neighbours, and Decision Trees have been shown in numerous studies to be successful in classifying plant diseases. These models can attain excellent classification accuracy when paired with suitable image preprocessing and feature extraction techniques. Robust disease prediction is nevertheless hampered by differences in lighting, noise in the background, leaf position and disease severity. As a result, research into creating a reliable and broadly applicable corn disease prediction algorithm is still ongoing. A maize leaf disease classification method was proposed by Dawood *et al.,* (2024) that uses the colour and texture feature extraction after image segmentation via K-means clustering. Diseases like common rust and grey leaf spot were successfully classified using Support Vector Machine and Artificial Neural Network classifiers. Fadhilla *et al.,* (2023) demonstrated the potential of deep learning in detecting disease patterns in tropical environments by implementing a CNN-based detection system for maize leaf diseases. In order to identify maize leaf disease, Çakmak (2024) designed an autonomous deep learning system that achieved good classification performance. Yang *et al.,* (2024) suggested an improved YOLOv8-derived model for maize leaf disease, such as leaf spot recognition.

Vimalkumar & Latha (2024) demonstrated that hybrid deep learning approaches can produce higher accuracy by combining DenseNet extraction of attributes with an LSTM classifier and meta-heuristic hyperparameter tuning for maize leaf disease diagnosis. Four CropNet, a deep learning system that can identify illnesses in a variety of crops, including corn, with excellent accuracy and scalability across different datasets, was presented by Khandagale *et al.,* (2025). Though many models and algorithms are available for disease prediction, there are still many drawbacks in corn disease prediction. Thus, this research proposes a machine learning-based method for leaf image-based corn disease prediction by incorporating different ML algorithms. Image preprocessing, feature extraction, and classification using appropriate machine learning techniques are all part of the methodology. Standard metrics like accuracy, precision, recall, and F1-score are used to assess the performance of the suggested model. The investigation shows that the suggested method can efficiently detect and categorise maize leaf illnesses with a high degree of accuracy, facilitating precision agricultural techniques for disease detection.

By offering an automated and affordable method of detecting maize disease, the suggested system seeks to support farmers and other agricultural stakeholders. This strategy promotes increased crop yield, decreased pesticide use, and a sustainable agricultural future by facilitating intervention and optimal disease management.

MATERIALS AND METHODS

Leaf disease and classes

The data for this study were obtained from the PlantVillage database (Hughes and Salathe, 2015). The dataset is classified into four categories, viz. Healthy, Grey Leaf Spot, Common Rust, and Northern Leaf Blight. The authors termed healthy leaf as class 1; Grey Leaf Spot (GLS) as class 2; Common Rust (CR) as class 3, and Northern Leaf Blight (NLB) as class 4. Healthy leaves have adequate physiological development and excellent efficiency in photosynthesis, which is reflected in the uniform green hue and shiny, intact lamina of healthy corn leaves (class 1). On the other hand, rectangular dark grey to brown infections aligned transversely with plant veins are the signature of Grey Leaf Spot (GLS), which occurs due to *Cercospora zeae-maydis* (class 2). Under humid and warm circumstances, these spots may consolidate, significantly reducing the photosynthetic area of leaves and production (Ward *et al.,* 1999; APS, 2020). *Puccinia sorghi* is the cause of Common Rust (class 3), which manifests as tiny to extended reddish-brown cysts on both the top and bottom leaf surfaces. These pustules burst to produce granular urediniospores that are powdery, and in chilly, damp environments, they may cause earlier senescence of the leaves (Pataky *et al.,* 2009; FAO, 2018). *Exserohilum turcicum* causes Northern Leaf Blight (NLB) (class 4), which is characterised by lengthy, elliptic or cigar-shaped lesions that usually start on the bottom leaves and move up; serious infections under extended moisture in the leaves can result in significant foliar necrosis along with substantial production losses (CIMMYT, 2004; APS, 2021). Fig. 1 (a-d) shows the example images of healthy, GLS, CR, and NLB, respectively, obtained from the PlantVillage database.

Fig. 2 shows the overall flow of this study. At first, the data has been pre-processed before further analysis. In the pre-processing stage, all the images are processed into a uniform size. Then, the features such as color, texture, vegetation indices, and morphological features are extracted from all the images. After that, the data are normalised to maintain a uniform scale for all features. Then, all the features are fed into the individual classifier to classify the disease into four classes, viz., healthy leaf, grey leaf spot, common rust, and northern leaf blight. The performance of all individual classifiers has been evaluated using accuracy, precision, recall, and F1-score. The authors split the obtained database into a 70:30 ratio to train and validate the classifier, respectively. Also, the authors did a 5-fold cross-validation and evaluated its performance. They used four different types of machine learning algorithms, such as bagging, boosting, random forest, and ensemble method, to classify these images into four categories.

RESULTS AND DISCUSSIONS

Feature Extraction

The authors extracted colour, texture, vegetation indices and lesion morphology features from the leaf image. They have extracted mean, median, variance and skew from each RGB (Red, Green, Blue) channel; mean from HSV (Hue, Saturation, Variance) channel, mean of EXG (Excess-green), EXR (Excess-red), GR (Green Red), RG (Red, Green), NDVI; Haralick features such

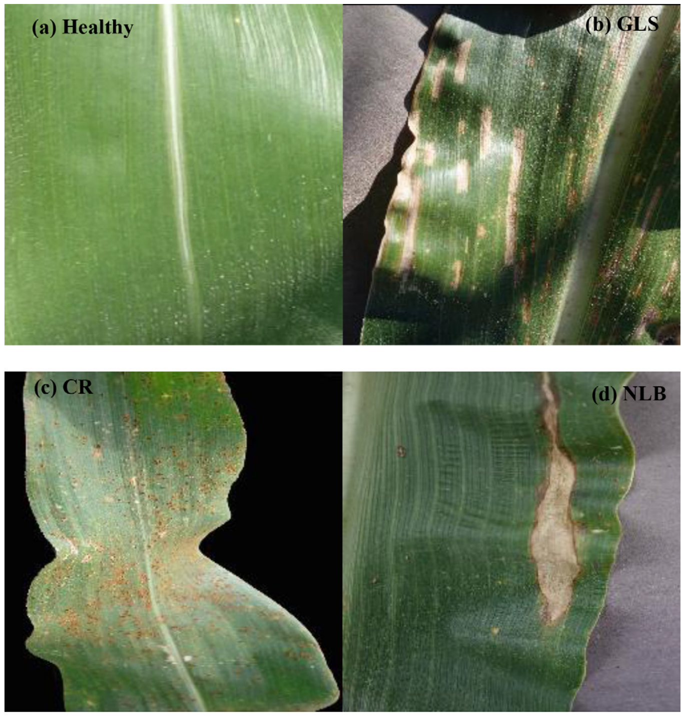

Fig. 1: Example image of crop disease classification (a) Healthy (class 1); (b) Grey Leaf Spot (class 2); (c) Common Rust (class 3); and (d) Northern Leaf Blight (class 4)

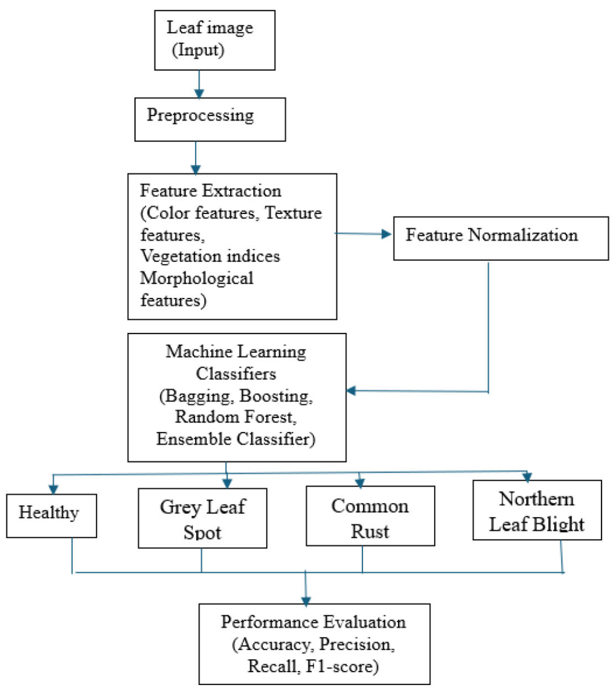

Fig. 2: Framework of this study

as contrast, correlation, energy, homogeneity, entropy, lbphist, total leaf area, lesion area, lesion fraction, number of lesions, standard deviation of leaf area, max of leaf area, mean of leaf area, perimeters, circularity, solidity, eccentricity, aspect ratio, and boundary irregularity from each images. Fig. 3 shows an example of a common rust input image and its HSV and grey scale images.

Mean EXG means excess green in the plant, and mean EXR means excess red in the plant, which is essential for rust detection. Fig. 4 (a-b) shows the result of EXG and EXR of healthy and GLS plants, respectively. A second- order method of statistics for capturing spatial correlations between the intensities of pixels in an image is the Grey Level Co-occurrence Matrix (GLCM). It calculates the frequency of a grey level I^{th} pixel occurring with a grey level J^{th} pixel at a particular distance and direction (0°, 45°, 90°, 135°). To measure textural qualities, Haralick features such as

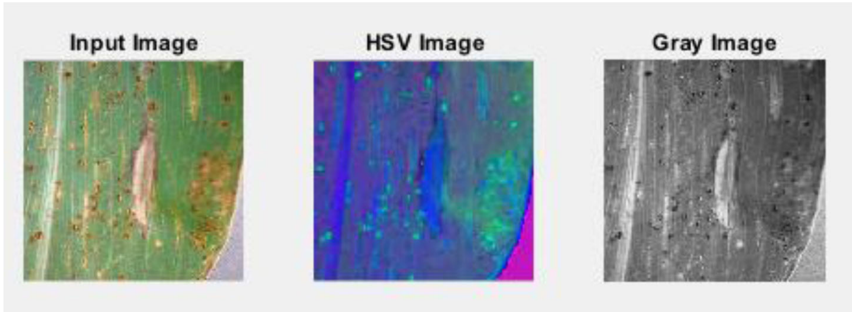

Fig. 3: Input image, common rust disease classification, and its HSV and grey scale image conversion

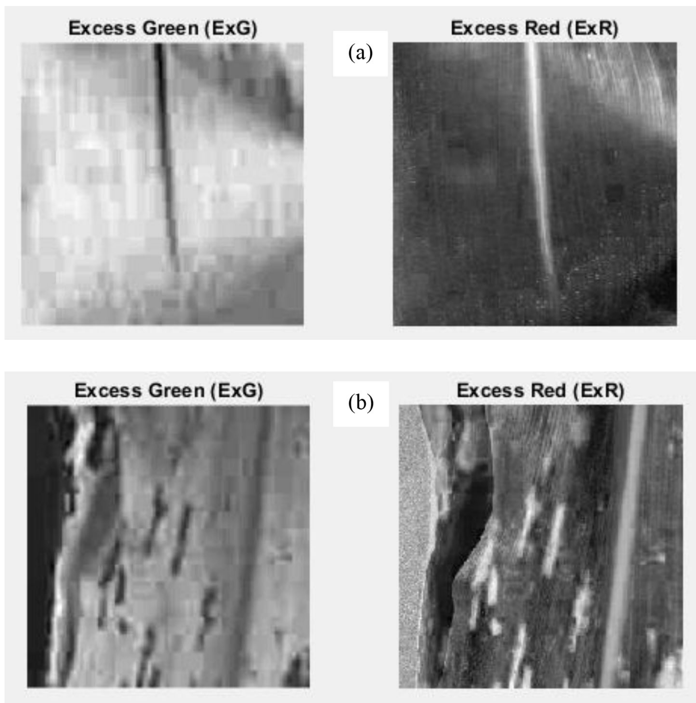

Fig. 4: Excess-EXG and Excess-EXR of (a) a healthy plant and (b) GLS plant

contrast, correlation, energy, homogeneity and entropy are extracted from the GLCM (Thirumala Lakshmi & Usha Kingsly Devi, 2020). Because plant diseases and conditions of stress mostly appear as local texture anomalies on the exterior of the leaf, such as spots, lesions, uneven areas, and growth of fungi, Local Binary Pattern (LBP) features are employed to classify leaf health. By preserving the association between a single pixel and its adjacent pixels, LBP efficiently detects these micro-texture changes, making it possible to distinguish between healthy and diseased leaf patches. All these features are extracted from gray level image.

LBP-hist is resilient to illumination changes frequently seen in exterior agricultural sensing since it is based on the relative brightness differences between nearby pixels. Additionally, despite variations in leaf position and size, the histogram-based approach ensures constant texture characterisation by offering rotational invariance and spatial resilience. LBP-hist is a dependable and effective feature for precise leaf health classification due to its computational efficiency and discriminative capability.

Quantified structural and lesion specific features viz. total leaf area, lesion area, lesion fraction that is the ratio of lesion area and leaf area, lesions number, mean, standard deviation and maximum of lesion area, mean perimeter, circularity, solidity, eccentricity, aspect ratio, and boundary irregularity are crucial for to classify the leaf health efficiently as they provides simple measures of disease infection and structural modifications imposed by pathogens. Lesion area and lesion percentage are two examples of metrics that are commonly used to objectively measure the severity of diseases and increase diagnostic uniformity across samples. These metrics describe the extent and the percentage of diseased leaf tissue (Bi *et al.,* 2025).

Geometric characteristics like perimeter, circularity, solidity, and eccentricity reflect morphological changes brought on by pathogen activity, while statistical metrics of lesion size variation (like mean, standard deviation, and maximum of lesion area) measure the variation associated with symptom behaviour and aid in differentiating slight stress from widespread disease (Javidan *et al.,* 2024). Lesion morphology is further characterised by additional shape parameters such as aspect ratio and boundary irregularities, which help distinguish disease types with various visual patterns.

Table 1: Rank of feature importance based on permutation score

Rank	Feature	Importance Score
1	NDVI	0.182
2	ExG	0.165
3	Lesion Fraction	0.152
4	Lesion Area	0.141
5	GLCM Texture Features	0.128
6	LBP Histogram	0.115
7	Mean (RGB)	0.098
8	Variance (RGB)	0.085
9	Standard Deviation (Leaf)	0.079
10	Perimeter	0.072
11	Circularity	0.066
12	ExR	0.049
13	GR Ratio	0.043
14	RG Ratio	0.039
15	Median (RGB)	0.033
16	Skewness (RGB)	0.028
17	Aspect Ratio	0.022
18	Boundary Irregularity	0.018

These manually created features, which are extracted following the separation of the leaves and lesion areas, convert intricate visual warning signs into numerical indicators. This improves the automatic plant pathogen recognition and severity evaluation system accuracy for machine learning-based classification algorithms (Enow *et al.,* 2025). All these extracted features are fed into the machine learning algorithms for further classification. Fig. 5 shows an example of labelled lesions of the NLB image. It is observed from Fig. 5 that the boundary of the leaf shape is extracted well.

Feature analysis based on Permutation importance

The authors have employed four distinct feature categories: vegetation indices (ExG, ExR, GR, RG, NDVI), texture features (GLCM, LBP histogram), color (mean, median, variance, skewness of RGB channel, mean of HSV channel, and standard deviation of leaf), and morphological features (leaf area, lesion area, total area, mean of leaf area, perimeter, circularity, aspect ratio, boundary irregularity). The significance of features in model performance has been analyzed using the permutation importance. The features are shuffled at random to see how much the algorithm's accuracy drops. A higher value of the permutation score indicates the most important feature for disease prediction. It has been calculated by

$$\textit{Permutation importance } (f_i)=\textit{Performance}_{baseline}-\textit{Performance}_{(shuffled\ (f_i))} \quad (1)$$

The ensemble classifier's permutation relevance is shown in Table 1. Equation (1) has been used to estimate the important score listed in Table 1. For instance, when the NDVI features are randomly permuted, the classifier's accuracy drops from 91.9% to 91.718%. If the ExG feature is randomly permuted, the accuracy drops with a deviation of 1.65%. Table 1 reveals that characteristics like NDVI, ExG, lesion fraction, and lesion area are the most significant and have an immense effect on the classification of diseases. The most significant characteristic of the classifier is implied by the greatest feature value. ExG indicates the existence of green pigment in an image, while NDVI features rely on the amount of chlorophyll and plant health. Lesion characteristics, such as lesion area and lesion fraction, provide information on the extent of the leaf's surface infection. As a result, these four characteristics are important for classifying leaf diseases. The authors have selected all features listed in Table 1 for disease prediction.

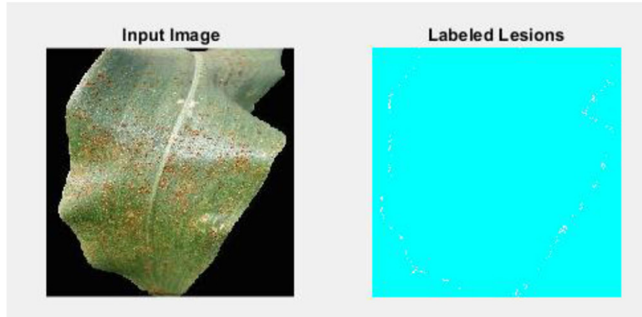

Fig. 5: Output of labelled lesion extraction of the NLB class. The cyan colour region represents the segmentation mask generated using MATLAB's default visualization. The apparent low visibility of the mask is due to rendering and transparency effects, and the segmentation quality is verified via the extracted contours shown alongside.

Machine learning techniques

They have used four different ML algorithms, such as bagging, boosting, random forest and ensemble learning. Ensemble learning techniques like bagging, boosting, and random forest have been frequently used because they minimise variance and bias by aggregating several models, which enhances the accuracy of predictions and generalisation when compared with individual models. Bagging improves robustness towards overfitting and distortion in leaf image attributes derived from texture, shape, and lesion parameters by training several initial learners on various bootstrapping samples of the training data and pooling their predictions (Timilsina *et al.,* 2025). A modified version of bagging, random forest builds a combination of decision trees using samples for training and randomly selected subsets of attributes. This allows for effective management of feature spaces with high dimensions frequently encountered in the analysis of plants and offers predefined evaluations of feature significance that help understand leaf health metrics (Hazra *et al.,* 2021). Boosting techniques emphasise hard-to-classify samples while progressively training weak learners. This improves categorisation of difficult categories of diseases and increases sensitivity to modest fluctuations in leaf symptoms. Overall ensemble approaches take advantage of the complementary capabilities of individual learners and are especially well-suited for challenging tasks involving classification, like leaf health evaluations, where there is significant intra-class variation and data heterogeneity. The performance of the classifier has been evaluated by precision, recall, accuracy, and F1-score.

The investigation shows that the random forest classifier performed the best overall across the individual ensemble methods,

Table 2 : Confusion matrix of bagging, boosting, RF and ensemble classifier

Actual/ Predicted	Healthy	Grey Leaf Spot	Common Rust	Northern Leaf Blight
Bagging classifier				
Healthy	1030	40	55	37
Grey Leaf Spot	60	390	35	28
Common Rust	48	42	1035	67
Northern Leaf Blight	55	30	78	822
Boosting classifier				
Healthy	1045	35	48	34
Grey Leaf Spot	45	415	30	23
Common Rust	40	38	1065	49
Northern Leaf Blight	46	28	65	846
RF classifier				
Healthy	1070	28	40	24
Grey Leaf Spot	38	435	22	18
Common Rust	32	30	1085	45
Northern Leaf Blight	35	20	50	880
Ensemble classifier				
Healthy	1090	22	32	18
Grey Leaf Spot	30	455	15	13
Common Rust	25	22	1110	35
Northern Leaf Blight	28	15	35	907

exhibiting good generalisation ability among all four of the classes. This is explained by its capacity to manage intricate, nonlinear interactions between retrieved texture and morphological data and to minimise variation using bootstrapped sampling. When compared to a single decision tree, bagging-based classifiers demonstrated steady and consistent output, especially for the Healthy and Common Rust classes. For the Grey Leaf Spot class, which includes relatively fewer data, boosting algorithms demonstrated increased recall and sensitivity against misclassified data.

The ensemble method, which integrated the predictions from all three individual classifiers, produced a good classification performance, with better class-wise balance as well as less misclassification between visually equivalent disease classes such as Grey Leaf Spot and Northern Leaf Blight. The performance of the classifiers is validated with two approaches of dataset splitting: one is a Hold-out validation (70:30 ratio), and the other is 5-fold cross-validation.

Hold-out validation

In Hold-out validation, the database is split into a 70:30 ratio for training and testing, respectively. Table 2 shows the confusion matrix of bagging, boosting, random forest, and an ensemble classifier, respectively.

Four basic metrics are frequently used to assess a model's performance in classification problems, viz. True Positive (TP), True Negative (TN), False Positive (FP), and False Negative (FN). When the classifier accurately selects an image that actually belongs to the positive class, this is known as a True Positive (TP). When an image is correctly identified as belonging to the negative class, it is called a True Negative (TN). False Positive (FP), commonly referred to as a Type-I error, happens when the classifier mistakenly classifies a negative image as positive. A Type-II error, also known as a False Negative (FN), happens when the classifier fails to recognise a positive image and mistakenly labels it as negative. Table 3 shows the TP, TN, FP, and FN of the classifier. It is observed from Table 3 that the bagging classifier predicts the actual classes 1, 2, 3, and 4, in about 88.6 %, 76.02 %, 86.82 %, and 83.45 %, respectively. The boosting classifier predicts the actual classes 1, 2, 3, and 4, in about 89.9 %, 80.89 %, 89.34 %, and 85.88 %, respectively. The RF classifier predicts the actual classes 1, 2, 3, and 4, in about 92.1 %, 84.8 %, 91.03 %, and 89.34 %, respectively. The ensemble classifier predicts the actual classes 1, 2, 3, and 4, in about 93.8 %, 88.69 %, 93.12 %, and 92.03 %, respectively. Thus, the investigation shows that the ensemble classifier predicts all true classes with better accuracy than individual classifiers. The analysis of individual classifiers shows that the prediction of the true classes is higher in RF, followed by boosting and bagging.

The class-wise performance of all classifiers is shown in Fig. 6 (a–d). When it comes to classifying the Common Rust (CR) class, the bagging classifier performs better than the other classifiers. For the Healthy and Grey Leaf Spot (GLS) classes, the boosting classifier exhibits higher classification accuracy. The class-wise NLB accuracy is 95.7 % and 96.5 %, respectively for random forest and ensemble model classifier.

The Bagging classifier shows consistent predictions for the Healthy and Common Rust classes; however, there is a discernible misclassification that occurs for Grey Leaf Spot and Northern Leaf Blight. The Boosting classifier reduces false negatives by iteratively focusing on tricky-to-classify samples, demonstrating improved discrimination performance, especially for the Grey Leaf Spot class. Because of feature unpredictability and ensemble variation, the random forest classifier exhibits better diagonal superiority than all individual classifiers among all classes, indicating enhanced classification and diminished inter-

Table 3: TP, TN, FP, FN of classifier

Classifier	Class	TP	FP	FN	TN
Bagging	Healthy	1030	163	132	2550
Bagging	GLS	390	112	123	3250
Bagging	CR	1035	168	157	2515
Bagging	NLB	822	132	163	2758
Boosting	Healthy	1045	131	117	2582
Boosting	GLS	415	101	98	3261
Boosting	CR	1065	143	127	2540
Boosting	NLB	846	106	139	2784
RF	Healthy	1070	105	84	2616
RF	GLS	435	80	98	3262
RF	CR	1085	112	112	2570
RF	NLB	880	87	105	2803
Ensemble	Healthy	1090	85	70	2630
Ensemble	GLS	455	59	73	3262
Ensemble	CR	1110	92	82	2581
Ensemble	NLB	907	68	71	2810

class ambiguity. With the best precise categorisation rates across all four categories and a minimum of off-diagonal deviations, the mixed ensemble approach provides an optimally balanced result. This demonstrates that combining several ensemble approaches successfully makes use of complementary decision limits, leading to improved consistency and scalability for the categorisation of leaf health. Thus, the authors used an ensemble approach in this study. The reason behind this advantage of an ensemble classifier is that it learned from three base learners, such as bagging, boosting, and random forest. By leveraging the advantage of these classifiers, the ensemble classifier approach predicts the leaf disease better than an individual base classifier. The ensemble approach improves the generalisation ability as it predicts the disease based on aggregation to minimise the bias and variance. This approach combined several decision boundaries suggested by all base classifiers to handle the variation in the feature space vector more precisely. This plays a vital role in leaf disease prediction as the features, such as color, morphology, and texture, might show similarity between different disease classes of an image. When compared to an individual classifier, the ensemble classifier shows high accuracy and precision for both 5-fold cross-validation and 70:30 ratio validation process. This approach also lessens the drawback of individual classifiers, including the random forest's overfitting and the noise sensitivity of the boosting classifier. The time taken by the ensemble approach for disease prediction is higher than that of the remaining individual classifiers. Also, the computational complexity is higher for the ensemble learning approach. However, the ensemble approach balances accuracy and robustness to predict the disease in a real-time agriculture system. The overall classifier accuracy is 84.6 %, 86.9 %, 89.6 %, and 91.9 % for bagging, boosting, RF, and the ensemble classifier, respectively.

Cross-validation

The authors have used a 5-fold cross-validation to evaluate the performance metrics of the classifier. In this, the authors split the entire dataset into 5 equal sub-datasets and trained the model. They trained the model by using 4 sub-datasets and tested it on 1 sub-dataset. Each fold has been used once for testing and training four times. The average of all 5-fold accuracy has been considered as the model's accuracy. Table 4 shows the accuracy of the 5-fold validation of all classifiers. Like the 70:30 ratio dataset, the accuracy is higher for the ensemble classifier, followed by the random classifier.

Table 4: Accuracy of 5-fold cross-validation

Fold	RF (%)	Bagging (%)	Boosting (%)	Ensemble (%)
1	95.8	92.1	93.6	96.0
2	96.1	92.5	94.0	96.4
3	95.6	91.9	93.5	95.8
4	96.4	92.8	94.3	96.8
5	96.0	92.4	94.1	96.5
Average	95.9	92.3	93.9	96.3

The mean and standard deviation of the 5-fold cross-validation of all classifiers are mentioned in Table 5. It is observed from Table 5 that the mean and standard deviation are higher in the ensemble approach, which implies the stability and robustness of the algorithm. This results in a high degree of algorithmic generalisation.

Measurement of inference time

The authors used a MATLAB R2025 version to train the machine learning algorithms on a PC with an Intel Core i5–1155G7 processor and 8 Gigabytes of RAM running on Windows 11 (64-bit) operating system. The in-built MATLAB functions, such as "tic" and "toc", are used to measure the time taken by an algorithm to predict the crop disease class. During the training stage, 70 % of samples are given as input, and the time required to execute the output was recorded for all four different ML algorithms. The algorithm has been trained up to 45 iterations, and the average time was estimated. The average time taken by the ensemble classifier is 6.89 milliseconds (ms). Table 6 shows the average prediction time and total training time of each classifier. It is observed from Table 6 that both training time and prediction time are higher for the ensemble classifier than for the remaining classifiers. The prediction time of bagging and RF is faster than that of boosting and the ensemble approach.

In plant disease analysis, feature extraction and machine learning algorithms pose more difficulties than deep learning techniques. Because handcrafted elements like color, vegetation indices, texture, and morphological features are derived using predetermined formulas recommended by specialized researchers and domain experts, they may not be sufficient to recover the non-linear patterns of the disease-infected leaf. Additionally, background clutter, light fluctuations, and leaf opacity cause the ML approach's performance to lag in real-world agricultural systems. Because handcrafted methods cannot obtain hierarchical and universal

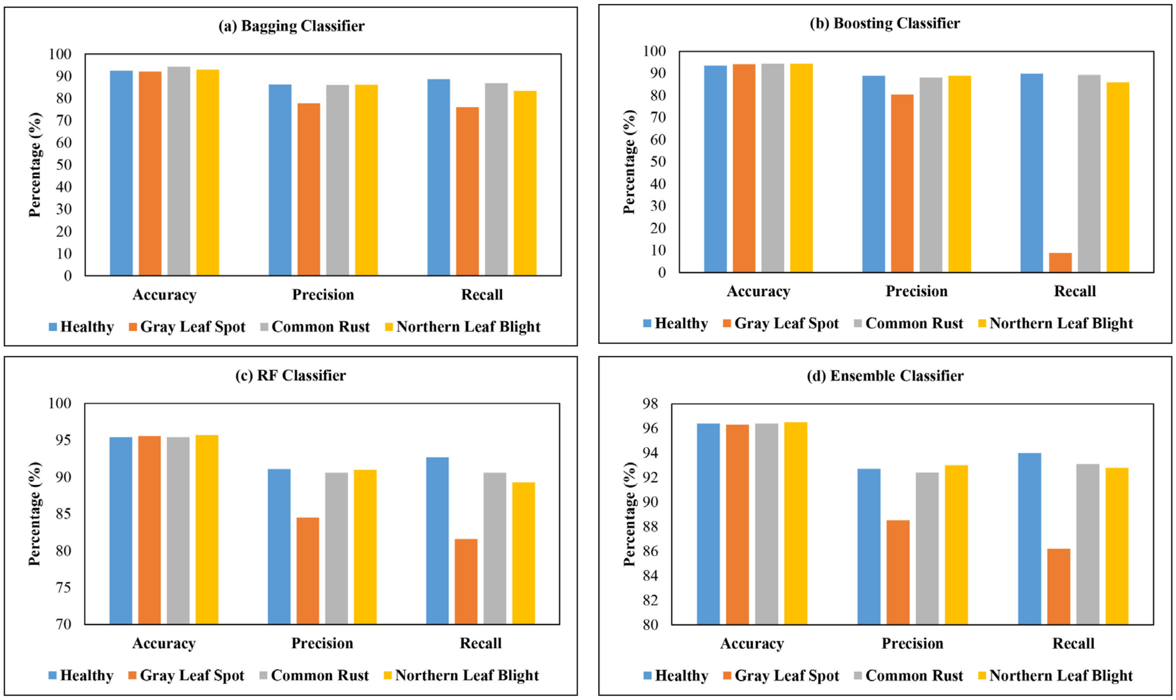

Fig. 6: Precision, recall and accuracy of all 4 disease classifications (a) Bagging, (b) Boosting, (c) Random forest, and (d) Ensemble classifier

representation, they are less generalizable than deep learning systems over a wide range of crops, disease kinds, and imaging circumstances (Mohanty *et al.,* 2016; Ferentinos, 2018). However, the ML model works well with low GPU and computational resources, less computational complexity, minimum hyperparameter tuning and less time for training.

The proposed machine learning techniques can be effectively incorporated into real-world agricultural models, as their computational complexity is low. Farmers can use smartphones to take pictures of leaves in a mobile application-driven system. The learned model can then process the images taken on-device or via cloud-based services to deliver an immediate diagnostic and damage assessment. This facilitates quick decision-making, especially in remote locations where access to professional advice may be restricted. The technology can be used with drone-driven imaging for extensive agricultural surveillance, whereby aerial views of crop fields are taken and examined to calculate vegetation indices like NDVI and pinpoint areas impacted by disease. By allowing for disease diagnosis and focused instruction, this promotes precision agriculture and lessens the overuse of pesticides. Additionally, the pipeline may be integrated into IoT-enabled automated farming platforms that continuously gather crop and climatic data using cameras and sensors.

Through linked platforms, four types of disease prediction and notifications in real time to farmers are made possible by the incorporation of features based on images. Because the suggested method is portable, it may be implemented on edge devices such as standard embedded systems and low-powered CPUs, guaranteeing operation in real time without the need for expensive processing resources. Even though there are obstacles such as different lighting conditions, noise in the background, and database consistency, they can be lessened with careful preprocessing and feature selection.

Dataset Limitation

The PlantVillage dataset, which includes images taken in controlled laboratory environments with standardized lighting and backgrounds, is used in the study. Although this provides for excellent classification precision as well as effective feature extraction techniques, it might not accurately depict actual agricultural conditions. Variations in lighting, complicated background colors, shadow effects, leaf obscurity, and discrepancies in image collecting equipment can all have a substantial impact on model performance in real-world field settings. When the developed algorithm is used in real agricultural environments, these differences could result in a decreased capacity for generalization. This limitation should be considered when evaluating the provided results. Future research will concentrate on integrating field-gathered databases, using data-augmenting approaches that replicate real-world unpredictability, and creating more reliable preprocessing techniques to enhance model flexibility under various environmental situations in order to overcome this problem.

CONCLUSIONS

In this study, the authors attempted to predict leaf disease by classifying the leaf images into four categories using different machine learning algorithms. This study suggested and assessed a reliable method for detecting plant diseases using machine learning classifiers and a handcrafted feature extraction technique. They have used bagging, boosting, random forest and ensemble learning algorithms, and evaluated their performance to know the most effective model for leaf disease prediction. A hybrid performance evaluation approach by combining Hold-out and 5-fold cross-validation has been done to ensure the model's stability and

Table 5: Mean and standard deviation of 5-fold cross-validation

Classifier	Accuracy (%)	Precision (%)	Recall (%)	F1-Score (%)
Random Forest	95.98 ± 0.29	95.62 ± 0.36	95.82 ± 0.28	95.72 ± 0.32
Bagging	92.34 ± 0.32	91.92 ± 0.33	92.16 ± 0.31	92.04 ± 0.32
Boosting	93.90 ± 0.31	93.56 ± 0.34	93.70 ± 0.30	93.63 ± 0.32
Ensemble	96.30 ± 0.36	95.90 ± 0.38	96.06 ± 0.34	95.98 ± 0.36

Table 6: Average prediction time and training time of ML algorithms

Classifier	Average prediction time	Total images training time
Bagging	1.2 ms	4.65 s
Boosting	2.1 ms	8.14 s
Random Forest	1.5 ms	5.81 s
Ensemble	6.89 ms	10.07 s

generalization. The investigation shows that all the individual classifiers predict healthy and CR classes better than the other two classes. The random forest predicts all four classes better than bagging and boosting classifiers; however, the ensemble method classifies better than individual classifiers. The overall classifier accuracy is 84.6 %, 86.9 %, 89.6 %, and 91.9 % for bagging, boosting, RF, and the ensemble classifier, respectively. The prediction time of bagging and RF is faster than that of boosting and the ensemble approach. The significant contribution of this study is the development of hybrid features by combining color, texture, vegetation indices and morphological features. The permutation importance has been done for these combined features and finds the most discriminative features, emphasizing the relevance of lesion-based characteristics such as lesion area and lesion fraction; NDVI, and ExG. Overall, the key contribution of this research is the development of a robust ensemble-based machine learning approach for leaf disease prediction. The results of the experiment verify that the suggested method offers an accurate and comprehensible way to classify plant diseases. Future research will concentrate on enhancing the model's resilience in real-world scenarios and incorporating it into workable agricultural systems.

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