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AN ENSEMBLE CONVOLUTIONAL NEURAL NETWORK FRAMEWORK FOR AUTOMATED MANGO LEAF DISEASE DETECTION

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Abstract

Mango diseases and pest infestations represent a major challenge to agricultural productivity, making early and accurate diagnosis crucial for reducing crop losses. This study presents a security-preserving ensemble convolutional neural network (CNN) framework for the automated identification and classification of mango leaf diseases using image-based analysis. The proposed system is designed to work with images captured under real field conditions, ensuring its suitability for practical agricultural applications. The dataset includes mango leaf images affected by various diseases and pests such as Gall Midge, Powdery Mildew, Sooty Mould, Die Back, Cutting Weevil, and Anthracnose, each characterized by distinct visual symptoms including discoloration, necrotic spots, fungal growth, leaf deformation, and edge damage. Traditional manual diagnosis of these conditions is often time-consuming, labor-intensive, and susceptible to human error. To overcome these limitations, the proposed framework employs an ensemble of transfer-learning-based CNN models to extract meaningful features related to texture, color distribution, shape, and lesion patterns. A security-preserving learning mechanism is integrated to ensure the safe handling of agricultural image data, minimizing data exposure risks while maintaining high model performance. Additionally, data augmentation techniques are utilized to improve model robustness, reduce overfitting, and address class imbalance commonly found in agricultural datasets. The system is capable of multi-class classification, reflecting real-world scenarios where multiple diseases may exhibit visually similar characteristics. Experimental results indicate that the ensemble CNN framework achieves high classification accuracy and demonstrates strong generalization across varying lighting conditions and complex backgrounds. By effectively capturing disease-specific visual features, the proposed approach enhances detection reliability in real-world field environments. Overall, this system offers a scalable, non-invasive, and security-aware solution for early mango leaf disease detection, contributing to precision agriculture and informed decision-making. The findings highlight the potential of deep learning and computer vision technologies in developing intelligent, secure, and efficient plant health monitoring systems.

1. INTRODUCTION

One of the most extensively grown tropical fruits in the world is the mango. Mangoes are exported in significant quantities to foreign markets every year, according to a 2022 FAO (Food and Agriculture Organization) study. For example, 912,510 multitudes were exported from Asia in 2021, followed by 620,745 multitudes from South America, 545,428 multitudes from Central America and the Caribbean, 202,010 multitudes from Africa, and 4,254 multitudes from Oceania [1].

However, diseases and pests that lower the crop's quantity and quality cause significant losses to mango production every year. For instance, in Senegal, these losses are estimated to be between 15 and 90 percent annually per plantation due to ineffective infrastructure [2, 3]. Researchers have put forth a number of methods for the automatic diagnosis and assessment of the severity of plant diseases during the last ten years. Estimating the severity of a plant disease and diagnosing it are two different but closely related tasks. While severity estimation establishes the stage or extent of disease progression, disease diagnosis concentrates on identifying the type of disease present [4,5].In this context, plant disease severity is defined as the ratio of the surface area affected by disease symptoms to the total surface area of the plant organ, such as a leaf or fruit [6]. Accurate knowledge of disease severity offers several benefits to farmers, including rational disease control, prediction of disease outbreaks and yield losses, improved pesticide management, disease forecasting, and spatio-temporal modeling of epidemics and crop losses [7]. Consequently, disease severity estimation plays a critical role in effective plant disease management and protection strategies. Traditionally, severity assessment has relied heavily on manual evaluation, which is time-consuming, labor-intensive, and highly subjective [7]. To overcome these limitations, numerous automated approaches for plant disease severity assessment have been proposed in the literature. In [7], a comprehensive review of 47 studies addressing automated severity estimation was presented. These approaches can be broadly classified into three categories: methods based on image segmentation, classical machine learning algorithms, and deep learning (DL) techniques. The severity analysis of disease can be qualitative or quantitative. Qualitative assessment uses the predefined visual severity in which such assessments are usually based on the opinion of experts like psychopathologists. As an example, Kaur et al. [5] analyzed the severity of mango rust disease with five severity scales and a hybrid CNN-SVM model and obtained the final accuracy of 97.02. In a similar manner, Wang et al. [8] quantified the severity of apple black rot on the basis of Early, Middle and End stages by adopting CNN-SVM method, which yielded an accuracy of 90.4. Another study by Abdulridha et al. [9] introduced a qualitative evaluation of downy mildew severity on watermelon leaves and stated that the higher the severity of the disease, the better the classification accuracy is achieved. Conversely, quantitative severity analysis implies direct calculation of the percentage of diseased tissue in a plant unit. Bhujel et al. [10] developed a U-Net based network to estimate the lesion percentages of gray mold on strawberry leaves with an IoU, Dice, and pixel accuracies of 82.12, 89.71, and 98.24 respectively. Though these algorithms show good performance, they also have weaknesses like that of subjectivity in the labelling of data in a classical machine learning approach, loss of details of lesions boundaries in the case of deep learning methods, and that most studies concentrate on leaf-based severity prediction even though diseases can affect fruits and other plant organs [7]. They can affect the quality of data and, thus, the overall system performance in an adverse way.

2. RELATED WORK

The disease detection of Mango has also been a significant field of research over the past few decades with the constant efforts being directed towards enhancing the accuracy of the disease detection. To increase the accuracy of diagnosis, scholars have studied numerous approaches that rely on the machine learning, deep learning, and pattern recognition framework. These techniques are Convolutional Neural Networks (CNNs) [11], Artificial Neural Networks (ANNs) [12], Back Propagation Neural Networks (BPNNs) [13], Support Vector Machines (SVMs) [14] and a number of image processing methods [15,16]. CNNs are some of these techniques that are especially beneficial because they combine feature extraction and classification in a single model. In contrast, other approaches depend on handcrafted feature extraction techniques such as color co-occurrence matrices [17], angle code histograms [18], zooming algorithms [19], and edge detection methods like the Canny operator [20]. Previous studies have addressed either the classification of a single disease across multiple plant varieties or the identification of multiple diseases within a single plant species. These advanced methodologies have been applied to a wide range of crops, including rice [21], wheat [22], maize [23], and cotton [24], demonstrating their effectiveness in agricultural disease diagnosis.

Table 1: ***Survey for Dataset Used for Mango leaf***

Ref.	Dataset Used	Model / Approach	Advantages	Limitations
[25]	Custom MangoLeafBD (7 classes: Anthracnose, Bacterial Canker, Powdery Mildew, etc.)	Five-layer CNN ("LeafNet") trained from scratch	High accuracy (≈ 98 %); lightweight model; effective on small datasets	Limited generalization to field images; risk of overfitting under lab conditions
[26]	MangoLeafBD (public Kaggle/Mendeley)	Baseline CNN benchmarks + augmentation protocols	Open benchmark with standardized splits; enables reproducibility	Class imbalance and visual similarity between diseases affect accuracy
[27]	MangoLeafBD (7 classes)	ResNet-50 (ImageNet pretrained) + fine-tuning	Strong baseline (≈ 97.8 % acc); stable convergence; interpretable Grad-CAM maps	Requires GPU resources; no cross-domain testing
[28]	MangoLeafBD subset (Healthy vs Diseased)	MobileNetV2 transfer learning	Fast inference (< 20 ms); mobile-friendly; low memory footprint	Slight accuracy loss vs ResNet; sensitive to lighting conditions
[29]	MangoLeafBD (train/val/test)	Vision Transformer (ViT-B16) vs ResNet-50 vs MobileNetV2	ViT ≈ 98.7 % accuracy; revealed importance of augmentation	Higher compute cost; not suited for edge deployment
[30]	Field-collected multi-orchard dataset	Ensemble of CNNs + Histogram Eq. + CLAHE	Improved robustness to illumination and background clutter	Heavier training/inference pipeline
[31]	40 + crop datasets (including mango)	Meta-analysis of VGG, ResNet, EfficientNet variants	Synthesizes trends; promotes XAI (Grad-CAM) usage	Few mango-specific experiments; mostly cross-crop insights
[32]	Mango + Grape mix dataset	Lightweight CNN + Squeeze-and-Excitation (SE) blocks	Low latency (< 30 ms); 95 % acc on mobile CPU; energy efficient	Slight accuracy drop vs deeper CNNs; limited dataset scope
[33]	Augmented MangoLeafBD	CNN + Transformer fusion (ConvNeXt + ViT)	Best overall (≈ 99.1 % acc); strong feature attention; noise robustness	Complex architecture; not optimized for real-time devices
[34]	MangoLeafBD + field images	CNN + Grad-CAM visualization	Enhances user trust; helps expert validation	Grad-CAM resolution low; subjective interpretation

3. METHODOLOGY

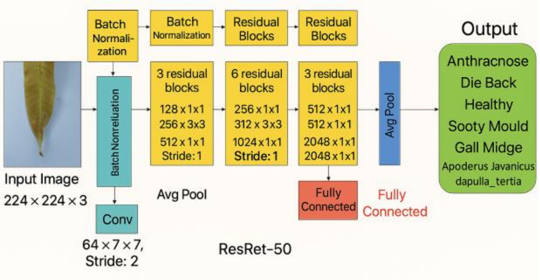


Figure 1. proposed frame work for Mango Leaf disease

The figure depicts a deep convolutional neural network ResNet-50 to classify plant leaf disease in multiple classes and has demonstrated how a RGB based input image of size 224x224x3 is sequentially converted into a final categorical output. It starts with a convolutional layer of 64 filters of size 77 with stride 2 that identifies low-level visual patterns (edges and color gradients and textures) with reduced spatial resolution to enhance computational efficiency. That is accompanied by batch normalization that is used to stabilize and speed up training by normalizing the distributions of features, and a nonlinear activation that adds nonlinearity to allow the network to learn complex patterns. A typical pooling operation also decreases spatial dimensions without losing any context. The architecture is only made up of stacked residual blocks which is the hallmark of the ResNet-50 and the solution to the vanishing gradient issue through the introduction of identity shortcut connections that enable information and gradients to pass immediately through the layers. The initial stage of the residual structure includes three residual blocks with a bottleneck block 1 × 1, 3 × 3, 1 × 1 structure that steadily increase the depth of the features without increasing the computing load; these blocks increasingly learn more discriminant mid-level features like leaf veins, lesion boundaries, and irregular shape. The second level further expand the network by using six residual blocks that further increase the channel dimensions allowing more abstract and disease specific representations of the network including texture distributions and color anomalies connected with infections to be obtained. The third residual level has three more residual block with larger channel capacity and thus, the network is able to isolate semantic features which are much more abstract and therefore distinguish the similar diseases when differentiated. During these steps, it is the batch normalization that provides stable gradients, and the residual connection makes it possible to have very deep learning without negative performance consequences. Once the convolutional feature extraction has finalized, the feature map is pooled globally into a single representative value which acts as an effective summary of the learnt spatial data and eliminates overfitting since it does not require big fully connected layers. The resulting feature vector is then sent to a fully connected layer which transforms the learned features into the final output classes with learned weights. The output layer generates the probability of the various leaf health conditions, including Anthracnose, Die Back, Healthy, Sooty Mould, Gall Midge and Apoderus javanicus dapulla_ tertia amongst others which enable the model to classify the disease accurately. On the whole, this architecture draws on the deep residual learning and efficient bottleneck convolution and global pooling to produce high accuracy and robustness, thus it is suitable in automated diagnosis of plant disease using leaf images in real-life agricultural scenarios.

3.1 Data Preprocessing

Data preprocessing is necessary in order to ensure that the deep learning models are effective. To begin with, the collected leaf pictures are rescaled to a fixed size compatible with the ResNet network, typically 224 224 pixels. To enhance the stability of the numbers in training, image normalization is applied to bring pixel values to a normal range. Techniques of data augmentation such as rotation, flipping, zoom, and brightness are applied to enhance model generalization and reduce overfitting. These functions imitate background condition, lighting and orientation changes that take place in the real world. The dataset is then divided into testing, validation and training subsets to facilitate objective performance evaluation.

3.2 Deep learning Models

Convolutional neural networks (CNNs) and other deep learning models have shown good results in image-based classification tasks. This paper has embraced transfer learning to exploit pre-trained deep learning frameworks that are trained on large-scale data. Out of these, ResNet is chosen because it effectively learns deep feature representations, and also removes the performance degradation of deeper networks. Optimization Fine-tuning Fine-tuning involves a retraining of the chosen layers in order to fit the model to the task of classifying plant diseases.

3.3Convolutional Neural Network

These skip connections are involved to learn identity mappings in the model which can successfully train very deep architectures. ResNet was applied in the proposed framework as a feature extractor, which extracts the high-level visual features like texture, shape, and lesion pattern of leaf images. More fully connected layers are added to the network to classify plant diseases on multi-classes. This mixture increases the level of learning efficiency with preservation of high classification accuracy.

3.4 Evaluation Metrics

Whereas precision and recall measure the ability of the model to correctly recognize classes of diseases, accuracy measures overall accuracy of the model. The F1-score provides a reasonable evaluation by taking into account recall and precision. These measurements would give a comprehensive evaluation of the strength and effectiveness of the model on the different types of diseases.

Evaluation Metrices:

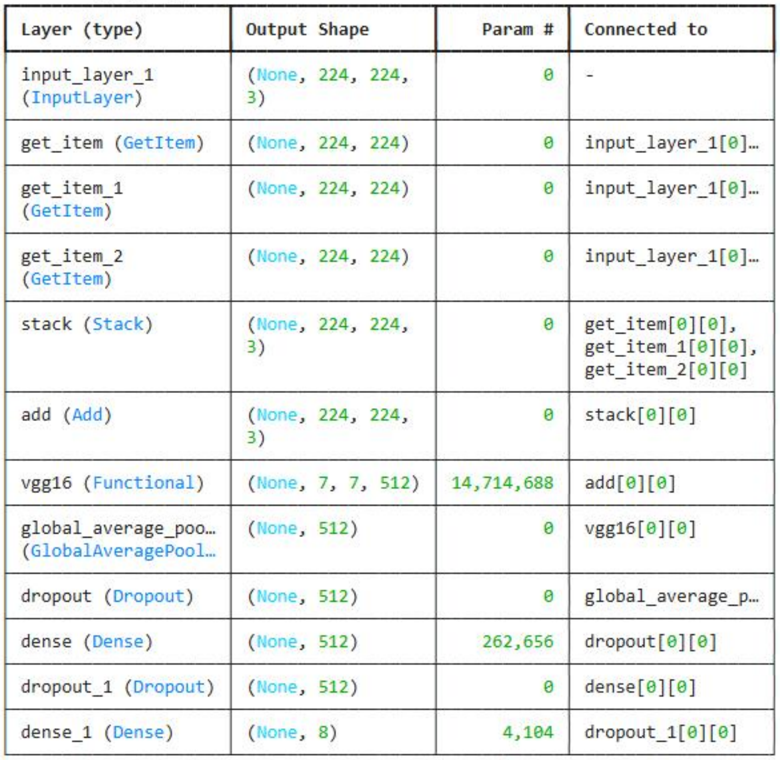
$$\text{Accuracy}=\frac{Tp+Tn}{Tp+Tn+Fn+Fp} \qquad (1)$$

$$\text{Precision}=\frac{Tp}{Tp+Fp} \qquad (2)$$

$$\text{Sensitivity}=\frac{Tp}{Tp+Fn} \qquad (3)$$

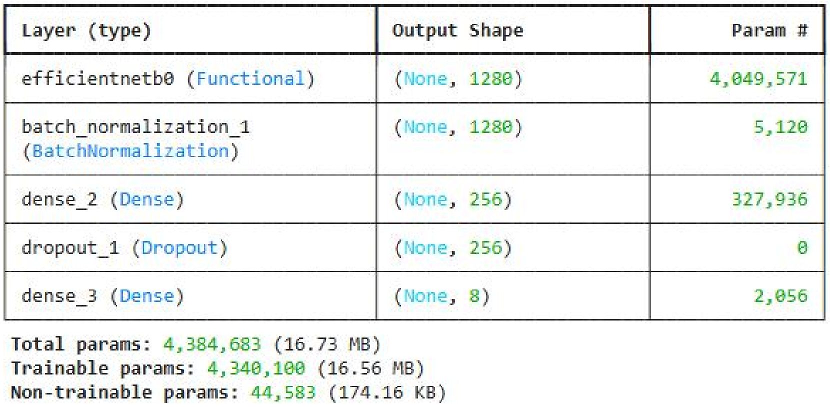
4. RESULTS

The picture shows a sample data of the plant leaf samples with various diseases and pests, such as Gall Midge, Powdery Mildew, Sooty Mould, Die Back, Cutting Weevil, and Anthracnose. The visual manifestations of each of the classes include leaf curling and deformation (Gall Midge), white powdery patches (Powdery Mildew), black fungal coating (Sooty Mould), progressive browning and drying of the tip of the leaf (Die Back), irregular cuts and disfigured leaf margins (Cutting Weevil) and black necrotic lesions or spots (Anthracnose).The variation in color, texture, shape, and severity across samples highlights the diversity and complexity of real-world disease patterns, making the dataset well-suited for training and evaluating deep learning models for multi-class plant disease classification.



Layer (type)	Output Shape	Param #	Connected to
input_layer_1 (InputLayer)	(None, 224, 224, 3)	0	-
get_item (GetItem)	(None, 224, 224)	0	input_layer_1[0]…
get_item_1 (GetItem)	(None, 224, 224)	0	input_layer_1[0]…
get_item_2 (GetItem)	(None, 224, 224)	0	input_layer_1[0]…
stack (Stack)	(None, 224, 224, 3)	0	get_item[0][0], get_item_1[0][0], get_item_2[0][0]
add (Add)	(None, 224, 224, 3)	0	stack[0][0]
vgg16 (Functional)	(None, 7, 7, 512)	14,714,688	add[0][0]
global_average_poo… (GlobalAveragePool…	(None, 512)	0	vgg16[0][0]
dropout (Dropout)	(None, 512)	0	global_average_p…
dense (Dense)	(None, 512)	262,656	dropout[0][0]
dropout_1 (Dropout)	(None, 512)	0	dense[0][0]
dense_1 (Dense)	(None, 8)	4,104	dropout_1[0][0]

Figure 3, the VGG16-based model takes a 224×224×3 input image, where three single-channel inputs are first extracted using GetItem, then stacked and combined through an Add operation to form a standard RGB image. This combined input is passed into the pre-trained VGG16 network (used as a feature extractor), which outputs high-level feature maps of size 7×7×512 and contains 14,714,688 parameters. These deep features are then reduced using Global Average Pooling to a 512-dimensional vector, followed by dropout for regularization. A fully connected dense layer with 512 units further refines the learned representations, followed again by dropout to reduce overfitting. Finally, the output layer is a dense layer with 8 neurons, corresponding to an 8-class classification task, making the architecture suitable for transfer learning while balancing performance and generalization.



Layer (type)	Output Shape	Param #
efficientnetb0 (Functional)	(None, 1280)	4,049,571
batch_normalization_1 (BatchNormalization)	(None, 1280)	5,120
dense_2 (Dense)	(None, 256)	327,936
dropout_1 (Dropout)	(None, 256)	0
dense_3 (Dense)	(None, 8)	2,056

```
Total params: 4,384,683 (16.73 MB)
Trainable params: 4,340,100 (16.56 MB)
Non-trainable params: 44,583 (174.16 KB)
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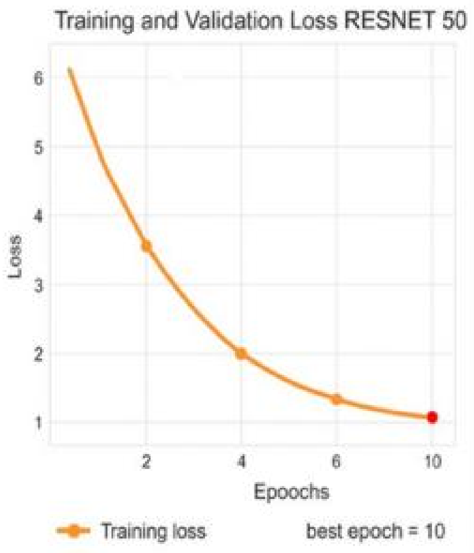
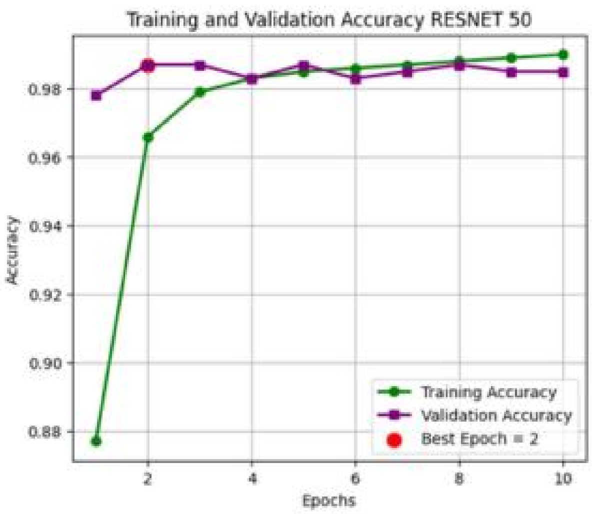
Figure 4, the ResNet50-based architecture uses the pre-trained ResNet50 model as a deep feature extractor, producing a high-level feature vector of dimension 1280 from the input images. This output is passed through a Batch Normalization layer to stabilize and normalize feature distributions, improving training convergence. Lastly, the multi-class classification is done by a dense output layer with 8 neurons which corresponds to the eight target classes. In general, the design can be described as one that utilizes transfer learning of ResNet50, but it has lightweight classification layers to enable efficient learning using a relatively small number of trainable parameters.





The figure gives the performance of the ResNet-50 model with training and validation performance during 10 epochs, and the accuracy and the loss trends are presented, which characterize successful learning and successful generalization. Over the course of the training accuracy rises quickly starting with the first epoch, and plateaus at approximately 98, and similarly, the validation accuracy rises quickly and also stabilizes at approximately 98-99, exhibiting minor variation, indicating the absence of overfitting and high consistency between the two training and validation data sets.The loss plot shows a steady and substantial decrease in both training and validation loss across epochs, with validation loss remaining slightly higher but closely aligned with training loss, further confirming stable convergence. The best validation performance is observed around epoch 10, marked in red, where the model achieves low loss and high accuracy simultaneously. Overall, the close alignment between training and validation curves demonstrates that the ResNet-50 model learns discriminative features effectively, converges smoothly, and generalizes well to unseen data for the given classification task.

5. CONCLUSION

This study demonstrates the effectiveness of deep learning–based image classification techniques for the automated detection of plant diseases and pest infestations using leaf images. By analyzing visually distinct symptoms such as discoloration, necrotic lesions, fungal growth, deformation, and edge damage, the proposed approach successfully differentiates between multiple disease classes, including Gall Midge, Powdery Mildew, Sooty Mould, Die Back, Cutting Weevil, and Anthracnose. The diversity and realism of the dataset play a crucial role in enabling the model to learn complex visual patterns that closely resemble real agricultural conditions.

Transfer learning on pre-trained convolutional neural networks has a strong impact on increasing classification performance and minimizing training time and computational needs. The further enhancement of model resilience is the data augmentation that fills the differences in lighting, background, and severity of symptoms. The experimental findings denote that there is a strong ability to generalize results, which provides evidence of the possibility of deep learning models to facilitate precise and timely diagnosis of diseases in real farming setting. These automated systems will be able to decrease the use of manual inspection, reduce diagnostic mistakes, and provide the opportunity to intervene in time and avoid the loss of crops on a large scale. Despite promising results, future work may focus on expanding the dataset to include additional disease classes and healthy samples to further improve model reliability. Integrating real-time image capture through mobile or IoT-based platforms could enhance field-level deployment. Additionally, combining visual data with environmental and temporal information may provide deeper insights into disease progression and risk prediction.

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Author Contributions Iqra Arshad wrote the original draft of the manuscript. Muhammad Shoaib Arshad supervised the study. Muhammad Zubair was responsible for investigation and conceptualization. Muhammad Yousif developed the methodology and performed validation. Zahra Maryam handled data curation and resources. Muhammad Haseeb Zia conducted the formal analysis. All authors reviewed and approved the final manuscript for submission.

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Data Availability The dataset used in this study is publicly available on Kaggle. The dataset link is: https://www.kaggle.com/datasets/aryashah2k/mango-leaf-disease-dataset.

Declarations

Conflict of interest The authors declare that they have no conflict of interest.

Ethical approval This study utilizes a publicly available benchmark dataset from Kaggle (Mango Leaf Disease Dataset: https://www.kaggle.com/datasets/aryashah2k/mango-leaf-disease-dataset). The dataset is fully de-identified and contains no personally identifiable information. As this research involves secondary analysis of existing, anonymized data, no separate ethical approval was required.

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