Original Research

Automated Identification of Mango Leaf Diseases Using Deep Convolutional Neural Networks

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Abstract

Mango, a widely cultivated tropical fruit, is susceptible to various foliar diseases that adversely affect yield, quality, and market value. Early and exact disease identification is crucial for effective crop management and sustainable production. Conventional diagnostic methods, primarily dependent on manual visual inspection, are often inefficient and liable to error. To overcome these challenges, the current study proposes a lightweight convolutional neural network (CNN) model for automated detection and classification of mango leaf diseases using image data. A dataset of 4,000 images comprising 3,500 diseased and 500 healthy samples across 8 categories, including anthracnose, die back, bacterial canker, and powdery mildew. Comparative analyses with pretrained models (DenseNet169, DenseNet121, and InceptionV3) showed high accuracies. Among them, DenseNet121 and InceptionV3 reach approximately 99.92%. A custom 13-layer CNN with 55,184 trainable parameters was developed, achieving 100% accuracy and outperforming all benchmark models in precision, recall, and F1-score. The proposed model demonstrates strong diagnostic effectiveness and computational efficiency, offering a practical solution for real-time, field-level disease monitoring in mango cultivation. The proposed approach combines high diagnostic accuracy with computational efficiency, making it practical for real-time, field-level disease monitoring. This progress supports precision agriculture by providing accessible and user-friendly plant health assessment tools that promote sustainable mango production.

Keywords: mango leaf diseases, plant disease detection, precision agriculture, automated diagnosis, lightweight CNN

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Introduction

Agriculture-dependent countries face serious risks and significant losses due to plant diseases. This reduces the yield and quality of fruits and crops. Pakistan is a country that earns a lot of income by producing and exporting these agricultural products, vegetables, and fruits cultivated around the nation [1]. As a result, it is necessary to use computer vision and image processing technology to identify diseased plants [2, 3]. Early diagnosis of plant diseases may increase the likelihood of cure, thereby reducing crop damage. In some circumstances, diseases have no obvious indications and respond too late to their surroundings; however, certain diseases have clear signs based on their signs [4]. To preserve the agricultural product in time, an early disease detection system is also required [5].

Mangoes are an extensively consumed fruit that is readily available during the summer. It is significant in Pakistan's agricultural industry due to its large quantity of output [6]. The cultivation of mangoes is crucial to the world's agricultural industry. One of the most well-known and extensively consumed tropical fruits, mangoes, has a long cultural history and significance across many locations. They are valued for their nutritional advantages in addition to their exquisite taste. Mango is an important part of a healthy diet because it is a good source of vitamins, minerals, and dietary fiber [7]. Currently, the farmers in this area are concerned about the effects of numerous diseases on mango plants, which are caused by climate change and other causes. Therefore, it is essential to maintain this fruit plant to ensure the continued availability of nutritious and delicious mangoes for the rest of the world [8]. Several ailments afflict mango trees, including: Mango deformity disease, bacteriological flower disease, anthracnose, sooty mold, bacterial black spot disease, Golmachi disease, red rust disease, Moricha disease, apical bud necrosis, lichens, powdery mildew, root rot disease, damping off, and ganoderma root rot disease [9]. Powdery mildew disease is estimated to be responsible for almost 23% damage to mango plants and their economy worldwide. Anthracnose is responsible for up to 39% of mango tree damage globally [7]. Image processing techniques and strategies play an important role in providing guidance for farmers based on leaf image analysis for early disease detection. As a result, the farmer can execute the necessary steps.

Researchers have proposed several new computer methods, deep learning procedures [10-14], artificial intelligence tools, and machine learning, as well as optimization methods for the classification of mango leaf diseases. These solutions offer an excellent foundation for mango plant strengthening, care, disease identification, and efficiency improvements [15]. Effective results have recently been developed by applying Deep learning (DL) approaches, especially Convolutional Neural Networks (CNNs), for the classification of plant diseases [16]. These methods and purposes use images as input to classify leaves as healthy or diseased, allowing them to detect leaf diseases early. This approach, however, processes detailed images captured under beneficial quality and environmental conditions [17]. Accurate and prompt recognition and classification of mango leaf infections are essential to reducing their negative impacts. This is where the use of cutting-edge technologies, like CNN algorithms, can be extremely useful. By developing an automated mango leaf disease classification system using CNNs, it becomes possible to detect diseases early, provide appropriate interventions, and effectively manage mango tree health, ultimately safeguarding fruit quality, yield, and the economic sustainability of mango production [18].

The study [19] presented a novel categorization approach for mango leaf diseases. The suggested system consists of 4 stages: data preparation, feature selection, learning and categorization, and performance assessment. We found 1,536 photos in both the healthy and diseased categories. The open Kaggle database was used to obtain the dataset for this study. Accuracy and sensitivity are evaluation measures that help discover the best-performing design. A few extra performance metrics were also used. The top model has a sensitivity of 96.2 and an accuracy of 97.9.

This research [20] provides a deep learning-based strategy for categorizing disorders of mango leaves. Deep learning-based categorizing algorithms, such as Support Vector Machines (SVM), categorize multiple image datasets and provide the greatest classification results. In this paper, we suggested a technique for extracting deep characteristics from images by enhancing the SVM and then using the SVM and Stochastic Gradient Descent (SGD) hybrid method. This study looks at the uses of the primary Harumanis Mango Leaves 2021 Dataset. These experimental findings illustrate that the proposed method has a 97.7% precision.

In this work [21], three ML algorithms are used to detect mango diseases. A dataset with pictures of diseased and healthy mango fruits and leaves in 20 different classifications has been developed. We obtained our dataset from various websites, including Krishi Batayon. We generated 20 categories for our raw data, 11 of which feature images of diseased mango leaves and 7 of which include shots of miserable mango fruit. The other additional classes show images of healthy mangoes and healthy fruits. DenseNet169 achieves the greatest accuracy rate of 97.81% across various machine Learning techniques, with precision, recall, and F1-scores of 97%, 96%, and 96%, respectively.

Manual detection systems for mango leaf diseases face challenges such as a shortage of experts, high costs, and diverse symptomatology [22]. They present an automated approach in which input pictures are collected from standardized supplies, using contrast enhancement, and segmented using optimal Fuzzy C Means (FCM). The Deviation-based Updated Dingo Optimizer (D-UDOX) is used for improving

parameters. D-UDOX handles a balanced choice of features. The balanced data are fed into the Optimized Recurrent Neural Network (WO-RNN) classifier. Deep features are also extracted from a divided image using ResNet-150. WO-RNN performs the classification using the obtained deep characteristics. D-UDOX is used to modify the parameters of RNN and ResNet-150. The suggested method obtains 96% accuracy and 93% F1 score.

This study [23] focuses on the classification of typical mango leaf disorders in Bangladesh using image processing and a deep neural network. In this article, we presented a Lightweight Convolutional Neural Network (LCNN) to perfectly categorize healthy mango leaves and seven different mango leaf diseases very accurately. This study makes use of the Mango Leaf BD dataset. It is Bangladesh's first complete mango leaf infection dataset. The results of the proposed LCNN model are contrasted with those of many pre-trained models, including VGG16, Resnet50, Resnet101, and Xception, and it is discovered that LCNN obtains the highest testing accuracy of 98%.

In this study [5], the researchers use an Artificial Neural Network (ANN) approach to identify signs of disease on the surface of plants with microscopic disease chunks that can only be seen with better-resolution pictures. Their data collection contains 450 photos of mango leaves of 4 different types (three unhealthy and one healthy): Gall Midge, Powdery Mildew, Anthracnose, and Healthy. They evaluate the results produced with our approaches to those achieved with a different approach that employs prominent CNN models (AlexNet, VGG16, and ResNet-50), improved with the use of transfer learning. The findings of the ANN outperform those of CNNs with a smaller network structure (89.41%, 78.64%, 79.92%, and 84.88%, respectively).

This study [24] describes a unique deep learning CNN design for identifying mango Anthracnose sickness. Validation is based on a real-time dataset gathered from farms in Karnataka, Maharashtra, and New Delhi. It contains 2 types of photos of mango plant leaves (healthy and damaged leaves). The 2 datasets of mango leaf pictures are presented in this research work. A 3500 photo dataset was utilized (with 80% for training and 20% for validation). Compared to other cutting-edge algorithms, the suggested method achieves a recognition accuracy of approximately 96.16%.

Convolutional Neural Networks are used in the study to identify and recognize mango leaf disorders efficiently and reliably, boosting their applications in image identification, object classification, and segmentation. In the suggested research [25], they construct a Convolutional Neural Network-based model for timely classification and identification of mango leaf diseases. SKUAST-J provides a dataset of 980 pictures. The information collected is divided into 4 categories: normal, anthracnose, red rust, and powdery mildew. A developed convolutional neural network algorithm is being used on greater data to recognize and classify diseased mango leaves. The suggested CNN-based model achieves 90.36% precision.

This research [6] presents a novel recognition approach based on the leaf's blood vessel structure, which is proposed to identify the sick area. The leaf vein pattern is segmented using this leaf vein-seg method. The data set utilized for this research was assembled for self-collected photographs taken with various sorts of image-capturing devices. The RGB photos were obtained from various mango-farming districts in Pakistan, including Multan, Lahore, and Faisalabad. Then, characteristics are identified and merged using Canonical Correlation Analysis (CCA). The cubic support vector machine (SVM) is used to validate the results obtained from the classification phases. The suggested model's obtained accuracy is 95.5%, proving its great value to growers of mango plants for the prompt detection and recognition of disease. Table 1 describes the summary of the existing literature review.

The current study focuses on developing an efficient and applied protocol for identifying mango leaf diseases using a lightweight convolutional neural

Table 1. Summary of reviewed literature.

Reference	Method	Dataset	Accuracy
[19]	DNN	Mango leaf species	97.9%
[20]	SVM and SGD	Harumanis Mango Leaves 2021	97.7%
[21]	DenseNet169	Mango leaf disease dataset	97.81%
[22]	RNN	Customized dataset	96%
[23]	LCNN	MangoLeafBD	98%
[5]	CNN	Plant village dataset	89.41%,
[24]	CNN	Customized dataset	96.16%
[25]	CNN	Customized dataset	90.36%
[6]	SVM	Customized dataset	95.5%

network (CNN). Key objectives include standardizing CNN architecture, applying transfer learning strategies, and evaluating potential through standard metrics. A customized model was compared with advanced architectures like DenseNet121, DenseNet169, and InceptionV3, displaying high accuracy in categorizing multiple disease types. The suggested system provides a practical solution in the field for early disease diagnosis to reduce dependence on manual inspection and support improved crop health management in mango production on a sustainable basis.

Materials and Methods

The mango leaf disease dataset is a publicly available collection of mango leaf images sourced from the Kaggle website (https://www.kaggle.com/datasets). This dataset comprises a total of 4,000 images, covering 8 distinct diseases (Anthracnose, Bacterial canker, cutting weevil, Die back, Gall midge, Healthy, Powdery mildew, and Sooty mould) found in mango trees. Fig. 1 illustrates the representative samples of mango diseases. Each of the eight categories in the dataset comprises 500 images, making it a valuable resource for research and applications related to mango leaf disease detection and classification. The dataset is highly balanced, with an equal distribution of 500 images for each of the 8 distinct disease categories.

Image Preprocessing

Preprocessing was conducted to enhance image quality, standardize inputs, and improve model performance. All images were originally sized at 240×320 pixels and were resized to 224×224 pixels to conform to the input requirements of convolutional neural networks (CNNs). This dimension is widely adopted in deep learning applications due to its computational efficiency while retaining essential features [26].

Pixel values were normalized to the range [0,1] by dividing each pixel's intensity value by 255. Normalization ensures consistent feature scaling across inputs, accelerates convergence, and prevents numerical instability during training [27].

To reduce overfitting and improve generalization, data augmentation was applied to the training set. Random rotations, horizontal flips, and zoom transformations were performed to artificially expand dataset variability. Such augmentation techniques have been demonstrated to significantly improve CNN robustness in image classification [28].

Finally, the dataset was partitioned into training (80%) and testing (20%) subsets, ensuring unbiased model evaluation on unseen samples. The overall preprocessing and methodological pipeline are illustrated in Fig. 2.

CNN Architecture

Convolutional neural networks (CNNs) were employed to automatically learn discriminative features from mango leaf images. CNNs have been extensively applied in plant disease recognition due to their ability to capture complex spatial and texture patterns [26, 29, 30]. A standard CNN typically comprises convolutional, activation, pooling, and fully connected layers, which together enable hierarchical feature extraction and classification. In this study, we adopted a custom deep CNN architecture tailored for mango leaf disease classification.

The proposed architecture (Fig. 3) consists of seven convolutional layers activated by the rectified linear unit
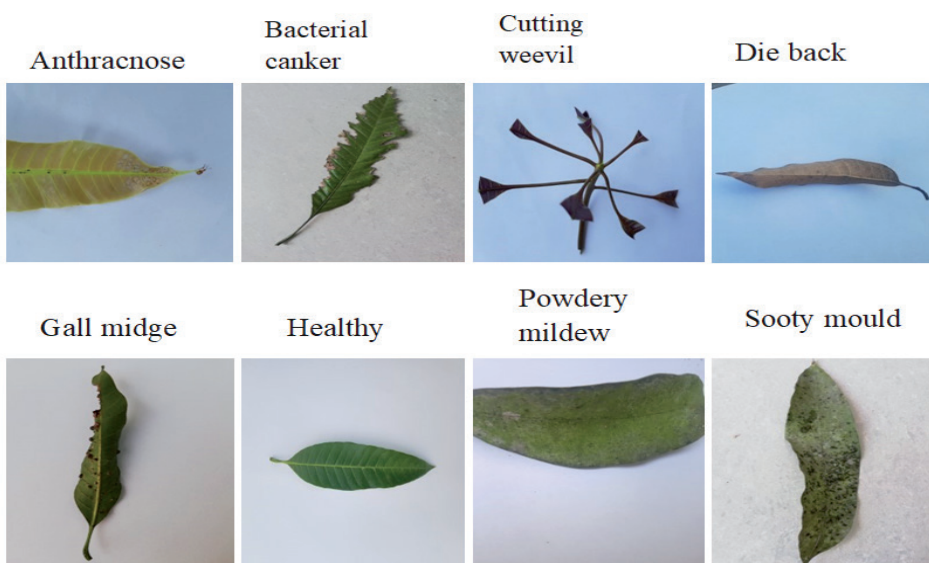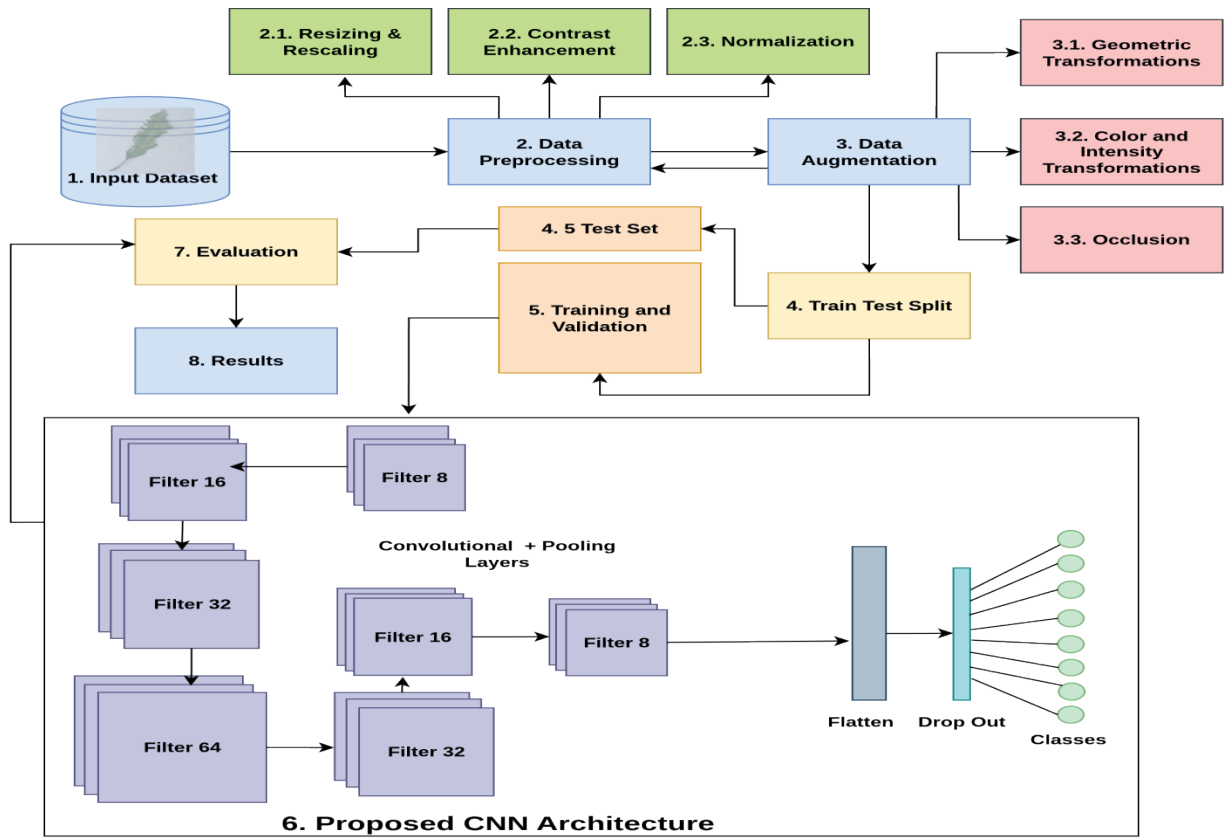

Fig. 1. Sample images from the dataset.

Fig. 2. Block diagram of the proposed methodology.

(ReLU) [31], interleaved with 4 max-pooling layers to progressively reduce spatial dimensions while retaining salient features. A flattening layer transforms the feature maps into a one-dimensional vector, which is then processed by a fully connected dense layer. The final output layer applies a Softmax activation function to predict the probability distribution across the 8 disease categories. Detailed configurations of the architecture are summarized in Table 2.

Proposed Deep CNN Architecture

In this research, we provide a deep CNN architecture for classifying mango leaf disorders. The simulation parameters of the proposed deep CNN architecture are shown in Table 2, while the parameters and their tuned values are shown in Table 3. The model comprises 7 convolutional layers with RELU activation, 4 max-pooling layers, and 1 dense layer with Softmax activation. To improve deep CNN efficiency, a hidden layer called flatten is utilized, which generates a 1D array using the image as input, making it easier to deal with huge amounts of input. The model presented features an API architecture containing multiple hierarchical layers that extract and process features from the input image. The first layer consists of eight convolution layers, which follow RELU activation. The max pooling layer is the second layer with a pool dimension of 2×2, which decreases the dimension of

the image that is provided in it. Convolution layers with 16 and 32 filters are used in the third and fourth layers, which are subsequently followed by RELU functions.

The following layer is another maximum pooling layer with a similar pool size. As shown in Fig. 3, another layer is added called flatten, which flattens the outcomes from the previous layers and returns features from each input it receives. The class label presented is the layer's output, which is used to assess the overall correctness of the model being suggested.

Evaluation Measures

Equation (1) demonstrates how different performance metrics, including recall, accuracy, precision, confusion matrix, and F1 score, are utilized to validate the expected output of mango leaf disease detection.

$Accuracy$

$$= \frac{\text{True positive} + \text{True negative}}{\text{True positive} + \text{True negative} + \text{False positive} + \text{False nagative}}$$

$$(1)$$

Where accuracy is the fraction of correctly classified instances in the test set.

The instances that are truly positive in the test set yet are accurately classified as such by the classifier are known as true positives (TP). Cases that are truly negative in the test set yet are accurately classified

Table 2. Parameter details of the proposed CNN architecture.

Layer (type)	Output Shape	Param #	Kernel Size/Stride
Input Layer	(224, 224, 3)	0	-
Rescaling (1/255)	(224, 224, 3)	0	-
Conv2D	(222, 222, 8)	224	3×3 / 1
MaxPooling2D	(111, 111, 8)	0	2×2 / 2
Conv2D	(109, 109, 16)	1,168	3×3 / 1
Conv2D	(107, 107, 32)	4,640	3×3 / 1
MaxPooling2D	(53, 53, 32)	0	2×2 / 2
Conv2D	(51, 51, 64)	18,496	3×3 / 1
Conv2D	(49, 49, 32)	18,464	3×3 / 1
MaxPooling2D	(24, 24, 32)	0	2×2 / 2
Conv2D	(22, 22, 16)	4,624	3×3 / 1
Conv2D	(20, 20, 8)	1,160	3×3 / 1
MaxPooling2D	(10, 10, 8)	0	2×2 / 2
Flatten	(800)	0	-
Dropout (0.5)	(800)	0	-
Dense	(8)	6,408	-
Total		55,184	

as such by the classifier are called true negatives (TN). Cases that are truly negative in the test set but are mistakenly classified as positive by the classifier are called false positives (FP). False negatives (FN) are examples that are positive in the test set but are incorrectly labeled as negative by the classifier.

As a result, the positive or healthy mango leaf samples are P, whereas the negative or unhealthy mango leaf samples are N, as shown in Equations (2) and (3). The specificity and sensitivity formula are as follows:

$$Specificity = \frac{True\ positive}{True\ positive + False\ negative} \quad (2)$$

$$Sensitivity = \frac{True\ negative}{True\ negative + False\ positive} \quad (3)$$

Table 3. Parameters and their tuned values.

Parameters	Values
Convolutional layer	7 (3*3)
Pooling layer	4 (2*2)
Optimizer	Root Mean Square Propagation (rmsprop)
Epochs	100
Batch size	32
Learning rate	0.001

The percentage of actual positive examples among all occurrences that the classifier predicts to be positive is known as precision, as shown in Equation (4). Dividing the actual number of successes by the classifier's predicted number of successes, one can assess precision.

$$Precision = \frac{True\ positive}{True\ positive + False\ positive} \quad (4)$$

The percentage of genuine positive cases in the test set that truly are positive is known as recall, as shown in Equation (5).

$$Recall = \frac{True\ positive}{True\ positive + False\ negative} \quad (5)$$

Equation (6) demonstrates that the F1 score, which provides a combined measure of precision and recall; is the harmonic mean of precision and recall.

$$F1\ score = 2 * \frac{Precision * Recall}{Precision + Recall} \quad (6)$$

Experiment Setup

The efficiency of the proposed mango leaf disease classification framework is validated using several types of evaluation criteria and comparisons with other models. TensorFlow and Python programming are
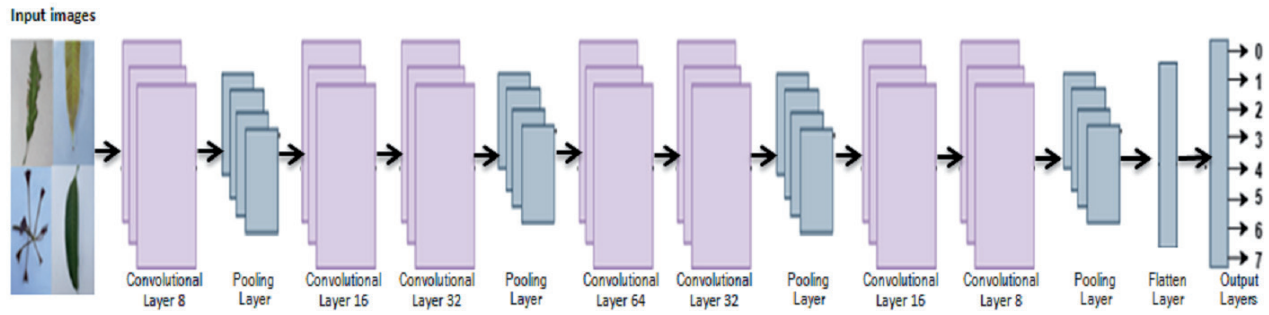
Fig. 3. The proposed deep CNN architecture.

utilized to carry out the model mentioned in the present research. The complete experimental setup was done in Python using Anaconda. For constructing, compiling, and testing the Model, the Keras libraries are used. to build, compile, and test the model. TensorFlow was used to develop models as a backend, as Python 3.12 on a computing environment was used in these experiments with a 2.20GHz Intel(R) Core (TM) i9-13950HX CPU, NVIDIA GeForce RTX 4060 GPU, and 64GB of RAM.

Results and Discussion

The dataset contained a total of 4000 images, and the instance images are separated into 2 sections, with one portion used for training and the second for testing. The dataset is divided into 2800 images for training and 1200 images for testing to obtain results, i.e., randomly split into an 80% training set and a 20% held-out test set.

Table 4 presents a comparative performance analysis between the proposed Deep CNN and other well-established pretrained models, i.e., DenseNet121, DenseNet169, and InceptionV3, for the multi-class classification of mango leaf diseases. To ensure a robust comparison, identical training strategies were applied to all pre-trained models. All layers were unfrozen and set to trainable to allow for full fine-tuning on the mango leaf dataset. The models were compiled with the Adam optimizer with a learning rate of 1e-4 and trained using early stopping with a patience of 10 epochs, monitoring the validation loss. The analysis is based on standard evaluation metrics, i.e., precision, recall, F1-score, and overall accuracy across eight disease classes. The model achieved an accuracy of 100% on the held-out test set. To further evaluate robustness, 5-fold cross-validation was also performed.

In comparison, DenseNet121, the best-performing pretrained model, achieved near-perfect performance with an overall accuracy of 99.92%, but still exhibited minor reductions in recall for Die Back (0.9933) and in precision for Powdery Mildew (0.9934), resulting in slightly diminished F1-scores (0.9967) for these classes. Similarly, DenseNet169 and InceptionV3 demonstrated strong but slightly inconsistent results, with recall

dropping as low as 0.90 for Gall Midge in the case of InceptionV3, indicating potential sensitivity to intra-class variability or overlapping visual features in certain categories.

The proposed Deep CNN model demonstrates clear superiority in classifying mango leaf diseases, achieving perfect performance across all 8 disease categories with precision, recall, and F1-score values of 1.00 and an overall accuracy of 100%. This exceptional performance significantly surpasses that of competitive pretrained models such as DenseNet121, DenseNet169, and InceptionV3, establishing the proposed model's supremacy in disease-specific feature extraction. Notably, the model is designed with a streamlined architecture comprising only 13 layers and a total of 55,184 trainable parameters, substantially fewer than most pretrained architectures, yet it outperforms them in both generalization and precision. This achievement is attributed to the model's end-to-end training on domain-specific data, allowing it to learn finely grained morphological and textural features critical for distinguishing between both visually distinct and subtly varying disease symptoms [32]. Furthermore, its ability to maintain class-wise balance, even in the presence of overlapping symptoms and intra-class variability, underlines its robustness against class imbalance and environmental noise. The lightweight yet highly expressive architecture ensures computational efficiency, making it suitable for real-time field deployment in precision agriculture and disease monitoring systems [33].

Fig. 4 provides a comprehensive visualization of the training and validation performance of DenseNet121, DenseNet169, InceptionV3, and the proposed Deep CNN model through accuracy and loss plots. Fig. 4a) displays the training and validation accuracy curves for DenseNet121, showing a steady rise and convergence towards high accuracy with minimal variance, indicating effective learning. Fig. 4b) illustrates the corresponding loss curves, where both training and validation losses decrease consistently, albeit with slight fluctuations, suggesting a well-trained yet marginally overfitted model. Fig. 4c) presents the DenseNet169 accuracy curves, reflecting strong learning behavior with high final accuracy, although the slightly wider

Table 4. Results obtained through the proposed deep CNN and other pretrained models.

Pre-trained models	Disease class	Precision	Recall	F1-score	Accuracy	Parameters (M)
DenseNet121	Anthracnose	1.0	1.0	1.0	99.92%	8.1M
	Bacterial Canker	1.0	1.0	1.0		
	Cutting Weevil	1.0	1.0	1.0		
	Die Back	1.0	1.0	1.0		
	Gall Midge	1.0	1.0	1.0		
	Healthy	1.0	1.0	1.0		
	Powdery mildew	0.9934	1.0000	0.9967		
	Sooty Mould	1.0	1.0	1.0		
DenseNet169	Anthracnose	1.0	1.0	1.0	99.75%	14.3M
	Bacterial Canker	1.0	0.9933	0.9967		
	Cutting Weevil	1.0	1.0	1.0		
	Die Back	0.9934	1.0	0.9967		
	Gall Midge	1.0	1.0	1.0		
	Healthy	1.0	1.0	1.0		
	Powdery mildew	1.00	0.9867	0.9933		
	Sooty Mould	0.9868	1.0000	0.9934		
InceptionV3	Anthracnose	1.0	0.9933	0.9967	99.92%	23.9M
	Bacterial Canker	1.0	1.0	1.0		
	Cutting Weevil	1.0	1.0	1.0		
	Die Back	1.0	1.0	1.0		
	Gall Midge	0.9934	1.00	0.9967		
	Healthy	1.0	1.0	1.0		
	Powdery mildew	1.0	1.0	1.0		
	Sooty Mould	1.0	1.0	1.0		
The Proposed Deep CNN	Anthracnose	1.0	1.0	1.0	100%	5.5M
	Bacterial Canker	1.0	1.0	1.0		
	Cutting Weevil	1.0	1.0	1.0		
	Die Back	1.0	1.0	1.0		
	Gall Midge	1.0	1.0	1.0		
	Healthy	1.0	1.0	1.0		
	Powdery mildew	1.0	1.0	1.0		
	Sooty Mould	1.0	1.0	1.0		

gap between training and validation accuracy hints at potential overfitting. The loss trajectory in Fig. 4d) further supports this, with a sharp decline in training loss and relatively stable validation loss, indicating effective convergence but room for improvement in generalization. Fig. 4e) illustrates the accuracy plot of InceptionV3, where both curves closely follow each other and improve rapidly, highlighting the model's strong learning and generalization capabilities. Fig. 4f) shows the loss curves for InceptionV3, depicting a consistent decline in both training and validation losses, although a minor divergence near convergence suggests mild overfitting. Fig. 4g) showcases the training and validation accuracy curves of the proposed Deep CNN model, which exhibits a nearly perfect and synchronized rise, achieving perfect accuracy from the

early epochs, while Fig. 4h) shows that both training and validation losses reach near-zero values in a smooth and synchronized manner [34]. These observations clearly indicate the proposed model's stability, robustness, and optimal parameter learning, further validating its superior performance compared to the pretrained counterparts.

Fig. 5 presents the confusion matrices of DenseNet121, DenseNet169, InceptionV3, and the proposed Deep CNN model, offering insights into their classification performance across all mango leaf disease classes. Fig. 5a) shows that DenseNet121 achieves near-perfect predictions, with minor misclassifications in a few categories. Fig. 5b) illustrates DenseNet169's strong overall performance but reveals slightly more confusion between visually similar classes. Fig. 5c) indicates
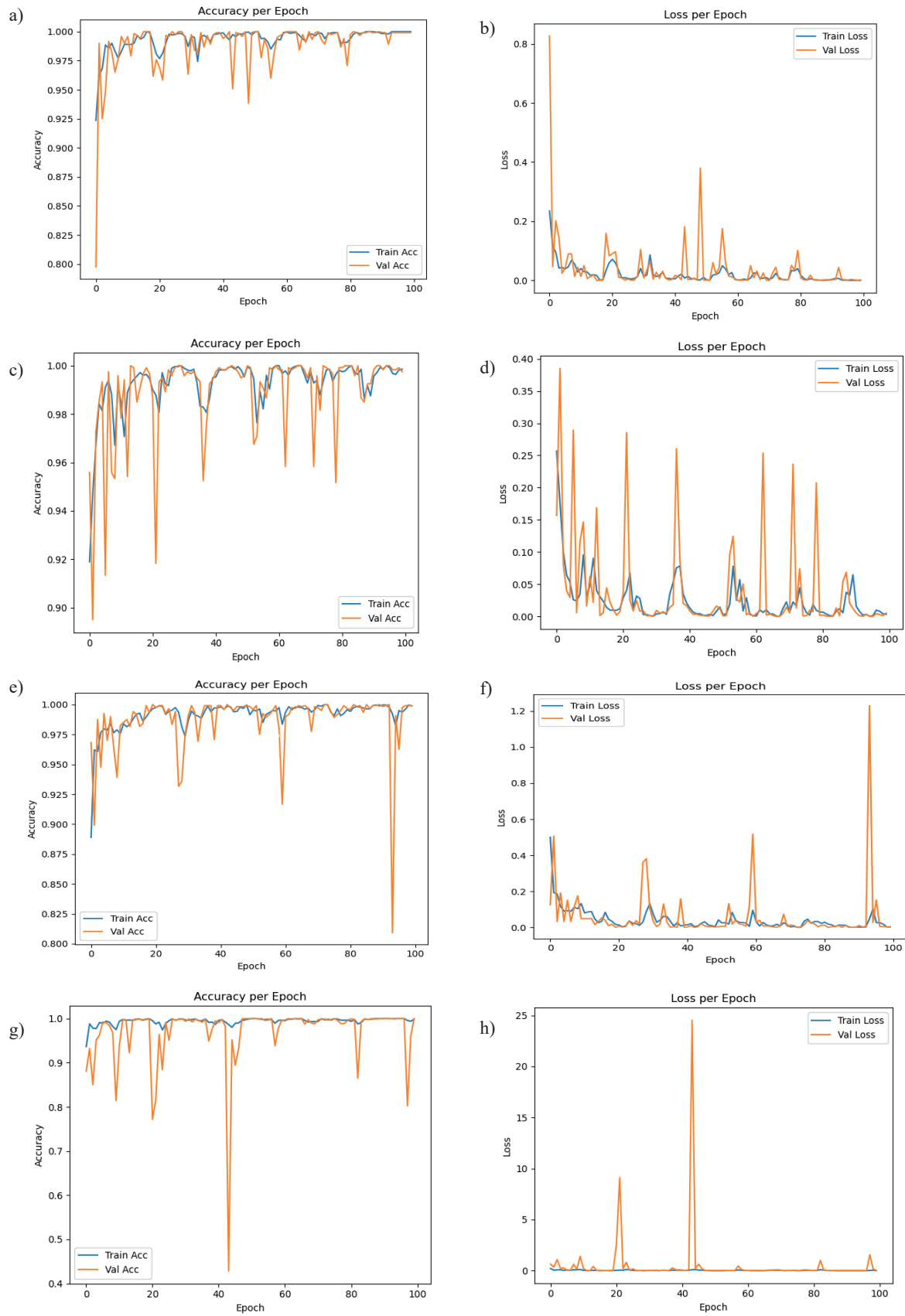
Fig. 4. Accuracy and loss plots of DenseNet121, DenseNet169, InceptionV3, and the proposed deep CNN model. a) Training and validation accuracy plot of the DenseNet121, b) Training and validation loss plot of DenseNet121, c) Training and validation accuracy plot of the DenseNet169, d) Training and validation loss plot of DenseNet169, e) Training and validation accuracy plot of the InceptionV3, f) Training and validation loss plot of InceptionV3, g) Training and validation accuracy plot of the proposed deep CNN Model, h) Training and validation loss plot of the proposed deep CNN Model.
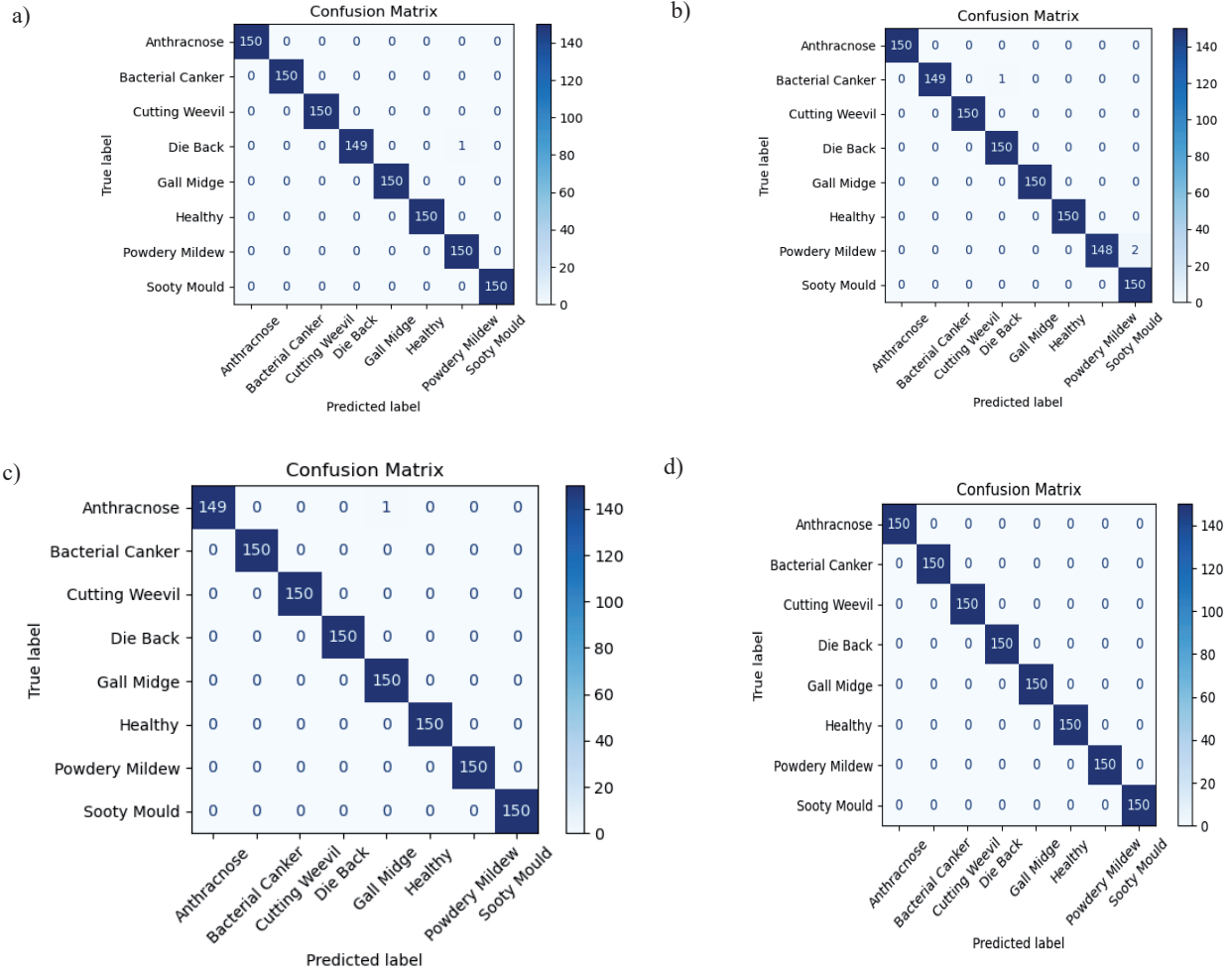
Fig. 5. Confusion matrices of the pretrained models, i.e., DenseNet121, DenseNet169, InceptionV3, and the proposed deep CNN model. a) Confusion matrix of the DenseNet121, b) Confusion matrix of the DenseNet169, c) Confusion matrix of the InceptionV3, and d) Confusion matrix of the proposed deep CNN model.

that InceptionV3 also performs well, though a few off-diagonal elements suggest occasional mislabeling. In contrast, Fig. 5d) demonstrates the proposed Deep CNN's perfect classification with zero misclassifications, reaffirming its superiority in recognizing all disease classes with complete precision [35].

Fig. 6 illustrates the ROC-AUC curves with 95% confidence intervals for DenseNet121, DenseNet169, InceptionV3, and the proposed Deep CNN model, offering a robust evaluation of each model's diagnostic reliability. Fig. 6a) reveals that DenseNet121 attains high AUC values across all classes, with narrow confidence intervals indicating consistent model behavior. Fig. 6b) shows similar trends for DenseNet169, although a slightly broader confidence band in certain classes points to marginal variability. Fig. 6c) presents the ROC-AUC curves for InceptionV3, which maintains strong discriminative performance but exhibits slightly wider intervals in a few cases, suggesting less stability under class-specific perturbations. In contrast, Fig. 6d) highlights the proposed Deep CNN model's exemplary performance, achieving AUC values approaching 1.0

across all classes with uniformly narrow confidence intervals. This underscores the model's exceptional ability to distinguish between healthy and diseased categories with high confidence and minimal uncertainty, making it a highly dependable tool for practical disease detection scenarios [36].

Comparison with Recently Published Studies

The suggested CNN model for mango leaf detection exhibits superior accuracy when compared to existing models. Leveraging advanced convolutional layers, the proposed model excels in capturing intricate features crucial for precise classification, outperforming traditional methods, as shown in Table 5. This enhanced accuracy underscores the potential of the proposed CNN model as a more reliable and effective tool for automated mango leaf detection [38].

A variety of machine [37] learning algorithms were applied to identify and categorize mango leaf illnesses [8], including a CNN that achieved 96% accuracy in diagnosing leaf diseases. The study [32] used VGG-Net
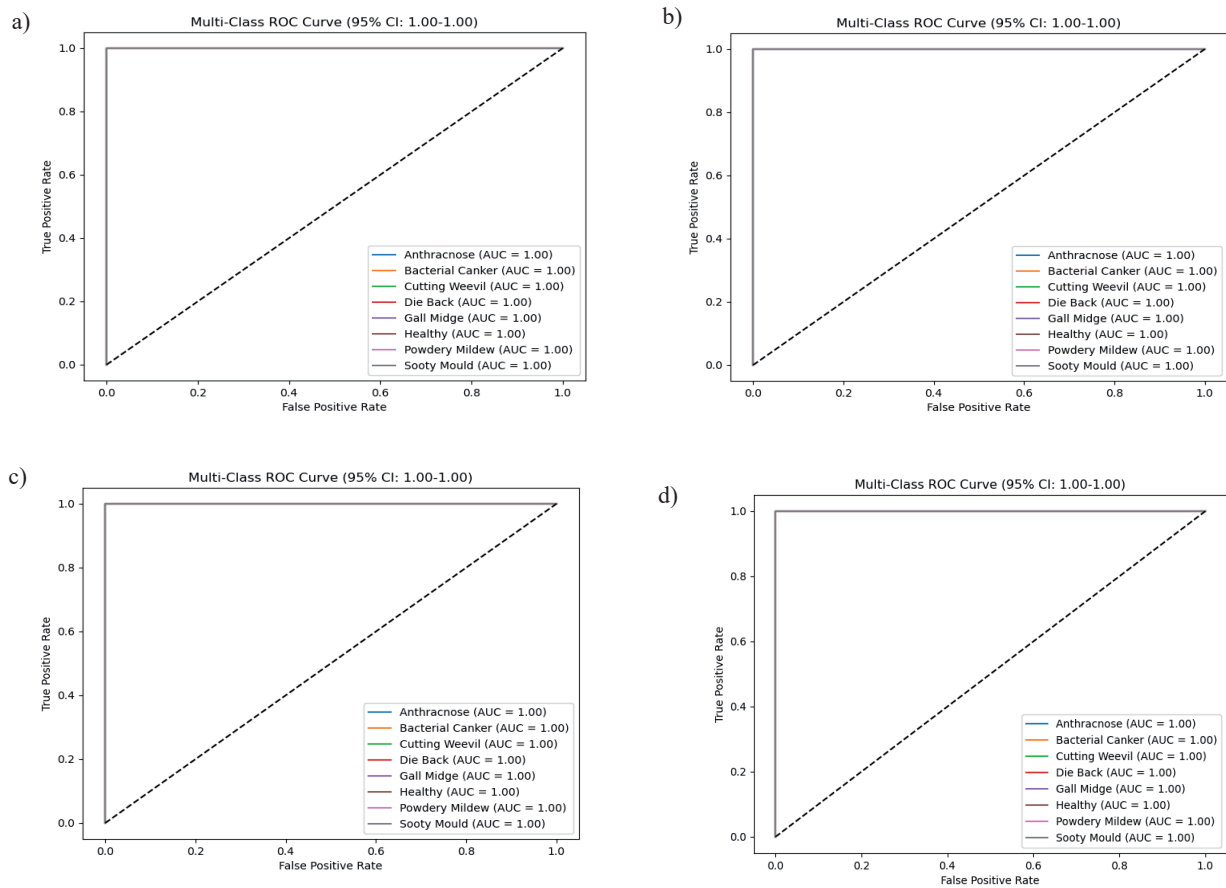
Fig. 6. ROC-AUC curves with 95% confidence intervals of the pretrained models, i.e., DenseNet121, DenseNet169, InceptionV3, and the proposed deep CNN model. a) ROC-AUC curves with 95% confidence intervals of the DenseNet121, b) ROC-AUC curves with 95% confidence intervals of the DenseNet169, c) ROC-AUC curves with 95% confidence intervals of the InceptionV3, and d) ROC-AUC curves with 95% confidence intervals of the proposed deep CNN model.

for the classification of the infected mango leaves dataset with 92% accuracy. The CNN model demonstrated exceptional performance in identifying mango leaves, attaining a 98% accuracy rate [33]. Mango leaf disease categorization and detection using a CNN-based approach showed a 90.36% accuracy rate [25]. The study [20] used SVM and SGD for the classification of mango leaf disease, achieving 97.7% accuracy. The study [21] utilized the DenseNet169-based CNN to detect mango leaf disease with 97.81% accuracy. [23, 39, 40] proposed a lightweight convolutional neural network for detecting mango leaf diseases, achieving 98% accuracy [41]. The proposed CNN model in this study outperformed all other methods, achieving an impressive 100% accuracy.

The perfect accuracy on the test set, while promising, may raise concerns of overfitting; however,

Table 5. Comparison of the results obtained with the proposed model and the published studies.

References	Technique	Description	Accuracy
[8]	CNN	Identify leaf disease	96%
[32]	CNN (VGGNet)	Classification of infected mango leaves	92%
[33]	CNN	Recognition of mango leaves	98%
[25]	CNN	Classification and detection of mango leaves	90.36%
[20]	SVM and SGD	Classification of mango leaf diseases	97.7%
[21]	CNN	Detection of mango leaf diseases	97.81%
[23]	CNN	Detection of mango leaf diseases	98%
Proposed model	CNN	Classification and detection of mango leaf diseases	100%

the consistently high performance achieved through 5-fold cross-validation (mean accuracy: 99.98%±0.02%) helps mitigate this concern and highlights the model's robustness.

Practical Deployment and Real-World Application

The proposed model's high accuracy and computational efficiency make it a prime candidate for real-world deployment of resource-constrained hardware. Two primary pathways are envisaged: integration into a mobile application, for instance, in-field farmer diagnosis, and deployment on edge devices coupled with drones for automated, large-scale crop monitoring. Future work will address practical challenges like varying field conditions and focus on developing a functional prototype to validate the model's efficacy in real-world scenarios.

Limitations and Future Work

Despite strong performance, this study has limitations. The model was trained in curated datasets, and its generalizability to the full variability of real-world field conditions requires further validation. Future work will focus on external validation with more diverse data, practical deployment via a mobile application prototype, architectural refinement to enhance robustness, and expanding the model's scope to include disease severity estimation.

Conclusions

This study successfully developed a lightweight deep convolutional neural network for the automated classification of mango leaf diseases. The model demonstrated exceptional performance, achieving high accuracy on a balanced, multi-class dataset, while maintaining significantly lower computational complexity than advanced pre-trained architectures. The primary contribution of this work is a highly accurate, yet resource-efficient model specifically designed for practical deployment. Its compact design makes it a viable candidate for integration into mobile or edge-computing devices, directly supporting the goals of precision agriculture by providing a tool for rapid, in-field disease diagnosis. This capability is crucial for enabling timely interventions, reducing crop losses, and promoting more sustainable orchard management practices, moving beyond theoretical applications to offer tangible benefits for mango cultivation. The lightweight CNN model is highly accurate, computationally efficient, and scalable, making it suitable for integration into mobile-based diagnostic systems for real-time mango leaf disease detection in the field.

Conflict of Interest

Acknowledgments

Data Availability

The datasets generated during the current study are available from the corresponding author on reasonable request.

Author Contributions

Muhammad Iqbal, Waheed Anwar and Hina Shafique: Conceptualization, supervise, methodology, investigation and data curation. Ghulam Gilanie, Maryam, Adel A. Rezk and Sezai Ercisli: Formal analysis and writing draft of manuscript. Adel A. Rezk, and Othman Al-Dossary: project management. Hossam S. El-Beltagi, Mohammed I. Aldaej, Bader Alsubaie and Jameel M. Al-Khayri: Review and editing and funding acquisition. Muhammad Iqbal and Waheed Anwar: Software application and technical support.

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