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Optimizing papaya yield: the evaluation of deep learning models for automated disease detection

Tejas Rana, Chintan Thacker
Department of Computer Science Engineering, Parul Institute of Engineering and Technology, Parul University, Gujarat, India

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ABSTRACT

The current research will create a robust and successful deep learning (DL) system to recognize and classify papaya leaf diseases. The traditional disease detection techniques are both time-consuming and unreliable, and extensively rely on expert knowledge, therefore limiting them in terms of scalability in agricultural practice. To tackle this issue, the convolutional neural network (CNN)-based method is suggested and tested on the BDPapayaLeaf that includes 2,159 images of papaya leaf with four disease categories and healthy papaya leaves, i.e., anthracnose, bacterial spot, leaf curl (reversal), and ring spot. The data was split into training 80%, validation 10%, and testing 10% data. Pictures were downscaled to 224×224 and normalized before training. Six trained CNN structures VGG16, VGG19, InceptionV3, DenseNet121, MobileNetV2, and ResNet50 were examined. The top model in terms of classification accuracy, according to them, was InceptionV3 with 89% in terms of classification accuracy, showing a high level of performance on true positive and false negative. The findings indicate that DL is an effective and precise method of automated detection of papaya leaf disease and is useful in improving precision and reliability in agricultural diagnostics.

Corresponding Author:

Tejas Rana
Department of Computer Science Engineering, Parul Institute of Engineering and Technology
Parul University
Waghodia, Vadodara, Gujarat, India
Email: tejas.rana24781@paruluniversity.ac.in

1. INTRODUCTION

Agriculture plays a vital role in ensuring global food security and economic stability. However, crop productivity is frequently affected by plant diseases that cause major reductions in yield and quality. Plant pathogens and pests can spread rapidly depending on environmental and seasonal conditions, resulting in significant agricultural losses. These infections directly affect food production systems at both national and international levels, leading to financial and social challenges for farmers and agricultural industries. According to the Food and Agriculture Organization (FAO), plant diseases are responsible for approximately $220 billion in economic losses worldwide each year [1], [2]. Therefore, early identification and proper management of plant diseases are crucial for minimizing crop damage and maintaining sustainable agricultural production.

Traditionally, farmers rely on chemical treatments such as insecticides, herbicides, and fungicides to protect crops from diseases and pests. Although these chemicals can help improve crop productivity, their excessive use may cause environmental pollution and health risks. Conventional plant disease detection methods often depend on manual observation by farmers or agricultural experts, which can be time-consuming and inaccurate due to limited expertise or delayed diagnosis. In many cases, disease symptoms become visible only after the infection has already spread, making early detection difficult. Consequently, there is an increasing demand for automated and intelligent systems that can detect plant diseases efficiently and accurately [3], [4].

In recent years, advancements in artificial intelligence (AI), machine learning (ML), and computer vision have significantly improved plant disease detection methods. Traditional ML techniques typically involve extracting features such as color, texture, shape, and patterns from plant images to classify healthy and diseased leaves. The k-nearest neighbors (KNN) technique is a nonparametric, supervised ML technique commonly applied to pattern recognition [5], [1]. However, these approaches require manual feature extraction and extensive preprocessing, which can limit their performance when dealing with complex datasets.

Deep learning (DL) has emerged as a powerful technique for image-based plant disease detection due to its ability to automatically learn hierarchical features from raw image data. Convolutional neural networks (CNNs) are widely used DL architectures that have demonstrated high accuracy in image classification tasks. Several DL models, including VGG19, ResNet50, InceptionV3, MobileNet, DenseNet, and YOLO-based architectures, have been successfully applied for detecting plant diseases from leaf images [6], [7]. These models are capable of identifying subtle visual differences between healthy and infected leaves, making them highly effective for agricultural applications.

Papaya is an economically important tropical fruit crop cultivated in many parts of the world. However, papaya plants are highly susceptible to various diseases that affect leaf health and crop productivity. Common papaya leaf diseases include anthracnose, bacterial spot, leaf curl, and papaya ring spot virus, which often appear as visible spots or discoloration on leaves. If not detected early, these diseases can spread rapidly and cause severe crop losses. Traditional inspection methods require farmers to examine each plant individually, which is impractical for large farms and can increase the risk of spreading infections [8]–[10]. With the advancement of image processing techniques, automated plant disease detection systems have gained significant attention. The detection process typically involves image acquisition, preprocessing, segmentation, feature extraction, and classification. Image preprocessing techniques such as resizing, noise removal, and data augmentation improve image quality and model performance. Techniques like principal component analysis (PCA) can also be used for extracting important features from plant images [11]–[14]. Furthermore, the integration of these technologies with precision agriculture tools such as drones and smart monitoring systems enables efficient crop monitoring and disease management.

Precision farming practices, including yield monitoring and field management, help farmers maintain crop health and reduce disease spread. Additionally, agricultural hygiene practices such as removing infected plants and maintaining clean fields play an important role in disease control. By combining traditional agricultural practices with modern AI techniques, it is possible to develop efficient plant disease detection systems that improve productivity and ensure sustainable agricultural development [15].

2. LITERATURE SURVEY

Mumo *et al.* [16] conducted a comprehensive study on viruses associated with papaya ringspot disease (PRSD) in Kenya using next-generation sequencing (NGS) and bioinformatics techniques. The study aimed to overcome the limitations of traditional detection methods, such as enzyme-linked immunosorbent assay (ELISA) and reverse transcription polymerase chain reaction (RT-PCR), which previously failed to conclusively identify the causative agent. A total of 48 leaf samples were collected from papaya plants across 22 counties in Kenya, including both symptomatic and asymptomatic samples. Symptoms such as fruit ringspots, mosaic patterns, mottling, and leaf deformation were initially identified through field observations. The NGS-based metagenomic approach enabled accurate identification and characterization of viruses associated with PRSD, providing valuable insights for effective disease management strategies.

Sharath *et al*. [17] proposed a CNN model for detecting diseases in fruits such as papaya, orange, pomegranate, and grapes using image analysis techniques. The dataset contained 15,363 images, including 12,891 for training and 2,472 for testing. The proposed CNN-based model achieved an accuracy of approximately 91% in disease classification. The authors highlighted the importance of integrating environmental parameters such as temperature, humidity, and rainfall to improve disease prediction and management. Habib *et al.* [18] presented a ML approach for papaya disease detection using image processing techniques and support vector machines (SVM). The methodology included image acquisition, preprocessing, segmentation using K-means clustering, and feature extraction using statistical and gray-level co-occurrence matrix (GLCM) features, and classification using SVM. The dataset consisted of 128 real-world papaya images containing both healthy and diseased samples.

Soni *et al.* [19] investigated the effects of papaya leaf curl virus using PCR analysis and physiological studies on infected leaves. Unlike other studies, this research focused on biological and biochemical analysis rather than ML techniques. Yashodharan *et al.* [20] developed a disease detection system using k-medoid clustering and a multilayer perceptron (MLP) classifier. Using the PlantVillage dataset containing healthy and diseased papaya leaf images, the model achieved an average accuracy of 94.61%.

Hossen *et al.* [21] applied DL techniques using a CNN model developed with the Keras API to classify papaya images as healthy or diseased. The dataset included 234 images collected from real-world sources and Kaggle, achieving an average accuracy of 91%. Maski and Thondiyath [22] proposed lightweight versions of the YOLO algorithm for detecting PRSD. Using a dataset of more than 2,000 papaya leaf images, the model demonstrated faster detection and suitability for deployment in mobile agricultural robots. Sari *et al.* [23] reviewed several ML and DL techniques such as fuzzy naive Bayes classifier, forward chaining, CNNs, and YOLO-based models for papaya disease detection. The study concluded that DL models outperform traditional ML methods due to their ability to automatically extract features from images and enable real-time disease monitoring. An overview of papaya disease diagnosis is presented in Table 1.

Table 1. Papaya disease diagnosis overview

Category	Description	Specific examples
Methods	Techniques are used to process and analyze data for disease diagnosis.	Digital processing of images, extraction of features, AI and DL, object detection, expert systems
Algorithms	Specific procedures used within each method.	K-means clustering, SVM, naive Bayes model, the decision tree, the random forest, and CNN, fuzzy logic
Datasets	Collections of images and/or Data utilized for the training and review of models.	Images of healthy and damaged papaya leaves, fruits, and stems; datasets may be publicly available or privately collected by researchers.
Disease diagnosis	The specific papaya diseases targeted for identification.	Anthracnose and the papaya ringspot infection, black spot, powdery mildew, phytophthora, leaf spot, fungus, leaf curl
Deep learning models	Specific architectures of CNNs used for papaya disease diagnosis.	ResNet50, EfficientNet, AlexNet, GoogLeNet, MobileNetV2, InceptionResNetV2
Evaluation parameters	Metrics employed to evaluate the efficacy of the models.	Accuracy, sensitivity, specificity, precision, false positive rate (FPR), false negative rate (FNR), mean average precision (mAP), receiver operating characteristic (ROC) curve

3. METHODOLOGY

Figure 1 shows the proposed system block diagram that employs a deep learning approach to classify papaya leaf diseases. The diagram illustrates the key methodological steps of the system. Here is a breakdown of those key steps.

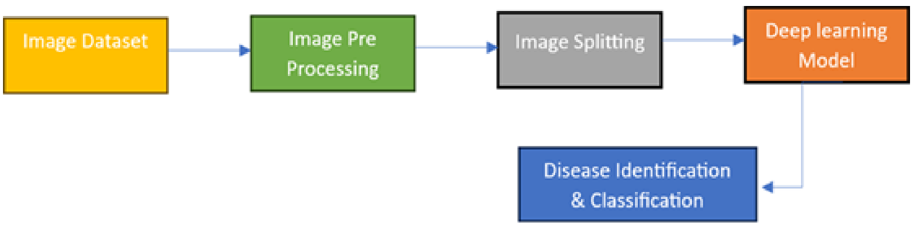

Figure 1. Proposed system block diagram

3.1. Dataset collection

The research makes use of the "BDPapayaLeaf" dataset [24], which contains 2,159 photos of papaya leaves. These photographs were taken in several locations throughout Bangladesh, offering a diverse portrayal of disease symptoms and environmental factors. Figure 2 depicts samples from a papaya leaf disease dataset, demonstrating leaves with varying diseases. Each subfigure in the collection depicts a separate leaf disease demonstrating the distinct visual traits associated with each ailment. The photos are grouped into subfolders based on their respective classes. The dataset includes 2,159 photos divided into five categories: anthracnose, curl, ring spot, bacterial spot, and healthy [25].

Table 2 presents the distribution and splitting of images in the dataset. The dataset is divided into three subsets: training, validation, and testing. About 80% of the images (1,726) are used for training, 10% (213) for validation, and 10% (220) for testing. The images were collected under varying conditions, such as lighting, resolution, backgrounds, poses, and alignments, ensuring reliable real-world disease detection [18], [21], [22].

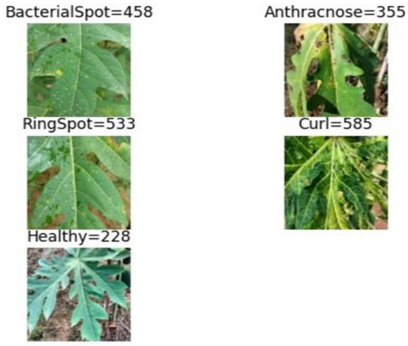

Figure 2. Dataset samples of papaya leaf disease

Table 2. Overview of dataset classes

Sr No.	Disease	Number of samples
1	Anthracnose	355
2	Bacterial spot	458
3	Curl	585
4	Ring spot	533
5	Healthy	228

3.2. Data preprocessing

Data preprocessing prepares raw data for DL models. In this study, images from the BDPapayaLeaf dataset are resized to 224×224 RGB format for consistent CNN input. Pixel values are normalized between 0 and 1 for stable training. Disease labels are converted into one-hot encoded vectors, enabling accurate multi-class classification of five papaya leaf diseases.

3.3. Model selection and training

The papaya plant disease classification dataset was used to train several CNN models. Each model has unique architectural characteristics that support the effective classification of diseases in papaya leaf images. The dataset was divided into five disease categories, and pretrained models were fine-tuned using the papaya leaf dataset to adapt their learned features to this specific classification task. In this study, five DL architectures were implemented and compared: VGG16, VGG19, DenseNet121, InceptionV3, and MobileNetV2.

VGG16, developed by the Visual Geometry Group at the University of Oxford, is a widely used CNN architecture known for its depth and simplicity. It contains 16 weighted layers, including 13 convolutional layers and 3 fully connected layers, and has demonstrated strong performance in image classification tasks through transfer learning [26]. Similarly, VGG19 extends this architecture to 19 layers, including 16 convolutional layers and 3 fully connected layers, enabling improved feature extraction for complex image recognition tasks [27].

InceptionV3 is a DL architecture designed to enhance computational efficiency by combining multiple convolution filters of different sizes within the same layer. This design allows the model to capture diverse visual patterns while maintaining high classification accuracy [28]. DenseNet121 introduces dense connections between layers, which promote feature reuse and improve gradient flow during training. The architecture consists of dense blocks, transition layers, and a final classification layer, enabling efficient feature propagation [29].

MobileNetV2 is a lightweight CNN architecture designed for mobile and embedded applications. It utilizes depthwise separable convolutions and inverted residual blocks to reduce computational cost while maintaining competitive performance. During training, model parameters were optimized by minimizing categorical cross-entropy loss using ground-truth disease labels. The models were evaluated using performance metrics such as accuracy, precision, recall, and F1-score to compare their effectiveness in detecting papaya leaf diseases.

3.4. Evaluation measures

Accuracy measures how often the model correctly predicts outcomes and is suitable for balanced datasets. Precision measures how many predicted positives are actually correct, reducing false positives. Recall measures how many actual positives are correctly identified, reducing false negatives. The F1-score represents the harmonic mean of precision and recall. Here, TP denotes true positive, TN denotes true negative, FP denotes false positive, and FN denotes false negative.

$$Accuracy = \frac{TP+TN}{TP+TN+FP+FN} \tag{1}$$

$$Precision\ (P) = \frac{TP}{TP+FP} \tag{2}$$

$$Recall\ (R) = \frac{TP}{TP+FN} \tag{3}$$

$$F1-score = \frac{2\times TP}{2\times TP+FP+FN} \tag{4}$$

4. RESULT AND DISCUSSION

The main intention of this research is to establish an effective model for recognizing and categorizing papaya plant illness. The 2,159 papaya leaf photos in the collection of data have been split into 1,726 training, 213 validation, and 220 testing images. We do our research using the "BDPapayaLeaf" dataset. The dataset provides a more comprehensive and diverse set of papaya leaf pictures, signifying a variety of illnesses and environmental circumstances. This variety enables a more accurate representation of problems seen in the real world.

The research tested CNN models that have already been trained, such as InceptionV3, VGG16, VGG19, DenseNet121, MobileNetV2, and ResNet50. Using the Adam optimizer and a learning rate of 0.001, each model was trained for a maximum of 100 epochs. The images are scaled to 224×224 pixels with three channels, a standard input size for CNNs. The photos and their labels are organized into lists. Labels are assigned according to the directory index. The photos are transformed into an array of numeric Python and normalized by scaling pixel values to the range [0, 1]. Labels are translated into a one-hot encoded format, which is required for multi-class categorization. There are two sets of the dataset: testing (20%) and training (80%). Applying TensorFlow and the Keras package to train a CNN. Dropout regularization is performed at a rate of 0.5. We employ rectified linear unit (ReLU), which increases nonlinearity in the model. Experiments are conducted on Google Colab. Figures 3 to 8 depicts the training accuracies and losses, and also shows the validation accuracies and losses of the models, where Figures 3 to 8 show VGG16, VGG19, InceptionV3, DenseNet121, MobileNetV2, and ResNet50, respectively. Meanwhile, Figure 9 summarizes the accuracy findings for the applied models.

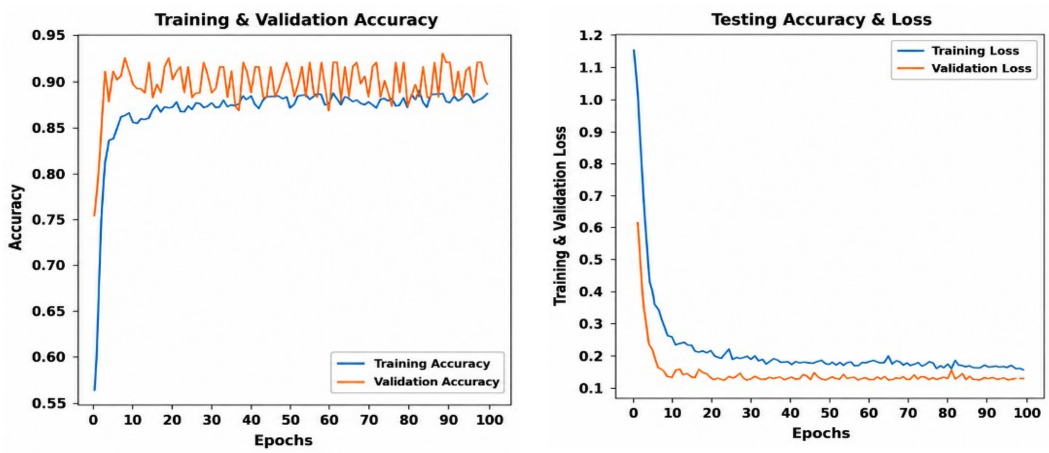

Figure 3. The training and validation accuracies as well as loss curves for CNN models of VGG16

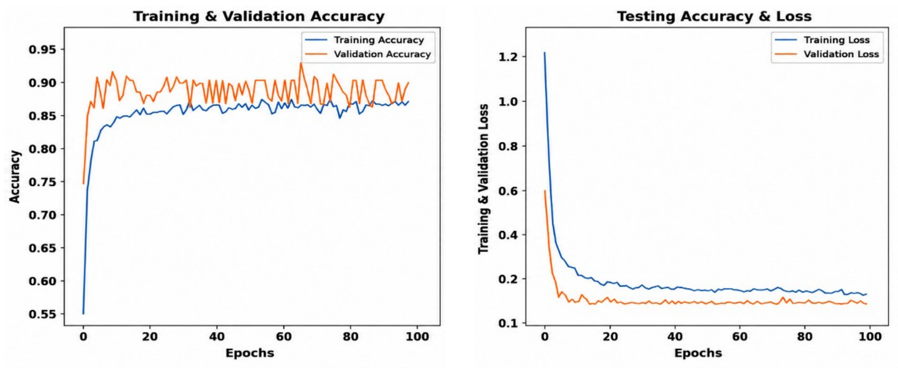

Figure 4. The training and validation accuracies as well as loss curves for CNN models of VGG19

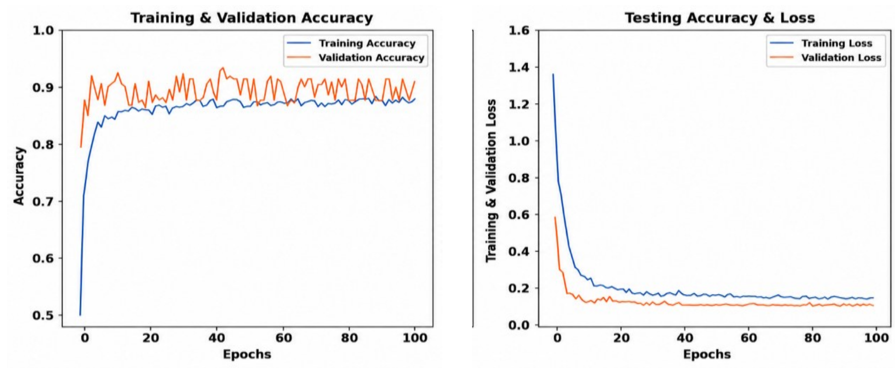

Figure 5. The training and validation accuracies as well as loss curves for CNN models of InceptionV3

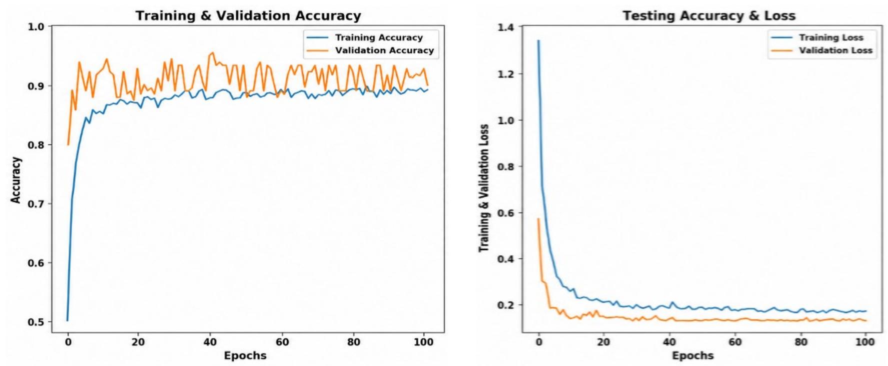

Figure 6. The training and validation accuracies as well as loss curves for CNN models of DenseNet121

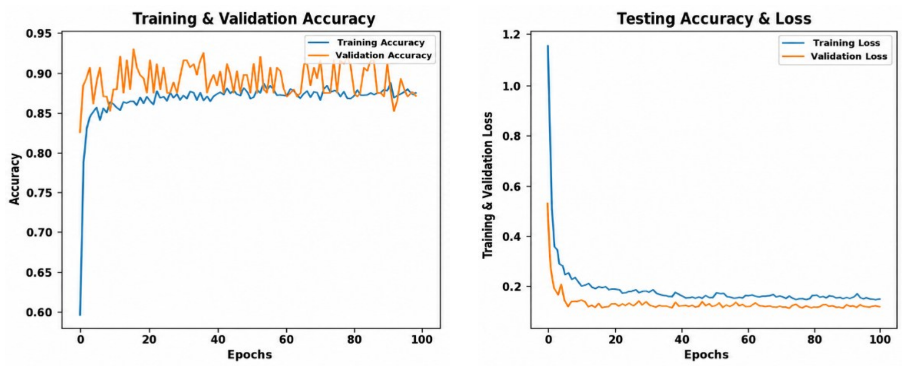

Figure 7. The training and validation accuracies as well as loss curves for CNN models of MobileNetV2

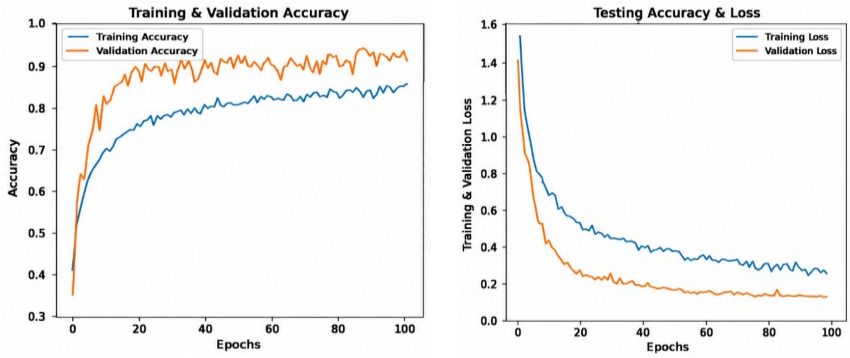

Figure 8. The training and validation accuracies as well as loss curves for CNN models of ResNet50

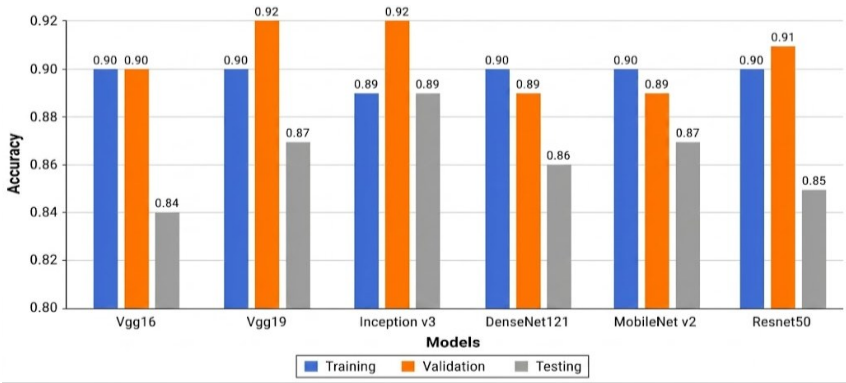

Figure 9. Training, validation, and test accuracy of fine-tuned models

Table 3 compares several CNN architectures, including VGG16, VGG19, InceptionV3, DenseNet121, MobileNetV2, and ResNet50 for papaya leaf disease classification. Among them, InceptionV3 achieved the highest accuracy of 87.95%, indicating superior prediction performance. It also showed high precision and recall across disease classes, reducing both false positives and false negatives. Consequently, InceptionV3 obtained the best F1-scores, demonstrating balanced and reliable classification performance even with possible class imbalance. The confusion matrix for each fine-tuned transfer learning model of CNN is shown in Figure 10, where Figures 10(a)–10(f) show, in order, VGG16, VGG19, InceptionV3, DenseNet121, MobileNetV2, and ResNet50. CNNs and other classification models can be evaluated for performance using the confusion matrix. It gives a thorough analysis of the model's performance by comparing expected results to actual outcomes.

Table 3. Demonstrates the metrics for fine-tuned pre-trained CNN models

	VGG16	VGG19	InceptionV3	DenseNet121	MobileNetV2	ResNet50
Accuracy (%)	0.84	0.88	0.89	0.86	0.87	0.85
			Precision (%)			
Ring spot	1	1	1	1	1	1
Curl	0.69	0.79	1	0.65	0.67	0.65
Healthy	1	1	1	1	1	1
Bacterial spot	0.67	0.74	0.69	1	0.96	0.83
Anthracnose	1	1	1	1	1	1
			Recall (%)			
Ring spot	1	1	1	1	1	1
Curl	0.72	0.76	0.6	1	0.98	0.91
Healthy	1	1	1	1	1	1
Bacterial spot	0.63	0.77	1	0.4	0.46	0.46
Anthracnose	1	1	1	1	1	1
			F1-score (%)			
Ring spot	1	1	1	1	1	1
Curl	0.71	0.77	0.75	0.79	1	0.76
Healthy	1	1	1	1	1	1
Bacterial spot	0.65	0.75	0.82	0.58	0.62	0.59
Anthracnose	1	1	1	1	1	1

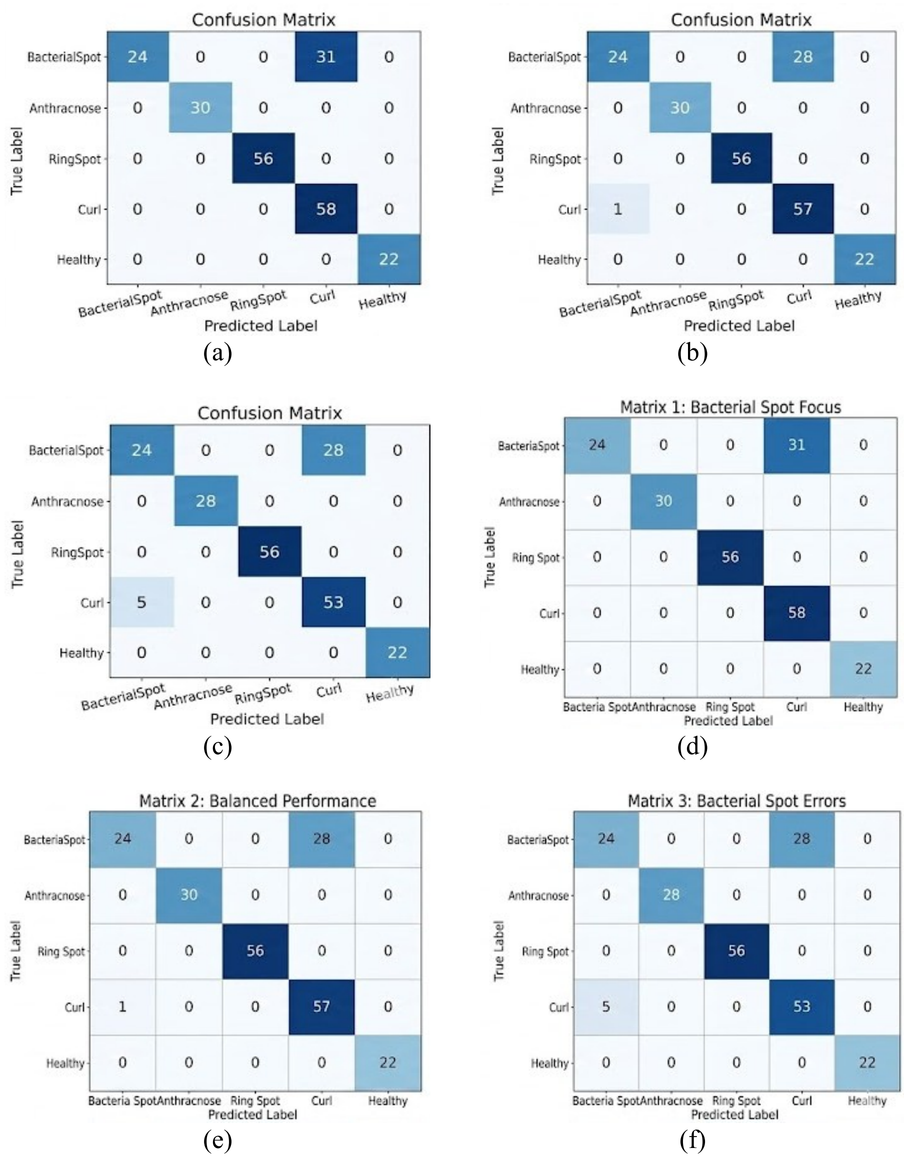

Figure 10. Confusion matrix of CNN base models employed in the work for (a) VGG16, (b) VGG19, (c) InceptionV3, (d) DenseNet121, (e) MobileNetV2, and (f) ResNet50

5. CONCLUSION

To maximize agricultural productivity, early and precise disease diagnosis is essential. Traditional approaches rely on human expertise, which is time-intensive and error-prone. The study provided in the sources investigates the potential for machine vision, namely DL, to control and optimize this procedure. The study focuses on classifying papaya leaf illnesses using a dataset of images that consists of both minty leaves with circle spots, twist, anthracnose, and microbial spots. CNN models with prior training were evaluated, such as VGG16, VGG19, InceptionV3, DenseNet121, MobileNetV2, and ResNet 50. The InceptionV3 model obtained 89% accuracy which is the highest among all models. Using pre-trained models speeds up training and, in many cases, improves performance. The study illustrates the approach's practical relevance in real-world agricultural settings, providing a potential solution for automated crop disease prediction and management. Future studies might apply to balancing the quantity of images in each class using augmentation to improve testing accuracy even more. Investigating the performance of various cutting-edge CNN designs or ensemble approaches may yield even better classification results. Integrating the disease categorization model with decision support systems could give farmers immediate and practical information into disease management.

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AUTHOR CONTRIBUTIONS STATEMENT

This journal uses the Contributor Roles Taxonomy (CRediT) to recognize individual author contributions, reduce authorship disputes, and facilitate collaboration.

Name of Author	C	M	So	Va	Fo	I	R	D	O	E	Vi	Su	P	Fu
Tejas Rana	✓	✓	✓	✓	✓	✓		✓	✓	✓			✓	
Chintan Thacker		✓				✓		✓	✓	✓	✓	✓		

C : **C**onceptualization
M : **M**ethodology
So : **So**ftware
Va : **Va**lidation
Fo : **Fo**rmal analysis
I : **I**nvestigation
R : **R**esources
D : **D**ata Curation
O : Writing - **O**riginal Draft
E : Writing - Review & **E**diting
Vi : **Vi**sualization
Su : **Su**pervision
P : **P**roject administration
Fu : **Fu**nding acquisition

CONFLICT OF INTEREST STATEMENT

Authors state no conflict of interest.

INFORMED CONSENT

We have obtained informed consent from all individuals included in this study.

DATA AVAILABILITY

Data availability is not applicable to this paper as no new data were created or analyzed in this study.

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BIOGRAPHIES OF AUTHORS

Tejas Rana received his Masters of Engineering Degree in Computer Science and Engineering from Parul Institute of Engineering and Technology, Gujarat Technological University in the year of 2014 and pursuing Ph.D. in Computer Science Engineering from Parul University, Vadodara, Gujrat. He has 11 years of experience in Academia. Currently, he serves as an assistant professor in Department of Computer Science and Engineering in Parul Institute of Engineering and Technology, Parul University. His Research interests are in the areas of machine learning, deep learning, image processing, cloud Computing. He can be contacted at email: tejas.rana24781@paruluniversity.ac.in or tej81781@gmail.com.

Chintan Thacker received the Ph.D. degree in the domain of AI and computer vision from Gujarat Technical University in the year 2022. He had served as head of the Department of Computer Science and Engineering at HJD Institute of Technical Education and Research, Kera, India. He has 1+ years of experience in industry and 12+ years of experience in academia. Currently, he serves as an assistant professor in Department of Computer Science and Engineering in Parul Institute of Engineering Technology, Parul University, Vadodara, Gujarat. In addition, he has also guided several doctorate students and has been active in conducting several workshops in the domain of computer vision. His research interests are in machine learning, AI, deep learning, and computer vision. He can be contacted at email: chintan.thacker19435@paruluniversity.ac.in.