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Research Article

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Optimizing papaya disease classification: A hybrid approach using deep features and PCA-enhanced machine learning

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Abstract: Computer vision has become an essential non-invasive technology for the automatic detection and classification of fruits and vegetables, driven by its speed, accuracy, and adaptability in meeting the demand for advanced food quality assessment systems. In this study, three methodologies were explored for papaya disease classification: (i) Transfer learning using a convolutional neural network (CNN) model, (ii) deep feature extraction followed by traditional machine learning (ML) models, and (iii) the application of principal component analysis (PCA) to retrieve deep features, using a best-performing model, ResNet101. Seven CNN architectures achieved over 90% classification accuracy, demonstrating the effectiveness of CNNs in fruit disease detection. The retrieved deep features combined with PCA further improved accuracy, with support vector machine achieving 99.87%, random forest classifier 99.54%, multilayer perceptron 99.08%, and k-nearest neighbors 91.63%. These outcomes highlight the advantages of integrating deep learning and traditional ML approaches. However, limitations include the exclusion of disease severity in classification and the lack of testing on large, diverse samples. Future research should concentrate on these by applying broader samples, considering environmental conditions, and exploring more advanced CNN architectures to enhance model robustness and generalizability for practical agricultural applications.

Keywords: papaya disease classification, deep learning, convolutional neural network, ResNet101, machine learning, principal component analysis

1 Introduction

The papaya (*Carica papaya* L.), a member of the family Caricaceae, is a tropical fruit characterized by its sweet, orange flesh and widely recognized for its nutritional and health benefits. In 2022, global production of papayas exceeded 13 million metric tons, reflecting its significance in both dietary consumption and agriculture [1]. Due to their flavor and health benefits, the demand for papayas keeps increasing, requiring consistent demand and supply. In this context, implementing novel methods in agricultural production and marketing

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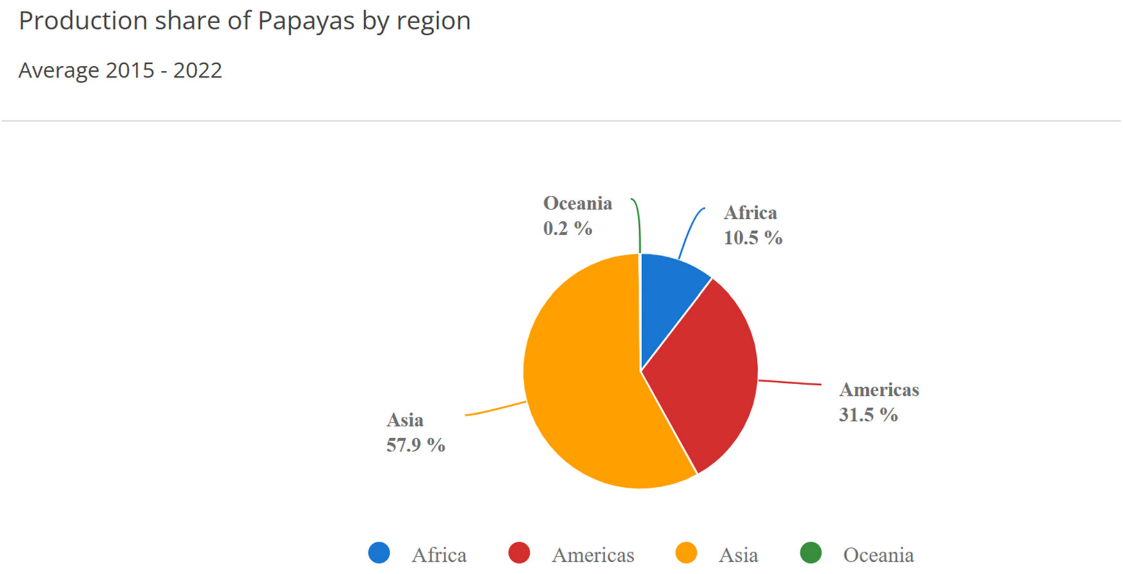


Figure 1: Region wise production quantity of papaya fruits (Source: FAOSTAT Statistical Database).

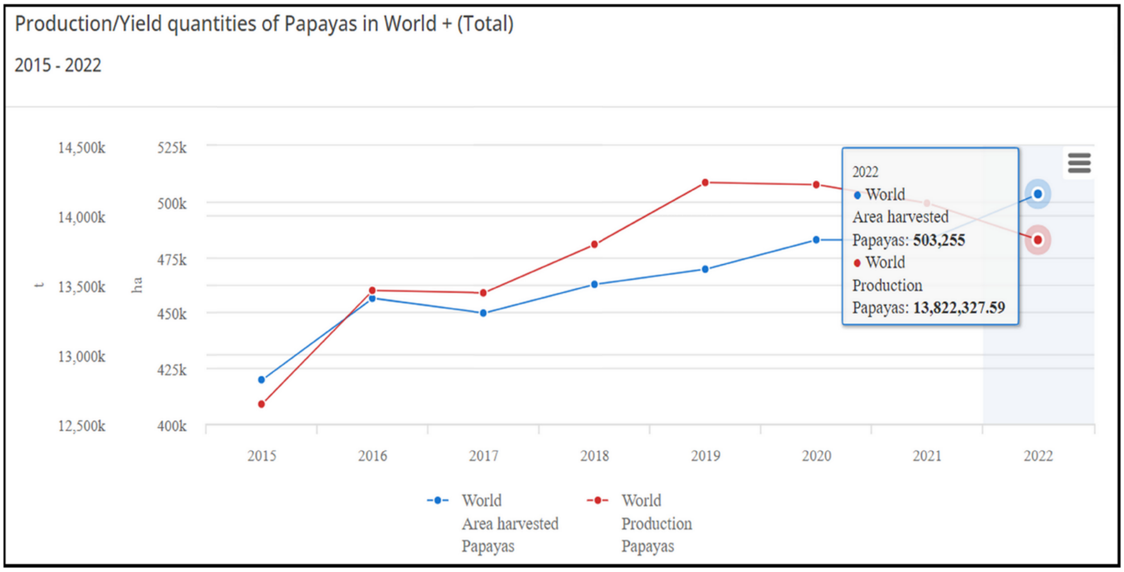


Figure 2: Year-wise production quantity of papaya fruits (Source: FAOSTAT Statistical Database).

strategies is crucial to satisfy increasing market demands and facilitate effective distribution [2]. Figure 1 illustrates the global contribution to papaya production, while Figure 2 provides statistical data on papaya production trends from 2015 to 2022 based on data obtained from FAOSTAT Database. Figure 2 shows a marginal decrease in papaya fruit production from 2019 to 2022. Papaya is susceptible to significant losses due to various diseases, making effective disease management crucial for minimizing these impacts. Diseases are seen as critical influences on lowering the production and commercial value of papaya. Throughout its growth stages, papaya is affected by several diseases, including anthracnose, phytophthora, black spot, powdery mildew, and ring spot. Therefore, implementing effective control measures against these defects is important to mitigate yield losses and preserve fruit quality. Prasad and Paul indicate that a major portion of the production goes into waste, which is reported to be around 40–60% of the total production at various papaya growing regions [3]. Manual disease inspections are susceptible to human error and variability due to factors like expertise, training, and environmental conditions. Automated recognition and classification systems, leveraging computer vision, offer superior speed, accuracy, and suitability for non-destructive fruit and vegetable quality assessment [4]. This technology enhances economic efficiency, reduces labor costs, and meets growing demand for food quality-sensing devices.

Image classification, a fundamental task in computer vision, has transitioned from traditional machine learning's (ML's) manual feature extraction to deep learning's (DL's) automated feature extraction and classification, particularly for fruits and vegetables. The quality of extracted features significantly impacts classifier performance [5]. Emergent computing power and algorithms for big data processing have fueled DL's popularity [6]. Particularly, convolutional neural network (CNN) automatically recognizes and classifies attributes, allowing for non-destructive and efficient sorting of fruits and vegetables, addressing the rising need for food quality assessment technologies [7]. By eliminating manual feature extraction or representation, CNNs optimize accuracy, robustness, and processing efficiency [8].

CNNs, a family of DL techniques, have shown improved performance across a variety of tasks within the food and agriculture sectors in recent studies [9–13]. Producing sorting and grading, classification of crop variety, and plant disease detection are some of these duties. The utilization of transfer learning (TL), especially through models that have been pre-trained on available images, has shown significant effectiveness in various applications, including the classification of crops and fruits. This approach enables the modification of pre-trained networks to recognize new patterns, which is particularly advantageous in situations where training data are scarce, making it a widely adopted strategy in the field [14]. The aims of this research are to evaluate the effectiveness of TL in classifying healthy and diseased papaya varieties. It also aims to find out the effects of integrating principal components (PCs) obtained from deep features with conventional ML models. As far as we are aware, the classification of papaya disease varieties has not yet been evaluated using this integration. As a result, the study will evaluate how these elements work together to improve classification efficacy and accuracy.

This study significantly advances the field of fruit disease classification by systematically exploring three methodologies for detecting papaya diseases: (i) TL utilizing a CNN model, (ii) deep feature extraction followed by traditional ML models, and (iii) the application of principal component analysis (PCA) on the derived deep features, specifically by using ResNet101 architecture.

Key contributions include:

- **High classification accuracy:** The research demonstrated that seven CNN architectures achieved over 90% classification accuracy, underscoring the effectiveness of CNNs for fruit disease detection.
- **Enhanced performance with PCA:** The integration of PCA with extracted deep features led to improved classification accuracy, with support vector machine (SVM) achieving an impressive 99.87%, followed by random forest classifier (RFC) at 99.54%, multilayer perceptron (MLP) at 99.08%, and k-nearest neighbors (KNN) at 91.63%.
- **Integration of approaches:** The study highlights the advantages of combining DL techniques with traditional ML approaches, paving the way for more robust disease classification systems.
- **Identification of limitations and future directions:** The work acknowledges limitations, such as the exclusion of disease severity and the lack of testing on large, diverse datasets, and outlines future research directions to address these issues. This includes the incorporation of broader datasets, consideration of environmental conditions, and exploration of advanced CNN architectures to enhance model robustness and generalizability for practical agricultural applications.

2 Review of literature

The papaya fruit holds economic importance throughout the world due to its tropical origins and widespread cultivation. Papaya fruit production and quality experience major losses due to various diseases. Throughout history, researchers have experimented with multiple strategies ranging from traditional techniques to advanced ML methods to diagnose and control diseases. This chapter examines current research employing DL models for papaya disease classification alongside contemporary top-performing methods used in identifying papaya diseases.

Munasingha et al. introduced a DL approach to identify papaya fruit diseases. The study achieved 92% accuracy in detecting five distinct papaya diseases through their model which demonstrated efficient disease identification [15].

Sari et al. enabled farmers to identify papaya diseases independently from expert intervention. The system converted expert knowledge expressed in linguistic terms to numerical values by applying fuzzy reasoning with the triangular fuzzy number membership function. The Naïve Bayes Classifier achieved 88% accuracy in disease classification while forward chaining search approaches reached 90% accuracy when compared against expert diagnoses [16].

Islam et al. introduced a smart ML technique for disease detection. Four separate algorithms were evaluated to identify papaya sickness. The researchers utilized CNN together with support vector classifier (SVC) and random forest (RF) algorithms plus *K*-mean clustering for their analysis. CNN achieved the highest accuracy level of 98.4% among all methods evaluated. In 2020, Hossen et al. proposed a DL-based approach for the detection and categorization of papaya diseases. Their study focused on both fruit and leaf diseases, encompassing a total of 234 samples. The CNN model developed in their experiment achieved a classification accuracy of 91%, demonstrating its effectiveness in identifying and classifying papaya diseases [18].

Habib et al. performed thorough investigations into multiple classifiers designed for papaya disease detection. The research tested nine different classifiers against 129 papaya disease samples. SVMs exhibited superior performance compared to other classifiers by achieving a 95.2% accuracy rate. Among the classifiers tested, the KNN classifier showed the weakest performance resulting in an accuracy of 71.11% [19].

Habib et al. developed a machine vision-based method to recognize diseases in papaya plants. They employed a group of ten features for their analysis process. The researchers employed k-means clustering to segment infected areas and identify important features. The authors implemented SVM and additional classification algorithms for their analysis. The testing results indicated that the method achieved an accuracy level of 90.15% when applied to a dataset of 126 samples [20].

Veeraballi et al. proposed using ResNet50 deep neural network architecture to identify and categorize papaya leaf diseases in 2020. To conduct their research, they utilized a dataset comprising 9,470 samples. The constructed model demonstrated 85.19% classification accuracy while achieving sensitivity and specificity rates of 90 and 61%, respectively [21].

Hridoy with Tuli developed a deep ensemble technique utilizing EfficientNet for papaya disease identification. The research involved training eight EfficientNet models (B0–B7) through TL to detect eight distinct papaya diseases. Eight papaya diseases required classification following training on a dataset of 138,980 images gathered through image collection augmentation. The EfficientNet models B5, B7, and B6 which showed the best performance were further fine-tuned before being used in an ensemble learning strategy. The models reached classification accuracies of 98.13, 96.93, and 96.87% on a test set of 6,931 images which shows their strong performance in disease identification [22].

Nagaraj et al. combined CNNs with fruit disease prediction and classification to innovate a new method. The CNN framework developed by Nagaraj et al. achieved 97% accuracy while using Inception as its foundational architecture. The model demonstrates high efficiency in diagnosing fruit diseases accurately according to the study [23].

Ratha et al. introduced a hybrid network combining wavelet transform with ConvNET to estimate papaya fruit maturity stages. The methodology extracted deep features from VGG16 architecture as well as higher-level features from discrete wavelet transform (DWT). The combined features were classified using SVM. Maturity stage classification reached a high effectiveness level with the proposed model achieving 98% accuracy [24].

de Moraes et al. created a papaya disease detection system using convolutional block attention modules (CBAM). The model received training from a dataset consisting of 23,158 samples, which were categorized into nine different classes encompassing eight disease types and one category for healthy fruit. The proposed detector demonstrated superior performance in disease detection compared to other models by reaching an average mean Average Precision (mAP) of 86.2%, which proves its effectiveness in accurate papaya disease identification [25].

Banarase and Shirbahadurkar created an innovative ML model for papaya fruit and leaf disease detection, which combines gray-level co-occurrence matrix (GLCM) feature extraction methods with classifier hyperparameter tuning. They derived 16 features from 8 different categories of healthy and sick papaya leaves and fruits using GLCM. SVM and RF with optimal hyperparameters outperformed other classifiers and prior methods by achieving 91.47 and 90.22% accuracy, respectively [26].

Mir et al. proposed a system to classify diseases in papaya leaves into six categories: The classification system includes six categories which are “Healthy,” “Papaya Ringspot Virus,” “Papaya Leaf Curl Virus,” “Powdery Mildew,” “Papaya Mosaic Virus,” and “Leaf Spot Diseases.” The classification system merges RF technology with CNN. The model’s accuracy ranged between 94.44 and 96.22% based on performance indicators, which demonstrated its effectiveness at distinguishing between various papaya diseases. State-of-art illustration is given in Table 1.

Table 1: State-of-the-art methods for papaya disease detection and classification

Author(s) and Year (Ref.)	Dataset	Adapted methods	Performance metrics
Munasingha et al. (2019) [15]	Papaya diseases (fruit)	CNN	Obtained a classification with an accuracy of 92%
Sari et al. (2020) [16]	Papaya diseases (fruit)	NBC with Forward chaining search method	Achieved a classification accuracy of 88% with Fuzzy Naive Bayes classifier and 90% with fuzzy cognitive strategy map
Islam et al. (2020) [17]	214 images of papaya diseases	CNN, SVC, RF, and K-mean clustering	Obtained a classification with accuracy of 98.4% with CNN
Hossen et al. (2020) [18]	234 images of papaya diseases (both fruit and leaf)	Keras API with CNN	Obtained a classification with an accuracy of 91% with CNN
Habib et al. (2020) [19]	129 images of papaya fruit diseases	SVM, Naïve Bayes, C4.5, Logistic regression, RF, kNN, BPN, CPN, RIPPER, etc.	Obtained a classification with an accuracy of 95.2% with SVM
Habib et al. (2020) [20]	126 images of papaya diseases (leaf and fruit)	K-mean clustering – segmentation, SVM – classification	Obtained a classification with an accuracy of 90.15% with SVM
Veeraballi et al. (2020) [21]	9,470 images of papaya diseases (leaf)	ResNet50	Obtained a classification with an accuracy of 85.19%, Sensitivity of 90% and Specificity of 61%
Hridoy and Tuli (2021) [22]	138,980 images of papaya diseases (leaf and fruit)	Eight EfficientNet models (B0–B7)	Achieved a classification accuracy of 98.13, 96.93, and 96.87%, with EfficientNet B5, B7, and B6
Nagaraj et al. (2022) [23]	Papaya diseases (fruit)	CNN (Inception)	Obtained a classification with accuracy of 97% with Inception CNN architecture
Ratha et al. (2023) [24]	Papaya fruit maturity classification	DWT, VGG16, and SVM	Obtained a classification with accuracy of 98% with the hybrid architecture
de Moraes et al. (2023) [25]	Papaya diseases (fruit)	CNN with CBAM	Proposed detector achieving an average mAP of 86.2%, highlighting its effectiveness in accurately identifying papaya diseases
Banarase and Shirbahadurkar (2023) [26]	Papaya diseases (fruit and leaf)	GLCM with SVM and RF	Achieved a classification accuracy of 91.47% with SVM and 90.22% with RF
Mir et al. (2024) [27]	Papaya diseases (leaf)	CNN with RF	Achieved a classification accuracy in between 94.44 and 96.22%

Table 1 offers a comprehensive summary of current progress in papaya fruit and leaf disease identification using DL and ML methods. Dominant techniques are CNN-based models, TL, and fusion techniques that benefit from feature extraction and optimization strategies. Accuracy, precision, recall, and *F*1-score measurements indicate remarkable gains, with a few models offering near-perfect accuracy. The research as a whole depicts a trend of combining cutting-edge architectures and optimization methods to improve disease classification and prediction. In general, the developments depict a promising path for more efficient and accurate disease detection in fruit production.

Our study focused on overcoming the shortcomings of current models in rice leaf disease classification through the use of a severity-based categorization system. This is made possible by a hybrid model that combines TL and deep-feature extraction methods, allowing for a balance between accuracy and robustness. The combination of these cutting-edge methodologies allows the model to be generalized across datasets, making it extremely versatile for real-world agricultural applications.

3 Materials and methods

3.1 Acquisition of healthy and diseased papaya fruit images

The database used in the current research involves images of both diseased and healthy papaya fruits. A sum of 983 images were collected, representing healthy and diseased fruit samples. The images were captured using a 15-megapixel camera under controlled conditions, ensuring consistent distance and lighting. A white background was employed to eliminate visual distractions and improve image clarity. Additionally, to avoid the effects of direct sunlight, natural daylight was used without direct illumination on the fruits during image capture. The distribution of images across the various disease classes, along with healthy samples, is presented in Table 2. For the purposes of model training 80% images used for training and 20% images are used for testing.

Table 2: Distribution of papaya fruit images among various classes

Papaya fruit disease class	Image	Number of image collected	Number of image taken for model training (80%)	Number of image taken for model testing (20%)
Anthracnose disease		165	132	33
Black spot disease		150	120	30
Ring spot disease		266	213	53
Phytophthora disease		148	118	30
Powdery Mildew disease		155	124	31
Healthy papaya (disease free)		99	79	20

3.2 Adopted methodology

In this study, three methodologies were proposed for papaya disease classification: (a) the application of TL using CNN, (b) ResNet101 deep features extraction followed by training of ML models, and (c) the application of PCA for the extracted ResNet101 deep features, where ML models were trained using the PCs whose eigenvalues (>1) are illustrated in Figure 3.

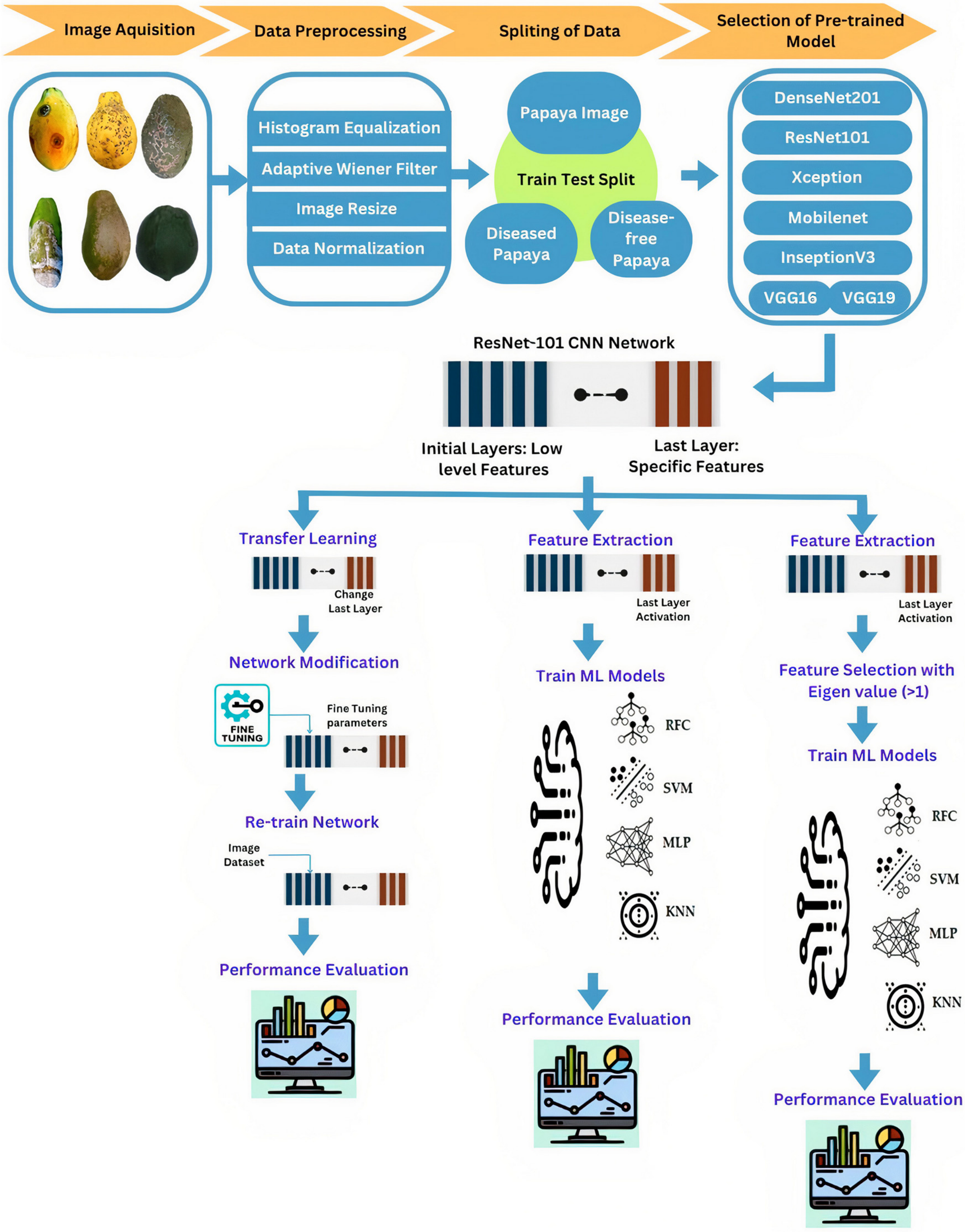


Figure 3: An overview of the three stages of the suggested methodology (Source: Created by the Author).

3.3 Image preprocessing

Preprocessing is a critical phase in computer vision systems, aimed at improving image quality and ensuring accurate analysis. Techniques such as noise removal, image enhancement, resizing, and data normalization are commonly employed. These methods help to highlight defects on the surface of fruits by reducing irrelevant information, improving contrast, and standardizing image inputs, thereby facilitating more precise detection and classification of surface anomalies.

3.3.1 Adaptive wiener filter

By reducing mean squared error, a linear filter – like the Adaptive Wiener Filter – works well for denoising and smoothing images. This filter applies a variable amount of smoothing, based on the local variation of the image. Less smoothing is applied to high variance regions and more smoothing is applied to low variance regions. Local neighborhoods are covered by this low-pass filter, usually in 3 × 3 pixel blocks. Because the Adaptive Wiener Filter retains high-frequency components and edge information in the image, it is very helpful for lowering background noise without creating blurring.

3.3.2 Histogram equalization

Histogram equalization is a commonly utilized preprocessing technique designed to improve the quality of images by improving contrast. This method works by redistributing the pixel intensity values of an image, aiming for a more uniform distribution across the intensity range [28]. Histogram equalization achieves this by spreading out the most frequent pixel values, thus increasing the contrast in areas with low dynamic range and making details more visible.

3.3.3 Image resizing

The initial dataset is composed of colored images of different papaya fruit types, taken in varied formats and dimensions. In an attempt to normalize the dataset, every image is accurately resized to a resolution of 224 × 224 pixels with three color channels (RGB). After resizing, the images are labeled and deposited in discrete directories for further analysis and processing.

3.3.4 Normalization of data

As a preprocessing step, the mean value and standard deviation (SD) of every image in the dataset are calculated. Each image is initially converted to RGB format, and the pixel values are scaled so that they lie between 0 and 1. The square root of variance is used to obtain the standard deviation, which is the outcome of normalizing the pixel values by determining their mean and variance. The pixel intensities are then normalized based on these statistics. The pixel values are normalized to the 0–1 range by dividing them by 255 in an effort to minimize computing complexity. The pixel intensity ranges in the dataset are normalized by this process [29].

3.4 TL of CNN

Training CNNs usually needs heavy data because they have deep, interconnected layers responsible for their powerful performance. Unfortunately, if the CNNs are trained on tiny datasets, then there is high risk of overfitting, resulting in weak and unreliable performance [30]. Deep CNNs' training also causes issues like computationally intensive with high cost and slow processing times [31]. To overcome such limitations, TL is widely utilized. TL is a DL method that makes use of information from a previously trained model on a similar task to transfer to a new issue [32]. Through the transfer of applicable information from the pre-trained model, TL minimizes the training duration and enhances performance on the target task [33].

Seven well-known architectures – DenseNet201, ResNet101, Xception, InceptionV3, MobileNet, VGG16, and VGG19 – were employed in this study's methodology. These models were trained in MATLAB. The architectures are described as follows: DenseNet201, with 201 layers, features dense connectivity between layers [34]. ResNet101, with 347 layers, uses residual connections to aid training [35]. InceptionV3 (48 layers) and Xception (71 layers) are known for inception modules that perform parallel convolutions [36]. MobileNet (53 layers) uses depthwise separable convolutions for efficiency [37]. VGG16 and VGG19 have 13 and 16 convolutional layers, respectively, plus 5 max-pooling layers. Both VGG models follow a simple, sequential design [38].

3.5 Extraction of deep features

Deep neural networks learn high-level representations of incoming data, like text or images, which are referred to as deep features. Because they capture deep and complex connections between the input data and output labels, these characteristics are more accurate and effective [39]. Deep features are important for a number of ML tasks, i.e., natural language processing, image recognition, and its classification.

After applying the TL technique in this work, we extracted 1,920 deep feature vectors from ResNet101. These deep features were then used to train traditional ML models for further analysis as shown in Figure 3.

3.6 ML

The deep features that were retrieved by using ResNet101 were used to train ML models. Five-fold stratified cross-validation (SCV) was used to train four ML models: RFC, SVM, KNN, and MLP, as illustrated in Figure 4.

SCV is essential for managing unequal data distributions across classes, as illustrated in Figure 4. SCV improves the robustness of model evaluation by guaranteeing that each fold retains the same percentage of class labels as in the original dataset. This helps to avoid biased performance measurements that might result from unequal class representation in conventional cross-validation.

3.7 PCA

PCA reduces the dimensionality of multi-dimensional data by identifying dependencies between variables and transforming them into a lower-dimensional form while preserving significant information. The primary objective of PCA is to minimize redundancy (measured by covariance) and maximize information retention (measured by variance).

PCA generates principal components that are uncorrelated linear combinations of the original variables, effectively removing redundant information. This multivariate unsupervised technique is widely employed for feature selection in various applications, including data compression and pattern recognition. In this study, PCA was applied to the 1,920 deep features using MATLAB. Based on the eigenvalues, 108 PCs with eigenvalues (>1) were selected for training the RFC, SVM, MLP, and KNN models.

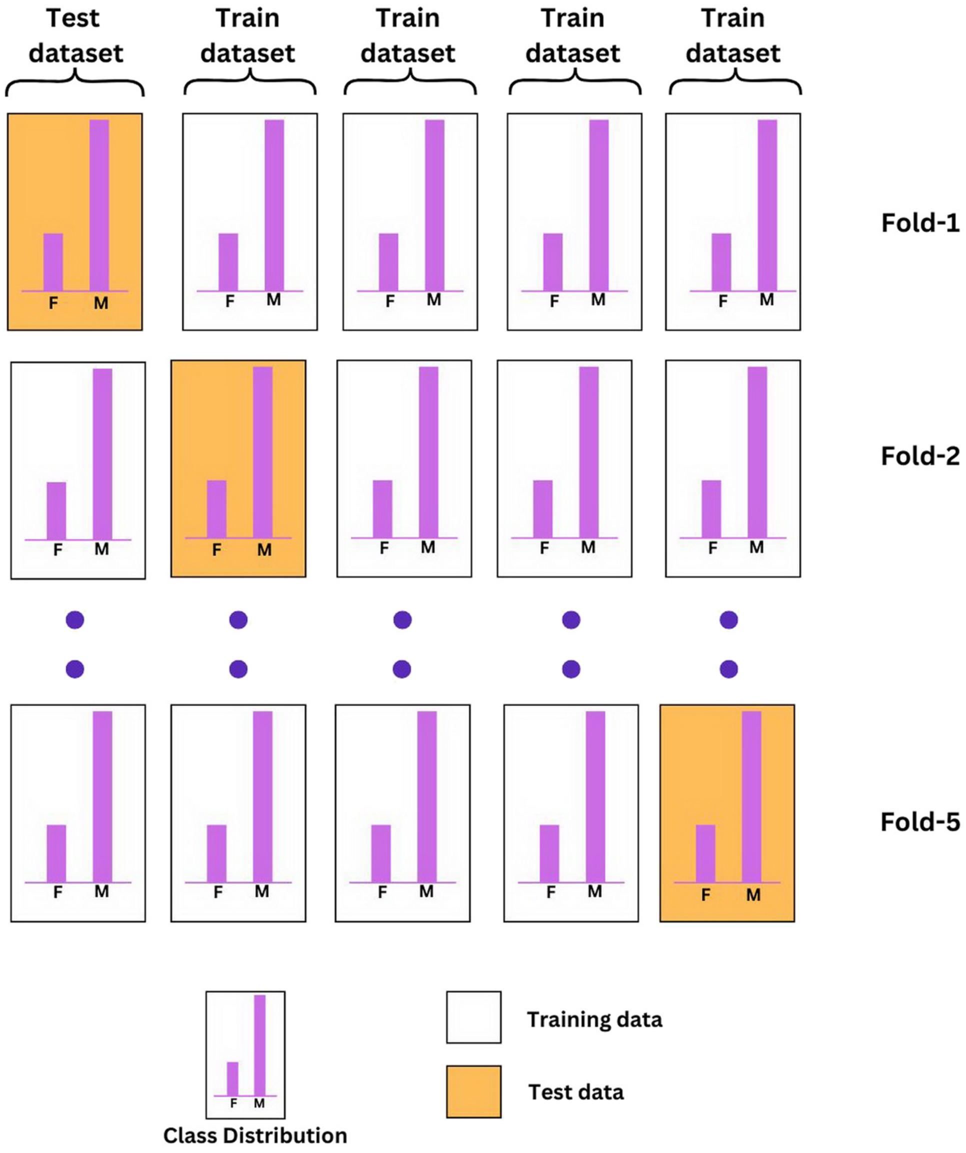


Figure 4: Five-fold SCV (Source: Created by the Author).

3.8 Matrices used for performance evaluation of the model

Accuracy, precision, recall, specificity, *F*1-score, and the AUC were among the measures used to assess each model's performance. These metrics assess the trade-off between the True positive rate (TPR) and the False positive rate (FPR) across different classification thresholds. The mathematical formulations for each metric are provided below:

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

$$\text{Precision} = \frac{\text{TP}}{\text{TP} + \text{FP}}, \tag{2}$$

$$\text{Sensitivity or Recall} = \frac{\text{TP}}{\text{TP} + \text{FN}}, \tag{3}$$

$$\text{Specificity} = \frac{\text{TN}}{\text{TN} + \text{FP}}, \tag{4}$$

$$F1\ \text{score} = \frac{2 \times (\text{Precision} \times \text{Recall})}{\text{Precision} + \text{Recall}}, \tag{5}$$

where TP is true positive; TN is true negative; FP is false positive; and FN is false negative.

4 Results and discussion

4.1 Experimental setup

MATLAB software was utilized to conduct the empirical assessments of the suggested DL model on a machine that was equipped with an NVIDIA GTX3050 graphics card and a Core i5 processor operating at 2.50 GHz. Together with 16GB of RAM, this setup offered sufficient processing power for examining the algorithm's classification results for diseased and healthy papaya fruit varieties. To conform the dependability when assessing the suggested network models, a fivefold SCV was also used in every experiment.

4.2 Training and testing of network classifier

In this study, three methodologies were proposed for papaya disease classification: (a) the application of TL using CNN model; (b) extraction of deep features from ResNet101 followed by training of traditional ML models; and (c) the application of PCA for the extracted deep features, where ML models were trained by using the PCs whose eigenvalues were >1. Tables 3–5 provide a summary of the performance metrics for the respective proposed methods.

Table 3: Performance assessment of widely-used CNN models employing TL

CNN model	Accuracy	Precision	Recall	Specificity	*F*1-score	AUC-ROC
DenseNet201	94.84	95.26	94.84	99.42	94.76	99.89
ResNet101	97.50	97.54	97.48	99.72	97.48	99.98
Xception	93.47	93.97	93.47	99.27	93.39	99.79
InceptionV3	92.44	92.74	92.51	99.16	92.45	99.77
MobileNet	96.45	96.61	96.45	99.61	96.44	99.96
VGG16	91.87	92.44	91.87	99.09	91.85	99.72
VGG19	94.16	94.55	94.16	99.35	94.18	99.76

Table 4: Metrics for ML model evaluation

ML models	Accuracy	Precision	Recall	Specificity	*F*1-score	AUC-ROC
RFC	91.86	91.65	91.69	90.14	91.62	99.56
SVM	98.05	97.99	97.95	96.47	97.96	99.96
MLP	98.30	98.32	98.10	97.67	98.18	99.88
KNN	89.33	91.59	88.93	98.46	89.04	98.59

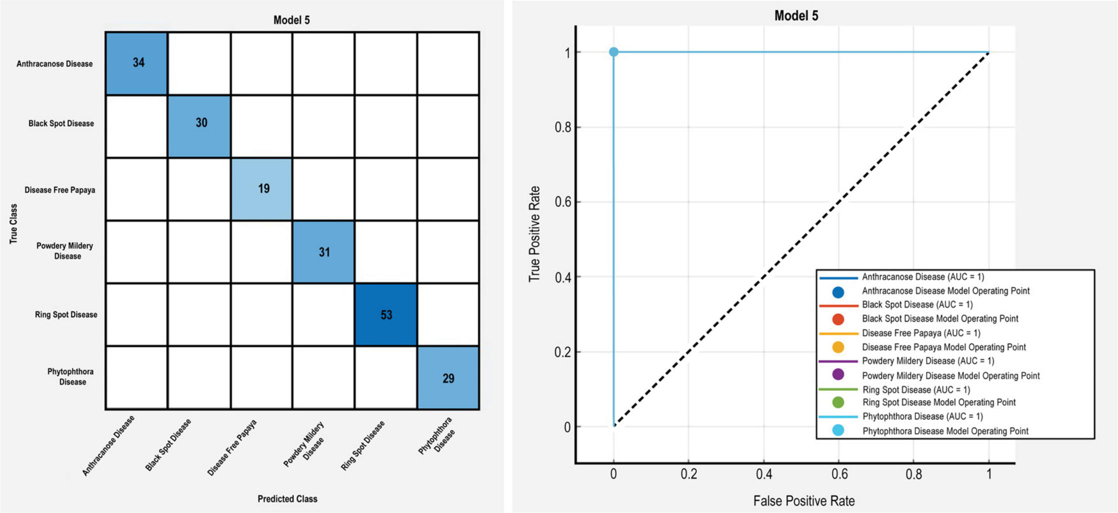
Table 5: Evaluation metrics for ML models trained with PCA

ML models	Accuracy	Precision	Recall	Specificity	*F*1-score	AUC-ROC
RFC	99.54	99.57	99.55	100	99.99	99.99
SVM	99.87	99.78	99.75	100	99.99	1.00
MLP	99.08	99.06	99.05	97.70	99.05	99.93
KNN	91.63	92.35	91.26	98.70	99.70	99.70

The performance parameters show that ResNet101 is the best by achieving the maximum 97.50% of accuracy in classifying diseased and healthy papaya fruit varieties, as shown in Table 3. The effectiveness of the ML models (RFC, SVM, KNN, and MLP) trained and evaluated using the 1,920 features taken from the ResNet101 CNN (as shown in Table 4) showed that the MLP outperformed the other models with the maximum accuracy of 98.30%.

Different ML models (RFC, SVM, KNN, and MLP) evaluated through training and testing on a set of 1,920 features derived from the ResNet101 CNN revealed distinct performance results. Among all models tested in this study, the MLP showed the highest effectiveness by attaining an accuracy of 98.30%. The MLP showed strong classification abilities as reflected by its precision rate of 98.32%, recall rate of 98.10%, specificity rate of 97.67%, and *F*1-score of 98.18%. The SVM demonstrated competitive performance through its 98.05% accuracy rate, 97.99% precision rate, 97.95% recall rate, 96.47% specificity rate, and 97.96% *F*1-score rate. The RF classifier achieved 91.86% accuracy along with 91.65% precision, 91.69% recall, 90.14% specificity, and an *F*1-score of 91.62%. The KNN model performed the worst compared to others with an accuracy of 89.33%, precision of 91.59%, recall of 88.93%, specificity of 98.46%, and an *F*1-score of 89.04%. The results confirm that selecting the right model architecture and choosing appropriate models leads to optimal classification performance while advanced feature extraction methods like ResNet101 boost ML models' predictive capabilities.

Following the use of PCA to lower the dimensionality of the feature set to 108 principal components, The SVM model performed better with an impressive 99.87% of classification accuracy as evident in Table 5. Such performance is significant since it beats all other models that were tested, including RFC, MLP, and KNN. The RFC attained 99.54% accuracy with precision of 99.57% and *F*1-score of 99.99%, whereas the MLP attained 99.08% accuracy with precision of 99.06% and *F*1-score of 99.05%. KNN performed poorer with an accuracy of 91.63%, precision of 92.35%, and *F*1-score of 99.70%. Confusion matrix and ROC of the test set of the proposed method 3 is shown in Figure 5.



	Anthracanose Disease	Black Spot Disease	Disease Free Papaya	Powdery Mildery Disease	Ring Spot Disease	Phytophthora Disease
Anthracanose Disease	34					
Black Spot Disease		30				
Disease Free Papaya			19			
Powdery Mildery Disease				31		
Ring Spot Disease					53	
Phytophthora Disease						29

Figure 5: Confusion matrix and ROC of the test set of the proposed method 3 (Source: Created by the Author).

The comparison to related works displays remarkable improvements in papaya classification accuracy in Table 6. Earlier models proposed by Habib et al. [19,20] with *K*-means clustering based on SVM was 90.15%, and Islam et al. [17] integrated CNN, RF, and SVC at a rate of 98.04%. Other works like Veeraballi et al. [21] with ResNet-50 posted lower accuracy rates at 89.15%.

Conversely, the suggested techniques, based on sophisticated methods, greatly surpassed the above models. The TL-based ResNet101 approach had 97.50% accuracy, whereas ResNet101 deep features combined

Table 6: Analysis of the proposed method with other related studies

References	Classification	Used methodology with accuracy
[17]	Papaya (fruit) – 214 numbers	*K*-mean clustering with SVC, CNN, and RF classifier. Accuracy of 98.04%
[18]	Papaya (both leaf and fruit) – 234 numbers	CNN, accuracy of 91%
[20]	Papaya (both leaf and fruit) – 126 numbers	*K*-mean clustering with SVM classifier, accuracy of 90.15%
[21]	Papaya (leaf) – 9,470 numbers	ResNet-50, accuracy of 89.15%
[23]	Papaya (fruit)	Inception CNN, accuracy of 97%
[26]	Papaya (both fruit and leaf)	SVM & RF, Accuracy of 91.47 and 90.22%
Proposed method	Papaya (fruit) – 983 numbers	ResNet101 deep features, PCA, and ML-SVM with an accuracy of 99.87%

with ML using MLP classifiers had 98.30% accuracy. The best-performing model, based on ResNet101deep features, PCA, and ML with SVM classifiers, had a spectacular accuracy of 99.87%. This shows the efficacy of the proposed techniques, particularly when DL, feature reduction, and conventional classifiers are used together for better performance in papaya classification.

5 Findings and future research

In recent years, ML has played a pivotal role in addressing agricultural challenges, such as the classification and grading of fruit varieties. TL, in particular, has gained prominence as an effective approach for the classification of fruit diseases, including the identification of papaya diseases. Here we experimented with seven prominent CNN models from different families, each with a classification accuracy greater than 90%. The success of the models in classifying papaya diseases using CNN-based models reaffirms the robustness of the approach. Still, this study goes beyond traditional CNN methods since it incorporates deep feature extraction, PCA, and classical ML algorithms to classify papaya disease, bringing novelty to the domain. The approach consisted of extracting deep features from CNN models and performing PCA for reducing dimensions. Next four classical ML models were utilized: RFC, SVM, MLP, and KNN. The performance of the models was tested using SCV for stable classification. The findings indicated exemplary classification accuracies, with the highest accuracy recorded by SVM at 99.87%, followed by RFC (99.54%), MLP (99.08%), and KNN (91.63%). These results highlight the dramatic improvement in classification performance obtained by combining deep feature extraction with PCA when used for image-based tasks.

Apart from aiding better classification performance, the results of this study have real-world applications for end users, especially in helping them determine the kind of disease that is impacting papaya crops. This enables corrective actions to be taken in a timely manner during the cultivation process. One drawback of this research, however, is that the severity of the diseases was not factored into the classification process. In addition, the research was not able to evaluate the performance of the developed models on large, high-volume datasets, as well as the consideration of the existence of other flaws in papaya leaves and plants under different environmental conditions. Such a limitation offers a significant direction for future research.

5.1 Future research directions

Subsequent work will remediate these shortfalls by highlighting a number of important areas. First, integration of a greater number of samples with a larger variety of disease severity and potential flaws will provide a more realistic assessment of model performance. Moreover, the influence of varied environmental conditions on papaya disease categorization should be explored to further enhance model generalizability. Future research can also investigate the combination of state-of-the-art CNN architectures and dimensionality reduction methods to further improve classification accuracy. Through solving these challenges, future research will lead to more stable and dependable papaya disease classification systems for agricultural applications.

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