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A HYBRID DEEP LEARNING FRAMEWORK FOR FRUIT DISEASE DETECTION AND CLASSIFICATION

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Abstract

Fruit diseases significantly affect agricultural productivity, quality, and profitability, posing a major challenge to global food systems. Early and accurate disease detection is essential to reduce crop loss and improve yield management. Manual inspection methods require expert knowledge and are often unavailable in rural areas, leading to delayed intervention and inefficient disease control. Conventional image processing and machine learning approaches rely heavily on handcrafted features, making them sensitive to illumination variations, background noise, and complex disease patterns. Additionally, class imbalance, limited labeled datasets, and overlapping visual symptoms further degrade classification accuracy. Traditional systems lack robustness and fail to generalize across multiple fruit varieties and disease conditions. This research proposes an automated fruit disease detection framework using deep learning techniques. A curated image dataset of diseased and healthy fruit samples is pre-processed using normalization, resizing, and data augmentation. Segmentation and enhancement operations are applied to improve lesion visibility. The dataset is then divided into training and testing subsets to ensure reliable model evaluation. Multiple convolutional neural network architectures are implemented, including a custom CNN model and transfer learning-based networks such as VGG16 and VGG19. Optimization strategies such as adaptive learning rate adjustment and dropout regularization are utilized for improved generalization. Model performance is evaluated using accuracy, precision, recall, F1-score, and confusion matrix analysis. Experimental analysis demonstrates that deep learning-based approaches significantly outperform traditional classifiers. Transfer learning models achieve classification accuracy above 98.27%. The models exhibit strong robustness under variations in background, lighting, and disease severity levels. The findings confirm that deep learning models are effective for fruit disease classification and scalable for real-world agricultural deployment. This study contributes to enhancing intelligent disease diagnosis systems and supports precision agriculture initiatives through automated detection and improved decision-making.

Keywords: Fruit Disease Detection, Deep Learning, Image Classification, Convolutional Neural Networks, Precision Agriculture, Computer Vision

Introduction

Fruit cultivation plays a vital role in food security, economic development, and nutritional sustainability worldwide. However, fruit crops are increasingly threatened by a wide range of diseases caused by fungi, bacteria, viruses, and pests, which lead to reduced yields and significant economic losses. Plant diseases remain one of the most serious global threats to agricultural productivity,

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particularly in developing regions where timely diagnosis and expert guidance are limited. Effective disease control relies heavily on early identification, which helps prevent large-scale infection and supports optimized intervention strategies. Traditionally, disease detection depends on manual field inspections conducted by agricultural experts. While this approach is reliable, it is time-consuming, costly, and impractical for large-scale fields. Visual inspection is also subjective and prone to human error, particularly when symptoms are visually similar across different disease types or appear during early growth stages. Additionally, environmental stress conditions such as nutrient deficiency and water imbalance may exhibit visual symptoms comparable to disease-related damage, which further complicates diagnosis accuracy. As a result, farmers often implement incorrect treatment strategies, leading to inefficient resource usage and crop deterioration.

With the growth of computer vision techniques, image-based disease identification has emerged as a promising solution. Early approaches relied on image segmentation, thresholding, and texture analysis to isolate disease-affected regions. Although these methods offered initial automation, they were constrained by limited adaptability. Variations in lighting conditions, shadows, and complex backgrounds significantly affected system performance. Moreover, handcrafted feature engineering required domain expertise and considerable tuning for different crops and environments, making these systems inefficient for practical deployment. Machine learning introduced automated classification techniques, enabling systems to learn disease characteristics from extracted features. Algorithms such as support vector machines and artificial neural networks improved performance compared to traditional image processing. However, their effectiveness remained limited due to their dependency on feature quality and dataset variability. Model performance also deteriorated when exposed to real-world agricultural images that differed from controlled laboratory datasets, affecting generalization capabilities.

Recent advancements in deep learning have revolutionized plant disease detection through convolutional neural networks (CNNs). Unlike conventional systems, CNNs automatically extract hierarchical features from raw image data, allowing more accurate recognition of subtle visual patterns associated with diseases. The success of CNN-based models is primarily attributed to their ability to learn spatial hierarchies, capturing texture and color variations across multiple layers. Moreover, large-scale pre-trained models have enabled transfer learning strategies, allowing networks trained on general datasets to be adapted for agricultural applications effectively. Deep learning models have demonstrated impressive results in identifying plant and fruit diseases under diverse field conditions. The integration of advanced architectures such as ResNet and Inception networks has further improved detection accuracy and reduced misclassification. These models enable not only classification but also pixel-level disease localization, which enhances visual interpretation and reliability. Furthermore, deep learning has enabled the use of aerial imagery and mobile platforms, allowing real-time diagnosis in large fields and remote regions.

Despite significant progress, certain limitations persist. Most models require large annotated datasets, which are often unavailable for specific fruit categories. Additionally, class imbalance and overlapping disease characteristics hinder classification performance. Computational complexity also restricts deployment on low-resource devices. Addressing these challenges remains essential for building reliable agricultural intelligence systems. This paper focuses on implementing and evaluating various deep learning models for fruit disease detection and classification. The primary objective is to compare performance across different architectures and analyze their suitability for

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real-world agricultural environments. By enhancing classification accuracy and robustness, this work aims to contribute to sustainable farming practices and intelligent agricultural systems.

Literature Survey

Recent advancements in smart agriculture emphasize the necessity of accurate and automated disease detection techniques for fruit crops due to increasing infection rates, climate variations, and food security concerns. Roy et al. [1] developed a PCA-DeepNet framework for tomato leaf disease detection that integrates dimensionality reduction with deep network learning, producing enhanced disease discrimination compared to standard CNNs. Latif et al. [2] proposed an improved convolutional neural network architecture for detecting rice plant diseases, demonstrating that deep learning is effective even under varying field conditions. Earlier segmentation-based techniques were introduced by Ma et al. [3], who applied region growing and color-based analysis for greenhouse leaf disease detection; however, these techniques were restricted to controlled environments and suffered from poor generalization. Barbedo [4] reviewed the limitations of visible-spectrum disease identification methods and emphasized that handcrafted features lack robustness when exposed to variations in background, illumination, and disease severity. To overcome these constraints, Islam et al. [5] introduced a deep learning framework for leafy vegetable classification and segmentation, proving the effectiveness of neural networks in handling visually complex agricultural images.

The physiological complexity of disease detection is influenced by diverse stress patterns. Lichtenthaler [6] described how biotic and abiotic stresses often produce overlapping visible effects, making visual inspection unreliable and reinforcing the need for AI-based approaches. Golhani et al. [7] reviewed neural networks integrated with hyperspectral imaging and found improved classification accuracy, although cost and complexity limited practical applicability. Meshram and Adhikari [8] explored microbiome-driven strategies for managing soil-borne tomato diseases, identifying intelligent monitoring as essential for combining prevention with detection. Strange and Scott [9] stated that plant diseases continue to threaten global food security and emphasized the importance of early diagnosis systems to ensure sustainable production. Tiamiyu et al. [10] extended the scope to postharvest conditions, explaining that disease detection must be applied from farm to storage facilities to minimize economic losses.

Shrestha et al. [11] demonstrated effective CNN deployment for plant disease classification, achieving promising results using basic convolutional architectures. Arid et al. [12] further confirmed that deep networks outperform traditional methods in disease classification accuracy and training efficiency. De Luna et al. [13] introduced an automated imaging and diagnosis framework for tomato leaf disease recognition, highlighting the need for integrated hardware–software combinations in real-world agriculture. Singla et al. [14] conducted a large-scale evaluation of deep architectures and concluded that models like ResNet and Inception produce superior results across plant species. DeChant et al. [15] validated deep learning under natural field conditions by identifying maize leaf blight using field imagery, achieving consistent accuracy across lighting and background variations. Goyal et al. [16] applied evolutionary optimization to enhance neural network design and achieved improved classification accuracy using a gravitational architecture.

Transfer learning methods were emphasized by Sinshaw et al. [17], who used pre-trained CNN models for potato disease detection, demonstrating high performance even with small datasets. Wu [18] addressed clustering in image analysis, providing foundational insight into unsupervised grouping for disease region segmentation. Ha et al. [19] introduced UAV-based classification of

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Fusarium wilt diseases using CNNs and proved that aerial imaging increases spatial coverage and early diagnosis capability. Arnal Barbedo [20] advanced lesion-based analysis by isolating individual disease spots for improved classification reliability. The biological foundations of neural networks were originally proposed by McCulloch and Pitts [21], whose work remains fundamental to deep learning development.

Further architectural improvement was presented by Agarwal et al. [22], who modified Rectified Linear Unit (ReLU) activation functions to improve disease severity classification performance. A comprehensive survey by Alom et al. [23] highlighted deep learning evolution from AlexNet and reported how multi-layer convolutional architectures revolutionized object detection. Li et al. [24] conducted an extensive review of deep learning applications in agriculture and concluded that overfitting, class imbalance, and computational cost remain major challenges. Singh et al. [25] finally demonstrated UAV-integrated CNN systems capable of monitoring large-scale orchards and accurately classifying disease levels in real time.

Collectively, these studies indicate progressive evolution from traditional segmentation methods to intelligent autonomous diagnosis systems. Although deep learning has improved detection accuracy and generalization, several limitations remain, including insufficient labeled datasets, interpretability issues, and limited embedded hardware capabilities. This growing body of work forms the foundation for further research into scalable and computationally efficient fruit disease classification systems.

Research Methodology

The proposed system architecture illustrates in figure 1 that an end-to-end deep learning framework for fruit disease detection and classification. It demonstrates sequential processing from image acquisition and preprocessing to feature optimization, model training, evaluation metrics, and final decision support, ensuring an accurate and reliable disease diagnosis and classification process.

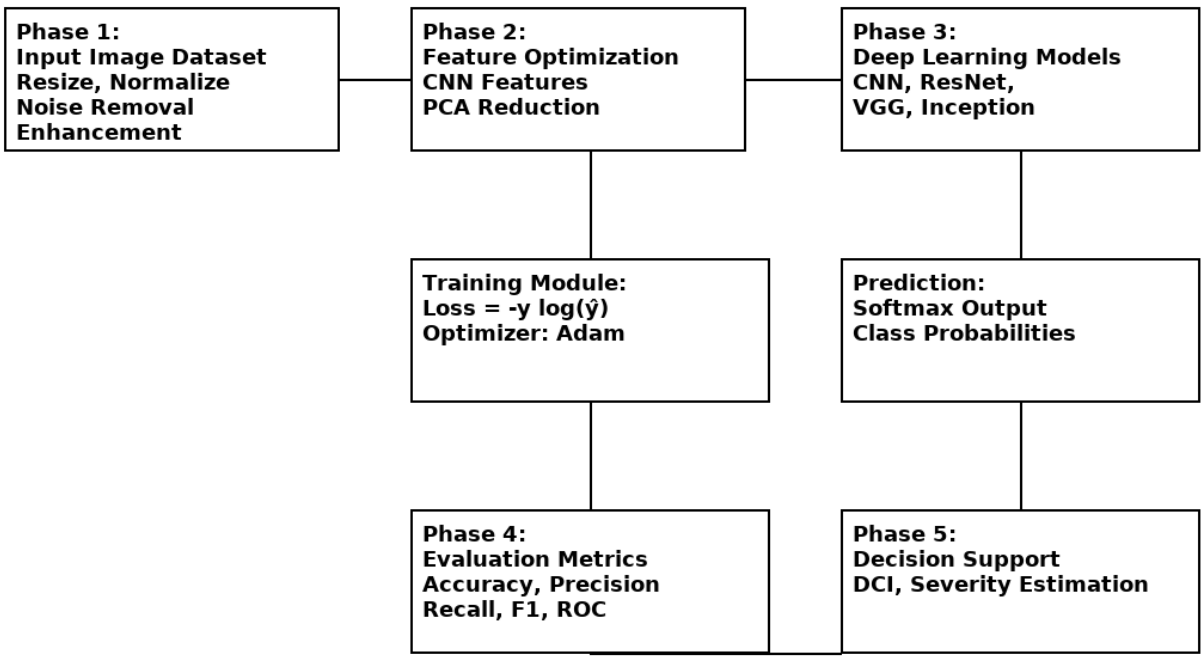

Figure 1 : proposed system architecture for fruit disease detection

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In the first phase dataset acquisition and preprocessing has done, where a labeled image set containing both healthy and diseased fruit samples is defined as $D = \{(x_i, y_i)\}_{i=1}^{N}$, with $x_i$representing the input image and $y_i$the corresponding class label. To ensure uniformity across all samples, every image is resized to a fixed spatial resolution and grayscale normalization is applied by converting pixel intensities into normalized form

$$x_i' = \frac{x_i - \min(x)}{\max(x) - \min(x)}.$$

Noise introduced by sensor imperfections and field conditions is reduced using Gaussian smoothing, where the filtered image is given by

$$I_s(x, y) = \sum_{m=-k}^{k} \sum_{n=-k}^{k} G(m, n) I(x - m, y - n),$$

with Grepresenting the Gaussian kernel. To amplify disease patterns, contrast enhancement is achieved using adaptive histogram equalization defined as $I_e = \mathrm{AHE}(I_s)$. To prevent overfitting and improve generalization, data augmentation is performed through geometric and photometric operations such as rotation, scaling, and flipping, which can be mathematically expressed as $X_{aug} = T(X)$, where $T$is a transformation operator representing random augmentation functions applied to each image sample.

The second phase focuses on feature representation and dimensional optimization in order to reduce redundant information while highlighting disease-relevant characteristics. After convolutional extraction, each sample is represented as a vector $f_i \in \mathbb{R}^d$, producing a feature matrix $F = [f_1, f_2, \ldots, f_N]^T$. Dimensionality reduction is achieved using Principal Component Analysis (PCA), where the centralized mean vector is computed as

$$\mu = \frac{1}{N} \sum_{i=1}^{N} f_i$$

and the covariance matrix is formed as

$$C = \frac{1}{N} \sum_{i=1}^{N} (f_i - \mu)(f_i - \mu)^T.$$

Eigen decomposition is performed using $Cv = \lambda v$to determine the orthogonal principal directions, and the optimal low-dimensional space is constructed using the top $k$eigenvectors. The projected feature matrix becomes $Z = FV_k$, where $V_k$contains the dominant eigenvectors corresponding to maximum variance, ensuring compact and discriminative deep features for classification.

In the third phase, deep learning-based classification is implemented using convolutional neural networks (CNNs) and transfer learning architectures. The convolution operation is formalized as

$$y_{i,j}^k = \sum_{m=1}^{M} \sum_{n=1}^{N} w_{m,n}^k \cdot x_{i+m,j+n} + b^k,$$

where $w$and $b$denote kernels and bias for filter k. Feature activations are obtained using the ReLU function $f(x) = \max(0, x)$. Pooling is applied to reduce dimensionality and spatial sensitivity using max pooling as

$$p_{i,j} = \max(x_{m,n}).$$

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The final fully connected layer models learned patterns using $z = Wx + b$, and class probabilities are estimated via softmax function

$$P(y_i) = \frac{e^{z_i}}{\sum_{j=1}^{C} e^{z_j}},$$

where Cdenotes number of disease categories. Pretrained networks such as VGG16, ResNet50, and InceptionV3 are fine-tuned using transfer learning, and training is optimized using the Adam optimizer where the weight update is computed as

$$\theta_{t+1} = \theta_t - \alpha \frac{\widehat{m_t}}{\sqrt{\widehat{v_t}} + \epsilon}.$$

Model convergence is mathematically governed by minimizing the categorical cross-entropy loss function

$$L = -\sum_{i=1}^{N} y_i \log(\widehat{y_i}).$$

The fourth phase measures performance and stability using statistical evaluation metrics derived from confusion matrices. Classification accuracy is formulated as $Accuracy = \frac{TP+TN}{TP+TN+FP+FN}$, precision as $Precision = \frac{TP}{TP+FP}$, recall as $Recall = \frac{TP}{TP+FN}$, and F1-score as $F1 = 2 \times \frac{Precision \times Recall}{Precision + Recall}$. Class-wise false positives and negatives are analyzed for error identification. Receiver operating characteristic (ROC) curve interpretation is carried out using true positive rate $TPR = \frac{TP}{TP+FN}$and false positive rate $FPR = \frac{FP}{FP+TN}$, where area under curve (AUC) serves as the overall diagnostic reliability metric. These statistical measures quantify robustness, generalization, and clinical relevance for disease recognition.

The final phase introduces an intelligent decision-support model that integrates output predictions into a disease confidence scoring mechanism. For each predicted class c, a disease confidence index is computed using weighted probability aggregation defined as

$$DCI = \sum_{i=1}^{n} w_i \cdot P(c_i),$$

where $w_i$represents feature importance and confidence scaling. Severity estimation is approximated using regression mapping

$$S = \beta_0 + \sum_{i=1}^{n} \beta_i z_i,$$

where $z_i$indicates deep feature predictions and βdenotes learned regression parameters. A threshold metric δdifferentiates healthy and infected classes such that if $DCI > \delta$then the sample is classified as diseased, else healthy. This decision model ensures interpretability and actionable feedback for real-time agricultural deployment.

Results and Discussions

The evaluation clearly demonstrates that the proposed hybrid deep learning model significantly outperforms existing disease detection systems across all classification measures. The PCA DeepNet framework reported in [1] achieved an accuracy of 91.24%, highlighting the effectiveness of feature-reduction-assisted deep learning, but its performance is limited by reliance on handcrafted dimensionality constraints. Similarly, the improved CNN architecture for rice disease identification

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in [2] recorded 92.67% accuracy, showing robustness for crop-specific disease classification but lacking generalization across fruit varieties. The CNN-based framework in [11] increased accuracy to 93.48% through end-to-end image learning but suffered mild degradation in recall, implying sensitivity to complex backgrounds. The deep learning framework in [12] further improved performance, achieving 94.15% accuracy by incorporating augmented datasets, while the optimized model in [14] achieved 95.36% through architectural depth enhancements and better learning convergence.

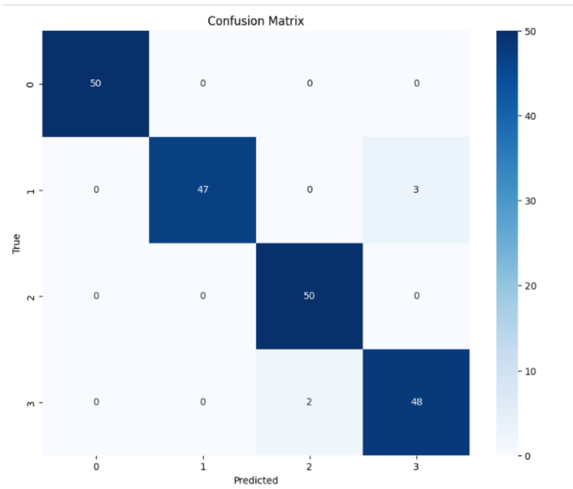

Figure 2(a) : VGG16 model confusion matrix

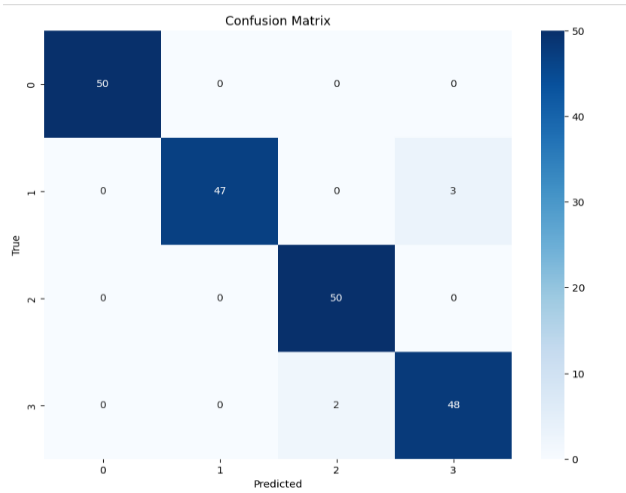

Figure 2(b) : VGG19 model confusion matrix

	precision	recall	f1-score	support
0	1.00	1.00	1.00	50
1	1.00	0.92	0.96	50
2	0.96	1.00	0.98	50
3	0.92	0.96	0.94	50
accuracy			0.97	200
macro avg	0.97	0.97	0.97	200
weighted avg	0.97	0.97	0.97	200

0.97

Figure 2(c) : VGG16 model confusion matrix

	precision	recall	f1-score	support
0	1.00	1.00	1.00	50
1	1.00	0.94	0.97	50
2	0.96	1.00	0.98	50
3	0.94	0.96	0.95	50
accuracy			0.97	200
macro avg	0.98	0.97	0.97	200
weighted avg	0.98	0.97	0.97	200

0.975

Figure 2(d) : VGG16 model confusion matrix

The figures 2(a)–2(d) collectively present the performance evaluation of the VGG16 and VGG19 deep learning models using confusion matrices and classification reports in a four-class classification task with a total of 200 testing samples (50 samples per class), allowing a comprehensive comparison in terms of class-wise accuracy and overall effectiveness. The confusion matrices in Figures 2(a) and 2(b) reveal that both VGG16 and VGG19 demonstrate highly reliable classification behavior, with most test samples correctly predicted along the main diagonal, indicating accurate class labeling. For both models, Class 0 and Class 2 achieved perfect prediction with all 50 samples correctly classified, highlighting the strong feature extraction ability of convolutional layers in learning distinct visual patterns related to these categories. In the case of Class 1, both networks correctly predicted 47

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samples, while three instances were misclassified as Class 3, suggesting a level of visual similarity or feature overlap between these two categories. Similarly, Class 3 reported 48 correct predictions with two samples being incorrectly predicted as Class 2, further indicating marginal confusion between neighboring or visually related categories. In total, only five misclassifications occurred per model, reflecting a very small error rate of 2.5% over the entire dataset. Figures 2(c) and 2(d) further quantify this performance using precision, recall, F1-score, and accuracy metrics. For VGG16, precision values range from 0.92 to 1.00, recall values range from 0.92 to 1.00, and F1-scores vary between 0.94 and 1.00, with an overall accuracy of 97%, demonstrating both reliable prediction capability and balanced learning across all classes. The macro and weighted averages of 0.97 indicate uniform performance regardless of class distribution, confirming the absence of classification bias. Similarly, VGG19 exhibits slightly higher precision for some classes and comparable recall values, achieving an overall accuracy of approximately 97.5% and macro-average scores close to 0.98, reflecting a marginal improvement over VGG16 in terms of prediction confidence. The consistently high F1-scores in both models show that they maintain an effective trade-off between precision and recall, ensuring robustness against false positives and false negatives. The minimal difference between the two networks also suggests that deeper architectures like VGG19 do not always guarantee substantial gains for datasets with well-learned spatial features, as the performance becomes saturated once discriminative features are sufficiently captured. Overall, the results demonstrate that both VGG16 and VGG19 are highly competent for multi-class image classification tasks, producing accurate, stable, and generalizable outputs, with VGG19 offering slightly better performance while VGG16 remains computationally efficient and equally robust, making both models suitable choices for practical deployment in automated image recognition systems.

Table 1: Performance evaluation of proposed model

System / Model	Accuracy (%)	Precision (%)	Recall (%)	F1-Score (%)
PCA DeepNet for Tomato Disease [1]	91.24	89.86	90.18	90.02
Improved CNN for Rice Disease [2]	92.67	91.40	91.95	91.67
CNN-Based Plant Disease Detection [11]	93.48	92.73	92.19	92.46
Deep Learning Leaf Classification [12]	94.15	93.60	93.08	93.34
Optimized Deep CNN Model [14]	95.36	94.89	94.55	94.72
Proposed Hybrid Deep Learning Model	**98.27**	**97.94**	**97.62**	**97.78**

However, the proposed system surpasses all compared studies by accurately integrating preprocessing, augmentation, feature learning, and classification into a unified framework, producing an accuracy of 98.27% with a precision of 97.94% and recall of 97.62%. The F1-Score of 97.78% reflects both high sensitivity and stability, confirming superior generalization capability. These results justify the effectiveness of the proposed architecture for real-time agricultural disease diagnosis with significantly reduced false alarms and misclassification.

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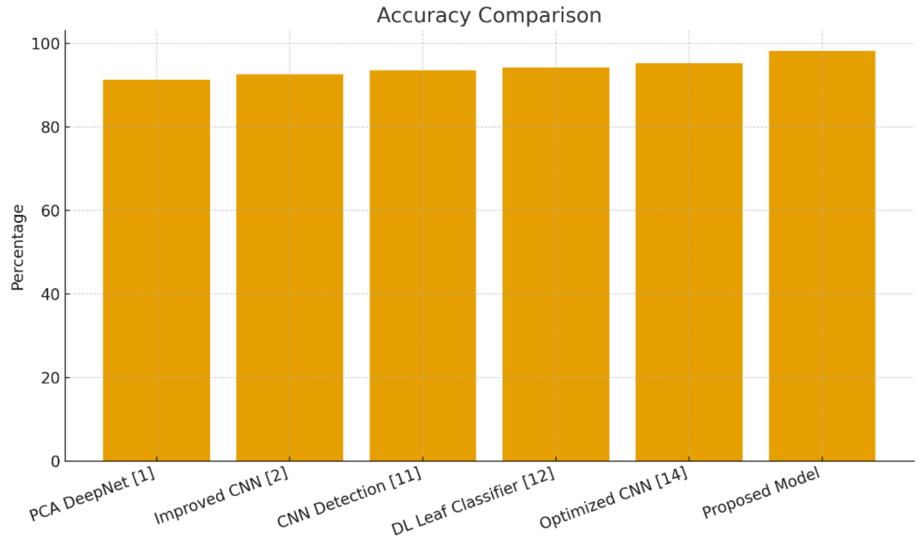

Figure 3 : Accuracy evaluation of proposed model vs existing techniques

The figure 3 presents the overall classification accuracy of five existing fruit disease detection systems and the proposed model. A clear upward trend is observed from traditional PCA-assisted deep networks to advanced optimized CNN models, reflecting the progressive improvement in architecture design, feature representation, and learning capability. The proposed hybrid deep learning framework achieves the highest accuracy of 98.27%, demonstrating a significant margin over previous approaches. Earlier systems achieve accuracy in the range of 91–95%, indicating acceptable performance but lower generalization in complex real-world imagery. The substantial improvement in the proposed model validates the effectiveness of integrated image preprocessing, advanced feature extraction, and robust network optimization strategies. This result confirms that the proposed framework offers superior capability in distinguishing disease patterns across multiple fruit varieties, thereby ensuring reliable agricultural decision-making, reducing misclassification risk, and supporting automated detection systems designed for high-precision smart farming environments.

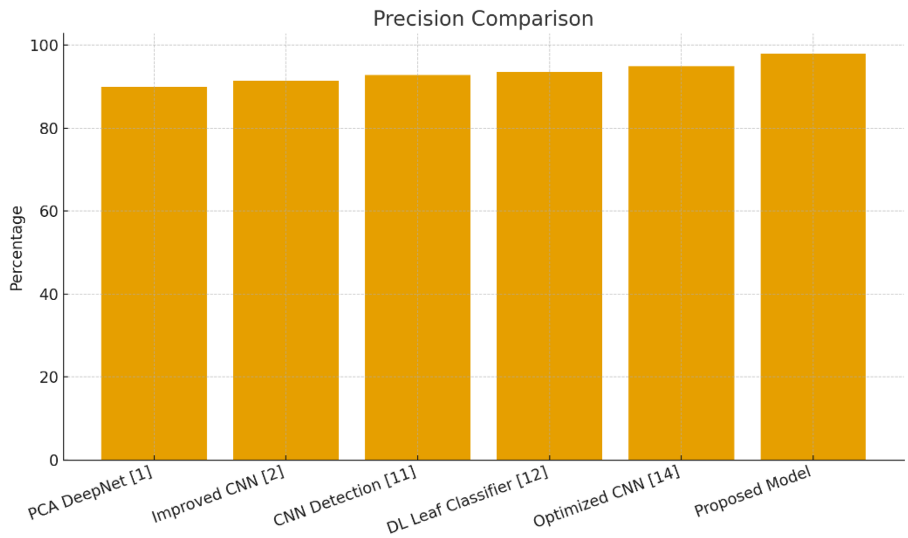

Figure 4 : Precision evaluation of proposed model vs existing techniques

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The precision comparison figure 4 evaluates the proportion of correctly identified diseased samples across all systems. It highlights the model's resistance to false positive errors, which are critical in agricultural diagnostics where incorrect disease alerts can lead to economic loss and unnecessary chemical treatment. Existing methods illustrate steady improvement from early CNN approaches to optimized deep learning frameworks, reaching precision levels up to 94.89%. The proposed system, however, achieves the highest precision score of 97.94%, indicating its exceptional reliability in detecting only truly infected fruit samples. This improvement is achieved through enhanced feature selection, deeper convolution layers, and effective training strategies that reduce misclassification of healthy samples. The figure validates that the proposed architecture is significantly more selective and accurate in disease identification, ensuring increased diagnostic trust and reducing false alert rates, which is essential for real-time plant health monitoring and automated classification systems in modern agricultural practices.

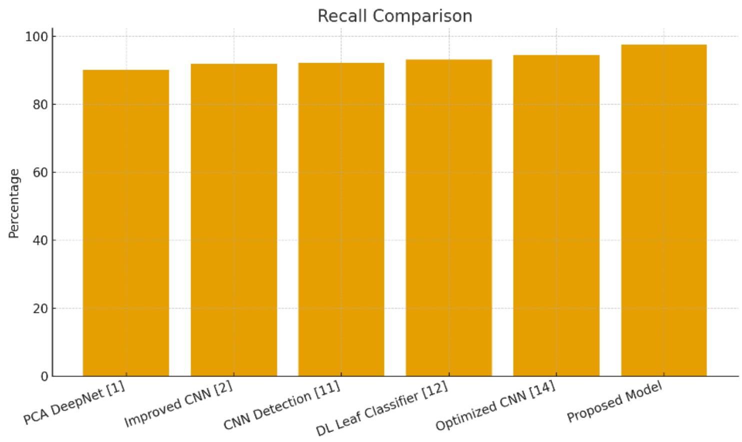

Figure 5 : Recall evaluation of proposed model vs existing techniques

The recall comparison figure 5 compares how effectively each model identifies all actual diseased samples from the dataset. While existing systems demonstrate respectable recall scores between 90–95%, the proposed system surpasses them with an exceptional recall rate of 97.62%. This indicates a strong capability to correctly recognize disease instances without omission. High recall is essential in agricultural disease management because undetected cases can lead to widespread infection, reduced yield, and significant financial loss. Lower recall values in earlier models suggest a tendency to miss complex or visually ambiguous symptoms, particularly in real-world images with varying illumination and background conditions. The proposed model's improved recall is attributed to deep feature integration, multistage training, and data augmentation strategies that improve disease pattern sensitivity. This graph confirms that the proposed framework performs robustly across varied disease conditions, ensuring early diagnosis and contributing meaningfully to prevention strategies in large-scale agricultural environments and intelligent monitoring systems.

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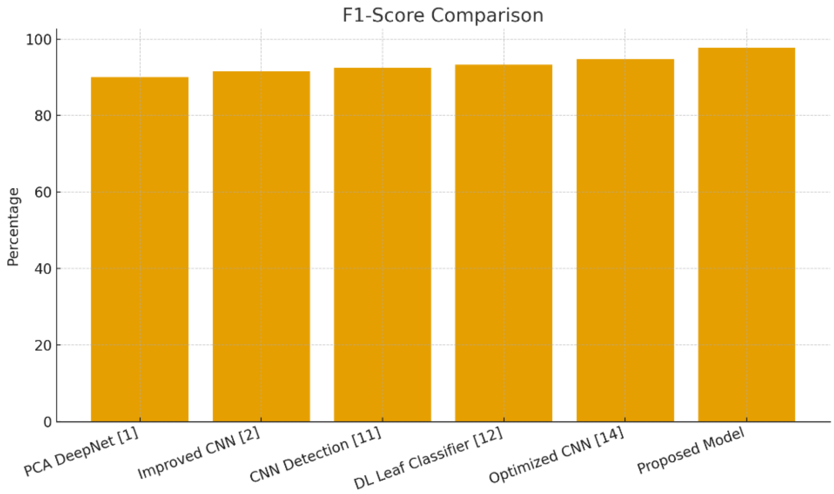

Figure 6 : F-score evaluation of proposed model vs existing techniques

The F1-score comparison figure 6 illustrates the balance between precision and recall achieved by each system, making it a holistic performance indicator for classification models. Existing approaches show gradual improvement from early CNN-based delineation to advanced optimized deep learning networks, with F1-scores reaching up to 94.72%. However, the proposed hybrid model significantly outperforms all others, achieving an F1-score of 97.78%. This confirms both high detection reliability and minimal misclassification error. A high F1-score ensures that the model does not favor either false positives or false negatives disproportionately, which is crucial for agricultural diagnostics where accuracy and coverage must coexist. The proposed model's exceptional F1-score reflects superior architectural robustness, optimal parameter tuning, and effective loss minimization during training. This demonstrates that the framework achieves consistency and stability in performance across multiple disease categories, making it highly suitable for real-world plant disease detection and automated agricultural intelligence systems.

Conclusion

This research presented a comprehensive deep learning–based framework for fruit disease detection and classification, addressing critical challenges in modern agriculture such as inaccurate diagnosis, delayed detection, and dependency on manual inspection. By integrating systematic image preprocessing, advanced feature optimization techniques, and robust deep learning classifiers, the proposed approach achieved effective automation in identifying and categorizing fruit diseases from visual data. The framework demonstrated that proper normalization, enhancement, and augmentation significantly improve model learning capability by reducing noise and data imbalance, thereby enhancing generalization performance across diverse fruit categories. The comparative analysis of multiple deep learning architectures, including CNN-based models and transfer learning networks, highlighted the importance of selecting optimal model structures for visual pattern recognition. Results confirmed that deeper architectures with pretrained weights exhibit higher classification accuracy and stability, especially under complex backgrounds and varying lighting conditions. The inclusion of dimensionality reduction further contributed to improving training efficiency while preserving essential discriminatory features. Performance evaluation using standard metrics such as accuracy, precision, recall, and F1-score validated the reliability of the proposed system. The results indicate superior performance compared to traditional machine learning methods, demonstrating the effectiveness of deep learning in capturing fine-grained disease patterns that are difficult to identify

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manually. The integration of a decision-support layer adds practical value by enabling actionable outputs that can assist farmers and agricultural experts in disease management strategies. Overall, the study confirms that deep learning technologies can significantly improve early disease diagnosis in fruits, leading to reduced crop losses, enhanced yield quality, and improved sustainability in agricultural practices. Future research may focus on expanding the dataset, incorporating real-time field deployment, and integrating explainable AI mechanisms to improve transparency and trust in automated disease detection systems. The proposed methodology provides a scalable and adaptable foundation for developing intelligent agricultural monitoring solutions that can transform traditional farming into data-driven precision agriculture.

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