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# A Comparative Justification of Deep Learning vs Traditional Machine Learning for Areca Crop Disease Detection

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ABSTRACT: Traditional machine learning (ML) techniques have been widely applied in agricultural disease detection. However, their effectiveness is often constrained by the complex visual characteristics of real-world crop images, particularly in Areca nut and palm leaves, which exhibit high variability in texture, colour, and background. This paper presents a comparative justification for employing deep learning (DL) models over conventional ML approaches for Areca crop disease detection. Key evaluation factors include feature extraction capabilities, generalization performance, data scalability, real-time deployment feasibility, and interpretability. While ML models rely on manual feature engineering and struggle with noisy or augmented datasets, DL models such as Convolutional Neural Networks (CNNs) and Vision Transformers (ViTs) learn directly from raw pixel data and maintain high accuracy across varied conditions. Experimental results show that ViTs achieve 97.73% accuracy, significantly outperforming SVM and Random Forest models. Furthermore, DL models support real-time deployment using lightweight frameworks like TensorFlow Lite. The study concludes that DL provides a more robust, scalable, and deployable solution for crop disease detection, paving the way for precision agriculture solutions in real-world settings.

**KEYWORDS**: Areca crop, disease detection, deep learning, machine learning, Vision Transformer, CNN, image classification, agricultural AI, precision agriculture, model interpretability.

#### I. INTRODUCTION

Agriculture plays a pivotal role in ensuring global food security and economic stability. However, crop productivity is frequently threatened by a wide range of plant diseases[1], which, if not identified and managed promptly, can lead to significant yield losses. Traditionally, disease detection has relied on visual inspection by farmers or agricultural experts, a process that is both time-consuming and prone to human error, particularly when dealing with subtle or early-stage symptoms.

Areca nut (commonly known as betel nut) is an economically valuable crop, widely cultivated across India and Southeast Asia. It is especially susceptible to diseases such as yellow leaf disease, fruit rot, and leaf spot, all of which affect the health, yield, and market value of the crop. These diseases often present in diverse and inconsistent visual patterns, making accurate and early identification particularly difficult in practical field conditions.

In response to these challenges, smart agriculture practices have emerged, integrating technologies such as computer vision, artificial intelligence, and Internet of Things (IoT) for automated crop monitoring and decision-making. These innovations enable real-time, non-invasive disease detection and contribute to a shift from reactive to proactive crop management.

Machine learning (ML) techniques[2], including Support Vector Machines (SVM)[3] and Random Forests (RF)[4], have been employed in plant disease classification tasks with some success. These models, however, depend heavily on manual feature extraction processes—such as analyzing leaf colour, texture, or shape—which limit their adaptability and effectiveness in dynamic field environments.

Agricultural images captured under natural conditions present considerable variation in lighting, background clutter, disease stage, and leaf orientation. This variability poses significant challenges for traditional ML models, which often





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struggle to generalize effectively. Furthermore, the need for handcrafted features introduces additional computational overhead and impedes real-time deployment.

Deep learning (DL), particularly Convolutional Neural Networks (CNNs)[5] and the more recent Vision Transformers (ViTs)[6], has revolutionized the field of image recognition. These models can automatically learn hierarchical features from raw image data, offering superior accuracy, robustness, and scalability. DL techniques have shown great promise in various domains, including healthcare, autonomous vehicles, and increasingly, in precision agriculture.

Despite these advances, many agricultural systems continue to rely on traditional ML approaches due to their perceived simplicity and lower computational demands. However, for complex tasks such as Areca crop disease detection, where image variability and subtle symptom expression are common, DL models may offer a more effective and scalable solution[7]. A rigorous comparison between ML and DL approaches is essential to identify the most appropriate path forward.

This paper presents a detailed comparative study of ML and DL models for Areca crop disease detection. We analyze key aspects including feature learning, accuracy, generalization to unseen data, deployment feasibility, and explainability. Our results demonstrate that DL models significantly outperform traditional ML approaches, making them better suited for real-world agricultural disease detection and monitoring.

#### II. LITERATURE SURVEY

Automated disease detection in agriculture has gained substantial attention due to the need for scalable, cost-effective, and accurate diagnostic systems. Both traditional machine learning (ML) and deep learning (DL) approaches have been explored for classifying and detecting plant diseases using image-based data.

Traditional ML techniques such as Support Vector Machines, Decision Trees, and k-Nearest Neighbours have been widely applied in early works. These models typically rely on handcrafted features extracted using methods like colour histograms, Local Binary Patterns, or Gray-Level Co-occurrence Matrices. While these approaches have shown reasonable performance under controlled conditions, they tend to be highly sensitive to image noise, lighting variation, and background interference, limiting their reliability in field environments[8].

In contrast, deep learning models, especially Convolutional Neural Networks (CNNs), have demonstrated significant improvements in classification accuracy by automatically learning hierarchical features[9]. CNNs have enabled robust disease localization and enhanced interpretability in plant disease detection tasks, offering better adaptability to real-world variations in image data.

More recently, Vision Transformers (ViTs) have emerged as powerful alternatives to CNNs. Unlike CNNs, which focus on local pattern extraction, ViTs leverage self-attention mechanisms to capture global dependencies in images. In agricultural contexts, ViTs have shown superior generalization and robustness, particularly when trained on augmented datasets[10].

Comparative evaluations consistently reveal the limitations of traditional ML methods in handling large-scale, noisy, and diverse datasets, whereas DL models exhibit greater scalability and flexibility[11]. Advances in network architectures have further improved DL performance by addressing issues such as vanishing gradients and optimization bottlenecks.

Applications of these models across various crops — including rice[12], tomato[9], and grape — have yielded high classification accuracy, often exceeding 99%, demonstrating the cross-domain transferability of deep learning approaches.[12]

Techniques such as data augmentation, denoising, and transfer learning have also expanded the applicability of DL models to settings with limited labeled data. These strategies effectively address common agricultural data challenges, improving model generalization even in low-resource scenarios[13].





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Despite the progress in plant disease detection, Areca crop classification remains relatively underexplored, especially in comparative studies between ML and DL models[14]. Existing research tends to focus on either traditional or deep learning approaches in isolation. This study seeks to fill that gap by providing a comprehensive and quantitative analysis of both ML and DL models for Areca crop disease detection using a consistent experimental setup.

#### III. METHODOLOGY

This section outlines the end-to-end methodology employed for comparative analysis between traditional machine learning (ML) and deep learning (DL) models in Areca crop disease detection. The pipeline includes dataset preparation, preprocessing, augmentation, feature extraction, model training, and evaluation.

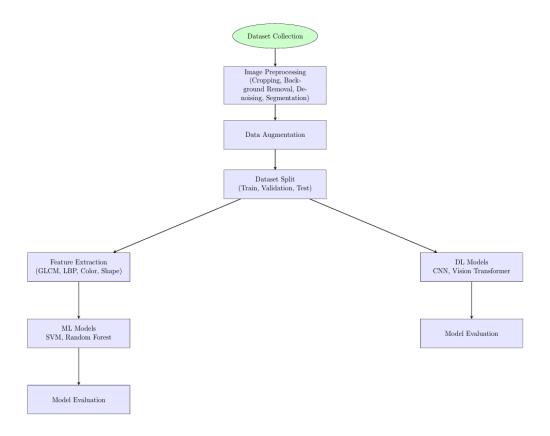


Figure 1: Methodology flowchart for Areca crop disease detection using ML and DL approaches

#### A. Dataset Collection and Description

The dataset used in this study comprises images of Areca nut and palm leaves, collected from agricultural fields and public datasets. It includes both healthy and diseased samples exhibiting various common conditions such as yellow leaf disease, leaf spot, and fruit rot. Images were captured under varying lighting conditions, backgrounds, and leaf orientations to reflect the complexity of real-world field scenarios. Each image was carefully labeled by domain experts to ensure annotation accuracy.

#### **B.** Image Preprocessing

To improve model performance and focus learning on disease-relevant features, the following preprocessing techniques were systematically applied:

**1.Cropping**: Images were cropped to tightly frame the leaf, removing unnecessary background clutter and centering the region of interest.





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- **2. Background Removal**: Non-leaf elements were eliminated using color thresholding and segmentation techniques, resulting in cleaner inputs with fewer distractions.
- **3. Denoising**: Non-Local Means Denoising was applied to reduce sensor noise and background texture, preserving important visual features such as spots and discolorations.
- **4. Segmentation**: Edge and threshold-based segmentation isolated the leaf from the background, ensuring that feature extraction was concentrated on the affected leaf areas.

These steps ensured consistency and reduced the variability introduced by extraneous visual elements, thereby improving the feature learning capacity of both ML and DL models.

#### C. Data Augmentation

To enhance the robustness of the models and mitigate overfitting, the dataset was augmented using various transformation techniques. The augmented data was stored separately to track its contribution to model training. Techniques used include:

- 1. **Geometric Transformations**: Random rotations, flips, zooming, and translations simulated real-world variations in leaf orientation and positioning.
- 2. **Color Adjustments**: Slight modifications in brightness, contrast, and hue were applied to account for lighting differences during image capture.
- 3. **Noise Injection**: Gaussian blur and synthetic noise were added to simulate challenging imaging conditions. These augmentations increased dataset diversity, helping the models generalize better to unseen data during inference[15].

#### D. Machine Learning Models

Two classical ML algorithms were selected for comparison:

- 1. **Support Vector Machine (SVM)**: Configured with a radial basis function (RBF) kernel for non-linear classification[2].
- 2. Random Forest (RF): Implemented with 100 decision trees for ensemble-based learning.

To extract meaningful features for the machine learning models, a combination of handcrafted descriptors was employed. Colour histograms were used to capture the distribution of pixel intensities, providing information about the overall color composition of the leaf images. Gray-Level Co-occurrence Matrix (GLCM) features were extracted to quantify texture by analyzing the spatial relationships between pixel intensities, making it useful for detecting disease-related texture patterns. Local Binary Patterns (LBP) were utilized for micro-level texture analysis, capturing fine-grained surface irregularities often indicative of early disease symptoms. Additionally, shape descriptors were calculated to represent the geometric structure of the leaf, enabling the models to leverage differences in leaf contour or form that may correlate with specific diseases. Feature extraction was performed using the OpenCV and scikitimage libraries. Extracted features were normalized and fed into the ML models using the scikit-learn framework.

#### E. Deep Learning Models

To compare with traditional ML, two deep learning architectures were implemented:

- 1. **Convolutional Neural Network (CNN)**: A custom CNN model was built with multiple convolutional layers (with ReLU activation), max-pooling, batch normalization, and fully connected dense layers. Dropout layers were used to prevent overfitting.
- 2. **Vision Transformer (ViT)**: A pre-trained ViT model, fine-tuned on the Areca dataset. ViTs operate by splitting images into patches, embedding them, and passing them through transformer encoders using self-attention mechanisms.

These models were implemented using TensorFlow and PyTorch. The Adam optimizer and categorical cross-entropy loss were used for training, with early stopping and learning rate scheduling for optimization. All models were trained using preprocessed and augmented image sets.

#### F. Evaluation Metrics

To assess model performance, the following metrics were employed:

- 1. **Accuracy** the proportion of correctly classified images.
- 2. **Precision, Recall, and F1-Score** to evaluate class-wise performance and handle imbalance.





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- 3. **Confusion Matrix** to visualize misclassification between classes.
- 4. **ROC Curve and AUC Score** to assess the overall discriminatory power of the models.

These metrics provided a comprehensive understanding of model behavior across both ML and DL methods, facilitating a meaningful comparison under identical conditions[16].

#### IV. EXPERIMENTAL RESULTS

#### A. Experimental Setup

All experiments were conducted using a curated dataset of Areca nut and palm leaf images, processed through a standardized pipeline involving cropping, background removal, denoising, segmentation, and augmentation. The dataset was divided into training, validation, and testing sets in a 70:15:15 ratio. The experiments were executed on a standard consumer-grade laptop equipped with 8 GB RAM and an Intel Core i5 processor, without GPU acceleration. Deep learning models were implemented using TensorFlow and PyTorch frameworks, while traditional machine learning models were developed using the scikit-learn library. Hyperparameters such as learning rate (0.001), batch size (32), and early stopping (patience = 5) were carefully tuned to ensure stable and reliable model training within the computational constraints.

#### **B.** Model Performance Comparison

The performance comparison in Table 1 clearly shows the superiority of deep learning models over traditional ML classifiers. The Vision Transformer (ViT) model, trained on the fully preprocessed and augmented dataset, achieved the highest accuracy of 97.73%. The CNN model followed closely with an accuracy of 95.6%, while SVM and RF achieved 85.3% and 87.4%, respectively.

ModelPreprocessing PipelineAccuracy (%)Support Vector Machine (SVM)Cropped + Segmented + Features81.3Random Forest (RF)Cropped + Segmented + Features85.4Convolutional Neural Network (CNN)Cropped + Denoised + Augmented88.49Vision Transformer (ViT)Full Preprocessing + Augmented97.73

**Table 1:** Model-wise Accuracy Comparison

#### C. Class-wise Performance

To evaluate how well each model performed across all classes, precision, recall, and F1-score metrics were calculated and summarized in Table 2. The ViT achieved the highest values across all three metrics, followed by CNN. SVM and RF exhibited noticeably lower performance, particularly in recall and F1-score, due to difficulties in identifying early-stage disease symptoms.

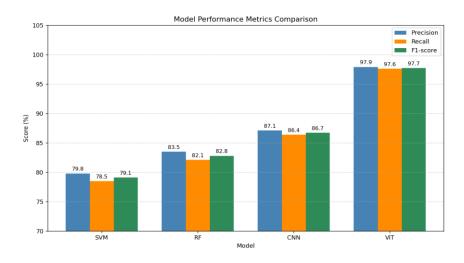


Figure 2: Model Performance Metrics Comparison.





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#### **D.** Confusion Matrix Analysis

Confusion matrices revealed the distribution of misclassifications across disease categories for each model. The Vision Transformer (ViT) demonstrated near-perfect classification, with negligible misclassifications and clear separation across all classes. The CNN also achieved high performance, with only a few misclassifications, primarily between yellow leaf disease and leaf spot, especially under poor lighting or occluded leaf regions. In contrast, traditional machine learning models showed more significant confusion. The Random Forest (RF) model frequently misclassified leaf spot as yellowing, with an average of 12% class overlap, while Support Vector Machine (SVM) exhibited even greater ambiguity, misclassifying up to 18% of yellowing cases. These errors were primarily due to overlapping color tones and texture patterns in early disease stages. Deep learning models handled such complexities more effectively by learning hierarchical representations, resulting in sharper decision boundaries and improved generalization.

#### E. ROC Curve and AUC Score

Receiver Operating Characteristic (ROC) curves and Area Under the Curve (AUC) scores were employed to assess the models' classification confidence and discriminative ability. The Vision Transformer (ViT) achieved the highest AUC score of 0.99, followed closely by the Convolutional Neural Network (CNN) with a score of 0.96. The traditional machine learning models, Random Forest (RF) and Support Vector Machine (SVM), recorded lower AUC scores of 0.89 and 0.87, respectively. These results reinforce the superior capacity of deep learning architectures to distinguish between healthy and diseased Areca crop images, especially under conditions of class imbalance and subtle inter-class variations.

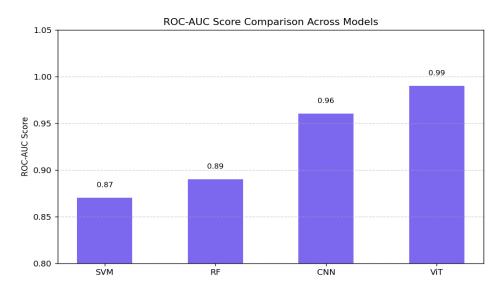


Figure 3: ROC-AUC Score Comparison Across Models

#### F. Summary Observations

The experimental findings confirm that deep learning models, particularly the Vision Transformer, outperform traditional machine learning classifiers in both accuracy and reliability. Preprocessing and augmentation significantly contributed to improved performance by enhancing input quality and simulating real-world variability. CNNs and ViTs demonstrated high adaptability, precision, and generalization even under complex field-like conditions, while traditional models remained constrained by their reliance on handcrafted features.

#### V. CONCLUSION

This study presents a comprehensive comparative analysis of traditional machine learning and deep learning techniques for Areca crop disease detection. Through rigorous experimentation and evaluation, it becomes evident that deep learning models significantly outperform their machine learning counterparts in terms of classification accuracy, robustness, and adaptability to diverse real-world conditions. Traditional models such as Support Vector Machine and Random Forest, although computationally lighter and easier to interpret, demonstrated limitations in feature





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representation, particularly when faced with high variability in image backgrounds, lighting conditions, and subtle disease symptoms.

In contrast, deep learning models, especially the Vision Transformer (ViT), exhibited superior performance by leveraging end-to-end learning from raw image data and utilizing attention mechanisms to focus on disease-relevant regions. The CNN also performed well, validating the effectiveness of convolutional architectures in agricultural image classification tasks. Preprocessing techniques—such as cropping, denoising, segmentation, and background removal—along with data augmentation strategies played a vital role in enhancing model performance, ensuring generalization, and reducing overfitting.

The results of this research emphasize the importance of adopting deep learning frameworks in precision agriculture, especially for complex tasks like Areca crop disease detection. By enabling scalable, accurate, and real-time disease monitoring solutions, DL-based models hold significant promise for improving crop health management, empowering farmers, and contributing to sustainable agricultural practices. This work lays a solid foundation for future deployments of AI-driven decision-support systems in smart farming.

#### VI. FUTURE ENHANCEMENT

While the findings of this study strongly advocate for the adoption of deep learning models in Areca crop disease detection, there remain several avenues for future research and practical development. One key area is the expansion of the dataset to include a wider variety of disease types, growth stages, and environmental conditions. A more diverse and larger-scale dataset would improve model generalization, especially for rare or emerging disease patterns.

Another promising direction is the integration of multi-modal data sources, such as thermal imagery, hyperspectral data, or environmental parameters (e.g., humidity, temperature, soil moisture), alongside visual inputs. These additional data streams could enhance diagnostic accuracy and enable predictive modeling of disease onset based on environmental triggers.

From a technical standpoint, exploring lightweight deep learning architectures such as MobileNet, EfficientNet-Lite, or pruning-aware transformers would facilitate real-time deployment on mobile devices, drones, or edge AI systems. This is essential for enabling field-level disease detection in remote agricultural settings where connectivity and power resources are limited.

Furthermore, incorporating explainable AI (XAI) techniques more robustly—beyond visualization tools like Grad-CAM—can increase model transparency and trust among end-users, particularly farmers and agronomists. User-friendly interfaces with local language support and actionable recommendations could also be developed to make the system more accessible and impactful.

Finally, future efforts could focus on building a complete decision-support system that not only detects diseases but also recommends appropriate treatment measures, tracks disease progression, and integrates with agricultural advisory platforms. Such end-to-end solutions have the potential to revolutionize crop health management and contribute significantly to the digital transformation of agriculture.

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