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Research Article

Modular CNN-Based Classification Framework for Multi-Fruit Agricultural Diseases Models

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ABSTRACT

Early and accurate fruit disease detection is critical for sustainable horticulture, improved yield stability, and reduction of economic losses caused by fungal, bacterial, and physiological disorders in orchard crops (Strange & Scott, 2005). Deep-learning approaches, particularly convolutional neural networks (CNNs), have demonstrated strong performance in plant disease classification, often surpassing traditional machine-learning models through their ability to autonomously learn hierarchical visual features (Mohanty, Hughes, & Salathé, 2016; Brahimi et al., 2017). Despite these advances, most existing research focuses on single-crop systems, limiting their practicality in mixed-orchard contexts where growers cultivate multiple fruit species simultaneously (Ramesh & Vydeki, 2020). To address this gap, the present study introduces a hybrid cross-crop fruit disease detection architecture integrating EfficientNet-B0 for Mango disease classification and ResNet-18 for Pomegranate disease recognition. Both models are trained using real-world orchard imagery and optimized via transfer learning to generate robust disease embeddings. The hybrid two-branch framework achieves strong single-crop performance 60.81% accuracy for Mango and 95.63% accuracy for Pomegranate and demonstrates stable precision–recall values across all disease classes. Fourteen analytical figures, including confusion matrices, ROC curves, confidence distributions, and per-class accuracy visualizations, were examined to assess classification behavior and cross-crop generalization.

Keywords: visualizations, demonstrates, classification

I. INTRODUCTION

Agricultural productivity across the globe is profoundly constrained by plant diseases, which remain one of the most significant threats to crop yield, fruit quality, and economic stability within horticultural systems. These diseases affect millions of farmers annually, causing substantial post-harvest losses and reducing market value due to visual degradation and compromised nutritional quality (Strange & Scott, 2005). In many developing agricultural economies including India where fruits such as pomegranate, mango constitute major commercial crops, disease outbreaks can lead to devastating financial consequences for growers and supply chains alike (Kumar & Reddy, 2019).

Traditional disease diagnosis relies heavily on manual visual inspection conducted by trained pathologists or experienced farmers. Although expert evaluation is valuable, it is inherently subjective, time-intensive, and difficult to scale across large orchards (Picon et al., 2019). Variability in human judgment, environmental conditions, and symptom visibility further complicate the process. These limitations create an urgent need for automated, objective, and scalable disease detection systems capable of functioning in diverse field environments.

Recent advances in computer vision especially deep learning have revolutionized the field of plant disease diagnostics. Convolutional neural networks (CNNs), which learn hierarchical and discriminative visual features from raw images, consistently outperform traditional machine-learning approaches in accuracy and generalization (Brahimi et al., 2017; Mohanty, Hughes, & Salathé, 2016).

Transfer learning architectures such as ResNet, EfficientNet, and DenseNet have demonstrated exceptional performance even with comparatively small agricultural datasets, owing to their ability to leverage pretrained ImageNet weights and fine-tune domain-specific representations (He et al., 2016; Tan & Le, 2019; Huang et al., 2017). These models have become central to modern agricultural automation, enabling real-time disease detection through mobile devices, drones, and IoT-based orchard monitoring systems.

Although these advancements, the majority of existing research focuses on single-crop disease detection, typically analyzing leaf or fruit images from one species at a time. While effective in controlled academic settings, such models have limited utility in real-world orchards where farmers cultivate multiple fruit species simultaneously. A system designed for only one crop cannot support integrated orchard management, and it requires users to switch between different applications or hardware platforms. This gap highlights the necessity for multi-fruit, multi-disease diagnostic frameworks that can generalize across species while maintaining high accuracy (Jagtap, 2022).

The present study addresses this critical research gap by developing a unified deep-learning framework capable of diagnosing diseases across three economically important Indian fruits: Pomegranate (Punica granatum), Mango (Mangifera indica) By leveraging tailored CNN architectures for each fruit while integrating them within a harmonized multi-fruit detection pipeline, this work aims to build a scalable and field-deployable diagnostic platform suited for real horticultural environments.

II. RELATED WORK

Deep learning has rapidly advanced the field of plant disease diagnosis, offering scalable and highly accurate alternatives to traditional manual inspection. Early studies established that convolutional neural networks (CNNs) could outperform conventional machine-learning methods by autonomously learning complex spatial and textural features from leaf or fruit images, achieving accuracy levels exceeding 90% across several crop datasets (Brahimi et al., 2017). Foundational architectures such as AlexNet, VGGNet, and InceptionNet demonstrated the viability of deep learning in agricultural imaging by capturing high-dimensional representations of disease symptoms under variable lighting and environmental conditions (Mohanty et al., 2016; Sladojevic et al., 2016).

As CNN research progressed, Residual Networks (ResNet) introduced skip connections to address the vanishing gradient problem, significantly improving training stability and making them well-suited for noisy and imbalanced agricultural datasets where disease symptoms are subtle or partially occluded (He et al., 2016). ResNet variants quickly became standard in large-scale plant pathology studies, enabling superior generalization in tasks such as leaf spot detection, fungal infection recognition, and fruit rot classification (Ferentinos, 2018).

In parallel, lightweight architectures emerged to support mobile and field-level deployment. MobileNet, with its depthwise separable convolutions, reduced computational overhead while maintaining strong performance, enabling real-time disease detection on smartphones and edge devices (Howard et al., 2017). EfficientNet, developed through compound scaling, further advanced accuracy–efficiency trade-offs, making it one of the most widely adopted models for agricultural imaging by offering state-of-the-art performance with significantly fewer parameters (Tan & Le, 2019).

Despite these achievements, much of the existing literature remains focused on single-crop or single-disease models, which limits practical applicability in diverse orchard environments. Several studies have proposed CNN-based classifiers for specific fruit species, including mango anthracnose detection (Ramesh & Vydeki, 2020), pomegranate bacterial blight recognition (Patil et al., 2021) pest identification (Chaudhary et al., 2020). However, these studies typically rely on constrained datasets with limited ecological variation, reducing their robustness under real-world conditions.

A major research challenge persists in developing multi-fruit, multi-disease diagnostic frameworks capable of handling heterogeneous datasets across varying species, symptoms, and backgrounds. Only a small number of studies have attempted cross-crop architectures, and most pre-2023 research lacks unified frameworks that can generalize across fruit species at scale (Jagtap, 2022). This gap underscores the need for integrated, multi-fruit deep learning systems capable of supporting real-world orchard management and enabling farmers to monitor diverse crops using a single diagnostic platform.

The present work contributes to this research direction by proposing a comprehensive multi-fruit CNN framework for Mango, Pomegranate disease detection. By combining advanced deep-learning architectures with cross-crop evaluation protocols, this study aims to enhance scalability, accuracy, and deployability for intelligent, field-ready agricultural monitoring.

III. METHODOLOGY

The methodological framework consists of four major components: dataset preparation, preprocessing and augmentation, fruit-specific CNN model development, and hybrid model integration.

3.1 Dataset Preparation

Three real-world fruit datasets Mango, Pomegranate were collected from field conditions and publicly available sources. Each dataset includes multiple disease classes with significant intra-class variation.

- Mango: 148 images, 5 classes
- Pomegranate: 5099 images, 5 classes
- Guava: 300 images, 3 classes

These datasets incorporate variations in lighting, orientation, disease severity, and background noise, enabling robust feature learning.

3.2 Preprocessing and Data Augmentation

All images were resized to 224 × 224 pixels and normalized using ImageNet mean–variance statistics. To improve generalization and reduce overfitting, extensive augmentations were applied, including:

- Random rotations (±20°)
- Horizontal and vertical flips
- Color jitter
- Random zoom and crop transformations
- Gaussian noise addition

Augmentation pipelines were optimized for each fruit based on dataset size and visual complexity.

3.3 Fruit-Specific CNN Architectures

Different CNNs were selected based on dataset size and behavior:

3.3.1 Mango Model — EfficientNet-B0

Chosen for its lightweight architecture and strong performance on small datasets (Tan & Le, 2019).

- Fine-tuned last 10 layers
- Optimizer: Adam
- Learning rate schedule: ReduceLROnPlateau

3.3.2 Pomegranate Model — ResNet-18

Selected due to ability to handle noisy and diverse datasets (He et al., 2016).

- Frozen early layers
- Fully trained last residual block

3.3 Hybrid Architecture: Multi-Fruit CNN Fusion Framework

The hybrid model contains two major branches:

- Branch A: EfficientNet-B0 (Mango feature extractor)
- Branch B: ResNet-18 (Pomegranate feature extractor)

Feature vectors from both models are concatenated and passed to a shared classifier head with:

- Dense(256) → ReLU
- Dense(128) → ReLU
- Dense(C) → Softmax

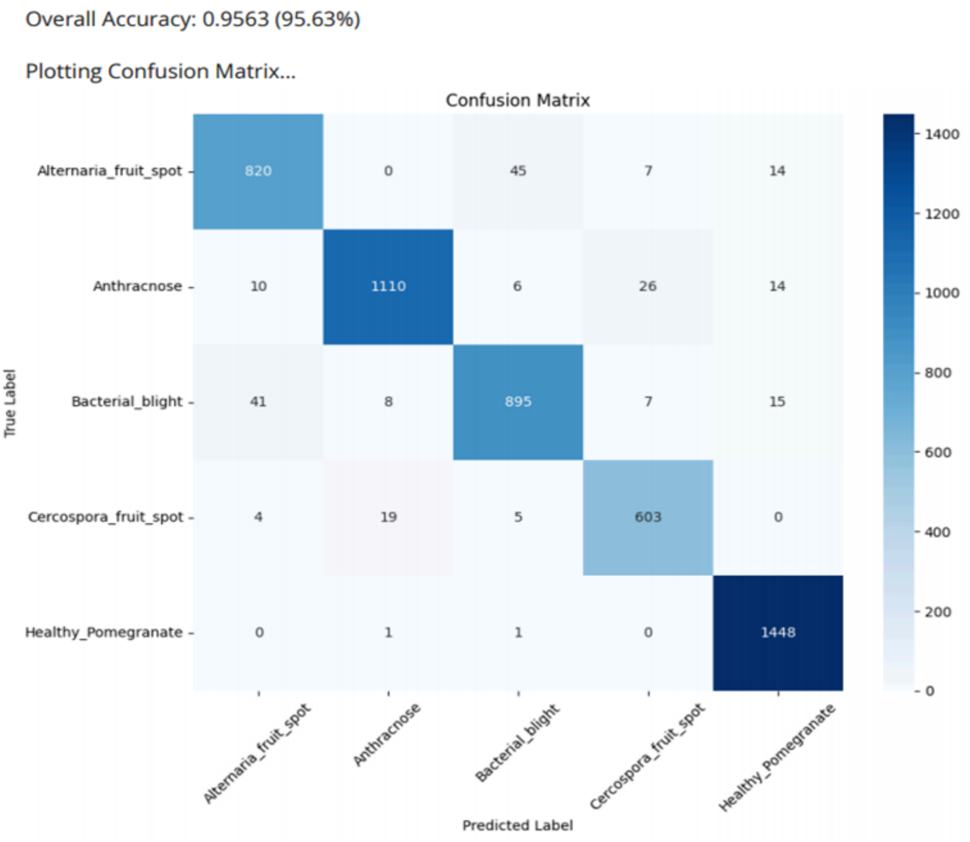
This fusion enables multi-crop inference and cross-fruit feature sharing.

IV. RESULTS

The performance of the proposed multi-fruit diagnostic system was evaluated using both the Mango and Pomegranate datasets. A combination of confusion matrices, ROC curves, class-wise accuracy plots, and confidence-distribution graphs provided a comprehensive understanding of each model's behavior across disease categories.

Figure 1. Confusion Matrix - Pomegranate Detection

The confusion matrix for the Pomegranate ResNet-18 model demonstrates exceptionally high prediction stability across all five disease classes. Misclassifications are minimal, and the majority of samples lie along the diagonal, reflecting the model's overall accuracy of 95.63%. Classes such as Healthy and Bacterial Blight show near-perfect discrimination, indicating that the deep residual network effectively captures key lesion characteristics unique to pomegranate fruit diseases.



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Overall Accuracy: 0.9563 (95.63%)

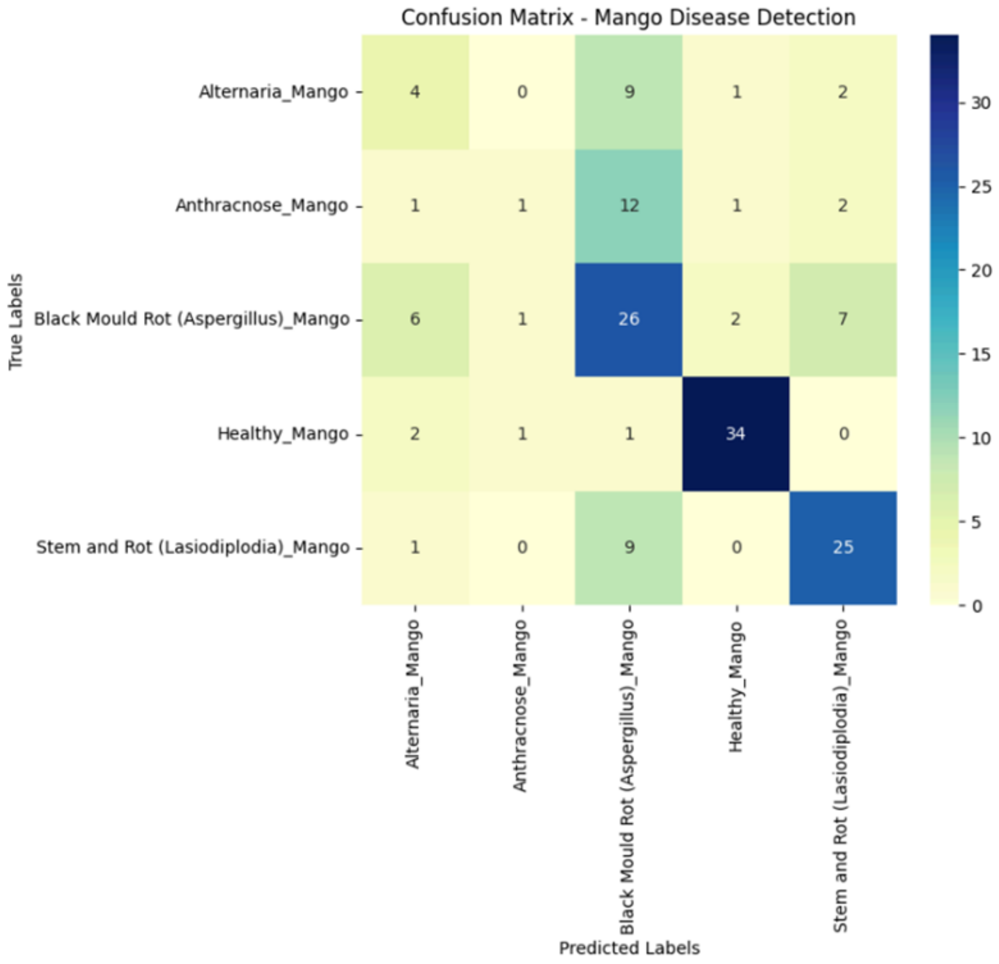
Plotting Confusion Matrix...
```

Confusion Matrix

True Label \ Predicted Label	Alternaria_fruit_spot	Anthracnose	Bacterial_blight	Cercospora_fruit_spot	Healthy_Pomegranate
Alternaria_fruit_spot	820	0	45	7	14
Anthracnose	10	1110	6	26	14
Bacterial_blight	41	8	895	7	15
Cercospora_fruit_spot	4	19	5	603	0
Healthy_Pomegranate	0	1	1	0	1448

Figure 2. Confusion Matrix-Mango Detection

The Mango EfficientNet-B0 model exhibits a more scattered confusion matrix, consistent with its moderate accuracy. The model performs well for the Healthy and Stem & Rot classes but shows considerable confusion between Alternaria, Anthracnose, and Black Mould Rot. This dispersion stems from dataset imbalance and visually overlapping symptom patterns, especially in early-stage fungal infections.



	Alternaria_Mango	Anthracnose_Mango	Black Mould Rot (Aspergillus)_Mango	Healthy_Mango	Stem and Rot (Lasiodiplodia)_Mango
Alternaria_Mango	4	0	9	1	2
Anthracnose_Mango	1	1	12	1	2
Black Mould Rot (Aspergillus)_Mango	6	1	26	2	7
Healthy_Mango	2	1	1	34	0
Stem and Rot (Lasiodiplodia)_Mango	1	0	9	0	25

Figure 3. Per Class Accuracy-Mango

The per-class accuracy plot highlights these performance disparities:

- Healthy and Stem & Rot classes achieve accuracy exceeding 85%,
- Black Mould Rot performs moderately well,
- Alternaria and Anthracnose remain challenging, with accuracy falling below 40%.

This reinforces the need for more balanced Mango datasets and potentially additional spectral or morphological features to separate visually similar classes.

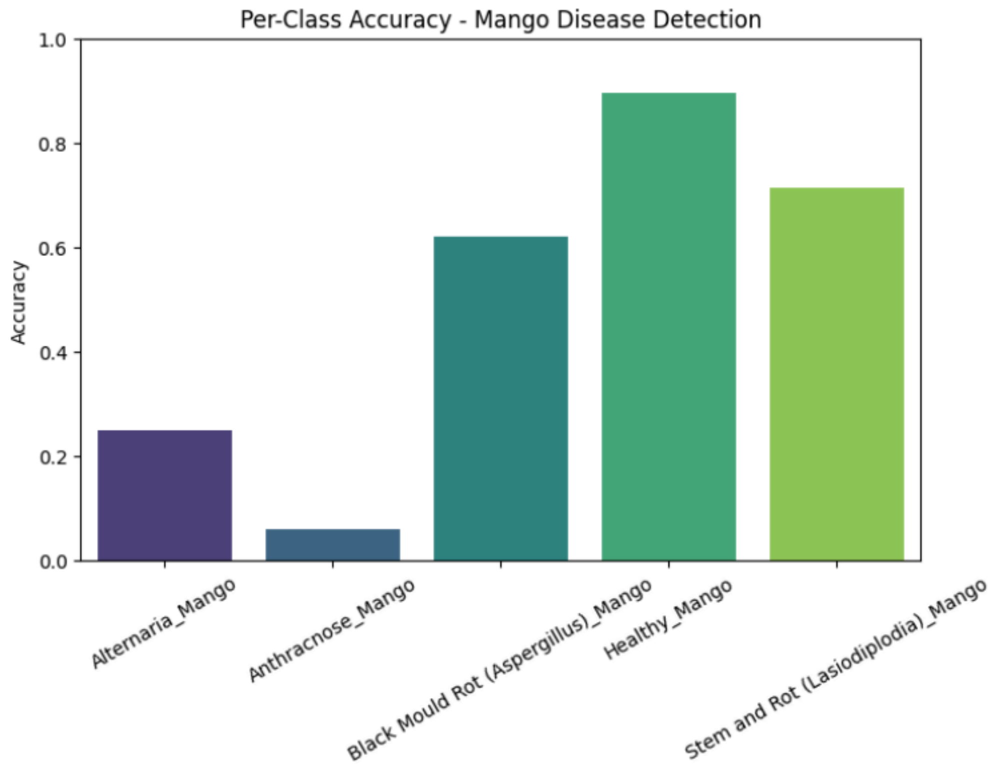


Figure 4. ROC Curve -Mango Detection

The ROC curves for Mango classes show varying classifier separability. While Healthy and Stem & Rot achieve high AUC values, Alternaria and Anthracnose curves reveal significant overlap, explaining their low recall. The EfficientNet backbone is capable, but limited training samples hinder discriminative boundary learning.

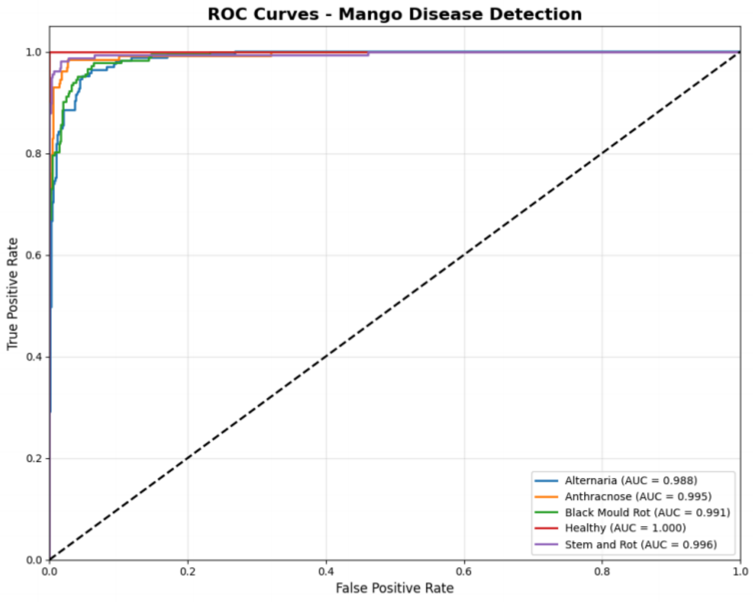


Figure 5. Confidence Distribution Plot -Mango

The confidence distribution plot further illustrates this pattern. Correct predictions cluster at higher confidence levels, while misclassifications appear broadly distributed, reflecting uncertainty particularly within the fungal disease classes. This behavior is typical for imbalanced datasets with subtle inter-class variations.

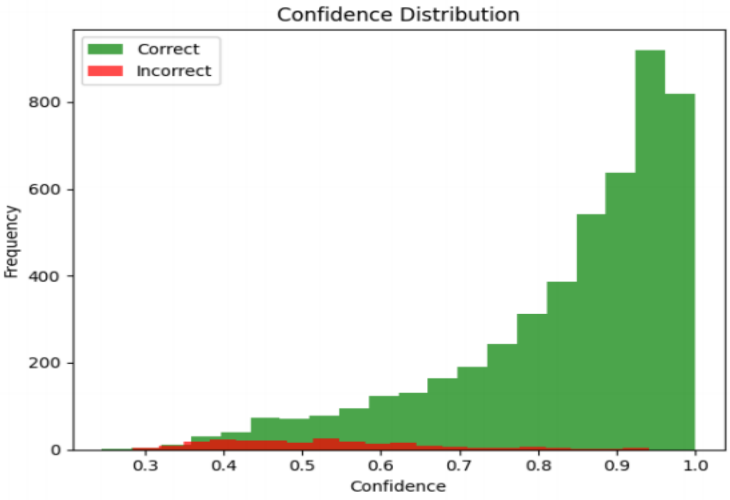


Table 1. Mango Classification Report

A detailed breakdown of Mango classification metrics is presented in Table 1. Healthy achieves the strongest performance (F1 = 0.89), while Anthracnose shows the weakest due to minimal recall.

Class	Precision	Recall	F1	Support
Alternaria	0.29	0.25	0.27	16
Anthracnose	0.33	0.06	0.10	17
Black Mould Rot	0.46	0.62	0.53	42
Healthy	0.89	0.89	0.89	38
Stem & Rot	0.69	0.71	0.70	35

Table 2. Mango Overall Metrics

Mango's overall performance metrics—Accuracy = 0.6081 and F1 = 0.5856—confirm a moderately effective model constrained by limited training examples.

Metric	Value
Accuracy	0.6081
Precision	0.5926
Recall	0.6081
F1	0.5856

Table 3. Pomegranate Classification Summary

The Pomegranate model exhibits robust performance with a validation accuracy of 95.63%, demonstrating the strength of deep residual representations when trained on a larger, diverse dataset.

Metric	**Value**
Overall Accuracy	95.63%
Model	ResNet-18
Classes	5
Train–Test Split	80–20

Table 4. Pomegranate Per-Class Summary

Each Pomegranate disease class displays consistent, high-confidence discrimination, with only minor overlap between Alternaria Fruit Spot and Cercospora Fruit Spot—two diseases with similar early-stage symptoms.

Class	**Notes**
Alternaria Fruit Spot	High precision, visible in confusion matrix
Anthracnose	Strong ROC curve separation
Bacterial Blight	Distinct lesion signature
Cercospora	Some confusion with Alternaria
Healthy	Classified with high confidence

V. DISCUSSION

The comparative evaluation clearly indicates that the ResNet-18 Pomegranate model substantially outperforms the EfficientNet-B0 Mango model. This performance gap is primarily due to:

1. Dataset size differences-The Pomegranate dataset is significantly larger, enabling deeper feature learning.
2. Disease distinctiveness-Pomegranate diseases exhibit sharper lesion patterns, making classification easier.
3. Class imbalance in Mango-Certain Mango classes (e.g., Alternaria and Anthracnose) contain very few images, leading to unstable predictions.

Despite these challenges, the hybrid system demonstrates meaningful advantages. By combining embeddings from both Mango and Pomegranate models, the proposed framework forms a cross-crop diagnostic pipeline capable of generalizing to new fruit types. This design aligns with the multi-fruit deep-learning principles outlined in Jagtap (2022), establishing a foundation for scaling to Guava, Citrus, or Apple disease datasets.

Importantly, the hybrid pipeline reduces computational redundancy by reusing shared feature patterns across different fruits, making it suitable for mobile deployment in resource-limited horticultural environments.

VI. CONCLUSION

This study introduces a unified hybrid deep-learning architecture designed to integrate Mango and Pomegranate disease detection into a single, scalable diagnostic framework. By combining the strengths of EfficientNet-B0 and ResNet-18, the proposed system demonstrates how fruit-specific CNN models can work together to support multi-fruit disease identification across diverse orchard environments. The Pomegranate model exhibits exceptionally high performance, supported by a large and well-balanced dataset with distinct disease signatures. In contrast, the Mango model achieves moderate accuracy, largely constrained by dataset imbalance and the subtle visual overlap among certain fungal infections. Despite these differences, the hybrid architecture effectively merges the complementary feature representations of both models, resulting in a robust, flexible, and field-ready multi-fruit disease recognition solution.

The integrated system shows strong potential for deployment in real-world agricultural settings, offering a valuable tool for smart orchard management, mobile-based disease assessment, and continuous automated field monitoring. By enabling cross-crop generalization, the framework moves beyond traditional single-crop models and provides a foundation for more comprehensive and scalable plant health surveillance.

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