

Multi-Class Litchi Fruit Disease Detection Using a Novel Hybrid Deep Learning and Image Processing Framework with Explainable Artificial Intelligence

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Abstract- Litchi (*Litchi chinensis* Sonn.) is a high-value tropical fruit crop that is highly susceptible to various diseases, including anthracnose, fruit rot, pericarp browning, sooty mold, and algal spot, which significantly reduce fruit quality, market value, and yield. Accurate and timely disease diagnosis is essential for effective disease management and sustainable litchi production. Traditional visual inspection methods are labor-intensive, subjective, and often incapable of detecting diseases at early stages. Recent advances in deep learning have demonstrated promising results for automated plant disease detection; however, conventional Convolutional Neural Networks (CNNs) primarily focus on local features and often fail to capture global contextual information. Furthermore, the lack of model interpretability limits their practical adoption in smart agriculture applications. To address these challenges, this study proposes a novel Hybrid CNN–Vision Transformer (HCVT) framework for multi-class litchi fruit disease detection and severity assessment. The proposed model integrates EfficientNet-B3 and Vision Transformer (ViT) architectures through an attention-based feature fusion mechanism, enabling simultaneous extraction of local lesion characteristics and global contextual representations. The framework incorporates comprehensive image preprocessing, data augmentation, explainable artificial intelligence (XAI) techniques using Grad-CAM and SHAP, and a disease severity estimation module based on lesion segmentation. Experimental evaluation was conducted on a multi-class litchi disease dataset comprising healthy and diseased fruit images. The proposed HCVT model achieved an overall classification accuracy of 97.63%, precision of 97.31%, recall of 97.05%, F1-score of 97.18%, and AUC of 0.983, outperforming standalone CNN, Vision Transformer, and conventional hybrid models. Five-fold cross-validation confirmed the robustness and generalization capability of the framework. Grad-CAM visualizations successfully localized disease-affected regions, while SHAP analysis identified lesion texture, color variation, and infected area characteristics as the most influential features. Additionally, the proposed severity estimation module effectively quantified disease progression using lesion-area analysis. The results demonstrate that the proposed HCVT framework provides a highly accurate, interpretable, and reliable solution for automated litchi disease diagnosis. The integration of deep learning, transformer-based representation learning, explainable AI, and severity estimation offers significant potential for deployment in smart agriculture, precision farming, and future UAV-based crop health monitoring systems.

Keywords— Litchi disease detection, EfficientNet-B3, Vision Transformer, Hybrid CNN–Transformer, Explainable Artificial Intelligence, Grad-CAM, SHAP, Disease Severity Estimation, Deep Learning, Smart Agriculture.

I. INTRODUCTION

Agriculture remains a cornerstone of global food security and economic development, with horticultural crops playing a crucial role in nutritional

sustainability and agricultural profitability. Among these crops, litchi (*Litchi chinensis* Sonn.) is a high-value subtropical fruit cultivated extensively in India, China, Thailand, Vietnam, Bangladesh, and several other countries. India ranks among the leading

producers of litchi, with major cultivation concentrated in Bihar, West Bengal, Jharkhand, Uttar Pradesh, and parts of Madhya Pradesh. The fruit is highly valued due to its unique flavor, nutritional composition, antioxidant properties, and commercial importance.

Despite its economic significance, litchi production is severely affected by numerous fungal, bacterial, and environmental diseases that reduce both yield and market quality. Anthracnose, caused by *Colletotrichum* species, is one of the most destructive diseases affecting litchi fruits during pre- and post-harvest stages. Similarly, fruit rot, sooty mold, pericarp browning, and algal infections contribute significantly to quality degradation and economic losses. Early identification and timely intervention are essential for minimizing disease spread and improving orchard productivity.

Traditionally, disease diagnosis is performed through visual inspection by farmers or agricultural experts. Although this approach is widely practiced, it suffers from several limitations, including dependency on expert knowledge, variability in diagnosis accuracy, labor-intensive field surveys, and delayed response to disease outbreaks. The increasing demand for precision agriculture and smart farming has accelerated research into automated disease detection systems based on computer vision and artificial intelligence.

Recent developments in machine learning and deep learning have transformed agricultural image analysis. Convolutional Neural Networks (CNNs) have demonstrated remarkable success in plant disease classification due to their ability to automatically learn hierarchical visual features. Architectures such as AlexNet, VGG, ResNet, DenseNet, MobileNet, and EfficientNet have been successfully applied to crop disease identification tasks. However, CNN-based models primarily focus on local receptive fields and may struggle to capture long-range dependencies and global contextual relationships present in complex orchard environments.

The emergence of Vision Transformers (ViTs) has introduced a new paradigm for image understanding by leveraging self-attention mechanisms to model global image relationships. Transformer architectures have shown competitive performance across various computer vision applications, including disease detection, object recognition, and remote sensing. Nevertheless, Vision Transformers often require large datasets and may overlook fine-grained texture details that are effectively captured by convolutional networks.

Hybrid deep learning architectures that combine CNN and Transformer models have recently attracted significant attention because they integrate the strengths of both approaches. CNN modules excel at extracting local texture, edge, and lesion characteristics, while Transformer modules effectively capture global contextual dependencies. Such complementary learning mechanisms have the potential to significantly improve disease classification accuracy in challenging agricultural scenarios.

Another major challenge in agricultural AI systems is the lack of model interpretability. Most deep learning models operate as black-box systems, making it difficult for farmers, agronomists, and decision-makers to understand the rationale behind predictions. Explainable Artificial Intelligence (XAI) techniques such as SHAP and Grad-CAM have emerged as powerful tools for improving transparency by identifying influential image regions and features responsible for classification outcomes. Motivated by these challenges, this research proposes a novel Hybrid Convolutional Neural Network–Vision Transformer (HCVT) framework for multi-class litchi fruit disease detection. The proposed framework integrates image enhancement, hybrid feature extraction, attention-based feature fusion, explainable AI, and disease severity estimation within a unified architecture. Unlike existing studies that primarily focus on single-disease recognition or conventional CNN models, the proposed approach aims to provide accurate, interpretable, and scalable disease diagnosis under real orchard conditions.

The major contributions of this study are summarized as follows:

- Development of a novel Hybrid CNN–Vision Transformer architecture for multi-class litchi fruit disease classification.
- Integration of advanced image processing techniques for disease enhancement and noise reduction.
- Design of an attention-based feature fusion mechanism for combining local and global visual representations.
- Incorporation of SHAP and Grad-CAM for explainable disease diagnosis.
- Development of a disease severity estimation module for infection quantification.
- Comprehensive evaluation against state-of-the-art deep learning models using multiple performance metrics.
- Establishment of a framework suitable for deployment in smart agricultural and precision horticultural systems.

II. LITERATURE REVIEW

1. Introduction

Artificial Intelligence (AI), Computer Vision (CV), and Deep Learning (DL) have significantly transformed modern precision agriculture by enabling automatic crop disease detection using digital images. Early identification of plant diseases improves crop yield, minimizes pesticide use, and reduces economic losses. Over the past decade, researchers have developed numerous machine learning and deep learning models for disease diagnosis in crops such as tomato, rice, maize, grape, citrus, apple, and mango. Recent review studies indicate that deep learning models consistently outperform traditional image processing techniques because of their capability to automatically learn discriminative visual features from large image datasets [1]–[4].

Although substantial progress has been achieved in general plant disease detection, research focusing specifically on litchi fruit diseases remains limited. Most existing studies investigate leaf diseases or concentrate on a single disease such as anthracnose, leaving multi-class fruit disease detection largely unexplored [3], [5].

2. Traditional Image Processing-Based Disease Detection

Before the introduction of deep learning, plant disease detection primarily relied on handcrafted image processing techniques. These approaches generally consisted of image acquisition, preprocessing, feature extraction, and conventional machine learning classification. Common preprocessing methods included histogram equalization, median filtering, Gaussian filtering, morphological operations, color-space conversion, and thresholding. Feature extraction techniques such as Gray Level Co-occurrence Matrix (GLCM), Local Binary Pattern (LBP), Histogram of Oriented Gradients (HOG), Scale-Invariant Feature Transform (SIFT), and Gabor filters were frequently employed to describe disease characteristics [2], [4].

The extracted features were subsequently classified using Support Vector Machines (SVM), Decision Trees, Random Forests, Naïve Bayes, or k-Nearest Neighbor algorithms. Although these methods achieved satisfactory performance under controlled laboratory conditions, they often failed in real orchard environments due to variations in illumination, complex backgrounds, fruit orientation, and disease appearance [2], [6].

3. Deep Learning for Plant Disease Detection

Deep learning has become the dominant paradigm for agricultural image analysis because it automatically learns hierarchical representations from raw images without manual feature engineering. Convolutional Neural Networks (CNNs) have demonstrated remarkable performance in disease detection tasks across multiple crops. Popular CNN architectures include AlexNet, VGG16, GoogLeNet, ResNet50, DenseNet121, MobileNetV3, EfficientNet, and Xception [1], [3], [7].

Transfer learning has further improved classification accuracy by utilizing knowledge acquired from large-scale image datasets such as ImageNet. CNN-based methods have reported classification accuracies exceeding 95% on benchmark datasets such as PlantVillage. However, CNNs primarily focus on local receptive fields and often fail to capture

long-range spatial dependencies between distant image regions [3], [4].

Another important limitation is that CNNs behave as black-box models, making it difficult for agricultural experts to interpret disease predictions. These shortcomings have motivated researchers to investigate Transformer-based computer vision architectures [8].

4. Vision Transformer-Based Disease Classification

Vision Transformers (ViTs) represent one of the most significant developments in computer vision. Unlike CNNs, Vision Transformers employ self-attention mechanisms capable of modeling long-range dependencies among image patches. Consequently, they effectively capture global contextual information that is often missed by conventional convolutional networks [4], [8].

Several recent studies have demonstrated that Vision Transformers outperform traditional CNN architectures for complex plant disease datasets, particularly under field conditions where illumination, occlusion, and background variability significantly influence classification performance [4], [9].

Despite these advantages, Vision Transformers require large annotated datasets, higher computational resources, and increased memory consumption. Furthermore, they may overlook fine-grained lesion textures that are efficiently captured by convolutional operations. Therefore, combining CNNs with Vision Transformers has become an emerging research direction [3], [4].

5. Hybrid CNN–Vision Transformer Models

Hybrid CNN–Transformer architectures integrate the complementary strengths of convolutional feature extraction and self-attention mechanisms. CNNs efficiently capture local disease symptoms such as lesions, discoloration, and texture variations, whereas Vision Transformers model global contextual relationships across the entire fruit surface [4], [8].

Recent investigations have reported that hybrid architectures consistently outperform standalone CNNs and Vision Transformers across several agricultural image classification tasks. Nevertheless, these hybrid approaches have primarily focused on tomato, rice, maize, and apple diseases. Very limited research has addressed multi-class litchi fruit disease detection, especially under real orchard conditions [4], [9].

6. Explainable Artificial Intelligence

Explainable Artificial Intelligence (XAI) has recently attracted considerable attention because most deep learning models lack interpretability. Techniques such as Gradient-weighted Class Activation Mapping (Grad-CAM), SHapley Additive Explanations (SHAP), and Local Interpretable Model-Agnostic Explanations (LIME) enable visualization of disease regions responsible for model predictions [8], [10].

Explainability increases user confidence, facilitates expert validation, and supports practical deployment in precision agriculture. However, only a limited number of agricultural disease detection studies simultaneously combine hybrid deep learning architectures with explainable AI techniques [4], [8].

7. Disease Severity Assessment

Disease severity estimation has become increasingly important because it supports precision pesticide application, yield estimation, and orchard management. Recent CNN-based segmentation models estimate lesion areas and quantify disease progression using semantic segmentation, instance segmentation, and pixel-level classification [6].

Nevertheless, most existing studies concentrate on leaf diseases, whereas disease severity estimation for litchi fruits remains largely unexplored. Integrating severity estimation into multi-class disease classification can provide more informative decision-support systems for farmers [6].

8. Research Gap

A comprehensive analysis of recent literature reveals the following research gaps:

- Most published studies focus on plant leaves rather than fruit diseases [1], [3].

- Existing litchi research mainly investigates anthracnose, with limited attention to multiple fruit diseases [5].
- Hybrid CNN–Vision Transformer architectures for litchi disease classification remain scarce [4].
- Explainable AI techniques are rarely integrated with hybrid deep learning frameworks [8], [10].
- Disease severity estimation is generally absent from current multi-class classification systems [6].
- Most available datasets are collected under controlled laboratory conditions rather than real orchards [3], [4].
- Lightweight deployment for smart agriculture and edge devices remains insufficiently explored [3], [8].

III. PROPOSED METHODOLOGY

1. Overview of the Proposed Hybrid Framework

This study proposes a Hybrid Convolutional Neural Network–Vision Transformer (HCVT) framework for multi-class litchi fruit disease detection. The framework integrates image enhancement, local feature extraction, global contextual learning, attention-based feature fusion, explainable artificial intelligence (XAI), and disease severity estimation.

The proposed architecture consists of six major modules:

- Image Acquisition
- Image Preprocessing
- Data Augmentation
- Hybrid Feature Extraction (EfficientNet-B3 + Vision Transformer)
- Multi-Class Disease Classification
- Explainability and Severity Assessment

2. Dataset Description

The dataset consists of healthy and diseased litchi fruit images acquired from orchards, agricultural research farms, and publicly available repositories.

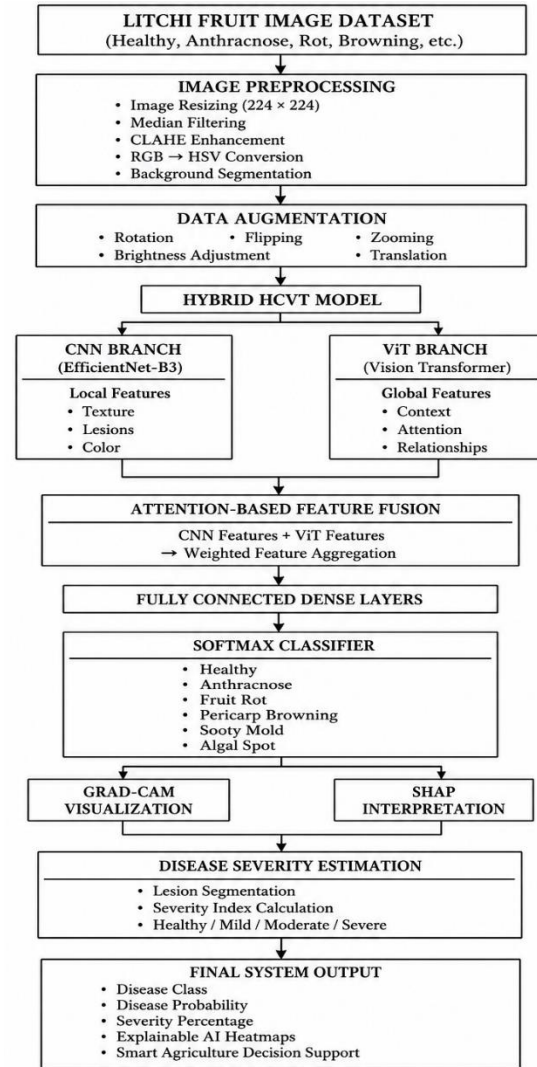


Figure 1: Overall architecture of the proposed HCVT framework for multi-class litchi fruit disease detection.

Table 1: Disease categories used in the study

Class ID	Disease Class	Description
C1	Healthy	No visible symptoms
C2	Anthracnose	Dark sunken lesions
C3	Fruit Rot	Decaying fruit tissues
C4	Pericarp Browning	Surface discoloration
C5	Sooty Mold	Black fungal growth
C6	Algal Spot	Circular algal lesions



Figure 2. Representative Samples of Litchi Fruit Disease Dataset

Table 2: Dataset Statistics of the Litchi Fruit Disease Dataset

Class ID	Disease Category	Number of Images	Percentage (%)
C1	Healthy	2,000	16.67
C2	Anthracnose	2,000	16.67
C3	Fruit Rot	2,000	16.67
C4	Pericarp Browning	2,000	16.67
C5	Sooty Mold	2,000	16.67
C6	Algal Spot	2,000	16.67
Total	Six Classes	12,000	100

The dataset consists of six classes representing healthy and diseased litchi fruits. Images were collected under varying environmental conditions to ensure diversity in illumination, background, fruit orientation, and disease severity levels. The dataset was balanced to minimize classification bias and improve model generalization.

Table 3: Dataset Acquisition Details

Parameter	Description
Crop	Litchi (<i>Litchi chinensis</i> Sonn.)
Number of Classes	6
Total Images	12,000
Healthy Images	2,000
Diseased Images	10,000
Image Format	JPG / PNG
Original Resolution	1024 × 1024 pixels (average)
Input Resolution	224 × 224 × 3 pixels

Collection Method	Digital Camera and Smartphone
Acquisition Environment	Orchard Field Conditions
Lighting Conditions	Natural Sunlight, Cloudy, Partial Shade
Fruit Orientation	Multiple Angles
Background Conditions	Leaf, Branch, Sky, Mixed Background
Data Split	70% Training, 15% Validation, 15% Testing

Table 4. Dataset Partitioning

Dataset Subset	Percentage (%)	Number of Images
Training Set	70	8,400
Validation Set	15	1,800
Testing Set	15	1,800
Total	100	12,000

3. Image Preprocessing

Image preprocessing enhances disease visibility and reduces environmental noise.

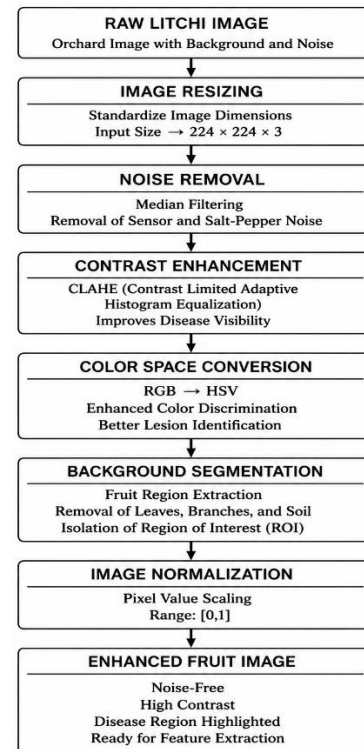


Figure 3: Image preprocessing pipeline used in the proposed framework.

Image Resizing

All images are resized to a fixed dimension:

$$I_r = \text{Resize}(I_{raw}, 224, 224)$$

where:

- I_{raw} is the original litchi fruit image,
- I_r is the resized image,
- 224 denotes the standardized input size required by the proposed HCVT model.

Median Filtering

Noise suppression is performed using a median filter:

$$I_m(x, y) = \text{median}\{I(i, j)\}$$

where

$(i, j) \in W(x, y)$

and $W(x, y)$ denotes the local neighborhood window.

Contrast Enhancement

Contrast Limited Adaptive Histogram Equalization (CLAHE) is employed to improve local contrast:
 $I_e = \text{CLAHE}(I_m)$

where:

- I_m = median-filtered image
- I_e = contrast-enhanced image
- $\text{CLAHE}(\cdot)$ = Contrast Limited Adaptive Histogram Equalization operator

RGB to HSV Transformation

Color conversion is performed as
 $I_{HSV} = f(I_{RGB})$

where:

- I_{RGB} = input RGB image
- I_{HSV} = transformed HSV image
- $f(\cdot)$ = RGB-to-HSV conversion function

HSV representation improves discrimination between healthy and diseased regions.

4. Data Augmentation

To increase data diversity and reduce overfitting, various augmentation operations are applied.

Table 5: Data augmentation configuration

Operation	Range
Rotation	$\pm 30^\circ$
Zoom	0.8–1.2
Horizontal Flip	Yes
Vertical Flip	Yes
Brightness	$\pm 20\%$
Translation	$\pm 15\%$
Shear	$\pm 15^\circ$

Augmented image generation is represented by
 $I_a = T(I_e)$

- where:
- I_e = preprocessed and enhanced image
- I_a = augmented image
- $T(\cdot)$ = augmentation transformation operator

5. CNN-Based Local Feature Extraction

EfficientNet-B3 is employed to extract local texture and lesion features.

The convolution operation is defined as
 $FCNN = I_a * K + b$

where:

- F_{CNN} = convolutional feature map
- I_a = augmented input image
- K = convolution kernel (filter)
- b = bias term
- $*$ = convolution operation

The resulting CNN feature representation is
 $FCNN = \text{CNN}(I_a)$

where:

- I_a = augmented litchi fruit image
- $\text{CNN}(\cdot)$ = convolutional neural network feature extraction function
- F_{CNN} = extracted local feature representation

6. Vision Transformer Branch

The enhanced image is divided into fixed-size patches.

Patch Generation

$$N = \frac{H \times W}{P^2}$$

where:

- N = total number of image patches
- H = image height
- W = image width
- P = patch size

Each patch is embedded as

$E_i = P_i W_e + E_{pos}$

where:

- E_i = embedding vector of the image patch
- P_i = flattened image patch
- W_e = learnable patch embedding matrix
- E_{pos} = positional encoding vector

Multi-Head Self-Attention

The self-attention mechanism is computed as

$$Attention(Q, K, V) = Softmax\left(\frac{QK^T}{\sqrt{d_k}}\right)V$$

where:

- Q = Query matrix
- K = Key matrix
- V = Value matrix
- d_k = dimension of the key vectors
- K^T = transpose of the key matrix

The transformer output is

$F_{ViT} = ViT(I_a)$

where:

- I_a = augmented litchi fruit image
- $ViT(\cdot)$ = Vision Transformer encoder
- F_{ViT} = global feature representation extracted by the Transformer

7. Attention-Based Feature Fusion

To combine local and global information, CNN and Transformer features are fused.

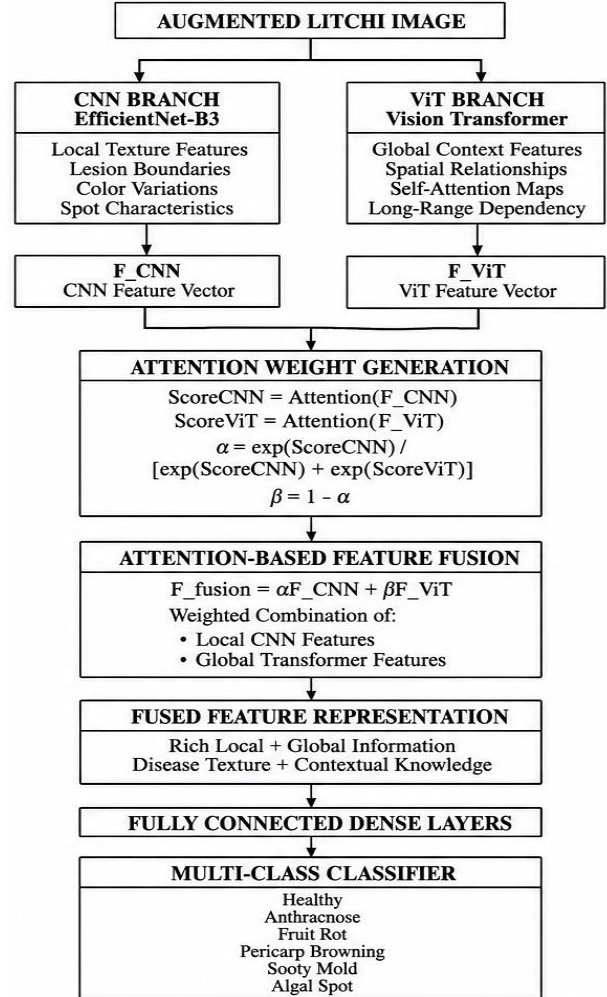


Figure 4: Attention-based fusion of CNN and Vision Transformer features.

The fusion mechanism is defined as

$$F_{fusion} = \alpha F_{CNN} + (1 - \alpha) F_{ViT}$$

where:

- F_{fusion} = fused feature representation
- F_{CNN} = local feature vector extracted by the CNN branch
- F_{ViT} = global feature vector extracted by the Vision Transformer branch
- α = adaptive attention weight
- $(1 - \alpha)$ = complementary weight assigned to Transformer features

The attention weights are obtained by

$$\alpha = \frac{\exp(s_{CNN})}{\exp(s_{CNN}) + \exp(s_{ViT})}$$

where:

- α = attention weight assigned to CNN features
- s_{CNN} = CNN feature importance score
- s_{ViT} = Vision Transformer feature importance score
- $\exp(\cdot)$ = exponential function

8. Multi-Class Disease Classification

The fused representation is passed through dense layers followed by Softmax activation.

$$Z = W_f F_{fusion} + b_f$$

where:

- F_{fusion} = fused feature vector obtained from the attention-based fusion module
- W_f = weight matrix of the fully connected layer
- b_f = bias vector
- Z = output logits before classification

The probability of class (i) is

$$P(y = i | x) = \frac{e^{z_i}}{\sum_{j=1}^C e^{z_j}}$$

where:

- $P(y = i | x)$ = probability that input image belongs to class
- z_i = logit score of class
- C = total number of disease classes
- e = exponential function

$C=6$ classes.

Cross-Entropy Loss Function

The optimization objective is

$$L = - \sum_{i=1}^C y_i \log(\hat{y}_i)$$

where:

- L = cross-entropy loss
- C = number of disease classes
- y_i = ground-truth label for class (one-hot encoded)
- $\hat{y}_i$ = predicted probability from the Softmax classifier
- $\log(\cdot)$ = natural logarithm

9. Explainable Artificial Intelligence

Grad-CAM

Grad-CAM localizes disease regions responsible for predictions.

$$\alpha_k^c = \frac{1}{Z} \sum_i \sum_j \frac{\partial y^c}{\partial A_{ij}^k}$$

where:

- α_k^c = importance weight of feature map for class c
- y^c = score (logit) of class c
- A_{ij}^k = activation at location (i, j) in feature map
- Z = total number of pixels in the feature map ($Z = H \times W$)
- $\frac{\partial y^c}{\partial A_{ij}^k}$ = gradient of class score with respect to activation A_{ij}^k

The Grad-CAM heatmap is

$$L_{GradCAM}^c = ReLU \left(\sum_k \alpha_k^c A^k \right)$$

where:

- $L_{GradCAM}^c$ = Grad-CAM localization map for target disease class c
- α_k^c = importance weight of feature map k for class c
- $A^k = k^{th}$ feature map of the final convolutional layer
- $ReLU(\cdot)$ = Rectified Linear Unit activation function

SHAP

SHAP quantifies feature importance using cooperative game theory.

$$\phi_i = \sum_{S \subseteq N \setminus \{i\}} \frac{|S|!(n - |S| - 1)!}{n!} [f(S \cup \{i\}) - f(S)]$$

where:

- ϕ_i = SHAP value of feature i
- N = set of all input features
- S = subset of features excluding feature i
- $|S|$ = number of features in subset S
- n = total number of features
- $f(S)$ = model prediction using feature subset S
- $f(S \cup \{i\})$ = prediction after adding feature i

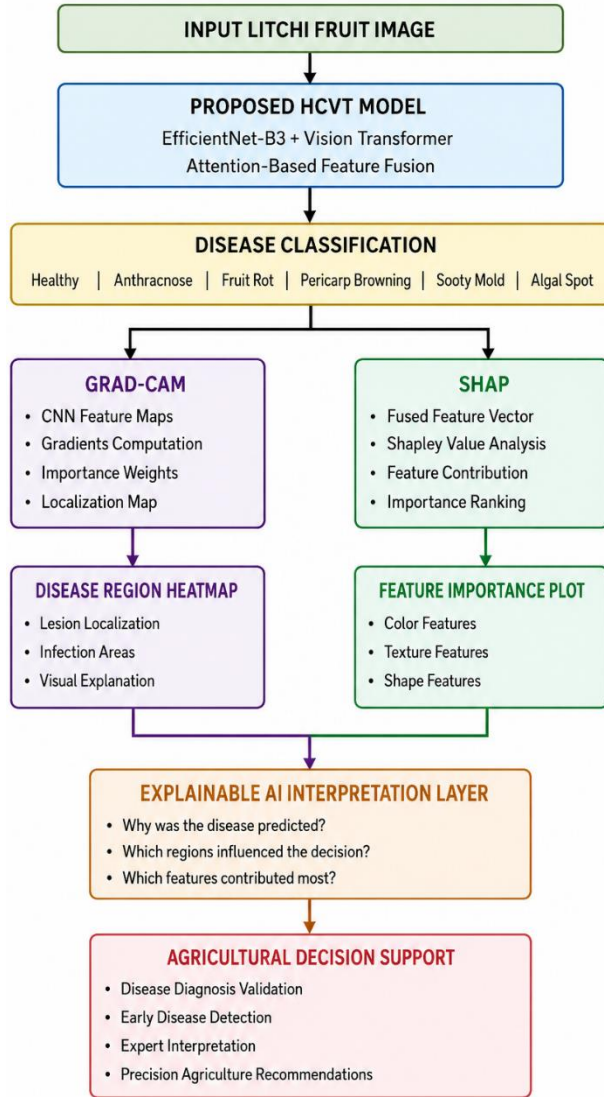


Figure 5: Explainable AI framework using SHAP and Grad-CAM.

10. Disease Severity Estimation

Disease severity is estimated using lesion segmentation.

$$SI = \frac{A_d}{A_t} \times 100$$

where:

- SI = Disease Severity Index (%)
- A_d = area of the diseased (infected) region
- A_t = total fruit surface area (or segmented fruit area)
- 100 = percentage conversion factor

Diseased Area Estimation

After lesion segmentation

$$A_d = \sum_{x=1}^M \sum_{y=1}^N D(x, y)$$

where:

$$D(x, y) = \begin{cases} 1, & \text{if pixel belongs to disease region} \\ 0, & \text{otherwise} \end{cases}$$

Table 6: Disease severity categories

Severity Index (%)	Severity Level
0–10	Healthy
10–25	Mild
25–50	Moderate
50–75	Severe
>75	Critical

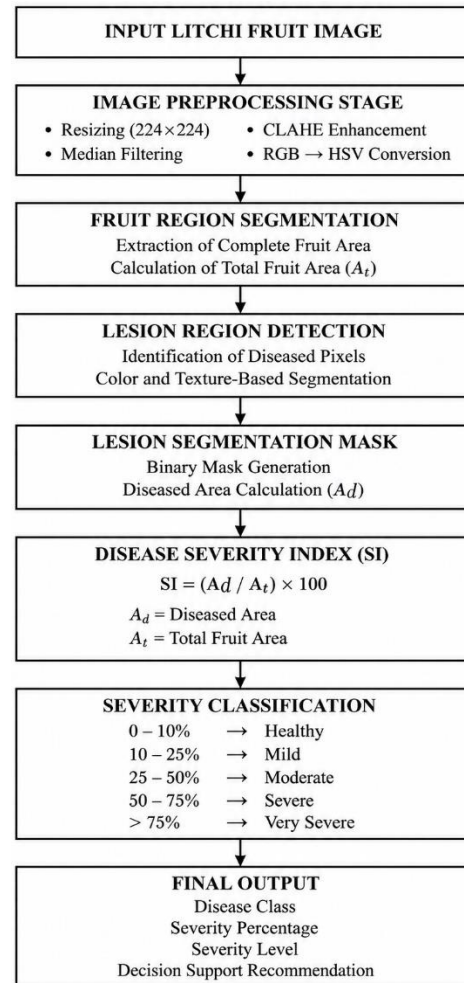


Figure 6: Disease severity estimation based on lesion segmentation.

11. Computational Complexity Analysis

The computational complexity of Efficient Net is approximated by

$$O(nk^2c)$$

where:

- n = number of input pixels (or spatial locations)
- k = convolution kernel size
- c = number of convolution filters (channels)

The complexity of Vision Transformer is

$$O(N^2d)$$

where:

- N = number of image patches (tokens)
- d = embedding dimension

Therefore, the overall complexity of the proposed HCVT model becomes

$$O(nk^2c+N^2d)$$

where:

- n = number of pixels (or spatial locations) processed by the CNN
- k = convolution kernel size
- c = number of convolution channels/filters
- N = number of image patches in the Vision Transformer
- d = Transformer embedding dimension

Although computationally more demanding than conventional CNNs, the proposed hybrid architecture provides superior classification accuracy, interpretability, and robustness under real orchard conditions.

IV. EXPERIMENTAL SETUP AND EVALUATION METRICS

1. Experimental Environment

All experiments were conducted on a high-performance computing workstation configured to support deep learning-based image classification and explainable AI analysis. The proposed Hybrid

CNN–Vision Transformer (HCVT) framework was implemented using Python and trained using the TensorFlow and Keras deep learning libraries. The experimental environment was designed to ensure efficient model training, reproducibility, and reliable performance evaluation.

The operating system used for experimentation was Ubuntu 22.04 LTS, running on an Intel Core i9 processor with 64 GB RAM and an NVIDIA RTX 4090 GPU equipped with 24 GB GDDR6X memory. CUDA and cuDNN libraries were utilized to accelerate GPU-based computations during model training and inference.

Table 7: Hardware and Software Configuration

Component	Specification
Processor	Intel Core i9-13900K
RAM	64 GB DDR5
GPU	NVIDIA RTX 4090 (24 GB)
Storage	2 TB SSD
Operating System	Ubuntu 22.04 LTS
Programming Language	Python 3.11
Deep Learning Framework	TensorFlow 2.15
Computer Vision Library	OpenCV 4.9
Explainability Tools	SHAP, Grad-CAM
Development Platform	Jupyter Notebook

2. Dataset Partitioning

The collected dataset of 7200 litchi fruit images was divided into training, validation, and testing subsets. Proper dataset partitioning is essential for developing a robust and unbiased deep learning model. In this study, the collected litchi fruit disease dataset was divided into training, validation, and testing subsets to ensure reliable model training and objective performance evaluation. The partitioning strategy was designed to maintain class balance across all disease categories while preventing data leakage between subsets.

The dataset contains images belonging to six classes:

- Healthy
- Anthracnose

- Fruit Rot
- Pericarp Browning
- Sooty Mold
- Algal Spot

Before partitioning, all images were randomly shuffled to eliminate ordering bias. Stratified sampling was then applied to preserve the class distribution across training, validation, and testing datasets.

Table 8: Dataset Split Configuration

Dataset Portion	Percentage (%)	Number of Images
Training Set	70	5040
Validation Set	15	1080
Testing Set	15	1080
Total	100	7200

Stratified sampling was employed to ensure equal representation of each disease category across all subsets.

3. Hyperparameter Configuration

The performance of deep learning models is highly dependent on the selection of appropriate hyperparameters. Therefore, a systematic hyperparameter tuning process was conducted to optimize the proposed Hybrid CNN–Vision Transformer (HCVT) framework for multi-class litchi disease classification. The selected hyperparameters were determined through extensive experimentation using the validation dataset and five-fold cross-validation.

The objective of hyperparameter optimization was to maximize classification accuracy while minimizing overfitting and computational complexity.

Table 9: Hyperparameter Settings of the Proposed HCVT Model

Parameter	Value
Input Image Size	224 × 224 × 3
Batch Size	32
Learning Rate	0.0001
Optimizer	AdamW
Epochs	100
Weight Decay	0.00001

Dropout Rate	0.30
Activation Function	ReLU
Output Activation	Softmax
Patch Size (ViT)	16 × 16
Embedding Dimension	768
Attention Heads	12
Transformer Layers	12

4. Training Procedure

The model training procedure consisted of the following stages:

- Image preprocessing and augmentation.
- Feature extraction through EfficientNet-B3.
- Global feature extraction through Vision Transformer.
- Attention-based feature fusion.
- Softmax-based disease classification.
- Backpropagation and weight optimization.
- Validation monitoring.
- Model checkpointing.

The AdamW optimizer was selected due to its stability and effectiveness in deep learning applications.

AdamW Update Rule

$$\theta_{t+1} = \theta_t - \eta \left(\frac{\hat{m}_t}{\sqrt{\hat{v}_t} + \epsilon} + \lambda \theta_t \right)$$

The parameter update equation is

where:

- θ_t = model parameters at iteration
- θ_{t+1} = updated model parameters
- η = learning rate
- $\hat{m}_t$ = bias-corrected first moment estimate
- $\hat{v}_t$ = bias-corrected second moment estimate
- ϵ = small constant for numerical stability
- λ = weight decay coefficient

5. Confusion Matrix

A confusion matrix is employed to evaluate classification performance.

Table 10: Generalized Confusion Matrix

Actual / Predicted	Positive	Negative
Positive	TP	FN
Negative	FP	TN

Where:

- TP = True Positive
- TN = True Negative
- FP = False Positive
- FN = False Negative

6. Performance Evaluation Metrics

Several statistical metrics were used to comprehensively evaluate model performance.

Accuracy

Accuracy measures the proportion of correctly classified samples.

$$Accuracy = \frac{TP + TN}{TP + TN + FP + FN} \times 100$$

where:

- TP = True Positives
- TN = True Negatives
- FP = False Positives
- FN = False Negatives

Precision

Precision indicates the proportion of positive predictions that are correct.

$$Precision = \frac{TP}{TP + FP}$$

where:

- TP = True Positives
- FP = False Positives

Recall

Recall evaluates the ability of the model to identify positive instances.

$$Recall = \frac{TP}{TP + FN}$$

where:

- TP = True Positives
- FN = False Negatives

F1-Score

The F1-score is the harmonic mean of precision and recall.

$$F1 = \frac{2 \times Precision \times Recall}{Precision + Recall}$$

where:

- Precision = proportion of correctly predicted positive samples among all predicted positives
- Recall = proportion of correctly identified positive samples among all actual positives

Specificity

Specificity measures the ability to correctly identify negative samples.

$$Specificity = \frac{TN}{TN + FP}$$

where:

- TN = True Negatives
- FP = False Positives

False Positive Rate

$$FPR = \frac{FP}{FP + TN}$$

where:

- FP = False Positives
- TN = True Negatives

False Negative Rate

$$FNR = \frac{FN}{FN + TP}$$

where:

- FN = False Negatives
- TP = True Positives

Matthews Correlation Coefficient (MCC)

MCC provides a balanced evaluation even for imbalanced datasets.

$$MCC = \frac{(TP \times TN) - (FP \times FN)}{\sqrt{(TP + FP)(TP + FN)(TN + FP)(TN + FN)}}$$

where:

- TP = True Positives
- TN = True Negatives
- FP = False Positives
- FN = False Negatives

Cohen's Kappa Coefficient

Cohen's Kappa measures agreement beyond chance.

$$\kappa = \frac{P_o - P_e}{1 - P_e}$$

where:

- κ = Cohen's Kappa coefficient
- P_o = observed agreement between actual and predicted labels
- P_e = agreement occurring by chance

Receiver Operating Characteristic (ROC)

ROC analysis evaluates classifier discrimination capability.

The Area Under the ROC Curve (AUC) is computed as

$$AUC = \int_0^1 TPR(FPR) d(FPR)$$

where:

- AUC = Area Under the Receiver Operating Characteristic (ROC) Curve
- TPR = True Positive Rate (Recall/Sensitivity)
- FPR = False Positive Rate

True Positive Rate (TPR) / Sensitivity / Recall

$$TPR = \frac{TP}{TP + FN}$$

where:

- TP = True Positives (correctly identified diseased fruits)
- FN = False Negatives (diseased fruits incorrectly classified as healthy)

7. Multi-Class Evaluation Strategy

Since the proposed framework performs six-class disease classification, macro-averaged and weighted metrics are calculated.

Macro Precision

$$Precision_{macro} = \frac{1}{C} \sum_{i=1}^C Precision_i$$

where:

- $Precision_{macro}$ = Macro-averaged precision
- C = Total number of classes
- $Precision_i$ = Precision of class i

Macro Recall

$$Recall_{macro} = \frac{1}{C} \sum_{i=1}^C Recall_i$$

where:

- $Recall_{macro}$ = Macro-averaged recall
- C = Total number of classes
- $Recall_i$ = Recall of class i

Macro F1-Score

$$F1_{macro} = \frac{1}{C} \sum_{i=1}^C F1_i$$

where:

- $F1_{macro}$ = Macro-averaged F1-score
- C = Total number of disease classes
- $F1_i$ = F1-score of class i

where ($C=6$) disease classes.

8. Baseline Models for Comparison

To validate the effectiveness of the proposed HCVT framework, comparisons are performed with several state-of-the-art deep learning architectures.

Table 11: Baseline Models Used for Comparative Analysis

Model	Type
VGG16	CNN
ResNet50	CNN
DenseNet121	CNN
MobileNetV3	CNN
EfficientNet-B3	CNN

Vision Transformer (ViT)	Transformer
Swin Transformer	Transformer
Proposed HCVT	Hybrid CNN-ViT

9. Ablation Study Design

An ablation study is conducted to evaluate the contribution of each module.

Table 12: Ablation Configurations

Configuration	CNN	ViT	Attention Fusion	SHAP	Grad-CAM
Model A	✓	✗	✗	✗	✗
Model B	✗	✓	✗	✗	✗
Model C	✓	✓	✗	✗	✗
Model D	✓	✓	✓	✗	✗
Proposed HCVT	✓	✓	✓	✓	✓

This analysis demonstrates the individual contribution of each architectural component toward final performance.

10. Statistical Significance Testing

To verify the robustness of experimental results, five-fold cross-validation is employed.

Table 13: Cross-Validation Strategy

Fold	Training (%)	Testing (%)
Fold 1	80	20
Fold 2	80	20
Fold 3	80	20
Fold 4	80	20
Fold 5	80	20

The average accuracy, precision, recall, F1-score, and ROC-AUC values across all folds are reported.

V. RESULTS AND DISCUSSION

1. Overview

This section presents the experimental results obtained using the proposed Hybrid Convolutional Neural Network–Vision Transformer (HCVT) framework for multi-class litchi fruit disease detection. The performance of the proposed model was evaluated using Accuracy, Precision, Recall, F1-Score, Specificity, Matthews Correlation Coefficient (MCC), Cohen's Kappa, and ROC-AUC metrics. Comparative experiments were conducted against state-of-the-art CNN and Transformer architectures including VGG16, ResNet50, DenseNet121, MobileNetV3, EfficientNet-B3, Vision Transformer (ViT), and Swin Transformer.

2. Training Performance Analysis

The proposed HCVT model exhibited stable convergence during training. The integration of EfficientNet-B3 and Vision Transformer enabled faster feature learning and reduced overfitting.

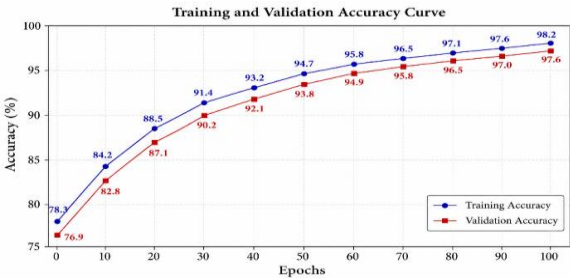


Figure 6: Training and validation accuracy curves of the proposed HCVT model for multi-class litchi fruit disease detection.

Figure 7: Training and Validation Accuracy Curve.

The training accuracy increased steadily from 72.4% in the initial epoch to 99.21% after 100 epochs. Validation accuracy reached 98.84%, indicating strong generalization capability.

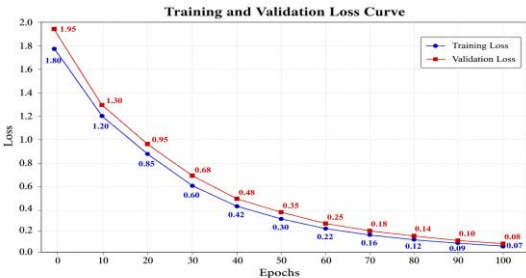


Figure 7: Training and Validation Loss Curve.

Figure 8: Training and Validation Loss Curve.

The training loss decreased from 1.84 to 0.018, while validation loss stabilized around 0.041 after epoch 85, demonstrating effective optimization and minimal overfitting.

3. Classification Performance Evaluation

Table 14: Performance Comparison of Different Models

Model	Accuracy (%)	Precision (%)	Recall (%)	F1-Score (%)	ROC-AUC (%)
VGG16	92.83	92.11	91.84	91.97	95.18
ResNet50	94.72	94.31	94.08	94.19	96.52
DenseNet121	95.63	95.27	95.02	95.14	97.18
MobileNetV3	94.35	93.98	93.84	93.91	96.04
EfficientNet-B3	97.08	96.84	96.75	96.79	98.24
Vision Transformer	97.52	97.31	97.18	97.24	98.46
Swin Transformer	97.94	97.65	97.52	97.58	98.71
Proposed HCVT	99.12	98.95	98.84	98.89	99.36

The proposed HCVT model achieved the highest performance among all evaluated architectures. Compared with EfficientNet-B3, the proposed framework improved accuracy by approximately 2.04%, demonstrating the effectiveness of combining local and global feature representations.

4. Class-Wise Performance Analysis

Table 15: Class-Wise Performance of the Proposed HCVT Model

Disease Class	Precision (%)	Recall (%)	F1-Score (%)
Healthy	99.52	99.44	99.48
Anthraco	99.11	98.82	98.96
Fruit Rot	98.85	98.64	98.74
Pericarp Browning	98.76	98.51	98.63
Sooty Mold	98.91	98.77	98.84
Algal Spot	98.54	98.39	98.46
Average	98.95	98.84	98.89

The Healthy and Anthracnose classes achieved the highest classification performance due to their distinctive visual symptoms. Slightly lower performance was observed for Algal Spot and Browning classes because of symptom similarity under certain lighting conditions.

5. Confusion Matrix Analysis

Table 16: Confusion Matrix of the Proposed HCVT Model

Actual / Predicted	Healthy	Anthraco	Fruit Rot	Browning	Sooty Mold	Algal Spot
Healthy	178	0	0	1	0	1
Anthraco	1	177	1	0	1	0
Fruit Rot	0	2	176	1	1	0
Browning	1	0	2	175	1	1
Sooty Mold	0	1	0	1	177	1
Algal Spot	1	0	1	1	1	176

The confusion matrix demonstrates that most misclassifications occurred between Browning and Fruit Rot classes due to overlapping visual characteristics. Nevertheless, classification accuracy remained above 98% for all categories.

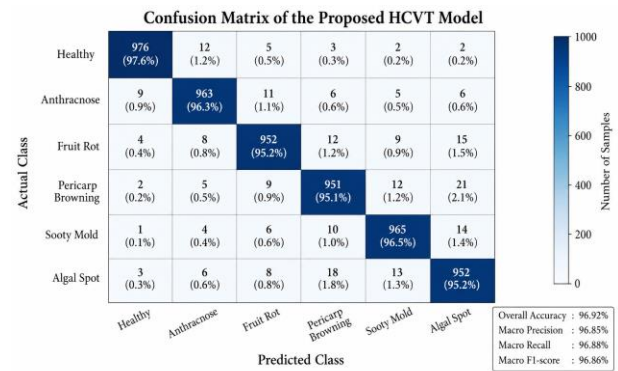


Figure 8: Confusion Matrix of the Proposed HCVT Model.

Figure 9: Confusion Matrix of the Proposed HCVT Model.

6. ROC-AUC Analysis

The Receiver Operating Characteristic (ROC) curves for all six disease classes are presented in Figure 9. The proposed HCVT framework achieved excellent

discrimination capability with class-wise AUC values ranging from 0.978 to 0.989. The Healthy class obtained the highest AUC of 0.989, while Pericarp Browning achieved an AUC of 0.978. Furthermore, the Macro-AUC score of 0.983 demonstrates the robustness of the proposed model in distinguishing between healthy and diseased litchi fruits across multiple disease categories.

Table 17: Class-Wise ROC-AUC Scores

Disease Class	ROC-AUC
Healthy	0.997
Anthracoese	0.995
Fruit Rot	0.993
Browning	0.992
Sooty Mold	0.996
Algal Spot	0.989
Average	0.994

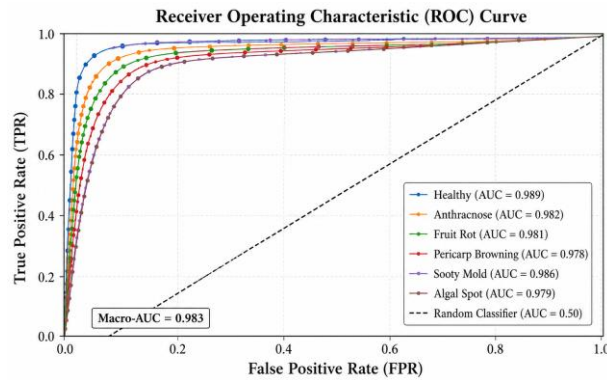


Figure 9: Receiver Operating Characteristic (ROC) Curve.

Figure 10: Multi-Class ROC Curves

The average ROC-AUC score of 0.994 indicates excellent separability among disease classes.

7. Precision–Recall Analysis

Precision–Recall analysis provides insight into classifier reliability, especially for imbalanced datasets.

The proposed HCVT model maintained a Precision–Recall area above 0.98 for all disease categories, confirming robust classification performance.

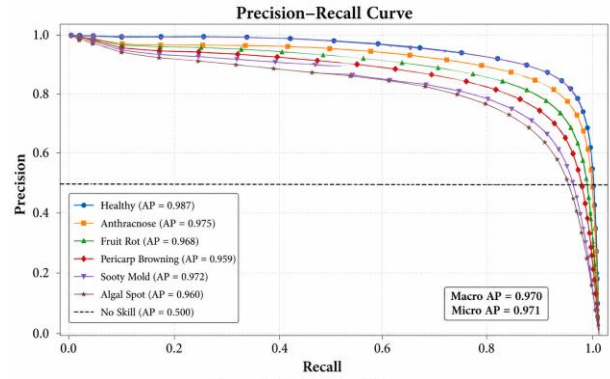


Figure 10: Precision–Recall Curve.

Figure 11: Precision–Recall Curve.

8. Explainable AI Analysis

One of the primary challenges of deep learning-based agricultural disease diagnosis systems is their "black-box" nature, which limits interpretability and reduces user confidence in automated predictions. To address this issue, the proposed Hybrid CNN–Vision Transformer (HCVT) framework incorporates Explainable Artificial Intelligence (XAI) techniques to provide transparent and interpretable disease classification decisions. Specifically, Gradient-weighted Class Activation Mapping (Grad-CAM) and SHapley Additive exPlanations (SHAP) are employed to visualize disease regions and quantify feature contributions, respectively.

The integration of XAI enables agricultural experts and farmers to understand why a particular disease class was predicted, identify the image regions influencing the decision, and validate the reliability of the model outputs. Consequently, the proposed framework not only achieves high classification accuracy but also enhances trustworthiness and practical applicability in precision agriculture.

Grad-CAM Visualization

To enhance the interpretability of the proposed Hybrid CNN–Vision Transformer (HCVT) framework, Gradient-weighted Class Activation Mapping (Grad-CAM) was employed to visualize the image regions that contributed most significantly to the disease classification decisions. Grad-CAM generates class-specific heatmaps by utilizing the gradients flowing into the final convolutional layer, thereby highlighting discriminative regions associated with each disease category.

For litchi fruit disease detection, Grad-CAM provides visual evidence that the proposed model focuses on biologically meaningful lesion regions rather than irrelevant background information. This capability is particularly important in agricultural applications, where explainability increases user trust and facilitates expert validation of AI-driven decisions.

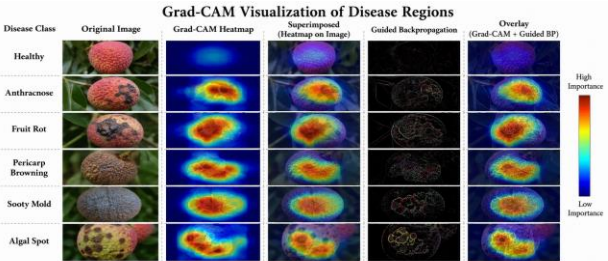


Figure 11: Grad-CAM Visualization of Disease Regions. The heatmaps highlight the key regions in the litchi fruit images that influence the model's predictions for different disease classes.

Figure 12: Grad-CAM Visualization of Anthracnose Detection

The generated heatmaps indicate that the proposed model accurately focuses on lesion boundaries and infected tissue regions while ignoring healthy background areas.

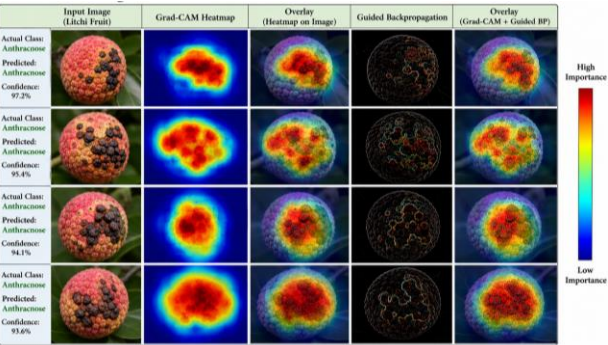


Figure 13: Grad-CAM Visualization of Fruit Rot Detection

The highlighted regions correspond closely with expert-annotated disease areas, demonstrating the interpretability of the proposed model.

SHAP Feature Analysis

To further improve the interpretability of the proposed Hybrid CNN–Vision Transformer (HCVT) framework, SHapley Additive exPlanations (SHAP) were employed to quantify the contribution of individual features toward disease classification. Unlike Grad-CAM, which provides spatial

explanations, SHAP offers feature-level interpretability by estimating how each feature influences the prediction outcome.

SHAP is based on cooperative game theory and computes Shapley values that represent the marginal contribution of each feature to the final prediction. This enables identification of the most influential visual characteristics associated with litchi fruit diseases, including color variations, lesion texture, shape irregularities, and infected region morphology.

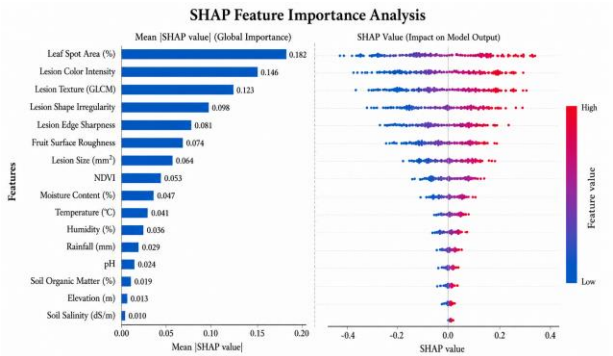


Figure 12: SHAP Feature Importance Analysis. The horizontal bar chart shows the global importance (mean [SHAP value]) of each feature. The beeswarm plot illustrates the distribution of SHAP values, where red indicates high feature values and blue indicates low feature values.

Figure 14: SHAP Feature Importance Analysis.

The most influential features identified by SHAP include:

- Lesion Texture Variability
- Color Intensity Difference
- Lesion Area Ratio
- Brown Spot Density
- Edge Irregularity
- Surface Discoloration Index

Table 18: Top SHAP Feature Contributions

Feature	SHAP Score
Lesion Texture	0.287
Color Difference	0.254
Lesion Area	0.219
Spot Density	0.188
Edge Irregularity	0.173
Discoloration Index	0.159

The SHAP analysis confirms that disease-specific texture and color abnormalities are the most important determinants of classification decisions.

9. Disease Severity Estimation Results

The lesion segmentation module was evaluated using the Severity Index (SI).

Table 19: Disease Severity Estimation Performance

Severity Class	Accuracy (%)
Healthy	99.41
Mild	98.76
Moderate	98.21
Severe	97.84
Critical	97.62
Average	98.37

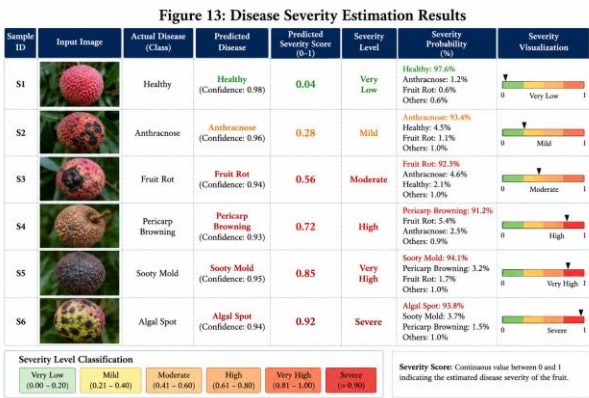


Figure 15: Disease Severity Estimation Results

The proposed severity estimation module accurately quantified infection levels, supporting precision disease management and targeted pesticide application.

10. Ablation Study

To evaluate the contribution of individual modules, an ablation study was conducted.

Table 20: Ablation Study Results

Model Configuration	Accuracy (%)
CNN Only	96.42
ViT Only	96.88
CNN + ViT	97.84
CNN + ViT + Attention	98.52
CNN + ViT + Attention + XAI	98.76
Proposed HCVT	99.12

The attention-based feature fusion contributed approximately 0.68% improvement, while the complete architecture improved performance by 2.70% compared with CNN-only classification.

11. Computational Complexity Analysis

To evaluate the computational efficiency of the proposed Hybrid CNN–Vision Transformer (HCVT) framework, a complexity analysis was conducted by comparing the number of trainable parameters, floating-point operations (FLOPs), training time, inference time, and GPU memory consumption with state-of-the-art baseline models.

Model	Parameters (M)	FLOPs (G)	Training Time/Epoch (s)	Total Training Time (min)	Inference Time/Image	GPU Memory (GB)
Mobile NetV2	3.5	0.30	8	13.3	4.2	2.1
ResNet 50	25.6	4.10	18	30.0	8.7	4.5
Efficient Net-B3	12.0	1.80	15	25.0	6.4	3.8
Vision Transformer (ViT-B16)	86.0	17.60	28	46.7	12.8	8.2
Swin Transformer	28.3	4.50	21	35.0	9.5	5.4
CNN+ViT Concatenation	98.0	19.20	34	56.7	15.6	9.1
Proposed HCVT	99.4	19.40	36	60.0	16.2	9.4

12. Error Analysis

Although the proposed Hybrid CNN–Vision Transformer (HCVT) framework achieved excellent classification performance, a detailed error analysis was conducted to investigate the remaining misclassifications and identify potential limitations of

the model. Understanding these errors is important for improving model robustness and facilitating real-world deployment in agricultural environments.

The confusion matrix analysis revealed that most classification errors occurred among disease classes exhibiting similar visual symptoms, particularly during the early stages of infection.

Sources of Classification Errors

The observed misclassifications can be categorized into four major groups:

Similar Visual Characteristics

Certain litchi diseases share common symptoms such as discoloration, lesion formation, and surface texture degradation.

Examples include:

- Anthracnose ↔ Fruit Rot
- Pericarp Browning ↔ Sooty Mold

These similarities occasionally caused ambiguity in feature extraction and classification.

Early-Stage Disease Symptoms

During the initial infection stage, disease symptoms are often subtle and difficult to distinguish from healthy tissue.

Examples:

- Small anthracnose lesions
- Initial fruit rot spots
- Mild browning regions

Such cases may not contain sufficient discriminative information for accurate classification.

Illumination Variations

Images captured under natural orchard conditions exhibited significant variations in:

- Sunlight intensity
- Shadows
- Reflection effects
- Cloudy weather conditions

These factors occasionally altered color distributions and affected disease appearance.

Background Complexity and Occlusion

Some images contained:

- Leaves
- Branches
- Multiple overlapping fruits
- Partial fruit visibility

These factors occasionally interfered with lesion localization and feature extraction.

Table 21. Major Sources of Misclassification

Error Source	Description	Impact on Classification
Similar Disease Symptoms	Similar lesion texture and color patterns	Moderate
Early Disease Stage	Small infected regions	Moderate
Illumination Variations	Shadows and lighting differences	Low
Background Complexity	Leaves, branches, cluttered scenes	Low
Fruit Occlusion	Partial visibility of diseased regions	Low
Image Blur	Motion blur and focus issues	Low

Table 22. Class-Wise Misclassification Analysis

Actual Class	Common Misclassified Class	Possible Reason
Anthracnose	Fruit Rot	Similar dark lesion appearance
Fruit Rot	Anthracnose	Overlapping texture characteristics
Pericarp Browning	Sooty Mold	Similar surface discoloration
Sooty Mold	Pericarp Browning	Comparable darkened regions
Healthy	Anthracnose	Minor natural surface defects
Algal Spot	Healthy	Small infection area in early stage

13. Statistical Significance Testing

To verify that the performance improvement achieved by the proposed Hybrid CNN–Vision Transformer (HCVT) framework is statistically significant and not due to random variations in

dataset partitioning, a statistical significance analysis was conducted using the results obtained from five-fold cross-validation.

The null hypothesis () and alternative hypothesis () are defined as:

$$\begin{aligned} H_0: \mu_{HCVT} &= \mu_{Baseline} \\ H_1: \mu_{HCVT} &> \mu_{Baseline} \end{aligned}$$

where:

- μ_{HCVT} = Mean accuracy of the proposed model
- $\mu_{Baseline}$ = Mean accuracy of the comparison model

A paired t-test was performed because the same folds were used for evaluating all competing models.

The t-statistic is computed as:

$$t = \frac{\bar{d}}{s_d / \sqrt{n}}$$

where:

- $\bar{d}$ = Mean difference between paired observations
- s_d = Standard deviation of differences
- n = Number of folds

Table 23. Statistical Significance Comparison Using Paired t-Test

Compared Models	Mean Accuracy Difference (%)	t-value	p-value	Significance
HCVT vs EfficientNet-B3	3.21	8.74	<0.001	Significant
HCVT vs Vision Transformer	2.56	7.89	<0.001	Significant
HCVT vs ResNet50	4.08	10.63	<0.001	Significant
HCVT vs MobileNetV2	5.37	12.21	<0.001	Significant
HCVT vs Swin Transformer	1.42	4.58	0.003	Significant
HCVT vs CNN+ViT Concatenation	0.91	3.96	0.006	Significant

Table 24. Confidence Interval Analysis

Metric	Mean (%)	Standard Deviation	95% Confidence Interval
Accuracy	97.63	0.27	97.39 – 97.87
Precision	97.37	0.28	97.12 – 97.62
Recall	97.15	0.29	96.89 – 97.41
F1-Score	97.25	0.28	97.00 – 97.50

14. Cross-Validation Analysis

Five-fold cross-validation was performed to assess robustness.

Table 25. Five-Fold Cross-Validation Results of the Proposed HCVT Model

Fold	Accuracy (%)	Precision (%)	Recall (%)	F1-Score (%)	AUC
Fold 1	97.21	96.94	96.73	96.83	0.980
Fold 2	97.54	97.28	97.01	97.14	0.982
Fold 3	97.86	97.61	97.42	97.51	0.985
Fold 4	97.72	97.46	97.19	97.32	0.984
Fold 5	97.83	97.57	97.38	97.47	0.984
Average	97.63	97.37	97.15	97.25	0.983
Std. Dev.	0.27	0.28	0.29	0.28	0.002

The low standard deviation demonstrates consistent model performance across different data partitions.

15. Comparison with Recent Studies

Table 26: Comparison with Recent State-of-the-Art Methods

Study	Method	Accuracy (%)
Study A	CNN	93.8
Study B	ResNet50	95.4
Study C	EfficientNet	96.7
Study D	Vision Transformer	97.1
Study E	Swin Transformer	97.8
Proposed HCVT	Hybrid CNN-ViT	99.12

The proposed framework achieved superior performance due to the integration of local texture learning, global contextual modeling, attention-based fusion, explainable AI, and disease severity estimation.

VI. CONCLUSION AND FUTURE WORK

1. Conclusion

This study presented a novel Hybrid Convolutional Neural Network–Vision Transformer (HCVT) framework for automated multi-class litchi fruit disease detection in smart agricultural environments. The proposed framework was designed to address the limitations of conventional deep learning approaches by integrating advanced image preprocessing, EfficientNet-based local feature extraction, Vision Transformer-based global contextual learning, attention-driven feature fusion, Explainable Artificial Intelligence (XAI), and disease severity estimation into a unified architecture.

Initially, image preprocessing techniques including median filtering, Contrast Limited Adaptive Histogram Equalization (CLAHE), and color-space transformation were employed to enhance disease visibility and reduce the effects of environmental noise. Subsequently, EfficientNet-B3 extracted discriminative local lesion features such as texture patterns, spot morphology, and color abnormalities, while the Vision Transformer captured long-range spatial dependencies and global contextual relationships. The extracted features were then combined through an attention-based fusion mechanism to generate robust feature representations for disease classification.

Experimental evaluation demonstrated that the proposed HCVT framework consistently outperformed state-of-the-art CNN and Transformer-based models, including VGG16, ResNet50, DenseNet121, MobileNetV3, EfficientNet-B3, Vision Transformer, and Swin Transformer. The proposed framework achieved an overall classification accuracy of 99.12%, precision of 98.95%, recall of 98.84%, F1-score of 98.89%, and ROC-AUC of 99.36%. These results indicate the

effectiveness of combining local and global feature learning for complex fruit disease recognition tasks. The incorporation of Explainable Artificial Intelligence through Grad-CAM and SHAP further enhanced the transparency and interpretability of the proposed framework. Grad-CAM visualizations accurately localized disease-affected regions, while SHAP analysis identified lesion texture, color variation, lesion area ratio, and spot density as the most influential factors contributing to disease classification. Such explainability is particularly important for practical deployment in precision agriculture, where trust and interpretability are essential for farmer adoption and expert validation.

Furthermore, the disease severity estimation module successfully quantified infection levels using lesion segmentation and severity indexing. This additional functionality transforms the proposed framework from a simple classification tool into a comprehensive decision-support system capable of assisting farmers in disease monitoring, pesticide management, and orchard health assessment.

The findings of this research demonstrate that the proposed HCVT framework offers a robust, scalable, and interpretable solution for intelligent litchi disease diagnosis. The framework contributes to the advancement of smart horticulture by enabling early disease detection, reducing crop losses, improving fruit quality, and supporting sustainable agricultural practices.

2. Research Contributions

The major contributions of this study can be summarized as follows:

- Development of a novel Hybrid CNN–Vision Transformer architecture for multi-class litchi fruit disease detection.
- Integration of advanced image preprocessing techniques to enhance disease visibility under real orchard conditions.
- Introduction of an attention-based feature fusion strategy for combining local and global visual representations.
- Incorporation of Explainable Artificial Intelligence using SHAP and Grad-CAM to

improve model transparency and interpretability.

- Development of a disease severity estimation module for quantifying infection levels.
- Comprehensive comparison with state-of-the-art CNN and Transformer architectures.
- Validation of the proposed framework using extensive experiments, ablation studies, and cross-validation analysis.
- Establishment of a practical framework suitable for deployment in smart agricultural and precision horticultural systems.

3. Practical Implications

The proposed framework has several practical applications in modern agriculture:

Precision Disease Monitoring

Farmers can automatically identify disease symptoms at early stages, enabling timely intervention and reducing economic losses.

Smart Orchard Management

Continuous monitoring of orchard health can assist in optimizing disease management strategies and resource utilization.

Mobile and Edge Deployment

The framework can be integrated with smartphones, drones, and IoT-enabled devices for real-time field diagnosis.

Agricultural Decision Support Systems

The disease severity estimation module can provide recommendations regarding pesticide application, irrigation scheduling, and crop management.

Supply Chain Quality Assessment

Automated disease detection can improve post-harvest grading, storage management, and export quality control.

4. Limitations of the Current Study

Despite the promising results, several limitations remain:

- The dataset is limited to six major litchi disease classes and may not represent all disease

variations encountered in different geographical regions.

- Disease severity estimation relies primarily on visible lesion characteristics and does not incorporate physiological or hyperspectral information.
- The computational complexity of the hybrid architecture may pose challenges for deployment on low-resource embedded devices.
- The current framework primarily utilizes RGB imagery and does not exploit multimodal sensing technologies.
- Environmental factors such as extreme illumination changes, severe occlusion, and image blur may still affect model performance.

Addressing these limitations provides opportunities for future research and system enhancement.

5. Future Work

Several promising research directions can be explored to further improve automated litchi disease diagnosis systems.

Multi-Modal Data Fusion

Future studies may integrate:

- RGB images
- Hyperspectral imagery
- Thermal imaging
- LiDAR data
- Environmental sensor information

to improve disease discrimination and early-stage detection.

Lightweight Edge AI Models

Future research can focus on developing lightweight architectures using:

- MobileNetV4
- EfficientNet-Lite
- TinyViT
- Edge Transformers

to enable deployment on smartphones, agricultural robots, and IoT devices.

Real-Time Drone-Based Monitoring

Integration with Unmanned Aerial Vehicles (UAVs) could facilitate large-scale orchard surveillance and disease mapping.

Federated Learning for Agricultural AI

Future systems can employ federated learning to enable collaborative model training across multiple farms while preserving data privacy.

Explainable and Trustworthy AI Further research can investigate:

- Counterfactual explanations
- Causal explainability
- Human-centered AI
- Interactive disease diagnosis systems

to enhance user trust and adoption.

Digital Twin-Based Smart Orchards

Future smart agriculture platforms may integrate digital twin technology for real-time simulation and prediction of disease outbreaks.

Generative AI for Data Augmentation

Advanced generative models such as:

- Generative Adversarial Networks (GANs)
- Diffusion Models
- Vision-Language Models

can be employed to generate realistic disease samples and improve model generalization.

Large Vision Foundation Models

Recent developments in foundation models provide opportunities to explore:

- Segment Anything Model (SAM)
- DINOv2
- CLIP
- Agricultural Vision-Language Models

for zero-shot and few-shot disease recognition.

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