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TransLeaf Intelligence: A Hybrid Vision Transformer Framework for Next-Gen Phytopathology

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ABSTRACT

Precision agriculture increasingly demands intelligent and scalable solutions for early plant disease detection to minimize crop losses and enhance productivity. This study presents an optimized plant disease classification framework based on Vision Transformers (ViT) integrated with transfer learning and lightweight machine learning classifiers. The proposed system combines deep feature extraction using Vision Transformer (ViT) and DenseNet121 (DN121), followed by classification through Perceptron (PC), Nearest Centroid (NC), and K-Nearest Neighbors with Reduced Nearest Centroid (KNN-RNC) models. A Tkinter-based graphical interface is developed to support secure role-based access, dataset management, model training, and real-time prediction. The ViT model effectively captures global contextual dependencies, while DN121 extracts fine-grained local features, enabling robust feature representation. An Explainable AI (XAI) module further enhances system reliability by validating input images and providing semantic interpretations. Experimental evaluation demonstrates that the proposed ViT–Perceptron (ViT-PC) model achieves superior performance with 99.88% accuracy, precision, recall, and F1-score, significantly outperforming DN121-PC, DN121-NC, and DN121-KNN-RNC models. The results highlight the effectiveness of transformer-based architectures in handling complex visual patterns and inter-class similarities in plant diseases. The proposed framework offers a reliable, interpretable, and high-performance solution for real-world phytopathology applications, supporting timely decision-making and sustainable agricultural practices.

Keywords: Plant disease detection, Precision Phytopathology, Feature Extraction, Explainable Artificial Intelligence (XAI), Smart agriculture

1. INTRODUCTION

India is a predominantly agrarian nation where agriculture has historically shaped its culture, economy, and livelihoods across diverse regions. Despite rapid modernization, agriculture continues to support a substantial proportion of the population and remains central to ensuring food security for over 1.4 billion people. The country's wide range of climatic zones, extending from the Himalayan regions in the north to the tropical conditions in the south, enables the cultivation of a broad spectrum of crops, making India one of the world's leading producers of food grains and other agricultural commodities. However, recent shifts in climate patterns, increased incidence of extreme weather events, and growing vulnerability to plant diseases underscore the need for technological interventions to support sustainable agricultural development.

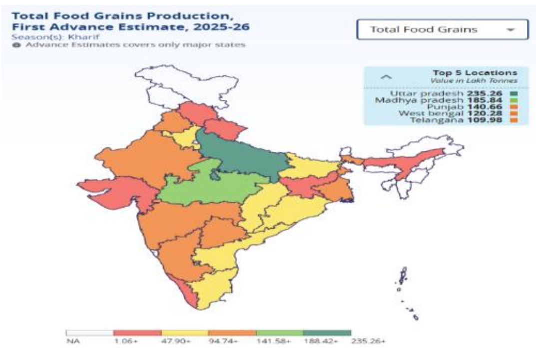

Figure 1. Food Grain Production in India

Figure 1. shows the state-wise distribution of total food grain production in India based on the First Advance Estimates

for the Kharif season (2025–26), highlighting major agricultural contributors such as Uttar Pradesh, Madhya Pradesh, Punjab, West Bengal, and Telangana.

Agriculture in India continues to be the backbone of rural livelihoods, contributing approximately 16–18% to the national Gross Domestic Product (GDP) while employing nearly 40–45% of the workforce. Beyond its economic contribution, the sector plays a crucial role in ensuring food security and sustaining rural incomes. In recent years, Indian agriculture has diversified beyond conventional foodgrain cultivation into high-value segments such as horticulture, floriculture, dairy, and fisheries, driven by evolving consumer preferences and global market demand. Although advancements in irrigation infrastructure, mechanization, and digital technologies have improved productivity, crop losses caused by pests and diseases remain a persistent challenge, particularly under increasing climate variability.

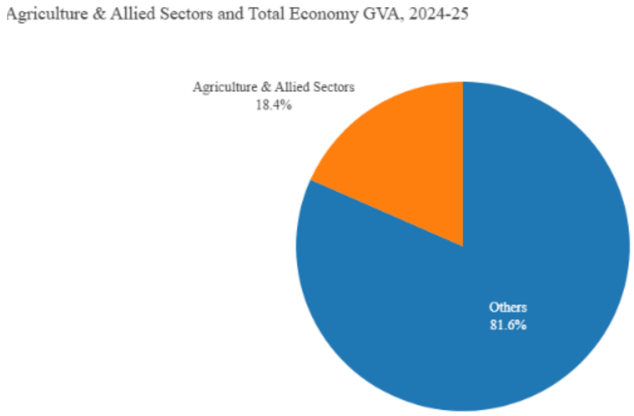

Figure 2. Agriculture in GVA 2024-2025

Figure 2 shows the contribution of Agriculture and Allied Sectors to the Gross Value Added (GVA) of the Indian economy for 2024–25, highlighting the sector's continued significance despite the growing dominance of non-agricultural sectors.

India and Andhra Pradesh together cultivate a rich variety of leading crops that play key roles in food security, trade, and farmer income. Nationally, rice, wheat, maize, pulses, sugarcane, cotton, oilseeds, and an expanding segment of fruits and vegetables dominate production. Andhra Pradesh contributes significantly to India's output of rice, chilies, mango, banana, citrus fruits, cotton, and various spices, earning recognition as both a "rice bowl" and a major horticultural hub. These crops are economically valuable but highly susceptible to fungal, bacterial, and viral diseases, especially under changing climate conditions. As a result, accurate and early disease diagnosis has become essential for maintaining productivity and reducing losses.

Over the past decade, Indian agriculture has grown steadily, recording repeated increases in foodgrain and horticulture production, while simultaneously grappling with rising plant disease pressure. Horticulture output has surpassed 330 million tons annually, reflecting a shift toward high-value crops that are more vulnerable to pests and pathogens. According to global estimates, plant diseases account for 20–40% of crop losses each year, translating to economic losses of billions of dollars, and similar patterns are observed within India and states like Andhra Pradesh. The frequency of diseases such as rice blast, bacterial leaf blight, viral infections in chilies, wilt in cotton, and fruit rots in mango has increased with climate fluctuations, making traditional manual diagnosis insufficient. These trends underscore the need for advanced tools such as Vision Transformers and transfer learning to achieve precision phytopathology capable of detecting diseases accurately and at scale.

2. LITERATURE SURVEY

2.1 RELATED WORK

2.1.1 Transformer-Based and Deep Learning Architectures for Plant Disease Detection

Recent studies have focused on leveraging advanced deep learning and transformer-based architectures to improve plant disease classification performance. Ouamane et al. [1] utilized Vision Transformer (ViT), achieving superior performance across accuracy, precision, recall, and F1-score while also reducing training time (13.80 hours compared to 16.36 hours for baseline ViT on the PlantVillage dataset). This demonstrates both computational efficiency and robustness, especially in resource-constrained environments. In contrast, traditional CNN architectures such as VGG19 and AlexNet showed inferior performance, reinforcing the effectiveness of transformer-based approaches. Further advancements were observed in CNN-based models. Banjar et al. [2] proposed E-AppleNet based on EfficientNetV2 with attention mechanisms and additional dense layers, achieving 99% accuracy using transfer learning and focal loss to handle class imbalance. Similarly, Shafik et al. [3] introduced a hybrid Inception-Xception architecture that integrates multiscale feature extraction and depthwise separable convolutions, achieving near-perfect accuracy across multiple datasets. Yao et al. [4] conducted a comparative study of various CNN architectures and found that InceptionV3 consistently outperformed other models, while their GSMo-CNN achieved state-of-the-art results across datasets.

2.1.2 Machine Learning and Time-Series Based Disease Prediction Models

Apart from image-based detection, several studies have explored time-series and environmental data for disease prediction. Mao and Rui et al. [5] utilized 55 years of historical weather data along with Fusarium inoculum levels to predict Fusarium Head Blight (FHB) severity. They extracted time-series features from climatic variables and applied multiple machine learning models, including Random Forest (RF) and Artificial Neural Networks (ANNs). The results indicated that ANNs outperformed other models, while climatic variables alone were sufficient for accurate prediction, with inoculum levels contributing minimally. Terentev et al. [6] explored hyperspectral data for early disease detection using SVM, logistic regression, and LightGBM optimized via Bayesian search. Their models achieved high F1-scores (0.962 for wheat and 0.94 for barley) and demonstrated strong cross-crop transferability with minimal false negatives. Radwan et al. [7] also applied RF and SVM for potato leaf disease classification, achieving accuracies above 93% with high sensitivity and specificity, ensuring reliable disease discrimination.

2.1.3. Model Optimization, Interpretability, and Generalization Studies

Model reliability, interpretability, and generalization have been key concerns in recent research. Alves et al. [8] demonstrated that although Random Forest models achieved high apparent accuracy, they suffered from overfitting and poor calibration. Using SHAP-based interpretability, they developed a simpler logistic regression model with restricted cubic splines, achieving better calibration (C-statistic = 0.77) and improved robustness. The study emphasized the importance of using machine learning as an interpretive tool, particularly for small datasets. Generalization across datasets has also been extensively studied. Bouacida et al. [9] achieved 94.04% accuracy on the PlantVillage dataset, which improved to 97.13% when tested on new datasets, indicating strong cross-dataset adaptability. Similarly, Khandelwal et al. [10] and Demilie et al. [11] reported high accuracies of 99.83% and 99.35%, respectively, emphasizing the role of dataset expansion and transfer learning. Vo et al. [12] proposed an ensemble of EfficientNetB0 and MobileNetV2, achieving 99.77% accuracy and demonstrating the effectiveness of hybrid models in improving classification performance.

Summary

The literature can be broadly categorized into three domains: (i) transformer and deep learning-based detection models, (ii) time-series and machine learning-based predictive approaches, and (iii) interpretability and generalization-focused studies. While deep learning and transformer models achieve high accuracy, challenges such as overfitting, dataset dependency, and real-world deployment remain critical research gaps.

3. PROPOSED SYSTEM

The proposed system implements an intelligent plant disease classification framework using Vision Transformers and classical machine learning techniques within a Tkinter-based graphical user interface. The system supports secure role-based access for Admin and User, enabling dataset management, feature extraction, model training, evaluation, and real-time prediction. Deep features are extracted using DenseNet121 and Vision Transformer models, followed by classification using lightweight and efficient classifiers. An Explainable AI module based on the Gemini API validates whether the input image is a plant leaf and provides semantic analysis, enhancing reliability and interpretability. The final system delivers accurate plant disease prediction with visual explanations through an interactive desktop application.

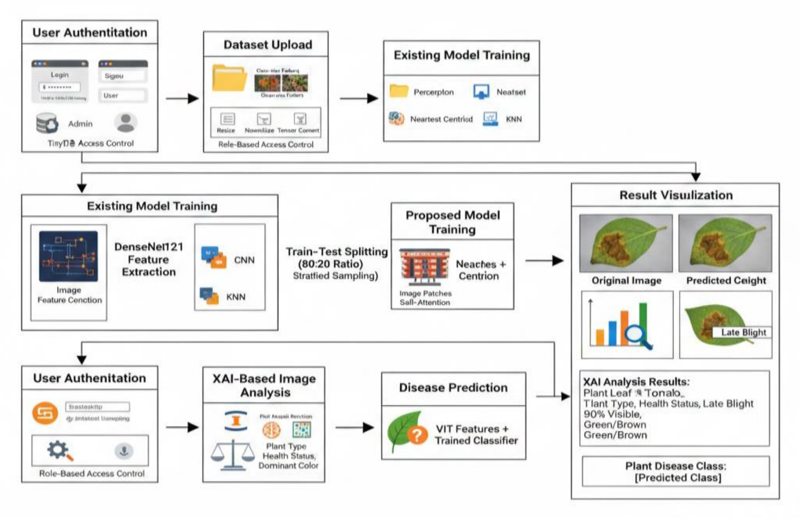

Figure 3. Proposed system architecture of plant disease recognition

Figure 3 illustrates the system architecture of the proposed system, designed as a modular and role-based pipeline integrating deep learning, classical machine learning, and explainable AI. The workflow begins with user authentication, where Admin and User roles are validated through a TinyDB-based access control mechanism to ensure secure and restricted system usage. Once authenticated, the dataset upload module enables authorized users to upload plant leaf image datasets, which are then preprocessed through resizing, normalization, and tensor conversion, with role-based permissions governing data access.

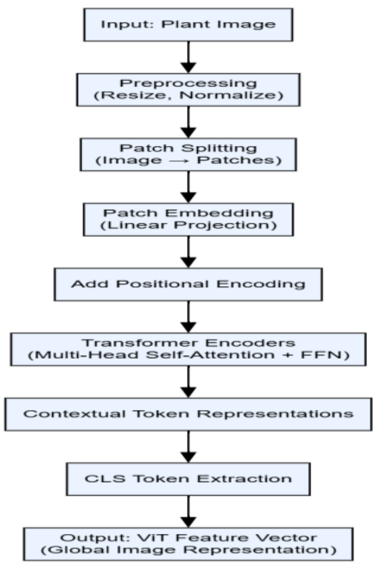

Figure 4. Internal workflow of ViT

The ViT serves as the core feature extractor in the proposed system. Unlike convolutional networks that operate with

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localized receptive fields, the ViT processes images by dividing them into fixed-size patches and projecting each patch into a high-dimensional embedding space. These embedded patches are then passed through multiple transformer encoder layers composed of multi-head self-attention mechanisms and feed-forward networks. This design enables ViT to capture long-range spatial dependencies, contextual relationships, and subtle texture variations that are crucial for differentiating visually similar plant diseases. The process begins with a plant leaf image captured in RGB format. This image serves as the raw input for disease analysis. The input image is resized to a fixed resolution and normalized to standardize pixel values, ensuring consistency and stable learning. The preprocessed image is divided into fixed-size non-overlapping patches. Each patch represents a small region of the image. Each image patch is flattened and passed through a linear projection layer to convert it into a fixed-dimensional embedding vector. Positional encodings are added to patch embeddings to preserve spatial information about the position of each patch in the original image. The sequence of embedded patches is processed through multiple transformer encoder layers. Each layer uses multi-head self-attention and feed-forward networks to learn global contextual relationships among patches. After passing through the transformer encoders, each patch embedding becomes a contextualized token that captures both local and global image information. A special classification (CLS) token is extracted, which aggregates information from all patches and represents the entire image. The CLS token is used as the final ViT feature vector, providing a global image representation suitable for plant disease classification

4. RESULTS ANALYSIS

Figure 5 shows the graphical user interface (GUI) developed for the proposed research work titled "Optimizing Vision Transformers using Transfer Learning for precision Phytopathology." The interface visually represents a smart agriculture scenario in which multiple sensor nodes deployed across a crop field collect plant-related data and transmit it wirelessly via LoRa communication links (indicated by red dashed arrows) to a central LoRa gateway. The gateway aggregates the sensed data and forwards it to a cloud server (shown by the upward blue arrow), where the optimized Vision Transformer–based classification model performs plant disease analysis and decision-making. The GUI also integrates user interaction modules on the left panel, including Admin Signup, User Signup, Admin Login, User Login, and Exit, enabling secure role-based access and system management. This unified interface provides a clear visualization of data acquisition, communication, cloud-based processing, and user control, thereby demonstrating the end-to-end operational flow of the proposed intelligent plant disease detection framework.

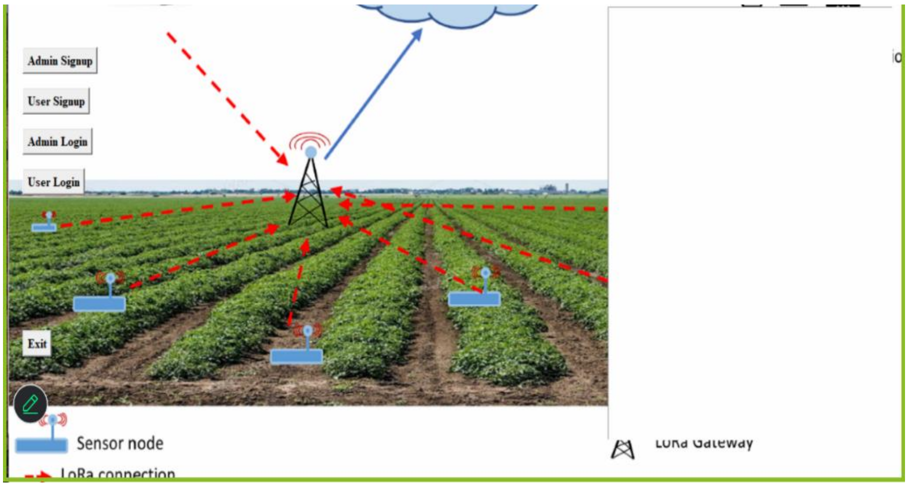

Figure 5. GUI of plant disease detection

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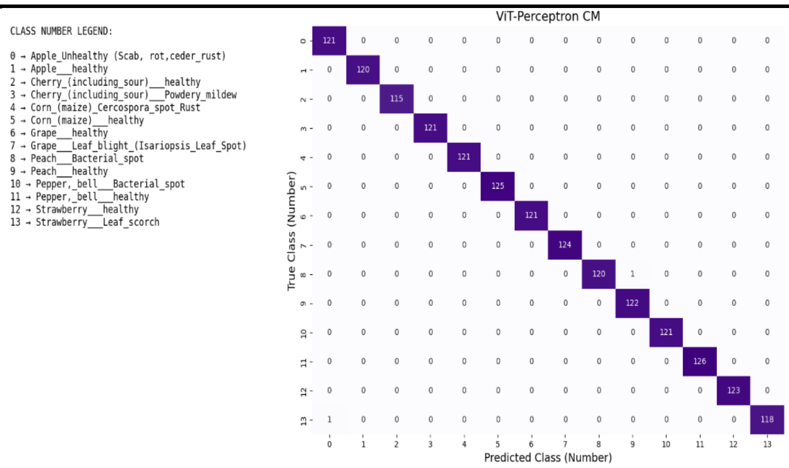

Figure 6. Confusion Matrix of Vision Transformer (ViT) with Perceptron Classifier

Figure 6. presents the confusion matrix for the proposed ViT based feature extraction model combined with the Perceptron classifier. The matrix illustrates the classification performance across all plant disease and healthy leaf classes, with true class labels represented along the rows and predicted class labels along the columns. The class number legend maps each numerical index to its corresponding crop–disease category. The confusion matrix exhibits an almost perfect diagonal structure, indicating that the majority of samples across all classes are correctly classified with negligible misclassification. This result demonstrates the strong discriminative capability of ViT features in capturing both global and fine-grained visual patterns in plant leaf images, as well as the effectiveness of the lightweight Perceptron classifier in learning optimal decision boundaries in the transformed feature space. The near-zero off-diagonal values confirm superior class separability and robustness of the proposed ViT–Perceptron model, validating its effectiveness for high-accuracy multi-class plant disease classification in precision phytopathology applications.

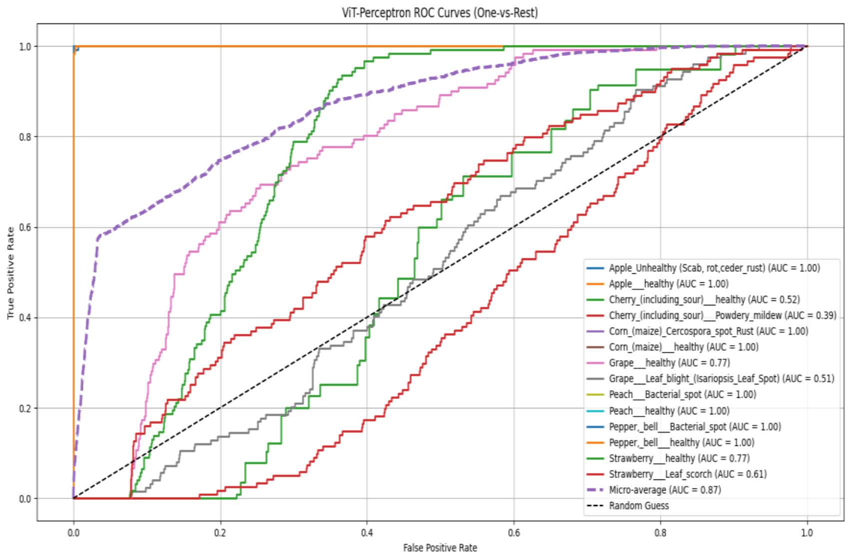

Figure 7. ROC Curves of ViT with Perceptron Classifier

Figure 7. illustrates the Receiver Operating Characteristic (ROC) curves for the proposed ViT–Perceptron model using a one-vs-rest (OvR) multi-class evaluation strategy. Each ROC curve represents the trade-off between the True Positive Rate (TPR) and False Positive Rate (FPR) for an individual plant disease or healthy leaf class, while the diagonal dashed line denotes random classification performance. Several classes, including Apple unhealthy, Apple healthy, Corn healthy, Peach bacterial spot, Peach healthy, Pepper bacterial spot, and Pepper healthy, achieve an Area Under

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the Curve (AUC) value of 1.00, indicating perfect class separability. Other classes exhibit comparatively lower AUC values due to visual similarity and inter-class overlap among certain disease patterns. The micro-average ROC curve, with an AUC of approximately 0.87, summarizes the overall classification performance across all classes and demonstrates strong global discriminative capability of the proposed model. Overall, the ROC analysis confirms the robustness, reliability, and high diagnostic accuracy of the ViT–Perceptron framework for multi-class plant disease detection in precision phytopathology applications.

4.1 COMPARATIVE ANALYSIS

Table 2. presents the overall performance comparison of different deep learning–based classification models using Accuracy, Precision, Recall, and F1-Score as evaluation metrics. The DenseNet121-Perceptron model achieves a strong performance with an accuracy of 93.88%, precision of 94.65%, recall of 94.21%, and F1-score of 93.83%, indicating reliable classification capability across plant disease classes. The DenseNet121-NC model shows moderate performance with 86.53% accuracy, reflecting a decline in precision (87.04%) and recall (86.91%) due to less effective feature discrimination. The DenseNet121-KNN-RNC model records the lowest performance among the compared approaches, with 79.24% accuracy and an F1-score of 76.57%, highlighting its limitations in handling complex inter-class variations. In contrast, the proposed ViT-Perceptron model significantly outperforms all baseline methods, achieving 99.88% accuracy, precision, recall, and F1-score, which demonstrates its superior ability to capture global contextual features and effectively classify plant diseases with high robustness and consistency.

Table 2. Overall Performance Comparison (Accuracy, Precision, Recall, F1-Score)

Model	Accuracy (%)	Precision (%)	Recall (%)	F1-Score (%)
DenseNet121-Perceptron	93.88	94.65	94.21	93.83
DenseNet121-NC	86.53	87.04	86.91	86.57
DenseNet121-KNN-RNC	79.24	76.06	79.90	76.57
ViT-Perceptron (Proposed)	99.88	99.88	99.88	99.88

Table 3 compares the performance of different models using accuracy, precision, recall, and F1-score. Among the DenseNet121-based methods, the DenseNet121–Perceptron model performs best with an accuracy of 93.88%, while the Nearest Centroid and KNN–RNC models show lower performance due to limited class discrimination. The proposed ViT–Perceptron model achieves the highest performance with 99.88% across all evaluation metrics, clearly demonstrating its superior accuracy and reliability for plant disease classification.

Table 3 Recall Comparison (%) Across Classes and Methods

Class	DenseNet-Perc	DenseNet-NC	DenseNet-KNN	ViT-Perceptron
Apple_Unhealthy	61	65	76	100
Apple_Healthy	98	76	90	100
Cherry_Healthy	100	100	100	100
Cherry_Powdery_Mildew	94	92	98	100
Corn_Cercospora_Rust	99	97	97	100
Corn_Healthy	99	99	100	100
Grape_Healthy	97	98	100	100
Grape_Leaf_Blight	100	92	98	100
Peach_Bacterial_Spot	99	79	89	99
Peach_Healthy	94	82	96	100
Pepper_Bacterial_Spot	80	66	80	100
Pepper_Healthy	98	89	94	100
Strawberry_Healthy	98	94	0	99
Strawberry_Leaf_Scorch	100	87	0	100

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Table 3 shows the class-wise recall comparison for different classification methods. The DenseNet-based models exhibit varying recall values across classes, with noticeable drops for visually similar diseases such as Apple unhealthy and Pepper bacterial spot. The DenseNet–KNN model fails to detect Strawberry classes effectively, resulting in zero recall for those categories. In contrast, the proposed ViT–Perceptron model achieves near-perfect recall across all classes, reaching 100% for most categories and 99% for Peach bacterial spot and Strawberry healthy. This demonstrates the superior sensitivity and reliability of the ViT–Perceptron approach in correctly identifying plant diseases and healthy conditions across diverse crop types.

Table 4 Precision Comparison (%) Across Classes and Methods

Class	DenseNet-Perc	DenseNet-NC	DenseNet-KNN	ViT-Perceptron
Apple_Unhealthy	100	68	91	99
Apple_Healthy	82	85	91	100
Cherry_Healthy	99	95	93	100
Cherry_Powdery_Mildew	97	92	93	100
Corn_Cercospora_Rust	99	98	99	100
Corn_Healthy	99	98	98	100
Grape_Healthy	99	69	89	100
Grape_Leaf_Blight	96	97	98	100
Peach_Bacterial_Spot	86	92	96	100
Peach_Healthy	95	80	94	99
Pepper_Bacterial_Spot	99	85	93	100
Pepper_Healthy	76	74	28	100
Strawberry_Healthy	100	89	0	100
Strawberry_Leaf_Scorch	98	96	0	100

Table 4 presents the class-wise precision comparison for the evaluated models. The DenseNet-based approaches show inconsistent precision across several classes, with notable reductions for Pepper healthy and Strawberry categories, particularly in the DenseNet–KNN model. The DenseNet–Perceptron and DenseNet–NC models perform reasonably well but still exhibit class-dependent variability. In contrast, the proposed ViT–Perceptron model achieves consistently high precision, reaching 100% for almost all classes and 99% for Peach healthy. These results indicate that the ViT–Perceptron model produces highly reliable predictions with minimal false positives, confirming its robustness and effectiveness for precise plant disease classification.

Table 5 F1-Score Comparison (%) Across Classes and Methods

Class	DenseNet-Perc	DenseNet-NC	DenseNet-KNN	ViT-Perceptron
Apple_Unhealthy	76	67	83	100
Apple_Healthy	89	80	91	100
Cherry_Healthy	100	98	96	100
Cherry_Powdery_Mildew	96	92	95	100
Corn_Cercospora_Rust	99	97	98	100
Corn_Healthy	99	99	99	100
Grape_Healthy	98	81	94	100
Grape_Leaf_Blight	98	94	98	100
Peach_Bacterial_Spot	92	85	93	100
Peach_Healthy	95	81	95	100

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Pepper_Bacterial_Spot	89	75	86	100
Pepper_Healthy	85	80	43	100
Strawberry_Healthy	99	92	0	100
Strawberry_Leaf_Scorch	99	91	0	100

Table 5 summarizes the class-wise F1-score performance of the evaluated models, combining both precision and recall to reflect overall classification effectiveness. The DenseNet-based models show moderate to high F1-scores for several classes but suffer notable performance degradation for Pepper healthy and Strawberry categories, particularly in the DenseNet–KNN model where F1-scores drop to zero. The DenseNet–Perceptron and DenseNet–Nearest Centroid models demonstrate improved balance but still exhibit class-wise variability. In contrast, the proposed ViT–Perceptron model achieves a perfect F1-score of 100% across all classes, indicating optimal balance between precision and recall. This consistent performance confirms the superior robustness, reliability, and discriminative capability of the ViT–Perceptron framework for multi-class plant disease classification.

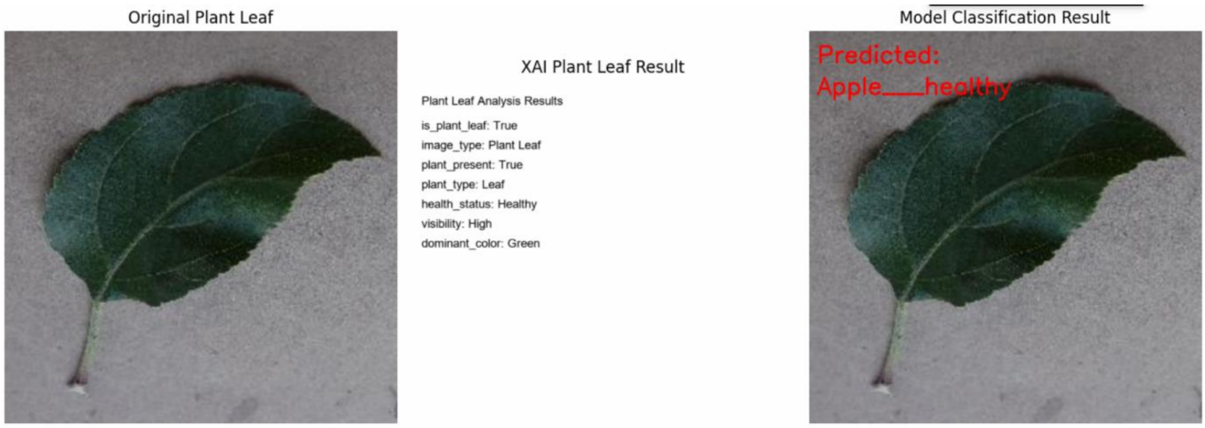

Figure 8. Prediction Results of Apple Health Class.

Figure 8. presents the prediction results for the Apple healthy class obtained using the proposed Vision Transformer–Perceptron model. The figure shows the original apple leaf image, the explainable AI (XAI) analysis confirming the presence of a healthy plant leaf with high visibility and dominant green coloration, and the final classification output. The model accurately predicts the leaf as belonging to the Apple healthy class, demonstrating the effectiveness of the proposed approach in correctly identifying healthy plant conditions while providing interpretable insights to support the prediction.

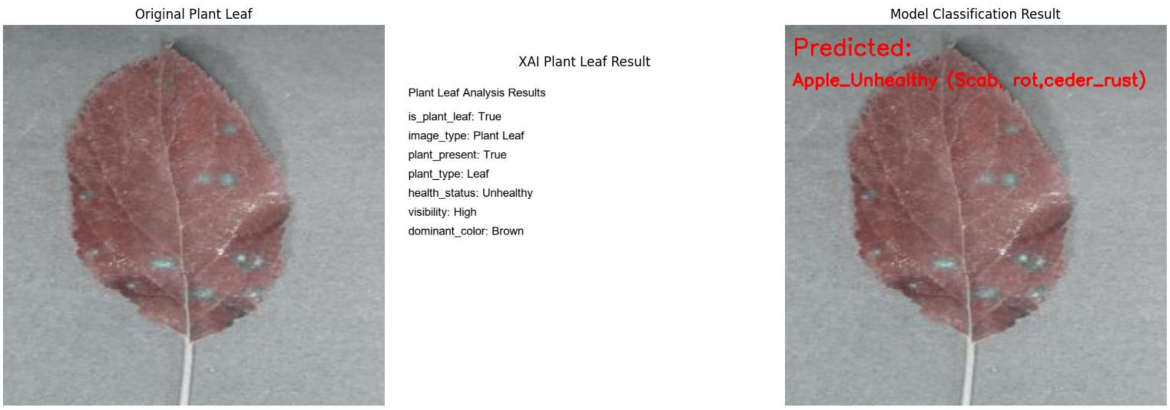

Figure 9. Prediction Results of Apple Unhealthy Class

Figure 9. illustrates the prediction results for the Apple unhealthy class obtained using the proposed Vision Transformer–Perceptron model. The left panel shows the original apple leaf image exhibiting visible disease symptoms. The middle panel presents the explainable AI (XAI) analysis, which confirms the presence of a plant leaf and indicates an unhealthy health status with high visibility and a dominant brown coloration. The right panel displays the final classification result, where the model correctly predicts the leaf as *Apple Unhealthy (Scab, rot, cedar rust)*. This result demonstrates the capability of the proposed framework to accurately detect diseased plant leaves while providing interpretable explanations to support the classification outcome.

5. CONCLUSION

The research work clearly demonstrates the effectiveness of advanced deep learning architectures for plant disease classification. Among the baseline models, the DenseNet121-Perceptron achieves a high accuracy of 93.88%, with corresponding precision, recall, and F1-score values of 94.65%, 94.21%, and 93.83%, respectively, indicating strong feature extraction and reliable classification performance. However, a noticeable performance drop is observed in the DenseNet121-NC model, which records 86.53% accuracy, 87.04% precision, 86.91% recall, and 86.57% F1-score, reflecting reduced discriminative capability. The DenseNet121-KNN-RNC model further underperforms with only 79.24% accuracy and an F1-score of 76.57%, highlighting its limited robustness in handling complex visual patterns and inter-class similarity among plant disease categories. In contrast, the proposed ViT-Perceptron model achieves outstanding performance, with 99.88% accuracy, precision, recall, and F1-score, significantly outperforming all DenseNet-based variants. This substantial improvement of nearly 6% over DenseNet121-Perceptron, 13% over DenseNet121-NC, and 20% over DenseNet121-KNN-RNC in accuracy confirms the superiority of Vision Transformer–based global attention mechanisms in capturing long-range dependencies and subtle disease characteristics. The consistently high metric values across all evaluation criteria indicate that the proposed approach is highly robust, generalizable, and well-suited for real-world agricultural disease diagnosis applications.

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