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Automated Identification of Crop Diseases using Computer Vision

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Abstract
Early and accurate identification of crop diseases is essential for ensuring agricultural productivity, food security, and sustainable farming practices. This study presents an automated computer vision based framework for multi-crop disease classification using a lightweight deep learning architecture. The proposed system employs the ReXNet-1.5 convolutional neural network as the core feature extractor, integrating efficient hierarchical feature learning with low computational complexity. A publicly available multi-crop dataset comprising 13,324 images across 17 disease and healthy classes covering corn, rice, potato, wheat, and sugarcane is used for model training and evaluation. Experimental results demonstrate strong performance, achieving 97.45% accuracy and a macro-F1 score of 96.26%, indicating reliable class-balanced prediction under dataset imbalance. Grad-CAM based visual explainability is incorporated to provide interpretable disease localization, enhancing transparency and trust in model predictions. Additionally, the model exhibits high computational efficiency, enabling real-time inference suitable for deployment on resource constrained platforms. The proposed framework offers an accurate, interpretable, and deployable solution for real world crop disease diagnosis, supporting intelligent decision-making and scalable agricultural monitoring systems.

Keywords: Crop Disease Detection, Computer Vision, Deep Learning, Smart Agriculture, Image Processing

1. Introduction

Agricultural systems form the foundation of global food supply and socio-economic stability, particularly in regions where livelihoods are directly tied to crop productivity. Rapid population growth, climate variability, and increasing pressure on natural resources have intensified the demand for efficient and resilient food production systems. At the same time, crop health remains a persistent vulnerability, with plant diseases and pests causing widespread yield degradation, economic losses, and long term threats to food security and rural sustainability.

The ability to detect crop diseases at an early stage is critical for minimizing damage and enabling effective management strategies. However, timely diagnosis remains a major challenge in many agricultural regions due to limited access to infrastructure, delayed response mechanisms, and the scale at which monitoring is required. As agricultural landscapes become more complex and geographically dispersed, conventional monitoring approaches struggle to provide rapid, consistent, and scalable disease surveillance.

The integration of intelligent digital technologies into agriculture has created new opportunities for automated crop monitoring and decision support. Vision based systems powered by artificial intelligence enable continuous, data-driven assessment of plant health using imagery captured from mobile devices, drones, and low-cost sensors. Such systems offer the potential to shift agriculture from reactive disease control toward proactive and predictive management, allowing interventions before large scale damage occurs.

Despite the growing adoption of AI driven agricultural tools, practical deployment remains constrained by efficiency, reliability, and operational feasibility. Many existing solutions are difficult to deploy at scale due to high computational requirements, limited adaptability to diverse field conditions, and dependency on controlled data environments. These limitations highlight the need for intelligent systems that are not only accurate but also efficient, robust, and deployable in real world farming contexts.

This research addresses these challenges through the development of an optimized computer vision based framework for automated crop disease identification. The proposed approach emphasizes a balanced design that integrates diagnostic accuracy with computational efficiency and real world adaptability. By enabling fast, reliable, and early stage disease detection, the system aims to support informed decision making, reduce crop losses, and strengthen agricultural resilience. Ultimately, this work contributes to the advancement of scalable, intelligent agricultural technologies that support sustainable food production and long term global food security.

2. Literature Review

The identification of crop diseases is essential for maintaining agricultural productivity and ensuring global food security [1-3]. Traditionally, this process has relied on naked eye visual inspection by experts or farmers, which is often slow, labor intensive, costly, and prone to human error [4-6]. In many remote regions, the lack of access to trained specialists leads to late detection, causing rapid disease spread and significant financial damage [7, 8].

Early automated systems utilized traditional machine learning and image processing techniques [9]. These methods typically follow a pipeline involving image acquisition, pre-processing, segmentation, and hand crafted feature extraction [10-12]. Extracted visual characteristics such as color, texture, and shape were then used to train classifiers like Support Vector Machines, K-Nearest Neighbour, Random Forest, and Artificial Neural Networks [13]. While effective in controlled settings, these models often struggle with complex backgrounds and require significant human expertise for feature engineering [14].

The emergence of Deep Learning, specifically Convolutional Neural Networks, has revolutionized the field by enabling the automatic extraction of salient features directly from original leaf images [15]. CNN architectures like AlexNet, MobileNet, GoogLeNet (Inception), ResNet, and DenseNet have demonstrated superior ability in recognizing complicated spatial hierarchies in agricultural data [16-17]. Researchers have successfully applied these models to various crops, including tomato, rice, wheat, and maize [4, 18]. For instance, DenseNet-121 and ResNet-50 are frequently cited for achieving high classification accuracy while maintaining computational efficiency [4, 17].

One of the primary challenges in training robust deep learning models is the lack of large, labeled datasets [1, 3, 19]. To address this, researchers widely adopt Transfer Learning, which involves using pre-trained weights from massive datasets like ImageNet to provide a foundation for domain specific training [9, 20]. This technique reduces the required image count, prevents overfitting, and decreases training time [15]. Furthermore, data augmentation methods such as flipping, rotation, scaling, and the generation of synthetic images via Generative Adversarial Networks are used to enhance dataset diversity [21-22].

Recent advancements have focused on improving disease localization and severity estimation using object detection frameworks [17]. One-stage detectors like YOLO (You Only Look Once) and Single Shot MultiBox Detector (SSD) are favored for real-time deployment on mobile devices due to their speed [5]. Conversely, two-stage detectors such as Faster R-CNN offer higher accuracy [23-25]. To further enhance precision in real world environmental conditions, attention mechanisms (e.g., CBAM) are integrated into backbone networks to help models focus on disease specific spots while ignoring background noise.

While reported results indicate strong performance under controlled conditions, critical limitations remain in real world applicability. Many existing studies are based on images captured in controlled or semi-controlled environments with uniform backgrounds and limited environmental variability [26]. Consequently, models often exhibit reduced generalization when deployed in real-field conditions characterized by variable illumination, complex backgrounds, occlusions, and the presence of multiple diseases on a single leaf [27]. Current research therefore emphasizes the need for lightweight architectures suitable for deployment on resource constrained edge devices, as well as models capable of generalizing across diverse crop species, heterogeneous environments, and previously unseen disease patterns.

3. Dataset

The experiments in this study are conducted using a publicly available crop disease image dataset titled “Top Agriculture Crop Disease Dataset”, comprising 13,324 labeled RGB images distributed across 17 distinct classes, representing both healthy and diseased crop conditions. The dataset includes five major crops: corn, potato, rice, wheat, and sugarcane covering a diverse range of plant pathologies. Specifically, the disease categories include Common Rust, Gray Leaf Spot, and Northern Leaf Blight for corn; Early Blight and Late Blight for potato; Brown Spot, Leaf Blast, and Neck Blast for rice; Brown Rust and Yellow Rust for wheat; and Red Rot and Bacterial Blight for sugarcane, along with healthy classes for each crop type. This multi-crop, multi-disease composition introduces significant inter-class variability and real-world complexity, making the dataset well suited for evaluating the robustness and generalization capability of deep learning based crop disease prediction models. Representative sample images from different crop disease categories are shown in Figure 1 to illustrate the visual diversity, inter-class variability, and complexity of symptoms present in the dataset.

4. Methodology

This section describes the complete pipeline used for automated crop disease identification, including dataset preprocessing, model architecture, training strategy, evaluation methodology, and explainability integration.

4.1 Data Preprocessing

The dataset was randomly partitioned into training, validation, and test sets using a ratio of 90%, 5%, and 5%, respectively. This split ensures sufficient data for learning robust representations while preserving independent subsets for model validation and unbiased performance evaluation. Each image is resized to a fixed spatial resolution of 224 × 224 pixels to ensure compatibility with the convolutional neural network backbone. The images are then normalized, enabling stable convergence during training and effective transfer learning from pretrained weights.

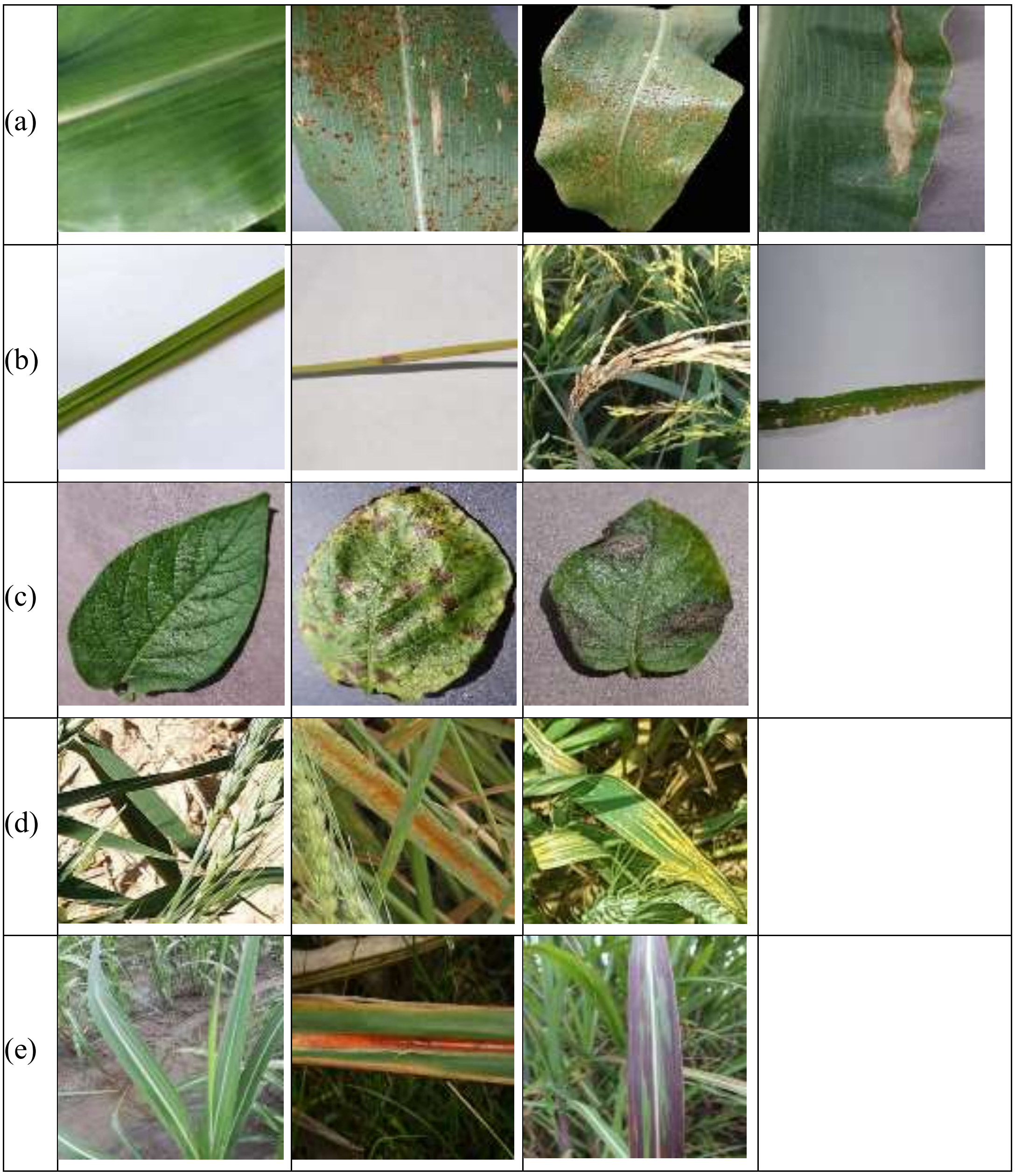


Figure 1: Representative sample images arranged in a structured grid layout. Rows (a-e) correspond to different crop types: (a) corn, (b) rice, (c) potato, (d) wheat, and (e) sugarcane. The first column shows healthy crop samples, while subsequent columns represent different disease conditions for each crop.

4.2 Model Architecture

The proposed system employs ReXNet-1.5 (rexnet_150) as the core feature extraction backbone. ReXNet is a lightweight convolutional neural network architecture based on progressive linear channel expansion, enabling efficient hierarchical feature learning with low computational overhead.

As illustrated in Figure 2, the network is composed of multiple functional components that collectively perform hierarchical representation learning and classification.

The architecture begins with a stem convolution layer, which performs initial low-level feature extraction and spatial downsampling. This is followed by the ReXNet feature extraction backbone, consisting of multiple stacked ReX blocks organized into progressive stages. The early stages focus on low-level texture and edge features, intermediate stages capture shape and structural patterns, and deeper stages learn high-level semantic representations.

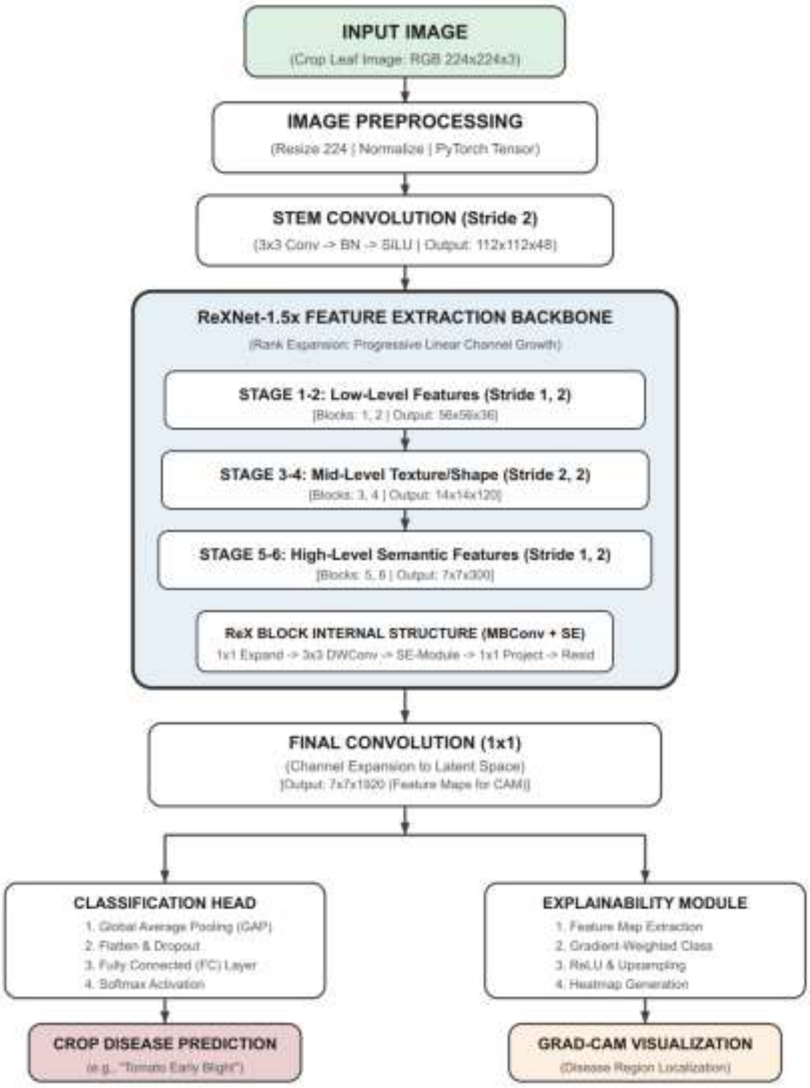


Figure 2: Abstracted architecture of the ReXNet-1.5 model for crop disease classification, illustrating the hierarchical feature extraction backbone, classification head, and Grad-CAM explainability module.

Each ReX block follows a MobileNet-inspired design consisting of a 1×1 expansion convolution, a 3×3 depthwise convolution, a squeeze-and-excitation (SE) attention module for channel-wise feature recalibration, and a 1×1 projection convolution, combined with residual connections for stable gradient propagation. Progressive channel expansion across layers enables efficient rank growth and enhanced representational capacity.

Global feature aggregation is achieved using a global average pooling layer, which compresses spatial feature maps into compact feature vectors. Finally, the classification head, implemented as a fully connected layer followed by a Softmax activation function, produces class probability distributions for multi-class disease prediction.

Transfer learning is employed by initializing the backbone with pretrained ImageNet weights and fine-tuning the network on the crop disease dataset, enabling faster convergence and improved generalization performance.

4.3 Model Training Strategy

The network is trained using the Adam optimizer with a learning rate of 3×10^{-4} and categorical cross-entropy loss as the objective function. Training is performed for a maximum of 10 epochs with early stopping based on validation loss monitoring to prevent overfitting.

Model checkpointing is applied, where the best performing model (based on minimum validation loss) is automatically saved. This ensures that the final deployed model represents the optimal generalization performance.

During training, model performance is monitored using training and validation loss, classification accuracy, and macro-averaged multi-class F1-score, enabling a balanced assessment of convergence, generalization, and class-wise predictive reliability.

4.4 Performance Evaluation

Model performance is evaluated on a held-out test set that is not used during training or validation. The evaluation metrics include:

- Accuracy for overall classification performance

$$Accuracy = \frac{1}{N}\sum_{i=1}^{N} 1(\hat{y}_i = y_i) \qquad (1)$$

- F1-score for balanced class-wise performance assessment

$$F1_c = \frac{2 \cdot Precision_c \cdot Recall_c}{Precision_c + Recall_c} \qquad (2)$$

$$F1_{macro} = \frac{1}{C}\sum_{c=1}^{C} F1_c \qquad (3)$$

- Learning curves to analyze convergence behavior and generalization stability

In the above equations, N denotes the total number of samples, and C represents the number of classes. For each sample i, y_i and $\hat{y}_i$ indicate the ground-truth label and predicted label, respectively.

The evaluation framework ensures objective measurement of the model's predictive reliability, robustness, and generalization performance.

4.5 Explainability and Visual Interpretation

To enhance interpretability and trustworthiness, a Grad-CAM (Gradient-weighted Class Activation Mapping) based explainability module is integrated into the proposed system. Grad-CAM generates class discriminative localization maps by computing the gradients of the predicted class score with respect to the final convolutional feature maps, producing heatmaps that are overlaid on the original input images to visually highlight disease relevant regions on crop leaves. This mechanism enables visual validation of the model's attention regions, supports the biological plausibility of predictions, improves transparency in the decision making process, and enhances user trust and system interpretability. Through this integration, the system functions not only as an accurate predictive model but also as a visual diagnostic support tool for reliable agricultural disease assessment.

5. Results and Discussion

5.1 Quantitative Performance Evaluation

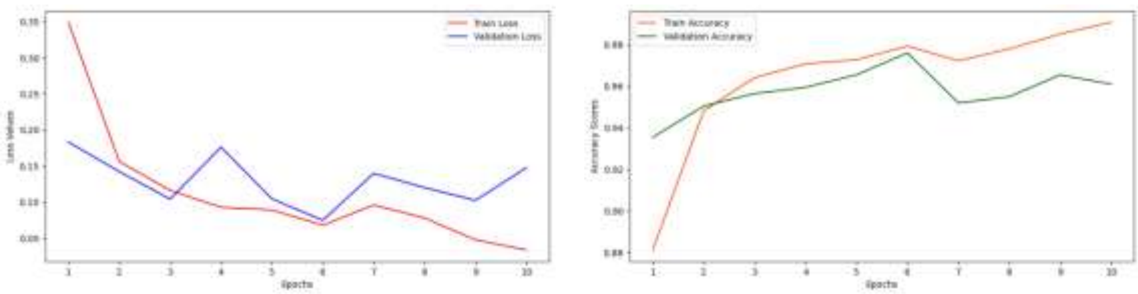
As summarized in Table 1, the model exhibits consistently strong generalization performance across all evaluation metrics, reflecting stable learning and balanced class wise discrimination. The high macro-averaged scores indicate robustness under class imbalance, while the overall performance confirms the suitability of the ReXNet-1.5 architecture for reliable multi class crop disease classification in real world agricultural scenarios.

Table 1: Overall Performance Metrics

Metric	Value
Accuracy	97.45%
Macro-Precision	95.78%
Macro-Recall	97.22%
Macro-F1 Score	96.26%

5.2 Learning Dynamics Analysis

Figure 3 presents the training and validation learning curves in terms of loss and accuracy across epochs. The model demonstrates stable convergence, with consistently decreasing training loss and increasing training accuracy. Validation curves show overall improvement with minor late stage fluctuations, indicating stable optimization and effective generalization.



(a) (b)

Figure 3: Training and validation learning curves of the proposed ReXNet-1.5 model showing (a) loss convergence and (b) classification accuracy across training epochs.

5.3 Class-wise Performance Evaluation

Table 2: Class-wise Performance Metrics

Class	Precision	Recall	F1-score	Support
Corn - Common Rust	1	1	1	62
Corn - Gray Leaf Spot	0.93	1	0.96	25
Corn - Healthy	1	1	1	60
Corn - Northern Leaf Blight	1	0.96	0.98	47
Potato - Early Blight	1	1	1	50
Potato - Healthy	1	1	1	8
Potato - Late Blight	1	1	1	48

Rice - Brown Spot	0.74	0.94	0.83	18
Rice - Healthy	0.95	0.93	0.94	88
Rice - Leaf Blast	0.91	0.86	0.89	50
Rice - Neck Blast	1	1	1	53
Sugarcane - Bacterial Blight	1	0.83	0.91	6
Sugarcane - Healthy	1	1	1	4
Sugarcane - Red Rot	0.75	1	0.86	3
Wheat - Brown Rust	1	1	1	45
Wheat - Healthy	1	1	1	50
Wheat - Yellow Rust	1	1	1	50

As summarized in Table 2,the class wise performance analysis demonstrates consistently strong predictive capability across all crop disease categories. Most classes achieve high precision, recall, and F1-scores, indicating robust discriminative learning and reliable disease identification. Minor performance variations are observed in visually similar disease categories, such as Rice Brown Spot and Rice Leaf Blast, where overlapping symptom patterns introduce limited ambiguity. Nevertheless, even in these cases, the model maintains high recall values, ensuring effective disease detection sensitivity. The strong performance across minority classes, including sugarcane and potato disease categories with limited sample support, highlights the model's generalization ability and robustness under class imbalance. This comprehensive class wise evaluation confirms the stability, reliability, and practical applicability of the proposed ReXNet-1.5-based framework for real world multi crop disease diagnosis.

5.4 Explainability Analysis

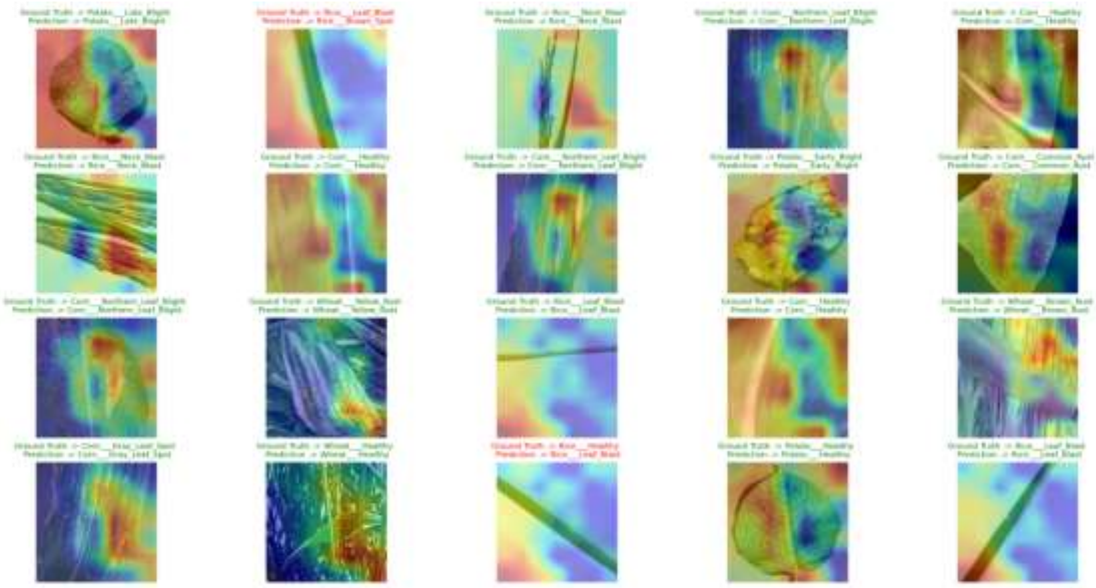


Figure 4: Grad-CAM Visualizations for Disease Localization

To enhance model interpretability, Grad-CAM based visual explanations were generated for test samples. As illustrated in Figure 4, Grad-CAM based visual explanations highlight that the model consistently focuses on disease affected regions of crop leaves, including lesions, discoloration patterns, and texture irregularities. This spatial alignment between model attention and biologically meaningful disease symptoms validates the semantic correctness of the learned representations and enhances the interpretability and trustworthiness of the proposed framework for real world agricultural deployment.

5.5 Computational Efficiency

As summarized in Table 3, the proposed model demonstrates high computational efficiency with a compact parameter size and low inference latency, enabling real time performance. These characteristics support its suitability for deployment in resource constrained environments, including edge devices and mobile platforms, facilitating practical adoption for real time, field level crop disease monitoring and decision support.

Table 3: Computational Performance

Metric	Value
Total Parameters	7.84 M
Model Size	29.9 MB
Inference Time	0.023 s/image
Throughput	42 FPS

Conclusion

This study presents an efficient and reliable computer vision based framework for automated multi crop disease identification using a lightweight deep learning architecture. By leveraging the ReXNet-1.5 model, the proposed system achieves strong classification performance while maintaining low computational complexity, enabling practical deployment in real world agricultural environments. Experimental results demonstrate high accuracy and robust class-balanced performance across diverse crop and disease categories, confirming the model's generalization capability under real world data variability and class imbalance. The integration of Grad-CAM based visual explainability further enhances system transparency by providing biologically meaningful disease localization, improving interpretability and user trust. In addition, the model's low inference latency and compact size support real time deployment on resource constrained platforms such as mobile devices and edge systems. Overall, the proposed framework offers a scalable, interpretable, and deployable solution for intelligent crop disease diagnosis, contributing to sustainable agriculture through early disease detection, improved decision making, and efficient field level monitoring. Future work will focus on real field data collection, multi disease detection per leaf, severity estimation, and integration with IoT based smart farming ecosystems.

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