

An Interpretable Feature-Enhancement Deep Ensemble Classifier for Brinjal Disease Detection

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Abstract

Artificial intelligence has become an effective tool for improving agricultural productivity through automated crop disease diagnosis. Brinjal (eggplant) cultivation suffers substantial yield losses from diseases such as Shoot and Fruit Borer, Wet Rot, Fruit Cracking, and Phomopsis Blight, yet reliable field-based diagnostic systems remain limited. To address this challenge, we introduce *BrinjalFruitX*, a real-world dataset comprising 1,823 annotated images collected under natural farming conditions in Bangladesh across four disease classes and one healthy class. We propose an interpretable hybrid feature-enhancement deep ensemble framework that integrates image preprocessing, transfer learning, traditional machine learning, class imbalance mitigation, and explainable artificial intelligence. Three preprocessing techniques, Gaussian, Laplacian, and Unsharp Masking, are systematically evaluated, while deep features extracted using pre-trained VGG and ResNet models are classified by Random Forest, K-Nearest Neighbors, and a classifier-level ensemble. The optimal Unsharp-ResNet-Random Forest configuration achieved 80.0% accuracy with an F1-score of 87.0%. ADASYN applied in the deep feature space improved minority-class sensitivity, while Grad-CAM and Grad-CAM++ enhanced model interpretability. The proposed framework provides an effective and transparent solution for practical field-level brinjal disease detection and precision agriculture.

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Keywords: Brinjal Disease, BrinjalFruitX Dataset, Image Preprocessing, Deep Learning, Explainable AI, Precision Agriculture

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1. Introduction

Agriculture constitutes a fundamental pillar of global food security and economic stability, sustaining approximately 40% of the world's population and contributing significantly to the gross domestic product of developing nations [1]. Plant diseases and pests impose substantial constraints on agricultural productivity, causing annual yield losses ranging from 20% to 40% across major crops [2]. In horticultural crops such as brinjal (eggplant), a dietary staple in South and Southeast Asia, diseases including Shoot and Fruit Borer, Phomopsis Blight, Wet Rot, and Fruit Cracking severely diminish fruit quality and productivity [3]. Early and

precise disease detection is critical for mitigating these losses through timely intervention and sustainable agricultural management. Traditional disease diagnosis relies on visual inspection by agricultural experts, a method characterized by subjectivity, temporal inefficiency, and limited scalability [4]. Initial automated approaches employed machine learning techniques using handcrafted features, such as color, shape, and texture descriptors, classified through Support Vector Machines (SVM), K-Nearest Neighbors (KNN), and Random Forest (RF) algorithms [6]. While these methods achieved acceptable accuracy under controlled settings, they degraded substantially under real-field conditions characterized by illumination variability, occlusion, and

complex backgrounds [7], since handcrafted features inadequately capture the subtle disease manifestations essential for early-stage diagnosis.

The advent of deep learning and Convolutional Neural Networks (CNNs) has since transformed plant disease detection by enabling end-to-end feature extraction directly from raw imagery, learning hierarchical visual representations from elementary edges to complex disease patterns and yielding superior recognition performance [9, 10]. Despite this progress, existing approaches exhibit three critical limitations when applied to brinjal disease detection specifically. First, the majority of plant disease detection studies rely on controlled laboratory datasets such as PlantVillage [14], which fail to capture the illumination variability, occlusion, and background complexity characteristic of real agricultural fields; public, field-acquired brinjal datasets remain particularly scarce, and existing brinjal-focused studies predominantly address a limited subset of disease categories or rely on laboratory-acquired images. Second, class imbalance between common diseases, such as Shoot and Fruit Borer, and rare ones, such as Phomopsis Blight, remains under-addressed in brinjal-specific research, limiting model sensitivity for early-stage detection of less prevalent diseases. Third, the predominance of end-to-end deep learning approaches sacrifices interpretability for accuracy, reducing trust among farmers and agronomists who require transparent diagnostic reasoning to act on model predictions. Hybrid frameworks that combine image enhancement, deep feature extraction, and classical classification, offering a balance between accuracy, interpretability, and data efficiency, remain largely unexplored for brinjal disease detection, leaving the development of a generalized, explainable model for real-field deployment as an open challenge [13]. To address these gaps, this study makes the following contributions:

1. We introduce **BrinjalFruitX** [15], the first comprehensive field-acquired dataset for brinjal fruit disease detection, comprising 1,823 annotated images across five categories collected under real farming conditions in Bangladesh, capturing natural variation in illumination, background complexity, and disease severity.
2. We propose a **hybrid preprocessing and classification framework** integrating complementary image enhancement techniques (Unsharp Masking, Gaussian filtering, Laplacian filtering), deep feature extraction via pre-trained VGG and ResNet-50 architectures, and classical classifiers (Random Forest, KNN, Ensemble), with ADASYN oversampling to address class imbalance in the deep feature space.
3. We integrate **Grad-CAM and Grad-CAM++** for explainable AI visualization, enabling transparent localization of disease-relevant regions and supporting stakeholder trust in model predictions for practical field deployment.

The remainder of this paper is organized as follows. Section 2 reviews related work on crop disease detection, deep learning under field conditions, class imbalance, and explainable AI, and situates the identified research gap. Section 3 details the proposed hybrid framework, including dataset construction, image preprocessing, deep feature extraction, classification, and the explainability pipeline. Section 4 presents experimental results across all preprocessing, feature-extractor, and classifier configurations, together with the Grad-CAM/Grad-CAM++ analysis. Section 6 discusses the limitations of the proposed approach and directions for future work, followed by concluding remarks.

2. Literature Review

Crop diseases and pest infestations continue to threaten global food security by substantially reducing agricultural productivity and crop quality. Brinjal (eggplant), one of the most widely cultivated vegetable crops in South Asia, is particularly susceptible to diseases such as Shoot and Fruit Borer, Wet Rot, Fruit Cracking, and Phomopsis Blight, all of which contribute to considerable economic losses. Traditional disease diagnosis relies primarily on manual visual inspection, a process that is labor-intensive, subjective, and difficult to scale across large agricultural fields. Consequently, recent advances in machine learning (ML) and deep learning (DL) have accelerated the development of automated disease diagnosis systems capable of providing rapid, objective, and scalable crop monitoring. Although convolutional neural networks (CNNs) have demonstrated remarkable success in plant disease classification, their performance often deteriorates under real field conditions because of complex backgrounds, illumination changes, occlusions, and severe class imbalance. Moreover, the limited interpretability of deep learning models remains a significant obstacle to practical adoption by farmers and agricultural experts. This section reviews the progression of research from traditional disease detection to modern deep learning, explainable artificial intelligence (XAI), and smart agriculture, highlighting the remaining challenges that motivate the proposed framework.

2.1. Global Impact of Crop Diseases and Limitations of Traditional Detection

Crop diseases remain one of the leading causes of agricultural yield reduction worldwide. Jones and

Smith [1] quantified global crop losses caused by pests and diseases through a comprehensive meta-analysis, while Patel and Mehta [2] and Kumar and Gupta [3] documented the substantial economic impact of major brinjal diseases and emphasized the importance of integrated disease management strategies. Conventional diagnosis relies heavily on expert visual inspection, which is often inconsistent and impractical for large-scale farming. Lee and Tsao [4] demonstrated that automated image-based systems significantly improve diagnostic efficiency over manual inspection, and Singh et al. [5] further showed that ML-based approaches enable rapid and scalable plant stress phenotyping. These studies collectively establish the necessity of automated disease diagnosis but primarily focus on conventional methodologies without fully exploiting modern deep learning techniques for field-based brinjal disease detection.

2.2. Deep Learning for Plant Disease Detection

The emergence of deep learning has substantially improved automated plant disease recognition. Zhang et al. [6] demonstrated that transfer learning enables CNNs to achieve high classification accuracy even with relatively limited datasets, while Mohanty et al. [8] showed that CNN-based models consistently outperform traditional machine learning approaches across multiple crop species. Ferreira et al. [9] further compared several CNN architectures and analyzed the trade-off between network complexity and classification accuracy, providing valuable guidance for architecture selection. More recently, Yadav et al. [32] proposed a CNN-based framework for cauliflower disease classification, demonstrating the effectiveness of transfer learning for practical agricultural disease diagnosis under realistic conditions. Despite these advances, Liao et al. [7] reported that models trained under controlled laboratory conditions often fail to generalize to field environments characterized by varying illumination, cluttered backgrounds, and partial occlusion. These findings indicate that robust preprocessing, representative field datasets, and improved model generalization remain essential for practical deployment.

2.3. Dataset Quality, Class Imbalance, and Explainable AI

Recent studies have increasingly recognized that dataset quality, class imbalance, and model interpretability are equally important for reliable agricultural AI systems. Li et al. [10] demonstrated that data augmentation and resampling techniques significantly improve classification performance on imbalanced crop disease datasets, while Das and Kumar [13] highlighted the urgent need for diverse, field-collected

brinjal datasets to improve model robustness and generalization. Alongside data quality, explainable artificial intelligence has emerged as an important research direction for increasing user trust in deep learning systems. Mirza and Rehman [11] surveyed XAI techniques for precision agriculture, and Zhao and Su [12] proposed interpretable deep learning models specifically designed for plant disease diagnosis. Singh et al. [17] combined hyperspectral imaging with explainable 3D deep learning to improve both predictive accuracy and interpretability, while Kiriella et al. [20], Amara et al. [21], and Shafik et al. [22] further demonstrated the growing importance of explainability for transparent and sustainable agricultural decision-making. Similar trends have also been reported beyond agriculture. Hasan et al. [33] integrated deep ensemble transformers with Grad-CAM-based explanations for medical image diagnosis, illustrating that explainability substantially improves the transparency and reliability of complex deep learning systems. Nevertheless, existing studies generally address dataset imbalance or explainability independently, and very few integrate both within a unified framework validated on real field-acquired brinjal images.

2.4. Advances in Smart Agriculture

The broader smart agriculture literature demonstrates rapid progress toward practical AI-enabled crop monitoring systems. Kumar et al. [23] proposed a dedicated CNN architecture for crop disease detection. In contrast, Ahmed et al. [16] showed that hybrid preprocessing strategies significantly improve feature extraction from field-degraded images. Extending beyond single-crop applications, Munir et al. [24] developed a multi-crop disease detection framework, Sarangdhar et al. [27] introduced an automated CNN-based disease diagnosis system, and Munir et al. [28] proposed a hybrid CNN-CRF architecture for IoT-enabled smart agriculture. Recent studies published in EAI journals further reinforce these developments. Wen et al. [29] employed Random Forest classifiers combined with image preprocessing and segmentation for apple disease recognition, Khan et al. [30] utilized YOLOv8 for efficient pest detection to support food security, Moshayedi et al. [31] reviewed the transformative role of agricultural robotics in precision farming, and Sharma et al. [34] highlighted robust preprocessing, feature extraction, and dataset diversity as essential requirements for practical disease and pest detection systems. Similarly, Omer et al. [25] and Singh et al. [26] identified dataset scarcity, environmental variability, limited model generalization, and insufficient interpretability as persistent barriers to real-world deployment. Collectively, these studies demonstrate that robust preprocessing, deep feature

extraction, explainability, and intelligent deployment have each been investigated extensively. However, no existing work integrates these components into a unified hybrid framework specifically designed for field-acquired brinjal disease classification while simultaneously addressing class imbalance and model interpretability. This gap motivates the proposed study.

3. Methodology

The proposed methodology, illustrated in Figure 1, presents a hybrid framework addressing four challenges identified in Section 2: field-condition image degradation, class imbalance, data scarcity, and limited interpretability. Pre-trained VGG [35] and ResNet-50 [36] serve exclusively as feature extractors, while Random Forest, KNN, and a classifier-level ensemble via majority voting handle classification. This decoupled design enables robust learning under limited data while preserving interpretability and reducing computational overhead. Ensemble preprocessing techniques including Gaussian filtering, Laplacian filtering, and Unsharp Masking, are evaluated using PSNR, SSIM, and MSE. Class imbalance is mitigated using ADASYN in the deep feature space. Performance is assessed through accuracy, F1-score, TPR, TNR, FPR, FNR, precision, and error rate. Grad-CAM and Grad-CAM++ verify that predictions focus on pathologically relevant regions. Each component is described in detail in the following subsections.

3.1. Dataset Development and Initial Processing

Dataset quality and diversity were prioritized from the outset of this study. Field images were collected across two major agricultural regions of Bangladesh, Bogura and Dhaka, under natural lighting and varying environmental conditions to capture the real-world heterogeneity of brinjal disease presentation. A total of 2,273 raw images were captured by smartphone camera across five classes: Brinjal Fruit Cracking, Phomopsis Blight, Shoot and Fruit Borer, Wet Rot, and Healthy, with representative examples shown in Figure 2. To remove near-duplicate images and preserve dataset integrity, a perceptual hashing procedure (Algorithm 1) was applied, yielding a final curated dataset of 1,823 images. We refer to this dataset as BrinjalFruitX; its class distribution is Shoot and Fruit Borer (725), Healthy (514), Wet Rot (223), Brinjal Fruit Cracking (200), and Phomopsis Blight (161).

3.2. Data Balancing

To mitigate the impact of class imbalance inherent in real-field agricultural data, we employ the Adaptive Synthetic Sampling (ADASYN) technique. ADASYN operates in the deep feature space generated by CNN

Algorithm 1: Image Deduplication Using Perceptual Hashing (pHash)

Input: Image collection $\mathcal{I} = \{I_1, I_2, \dots, I_n\}$

Output: Deduplicated image set $\mathcal{U}$

```

1  $\mathcal{H} \leftarrow \emptyset;$ 
2  $\mathcal{U} \leftarrow \emptyset;$ 
3 foreach  $I_i \in \mathcal{I}$  do
4    $I_i^g \leftarrow \text{Gray}(I_i);$ 
5    $I_i^r \leftarrow \text{Resize}(I_i^g, h, w);$ 
6    $\mathbf{h}_i \leftarrow \text{pHash}(I_i^r);$ 
7   if  $\mathbf{h}_i \notin \mathcal{H}$  then
8      $\mathcal{H} \leftarrow \mathcal{H} \cup \{\mathbf{h}_i\};$ 
9      $\mathcal{U} \leftarrow \mathcal{U} \cup \{I_i\};$ 
10  else
11    // Duplicate image
12    discard  $I_i;$ 
12 return  $\mathcal{U}$ 

```

encoders, synthesizing minority samples with emphasis on regions that are difficult to classify. This strategy encourages balanced decision boundaries without altering the original image distribution. It is important to note that ADASYN is applied after feature extraction, not in the image domain. While this improves classifier sensitivity to underrepresented diseases, synthetic samples may not strictly conform to the original CNN feature manifold; therefore, all experiments are conducted on both original and ADASYN-balanced datasets, and performance gains are interpreted with caution to avoid overstating generalization improvements. While direct visualization of synthetic sample distribution (e.g., t-SNE plots) was beyond the scope of this study, indirect validation is provided through consistent performance improvement observed across multiple independent classifiers (Random Forest, KNN, and Ensemble) on the ADASYN-balanced dataset. If synthetic samples were distributional outliers, such consistent gains across heterogeneous classifiers would be unlikely. This limitation is acknowledged in Section 6, and future work will incorporate explicit feature-space validation of synthetic samples.

3.3. Image Filtering

Brinjal fruit images captured in field conditions often exhibit noise, uneven illumination, and blur, which obscure critical diagnostic features such as lesion boundaries and texture anomalies. To counteract these issues, we applied three complementary enhancement techniques: Gaussian filtering for noise reduction, Laplacian filtering for edge sharpening, and Unsharp

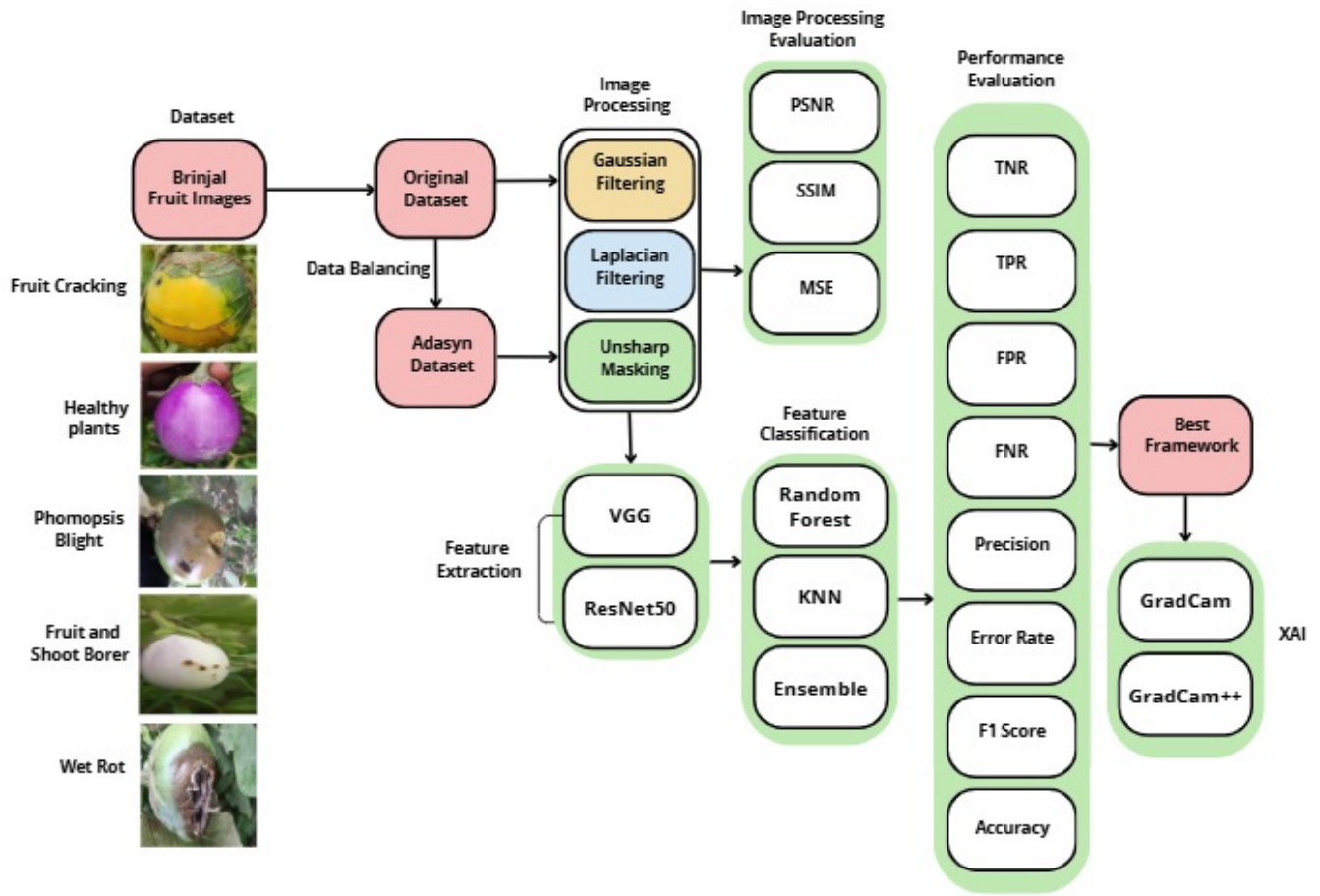


Figure 1. Overview of the proposed hybrid methodology for brinjal fruit disease detection, including data augmentation, preprocessing, feature extraction, classification, and explainability components



Figure 2. Representative examples from the BrinjalFruitX dataset illustrating the five disease classes: Shoot and Fruit Borer, Healthy, Wet Rot, Brinjal Fruit Cracking, and Phomopsis Blight

Masking for contrast enhancement. These methods collectively improve image quality, facilitating more reliable feature extraction and subsequent classification.

Gaussian Filter. The Gaussian filter is renowned for its efficacy in smoothing images while preserving structural integrity, making it ideal for preprocessing agricultural imagery affected by environmental noise. It applies a convolution kernel to attenuate high-frequency noise and correct illumination inconsistencies without overly blurring edges. In this study, the filter ensured that subtle disease symptoms remained

discernible, yielding more stable deep features. Mathematically, the Gaussian kernel is defined as:

$$G(x, y) = \frac{1}{2\pi\sigma^2} \exp\left(-\frac{x^2 + y^2}{2\sigma^2}\right). \quad (1)$$

In this study, the Gaussian filter was applied with a standard deviation of $\sigma = 1.0$, a commonly adopted value in agricultural image preprocessing that provides effective noise suppression while preserving structural integrity. This value was selected empirically based on visual quality assessment, validated through the PSNR and SSIM scores reported in Table 1.

Laplacian Filter. The Laplacian filter accentuates high-frequency components, such as edges and transitions, which are essential for delineating disease-induced irregularities in brinjal fruits. Computing the second-order derivative, it highlights areas of rapid intensity change, aiding in the detection of lesions and cracks. The Laplacian operator is expressed as:

$$\nabla^2 f(x, y) = \frac{\partial^2 f}{\partial x^2} + \frac{\partial^2 f}{\partial y^2}. \quad (2)$$

Consistent with its poor image-quality metrics (PSNR 6.194, SSIM 0.071, MSE 167.547; Table 1), Laplacian filtering degrades downstream classification performance across all configurations. Because the operator amplifies high-frequency noise alongside true edges, lesion boundaries become difficult to distinguish from background texture, and the loss of low-frequency structure removes the color and morphology cues that are especially important for diagnosing color-based symptoms such as Phomopsis Blight. A detailed breakdown of this effect on classification performance is provided in Section 4.

Unsharp Masking Filter. Unsharp Masking (USM) enhances perceived sharpness by subtracting a blurred version of the image from the original, amplifying contrast in mid-to-high frequency details. This technique proved particularly effective for revealing subtle texture variations indicative of diseases like Phomopsis Blight. Among the filters tested, USM offered the optimal trade-off between sharpness and artifact introduction. The formulation is given by:

$$I_{\text{sharp}} = I_{\text{orig}} + k \times (I_{\text{orig}} - I_{\text{blurred}}), \quad (3)$$

where k is the enhancement factor. The enhancement factor k was set to 1.5, a moderate value that amplifies mid-to-high frequency details without introducing excessive artifacts. This selection was guided by iterative visual inspection and confirmed by the highest PSNR (31.873) and SSIM (0.956) scores among all tested preprocessing methods, as reported in Table 1.

3.4. Deep Learning for Feature Extraction

Capturing the nuanced textural and structural variations in brinjal fruit images requires robust feature extraction. We leveraged pre-trained VGG and ResNet-50 architectures, fine-tuned on our dataset, to derive hierarchical representations. Transfer learning from ImageNet initialization expedites convergence and enriches feature quality, enabling the detection of disease-specific patterns from low-level edges to high-level semantics.

VGG. The VGG architecture, with its uniform stack of small 3×3 convolutional kernels, excels at extracting fine-grained features, ideal for discerning subtle brinjal disease manifestations. Progressive max-pooling layers downsample while retaining spatial hierarchies, allowing the model to learn increasingly abstract representations of fruit textures and anomalies.

ResNet-50. ResNet-50 addresses the vanishing gradient problem in deep networks via residual skip connections, facilitating the training of deeper models without degradation. These connections enable the network to learn residual functions, effectively capturing both local

details (e.g., surface cracks) and global contexts (e.g., overall fruit morphology) critical for accurate brinjal disease classification.

Both VGG and ResNet-50 architectures were initialized with ImageNet pre-trained weights and fine-tuned on the BrinjalFruitX dataset. The final fully connected layers were replaced to match the five-class output requirement. During fine-tuning, the convolutional base was partially frozen, retaining the first three blocks as fixed feature extractors while allowing the remaining layers to adapt to domain-specific disease patterns. Training was conducted using the Adam optimizer with a learning rate of 1×10^{-4} , a batch size of 32, and a maximum of 50 epochs with early stopping applied based on validation loss with a patience of 10 epochs. These hyperparameters were selected based on established practices in transfer learning for small agricultural datasets [6].

3.5. Machine Learning Models

Following deep feature extraction, we evaluated three classifiers: Random Forest (RF), K-Nearest Neighbors (KNN), and an Ensemble method. Each contributes uniquely to handling the high-dimensional feature space, balancing accuracy, interpretability, and computational efficiency.

Random Forest (RF). RF's ensemble of decision trees provides robustness against overfitting, making it suitable for the diverse, non-linear patterns in brinjal features. By aggregating predictions via majority voting, it yields stable classifications:

$$\hat{y} = \text{mode} \{h_1(\mathbf{x}), h_2(\mathbf{x}), \dots, h_T(\mathbf{x})\}, \quad (4)$$

where $h_t(\mathbf{x})$ denotes the prediction of the t -th decision tree.

K-Nearest Neighbors (KNN). KNN is a non-parametric, instance-based classifier that assigns the label occurring most frequently among the k nearest neighbors:

$$\hat{y} = \text{mode} \{y^{(1)}, y^{(2)}, \dots, y^{(k)}\}, \quad (5)$$

Ensemble Models. The ensemble combines the predictions of RF and KNN using majority voting:

$$\hat{y} = \text{mode} \{C_1(f(\mathbf{x})), C_2(f(\mathbf{x})), \dots, C_m(f(\mathbf{x}))\}, \quad (6)$$

where C_i are individual classifiers and $f(\mathbf{x})$ represents deep features. Majority voting was selected as the aggregation strategy due to its simplicity, robustness to individual classifier errors, and suitability for heterogeneous classifier combinations where confidence scores are not directly comparable across model types. Alternative strategies, such as weighted voting, where classifiers with higher individual accuracy contribute

more to the final decision, were considered but not implemented, as the relatively similar accuracy levels of RF and KNN on this dataset would yield marginal weighting differences. Furthermore, majority voting's interpretability aligns with the study's emphasis on transparency, as the decision rationale remains traceable to individual classifier outputs. Future work will explore weighted and probabilistic aggregation strategies to quantify potential performance gains.

3.6. Performance Evaluation

Model performance is evaluated using standard classification metrics, including Precision, Recall, F1-score, True Positive Rate (TPR), True Negative Rate (TNR), False Positive Rate (FPR), and False Negative Rate (FNR), computed as follows:

$$TPR = \frac{TP}{TP + FN}, \quad (7)$$

$$FPR = \frac{FP}{FP + TN}, \quad (8)$$

$$TNR = \frac{TN}{TN + FP}, \quad (9)$$

$$FNR = \frac{FN}{FN + TP}, \quad (10)$$

$$\text{Precision} = \frac{TP}{TP + FP}, \quad (11)$$

$$\text{Recall} = \frac{TP}{TP + FN}, \quad (12)$$

$$\text{F1-Score} = 2 \times \frac{\text{Precision} \times \text{Recall}}{\text{Precision} + \text{Recall}}, \quad (13)$$

$$\text{Accuracy} = \frac{TP + TN}{TP + TN + FP + FN}. \quad (14)$$

Accuracy is reported at the model level, reflecting overall classification correctness across all classes. Per-class performance is assessed using class-specific TPR, Precision, and F1-score to provide granular insight into disease recognition capability under class-imbalance conditions. Image enhancement quality is evaluated using PSNR, SSIM, and MSE solely as perceptual fidelity indicators; these metrics are not interpreted as direct predictors of classification performance, but rather as a means of comparing preprocessing effects on image quality prior to feature extraction.

3.7. Explainable AI (XAI)

To enhance transparency and qualitative interpretability, we employ Gradient-weighted Class Activation Mapping (Grad-CAM) and Grad-CAM++ on the CNN feature extractors. These methods generate class-discriminative localization maps by computing gradients of the predicted class scores with respect to the final convolutional feature maps. Importantly, Grad-CAM and Grad-CAM++ are applied only to the CNN

backbones and do not explain the decisions of the downstream RF or KNN classifiers, which are non-differentiable; instead, the generated heatmaps visualize salient image regions that most strongly activate disease-relevant deep features, providing insight into whether the CNN representations focus on pathological structures rather than background artifacts. Grad-CAM++ further improves localization by incorporating higher-order gradient information, making it particularly effective for subtle or spatially distributed disease symptoms. These visual explanations serve as qualitative validation of the learned representations and support interpretability for agricultural experts and other stakeholders.

4. Results

Classification performance is governed jointly by preprocessing choice, feature-extractor architecture, and classifier strategy. A comparative analysis of three image preprocessing techniques, Gaussian (G), Laplacian (L), and Unsharp (U) filtering, was performed to enhance brinjal fruit images prior to disease recognition. Each preprocessing technique was paired with two deep CNN feature extractors, ResNet (R) and VGG (V), and the resulting features were classified using three machine learning models: Ensemble (E), K-Nearest Neighbors (K), and Random Forest (R). Configurations are labeled by this three-letter code (e.g., GRE = Gaussian-ResNet-Ensemble) and evaluated on both the original and ADASYN-balanced datasets.

Unsharp masking consistently yields the highest-quality features and the strongest downstream classification accuracy; Gaussian filtering provides stable but comparatively moderate improvements; Laplacian filtering, despite sharpening edges, degrades global image structure and reduces sensitivity for minority disease classes. Across all configurations, Ensemble and Random Forest classifiers outperform KNN, particularly under ADASYN balancing, while Healthy Brinjal and Wet Rot are the most reliably detected classes and Brinjal Fruit Cracking and Phomopsis Blight remain the most difficult, exhibiting low recall despite high specificity, a pattern consistent with conservative decision boundaries on visually subtle, sparsely represented diseases.

Table 1. Evaluation of Image Enhancement Methods

Method	PSNR	SSIM	MSE
Unsharp	31.873	0.956	43.846
Gaussian	27.333	0.848	125.817
Laplacian	6.194	0.071	167.547

As shown in Table 1, Unsharp masking achieves the best overall image quality (PSNR 31.873, SSIM 0.956, MSE 43.846), effectively enhancing edge detail and diseased regions without introducing excessive noise. Gaussian filtering performs moderately (PSNR 27.333, SSIM 0.848), while Laplacian filtering severely degrades quality (PSNR 6.194, SSIM 0.071). This degradation directly explains Laplacian's downstream classification underperformance: because the Laplacian operator computes second-order derivatives, it amplifies high-frequency noise alongside true edges. In field-captured brinjal images this over-enhances lesion boundaries until they become indistinguishable from background texture (leaf veins, soil artifacts), while simultaneously suppressing the low-frequency global structure that encodes fruit morphology and color, information classifiers rely on to separate disease classes. The effect is most damaging for Phomopsis Blight, whose primary diagnostic signal is color gradient rather than sharp edges, consistent with the near-zero TPR (0.000) observed for the LRR and LVR configurations (Table 4).

4.1. Gaussian Filtering

On the original dataset (Table 2), GRE achieves the highest accuracy (0.718), with strong detection of Healthy Brinjal (TPR 0.881) and Wet Rot (TPR 0.904) but relatively weak recall for Phomopsis Blight (TPR 0.638) and Brinjal Fruit Cracking (TPR 0.712). These weaker classes are offset by high specificity (TNR >0.92). ROC analysis (Fig. 3) confirms this pattern: Healthy Brinjal and Wet Rot reach AUC 0.90–0.97, while Brinjal Fruit Cracking and Phomopsis Blight remain the most challenging. Ensemble and Random Forest-based classifiers (GRE, GRR, GVR) generally outperform KNN variants, with GRE and GRR showing the most stable performance across classes.

ADASYN balancing (Table 3) improves recall on minority classes; Brinjal Fruit Cracking TPR increases to 0.825 (GVK) and Phomopsis Blight reaches 0.781 (GRK). However, this comes at the cost of lower precision (as low as 0.380–0.462 for these classes), indicating a clear recall–precision trade-off. Wet Rot remains highly stable (TPR up to 0.911 with GRE). GRE and GRK provide the best overall balanced results on the balanced dataset, while GVR shows comparatively lower sensitivity due to elevated false-negative rates on some classes. ROC analysis (Fig. 4) again highlights Healthy Brinjal and Wet Rot as the strongest performers (AUC 0.90–0.97). Ensemble and Random Forest classifiers continue to outperform KNN variants in most scenarios.

4.2. Laplacian Filtering

Consistent with its poor image-quality metrics, Laplacian filtering yields the weakest classification results across all configurations (Table 4). On the original dataset, accuracy ranges only 0.553–0.644, and Phomopsis Blight recall collapses to 0.000 for LRR and LVR; the model fails to detect this class entirely under those settings. Healthy Brinjal (TPR 0.699–0.845) and Shoot and Fruit Borer (TPR 0.655–0.821) remain moderately detectable, but ROC AUCs for Brinjal Fruit Cracking and Phomopsis Blight fall to 0.60–0.75 (Fig. 5), confirming the class-specific breakdown described above rather than a general loss of discriminative power.

4.3. Cross-Configuration Summary

Three trends hold across the full experimental grid. First, preprocessing quality determines the classification ceiling: Unsharp masking outperforms Gaussian by roughly 6–8 percentage points in accuracy and Laplacian by up to 20 points, directly tracking the PSNR/SSIM gap in Table 1. Second, ResNet consistently outperforms VGG as a feature extractor across all preprocessing conditions, consistent with its residual connections supporting more discriminative hierarchical features from a limited, field-acquired dataset. Third, Random Forest and Ensemble classifiers consistently outperform KNN, especially after ADASYN balancing, where KNN's sensitivity to synthetic nearest neighbors in high-dimensional feature space reduces reliability. The best overall configuration is URR on the ADASYN dataset (accuracy 0.800, F1 0.870 for Wet Rot; see Table 7), combining high sensitivity for major classes (TPR 0.821–0.893) with moderate but improved minority-class detection (TPR 0.531–0.600) and strong specificity (TNR >0.85).

Brinjal Fruit Cracking and Phomopsis Blight remain the persistent weak points across every configuration, and this is not merely a data-volume artifact. Two class-specific factors compound the imbalance problem. First, both diseases present with diffuse, low-contrast visual symptoms, color and texture shifts rather than sharp lesion boundaries, so they benefit least from edge-oriented enhancement and are the classes most degraded by Laplacian filtering specifically. Second, ADASYN generates synthetic minority-class samples by interpolating in feature space between existing neighbors; when the true minority-class manifold is itself visually diffuse and overlaps with majority-class appearance (as with early-stage Phomopsis Blight resembling healthy discoloration), the synthetic samples inherit that ambiguity rather than resolving it, which explains why recall gains from ADASYN are consistently accompanied by precision

4.4. Unsharp Filtering

Unsharp masking produces the best results overall (Table 6), with URE reaching 0.795 accuracy on the original dataset and strong recall for Healthy Brinjal (TPR 0.893) and Wet Rot (TPR 0.800). Phomopsis Blight remains the weakest class (TPR 0.281–0.531) but still outperforms its Gaussian and Laplacian counterparts. ROC AUCs for Healthy Brinjal and Wet Rot reach

0.94–0.99 (Fig. 7), and Ensemble/RF classifiers again outperform KNN, with VGG-RF the strongest overall. ADASYN balancing on the Unsharp-filtered data delivers the study's best overall results: URR reaches 0.800 accuracy (Table 7), with Phomopsis Blight recall rising to 0.531–0.781 (URE, UVE) across the Unsharp-ADASYN configurations, a substantial improvement over both Gaussian- and Laplacian-based ADASYN runs. Brinjal Fruit Cracking recall similarly improves to 0.500–0.750. ROC AUCs remain high for Healthy Brinjal and Wet Rot (0.94–0.99, Fig. 8), with VGG-RF and the Ensemble/RF family again outperforming KNN.

4.5. Explainability of the Model Using XAI Methods

Figure 9 presents Grad-CAM and Grad-CAM++ visualizations for the URR model. Across all disease classes, the highlighted regions consistently align with the true pathological areas of the brinjal fruit rather than background artifacts, indicating that the model's predictions are driven by clinically meaningful features. This supports the framework's suitability for real-field brinjal disease diagnosis, though the persistent recall gap for Brinjal Fruit Cracking and Phomopsis Blight (Section 4.5) indicates that interpretability alone does not resolve the underlying minority-class detection limitation.

5. Discussion

The results in Section 4 allow the design choices motivated in Section 2 to be evaluated directly. The three limitations identified in the literature, reliance on controlled, non-field datasets; underaddressed class imbalance; and a general accuracy-interpretability trade-off in end-to-end deep learning, map onto the three components of the proposed framework, and each shows a measurable effect: preprocessing choice sets the achievable accuracy ceiling (Unsharp outperforming Gaussian by roughly 6–8 points and Laplacian by up to 20), ADASYN raises minority-class recall at a consistent cost to precision rather than resolving the imbalance outright, and Grad-CAM/Grad-CAM++ confirm that the URR model's predictions are grounded in pathologically relevant regions rather than background artifacts. Taken together, these results support the framework as

a viable middle ground between accuracy and interpretability, rather than a strict improvement over either objective in isolation.

On novelty, this study's contribution is best understood as the integration of preprocessing, deep feature extraction, imbalance correction, and explainability into a single pipeline validated on a real field-acquired brinjal dataset, rather than any single novel algorithmic component. Individually, hybrid CNN-plus-classical-classifier designs, ADASYN-based balancing, and Grad-CAM interpretability have each been explored elsewhere (Section 2); no prior brinjal-specific study combines all three under field conditions. A direct, quantitative comparison against re-implemented state-of-the-art end-to-end CNN classifiers on BrinjalFruitX was not performed in this work, since no such baselines currently exist on this dataset; we consider this an important next step and discuss it further in Section 6 rather than presenting an indirect comparison against numbers reported under different datasets and evaluation protocols, which would not be a fair basis for a performance claim.

The persistent recall gap for Brinjal Fruit Cracking and Phomopsis Blight (Section 4) also carries a broader theoretical implication beyond the immediate dataset: ADASYN and similar interpolation-based oversampling methods assume that the minority class occupies a separable region of feature space, an assumption that breaks down when a minority class's visual presentation is intrinsically diffuse and overlaps the majority class, as with early-stage Phomopsis Blight. This suggests that further gains for these classes are more likely to come from cost-sensitive learning, few-shot or metric-learning approaches, or additional targeted data collection than from further resampling of the existing feature space.

Two practical deployment considerations, raised but not analyzed in Section 4, deserve explicit discussion. First, on inference speed: the decoupled architecture separates a comparatively expensive CNN forward pass (VGG or ResNet-50) from a lightweight downstream classifier (RF, KNN, or their ensemble); on resource-constrained edge devices, the CNN forward pass is the dominant cost, and feature caching or model quantization would be necessary to support real-time or near-real-time field use, neither of which was benchmarked in this study. Second, on seasonal environmental interference: BrinjalFruitX was collected within a bounded data collection period, and seasonal variation in ambient lighting, humidity, and plant growth stage can shift the input image distribution in ways not represented in the current dataset; because Unsharp masking and Gaussian filtering are tuned to the noise and illumination characteristics of the images they were validated on, their effectiveness under substantially different seasonal conditions (e.g.,

Table 2. Performance of Brinjal Fruit Disease Classification Models Using Gaussian Filtering with Original Dataset

Model	Class	TPR	FPR	FNR	TNR	Error Rate	Precision	Accuracy	F1
GRE	Brinjal Fruit Cracking	0.712	0.072	0.288	0.928	0.095	0.552	0.718	0.622
	Healthy Brinjal	0.881	0.112	0.119	0.888	0.115	0.751	0.718	0.811
	Phomopsis Blight	0.638	0.079	0.362	0.921	0.105	0.429	0.718	0.513
	Shoot and Fruit Borer	0.592	0.071	0.408	0.929	0.208	0.819	0.718	0.687
	Wet Rot	0.904	0.015	0.096	0.985	0.026	0.898	0.718	0.901
GRK	Brinjal Fruit Cracking	0.661	0.129	0.339	0.871	0.149	0.395	0.655	0.495
	Healthy Brinjal	0.821	0.098	0.179	0.902	0.118	0.769	0.655	0.794
	Phomopsis Blight	0.765	0.105	0.235	0.895	0.117	0.418	0.655	0.541
	Shoot and Fruit Borer	0.512	0.046	0.488	0.954	0.222	0.851	0.655	0.639
	Wet Rot	0.742	0.031	0.258	0.969	0.061	0.776	0.655	0.758
GRR	Brinjal Fruit Cracking	0.415	0.028	0.585	0.972	0.088	0.628	0.748	0.499
	Healthy Brinjal	0.832	0.095	0.168	0.905	0.112	0.776	0.748	0.803
	Phomopsis Blight	0.608	0.021	0.392	0.979	0.053	0.719	0.748	0.659
	Shoot and Fruit Borer	0.781	0.148	0.219	0.852	0.168	0.758	0.748	0.769
	Wet Rot	0.874	0.046	0.126	0.954	0.054	0.739	0.748	0.801
GVE	Brinjal Fruit Cracking	0.685	0.105	0.315	0.895	0.125	0.451	0.711	0.544
	Healthy Brinjal	0.805	0.068	0.195	0.932	0.102	0.825	0.711	0.815
	Phomopsis Blight	0.641	0.069	0.359	0.931	0.095	0.458	0.711	0.535
	Shoot and Fruit Borer	0.668	0.075	0.332	0.925	0.179	0.829	0.711	0.740
	Wet Rot	0.809	0.022	0.191	0.978	0.042	0.845	0.711	0.826
GVK	Brinjal Fruit Cracking	0.809	0.131	0.191	0.869	0.135	0.438	0.671	0.569
	Healthy Brinjal	0.812	0.105	0.188	0.895	0.127	0.749	0.671	0.779
	Phomopsis Blight	0.578	0.058	0.422	0.942	0.091	0.475	0.671	0.521
	Shoot and Fruit Borer	0.558	0.059	0.442	0.941	0.211	0.835	0.671	0.670
	Wet Rot	0.741	0.035	0.259	0.965	0.063	0.758	0.671	0.749
GVR	Brinjal Fruit Cracking	0.392	0.027	0.608	0.973	0.091	0.615	0.739	0.478
	Healthy Brinjal	0.859	0.089	0.141	0.911	0.102	0.789	0.739	0.822
	Phomopsis Blight	0.422	0.029	0.578	0.971	0.076	0.558	0.739	0.480
	Shoot and Fruit Borer	0.805	0.138	0.195	0.862	0.152	0.775	0.739	0.790
	Wet Rot	0.809	0.055	0.191	0.945	0.072	0.682	0.739	0.740

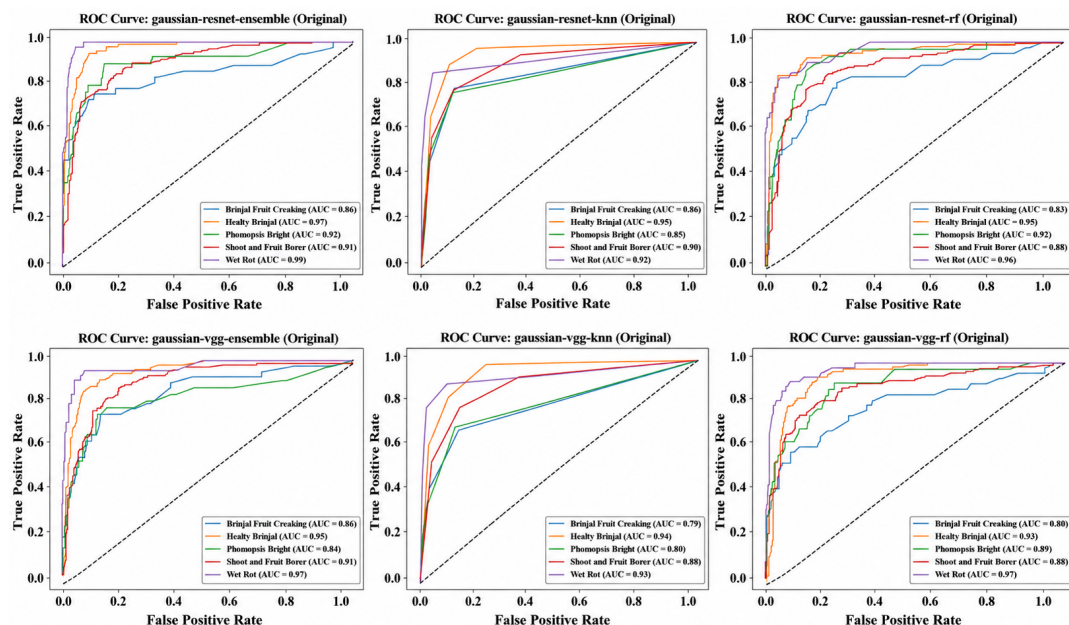
**Figure 3.** ROC Curves of Machine Learning Models Under Different Sampling and Preprocessing Techniques: (a) Gaussian–ResNet ensemble (ADASYN), (b) Gaussian–ResNet kNN (ADASYN), (c) Gaussian–ResNet Random Forest (ADASYN), (d) Gaussian–VGG ensemble (ADASYN), (e) Gaussian–VGG kNN (ADASYN), (f) Gaussian–VGG Random Forest (ADASYN)

Table 3. Performance of Brinjal Fruit Disease Classification Models Using Gaussian Filtering with ADASYN Dataset

Model	Class	TPR	FPR	FNR	TNR	Error Rate	Precision	Accuracy	F1
GRE	Brinjal Fruit Cracking	0.725	0.068	0.275	0.932	0.090	0.569	0.729	0.637
	Healthy Brinjal	0.893	0.107	0.107	0.893	0.107	0.767	0.729	0.825
	Phomopsis Blight	0.625	0.084	0.375	0.916	0.110	0.417	0.729	0.500
	Shoot and Fruit Borer	0.579	0.077	0.421	0.923	0.214	0.832	0.729	0.683
	Wet Rot	0.911	0.012	0.089	0.988	0.022	0.911	0.729	0.911
GRK	Brinjal Fruit Cracking	0.675	0.135	0.325	0.865	0.156	0.380	0.668	0.486
	Healthy Brinjal	0.835	0.092	0.165	0.908	0.112	0.782	0.668	0.808
	Phomopsis Blight	0.781	0.099	0.219	0.901	0.110	0.431	0.668	0.556
	Shoot and Fruit Borer	0.497	0.050	0.503	0.950	0.230	0.867	0.668	0.632
	Wet Rot	0.756	0.028	0.244	0.972	0.055	0.791	0.668	0.773
GRR	Brinjal Fruit Cracking	0.400	0.031	0.600	0.969	0.093	0.615	0.759	0.485
	Healthy Brinjal	0.845	0.088	0.155	0.912	0.107	0.791	0.759	0.817
	Phomopsis Blight	0.594	0.024	0.406	0.976	0.058	0.704	0.759	0.644
	Shoot and Fruit Borer	0.793	0.155	0.207	0.845	0.175	0.772	0.759	0.782
	Wet Rot	0.889	0.041	0.111	0.959	0.049	0.755	0.759	0.816
GVE	Brinjal Fruit Cracking	0.700	0.111	0.300	0.889	0.132	0.438	0.723	0.538
	Healthy Brinjal	0.816	0.061	0.184	0.939	0.096	0.840	0.723	0.828
	Phomopsis Blight	0.625	0.075	0.375	0.925	0.101	0.444	0.723	0.519
	Shoot and Fruit Borer	0.655	0.082	0.345	0.918	0.186	0.841	0.723	0.736
	Wet Rot	0.822	0.019	0.178	0.981	0.038	0.860	0.723	0.841
GVK	Brinjal Fruit Cracking	0.825	0.138	0.175	0.862	0.142	0.423	0.682	0.559
	Healthy Brinjal	0.825	0.099	0.175	0.901	0.121	0.766	0.682	0.794
	Phomopsis Blight	0.562	0.063	0.438	0.937	0.096	0.462	0.682	0.507
	Shoot and Fruit Borer	0.545	0.064	0.455	0.936	0.219	0.849	0.682	0.664
	Wet Rot	0.756	0.031	0.244	0.969	0.058	0.773	0.682	0.764
GVR	Brinjal Fruit Cracking	0.375	0.031	0.625	0.969	0.096	0.600	0.751	0.462
	Healthy Brinjal	0.874	0.084	0.126	0.916	0.096	0.804	0.751	0.837
	Phomopsis Blight	0.406	0.033	0.594	0.967	0.082	0.542	0.751	0.464
	Shoot and Fruit Borer	0.821	0.145	0.179	0.855	0.159	0.788	0.751	0.804
	Wet Rot	0.822	0.050	0.178	0.950	0.066	0.698	0.751	0.755

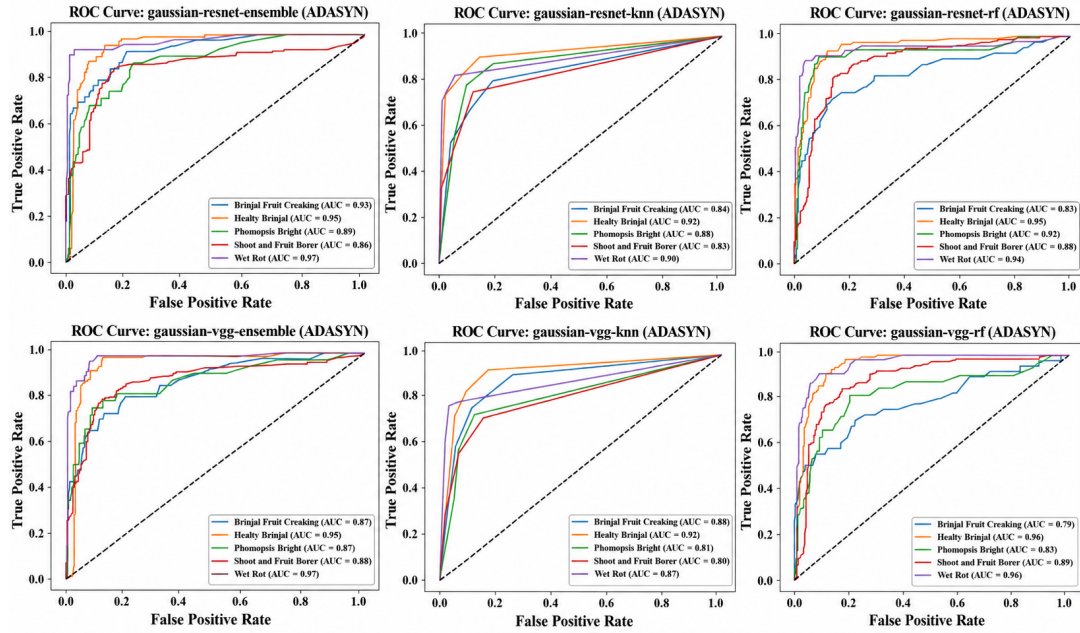

Figure 4. ROC Curves of Machine Learning Models Under Different Sampling and Preprocessing Techniques: (a) Gaussian–ResNet ensemble (ADASYN), (b) Gaussian–ResNet kNN (ADASYN), (c) Gaussian–ResNet Random Forest (ADASYN), (d) Gaussian–VGG ensemble (ADASYN), (e) Gaussian–VGG kNN (ADASYN), (f) Gaussian–VGG Random Forest (ADASYN)

Table 4. Performance of Brinjal Fruit Disease Classification Models Using Laplacian Filtering with Original Dataset

Model	Class	TPR	FPR	FNR	TNR	Error Rate	Precision	Accuracy	F1
LRE	Brinjal Fruit Cracking	0.100	0.034	0.900	0.966	0.129	0.267	0.603	0.145
	Healthy Brinjal	0.786	0.176	0.214	0.824	0.186	0.638	0.603	0.704
	Phomopsis Blight	0.125	0.024	0.875	0.976	0.099	0.333	0.603	0.182
	Shoot and Fruit Borer	0.766	0.345	0.234	0.655	0.301	0.594	0.603	0.669
	Wet Rot	0.444	0.012	0.556	0.988	0.079	0.833	0.603	0.580
LRK	Brinjal Fruit Cracking	0.250	0.089	0.750	0.911	0.162	0.256	0.644	0.253
	Healthy Brinjal	0.786	0.153	0.214	0.847	0.170	0.669	0.644	0.723
	Phomopsis Blight	0.250	0.036	0.750	0.964	0.099	0.400	0.644	0.308
	Shoot and Fruit Borer	0.779	0.205	0.221	0.795	0.211	0.715	0.644	0.746
	Wet Rot	0.511	0.012	0.489	0.988	0.071	0.852	0.644	0.639
LRR	Brinjal Fruit Cracking	0.025	0.003	0.975	0.997	0.110	0.500	0.608	0.048
	Healthy Brinjal	0.845	0.279	0.155	0.721	0.244	0.544	0.608	0.662
	Phomopsis Blight	0.000	0.000	1.000	1.000	0.088	0.000	0.608	0.000
	Shoot and Fruit Borer	0.786	0.295	0.214	0.705	0.263	0.637	0.608	0.704
	Wet Rot	0.444	0.012	0.556	0.988	0.079	0.833	0.608	0.580
LVE	Brinjal Fruit Cracking	0.225	0.034	0.775	0.966	0.115	0.450	0.573	0.300
	Healthy Brinjal	0.699	0.206	0.301	0.794	0.233	0.571	0.573	0.629
	Phomopsis Blight	0.156	0.030	0.844	0.970	0.101	0.333	0.573	0.213
	Shoot and Fruit Borer	0.738	0.336	0.262	0.664	0.307	0.591	0.573	0.656
	Wet Rot	0.356	0.022	0.644	0.978	0.099	0.696	0.573	0.471
LVK	Brinjal Fruit Cracking	0.250	0.123	0.750	0.877	0.192	0.200	0.553	0.222
	Healthy Brinjal	0.718	0.179	0.282	0.821	0.208	0.612	0.553	0.661
	Phomopsis Blight	0.188	0.054	0.812	0.946	0.121	0.250	0.553	0.214
	Shoot and Fruit Borer	0.655	0.236	0.345	0.764	0.279	0.646	0.553	0.651
	Wet Rot	0.378	0.019	0.622	0.981	0.093	0.739	0.553	0.500
LVR	Brinjal Fruit Cracking	0.025	0.000	0.975	1.000	0.107	1.000	0.573	0.049
	Healthy Brinjal	0.796	0.244	0.204	0.756	0.233	0.562	0.573	0.659
	Phomopsis Blight	0.000	0.006	1.000	0.994	0.093	0.000	0.573	0.000
	Shoot and Fruit Borer	0.821	0.409	0.179	0.591	0.318	0.569	0.573	0.672
	Wet Rot	0.156	0.000	0.844	1.000	0.104	1.000	0.573	0.269

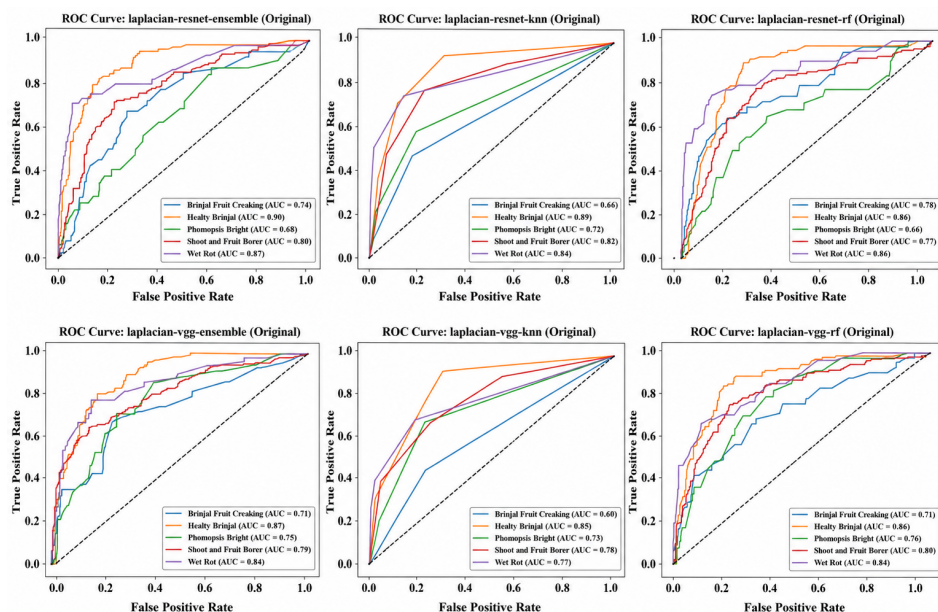
**Figure 5.** ROC Curves of Machine Learning Models Under Different Sampling and Preprocessing Techniques: (a) Laplacian–ResNet ensemble, (b) Laplacian–ResNet KNN, (c) Laplacian–ResNet Random Forest, (d) Laplacian–VGG ensemble, (e) Laplacian–VGG KNN, (f) Laplacian–VGG Random Forest

Table 5. Performance of Brinjal Fruit Disease Classification Models Using Laplacian Filtering with ADASYN Dataset

Model	Class	TPR	FPR	FNR	TNR	Error Rate	Precision	Accuracy	F1
LRE	Brinjal Fruit Cracking	0.475	0.126	0.525	0.874	0.170	0.317	0.559	0.380
	Healthy Brinjal	0.699	0.099	0.301	0.901	0.156	0.735	0.559	0.716
	Phomopsis Blight	0.438	0.147	0.562	0.853	0.184	0.222	0.559	0.295
	Shoot and Fruit Borer	0.428	0.091	0.572	0.909	0.282	0.756	0.559	0.546
	Wet Rot	0.822	0.078	0.178	0.922	0.090	0.597	0.559	0.692
LRK	Brinjal Fruit Cracking	0.475	0.154	0.525	0.846	0.195	0.275	0.493	0.349
	Healthy Brinjal	0.631	0.084	0.369	0.916	0.164	0.747	0.493	0.684
	Phomopsis Blight	0.469	0.174	0.531	0.826	0.205	0.205	0.493	0.286
	Shoot and Fruit Borer	0.345	0.036	0.655	0.964	0.282	0.862	0.493	0.493
	Wet Rot	0.689	0.147	0.311	0.853	0.167	0.397	0.493	0.504
LRR	Brinjal Fruit Cracking	0.350	0.037	0.650	0.963	0.104	0.538	0.633	0.424
	Healthy Brinjal	0.854	0.183	0.146	0.817	0.173	0.647	0.633	0.736
	Phomopsis Blight	0.031	0.036	0.969	0.964	0.118	0.077	0.633	0.044
	Shoot and Fruit Borer	0.724	0.227	0.276	0.773	0.247	0.677	0.633	0.700
	Wet Rot	0.511	0.038	0.489	0.962	0.093	0.657	0.633	0.575
LVE	Brinjal Fruit Cracking	0.350	0.172	0.650	0.828	0.225	0.200	0.493	0.255
	Healthy Brinjal	0.612	0.122	0.388	0.878	0.197	0.663	0.493	0.636
	Phomopsis Blight	0.594	0.117	0.406	0.883	0.142	0.328	0.493	0.422
	Shoot and Fruit Borer	0.386	0.127	0.614	0.873	0.321	0.667	0.493	0.489
	Wet Rot	0.622	0.094	0.378	0.906	0.129	0.483	0.493	0.544
LVK	Brinjal Fruit Cracking	0.550	0.262	0.450	0.738	0.282	0.206	0.455	0.299
	Healthy Brinjal	0.602	0.111	0.398	0.889	0.192	0.681	0.455	0.639
	Phomopsis Blight	0.469	0.138	0.531	0.862	0.173	0.246	0.455	0.323
	Shoot and Fruit Borer	0.276	0.027	0.724	0.973	0.304	0.870	0.455	0.419
	Wet Rot	0.600	0.103	0.400	0.897	0.140	0.450	0.455	0.514
LVR	Brinjal Fruit Cracking	0.175	0.037	0.825	0.963	0.123	0.368	0.595	0.237
	Healthy Brinjal	0.854	0.286	0.146	0.714	0.247	0.540	0.595	0.662
	Phomopsis Blight	0.031	0.027	0.969	0.973	0.110	0.100	0.595	0.048
	Shoot and Fruit Borer	0.690	0.214	0.310	0.786	0.252	0.680	0.595	0.685
	Wet Rot	0.467	0.016	0.533	0.984	0.079	0.808	0.595	0.592

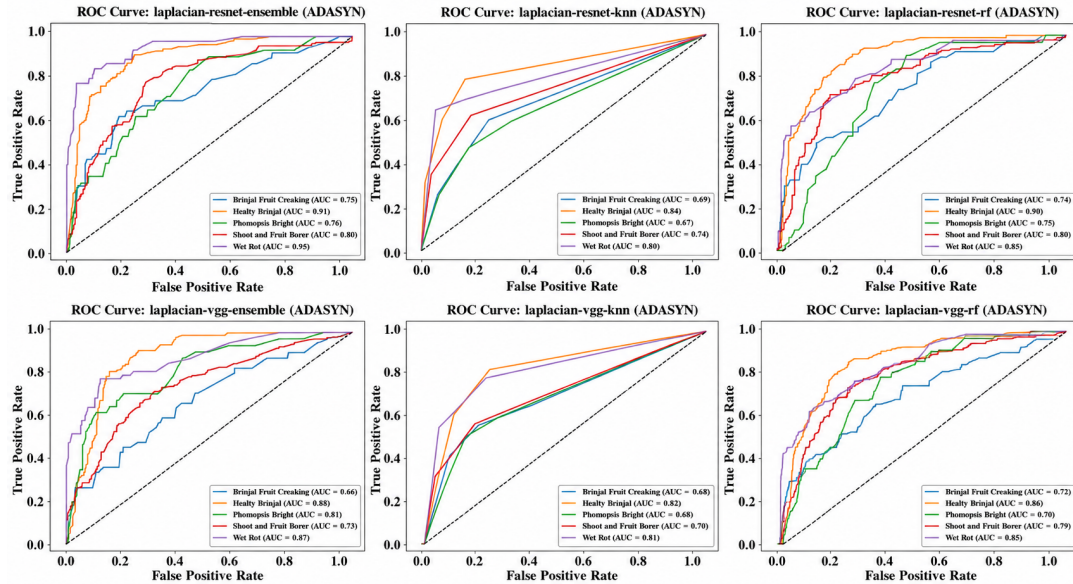

Figure 6. ROC Curves of Machine Learning Models Under Different Sampling and Preprocessing Techniques: (a) Laplacian–ResNet ensemble (ADASYN), (b) Laplacian–ResNet kNN (ADASYN), (c) Laplacian–ResNet Random Forest (ADASYN), (d) Laplacian–VGG ensemble (ADASYN), (e) Laplacian–VGG kNN (ADASYN), (f) Laplacian–VGG Random Forest (ADASYN)

Table 6. Performance of Brinjal Fruit Disease Classification Models Using Unsharp Filtering with Original Dataset

Model	Class	TPR	FPR	FNR	TNR	Error Rate	Precision	Accuracy	F1
URE	Brinjal Fruit Cracking	0.550	0.028	0.450	0.972	0.074	0.710	0.795	0.620
	Healthy Brinjal	0.893	0.095	0.107	0.905	0.099	0.786	0.795	0.836
	Phomopsis Blight	0.406	0.018	0.594	0.982	0.068	0.684	0.795	0.510
	Shoot and Fruit Borer	0.876	0.141	0.124	0.859	0.134	0.804	0.795	0.838
	Wet Rot	0.800	0.012	0.200	0.988	0.036	0.900	0.795	0.847
URK	Brinjal Fruit Cracking	0.500	0.065	0.500	0.935	0.112	0.488	0.764	0.494
	Healthy Brinjal	0.893	0.076	0.107	0.924	0.085	0.821	0.764	0.856
	Phomopsis Blight	0.406	0.024	0.594	0.976	0.074	0.619	0.764	0.491
	Shoot and Fruit Borer	0.828	0.127	0.172	0.873	0.145	0.811	0.764	0.819
	Wet Rot	0.756	0.028	0.244	0.972	0.055	0.791	0.764	0.773
URR	Brinjal Fruit Cracking	0.425	0.006	0.575	0.994	0.068	0.895	0.773	0.576
	Healthy Brinjal	0.922	0.095	0.078	0.905	0.090	0.792	0.773	0.852
	Phomopsis Blight	0.281	0.006	0.719	0.994	0.068	0.818	0.773	0.419
	Shoot and Fruit Borer	0.869	0.209	0.131	0.791	0.178	0.733	0.773	0.795
	Wet Rot	0.778	0.025	0.222	0.975	0.049	0.814	0.773	0.795
UVE	Brinjal Fruit Cracking	0.450	0.025	0.550	0.975	0.082	0.692	0.753	0.545
	Healthy Brinjal	0.874	0.095	0.126	0.905	0.104	0.783	0.753	0.826
	Phomopsis Blight	0.531	0.036	0.469	0.964	0.074	0.586	0.753	0.557
	Shoot and Fruit Borer	0.814	0.182	0.186	0.818	0.184	0.747	0.753	0.779
	Wet Rot	0.711	0.016	0.289	0.984	0.049	0.865	0.753	0.780
UVK	Brinjal Fruit Cracking	0.425	0.062	0.575	0.938	0.118	0.459	0.726	0.442
	Healthy Brinjal	0.864	0.073	0.136	0.927	0.090	0.824	0.726	0.844
	Phomopsis Blight	0.406	0.045	0.594	0.955	0.093	0.464	0.726	0.433
	Shoot and Fruit Borer	0.745	0.159	0.255	0.841	0.197	0.755	0.726	0.750
	Wet Rot	0.844	0.034	0.156	0.966	0.049	0.776	0.726	0.809
UVR	Brinjal Fruit Cracking	0.325	0.018	0.675	0.982	0.090	0.684	0.764	0.441
	Healthy Brinjal	0.932	0.099	0.068	0.901	0.090	0.787	0.764	0.853
	Phomopsis Blight	0.281	0.021	0.719	0.979	0.082	0.562	0.764	0.375
	Shoot and Fruit Borer	0.869	0.186	0.131	0.814	0.164	0.754	0.764	0.808
	Wet Rot	0.778	0.019	0.222	0.981	0.044	0.854	0.764	0.814

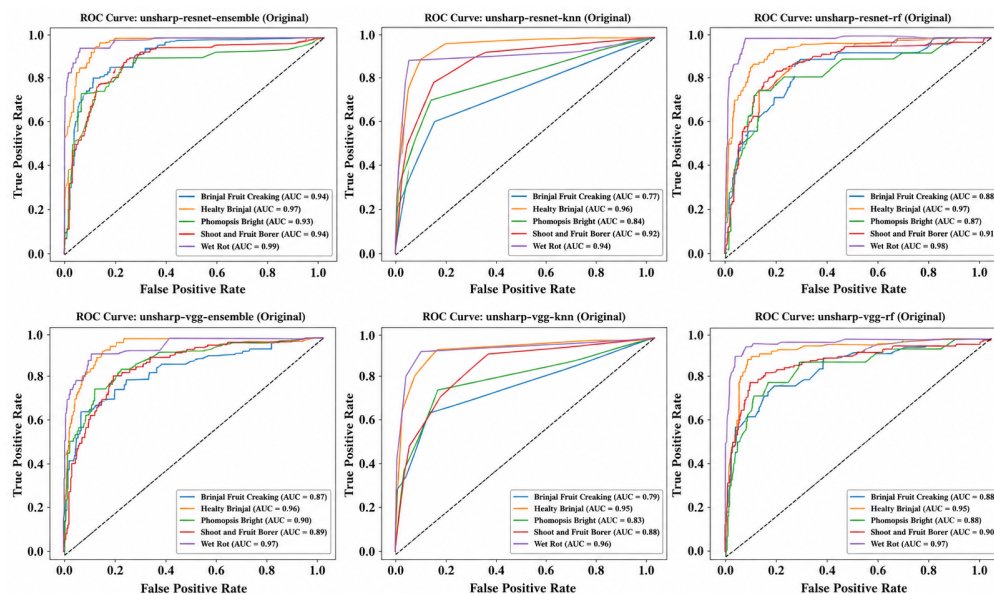
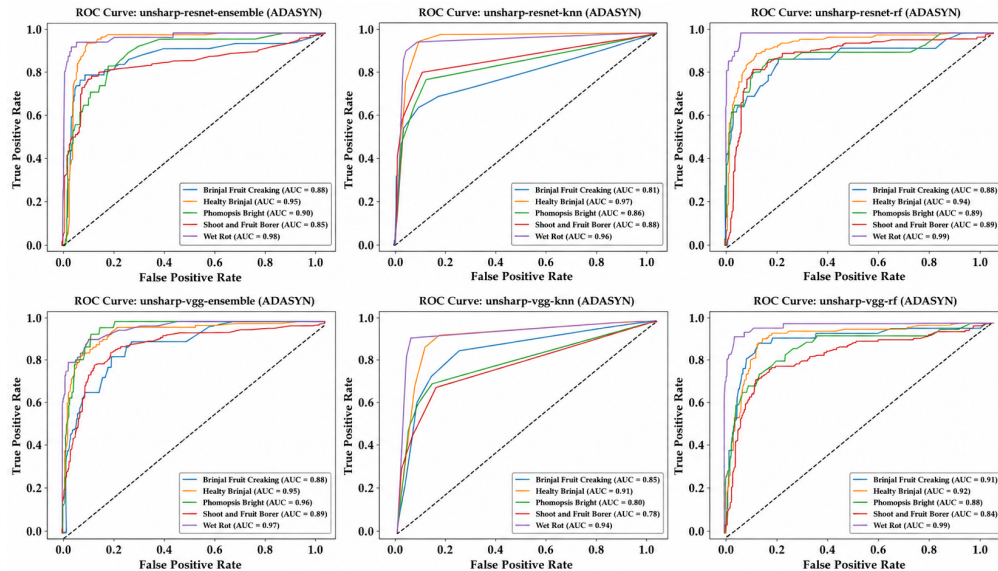
**Figure 7.** ROC Curves of Machine Learning Models Under Different Sampling and Preprocessing Techniques: (a) Unsharp-Resnet ensemble, (b) Unsharp-Resnet kNN, (c) Unsharp-Resnet Random Forest, (d) Unsharp-VGG ensemble, (e) Unsharp-VGG kNN, (f) Unsharp-VGG Random Forest

Table 7. Performance of Brinjal Fruit Disease Classification Models Using Unsharp Filtering with ADASYN Dataset

Model	Class	TPR	FPR	FNR	TNR	Error Rate	Precision	Accuracy	F1
URE	Brinjal Fruit Cracking	0.750	0.055	0.250	0.945	0.077	0.625	0.751	0.682
	Healthy Brinjal	0.893	0.084	0.107	0.916	0.090	0.807	0.751	0.848
	Phomopsis Blight	0.625	0.081	0.375	0.919	0.107	0.426	0.751	0.506
	Shoot and Fruit Borer	0.634	0.068	0.366	0.932	0.186	0.860	0.751	0.730
	Wet Rot	0.889	0.028	0.111	0.972	0.038	0.816	0.751	0.851
URK	Brinjal Fruit Cracking	0.675	0.092	0.325	0.908	0.118	0.474	0.753	0.557
	Healthy Brinjal	0.971	0.084	0.029	0.916	0.068	0.820	0.753	0.889
	Phomopsis Blight	0.656	0.066	0.344	0.934	0.090	0.488	0.753	0.560
	Shoot and Fruit Borer	0.593	0.023	0.407	0.977	0.175	0.945	0.753	0.729
	Wet Rot	0.911	0.034	0.089	0.966	0.040	0.788	0.753	0.845
URR	Brinjal Fruit Cracking	0.600	0.028	0.400	0.972	0.068	0.727	0.800	0.658
	Healthy Brinjal	0.893	0.099	0.107	0.901	0.101	0.780	0.800	0.833
	Phomopsis Blight	0.531	0.015	0.469	0.985	0.055	0.773	0.800	0.630
	Shoot and Fruit Borer	0.821	0.118	0.179	0.882	0.142	0.821	0.800	0.821
	Wet Rot	0.889	0.022	0.111	0.978	0.033	0.851	0.800	0.870
UVE	Brinjal Fruit Cracking	0.650	0.111	0.350	0.889	0.137	0.419	0.704	0.510
	Healthy Brinjal	0.845	0.095	0.155	0.905	0.112	0.777	0.704	0.809
	Phomopsis Blight	0.781	0.072	0.219	0.928	0.085	0.510	0.704	0.617
	Shoot and Fruit Borer	0.586	0.068	0.414	0.932	0.205	0.850	0.704	0.694
	Wet Rot	0.756	0.025	0.244	0.975	0.052	0.810	0.704	0.782
UVK	Brinjal Fruit Cracking	0.725	0.148	0.275	0.852	0.162	0.377	0.663	0.496
	Healthy Brinjal	0.864	0.099	0.136	0.901	0.110	0.774	0.663	0.817
	Phomopsis Blight	0.594	0.072	0.406	0.928	0.101	0.442	0.663	0.507
	Shoot and Fruit Borer	0.441	0.050	0.559	0.950	0.252	0.853	0.663	0.582
	Wet Rot	0.911	0.044	0.089	0.956	0.049	0.745	0.663	0.820
UVR	Brinjal Fruit Cracking	0.500	0.046	0.500	0.954	0.096	0.571	0.729	0.533
	Healthy Brinjal	0.893	0.141	0.107	0.859	0.132	0.713	0.729	0.793
	Phomopsis Blight	0.375	0.030	0.625	0.970	0.082	0.545	0.729	0.444
	Shoot and Fruit Borer	0.717	0.145	0.283	0.855	0.200	0.765	0.729	0.740
	Wet Rot	0.844	0.016	0.156	0.984	0.033	0.884	0.729	0.864

**Figure 8.** ROC Curves of Machine Learning Models Under Different Sampling and Preprocessing Techniques: (a) Unsharp–Resnet ensemble (ADASYN), (b) Unsharp–Resnet kNN (ADASYN), (c) Unsharp–Resnet Random Forest (ADASYN), (d) Unsharp–VGG ensemble (ADASYN), (e) Unsharp–VGG kNN (ADASYN), (f) Unsharp–VGG Random Forest (ADASYN)

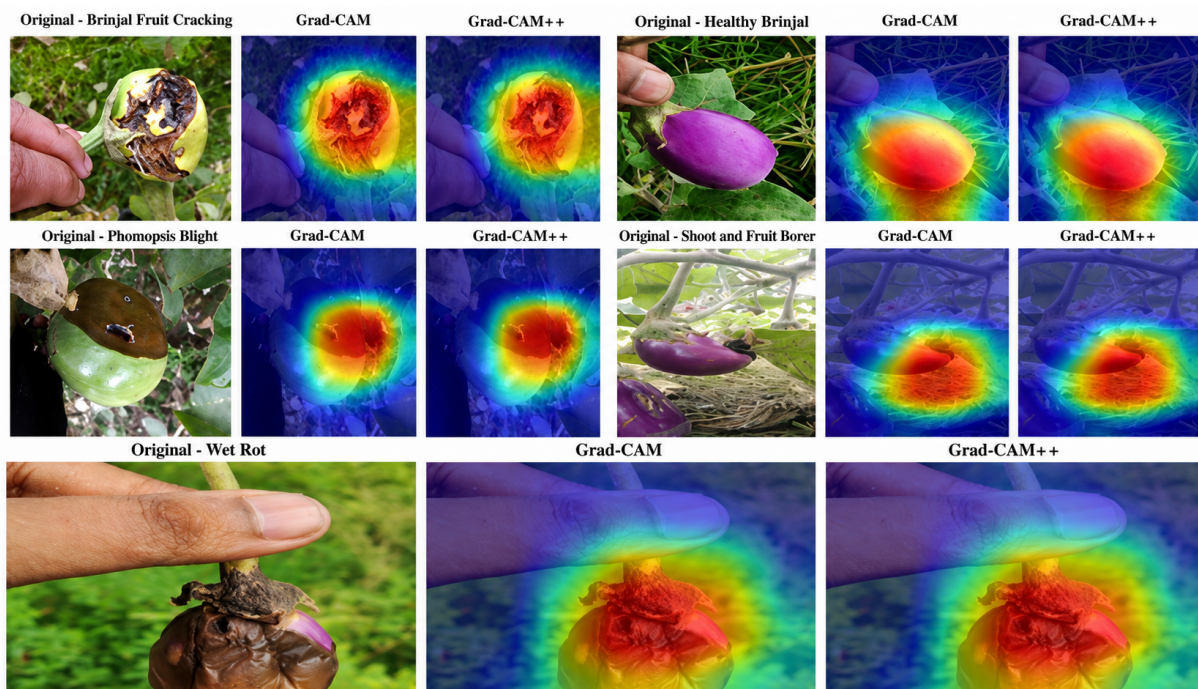


Figure 9. Visualization of GradCam and GradCam++ for the URR model

monsoon versus dry season) has not been established and would need to be re-validated before year-round deployment.

6. Limitations and Practical Considerations

Despite promising results, several limitations must be acknowledged. First, the dataset size remains modest, and the single-country, bounded-period collection window limits confidence in generalization to more complex field environments, different brinjal varieties, and other growing seasons (Section 5). Second, ADASYN-generated samples in the deep feature space may introduce distributional artifacts, potentially inflating minority-class performance. Third, explainability is limited to CNN feature representations and does not directly interpret classical classifier decisions. Fourth, inference speed and robustness under seasonal environmental variation were not directly benchmarked in this study, and both are prerequisites for continuous field deployment (Section 5). Fifth, this work does not include a direct quantitative comparison against re-implemented state-of-the-art end-to-end deep learning classifiers on BrinjalFruitX; establishing such a baseline is necessary to precisely quantify the accuracy–interpretability trade-off the proposed framework is intended to offer.

From a deployment perspective, the decoupled design reduces inference overhead compared to end-to-end deep learning models, making it suitable for low-cost edge devices. The preprocessing pipeline is

compatible with standard smartphone camera inputs, requiring no specialized imaging hardware. A typical field deployment workflow would involve: (1) image capture via smartphone, (2) preprocessing and feature extraction on an edge device or cloud endpoint, and (3) classification output with Grad-CAM visualization delivered via a mobile interface. The framework also complements existing Integrated Pest Management (IPM) practices by providing early, class-specific disease alerts that guide targeted pesticide application, and is compatible with IoT-based smart farming systems supporting real-time crop monitoring workflows [24].

While BrinjalFruitX was collected from Bangladesh, the framework generalizes across brinjal-growing regions through retraining on locally acquired data, and is crop-agnostic by design, with potential extension to tomato, pepper, and okra. The modular architecture facilitates long-term maintenance, as new disease classes can be incorporated by retraining only the classical classifier layer without retraining the CNN feature extractor. Future work will address these limitations through larger multi-region, multi-season datasets; image-domain augmentation strategies that complement feature-space ADASYN balancing; quantized or distilled CNN backbones for on-device inference benchmarking; and direct comparison against re-implemented state-of-the-art end-to-end classifiers to formally quantify the accuracy–interpretability trade-off proposed in this work.

7. Conclusion

In this study, we developed a robust, field-adapted framework for brinjal fruit disease detection, addressing the complexities of real-world agricultural environments. The BrinjalFruitX dataset, comprising 1,823 images across five categories, Healthy Brinjal, Shoot and Fruit Borer, Phomopsis Blight, Wet Rot, and Fruit Cracking, was collected under natural farming conditions in Bangladesh, providing a realistic benchmark for AI-based disease recognition. Its diversity in lighting, texture, background variability, and disease severity supports the development of models suitable for practical field applications. Preprocessing proved critical to downstream feature quality: among all tested configurations, the Unsharp-ResNet-Random Forest (URR) pipeline achieved the best performance, with 80.0% accuracy and a Wet Rot F1-score of 0.870, as Unsharp masking preserved fine-grained lesion boundaries that enabled ResNet to learn discriminative hierarchical features while Random Forest provided stable, generalized classification. Gaussian and Laplacian filtering improved feature clarity to a lesser degree and were less effective at emphasizing disease-specific patterns. ADASYN oversampling improved minority-class detection across categories, though, as discussed in Section 5, this gain was consistently accompanied by reduced precision rather than an unambiguous improvement. Grad-CAM and Grad-CAM++ visualizations further supported model transparency, consistently highlighting true pathological regions across all disease classes and confirming that URR's predictions were guided by meaningful symptom cues rather than background noise. Overall, the proposed framework demonstrates that combining sharpening-based preprocessing, deep residual feature extraction, and ensemble classification provides an accurate and interpretable basis for automated brinjal fruit disease diagnosis. The BrinjalFruitX dataset and the accompanying explainable, field-validated model establish a foundation for future work in precision agriculture, intelligent crop health monitoring, and scalable field-level disease detection, with the specific extensions outlined in Section 6.

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