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A Multi-Resolution Meta-Learning Framework with Attention-Based Feature Fusion for Rice Leaf Disease Classification

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Abstract: *In precision agriculture, the timely and precise identification of plant leaf diseases is of prime importance in reducing crop loss and in optimizing treatment plans. This work introduces a new deep learning architecture specifically developed for the diagnosis of rice leaf diseases based on multi-resolution image features and meta-learning strategies. The suggested system combines dual-resolution convolutional neural networks (CNNs), attention-based feature augmentation, and a model-agnostic meta-learning (MAML) framework to provide resilience to different data and environment types. A dataset of 2,627 rice leaf images from six disease classes Bacterial Leaf Blight, Brown Spot, Leaf Blast, Leaf Scald, Narrow Brown Spot, and Healthy is used. All images are preprocessed with histogram equalization and Gaussian filtering, and resized into two scales of 128×128 for preserving global structures and 512×512 for detailed texture information. These images are separately processed by shallow and deep CNNs to extract complementary feature maps. A Squeeze-and-Excitation (SE) block is incorporated to carry out channel-wise feature recalibration, elevating discriminative capacity with attention-guided feature fusion.*

In order to counter the problem of limited annotated examples in real-world applications, a MAML-based meta-learning strategy is utilized. The model is learned over synthetic few-shot tasks that are created to mimic various field conditions like occlusions, lighting variations, and partial leaves. This allows the classifier to rapidly adjust to new variations with little more data. The last classification network is trained using traditional supervised learning to achieve optimal performance on actual test sets. A large number of experiments illustrate that the new model much surpasses traditional single-resolution CNNs and baseline classifiers. The model reaches top-classification accuracy, precision, recall, and F1-score, and shows robust resistance under low-data scenarios. Also, adopting Grad-CAM visualization verifies that the model always pays attention to biologically meaningful areas of the leaf surface. The whole pipeline from image loading and preprocessing to feature extraction, classification, and result visualization is packaged in a friendly Graphical User Interface (GUI) coded using Python's Tkinter library. This renders the system usable and feasible for deployment by farmers and agricultural experts.

Keywords: *Rice leaf disease, Multi-resolution image features, Dual-resolution convolutional neural networks, Attention-based feature enhancement, Model-agnostic meta-learning, Squeeze-and-Excitation block, Synthetic few-shot tasks, Graphical User Interface*

1. Introduction

Rice (Oryza sativa) is perhaps the most important staple crop worldwide, supporting over half of the globe's population. Early and precise identification of rice leaf diseases is necessary to protect yield and achieve food security. Mechanically based diagnosis like visual inspection or lab testing is time-consuming, calls for expert skills, and fails to scale up for large-scale agrifarming operations. Consequently, there has been increasing need for automated, smart disease detection systems that are capable of functioning effectively and dependably under field environments. In the recent past, the introduction of deep learning methods, specifically convolutional neural networks (CNNs), has considerably boosted plant disease detection. State-of-the-art CNNs have been used with success to diagnose a variety of rice leaf diseases at an accuracy rate as high as 99.99% utilizing transfer learning frameworks such as ResNet-50, DenseNet-121, and EfficientNet B0 [1]. Light-weight models like MobileNet-V2 and EfficientNet-B0 have also shown viability for mobile and edge-device deployment without compromising accuracy significantly [2]. The tendency towards Green AI models that provide high accuracy at reduced computational costs is especially significant in resource-scarce agro ecosystems [3].

However, existing CNN-based approaches still face challenges:

1. **Limited generalizability**: Models do not easily adapt to fresh conditions because of differences in illumination, occlusion, or growth phases.
2. **Data scarcity**: Most rice leaf disease datasets have a limited number of annotated images per class, which can result in overfitting and insufficiency.

3. **Scalability constraints**: Even with high accuracy, most methods use large architectures, which puts restriction on deployment in low-resource or mobile environments.

To overcome these challenges, scientists have started investigating few-shot learning paradigms for plant disease detection [4]. For instance, meta-learning approaches like LFM CNAPS have obtained more than 97% average accuracy on novel plant disease categories with excellent generalizability under scarce data conditions. Meta-learning is well suited for agriculture, where samples per disease can be few and expensive to annotate [5].

The work presents a multi-resolution meta-learning approach with attention-based feature fusion for enhancing classification robustness and flexibility. The main innovations are:

- **Dual-resolution feature extraction**: Employing both coarse (128×128) and detailed (512×512) image scales, which are processed through shallow and deep CNNs, respectively, to extract complementary textures and patterns.
- **Attention-driven feature fusion**: Utilizing Squeeze-and-Excitation (SE) blocks to re-weight channel-wise importance so that discriminative features are highlighted.
- **Model-Agnostic Meta-Learning (MAML)**: Few-shot task simulation to train the model to quickly learn to adapt to novel disease classes in various environmental conditions.
- **Fine-tuning with traditional supervised learning**: Fine-tuning the meta-learned model on real rice leaf disease samples to achieve peak performance in real-world deployment.

These integrated approaches are meant to overcome the three important limitations of existing literature: generalizability across different conditions, efficient learning using sparse data, and feasibility of field deployment.

2. Related works

Li Z. et al. [6] introduce TLI-YOLO, a high-performance model for rice disease detection with mobile compatibility in mind. Their system provides high accuracy in real-time detection by combining compact neural designs, which are appropriate for execution on handheld systems. Yuhai Li et al. [7] introduce a multi-class classification method utilizing deep learning for rice plant diseases and apply convolutional neural networks to effectively identify leaf-specific patterns of diseases. Fang K. et al. [8] present RLDD-YOLOv11n, a YOLOv11 variant designed specifically for rice leaf disease detection. Their model improves detection speed as well as accuracy through optimal anchor box and feature extraction module optimization. Pandiyaraju V. et al. [9] present a channel attention-driven hybrid CNN model for enhancing paddy leaf disease identification. Their proposed model shows enhanced generalization on novel data by selective feature boosting through attention layers. Kayne Uriel K. Rodrigo et al. [10] suggest a CNN upgrade for rice leaf disease classification, specifically designed for mobile use. The research emphasizes the practical feasibility of deep learning in limited environments. Sadia Afrin Rimi et al. [11] present the RiceLeafBD dataset and evaluate different deep models through transfer learning. Their work emphasizes the significance of filtered datasets and the selection of best models for diagnosis. Ayyappan A. B. et al. [12] create a CNN-based system for detection of rice plant disease with an emphasis on architectural simplification without compromising classification accuracy. Zhou C. et al. [13] enhance YOLOv5s for real-world field image detection of rice leaves by improving spatial resolution and understanding context for practical use. Samia Mehnaz and Md. Touhidul Islam [14] provide a comparative assessment between CNNs, Transformers, and conventional methods, determining the advantage of deep networks in feature-rich plant disease classification.

Y. Cao [15] specializes in detection of pests and diseases in rice leaf images, providing an ensemble of deep learning models with robust performance under changing illumination and noise environments. C. G. Simhadri and H. K. Kondaveeti [16] utilize transfer learning mechanisms to enhance path and disease differentiation classification accuracy under restricted training conditions. J. Arcila-Diaz et al. [17] design a real-time CNN-based identification system for rice diseases. Their model supports low-latency predictions with reliable image processing pipelines, aimed at in-field diagnosis. M. Jothika and S. Nathiya [18] propose an effective model that fuses Inception V3 with transfer learning. Their findings emphasize the model's performance in high-velocity and precise classification, suited best for precision agriculture. P. S. Seelwal and T. R. Rohilla [19] suggest a lightweight model optimized for rice disease recognition with less computational overhead. Their approach is efficient and accurate for embedded systems. B. Paneru [20] investigates multi-featured CNN architectures and offers real-world suggestions to farmers depending on the type of diseases predicted, integrating model predictions with actionable insights. K. K. Kumar et al. [21] develop a deep learning pipeline based on CNNs to identify rice diseases in Indian agricultural farms. Their findings confirm the consistency of deep learning across different geographies. Lastly, S. Sistla et al. [22] utilize the KERTL-BME ensemble for rice leaf disease diagnosis with better performance over standalone learners using intelligent ensemble fusion.

3. The proposed model

The suggested model "Multi-Resolution Meta-Learning with Attention-based Feature Fusion for Rice Leaf Disease Classification" (MRMLAFF-RLDC), introduces a strong and adaptive deep learning architecture for rice leaf disease classification. The framework starts with a two-resolution image preprocessing followed by two independent CNNs based feature extraction. The middle features of both streams are combined by applying a Squeeze-and-Excitation (SE) attention mechanism to highlight the most informative channels. For increasing generalizability under few-shot conditions, the model utilizes Model-Agnostic Meta-Learning (MAML), learning from synthetically generated tasks that mimic real-world variations like occlusion and lighting changes. The meta-learned model is fine-tuned using supervised learning for optimization on the complete training set. Last but not least, a GUI-based interface facilitates real-time disease prediction from new test images. Figure 1 provides the block diagram of the whole framework.

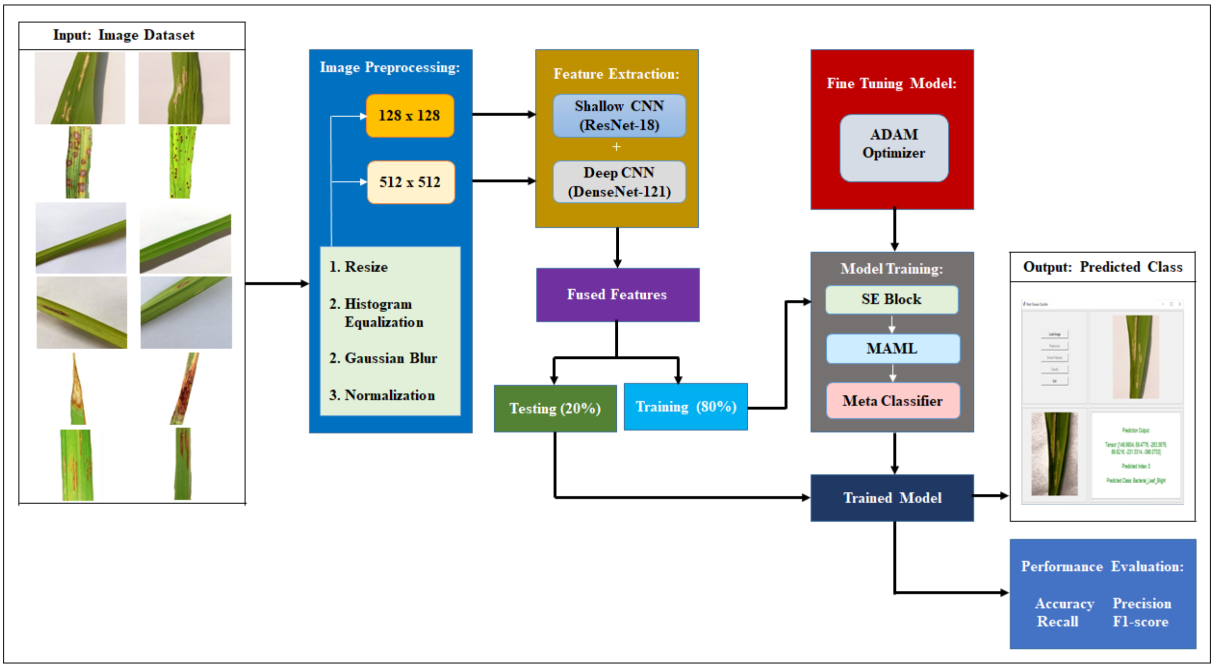


Figure 1. The Block Diagram of the proposed MRMLAFF-RLDC Framework

3.1 Image Pre-processing

Image preprocessing is an essential part of this research since it has a direct impact on the quality and efficiency of the feature extraction and classification processes. In agricultural image analysis, particularly in detecting plant leaf diseases, raw images tend to have problems with variations in lighting, noise, blurring, and non-uniform backgrounds, which can be detrimental to model performance. In this paper, image preprocessing plays an important part in improving the quality and uniformity of the input data for efficient feature extraction and classification. The raw rice leaf images are resized to two resolutions 128×128 pixels for global structural pattern capture and 512×512 pixels for capturing fine-grained disease properties. Each image is histogram equalized on the luminance channel to enhance contrast and emphasize disease-affected areas, and then Gaussian-blurred to denoise without eliminating crucial edges. The pixel values are also normalized to keep intensity scaling consistent across samples. Such preprocessing pipeline preserves both low-resolution and high-resolution inputs with complementary visual information required for the dual-stream convolutional architecture, resulting in more accurate and discriminative feature representation at subsequent stages of the model.

Step 1: Image Resizing (Dual Resolution)

To enable multi-scale feature learning, each original image $I(x, y)$ is resized into two different resolutions:

$I_{128}(x', y') = Resize(I(x, y), 128 \times 128)$

$I_{512}(x', y') = Resize(I(x, y), 512 \times 512)$

This is achieved using bilinear interpolation, mathematically defined as:

$$I_{resized}(x', y') = \sum_{i=0}^{1} \sum_{j=0}^{1} w_{ij} \cdot I(x_i, y_j) \quad (1)$$

Where w_{ij} are the interpolation weights and (x_i, y_j) are the four neighboring pixels around (x', y') in the original image.

The 128×128 image supports shallow CNNs for faster computation and global structure analysis, and the 512×512 image feeds into deeper CNNs to extract fine-grained textural details of leaf lesions.

Step 2: Color Space Conversion (BGR to YUV)

To prepare for histogram equalization, the image is transformed from the BGR to the YUV color space:

$$\begin{bmatrix} Y \\ U \\ V \end{bmatrix} = \begin{bmatrix} 0.299 & 0.587 & 0.114 \\ -0.14713 & -0.28886 & 0.436 \\ 0.615 & -0.51499 & -0.10001 \end{bmatrix} \cdot \begin{bmatrix} R \\ G \\ B \end{bmatrix} \quad (2)$$

Equation (2) separates the luminance component Y from chrominance components U and V, enabling targeted contrast enhancement.

Step 3: Histogram Equalization on Luminance Channel

Histogram equalization is performed on the Y channel to improve contrast by redistributing pixel intensities. Given a pixel intensity histogram $p(i)$, the cumulative distribution function (CDF) is:

$$CDF(i) = \sum_{j=0}^{i} p(j) \quad (3)$$

The transformation function applied to each pixel intensity i is:

$$i_{equalized} = round\left(\frac{CDF(i) - CDF_{min}}{(M \times N) - CDF_{min}} \times (L - 1)\right) \quad (4)$$

Where, $M \times N$ is the image size, L is the number of gray levels, and CDF_{min} is the smallest non-zero value of CDF. It enhances lesion visibility by amplifying intensity differences in affected areas.

Step 4: Denoising using Gaussian Blur

Gaussian filtering reduces high-frequency noise introduced by lighting and camera artifacts without degrading disease-related edges. To suppress noise while preserving edges, It is applied using a kernel $G(x, y)$ defined as:

$$G(x, y) = \frac{1}{2\pi\sigma^2} \cdot exp\left(-\frac{x^2 + y^2}{2\sigma^2}\right) \quad (5)$$

The blurred image $I_{blur}(x, y)$ is computed as:

$$I_{blur}(x, y) = \sum_{i=-k}^{k} \sum_{j=-k}^{k} G(i, j) \cdot I(x - i, y - j) \quad (6)$$

In practice, a 3×3 kernel with $\sigma \approx 1$ is used.

Step 5: Normalization

Each of the preprocessed images is normalized to a uniform intensity range to provide stable convergence in CNN training. It provides equal pixel intensity spread throughout the dataset to avoid skewed learning. Min-max normalization is used as:

$$I_{norm}(x,y) = \frac{I(x,y) - I_{min}}{I_{max} - I_{min}} \cdot 255 \quad (7)$$

Where, I_{min} and I_{max} are the minimum and maximum intensity values in the image.

Alternatively, for CNNs expecting input in [0, 1] or zero-centered data, z-score normalization may be used:

$$I_{zscore} = \frac{I - \mu}{\sigma + \epsilon} \quad (8)$$

Where, μ is the mean, σ the standard deviation, and ϵ a small constant to prevent division by zero.

The preprocessed images are stored in a organized directory under two resolution directories (128×128 and 512×512) with six subdirectories corresponding to the six rice disease classes.

3.2 Feature Extraction

Feature extraction is the core of image classification in deep learning. In this work, a multi-resolution dual-stream CNN structure is adopted to extract both global and fine-grained features from rice leaf images. The system processes an image of 128×128 and 512×512 resolutions with shallow and deep CNNs, respectively. Intermediate feature maps of both streams are concatenated through attention mechanisms to achieve a compact and discriminative representation, which is utilized for disease classification. Two pre-processed different resolution images are initially provided to the feature extraction technique.

Step 1: Feature Map Generation Using Dual-Stream CNNs

A shallow CNN operates on the 128×128 image to extract semantic (global) features and a deep CNN operates on the 512×512 image to extract high-resolution (local) features.

Let, f_s be the shallow CNN with parameters θ_s, and f_d be the deep CNN with parameters θ_d. Then,

$$F_s = f_s(I_{128};\ \theta_s),\ F_d = f_d(I_{512};\ \theta_d) \quad (9)$$

Where, $F_s \epsilon\ \mathbb{R}^{B\times C_1\times H_1\times W_1}$ and $F_d \epsilon\ \mathbb{R}^{B\times C_2\times H_2\times W_2}$

Each layer of a CNN uses convolution defined as:

$$F^{(l)}(x,y) = \sigma\left(\sum_{i=1}^{k}\sum_{j=1}^{k} W_{ij}^{(l)} \cdot F^{(l-1)}(x+i, y+j) + b^{(l)}\right) \quad (10)$$

Where, σ is the activation function and k is the kernel size.

Step 2: Flattening and Feature Vector Construction

Flattening is an intermediary step between feature extraction and classification. The quality of the flattened feature vectors contributes significantly to the overall prediction performance. Following the image going through the convolutional layers of the shallow CNN and deep CNN, the ensuing output is a multi-channel feature map a 3D tensor of the form: $F \epsilon\ \mathbb{R}^{C\times H\times W}$. Where, C is the number of channels, and $H \times W$ is the spatial dimension of each feature map.

Because classifiers such as fully connected (dense) layers or attention modules usually require 1D feature vectors instead of 3D tensors, these feature maps need to be flattened into vectors. The feature vectors that are flattened are:

$$v_s = Flatten(F_s)\ \epsilon\ \mathbb{R}^{C_s\cdot H_s\cdot W_s} \text{ and } v_d = Flatten(F_d)\ \epsilon\ \mathbb{R}^{C_d\cdot H_d\cdot W_d} \quad (11)$$

This is simply a reshaping of the 3D tensor to a 1D vector by concatenating all elements in row-major order.

Step 3: Feature Fusion

The vectors from the two streams are concatenated to form a joint feature representation:

$$v_{fused} = [v_s || v_d]\ \epsilon\ \mathbb{R}^{C_s + C_d} \quad (12)$$

This combined feature comprises both global and fine-grained spatial information, enhancing robustness and classification accuracy.

Step 4: Channel-Wise Attention via SE Block

The Squeeze-and-Excitation (SE) Block is a light but efficient attention mechanism that is used to enhance the representational power of a convolutional neural network to learn channel-wise dependencies. Rather than equally treating all feature channels, SE blocks learn to dynamically adapt the importance of each channel using global context. This process significantly boosts discriminative features but reduces the less informative ones - critical in achieving accurate plant leaf disease classification.

Let the input feature vector be: $v_{fused} \epsilon \mathbb{R}^{C}$, where C is the number of channels in the fused feature vector v_{fused} obtained after flattening and concatenation from the dual-resolution CNN streams.

a) Squeeze (Global Information Embedding)

Use Global Average Pooling (GAP) to encode the global context of the feature map:

$$z_c = \frac{1}{H \cdot W} \sum_{i=1}^{H} \sum_{j=1}^{W} F_c(i, j) \quad \text{for each channel c} = 1, \dots, \text{C} \tag{13}$$

Since, already working with flattened feature vectors, the squeeze operation becomes a simple identity, $z = v$.

b) Excitation (Fully Connected MLP)

Now, use a two-layer neural network to generate per-channel modulation weights:

$$s = \sigma(W_2 \cdot \delta(W_1 \cdot z)) \tag{14}$$

Where, $W_1 \epsilon \mathbb{R}^{\frac{C}{r} \times C}$, $W_2 \epsilon \mathbb{R}^{C \times \frac{C}{r}}$, r is reduction ratio to reduce computation, δ is ReLU activation, σ is Sigmoid activation, and $s \epsilon \mathbb{R}^{C}$ is channel-wise attention weights.

The goal of this MLP is to capture non-linear relationships between channels, assisting the model in determining which feature channels are informative and which can be discarded.

c) Reweight (Feature Recalibration)

The input feature vector v is recalibrated by element-wise multiplication with the attention weights s:

$$\hat{v} = s \odot v \tag{15}$$

Where, $\odot$ denotes Hadamard (element-wise) product.

The SE output $\hat{v}$ is used as the input to the meta-classifier, ensuring only the most relevant channel-level information is passed for final decision-making.

Table 1. Layer wise architecture of the Shallow CNN (ResNet-18) Stream (128×128 Input)

Layer Type	Output Shape	Details
Input	128×128×3	Original RGB image
Conv2D + ReLU	128×128×32	3×3 kernel, stride 1, padding 1
MaxPooling	64×64×32	2×2 pool size
Conv2D + ReLU	64×64×64	3×3 kernel, stride 1, padding 1
MaxPooling	32×32×64	2×2 pool size
Conv2D + ReLU	32×32×128	3×3 kernel, stride 1, padding 1
GlobalAveragePooling	128	Flattened vector

Table 2. Layer wise architecture of the Deep CNN (DenseNet-121) Stream (512×512 Input)

Layer Type	Output Shape	Details
Input	512×512×3	Original RGB image
Conv2D + ReLU	512×512×64	7×7 kernel, stride 2, padding 3
MaxPooling	256×256×64	3×3 pool size, stride 2
ConvBlock (DenseNet)	128×128×128	Multiple dense connections or mobile blocks
Transition Layer	64×64×256	1×1 conv + average pooling
ConvBlock	32×32×512	Further deep conv layers
GlobalAveragePooling	768	Flattened vector

The shallow and deep CNN streams' outputs are concatenated to create a fused feature vector. It creates a final 1536-sized feature vector (128 for shallow stream + 768 for deep stream). This vector gets fed into the classification phase after re-weighting using attention.

3.3 Classification

The last step in the envisioned rice leaf disease detection system is the classification process, in which the extracted and boosted features are utilized to classify the category of disease. It employs a MetaClassifier boosted by a Squeeze-and-Excitation (SE) block and fully connected layers. It is also trained with a meta-learning (MAML) approach and fine-tuned through conventional supervised learning.

The MetaClassifier is the last and most important step in the proposed rice leaf disease detection system. Its purpose is to transform the processed and fused feature vectors into the corresponding disease category. The classifier is not crafted as a regular feedforward neural network, but as an attention-augmented, meta-learning-friendly architecture capable of well generalizing to both traditional and few-shot learning environments.

Step 1: Fully Connected Layers

The attention-weighted vector $v_{attn} \epsilon \mathbb{R}^{1536}$ is passed through a two-layer dense neural network for classification:

a) First Dense Layer

$$h_1 = \delta(W_3 \cdot v_{attn} + b_3) \quad where\ W_3 \epsilon \mathbb{R}^{512 \times 1536} \tag{16}$$

This step compresses the feature dimension and introduces non-linearity.

b) Batch Normalization and Dropout

$$h_1^{norm} = BatchNorm(h_1) \tag{17}$$

$$h_1^{drop} = Dropout(h_1^{norm}, p = 0.4) \tag{18}$$

These regularization techniques ensure the Stabilize learning and Reduce overfitting.

c) Final Output Layer

$$z = W_4 \cdot h_1^{drop} + b_4 \quad where\ W_4 \epsilon \mathbb{R}^{6 \times 512} \tag{19}$$

This produces the raw scores (logits) for each class.

Step 2: Softmax Activation

Softmax activation function is a mathematical function that converts a vector of raw scores into a vector of probabilities. It is usually applied to the output layer of a classification neural network, particularly in multi-class cases, where it assists in finding the most probable class out of various possibilities. The softmax function $\sigma(z)$ converts these into probabilities p_i using the formula:

$$\sigma(z_i) = \frac{e^{z_i}}{\sum_{j=1}^{K} e^{z_j}} \quad for\ i = 1,2,\dots,K \tag{20}$$

Where, e is Euler's number, z_i is the score for class i, and the denominator ensures that the output values sum to 1.

Step 3: Loss Function and Optimization

For classification, the standard categorical cross-entropy loss is used:

$$L_{CE} = -\sum_{i-1}^{C} y_i \, log\,(\hat{y}_i) \tag{21}$$

Where, y_i is ground truth and $\hat{y}_i$ is predicted probability from softmax.

Step 4: Meta-Learning Integration (MAML)

Meta-learning, or "learning to learn", is an artificial learning paradigm in which models learn to adapt to new tasks with little data. Among the most effective and popular meta-learning algorithms is Model-Agnostic Meta-Learning (MAML), which seeks to make a model readily adaptable to new tasks by making minimal gradient updates. In this work of research, MAML is employed for the purpose of allowing the classifier to generalize well across disease classes and learn rapidly under changing environment, image quality, and data limitations.

MAML seeks to find an optimal set of model parameters θ such that for any new task T_i, a few gradient descent steps will lead to good performance:

$$\theta^* = arg\,\min_{\theta} \sum_{T_i \sim p(T)} L_{T_i}\big(\theta - \alpha \nabla_\theta L_{T_i}^{train}(\theta)\big) \tag{22}$$

Where, $L_{T_i}^{train}$ is the loss on training data for task T_i, L_{T_i} is the loss on validation data for task T_i, α is the inner-loop learning rate, and θ is the model's initial parameter set.

The processes involved in MAML are explained below:

a) Task Sampling

From a distribution over tasks $p(T)$, sample a batch of tasks. In this work, a synthetic few-shot task for each disease is generated by imposing variations such as blur, occlusion, illumination variation.

b) Inner Loop – Task-Specific Adaptation

For each task T_i, the model performs a few gradient descent steps using the support set: $\theta_i' = \theta - \alpha \nabla_\theta L_{T_i}^{train}(\theta)$. This step simulates learning on a small number of examples from a new task.

c) Outer Loop – Meta-Update

Evaluate the updated model θ_i' on the query set. Update the meta-parameters θ using the gradient of this loss:

$$\theta \leftarrow \theta - \beta \nabla_\theta \sum_{T_i} L_{T_i}^{test}(\theta_i') \tag{23}$$

Where, β is the outer-loop learning rate. The meta-objective is to minimize the post-adaptation loss across all tasks.

d) Iterative Training

Repeat steps 1–3 across numerous episodes until convergence. In this research, 10 meta-epochs are employed in training the MetaClassifier for robust generalization across unseen variations.

Step 5: Fine-Tuning and Evaluation

Following Model-Agnostic Meta-Learning (MAML) training of the classification model, the subsequent key phase in the devised rice leaf disease detection system is the Fine-Tuning and Evaluation phase. This phase fine-tunes the model for eventual deployment and validates its effectiveness via quantitative performance evaluation.

a) Fine-Tuning

That is fine-tune the meta-trained model parameters more accurately to the entire training dataset for improved real-world performance and to compensate for any last-minute discrepancies. This is accomplished by the following steps:

Model Initialization: Load the pre-trained MetaClassifier model with weights from the meta-learning phase.

Dataset Preparation: Fine-tune using the entire training set (80% of the merged feature dataset). Each input is a 1536-dimensional feature vector output by multi-resolution CNN feature fusion.

Loss Function: Optimization is done using cross-entropy loss for maximizing classification performance.

Optimizer and Learning Rate: Adam optimizer with a low learning rate for guaranteed stable convergence.

Regularization: Use dropout and batch normalization in the fully connected layers to minimize overfitting and stabilize training.

Epochs: Fine-tune the model for 20 epochs based on convergence behavior and validation performance.

b) Evaluation

The testing phase in the envisioned MRMLAFF-RLDC approach is a key phase to validate the performance, efficacy, and reliability of the MetaClassifier model after fine-tuning on new unseen test samples. It assists in quantifying overall classification performance based on statistical measures, determining model strengths and limitations by disease type, and displaying classification performance with graphical tools such as confusion matrices and ROC curves.

The assessment is performed on the 20% test split of the entire dataset of combined features, such that data seen at training or fine-tuning time is never exposed in this phase. Each sample is encoded as a 1536-dimensional feature vector extracted from dual-resolution CNN streams. To assess model performance, the following standard classification measures are calculated:

Accuracy: Measures the proportion of correct predictions over total predictions

Precision: Indicates how many predicted positives are actually positive

Recall: Indicates how many actual positives are correctly identified

F1-Score: Harmonic mean of precision and recall

Confusion Matrix: A confusion matrix is used to graphically represent per-class prediction performance, indicating the number of images in each true class that were correctly or incorrectly labeled.

ROC Curve: For every class, a Receiver Operating Characteristic (ROC) curve is used to plot True Positive Rate vs. False Positive Rate at different thresholds.

Table 3. Layer wise architecture of the classification model of MRMLAFF-RLDC framework

Layer Name	Layer Type	Output Shape	Description
Input	Input Vector	1536	Fused feature vector from 128x128 and 512x512 images
SE Block - FC1	Linear	96	Reduces dimensionality (1536 → 96) for channel attention
SE Block - ReLU	Activation	96	Applies non-linearity
SE Block - FC2	Linear	1536	Restores dimension (96 → 1536), learns attention weights
SE Block - Sigmoid	Activation	1536	Normalizes weights to [0, 1]
SE Scaling	Element-wise Multiply	1536	Applies attention weights to original input
FC Layer 1	Linear	512	Projects to lower dimension
BatchNorm1	BatchNorm	512	Normalizes activations
ReLU	Activation	512	Applies ReLU activation
Dropout	Dropout(0.4)	512	Reduces overfitting
Output Layer	Linear	6	Final classification layer for 6 disease classes
Softmax	Activation	6	Converts logits to class probabilities

3.4 GUI-based Testing for the MRMLAFF-RLDC Framework

The GUI framework implemented for the MRMLAFF-RLDC system is an interactive, intuitive interface for validating the trained model of rice leaf disease classification for new images. Using a user-friendly interface layout, the GUI is made up of a two-row and two-column grid with five sequentially triggered buttons: 'Load Image', 'Preprocess', 'Extract Features', 'Classify', and 'Exit'. The user starts by loading a test image through the 'Load Image' button, which shows the loaded image. This is succeeded by the 'Preprocess' process that normalizes and enhances the image using the same image normalization and enhancement methods used in training, resulting in 128×128 and 512×512 images of the image. The preprocessed images are shown for confirmation.

In the second step, the 'Extract Features' button initiates the dual-resolution feature extraction process, combining the 128×128 and 512×512 image features into a single feature vector, under the guidance of attention mechanisms. A progress bar and message box are used for user feedback. After extracting features, the 'Classify' button calls the MetaClassifier model, instantiated from the trained weights, and gives back the predicted disease class name as per the output of the model. The outcome is presented distinctly in the GUI. This visually-oriented, modular tool is incredibly useful for farmers and agricultural researchers alike as it allows non-expert users to detect diseases rapidly and accurately without intervention, making it perfectly suited for application in real-time precision agriculture use cases.

The entire proposed MRMLAFF-RLDC framework is described in the following algorithm.

Algorithm: Multi-Resolution Deep Learning for Rice Leaf Disease Detection and Classification
Input: - Rice leaf image dataset (2627 images, 6 classes) - Pre-trained CNN models (ResNet-18, DenseNet-121)

- Training hyperparameters (epochs, batch size, learning rate)
Output: - Trained deep learning model for classification - GUI for disease prediction on new images
1. Dataset Preparation a. Collect and combine Internet-based and independent rice leaf disease images. b. Assign class labels and organize dataset into class folders. 2. Image Preprocessing a. Resize each image into 128x128 and 512x512 resolutions. b. Apply histogram equalization, Gaussian blur, and normalization. c. Store preprocessed images in corresponding folders. 3. Multi-Resolution Feature Extraction a. Use shallow CNN (ResNet-18) on 128x128 images. b. Use deep CNN (DenseNet-121) on 512x512 images. c. Extract and concatenate feature vectors from intermediate layers. 4. Feature Fusion and Attention a. Apply Squeeze-and-Excitation (SE) block on fused feature vectors. b. Compute attention-weighted features. 5. Classification using MetaClassifier a. Define a fully connected network with dropout and batch normalization. b. Train with cross-entropy loss and Adam optimizer. 6. Meta-Learning (MAML) a. Generate synthetic few-shot tasks with augmentation. b. Train base model for quick adaptation to new tasks. 7. Fine-Tuning and Evaluation a. Fine-tune MetaClassifier on full training data. b. Evaluate using Accuracy, Precision, Recall, F1-score. c. Generate confusion matrix and ROC curve. 8. GUI Development for Testing a. Design GUI with buttons: Load Image, Preprocess, Extract Features, Classify, Exit. b. Display input and preprocessed images and show classification result. 9. Output a. Trained model in .h5 format. b. Performance reports and visualizations saved to disk. c. GUI for real-time prediction of rice leaf diseases.

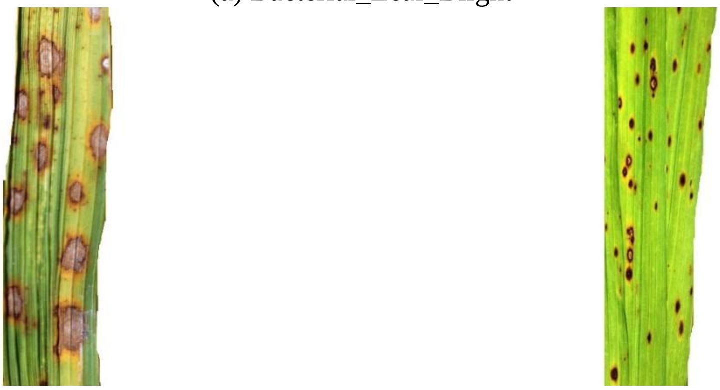
4. Experimental Validation

The efficacy of the suggested MRMLAFF-RLDC paradigm was evaluated on the basis of a publicly downloadable rice leaf disease dataset [23] obtained from the Kaggle website. The dataset comprises a total of 2,580 images, including five primary rice plant leaf disease classes and a healthy leaf class. For experimental validation with rigor, the dataset was categorically divided into training and testing subsets with an 80:20 ratio. Particularly, 80% of the images, i.e., 2,064 images, were used for model training, and the other 516 images (20%) were used to test the model's generalization on unseen data. The model's performance was tested based on commonly used performance metrics such as accuracy, precision, recall, and F1-score. An overview of the distribution of the dataset is presented in Table 4, and a representative sample of the disease classes is shown in Figure 5. This systematic evaluation method guarantees exhaustive investigation of the classification ability of the suggested model under practical conditions.

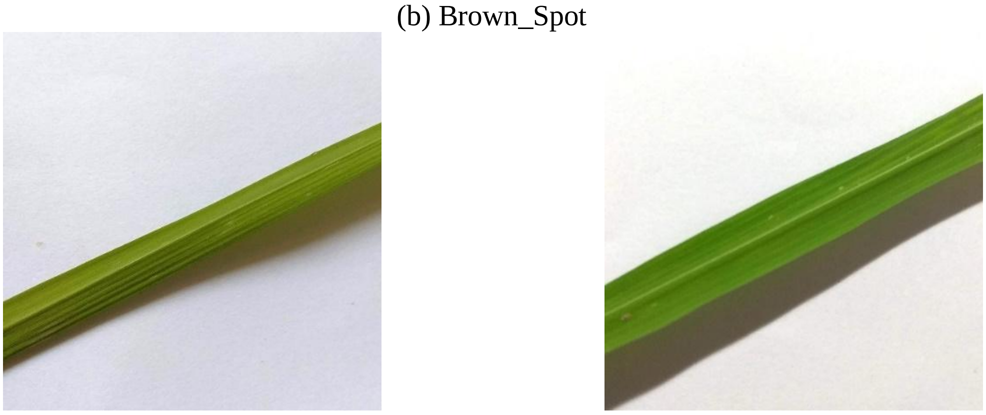
Table 4. Dataset details

Sl. No.	Classes	No. of Images
1.	Bacterial_Leaf_Blight	430
2.	Brown_Spot	430
3.	Healthy	430
4.	Leaf_Blast	430
5.	Leaf_Scald	430
6.	Narrow_Brown_Spot	430
	Total	2,580

(a) Bacterial_Leaf_Blight



(b) Brown_Spot



(c) Healthy

(d) Leaf_Blast

(e) Leaf_Scald

(f) Narrow_Brown_Spot

Figure 2. Sample rice leaf images for different classes

The following table presents the parameters of main simulations and their respective values utilized during development, training, and evaluation of the suggested MRMLAFF-RLDC model.

Table 5. Simulation Variables

Sl. No.	Simulation Variable	Value
1.	Total Images	2,580
2.	Number of Classes	6 (5 diseases + 1 healthy)
3.	Image Resolutions Used	128x128 and 512x512
4.	Training-Testing Split	80:20
5.	Training Images	2,064
6.	Testing Images	516
7.	Feature Vector Length	1536 (768 from 128x128 + 768 from 512x512)

8.	Batch Size	32
9.	Epochs (Fine-Tuning)	20
10.	Epochs (MAML Training)	10
11.	Learning Rate (Outer Loop)	0.001
12.	Learning Rate (Inner Loop)	0.01
13.	Optimizer	Adam
14.	Loss Function	Cross-Entropy Loss
15.	Dropout Rate	0.4
16.	Activation Function	ReLU, Softmax (final layer)
17.	Attention Mechanism	Squeeze-and-Excitation (SE) Block
18.	Classifier Input Dimension	1536

Figures 3 to 8 show the graphical user interface (GUI) developed for rice leaf disease classification based on the proposed MRMLAFF-RLDC model. The intuitive and interactive GUI enables users to choose and classify test images into respective disease categories. As Figure 3 illustrates, the GUI's front page consists of five major buttons 'Load Image', 'Preprocess', 'Extract Features', 'Classify', and 'Exit' on the left panel and individual areas for displaying the chosen image, preprocessed results, and classification results.

On clicking the "Load Image" button, the file dialog box is initiated, enabling the user to browse and open a test image from their system. After one image is chosen, it appears in the specified window, the "Load Image" button is disabled automatically, and the "Preprocess" button becomes active to lead the user to the next process. When the "Preprocess" button is clicked, the chosen image is preprocessed, including resizing, contrast adjustment, noise removal, and normalization, and the obtained processed images appear in the respective display area. The GUI then disables the "Preprocess" button and enables the "Extract Features" button. On clicking "Extract Features", the system extracts a fused feature vector from the multi-resolution inputs using the trained dual-stream model, and a confirmation message informs the user once completed. Lastly, when the "Classify" button is clicked, the GUI loads the pre-trained MetaClassifier model and predicts the disease category, printing the class label in the result window. This sequential and guided workflow simplifies the testing process for end-users, ensuring both ease of use and diagnostic accuracy.

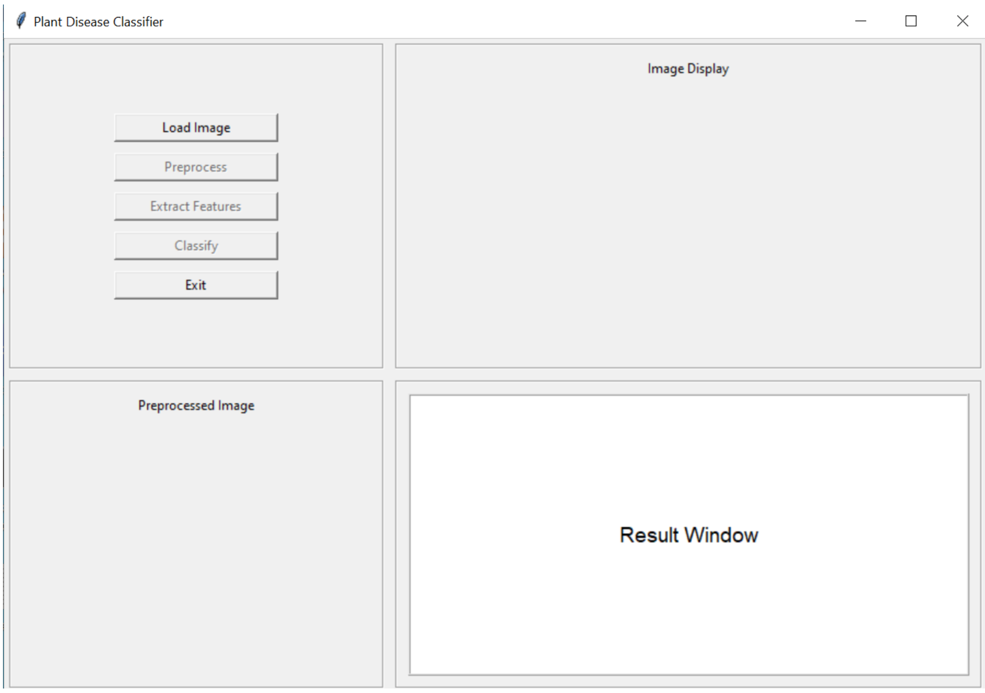


Figure 3. The GUI design for MRMLAFF-RLDC Framework

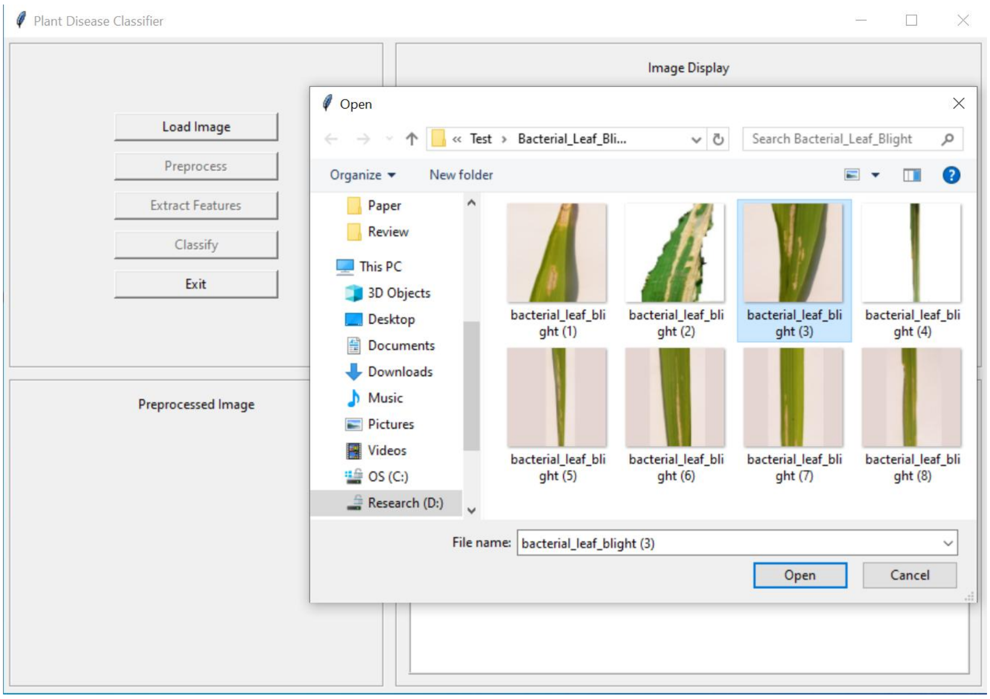


Figure 4. The GUI shows a dialog box to select an image

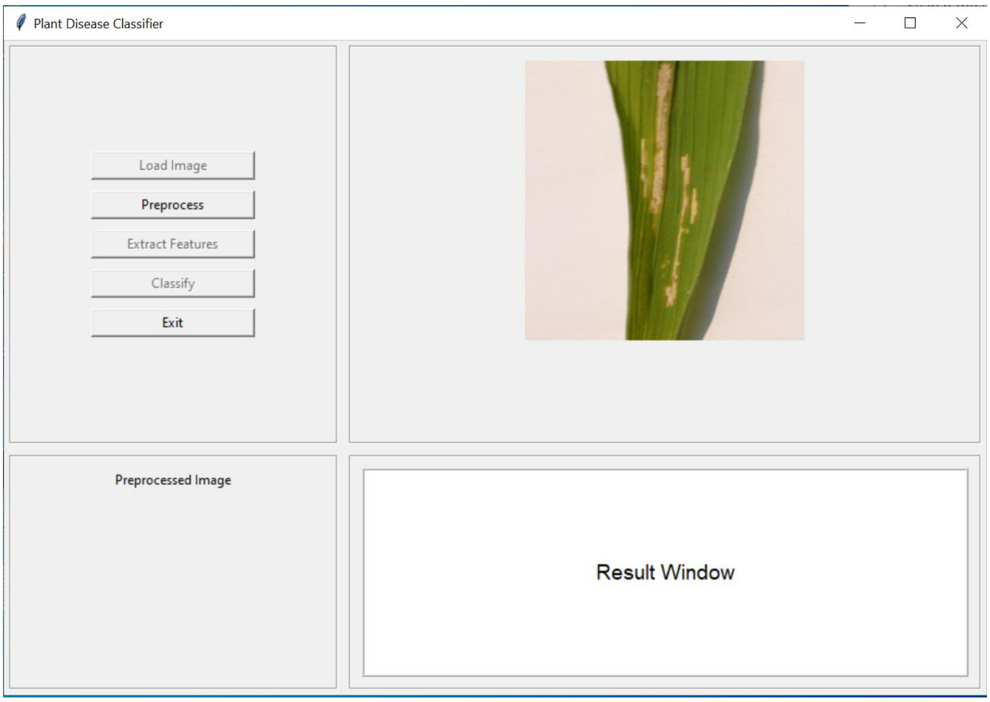


Figure 5. The GUI shows the loaded original image

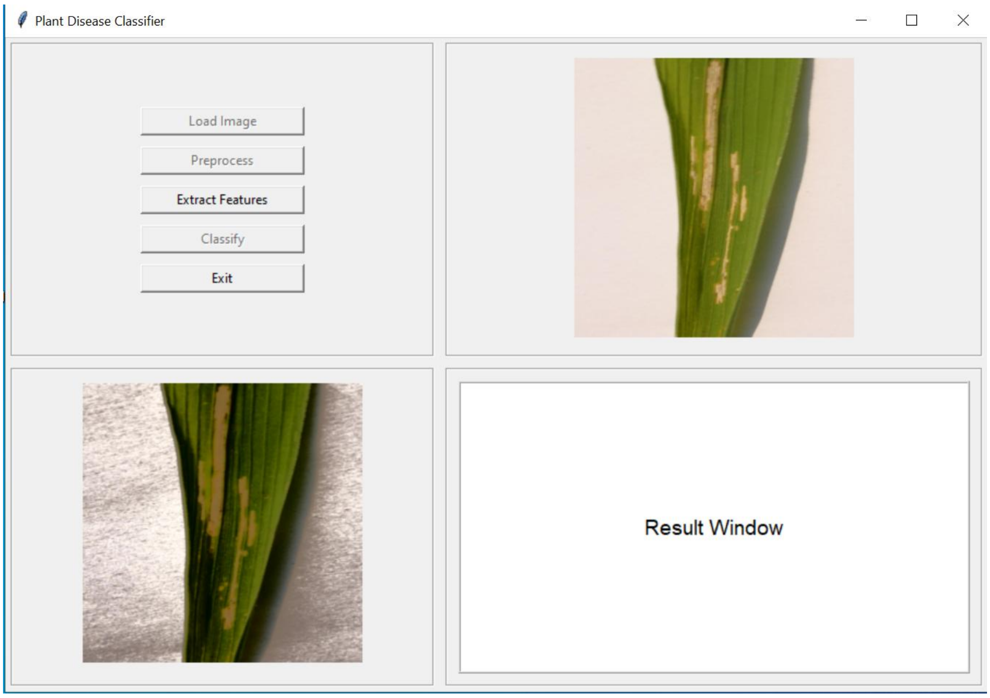


Figure 6. The GUI displays the original and preprocessed images

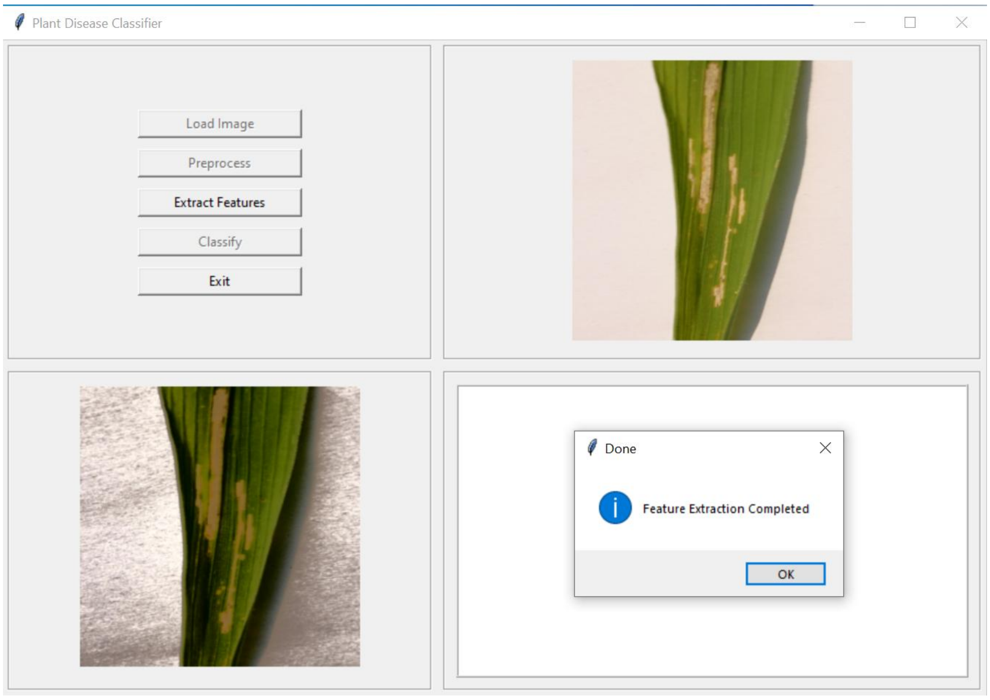


Figure 7. The GUI displays the confirmation of the feature extraction message

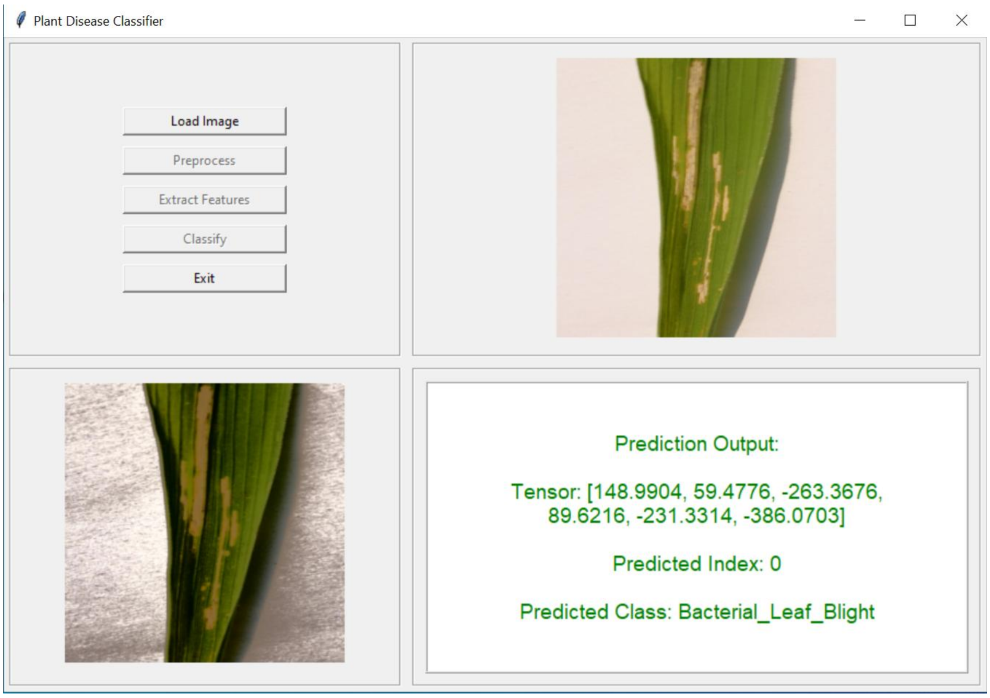
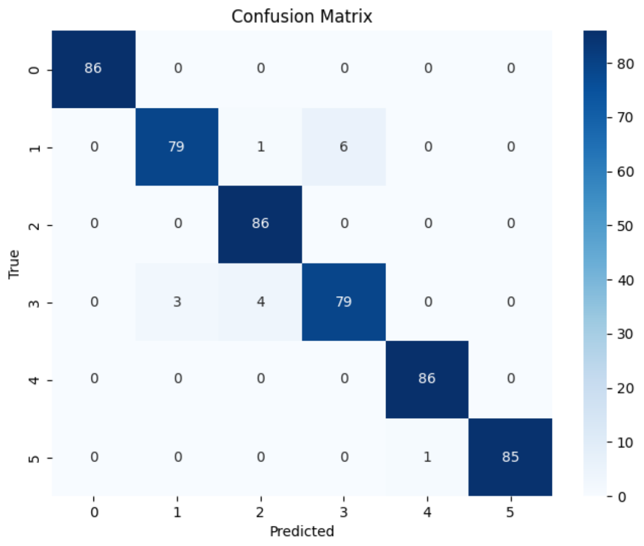


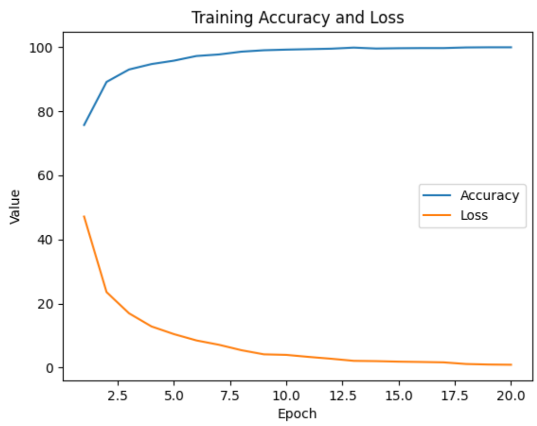
Figure 8. The GUI displays the predicted label in the result window

Figure 9 shows the classification results of the suggested MRMLAFF-RLDC framework on the test dataset. In particular, Figure 9(a) shows the confusion matrix plotted by the classifier, outlining the model's stable predictive performance for all six classes. The MRMLAFF-RLDC model precisely predicted 86 cases of Bacterial Leaf Blight, 79 cases of Brown Spot, 86 cases of Healthy leaves, 79 cases of Leaf Blast, 86 cases of Leaf Scald, and 85 cases of Narrow Brown Spot. The regular distribution of accurately predicted samples in this figure is indicative of the model's performance consistency across disease classes.

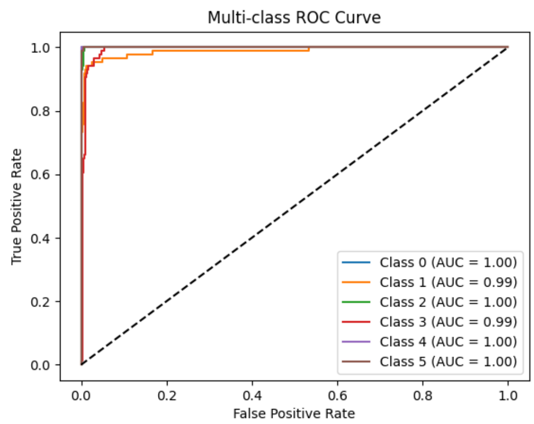
In addition, Figure 9(b) shows the accuracy-loss curve, depicting the training process of the model and its stability in convergence. The visualization proves that the model had quick convergence with little overfitting. The Receiver Operating Characteristic (ROC) curves for all disease classes are also presented in Figure 9(c). ROC analysis proves the discriminative power of the classifier based on high Area Under the Curve (AUC) values for all classes. Collective results identify MRMLAFF-RLDC model as effective for achieving accurate and reliable disease classification in multiclass agricultural image datasets. Table 6 and Figure 10 present the overall classification performance of the proposed MRMLAFF-RLDC model.



(a)



(b)



(c)

Figure 9. Result Analysis of MRMLAFF-RLDC approach
(a) Confusion Matrix (b) Accuracy-Loss Graph (c) ROC Curve

Table 6 and Figure 10 present the overall classification performance of the proposed MRMLAFF-RLDC model. The experimental results clearly establish the superior performance of the model on all major evaluation measures. In particular, the MRMLAFF-RLDC model achieved an impressive classification accuracy of 97.09%, besides a precision of 97.11%, recall of 97.09%, and F1-score of 97.08%. These outstanding values highlight the model's accuracy in predicting the proper class labels for the diverse leaf disease types even under differences in image conditions and complexities.

The overall high precision and recall values additionally support the model's strength and reliability in detecting disease patterns without repeated false positives or missed alarms. Such equilibrated performance across measures indicates the robustness of the framework in generalization and its resistance to visual variation within the data set. Overall, these findings confirm the practical utility of the MRMLAFF-RLDC architecture as an effective and trustworthy solution for precision agriculture. Its ability to support farmers in early and precise disease detection highlights its potential use in actual practice to enhance crop health monitoring and management.

Table 6. Result analysis of MRMLAFF-RLDC approach with distinct measures

Metrics	MRMLAFF-RLDC (%)
Accuracy	97.09
Precision	97.11
Recall	96.09
F1-Score	97.08

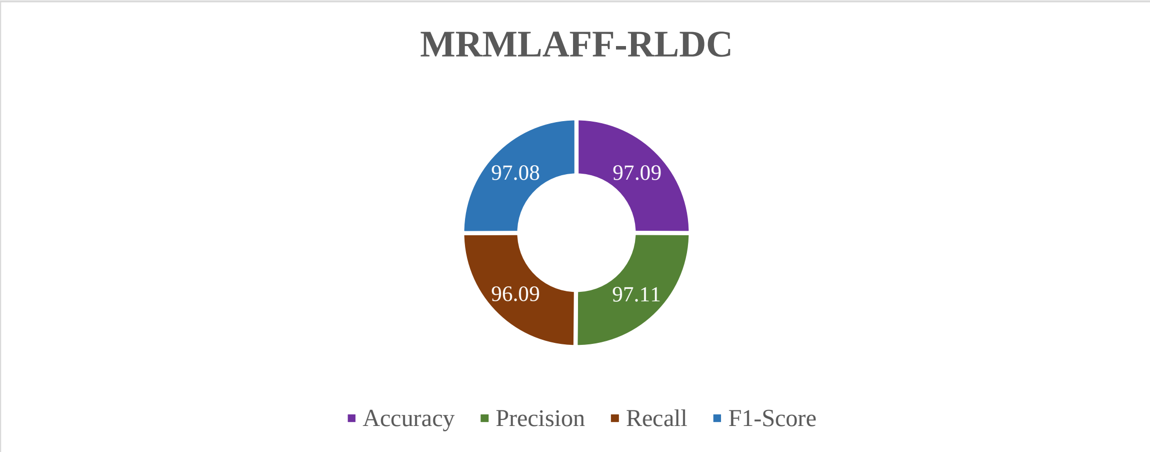


Figure 10. Result analysis of different metrics

Table 7 and Figure 11 show the outcomes of a thorough comparative assessment, highlighting the better performance of the presented MRMLAFF-RLDC model compared to some state-of-the-art strategies The experimental study indicates that standard architectures like the standard CNN and ResNet-18 attained comparatively low classification accuracies of 89.72% and 91.56%, respectively. Higher-level deep models, such as Inception-v3 and Vision Transformer (ViT), showed better performance with accuracy rates of 93.82% and 95.14%, which proved their efficiency in processing complex visual data. Nevertheless, the suggested MRMLAFF-RLDC framework surpassed all the baseline models with an exceptional classification accuracy of 97.09%. This notable margin of improvement demonstrates the power of the multi-resolution and attention-based feature fusion and meta-learning approaches utilized in the MRMLAFF-RLDC architecture. The comparative results unequivocally confirm MRMLAFF-RLDC as a highly accurate, robust, and reliable model for plant leaf disease detection, supporting its potential as a state-of-the-art solution for real-world agricultural diagnostics and precision farming.

Table 7. Accuracy analysis of MRMLAFF-RLDC model with existing approaches

Methods	Accuracy (%)
CNN	89.72
ResNet-18	91.56
Inception-V3	93.82
ViT	95.14
MRMLAFF-RLDC	97.09

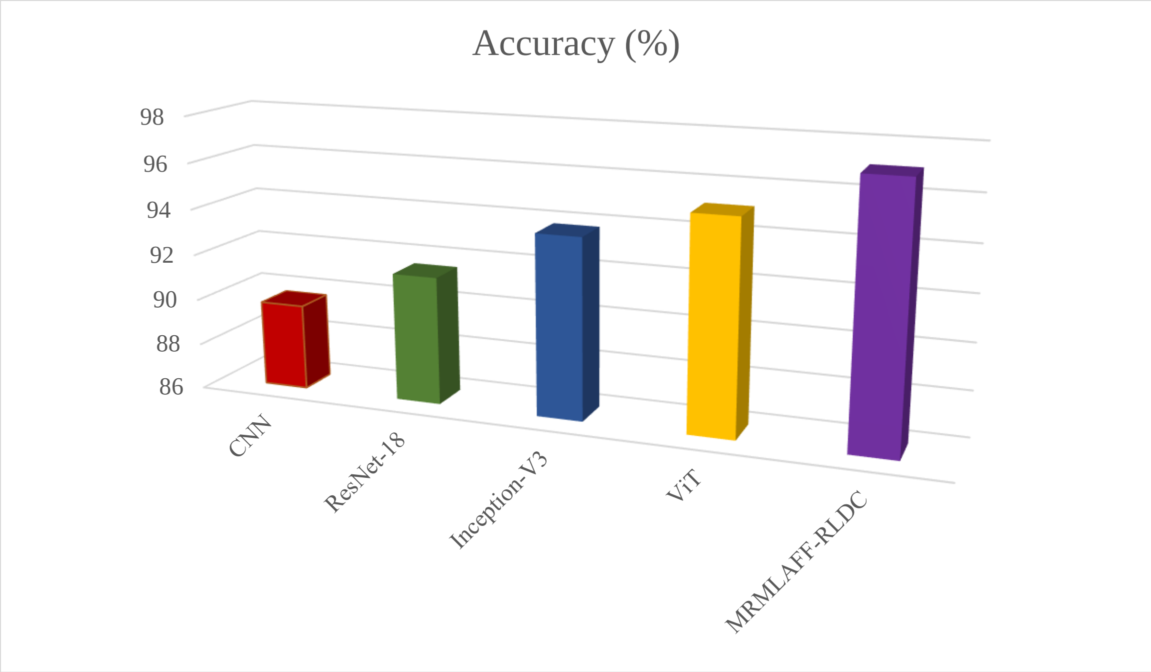


Figure 11. Accuracy analysis of MRMLAFF-RLDC approach with existing techniques

5. Conclusion

In this study, a new deep learning-based approach, MRMLAFF-RLDC (Multi-Resolution Meta-Learning with Attention-based Feature Fusion for Rice Leaf Disease Classification), was proposed to address the challenges of precise and effective plant leaf disease diagnosis. The suggested architecture combines efficient dual-resolution image processing, channel-wise attention mechanisms, and a meta-learning strategy to improve classification adaptability and accuracy. The preprocessing systematically, advanced feature extraction using two-stream CNNs, and feature fusion using SE blocks have collectively helped enhance the discriminative nature of the model. Additionally, utilization of a meta-classifier using fine-tuning helps maintain the stability of the framework under various and complex patterns of leaf diseases. Experimental verification, performed with the help of a well-prepared public rice leaf dataset, proved the efficacy of the proposed model as compared to other deep learning models in terms of accuracy, precision, recall, and F1-score.

In addition, the creation of an easy-to-use GUI for end-user interaction further highlights the real-world practical applicability of the system in farming practices. Through the identification of diseases at an early stage and at an accurate level, MRMLAFF-RLDC can support farmers in making timely decisions and managing crops. This work provides the basis for future research on AI-based smart farming systems, with potential extensions towards multi-crop disease classification, real-time deployment on mobile phones, and compatibility with recommendation systems for proper treatment recommendations.

Conflicts of Interest

The authors declare that they have no conflicts of interest to report regarding the present study.

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Declarations

- **Ethics approval and consent to participate**

  Not applicable. The study does not involve human participants, animals, or sensitive data requiring ethics approval.
- **Consent for publication**

  Not applicable. No identifiable personal data is included in this manuscript.
- **Availability of data and material**

  The dataset used in this study is publicly available and can be accessed through the Kaggle platform. Specific preprocessing steps and code are available upon request from the corresponding author.
- **Competing interests**

  The authors declare no competing interests related to this work.
- **Authors' contributions**

  S.P. Balamurugan : Conceived the study, performed data preprocessing, experimental analysis and prepared visualizations.

  CB. Sudhersun : Designed the model architecture, wrote the manuscript, and conducted the statistical evaluation.

  Both authors read and approved the final manuscript.

REFERENCES

[1] Simhadri C. G., Kondaveeti H. K., “Automatic Recognition of Rice Leaf Diseases Using Transfer Learning,” Agronomy, vol. 13, no. 4, p. 961, 2023.

[2] Muhammad S. Memon, Mumtaz Qabulio, Asia K. Soomro, “Deep Learning Based Effective Rice Leaf Disease Classification using MobileNet-Attention,” Asian Bulletin of Big Data Management, vol. 4, no. 4, 2024.

[3] Khairun Saddami, Yudha Nurdin, Mutia Zahramita, Muhammad Shahreeza Safiruz, “Advancing Green AI: Efficient and Accurate Lightweight CNNs for Rice Leaf Disease Identification,” arXiv e-prints, Aug. 2024.

[4] De’Silva T., Li G., Zheng Y., He R., Su J., “Meta-Learning for Few-Shot Plant Disease Detection”, Food, vol. 10, no. 10, pp. 2236–2252, 2021.

[5] Md. Shohanur Islam Sobuj, Md. Imran Hossen, Md. Foysal Mahmud, Mahbub U. I. Khan, “Leveraging Pre-trained CNNs for Efficient Feature Extraction in Rice Leaf Disease Classification,” arXiv e-prints, Feb. 2024.

[6] Li Z., Wu W., Wei B., Li H., Zhan J., Deng S., Wang J., "Rice Disease Detection: TLI-YOLO Innovative Approach for Enhanced Detection and Mobile Compatibility", Sensors, vol. 25, no. 8, art. 2494, 2025.

[7] Yuhai Li, Xiaoyan Chen, Lina Yin, Yue Hu, "Deep Learning-Based Methods for Multi-Class Rice Disease Detection Using Plant Images", Agronomy, vol. 14, no. 9, p. 1879, 2024.

[8] Fang K., Zhou R., Deng N., Li C., Zhu X., "RLDD-YOLOv11n: Research on Rice Leaf Disease Detection Based on YOLOv11", Agronomy, vol. 15, no. 6, art. 1266, 2025.

[9] Pandiyaraju V., Shravan Venkatraman, Abeshek A., Pavan Kumar S., Aravintakshan S. A., Senthil Kumar A. M., Kannan A., "A Channel Attention-Driven Hybrid CNN Framework for Paddy Leaf Disease Detection", arXiv preprint, 2024.

[10] Kayne Uriel K. Rodrigo, Jerriane Hillary H. Marcial, Samuel C. Brillo, Khatalyn E. Mata, Jonathan C. Morano, "An Enhancement of CNN Algorithm for Rice Leaf Disease Image Classification in Mobile Applications", arXiv preprint, 2024.

[11] Sadia Afrin Rimi, Md. Jalal Uddin Chowdhury, Rifat Abdullah, Iftekhar Ahmed, Mahrima Akter Mim, Mohammad Shoaib Rahman, "Empowering Agricultural Insights: RiceLeafBD – A Novel Dataset and Optimal Model Selection for Rice Leaf Disease Diagnosis through Transfer Learning Technique", arXiv preprint, 2025.

[12] Ayyappan A. B., Gobinath T., Kumar M., et al., "Rice Plant Disease Detection using Convolutional Neural Networks", Discovery Artificial Intelligence, vol. 5, no. 1, p. 50, 2025.

[13] Zhou C., Zhou C., Yao L., Du Y., Fang X., Chen Z., Yin C., "An Improved YOLOv5s-based Method for Detecting Rice Leaves in the Field", Frontiers in Plant Science, vol. 16, art. 1561018, 2025.

[14] Samia Mehnaz, Md. Touhidul Islam, "Rice Leaf Disease Detection: A Comparative Study Between CNN, Transformer and Non-neural Network Architectures", arXiv preprint, 2025.

[15] Y. Cao, "Detection and Classification of Pests and Diseases in Rice Leaf Images Based on Deep Learning Algorithms", Applied and Computational Engineering, vol. 74, no. 219, pp. 219–224, 2024.

[16] C. G. Simhadri, H. K. Kondaveeti, "Automatic Recognition of Rice Leaf Diseases Using Transfer Learning", Agronomy, vol. 13, no. 4, p. 961, 2023.

[17] J. Arcila-Diaz, D. Altamirano-Chavez, L. Arcila-Diaz, C. Valdivia, "Real-Time Identification of Rice Leaf Diseases Using Convolutional Neural Networks", International Journal of Computing, vol. 23, no. 4, pp. 709–714, 2024.

[18] M. Jothika, S. Nathiya, "Efficient Categorization and Prediction of Rice Leaf Diseases Using Machine Learning and Inception V3 with Transfer Learning", International Journal of Intelligent Systems and Applications in Engineering, vol. 11, no. 1, pp. 95–109, 2024.

[19] P. S. Seelwal, T. R. Rohilla, "Optimized Light-Weight Deep Learning Model for Rice Disease Identification", International Journal of Intelligent Systems and Applications in Engineering, vol. 12, no. 2 (special), pp. 657–664, 2024.

[20] B. Paneru, "Analysis of Convolutional Neural Network-Based Image Classifications: A Multi-Featured Application for Rice Leaf Disease Prediction and Recommendations for Farmers", Indonesian Journal of Electronics, Electromedical Engineering, and Medical Informatics, vol. 6, no. 3, pp. 1–? (article unspecified), 2024.

[21] K. K. Kumar, S. Sasikala, G. Maheswari, B. Kumar, S. Suthar, P. Sridevi, D. Kavitha, T. Vengatesh, "A Convolutional Neural Network Approach for Rice Leaf Disease Detection in India Using Deep Learning", Journal of Neonatal Surgery, vol. 14, no. 4 (S), pp. 1024–1028, 2025.

[22] S. Sistla, V. Vallabhajosyula, V. K. K. Kolli, "Advanced Diagnosis of Common Rice Leaf Diseases Using KERTL-BME Ensemble Approach", Journal of Real-Time Image Processing, 2024.

[23] https://www.kaggle.com/datasets/dedeikhsandwisaputra/rice-leafs-disease-dataset

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