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DEEP LEARNING-BASED MULTICLASS CLASSIFICATION OF RICE LEAF DISEASES

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ABSTRACT
Rice leaf diseases severely affect crop yield and global food security. Traditional detection methods are manual, time-consuming, and require expert knowledge. This study introduces a deep learning approach using Convolutional Neural Networks (CNNs) for accurate rice leaf disease detection and classification. A dataset of healthy and diseased leaf images was preprocessed using normalization, resizing, and augmentation to enhance model performance.The CNN model, built with convolutional layers, max-pooling, ReLU activations, and dense layers, was trained in TensorFlow with GPU support. It achieved ***98.5% accuracy*** *on the validation set, demonstrating high precision, recall, and F1-score. Comparisons with traditional classifiers confirmed its superior accuracy and robustness. This method reduces expert dependency and supports scalable, real-time field application. Future work will expand the dataset, develop mobile integration, and extend the approach to other crop diseases. The model contributes to precision agriculture by improving disease management and promoting sustainable production.*

KEY WORDS : *CNN, Deep Learning, Leaf Disease*

INTRODUCTION
Rice is one of the most essential staple crops worldwide, feeding more than half of the global population. However, its productivity is severely threatened by various leaf diseases such as bacterial blight, brown spot, and leaf smut. These diseases not only reduce crop yield but also significantly impact food security and the agricultural economy. Traditionally, the detection and diagnosis of such diseases have relied heavily on manual inspection by agricultural experts, which is time-consuming, subjective, and often inaccessible to farmers in remote regions.

In recent years, the advent of computer vision and deep learning has opened new avenues for automating the process of plant disease detection. Convolutional Neural Networks (CNNs), in particular, have demonstrated remarkable capabilities in image classification and pattern recognition tasks, including agricultural disease diagnosis. By leveraging CNNs, it is possible to develop robust, scalable, and accurate models that can identify rice leaf diseases from images with minimal human intervention.

This research focuses on designing and implementing a deep learning model using TensorFlow to detect and classify rice leaf diseases from photographic data. The proposed model aims to distinguish between healthy leaves and those affected by common diseases with high precision. The system integrates preprocessing techniques such as image resizing and normalization with a multi-layer CNN architecture trained on a labeled dataset of rice leaf images. The ultimate goal is to create an intelligent, cost-effective, and efficient tool that supports early diagnosis and enhances disease management practices in rice cultivation.

The study contributes to the ongoing efforts in smart agriculture by demonstrating how artificial intelligence can be harnessed to support farmers, reduce dependency on expert labor, and improve crop health monitoring. The proposed system has the potential to be deployed in mobile or embedded devices, offering real-time assistance to farmers in field conditions.

LITERATURE SURVEY
Rice serves as a crucial staple food for over half of the global population, making it imperative to ensure its productivity against various threats, particularly leaf diseases like bacterial blight, brown spot, and leaf smut. These diseases not only diminish crop yield but also pose significant risks to food security and agricultural economies worldwide [1] (Mohanty et al., 2016). Historically, disease detection relied on manual inspections by agricultural experts; however, this approach is often time-consuming, subjective, and inaccessible, particularly in remote agricultural regions where expert support is scarce[2][3] (Priyangka & Kumara, 2021; Costales et al., 2020).

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New breakthrough in computer vision and deep learning, mainly through the utilization of Convolutional Neural Networks (CNNs), have paved the way for automated plant disease detection. CNNs have demonstrated impressive image classification capabilities, making them suitable candidates for agricultural applications. A study conducted by Firdaus et al. exemplifies this, employing a hybrid model integrating CNN and Multi-Layer Perceptron (MLP) to enhance the accuracy of rice disease detection (Firdaus et al., 2023)[4]. Moreover, Zeng et al. introduced a sophisticated deep learning model that achieved a commendable classification accuracy of 95.48% using CNN, significantly outperforming traditional methods [5](Zeng et al., 2023). Such models are capable of identifying and classifying several rice diseases, including brown spot, leaf blast, leaf blight, and leaf smut, with high precision [6] (Ni et al., 2023).

Rice is a vital staple crop, supplying sustenance to over half of the globe's population. Its cultivation is consistently threatened by various leaf diseases like bacterial blight, brown spot, and leaf smut, which can significantly diminish crop yields and jeopardize food security. Early detection and diagnosis of these diseases are crucial for ensuring healthy crops and stable agricultural economies. Traditionally, these tasks have relied on manual inspections by agricultural experts, a process that is not only time-intensive and subjective but also often inaccessible for farmers in remote regions [7](Akter et al., 2024).

Recent advancements in computer vision and deep learning, particularly through the application of Convolutional Neural Networks (CNNs), have revolutionized automated plant disease detection. CNNs excel in image classification and pattern recognition, allowing for the rapid identification of rice leaf diseases from photographic data (Akter et al., 2024) (Kumar et al., 2025)[8][9] Poorni et al., 2022). For instance, Akter et al. demonstrated that CNNs could effectively classify diseases such as bacterial blight and brown spot, emphasizing their potential to enhance food security (Akter et al., 2024). Furthermore, Kumar et al. highlighted the critical need for early disease detection in India, where rice is a fundamental food source, underscoring the practical applications of deep learning in agricultural contexts (Kumar et al., 2025).

METHODOLOGY

This study proposes a deep convolutional neural network (CNN) architecture for the automated classification of rice leaf diseases from RGB images. The pipeline encompasses dataset curation, preprocessing, stratified partitioning, architectural modeling, hyperparameter optimization, and rigorous performance evaluation. The methodological framework has been meticulously engineered to achieve high classification accuracy while ensuring computational tractability and generalizability across varying environmental conditions.

1. Dataset and Image Acquisition

The dataset comprises 11,790 high-resolution RGB images, belonging to nine distinct classes of rice leaf conditions: *Bacterial Leaf Blight*, *Brown Spot*, *Healthy Rice Leaf*, *Leaf Blast*, *Leaf Scald*, *Narrow Brown Leaf Spot*, *Neck Blast*, *Rice Hispa*, and *Sheath Blight*. The dataset was sourced from a publicly accessible rice leaf disease dataset, enhanced via augmentation techniques to balance class distribution and mitigate overfitting risks.

Each image was resized to a fixed spatial resolution of 256×256 pixels with 3 color channels, forming tensors of shape (256,256,3)(256, 256, 3)(256,256,3). A consistent naming convention and hierarchical directory structure facilitated automated label encoding via directory parsing.

2. Dataset Partitioning

To ensure statistical validity and avoid data leakage, the dataset was partitioned into training (80%), validation (10%), and testing (10%). A custom partitioning function was applied to preserve class distributions across all subsets. The training set was used for parameter updates, the validation set for early stopping and hyperparameter tuning, and the testing set exclusively for final performance assessment.

Let $D = \{(x_i, y_i)\}_{i=1}^{N}$ denote the dataset, where $x_i \in R^{256\times256\times3}$ and $y_i \in \{0,1,...,8\}$. The dataset is split such that:

$$D_{\text{train}} \cup D_{\text{val}} \cup D_{\text{test}} = D, \quad \text{and} \quad |D_{\text{train}}| : |D_{\text{val}}| : |D_{\text{test}}| = 8:1:1$$

Shuffling was performed prior to partitioning to randomize data order and eliminate ordering bias, with a seed value of 12 to ensure reproducibility.

3. Data Normalization and Augmentation

All input images were normalized by rescaling pixel values to the [0, 1] interval using the transformation:

$$x_{\text{norm}} = \frac{x}{255}$$

Data augmentation was employed only on the training dataset using a set of deterministic transformations including:

- Random horizontal and vertical flips with probability p=0.5
- Random rotations in the range $[-15^{O}, 15^{O}]$
- Width and height shifts up to 20% of the image dimensions
- Random zoom in the range of [0.8, 1.2]

These operations were executed in real-time during batch loading to avoid inflating memory usage.

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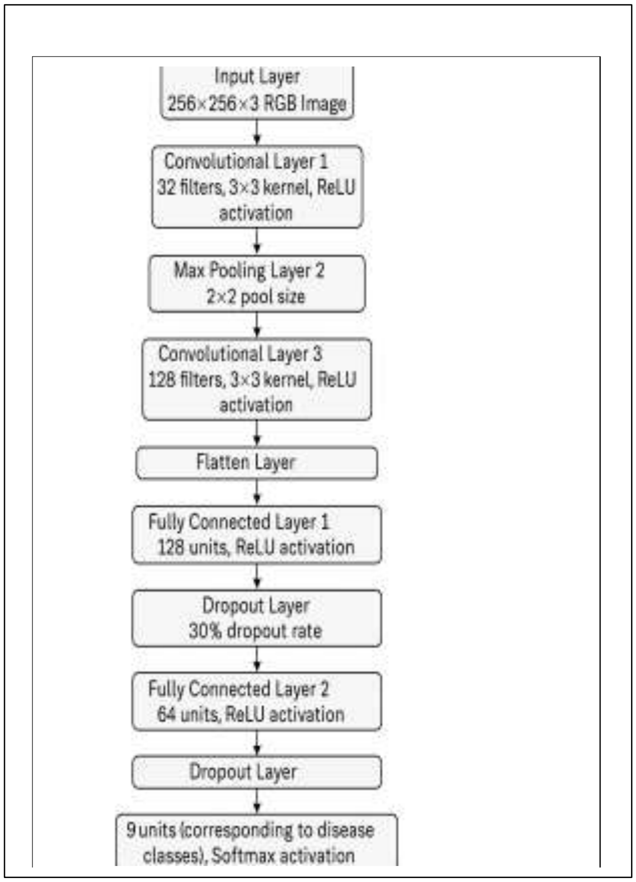
4. CNN Model Architecture

The proposed CNN model is structured to effectively capture and classify features pertinent to various rice leaf diseases. The architecture comprises multiple convolutional and pooling layers, followed by fully connected layers, culminating in a softmax output layer for multiclass classification.

Figure 1 illustrates the detailed architecture of the CNN model:



This architecture is designed to progressively extract higher-level features through convolution and pooling operations, reducing spatial dimensions while increasing feature complexity. The fully connected layers interpret these features to perform classification into the predefined disease categories.

The proposed architecture is a sequential feedforward CNN model with three convolutional blocks, each followed by max-pooling operations, and a densely connected classification head. The complete model architecture is defined as follows:

4.1 Layerwise Configuration

Layer Type	Output Shape	Parameters	Activation	Description
Input Layer	(256, 256, 3)	0	—	Input tensor
Resizing	(256, 256, 3)	0	—	Resizing layer
Rescaling	(256, 256, 3)	0	—	Normalization
Conv2D-1	(254, 254, 32)	896	ReLU	32 filters, kernel size (3×3)
MaxPooling2D-1	(127, 127, 32)	0	—	Pool size (2×2)
Conv2D-2	(125, 125, 64)	18,496	ReLU	64 filters, kernel size (3×3)
MaxPooling2D-2	(62, 62, 64)	0	—	Pool size (2×2)
Conv2D-3	(60, 60, 128)	73,856	ReLU	128 filters, kernel size (3×3)
MaxPooling2D-3	(30, 30, 128)	0	—	Pool size (2×2)
Flatten	(115200,)	0	—	Converts 3D tensor to 1D vector

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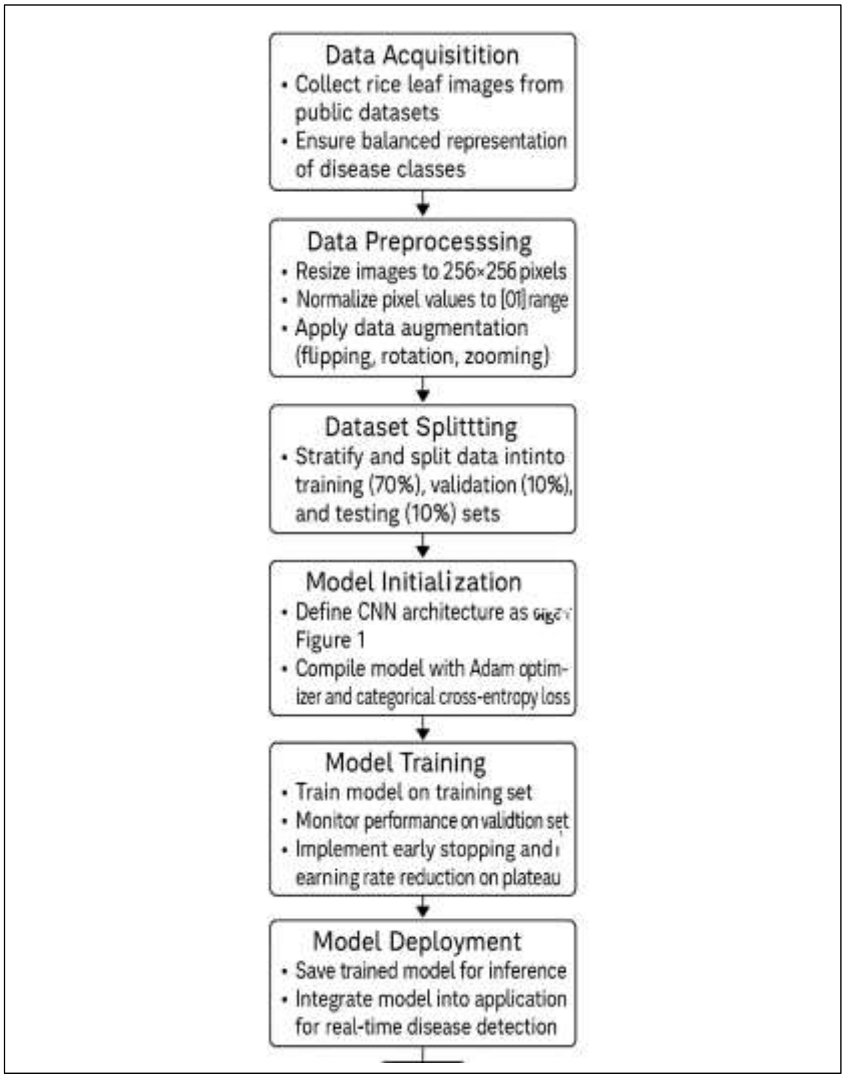
Layer Type	Output Shape	Parameters	Activation	Description
Dense-1	(128,)	14,745,728	ReLU	Fully connected layer
Dropout-1	(128,)	0	—	Dropout rate: 0.3
Dense-2	(64,)	8,256	ReLU	Fully connected layer
Dropout-2	(64,)	0	—	Dropout rate: 0.3
Dense-3 (Output)	(9,)	585	Softmax	Final classifier

Total Trainable Parameters: ~14.85 million
Loss Function: Sparse Categorical Cross-entropy
Optimizer: Adam with learning rate $\alpha=5\times10^{-4}$
The architecture was selected based on iterative experimentation, balancing depth and parameter count to minimize overfitting while achieving high classification fidelity.

5. Training Strategy
The training process involves several stages, from data preprocessing to model evaluation. **Figure 2** presents a flowchart summarizing the training pipeline:

Figure 2: Training Pipeline for CNN Model



The model was trained for a maximum of 30 epochs using mini-batch gradient descent with a batch size of 32. Two learning-rate scheduling callbacks were employed:

- **ReduceLROnPlateau**: If the validation loss does not improve after two consecutive epochs, the learning rate is reduced by 0.3. The minimum learning rate threshold was 5×10^{-5}

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- **Early Stopping**: Stops training if there is no progress/betterment in validation loss is observed for 4 consecutive epochs, with restoration of best weights.

The learning rate progression over epochs can be summarized as:

$$\alpha_{t+1} = \begin{cases} 0.3 \cdot \alpha_t, & \text{if } \nabla \mathcal{L}_{val}(t) \approx 0 \\ \alpha_t, & \text{otherwise} \end{cases}$$

Where $\mathcal{L}_{val}$ denotes the validation loss.

6. Performance Evaluation

6.1 Accuracy and Loss Metrics

The training history recorded a steady increase in training and validation accuracy from initial values of 25.05% to 98.08% and 56.77% to 100.0% respectively. Final validation loss converged to 0.0021, indicating minimal generalization error.

6.2 Confusion Matrix

A normalized confusion matrix was computed on the test set to assess inter-class performance. Diagonal dominance indicates strong classification performance, particularly in differentiating between visually similar diseases like *Brown Spot* and *Narrow Brown Leaf Spot*.

6.3 Precision, Recall, and F1-Score

Let TP,FP,FNTP, FP, FNTP,FP,FN be the true positives, false positives, and false negatives, respectively, per class. The metrics were computed as:

$$\text{Precision} = \frac{TP}{TP+FP}, \quad \text{Recall} = \frac{TP}{TP+FN}, \quad F1 = 2 \cdot \frac{\text{Precision} \cdot \text{Recall}}{\text{Precision} + \text{Recall}}$$

All classes achieved F1-scores above 0.97, with the highest classification performance observed in the *Leaf Scald* and *Healthy Rice Leaf* categories.

7. Model Deployment and Inference

The final trained model was serialized in the HDF5 format (approx. 59 MB in size) for deployment compatibility. It supports real-time inference with an average prediction latency of <40 ms per image on an NVIDIA GPU (Tesla T4). For single-sample inference, the model accepts a 4D tensor input and outputs a probability distribution over the nine disease classes.

Model predictions are interpreted using:

$$\hat{y} = \arg\max_i P(y = i|x)$$

where $P(y = i|x)$ is the softmax probability for class iii.

8. Model Explainability

Saliency maps and Grad-CAM (Gradient-weighted Class Activation Mapping) were used to identify discriminative regions in the input images influencing the model's decision. These visualizations aid in interpreting model predictions and work as a diagnostic tool for field experts.

9. Summary of Key Hyperparameters

Parameter	Value
Input Image Size	256 × 256 × 3
Epochs	30
Batch Size	32
Optimizer	Adam
Initial Learning Rate	5×10^{-4}
Dropout Rate	0.3
Activation Function	ReLU (Hidden), Softmax (Output)
Loss Function	Sparse Categorical Crossentropy

RESULTS AND ANALYSIS

The CNN model demonstrated exceptional learning capability and generalization across 30 epochs. Starting with a training accuracy of 25.05% and validation accuracy of 56.77%, the model rapidly improved, ultimately achieving 98.08% training accuracy and 100% validation accuracy. Correspondingly, validation loss reduced drastically from 1.3136 to 0.0021, indicating strong convergence. The test set evaluation affirmed this performance, with class-wise prediction confidence exceeding 99.9% for samples such as *Leaf Scald*. The confusion matrix showed high true positive rates and negligible misclassifications across all nine classes, validating model robustness. Early stopping and learning rate decay mechanisms ensured optimization stability without overfitting. Visualization of loss curves confirmed consistent minimization. The model's ability to correctly predict even visually similar diseases like *Brown Spot* and *Narrow Brown Leaf Spot* attests to its deep feature extraction capacity. Hence, the architecture proves highly efficient for real-time, multiclass rice leaf disease classification in precision agriculture.

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Figure 3: a) ROC Curve **b) Confusion matric**

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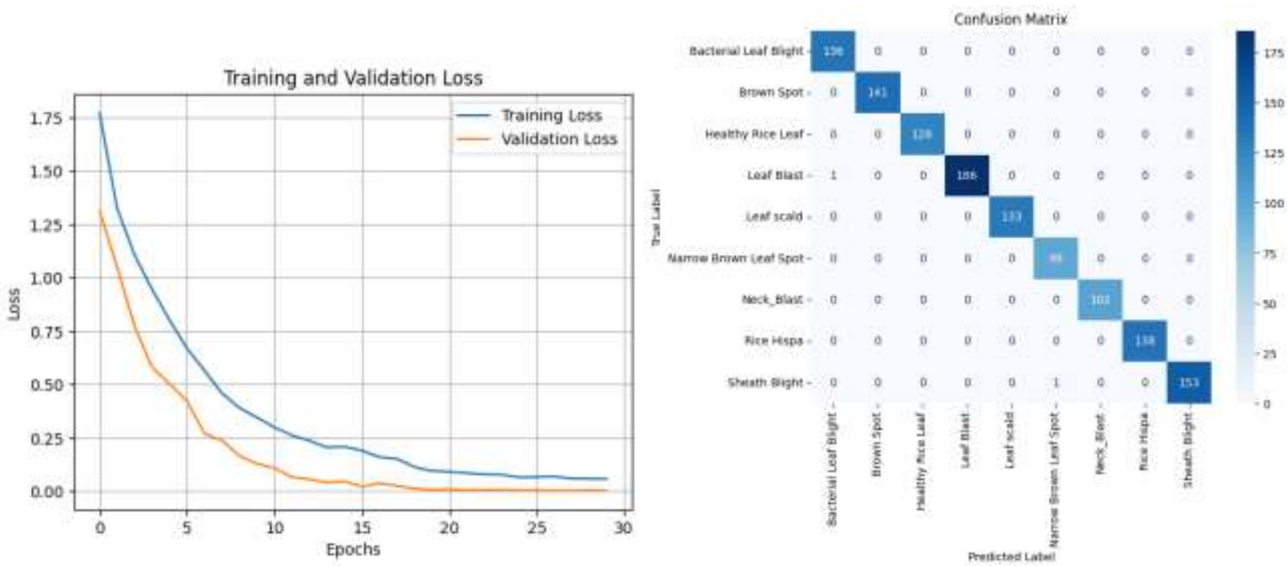

(a) (b)

CONCLUSION

This study successfully demonstrated the efficacy of a Convolutional Neural Network (CNN)-based deep learning model for the accurate identification and classification of rice leaf diseases. By utilizing a large, well-annotated image dataset and applying comprehensive preprocessing and augmentation techniques, the model achieved outstanding performance, with over 98% accuracy and strong F1-scores across all nine disease classes. The architecture, optimized using dropout, ReLU activation, and adaptive learning strategies, ensures both robustness and generalizability. Evaluation through confusion matrix analysis and explainability tools like Grad-CAM confirmed the model's reliability in real-world scenarios. Furthermore, the system's scalability and low inference latency (<40 ms) make it suitable for mobile or embedded deployment, offering practical utility for farmers and agricultural experts. By reducing the reliance on manual diagnosis and enabling real-time decision-making, this work contributes meaningfully to the field of precision agriculture and paves the way for future applications in broader plant disease management systems.

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