

A Novel Approach for Rice Disease Classification Under Intra-Class Variability

Mansi Negi¹, Prabh Deep Singh¹, Vikas Tripathi¹

1. Computer Science and Engineering, Graphic Era Deemed to be University, Dehradun, IND

Corresponding author: Mansi Negi, mansinegi366@gmail.com

Received 05/29/2025
Review began 07/07/2025
Review ended 07/31/2025
Published 09/02/2025

© Copyright 2025

Negi et al. This is an open access article distributed under the terms of the Creative Commons Attribution License CC-BY 4.0., which permits unrestricted use, distribution, and reproduction in any medium, provided the original author and source are credited.

DOI:

<https://doi.org/10.7759/s44389-025-07037-z>

Abstract

Agriculture is the foundation of India's economy, and India comes after China in the production of rice in the world. Rice disease can affect crops, leading to quantity-quality losses and capitalistic setbacks. Therefore, rice disease is a risk to food safety universally, so it requires effective and early detection. Currently, many deep learning techniques have been proposed for rice disease classification, although they have been restrained by low accuracy and data variety. Old authentic methods hang on manual detection, which is time-consuming and leads to increased errors, highlighting the need for an automated classification system. To address this issue, this research proposes a DenseNet121-based deep learning model optimized with Adam. The model was trained on a dataset of 5,932 images acquired from Mendeley Data. Experimental results demonstrate that the proposed model outperforms existing approaches. The result shows that DenseNet121 with Adam optimizer offers a solid solution for precise rice disease classification, achieving 95% accuracy along with balanced precision, recall, and F1-score across all disease classes. Future work will involve expanding the dataset and implementing the model in mobile or edge computing applications for deployment in the field.

Categories: Computer Vision, Machine Learning (ML), Deep Learning

Keywords: rice leaf diseases, classification, deep learning, accuracy, densenet121

Introduction

Hoing land to plant crops is referred to as agriculture. Roughly 20% of the country's GDP comes from the agricultural sector [1]. Asian and other countries consume over 90% of the global rice. Indians, or around 70% of the entire population, make their living through agriculture [2].

The most crucial contributor to the economy and society is the farmer, as they are the ones who till the soil. Approximately 319,598 farmers and agricultural laborers in India committed suicide between 2005 and 2020. In addition to pathogen-induced diseases, climatic factors such as temperature fluctuations, high humidity, and pest infestations significantly contribute to crop stress and yield loss in rice cultivation [3]. One major cause of the high rate of farmer suicides is crop failure. Therefore, timely identification and classification of crop diseases is essential to minimize crop loss, prevent suicides, and enable early treatment and prevention. Rice is one of the most essential staple foods in India and the whole world, but with the growing population and economic development, rice consumption is projected to reach 8 million tons in the foreseeable future [4]. Crop failure could lead to hunger and impairment. Given the increasing number of rice diseases, protecting the crop has become crucial. Traditional manual disease identification methods are outdated, labor-intensive, and prone to errors.

There have been numerous deep learning methods for rice disease detection and classification proposed in the last year. Despite their impressive results, deep learning has several drawbacks, such as low accuracy and data diversity. DenseNet demonstrates direct connections for L layers in this work. All layers in DenseNet take as input every preceding layer and provide their output to all subsequent ones. Among its numerous advantages, DenseNet drastically reduces the number of parameters, enhances feature propagation, encourages feature reuse, and addresses the vanishing-gradient problem [5]. DenseNet has several variations, including DenseNet121, DenseNet169, DenseNet201, and DenseNet264. Each variation has its strengths and weaknesses. Three DenseNet models, DenseNet121, DenseNet169, and DenseNet201, were utilized in recent studies by Saputra et al. [6] for rice disease classification, achieving accuracies of 93.2%, 94.6%, and 95.1%, respectively. However, it is not clear whether these results were achieved under identical training conditions, which could affect the fairness of the comparison [6].

In this research, DenseNet121 with the Adam optimizer is proposed to categorize four types of rice leaf disease (Figure 1). To improve classification performance, the proposed model uses the Adam optimizer. The deep learning-based classification model is trained on representative images, which also highlight the visual differences between the disease classes.

How to cite this article

Negi M, Singh P, Tripathi V (September 02, 2025) A Novel Approach for Rice Disease Classification Under Intra-Class Variability. Cureus J Comput Sci 2 : es44389-025-07037-z. DOI <https://doi.org/10.7759/s44389-025-07037-z>

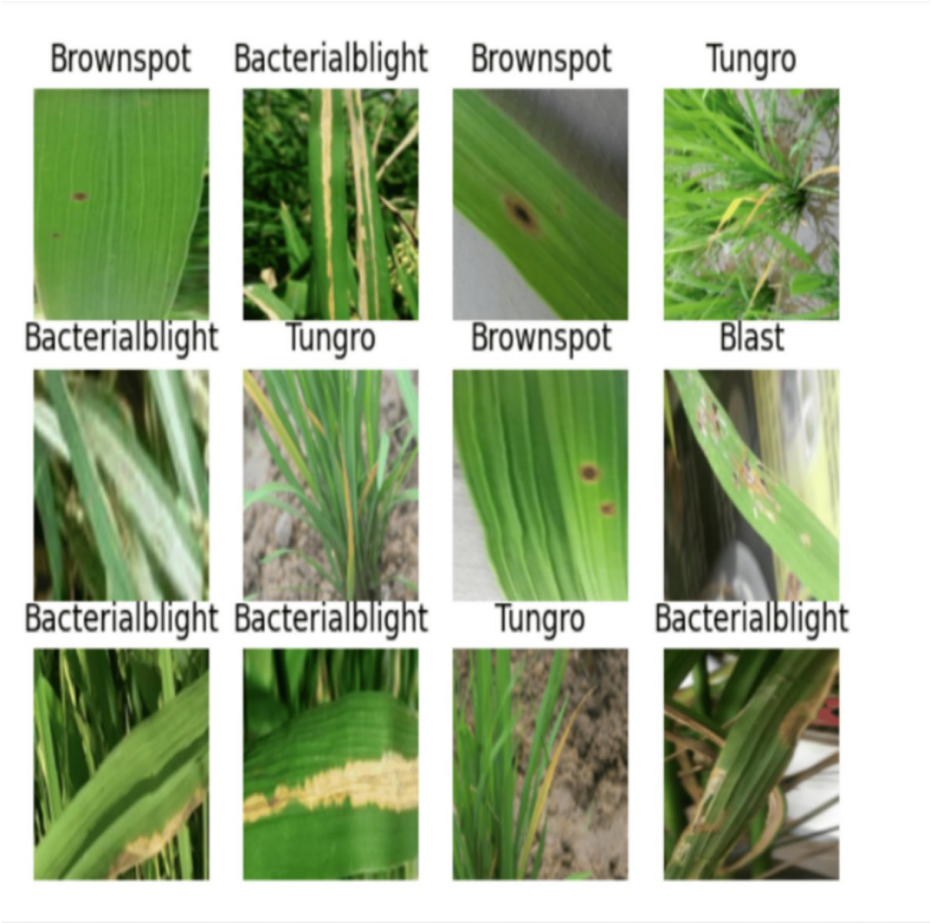


FIGURE 1: Rice Leaf Disease

Literature survey

Relevant literature is described in this section to support the development of a deep learning model that can provide improved classification accuracy for rice leaf diseases. Deep learning has been employed in recent research to classify rice leaf diseases, with various methods used to detect deteriorated rice leaf images.

Rukhsar and Upadhyay [1] utilized deep convolutional neural networks (CNN) and the InceptionV3 transfer learning model to identify rice diseases using a dataset from Kaggle containing four different disease types. Their results showed that the model achieved an accuracy of 90.50% with InceptionV3, compared to 63.40% with CNN.

Sachan et al. [7] evaluated several algorithms such as Support Vector Machine, VGG19, ResNet152V2, InceptionV3, and MobileNetV2 in conjunction with thermal imaging techniques for disease detection. Among these, InceptionV3 demonstrated strong performance with an accuracy of 92.34% in agriculture.

Sindhu et al. [8] employed ResNet50, InceptionV3, and MobileNetV2 for multi-class disease recognition, achieving accuracies of 91.89%, 82.79%, and 73.02%, respectively. Furthermore, a Stacking Classifier was deployed, which attained the highest accuracy of 96.09%, emphasizing the feasibility and effectiveness.

Van Ho et al. [9] integrated CNN with ResNet and DenseNet architectures in an ensemble approach. To enhance model generalization,, their dataset consisted of 3,355 preprocessed and improved images. With an F1-score of .096 in 10 trials, the proposed ensemble exhibited great precision and stability.

Liu et al. [10] proposed a combined model that integrates an attention-augmented DenseNet classifier and a strengthened U-Net for lesion region extraction. Rice leaf images were utilized to demonstrate the ability of the algorithm to detect disease regions. This approach demonstrates how a region-based attention process can significantly enhance disease identification accuracy by 96%.

Govindharaj et al. [11] proposed a CNN-RF hybrid model to improve the evaluation of rice crop health. The

CNN and RF models alone achieved accuracies of 88.2% and 86.7 %, respectively, and the hybrid model improved performance, achieving an accuracy of 93.5%

Saini et al. [12] developed a hybrid model by adding pre-trained MobileNetV2 and CNNs. Whereas Mobilenetv2 is employed to obtain features, the CNN model is applied for classification, and the model is employed at different epochs with a 32-batch size. This model achieved an accuracy rate of 92.17%.

Kavitha et al. [13] proposed EfficientNet for rice disease classification and compared it with other models like VGG16, ResNet50, and InceptionV3 based on various validation metrics. The proposed model achieved a precision of 94.4% and a recall of 92.9%, outperforming the others.

Finally, Mandwariya and Jotwani [14] applied a CNN and a 1,500-image dataset to self-classify three different diseases of rice: bacterial blight, blast, and brown mark. The accuracy of the model in classifying individual diseases was 78.44%, and its accuracy in distinguishing between healthy leaves and diseased ones was 94%.

Table 1 presents a comparative overview of significant studies on deep learning approaches for rice disease classification. Classical convolutional neural networks (CNNs) and transfer learning were commonly used in earlier works. For instance, Satoto et al. [15] employed GoogleNet and a custom neural network, achieving 80.94% accuracy. Kavin Kumar et al. [16] reached 89% accuracy using CNN with advanced image preprocessing on 4,112 rice leaf images from Kaggle.

Table 1 presents a comparative overview of significant research on the application of deep learning methods for rice disease classification. Classical CNNs and the transfer learning approach were utilized in earlier research. For instance, Satoto et al. [15] employed GoogleNet and a custom neural network and achieved an accuracy of 80.94%, while Kavin Kumar et al. [16] attained 89% accuracy utilizing CNN with advanced image preprocessing strategies on 4,112 images of rice leaves taken from Kaggle. Similarly, Ghosh et al. [17] applied a CNN to a large annotated image set containing 3,600 images of rice leaves and achieved a high accuracy of 92%. Further improvements were observed with the integration of preprocessing and segmentation techniques. Singh and Singh [18] combined preprocessing and segmentation techniques, which improved classification performance with 94.56% accuracy, 94% precision, and 94% recall. More recent works have focused on transfer learning and ensemble models. Barakala et al. [19] tested numerous architectures such as MobileNet, VGG16, InceptionV3, and ResNet50 with a dataset of 2,586 images. MobileNet had the greatest accuracy at 90%. Yasid et al. [20] utilized EfficientNetB3 with transfer learning, resulting in 79.43% accuracy and area under the curve (AUC) of 0.9321, although at the cost of considerable CPU resources. Hybrid and attention-enhanced models have also shown significant improvements. El-Shahat et al. [21] introduced a hybrid MobilNet Deep Network with an accuracy of 91.8% and an AUC of 0.949. Similarly, Singh and Kumar [22] integrated EfficientNetB4 with the convolutional Block Attention Module, achieving 93% accuracy and demonstrating the potential of attention mechanisms in improving disease prediction, although the dataset was limited to four classes.

Reference	Dataset	Methodology	Performance Metrics	Key Finding	Limitation
[15]	Rice Leaf Image (Kaggle)	GoogleNet and CustomNet	Accuracy: 80.94%	Data augmentation improved performance	Moderate accuracy, slow inference time
[16]	Dataset of 4,112 images (Kaggle)	CNN	Accuracy: 89%	Advanced image processing enhanced classification	Requires validation across diverse environments
[17]	Annotated dataset of 3,600 images (Kaggle)	CNN	Accuracy: 92%	High accuracy in disease detection	Requires extensive training data
[18]	Rice leaf images dataset	CNN with preprocessing and segmentation	Accuracy: 94.56%, Precision: 94%, Recall: 94%	Preprocessing improved classification accuracy	Needs validation on larger datasets
[19]	Rice Leaf Diseases dataset of 2,586 images (Kaggle)	MobileNet, VGG16, InceptionV3, ResNet50	Accuracy: 90%, Precision: 0.90, Recall: 0.89, F1: 0.90	MobileNet achieved the highest accuracy	Limited data diversity
[20]	Rice Leaf's dataset of 3,355 images (Kaggle)	EfficientNetB3 with transfer learning	Accuracy: 79.43%, AUC: 0.9321	Performed better than MobileNetV3 and InceptionV3	Requires high computational power
[21]	Paddy Doctor dataset (16,225 images)	HMobilenetDN (Hybrid MobileNet + DNN)	Accuracy: 91.8%, Precision: 91.8%, Recall: 90.7%, F1: 91.2%, AUC: 0.949	Reduced computing cost with improved capacity	Suffers from overfitting on small datasets
[22]	Rice Disease Image Dataset (3,355 images) (Kaggle)	Eff-CBAM (EfficientNetB4 + CBAM Attention)	Accuracy: 93%	Attention mechanism improved prediction	The dataset limited to four classes

TABLE 1: Comparision of Different Models for Rice Disease Classification

AUC, Area Under the Curve; CBAM, Convolutional Block Attention Module; CNN, Convolutional Neural Network; DNN, Deep Neural Network

Materials And Methods

Data collection

Four types of rice leaf diseases - Bacterial Blight, Brown Spot, Leaf Blast, and Tungro - are part of the dataset used in this work, obtained from Mendeley Data [23]. The dataset was stored on Google Drive for easy accessibility during training and testing, and it was imported using TensorFlow's 'pathlib' module. Table 2 shows the distribution of images, whereas the dataset was divided into two subsets: 80% for training and 20% for validation. The original dataset is publicly available at <https://data.mendeley.com/datasets/fwcj7stb8r/1>.

Classes	Total Images	Training	Validation
Bacterial Blight	1,584	1,268	316
Blast	1,440	1,152	288
Brown Spot	1,600	1,280	320
Tungro	1,308	1,047	261

TABLE 2: Distribution of Images Into Training and Validation Sets

Image preprocessing

To simulate the visual differences observed in rice fields in the real world, the augmentation methods were applied consistently across the dataset. TensorFlow's Keras API ImageDataGenerator was employed to preprocess the images. To improve model generalization, the preprocessing includes rescaling pixel values (divided by 255 to normalize them between 0 and 1) and applying data augmentation techniques. Zooming, rotation, brightness adjustments, width and height changes, and horizontal flipping are a few of these augmentations. All these parameters are shown in Table 3.

Parameter	Value
Zooming	0.5
Rotation	0.5
Brightness	[0.7, 1.3]
Width Shift	0.25
Height Shift	0.25
Horizontal Flip	True

TABLE 3: Augmentation Parameters

Proposed model

The flowchart of the proposed methodology, indicating the whole process from loading and preprocessing the dataset to model training and testing, is presented in Figure 2. It provides an exhaustive summary of the complete pipeline, which employs the DenseNet121 model with the Adam optimizer for classifying rice diseases. The proposed architecture is shown in Figure 3. The DenseNet121 model is utilized with ImageNet. For reducing dimensionality while preserving the important characteristics, a Global Average Pooling layer is employed. A fully connected layer of 256 neurons, ReLU activation, and L2 regularization $\lambda = 0.01$ is added along with a dropout layer (0.4) to prevent overfitting. The generalization is enhanced by the other dropout layer (0.3). Categorizing the images into four groups, Bacterial Blight, Blast, Brown Spot, and Tungro, is done by the fourth softmax layer that consists of four output neurons. DenseNet121 applies the following formula to build the output of each layer from all its preceding feature maps: The output of layer l is defined as:

$$x_l = H_l([x_0, x_1, \dots, x_{l-1}])$$

where H_l delineates a nonlinear transformation, and $x_0, x_1, \dots, x_{l-1}$ denotes the integration of all previous feature maps.

The feature map is represented by:

$$m_l = k_0 + k(l - 1)$$

where k_0 represents the number of starting feature maps, k is the growth rate, and l is the layer index.

Then, the transition layer uses 1×1 convolution before pooling to reduce dimensionality.

$$y = \text{Pool}(\text{Conv}_{1 \times 1}(x))$$

Here, 1×1 convolution is applied before the pooling operation to reduce the number of feature maps.

$$H_l(x) = \text{Conv}_{3 \times 3}(\text{ReLU}(\text{BN}(\text{Conv}_{3 \times 3}(x))))$$

Here, BN stands for Batch Normalization, and ReLU represents the Rectified Linear Unit activation function.

$$z_c = \frac{1}{H \times W} \sum_{i=1}^H \sum_{j=1}^W x_{i,j,c}$$

where, z_c is the final pooled value for the c -th channel, H and W represent the height and width of the

feature map, and the term $\frac{1}{H \times W}$ is the averaging factor to compute the mean value.

The final classification output is computed using the softmax function:

$$P(y = c|x) = \frac{e^{z_c}}{\sum_j e^{z_j}}$$

where $P(y = c|x)$ is the probability of class c given input z , and z_j delineates the pooled activation values for all classes.

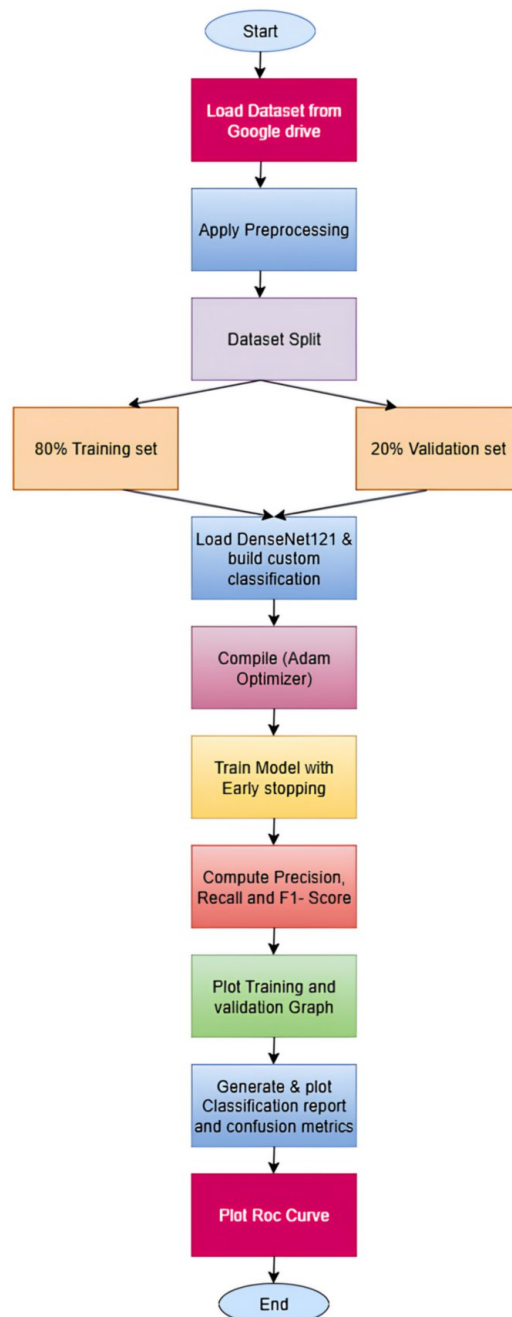


FIGURE 2: Flowchart

Optimization techniques

The Adam optimizer was utilized to train the model because of its effectiveness and capacity for adaptive learning rate. Adam is appropriate for sparse gradients and deep networks since it joins the buff of RMSProp and AdaGrad. The Adam optimizer, which dynamically adapts the learning rate using first-moment (mean) and second-moment (variance) approximations, is applied to construct the model. The model was trained for 30 epochs, with a batch size of 32, and a learning rate of $1e-4$ incorporating early stopping and learning rate reduction to prevent overfitting, enhance convergence, and save computational resources. During initial testing, the Adam optimizer outperformed other optimizers in terms of accuracy and convergence speed.

Evaluation metrics

Accuracy, recall, precision, F-score, and specificity are employed to measure performance, and the loss function applied is sparse categorical cross-entropy. In addition, a confusion matrix was created to indicate the correct and incorrect classifications. The confusion matrix was plotted using seaborn, and the performance evaluation of recall, precision, and F1-score was done using the confusion matrix. The classification performance was evaluated using the Receiver Operating Characteristic (ROC) curve, which was plotted for each class. AUC was also employed to measure how well the model distinguished among data at different thresholds. Weighted and macro averages were provided in order to measure the performance for all classes of diseases uniformly. The full implementation, model scripts, training pipeline, and performance results are made publicly available at <https://github.com/Mansinegii/rice-disease-classification> to ensure openness and reproducibility.

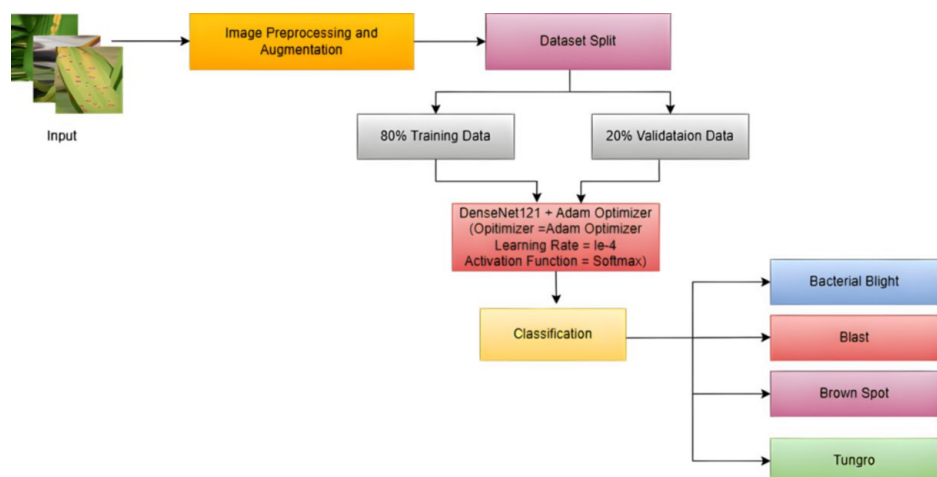


FIGURE 3: Proposed DenseNet121 Model With Adam Optimizer

Results

The extensive evaluation of the proposed model of rice disease classification is presented in this section. The hyperparameter setting used for model training is explained after the experimental environment and preparation of the dataset. Training and validation accuracy and loss patterns are employed to test the performance of the DenseNet121 model with the Adam optimizer.

Experimental setup

The experiments were regulated using Google Colab, exploiting its GPU acceleration for efficient deep learning model training. An Intel Core i5 processor was used, and the NVIDIA Tesla T4 GPU was utilized, provided by Google Colab. Software evaluation was carried out with the Keras library, TensorFlow, NumPy, Matplotlib, Seaborn, Scikit-learn, and Pathlib. The proposed model, DenseNet121 with Adam Optimizer, was trained using a T4 GPU. The programming language used is Python. Windows 10 operating system with 12GB was utilized.

Hyperparameters

The DenseNet architecture with the Adam optimizer was utilized with the adaptive learning rate to ensure stability during training, along with the ReduceLROnPlateau callback, which reduces the learning rate by half if the validation loss fails to improve after three consecutive epochs. L2 regularization was employed to improve the generalization ability of the fully connected layers. Additionally, dropout (40% after global average pooling and 30% in dense layers) was applied to prevent overfitting. The model was trained with a batch size of 32 for 30 epochs, incorporating early stopping to monitor the validation performance and

halt training once optimal performance was reached. The dataset was augmented using random rotation (up to 50 degrees), zooming (up to 50%), brightness variation (ranging from 0.7 to 1.3), width and height shifts (up to 0.25), and horizontal flipping to enhance the generalizability of the model.

Model performance

Figure 4 shows the graph that consists of the training and validation accuracy. The accuracy plot shows the performance improved over the epochs, where the blue line demonstrates training accuracy and the orange line specifies the validation accuracy. Twain's curves substantiate the upward trend, showing the model learned effectually. Figure 5 shows training and validation loss. Here, the loss plot shows that the model effectively minimized the errors during the training. The blue line represents the training loss, which decreased as the model learned, and the orange line represents the validation loss. In the validation loss, the fluctuation represents that the model learned more from training.

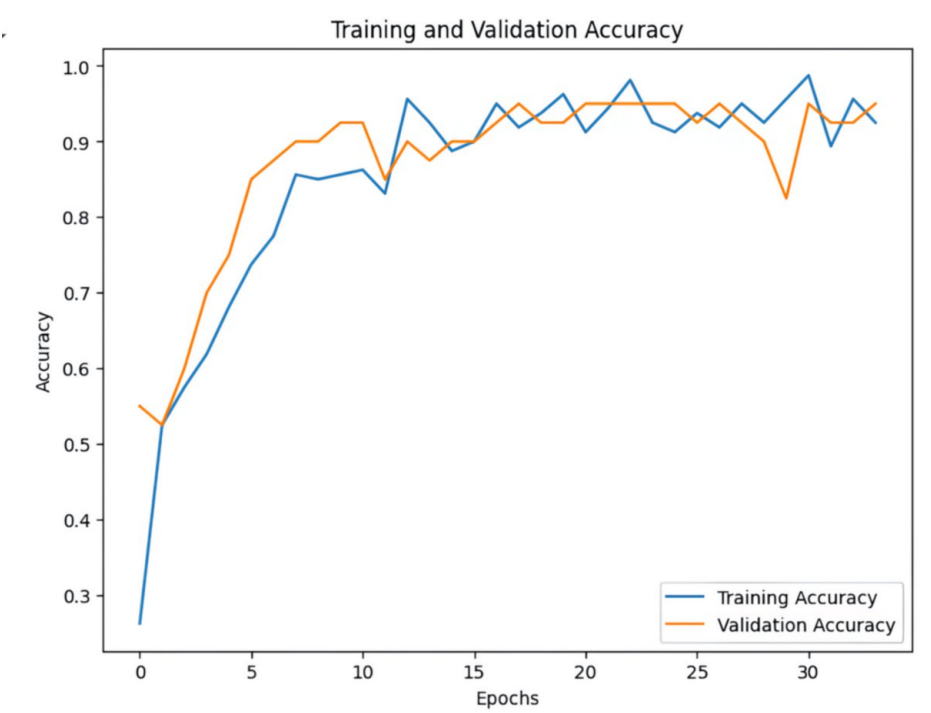


FIGURE 4: Training and Validation Accuracy



FIGURE 5: Training and Validation Loss

Analysis of classification report

The `classification_report` function from the `sklearn.metrics` module was utilized to generate a comprehensive classification report subsequent to the accuracy evaluation. By determining the following critical measures, this report provides a comprehensive assessment of the performance of the model in every class: precision, recall, F1-score, and support (the number of actual occurrences per class). The classification report shown in Table 4 emanates from the confusion matrix shown in Figure 6. It measures key performance metrics such as:

a) Accuracy: Accuracy of projected total cases and measured performance. The formula given by the equation can be utilized to calculate it:

$$\text{Accuracy} = \frac{TP + TN}{TP + TN + FP + FN}$$

where TP, TN, FP, and FN represent True Positive, True Negative, False Positive, and False Negative, respectively.

b) Macro Average: The average of all the classes is referred to as the Macro Average. All the classes are treated equally. It can be calculated using a formula based on an equation.

$$\text{Recall}_{\text{MacroAvg}} = \frac{1}{n} \sum_{i=1}^n \text{Recall}_i$$

where n is the number of class, and Recall_i represents recall score of i .

c) Macro Average Precision: The arithmetic mean of every per-class precision score, as mentioned in the equation, is utilized in order to find macro average precision scores.

$$\text{Precision}_{\text{MacroAvg}} = \frac{1}{n} \sum_{i=1}^n \text{Precision}_i$$

here, n shows total number of class, and Precision_i represent precision score of the i th class.

d) F1-Scores: F1-Score is the harmonic average of Precision and Recall. It provides a compromise between

the two and is especially useful when handling imbalanced datasets for classification problems. The formula for F1-Score is calculated by:

$$F1\text{-Score} = 2 \times \frac{\text{Precision} \times \text{Recall}}{\text{Precision} + \text{Recall}}$$

where, $F1\text{-Score}_i$ is the F1-Score of class i .

e) Weighted Average F1-Score: It is the mean of all per-class F1 scores for the dataset while considering each class's support.

$$\text{Weighted F1-Score} = \sum_{i=1}^n w_i \times F1\text{-Score}_i$$

where, w_i is the weight of class, and support_i is the number of true instances for class i .

Class	Precision	Recall	F1-Score	Support
Bacterial Blight	0.94	0.94	0.94	316
Blast	0.93	0.92	0.92	288
Brown Spot	0.93	0.95	0.94	320
Tungro	0.99	0.98	0.99	261
Accuracy	0.95 (Overall Accuracy)			
Macro Avg	0.95	0.95	0.95	1,185
Weighted Avg	0.95	0.95	0.95	1,185

TABLE 4: Classification Report

By contrasting the model's actual values with its anticipated values, it is counted. It is used to create the confusion matrix, in which off-diagonal components highlight the misclassification (False Positive and False Negative) while diagonal values represent the correctly classified values (True Positive). A summary of the model's accuracy in identifying each disease category is given in the classification report. The Adam Optimiser Densenet121 model used `model.predict(images)` to predict ahead using the validation dataset to generate the report. To calculate the maximum probability for every image, the class label predicted was considered using `np.argmax(preds, axis=1)`. Unlike the expected values (labels), the validation generator provides the actual label. Performance is tested by getting the values from the confusion matrix.

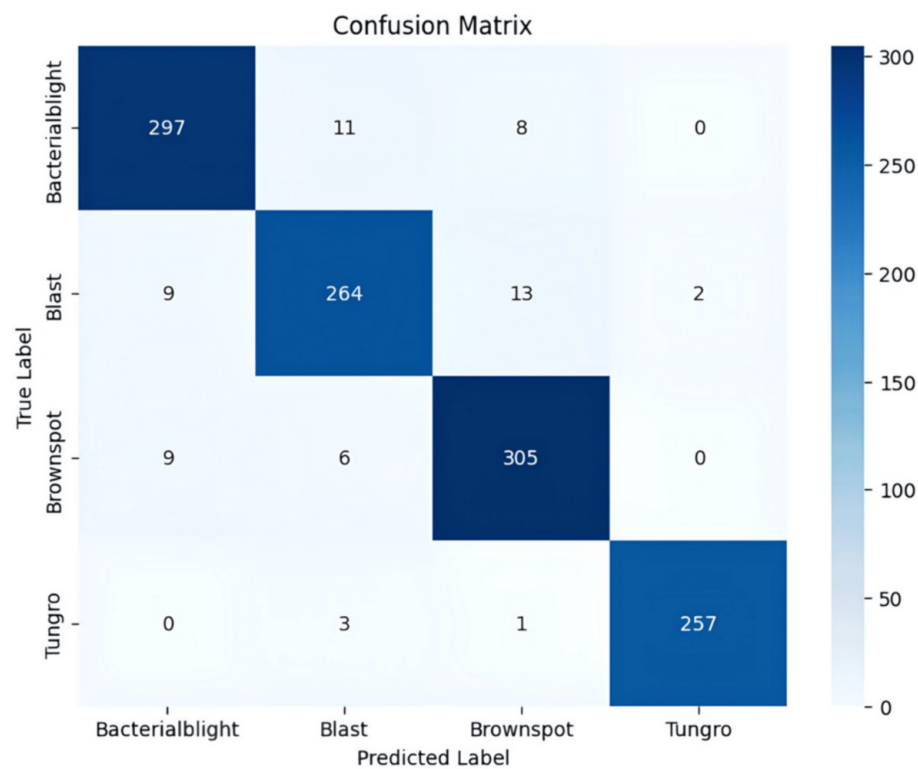


FIGURE 6: Confusion Matrix of Rice Disease Classification

Precision, recall, and F1-score analysis

The support column shows the total number of images in each class in the validation set in Table 4 and also shows that the model achieved high accuracy across all classes, with an accuracy of 95%. For the discrete class, Bacterial Blight achieved a precision and recall of 0.94. The blast has a precision of 0.93 and a recall of 0.92, which designates some misclassifications of actual blast cases. Brown Spot got a precision of 93% and a recall of 95%, showing better performance. Tungro shows a precision of 0.99, a recall of 0.98, and an F1-score of 0.99; it shows the best-performing classification of Tungro cases and indicates very few errors in classification. The macro average calculates the unweighted mean of all classes, achieving a precision, recall, and F1-score of 0.95. Then, the weighted average takes the sample sizes of each class and guarantees a proportionate contribution to the total score.

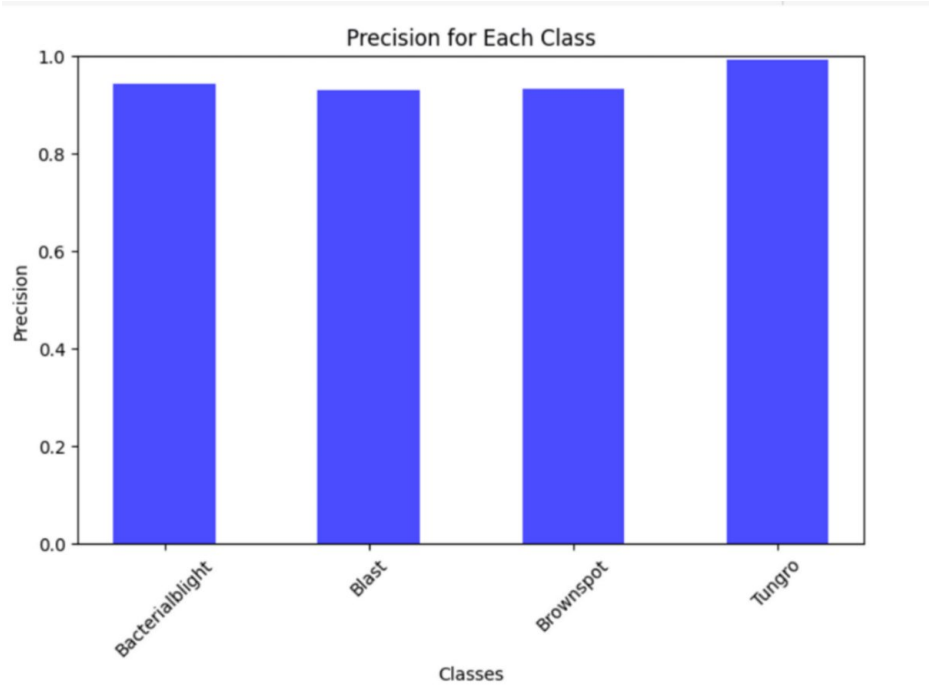


FIGURE 7: Precision

Figure 7 represents the precision, and Tungro shows the highest precision among all the classes.

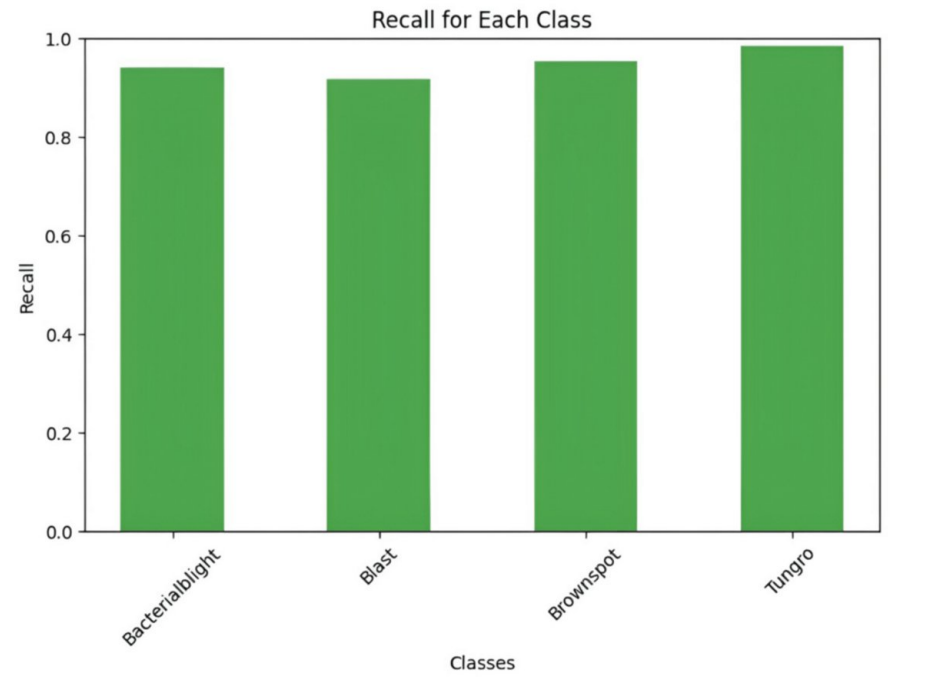


FIGURE 8: Recall

Figure 8 represents the recall, and Tungro shows the highest recall among all the classes.

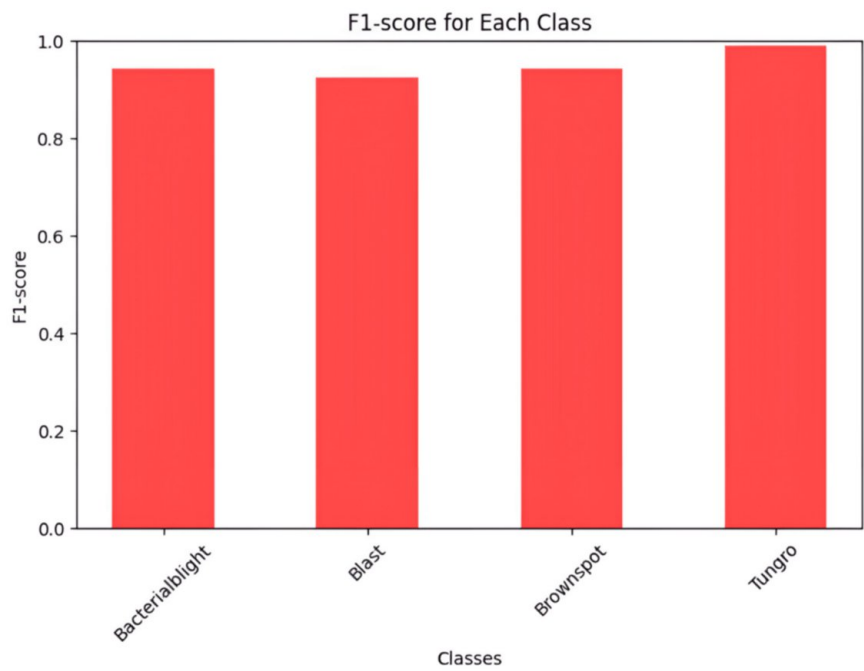


FIGURE 9: F1-Score

Figure 9 represents the F1-score, and Tungro shows the highest precision among all the classes.

ROC-AUC curve

The diagnostic ability of a classification model is illustrated by the ROC curve, which is a plot of the True Positive Rate (TPR) against the False Positive Rate (FPR) for varying threshold values. By applying methods such as micro and macro averaging, this curve can be stretched to a multiclass problem and is particularly useful for displaying a binary classifier's performance. Since this research involved a number of classes, the micro-averaged ROC curve was used to provide an overall view, especially when the sample distribution was relatively uniform across classes. ROC curves of each of the four rice disease categories are plotted in Figure 10. The TPR is plotted along the Y-axis, and the FPR along the X-axis. To quantify the model's ability to distinguish between different disease classes, the AUC was used as a measure of performance. The results show that the proposed DenseNet121 model worked extremely well on class level discrimination: Class 0 (Bacterial Blight) and Class 1 (Blast) both achieved an AUC of 0.99, whereas Class 2 (Brown Spot) and Class 3 (Tungro) achieved a perfect AUC of 1.00. These near-perfect and perfect AUC values attest to the robustness and strong predictive capability of the model in identifying rice leaf diseases.

These values illustrate how better the model can differentiate between various diseases and suggest robust classification. The ROC curves for all classes are nearly warped in the upper-left corner and show high sensitivity and specificity. The model produces a very low FPR, scores top-notch AUC, and supports its reliability for real-world application in rice disease classification.

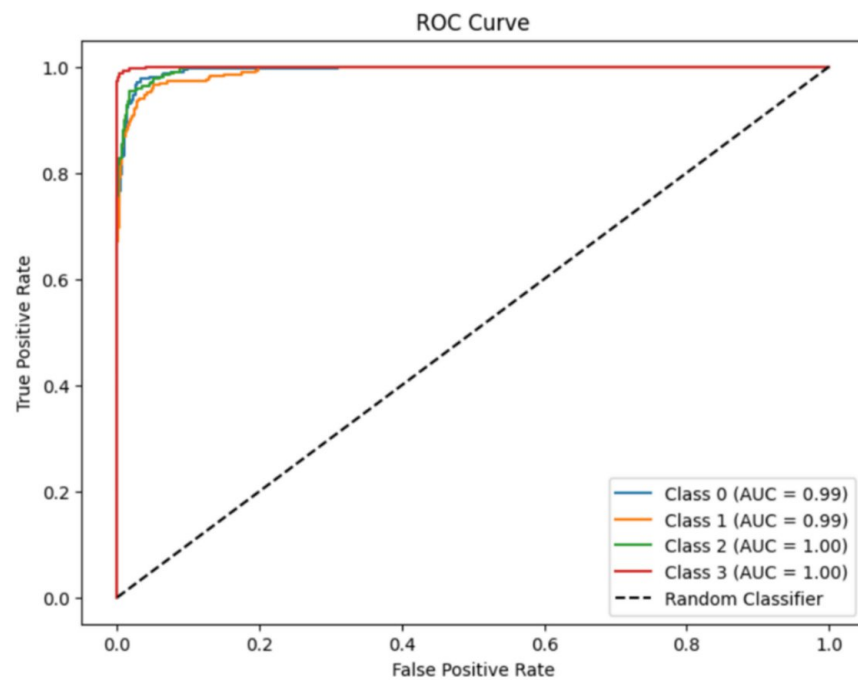


FIGURE 10: ROC Curve

AUC, Area Under the Curve; ROC, Receiver Operating Characteristic

With good precision, recall, and F1-scores across all classes, the experimental results show that the DenseNet121 model optimized with the Adam optimizer performs well in rice disease classification. The confusion matrix, precision-recall curves, and ROC analysis all validated the model's robust generalization and reliable training and validation results. These results support the suggested method's stability and dependability for real-world uses in the diagnosis of agricultural diseases.

Discussion

This section gives a detailed examination of the proposed model's performance and compares it with current approaches from earlier studies.

Comparison with previous work

The proposed model, DenseNet121 with the Adam optimizer, is more accurate than some other models in accuracy, efficiency, generalization, and robustness, even though most of them have great accuracy in rice disease classification. The comparison is illustrated in Table 5, and the proposed model has better accuracy than the others. The conventional CNN models possess a large number of parameters and are predominantly based on manual feature extraction. The DenseNet121 model, however, utilizes deep hierarchical features while conserving computational efficiency. In contrast to the former models that fail to counter dataset bias, our methods employ data augmentation as well as dropout to provide improved generalization. This reduces overfitting and enables the model to deal with visually similar diseases with minimal misclassification. Through the dynamic adjustment of learning rates, the Adam optimizer provides an extra boost to promote faster convergence and stable training. The proposed model possesses practically perfect AUC values (ranging from 0.99 to 1.00), good precision, recall, and F1-score with balanced performance on all four rice diseases.

Reference	Methodology	Accuracy
[1]	CNN, InceptionV3	63.40%, 90.50%
[6]	DenseNet121, DenseNet169, DenseNet201	91.67%, 91%, 88.33%
[8]	InceptionV3, MobileNet, ResNet 50	82.79%, 73.02%, 91.89%
[11]	CNN-RF	93.5%
[16]	CNN	89%
Proposed Model	DenseNet121 + Adam	95%

TABLE 5: Comparison With Other Work

CNN, Convolutional Neural Network; RF, Random Forest

Future ablation study consideration

Future research will include a particular ablation analysis in order to measure the contribution of each part, although this research indicates how much the proposed components (augmentation, dropout, and optimizer) are effective. This will give more insight into their individual roles in enhancing model performance.

Conclusions

This study suggested a DenseNet121 model optimized using the Adam optimizer to classify four rice leaf diseases, namely Bacterial Blight, Blast, Brown Spot, and Tungro. The stability and reliability of the model were shown by its high overall accuracy of 95%, well-balanced precision, recall, F1-score, and adequate AUC values in all disease classes. The better classifying performance of the model, particularly in dealing with intra-class variability, owed much to DenseNet121's strong feature extraction ability and the adaptive learning process of the Adam optimizer. The confusion matrix revealed some misclassifications, especially between visually close diseases such as bacterial blight and brown spot, even though the model performed very well overall. The better classifying performance of the model, particularly in dealing with intra-class variability, owed much to DenseNet121's strong feature extraction ability and the adaptive learning process of the Adam optimizer. The confusion matrix revealed some misclassification, especially between visually close diseases such as Bacterial Blight and Brown Spot, even though the model performed very well overall. These instances were difficult to explain, indicating that improved feature discrimination is needed to reduce these classification errors, and ROC analysis also supports its discriminative power. The loss on validation indicated minimal signs of overfitting despite optimistic outcomes. Future work can tackle this issue by utilizing more diverse datasets, regularization methods, or additional augmentation. To enable real-time detection, future projects can explore transfer learning and deployment of models into mobile or edge-based systems. Overall, this research presents a sound and efficient automated method for rice disease diagnosis in rice, inducing early intervention, improving crop management, and contributing to the goals of precision agriculture and food security.

Additional Information

Author Contributions

All authors have reviewed the final version to be published and agreed to be accountable for all aspects of the work.

Concept and design: Mansi Negi, Prabh Deep Singh

Acquisition, analysis, or interpretation of data: Mansi Negi, Vikas Tripathi

Drafting of the manuscript: Mansi Negi

Critical review of the manuscript for important intellectual content: Prabh Deep Singh, Vikas Tripathi

Supervision: Prabh Deep Singh, Vikas Tripathi

Disclosures

Human subjects: All authors have confirmed that this study did not involve human participants or tissue.

Animal subjects: All authors have confirmed that this study did not involve animal subjects or tissue.

Conflicts of interest: In compliance with the ICMJE uniform disclosure form, all authors declare the following: **Payment/services info:** All authors have declared that no financial support was received from any organization for the submitted work. **Financial relationships:** All authors have declared that they have no financial relationships at present or within the previous three years with any organizations that might have an interest in the submitted work. **Other relationships:** All authors have declared that there are no other relationships or activities that could appear to have influenced the submitted work.

References

1. Rukhsar N, Upadhyay SK: Rice leaves disease detection and classification using transfer learning techniques. 2022 2nd International Conference on Advance Computing and Innovative Technologies in Engineering (ICACITE), Greater Noida, India. 2022, 2151-2156. [10.1109/ICACITE53722.2022.9823596](https://doi.org/10.1109/ICACITE53722.2022.9823596)
2. Bhattacharya A: A novel deep learning based model for classification of rice leaf diseases. 2021 Swedish Workshop on Data Science (SweDS), Växjö, Sweden. 2021, 1-6. [10.1109/SweDS53855.2021](https://doi.org/10.1109/SweDS53855.2021)
3. Memdani L, Memdani A, Memdani AN: Farmers' suicides in India: a qualitative study of Andhra Pradesh (AP) and Telangana states of India. Indian Journal of Community Medicine. 2024, 49:629-632. [10.4103/ijcm.ijcm_206_22](https://doi.org/10.4103/ijcm.ijcm_206_22)
4. Mahajan G, Kumar V, Chauhan BS: Rice production in India. Rice Production Worldwide. Chauhan B, Jabran K, Mahajan G (ed): Springer, Cham; 2017. 53-91. [10.1007/978-3-319-47516-5_3](https://doi.org/10.1007/978-3-319-47516-5_3)
5. Huang G, Liu Z, Van Der Maaten L, Weinberger KQ: Densely connected convolutional networks. 2017 IEEE Conference on Computer Vision and Pattern Recognition (CVPR), Honolulu, HI, USA. 2017, 2261-2269. [10.1109/CVPR.2017.243](https://doi.org/10.1109/CVPR.2017.243)
6. Saputra AD, Hindarto D, Santoso H: Disease classification on rice leaves using DenseNet121, DenseNet169, DenseNet201. Sinkron. 2023, 7:48-55. [10.33395/sinkron.v8i1.11906](https://doi.org/10.33395/sinkron.v8i1.11906)
7. Sachan R, Kundra S, Dubey A: Paddy leaf disease detection using thermal images and convolutional neural networks. 2022 International Conference on Computational Intelligence and Sustainable Engineering Solutions (CISES), Greater Noida, India. 2022, 471-476. [10.1109/CISES54857.2022.9844413](https://doi.org/10.1109/CISES54857.2022.9844413)
8. Sindhu BVM, Badawadagi D, Bidargaddi AP, Chakalabbi S, Sirgond P: Paddy leaf disease detection using ensemble stacking. 2024 IEEE 9th International Conference for Convergence in Technology (I2CT), Pune, India. 2024, 1-7. [10.1109/I2CT61223.2024.10544089](https://doi.org/10.1109/I2CT61223.2024.10544089)
9. Van Ho S, Vuong HG, Nguyen BQ, Trinh QH, Tran MT: Ensemble of deep neural networks for rice leaf disease classification. 2022 RIVF International Conference on Computing and Communication Technologies (RIVF), Ho Chi Minh City, Vietnam. 2022, 238-243. [10.1109/RIVF55975.2022.10013858](https://doi.org/10.1109/RIVF55975.2022.10013858)
10. Liu W, Yu L, Luo J: A hybrid attention-enhanced DenseNet neural network model based on improved U-Net for rice leaf disease identification. Frontiers in Plant Science. 2022, 13:922809. [10.3389/fpls.2022.922809](https://doi.org/10.3389/fpls.2022.922809)
11. Govindharaj I, Rajput K, Garg N, Kukreja V, Sharma R: Enhancing rice crop health assessment: evaluating disease identification with a CNN-RF hybrid approach. 2024 International Conference on Innovations and Challenges in Emerging Technologies (ICICET), Nagpur, India. 2024, 1-5. [10.1109/ICICET59548.2024.10616297](https://doi.org/10.1109/ICICET59548.2024.10616297)
12. Saini A, Guleria K, Sharma S: An integrated MobileNetV2 with convolutional neural networks model for early categorization of rice leaf diseases. 2024 Second International Conference on Networks, Multimedia and Information Technology (NMITCON), Bengaluru, India. 2024, 1-5. [10.1109/NMITCON62075.2024.10698804](https://doi.org/10.1109/NMITCON62075.2024.10698804)
13. Kavitha M, Basha CH, Prashanth V, Senthilkumar S, Mohan V, Arunkumar P: An advanced rice plant disease classification through a modified EfficientNet deep learning model. 2024 Second International Conference on Networks, Multimedia and Information Technology (NMITCON), Bengaluru, India. 2024, 1-7. [10.1109/NMITCON62075.2024](https://doi.org/10.1109/NMITCON62075.2024)
14. Mandwariya D, Jotwani V: A deep learning approach for automated rice disease detection and classification. Journal of Advanced Zoology. 2024, 45:316-335. [10.53555/jaz.v45i3.4313](https://doi.org/10.53555/jaz.v45i3.4313)
15. Satoto BD, Anamisa DR, Yusuf M, Sophan MK, Alamsyah N, Irmawati B: Rice disease classification based on leaf damage using deep learning. 2022 6th International Conference on Informatics and Computational Sciences (ICICoS), Semarang, Indonesia. 2022, 42-47. [10.1109/ICICoS56336.2022.9930567](https://doi.org/10.1109/ICICoS56336.2022.9930567)
16. Kavin Kumar S, Kowshik T, Krishna Harini M, Kingsy Grace R: Disease classification in paddy crop leaves using deep learning. 2023 7th International Conference on Electronics, Communication and Aerospace Technology (ICECA), Coimbatore, India. 2023, 470-475. [10.1109/ICECA58529.2023.10395000](https://doi.org/10.1109/ICECA58529.2023.10395000)
17. Ghosh U, Rokoni S, Rahman MA, Rahman MS, Habib MT: CNN modeling for recognizing rice leaf diseases. 2024 15th International Conference on Computing Communication and Networking Technologies (ICCCNT), Kamand, India. 2024, 1-6. [10.1109/ICCCNT61001.2024.10725764](https://doi.org/10.1109/ICCCNT61001.2024.10725764)
18. Singh G, Singh R: Deep learning-based rice leaf disease diagnosis using convolutional neural networks. 2023 International Conference on Sustainable Computing and Smart Systems (ICSCSS), Coimbatore, India. 2023, 107-111. [10.1109/ICSCSS57650.2023.10169402](https://doi.org/10.1109/ICSCSS57650.2023.10169402)
19. Barakala M, Attada VR, Rajan C, Agnes SA: Rice plant leaf disease classification using deep residual learning. 2023 International Conference on Data Science, Agents & Artificial Intelligence (ICDSAAI), Chennai, India. 2023, 1-8. [10.1109/ICDSAAI59313.2023.10452625](https://doi.org/10.1109/ICDSAAI59313.2023.10452625)
20. Yasid A, Wahyuningrum RT, Ni'Mah AT, Ayani IH: Rice leaf diseases classification using deep learning based on EfficientNetB3 architecture with transfer learning. 2023 International Conference on Technology, Engineering, and Computing Applications (ICTECA), Semarang, Indonesia. 2023, 1-6. [10.1109/ICTECA60133.2023.10490596](https://doi.org/10.1109/ICTECA60133.2023.10490596)
21. El-Shahat D, Tolba A, Kumar AK: An improved deep learning model for detecting rice diseases. Optimization in Agriculture. 2024, 1:1-10. [10.61356/j.oia.2024.1194](https://doi.org/10.61356/j.oia.2024.1194)
22. Singh A, Kumar V: A deep learning attention approach for diagnosis of rice diseases. 2024 First International Conference on Electronics, Communication and Signal Processing (ICECSP), New Delhi, India. 2024, 1-5. [10.1109/ICECSP61809.2024.10698030](https://doi.org/10.1109/ICECSP61809.2024.10698030)
23. Sethy PK: Rice leaf disease image samples. Mendeley Data. (2020). Accessed: July 5, 2025:

<https://data.mendeley.com/datasets/fwcj7stb8r/1>.