

Deep Learning-Based Rice Leaf Disease Detection Using Custom CNN Models

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Abstract: Rice, a world food crop and one of the most essential elements of the food security chain, is highly susceptible to various leaf diseases, which have a devastating impact on production and quality. Some of the most widespread rice diseases include Bacterial Blight, Brown Spot, Tungro, and Blast, which can potentially cost the production and economy a lot when not detected early. To solve this problem, this paper will present a specific Convolutional Neural Network (CNN) model to perform the automated classification of four types of rice leaf disease, relying solely on diseased leaf images as available in the Kaggle dataset of 6,431 samples. The preprocessing of the images consisted of resizing the images to 224x224 pixels, normalization, and augmentation methods of rotation, flipping, and zooming to improve the generalization. The proposed CNN architecture includes several convolutional layers with ReLU activation, max-pooling that would reduce the dimension, dropout as a regularization technique, and fully connected dense layers with a softmax classifier. The model achieved 98% classification accuracy on a 70:30 train-test split, with high per-class precision, recall, and F1-scores, demonstrating its effectiveness and robustness. These findings underscore the possible applications of the suggested lightweight CNN as a low-cost and easily applicable system to effectively classify rice disease to facilitate early disease diagnosis and long-term control of the crop.

Keywords: Deep Learning; CNN; Image processing; Rice Leaf Disease Detection

1. Introduction

Agriculture is one of the most vital sectors worldwide, serving as the backbone of food security, rural livelihoods, and economic stability. It provides staple crops to feed the growing global population, supplies raw materials to various industries, and contributes significantly to international trade. As the issues of climate change, pest populations, and plant diseases grow, the agricultural industry is under pressure to be more productive and sustainable [1]. To address these, contemporary technologies like artificial intelligence, machine learning, and deep learning have emerged as the key to improving crop monitoring, disease detection, and precision farming.

The Pakistani agricultural industry is a key part of the Pakistani economy, which plays a role of about 23.5% in the country's GDP during fiscal year 2024-2025 and employs many labour force. It is a significant source of foreign exchange earnings and a primary source of raw materials needed by downstream industries and the central market of industrial products like fertilizers, pesticides, and machines [2]. Further, because almost two-thirds of the Pakistani population is rural, and most are directly and indirectly reliant on agriculture as their means of livelihood, the socio-economic significance of the sector is highlighted.

In recent years, agriculture has been transformed into a more innovative and efficient system due to the integration of modern technologies. Deep learning has become a disruptive technology, and it is now possible to automate agricultural processes, identify crop diseases early, communicate wirelessly with sensors, and make more sophisticated decisions based on cloud computing. The innovations have tremendous potential to boost productivity, guarantee sustainability, and reinforce agriculture's position in overall economic development.

Rice Leaf Diseases: Rice plants are vulnerable to numerous diseases throughout their growth cycle, and this study focuses on the most severe ones that significantly impact yield and quality.

- a) **Bacterial blight:** One of the most toxic diseases that impacts rice leaves and plants is bacterial blight. It has been known to destroy up to 70% of the grain crop and has also been known to destroy a large area of field covering hundreds of acres [3]. The disease attacks the plant in its early stages of growth. Powerful winds and rains significantly contribute to the dispersion of the bacteria on the fields. The first symptom of the disease is that infected rice leaves first appear yellow, then slowly roll up, and then the yellow color changes into a straw-like color. The proliferation of bacterial blight results in low-quality grains, and the yield is significantly decreased. However, this disease is treatable with practical, cost-effective, and trustworthy control mechanisms. Balanced use of nitrogen, timing irrigation, removing weeds at the right time, and keeping the fields clean can be applied to control this disease. In addition, the biological control methods, e.g., antagonistic pathogens, have worked quite well in controlling bacterial blight in rice crops.
- b) **Blast:** Rice blast is a fungal disease regarded as one of the biggest menaces to rice production worldwide, with yields of 10-30% losses. This disease is first found in small necrotic spots on the leaves, which then continue to increase and extend to the leaf blade and leaf sheath [4]. At an advanced stage, infection disrupts grain filling and can also get to the roots, inhibiting the overall progress of the plant. In a desirable environmental condition, the rice blast may destroy whole fields, causing a lot of crop losses. Common symptoms consist of spots of different sizes and shapes, which differ according to climatic factors. The control of this disease mostly depends on the usage of registered fungicides.
- c) **Brown spot:** Brown spot is a highly destructive rice disease caused by the fungus *Cochliobolus miyabeanus*. The disease mainly affects rice leaves, and its symptoms include spots that are different in size and color; they are small reddish-brown spots and large dark-brown oval spots. Serious infection may result in massive yield loss, approximately 60 to 90%. Nutrient deficiency, poor soil preparation, and poor drainage are among the factors that promote the disease in situations where there is poor crop management [5]. The core control strategies entail balanced fertilization, land leveling, correct soil management, placement of fungicide-treated seeds, and incorporation of disease management techniques.
- d) **Tungro:** Rice tungro disease is an infection that results from two viruses carried by rice hoppers. The ailment causes severe signs, such as leaf discoloration, mottling, stunted growth, and decreased yield. This is because losses have been realized up to 68%. The infected leaves turn orange-yellow to dark blue on the tip, and when they spread downward, they make the plant look striped or mottled. Infection during the growing period can be highly destructive, especially in the initial stages, since it can lead to the loss of complete rice acreage [6]. Tungro propagates very fast in cultivated rice fields, and this is mainly caused by the action of leafhoppers. Nutrient deficiencies, including nitrogen and zinc, and environmental stressors, including water scarcity or rat infestation, also contribute to the worsening of the disease. Tungro management techniques incorporate the use of insecticides to curb the population of leafhoppers and the adoption of proper nutrient and field management.

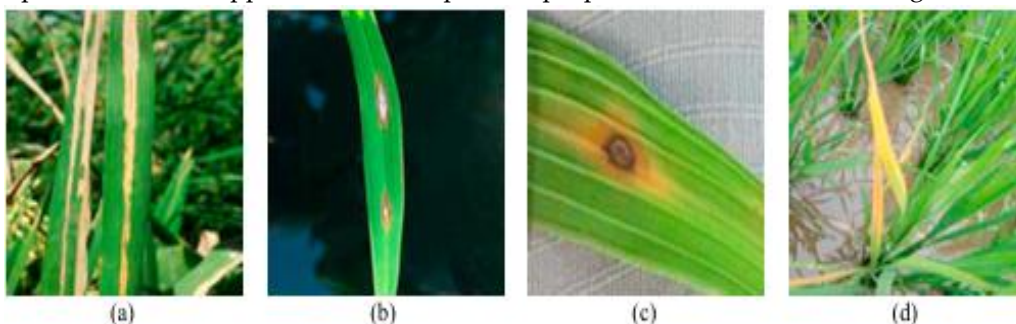


Figure 1. Image samples of all the rice plant diseases (a) Bacterial blight (b) Blast (c) Brown spot (d) Tungro

2. Literature review

Automated crop disease detection has been a highly developed field in recent years, and artificial intelligence (AI), in particular, deep learning, has been significantly applied to this area. Manual inspection processes can be tedious, subjective, and prone to error by humans, and it is here that automated methods are required. As a crop susceptible to bacterial blight, blast, brown spot, and tungro, rice has been the target of various studies on developing computer vision models to aid in early detection, minimize losses, and ensure food security. In the following section, we abide by the recent studies using CNNs, transfer learning, and hybrid deep learning models to detect rice leaf disease and discuss their datasets, methods, performance, and limitations.

Adoption of artificial intelligence and intense learning has contributed significantly to the automated detection of crop diseases. Rice is particularly susceptible to bacterial infections, such as bacterial blight, blast, brown spot, and tungro. Therefore, rice has been particularly interested in the recent literature on computer vision models that would help control the disease before its outbreak and decrease yield losses.

Designed a personalized CNN with MATLAB to detect four diseases of rice leaves and healthy leaves with 99.83% accuracy [7] However, the data set was restricted to field images in certain areas, the training was also limited to seven epochs, and the evaluation was limited to overall accuracy. This raises questions of overfitting and the absence of generalizability. We only used YOLOv5 on a 400-image Kaggle dataset. The model was exact (1.0) and recalls (0.94), although the mean average precision (mAP) was poor (0.62), which represented a limitation in robustness and scalability because of the small size of the dataset. [8].

Investigated the transfer learning models, including VGG19, ResNet101, and Inception-ResNet-V2, on 984 rice leaf images, with the highest result on 92.68 [9] Although the existing architectures were used, the dataset size was not very high, and the evaluation metrics were not exhaustive, so there are gaps in reliability.

Hybrid deep learning and machine learning methods were proposed, with an accuracy of less than 95%. Though novel, these models were computationally inexpensive, had poor consistency across datasets, and were less practically applicable in the real world. [10].

The Presented Detection Transformer (DHLC-DETR) with an improved model, combining Res2Net and a dense feature pyramid network, attains 97.44% accuracy on the IDADP dataset. They particularly worked with small-target detection; however, the method needed heavy augmentation (17,640 images) and was computationally intensive. [11].

Used CNNs and compared them with the conventional ML methods on the dataset of 1,600 images of four classes (Hispa, Brown Spot, Leaf Blast, Healthy). CNN had the highest accuracy of just 78.2, which demonstrates the weakness of shallow models and small datasets [12].

CNN architecture was assessed on a Kaggle dataset on four rice leaf diseases. Although the potential of CNNs was proven, the dataset was limited (fewer than 2,000 images), and the accuracy was under 85%, again highlighting the difficulty of dataset size and generalization.

Across the reviewed works, several common limitations emerge:

1. Small dataset sizes (often <2,000 images), limiting robustness.
2. It was evaluated based on the accuracy rather than precision, recall, F1-score, and the confusion matrix.
3. Limited disease coverage in some studies (only 3–4 classes).
4. Complex models (e.g., DETR, hybrids) that are difficult to deploy in resource-limited settings.

To address these gaps, the present research employs a custom CNN model trained on a comparatively large Kaggle dataset of 6,431 images, with four large rice leaf diseases (bact. blight, blast, brown spot, and tungro). Unlike many previous works, the model achieves 98% accuracy and provides a comprehensive assessment, such as precision, recall, F1-score, and confusion matrix. The proposed CNN is lightweight and scalable, making it applicable to practical use, such as mobile or IoT-based systems in agriculture.

Table 1. Summary of Related Work

Author & Year	Dataset	Diseases	Model	Accuracy / Results	Weakness	Difference (Our Study)
Singha et al. (2023)	Field images (India)	4 + Healthy	Custom CNN (MATLAB)	99.83% (7 epochs)	Small dataset, limited metrics	Larger dataset (6431), more epochs, full metrics
Jhatial et al. (2022)	400 (Kaggle)	4	YOLOv5	Prec=1.0, Recall=0.94, mAP=0.62	Very small dataset, low robustness	Larger dataset, higher accuracy, comprehensive metrics
Islam et al. (2021)	984 (Kaggle + UCI)	5	VGG19, ResNet101, Incep-ResNetV2	92.68%	Small dataset, lower accuracy	Larger dataset, improved accuracy (98%)
Elsevier (2025)	Public datasets	4–5	Hybrid DL+ML	<95%	Complex, inconsistent	Lightweight CNN, scalable, higher accuracy
Yang et al. (2023)	17,640 (augmented IDADP)	3	DHLC-DETR (Transformer)	97.44%	Heavy model, high computation	Simple CNN, less computational cost
Tejaswini et al. (2022)	1,600 (India)	4	CNN (5-layer, VGG16)	78.2% (best)	Low accuracy, shallow model	Better tuned CNN, 98% accuracy

The reviewed studies collectively demonstrate that deep learning approaches, particularly CNN-based models, have strong potential for rice disease detection. However, several challenges remain unaddressed. To begin with, the datasets of these studies are generally small: in many cases, they consist of less than 2,000 images, which restricts the stability of the trained models. Conversely, the paper uses over 6,000 pictures, providing more confident training and testing.

Second, earlier research used only accuracy as the performance metric, which is confounding when there is class imbalance or misclassification. Not many studies have given a detailed analysis of confusion matrices, precision, recall, and F1-scores. These metrics are expressly included in our work and provide a more detailed analysis of performance [13].

Third, other papers tried higher architectures like transformers or hybrid CNN-ML frameworks. Still, these were computationally intensive and not practically applicable to real-world agriculture in developed countries because developing countries have limited resources. Our CNN is a light but effective and scalable network suitable for precision agriculture applications that require a mobile and IoT-based network.

Lastly, one of the major lessons is that most previous works trained their models with tiny numbers of epochs (e.g., 7 epochs in [7]), which casts doubt on the stability and generalizability of findings. In comparison, our experiment trained the CNN model using 35 epochs and reached a steady convergence, presenting a high generalization potential with unknown data.

3. Materials and Methods

This part presents the dataset and the method of the suggested CNN structure of the study.

Dataset: The dataset used in this work was obtained from the Kaggle repository and consists exclusively of infected rice leaf images belonging to four major disease categories: Bacterial Blight, Blast, Brown Spot, and Tungro. In contrast to some of the earlier studies that have considered the diseased and

healthy samples of leaves, the current research focused on diseased samples only to develop disease-specific feature extraction and classification. There are 6,431 images in the dataset, which were gathered in various real-field conditions and provided by multiple sources on Kaggle, ensuring that they varied in terms of backgrounds, lighting, and orientations of the leaf.

Table 2. Dataset

Classes	Images	Training Image	Testing image
Bacterial Blight	2083	1519	564
Blast	1440	1007	433
Brown Spot	1600	1120	480
Tungro	1308	915	393
	6431	4561	1870

4. Methodology

The rice leaf disease images were acquired on Kaggle and consist of pictures taken in the field with different backgrounds, lights, and leaf positions. Every picture was scaled to 224x224 pixels and brought to the range of $[0, 1]$ as a normalization measure. There was no data augmentation before any data was split into training and testing sizes to avoid data leakage. Random rotation ($\pm 20^\circ$) and horizontal/vertical flipping and zooming (range 0.2) were only used in the training set to enhance the data diversity and model resilience. In the training, 20% of the training data was used internally by validation with the validation split option of Keras, which allows monitoring the model's performance without having a separate validation folder. Fixed random seed values (seed = 42) were used to ensure reproducibility of experimental results. This data preparation plan provided a valid assessment of the recommended CNN model.

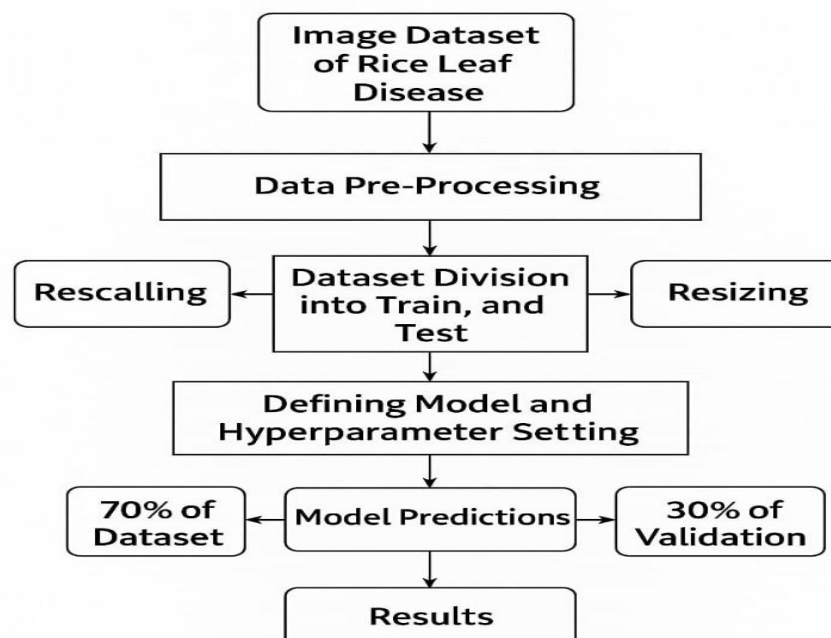


Figure 2. Propose Methodolgy

The proposed model is a tailor-made Convolutional Neural Network (CNN) used to predict four types of rice leaf diseases, such as Bacterial Blight, Blast, Brown Spot, and Tungro. The input images were made 224x 224x 3 and scaled in the range $[0, 1]$. The model represents three convolutional blocks, which are then succeeded by a fully connected layer and a softmax output. Individual convolutional layers employ a 3 x 3 kernel, a stride of 1, and the same padding to maintain spatial dimensions. ReLU was used

as an activation to add non-linearity, and MaxPooling (2×2) was utilized to reduce the number of feature maps. Regularization was done by having dropout layers to cut down on overfitting.

Table 3. Summary of the proposed CNN model architecture.

Layer	Filters / Units	Kernel	Parameters	Activation	Dropout
Input	224×224×3	–	–	Rescaling	–
Conv2D	32	3×3	896	ReLU	–
MaxPooling2D	–	2×2	0	–	0.3
Conv2D	64	3×3	18,496	ReLU	–
MaxPooling2D	–	2×2	0	–	0.3
Conv2D	128	3×3	73,856	ReLU	–
MaxPooling2D	–	2×2	0	–	0.4
Flatten	–	–	0	–	–
Dense	256	–	~6,425,600	ReLU	0.5
Output Dense	4	–	1,028	Softmax	–

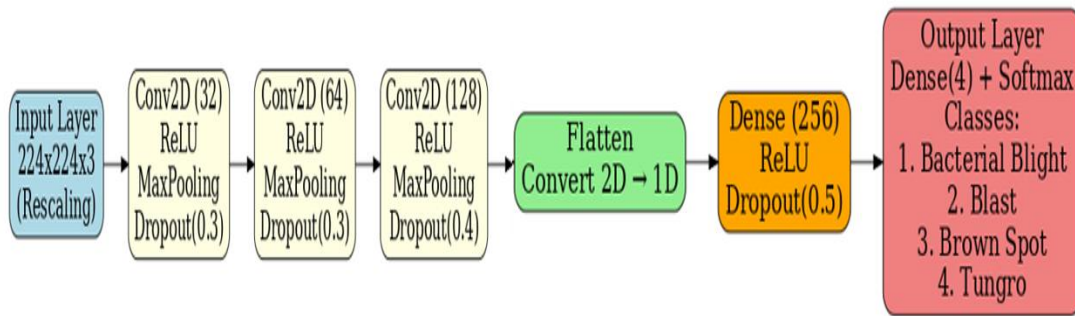


Figure 3. Proposed custom CNN architecture.

Convolution Layer: This constitutes the first layer of the neural network, which is the basic unit of the architecture. The convolutional layer that contains multiple feature detectors is referred to as a kernel or filters, which are dragged by a stride throughout the image to draw attention to the occurrence of the particular feature.

The Batch Normalization Layer decorrelates every layer's inputs, standardizing each mini-batch. This method averts the learning process and enables deep networks to train using much smaller epochs. [14]. Given a mini-batch $B = \{x_1, x_2, \dots, x_m\}$, each activation x_i is normalized using the batch mean μ_B and batch variance σ_B^2 as follows:

$$\hat{x}_i = \frac{x_i - \mu_B}{\sqrt{\sigma_B^2 + \epsilon}} \quad (1)$$

Lastly, linear transformation is used to recover the power of representation:

$$y_i = \gamma \hat{x}_i + \beta \quad (2)$$

where γ and β They are learnable parameters that scale and shift the normalized value, respectively.

Max Pooling Layer: The main reason the pooling layer is required is that it cuts in half the size of the output of the previously mentioned convolutional layer, making the computing cost of the following layer

less expensive. Max pooling is definitely the most popular pooling. It breaks down the picture into sub-region rectangles delimited by the kernel and will only output the maximum of every stage of the kernel. The proposed architecture is 2x2 in dimension, and its stride is 2.



Figure 4.. An example of max-pooling operation.

Activation Function Layer: The second layer is the activation function layer. The neural network is non-linear due to this layer. A choice in favor of non-linearity, one can either modify or cut off the layer's output before it. This is applied to restrict the output manufactured. Activation function of the Rectified Linear Unit (ReLU) has recently been applied in the works of CNN due to the possibility caused by a mixture of the following reasons:

$$g(z) = \max(0, z) \quad (3)$$

$$\frac{d}{dz}g(z) = \begin{cases} 1, & \text{if } z > 0 \\ 0, & \text{otherwise} \end{cases} \quad (4)$$

- a) Simplicity in function and derivative of the type in (3) and (4).
- b) Reduced the possibility of vanishing gradient.
- c) ReLU produces a sparser representation. The reason is that the zero in the gradient yields a complete zero.

Fully Connected Layer: The fully-connected layer is the same as the structure of neurons in traditional neural networks. This makes every neuron in the fully connected layer completely connected to all the neurons in the earlier and later layers. The drawback of the fully connected layer is that it possesses many parameters, which are very expensive to compute at any point during the training. Therefore, the proposed model employed a single connected layer to reduce complexity, yet many discriminative features were learned. In our implementation, the fully connected layer has 6,526,308 trainable parameters, demonstrating its computational intensity. And lastly, the result of this layer is overlaid with the Softmax activation function that transforms the real-valued outputs to a probability distribution of the four target classes (Bacterial Blight, Blast, Brown Spot, and Tungro).

Training the proposed custom CNN models: The CNN model was built based on Kaggle's data on four types of diseases of rice leaves: Bacterial Blight, Blast, Brown Spot, and Tungro. The data was divided into training and testing groups in a 70:30 ratio to regulate practical performance evaluation. All images were resized (224x224 pixels), normalized (to range [0,1]), and random rotations, flips, and zooming were added. These preprocessing steps assisted the model in extrapolating further and reduced the risk of overfitting.

Adaptive Moment Estimation (Adam): Our loss function was categorical cross-entropy, and model training was done using the Adam optimizer. To avoid overfitting, 35 epochs of training, a 32-batch size, and dropout layers (0.3, 0.4, and 0.5) were introduced on the different network levels.

The basic principles of the Adaptive Moment Estimation (Adam) algorithm update the gradient and squared gradient of the exponentially moving average using the hyperparameters. $\beta\beta_1, \beta\beta_2 \in [0,1]$

$$m_t = \beta_1 m_{t-1} + (1 - \beta_1) \nabla J(w_t) \quad (5)$$

The reason is that the moment estimates of the moving average are concentrated around zero, since they will be vectors of zeros. To overcome these biases, the writer of Adam calculates bias-corrected estimates $\hat{m}$ and $\hat{v}$.

$$\hat{m} = \frac{m_t}{1 - \beta_1^t}$$

(6)

$$\hat{v} = \frac{v_t}{1 - \beta_2^t} \quad \text{ie weights are updated with the following update rule in (8)} \quad (7)$$

$$W_{t+1} = W_t - \frac{\alpha \cdot \hat{m}_t}{\sqrt{\hat{v}_t + \epsilon}} \quad (8)$$

Experimental Setup: All experiments were conducted on a Windows 10 operating system computer. This computer had an Intel(R) Core i7-6600U CPU with a frequency of 2.60 GHz and 8 GB RAM. The model's implementation, training, and evaluation were conducted in Jupyter Notebook version with Python 3.9 and TensorFlow and Keras as a deep learning framework. All the data processing (resizing and normalization), model training, and evaluation metrics (accuracy, precision, recall, F1-score, and confusion matrix) were conducted in the same environment.

5. Results

Evaluation of the dataset of four classes of rice plant diseases. The experimental data set consisted of four types of courses of rice leaf disease: Bacterial Blight, Blast, Brown Spot, and Tungro. The suggested custom CNN has been trained through the Adam optimizer and validated through training and test data sets. This model was validated in the first epochs of training, and it demonstrated Adam's efficiency in refining the learning process.

An additional examination of the model performance to identify the predictions made on a class-by-class basis was conducted, assisted by a confusion matrix. The leading performance indicators, accuracy, precision, recall, and F1-score, were computed to make the model robust. It was determined that the model can reach a maximum test accuracy of 98 percent, which means it is overly generalized on unexplored data.

$$Accuracy = \frac{TN+TP}{TN+FP+FN+TP} \quad (9)$$

$$Precision = \frac{TP}{TP+FP} \quad (10)$$

$$Recall = \frac{TP}{TP+FN} \quad (11)$$

$$F1\ Score = 2 \times \frac{Precision \times Recall}{Precision + Recall} \quad (12)$$

Where, TN = true negative, TP= true positive, FP= false positive and FN = false negative

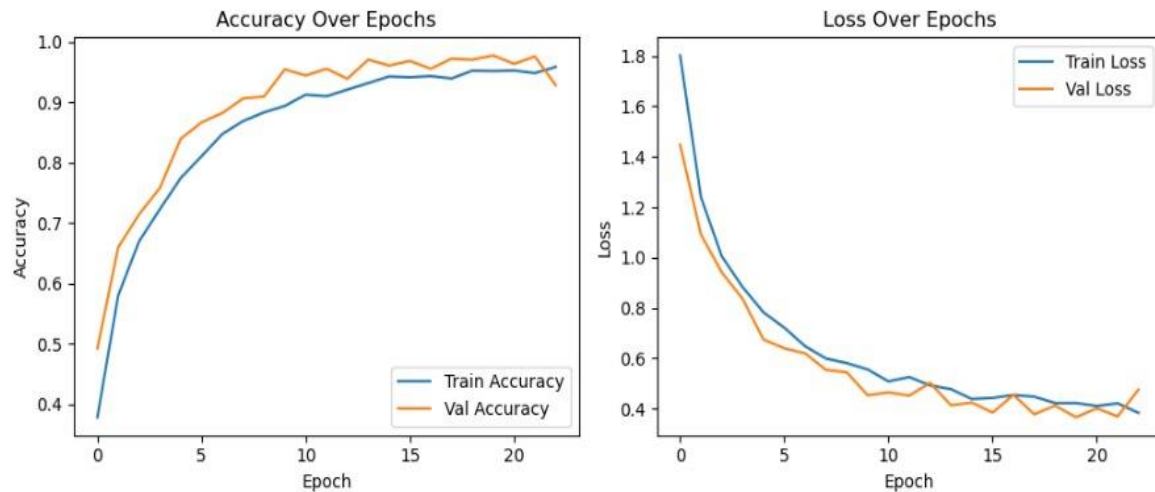


Figure 5. Accuracy and loss graph of Custom CNN

A Custom CNN was utilized to label rice leaf disease, with a test accuracy of 98%. The model was found to have a training accuracy of 96.34% and a validation accuracy of 97.75%, with minimal overfitting, as noticed during the training. The training and validation loss curves gradually decreased during an epoch of steady convergence and learning.

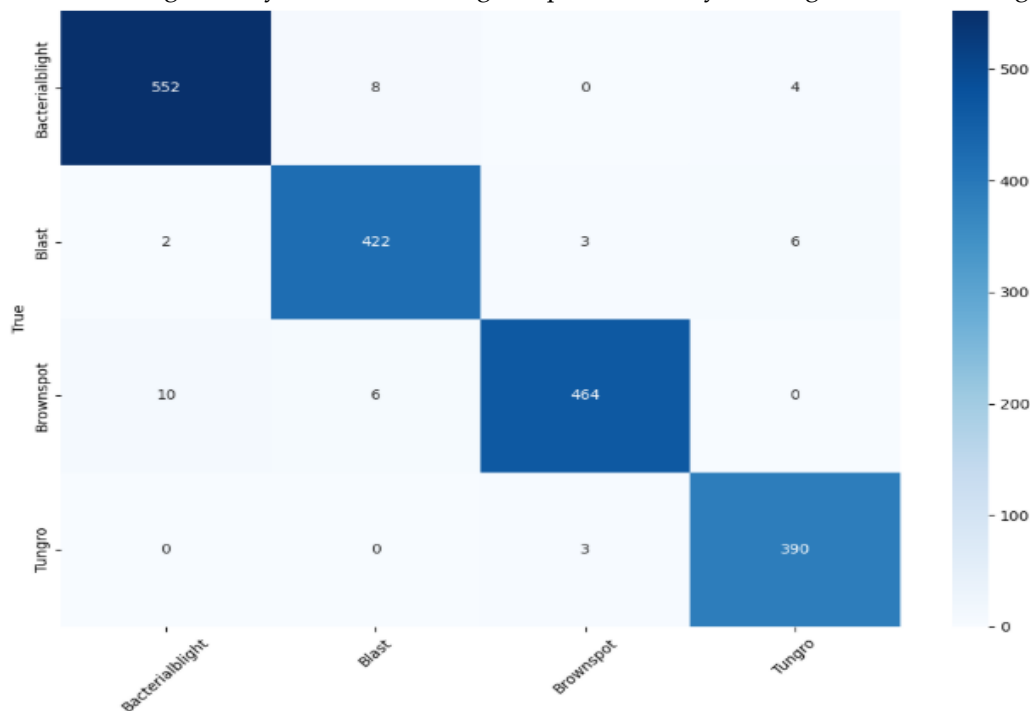


Figure 6. Confusion matrix of Custom CNN

The confusion matrix was used further to evaluate the CNN model's classification performance. The fact that most of the images were correctly classified in all four classes of rice leaf disease indicates that the model is correct. The diagonal values are high and represent high accuracy of each category, and the misclassifications are minimal, which testifies to the power and reliability of the model.

Table 4. Evaluation of Rice Leaf Diseases Identification

Disease Class	Precision (%)	Recall (%)	F1-Score (%)	Support
Bacterial Blight	0.98	0.98	0.98	564
Blast	0.97	0.97	0.97	433
Brown Spot	0.99	0.97	0.98	480
Tungro	0.97	0.99	0.98	393
Overall Accuracy			0.98	1870
Macro Average	0.98	0.98	0.98	1870
Weighted Average	0.98	0.98	0.98	1870

A detailed classification report was received to further evaluate the proposed CNN model's performance. This report's key performance indicators include precision, recall, F1-score, and support of the four target classes: Bacterial Blight, Blast, Brown Spot, and Tungro. These measures give more insight into the model's classification ability by each disease category rather than its general accuracy. The high scores in these indicators prove the model's ability to achieve accurate and reliable multi-class classification.

6. Conclusions

This paper expounded on a Custom Convolutional Neural Network (CNN) employed to develop an automated detection system for four rice leaf diseases: Bacterial Blight, Blast, Brown Spot, and Tungro. The data set was downloaded from Kaggle and pre-processed with resizing, normalization, and data augmentation to maximize the model's generalization. The CNN model comprising convolutional, pooling, dropout, and fully connected layers was trained on Adam optimization and categorical cross-entropy loss.

The test accuracy of the proposed model was found to be 98%, the training accuracy of the model was 96.34% and the validation accuracy was 97.75%. This implies that the model will generalise and possess excellent robustness. The loss curves of training and validation showed steady convergence without overfitting. Still, the confusion matrix and the classification report showed that the correct classification was well-founded in all four disease classes at high precision, recall, and F1-scores. The proposed model had a high performance and strength compared to the existing ones, which usually reported between 88 and 96 percent accuracy. This is an enhancement that highlights the study's input in the development of deep learning-based rice disease detection. To summarize, the proposed CNN model can be an effective, precise, and scalable way of diagnosing rice leaf diseases at an early stage. The model facilitates the production of precision agricultural practices by promoting yield protection, minimizing crop loss, and ensuring sustainable rice production through effective detection and intervention.

7. Future work

A large dataset with more rice diseases, healthy leaf samples, and actual rice can be considered in future studies. Images on fields to enhance generalization. The other direction worth pursuing is the creation of a lightweight CNN that can be deployed on mobile or edge devices, and this will allow farmers to diagnose diseases on-site in real-time. Lastly, the model can be expanded into a decision support system, which can not only identify rice leaf diseases but also provide farmers with an adequate management practice (e.g., using pesticides, adjusting nutrients, or managing the field), thus making the model more useful in precision agriculture

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Author contributions

All authors contributed equally to this research work

Competing of interest

The authors have declared no conflicts of interest.

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