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Research Article

ENHANCING REAL-TIME DETECTION OF RICE DISEASES USING AN OPTIMIZED DEEP LEARNING MODEL

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ABSTRACT

Rice is a vital staple food globally, but it is susceptible to a wide range of diseases. Early detection of leaf-related diseases is essential for ensuring its sustainability. Traditional disease identification methods often rely on manual techniques, which are time-consuming, labor-intensive, and inefficient. This study proposes a more efficient approach for detecting rice diseases using a customized *VGG16* convolutional neural network (CNN), addressing these limitations. The proposed model, which includes 14 convolutional layers and a depth of 512 layers, demonstrates enhanced classification effectiveness. A dataset consisting of 3,611 custom-generated images, along with benchmark datasets, was used for evaluation. The model's performance was assessed using five CNN-based algorithms: *DenseNet121, Inception V3, ResNet50*, *VGG16*, and a personalized *VGG* model. The proposed model achieved an accuracy of 96% on new data samples, outperforming current state-of-the-art models. These results highlight the proposed method's superior effectiveness in identifying rice diseases in real-world scenarios.

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INTRODUCTION

Rice is a staple food sustaining billions of people worldwide (Hasan et al., 2023). It plays a pivotal role in ensuring food security (Gogoi et al., 2023) and maintaining economic stability, particularly in Asia, where it serves as both a primary dietary component and a major source of employment (Chen et al., 2021). However, rice cultivation faces several challenges, including diseases such as bacterial leaf blight, sheath blight, brown spot, and leaf blast. These diseases, primarily caused by fungi, bacteria, and viruses, can spread rapidly, leading to significant yield losses, reduced grain quality, and economic hardship for farmers (Prajapati et al., 2017). In developing countries, where agriculture constitutes a crucial part of the economy, these rice diseases pose a severe threat to food security (Krishnamoorthy et al., 2021).

Traditional methods of disease detection, such as manual field inspections or the use of specialized equipment, are often time-consuming, labor-intensive, and require expert knowledge. These limitations make them inefficient for large-scale agricultural practices (Hajjar et al., 2023). Moreover, reliance on human expertise can result in inconsistent outcomes due to variations in skill levels and environmental conditions (Saleem et al., 2019). To address these challenges, there is an urgent need to develop innovative, scalable, and efficient solutions for timely and accurate disease detection to minimize crop losses and sustain agricultural productivity (Wang et al., 2021).

The integration of artificial intelligence (AI) and deep learning (DL) techniques has revolutionized plant disease detection (Trivelli et al., 2019). In particular, Convolutional Neural Networks (CNNs) have proven to be highly effective in analyzing plant leaf images for disease identification and classification. CNNs offer numerous advantages over traditional methods, including high accuracy, automation, and the ability to process large datasets efficiently (Lu et al., 2017). Despite these advancements, current models still face challenges such as overfitting, limited generalization to unseen data, and inefficiencies in extracting features from complex datasets. Addressing these issues is critical for the development of robust, scalable, and reliable disease detection systems.

In the present study, a novel approach for detecting rice diseases is proposed using a customized *VGG16* CNN architecture (Theckedath and Sedamkar, 2020). To enhance feature extraction capabilities (Yogeshwari and Thailambal, 2023) and improve classification performance, the *VGG16* model was upgraded with 14 convolutional layers, each with a depth of 512. Advanced data augmentation techniques, such as rotation and blurring, were applied to optimize the ability of the models to generalize to unseen data (Shorten and Khoshgoftaar, 2019). For robust evaluation and validation, an extensive dataset comprising 3,611 custom-generated and benchmark images of rice diseases was developed.

RELATED WORK

Farmers face daily challenges in agriculture, including the detection of crop diseases. This study reviews various research efforts on disease detection in rice using advanced techniques, focusing on deep learning models, pre-processing methods, and image analysis. Ritharson et al. (2024) proposed using deep learning for rice leaf disease classification. They developed a dataset of 5932 custom rice leaf images categorized into nine disease classes. Models like *ResNet50, DenseNet121,* and *InceptionV3* were evaluated, showcasing effective performance. Ahad et al. (2023) explored six CNN-based models (*DenseNet121, MobileNetV2, ResNet152V*, and others) for identifying nine rice diseases in Bangladesh. Their ensemble model achieved the highest accuracy, highlighting the potential of CNN for real-time agricultural applications. Tyagi et al. (2023) introduced a two-stage process with CLAHE for image pre-processing and hybrid segmentation (HSV and K-means). They integrated the model into an Android app for user-friendly rice disease diagnosis. Gogoi et al. (2023) utilized a transfer learning-based three-stage CNN with PReLU and progressive resizing to enhance model accuracy while minimizing training data needs. The approach was validated on a dataset of 8883 images.

Hasan et al. (2023) used k-means clustering to isolate affected areas in rice leaf images, identifying diseases like bacterial blight and leaf smut. Their model, trained on 2700 images, demonstrated real-world applicability via mobile integration. Velusamy et al. (2023) emphasized segmentation, augmentation, and feature engineering, achieving 3.1% improvement in classification accuracy (90.63%). Zhou et al. (2023) combined Faster R-CNN and FCM-KM for disease detection, achieving robust results after extensive training on 3010 images. Stephen et al. (2023) used *ResNet* architectures with self-attention mechanisms to enhance feature selection, achieving high multiclass classification accuracy. Bari et al. (2021) applied Faster R-CNN to detect healthy and diseased rice leaves (e.g., Hispa and brown spot) using Kaggle and custom datasets, leveraging the Caffe DL technique for training.

This review highlights the potential of deep learning, particularly enhanced *VGG* models, to improve disease classification accuracy and reliability. These approaches can be widely adopted across agricultural systems to address similar challenges effectively.

The main contributions of this paper are as follows:

1. The development of an enhanced *VGG16*-based CNN architecture tailored for precise and efficient rice disease detection.
2. Integration of data augmentation techniques to improve the robustness of the model and generalization across diverse datasets.
3. Demonstration of the proposed method’s superior performance through comprehensive experimental evaluations, benchmarking it against leading CNN models.
4. Utilization of rigorous experimental analyses and standard performance metrics to validate the results obtained from the datasets.

MATERIAL AND METHODS

This study employed automated methods to detect early signs of rice plant diseases. CNNs play a crucial role in this process due to their effectiveness in diagnosing plant diseases by accurately classifying and recognizing images. The training of CNN models heavily depends on the availability of quality data, making data accessibility a critical factor. Numerous researchers have utilized CNNs for plant disease detection because of their proven accuracy.

Figure 1 depicts the workflow of our proposed approach, which was evaluated using a self-generated database. For the training and validation tests, we employed pre-trained CNN models alongside a custom *VGG* model specifically designed for this study. Pre-trained CNNs leverage spatial correlations between image pixels to extract valuable features, enhancing the accuracy of image classification tasks.

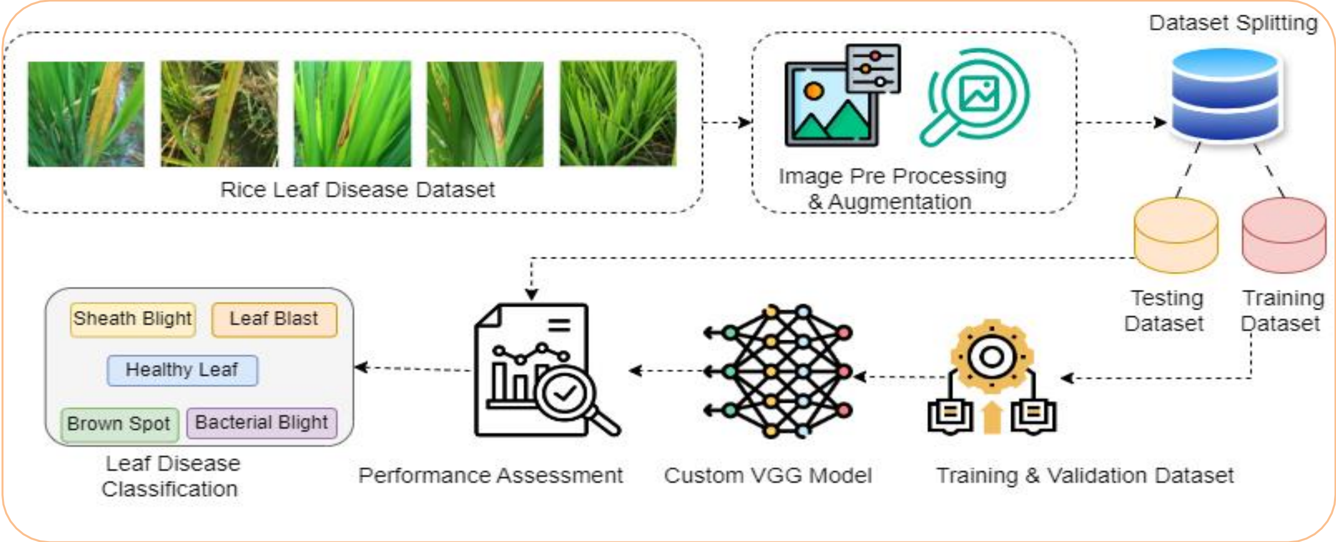

Figure 1. Proposed methodology for rice disease classification.

Classification of rice diseases using deep learning

The detection and classification of plant diseases, including rice diseases, can be effectively achieved using deep learning architectures such as *DenseNet121* (Huang et al., 2017), *Inception V3* (Chollet, 2017), *VGG16* (Chen et al., 2021), and *ResNet50* (Rawat et al., 2023). These architectures have successfully addressed challenges related to visual object recognition and are widely used in tasks such as semantic segmentation, image retrieval, video classification, region-of-interest extraction, and image indexing. Their effectiveness is largely attributed to transfer learning and fine-tuning of parameters.

In a study focused on rice disease classification, *DenseNet121, Inception V3, ResNet50,* and *VGG16* were compared, with the customized *VGG* model serving as a benchmark. *DenseNet121* enhances classification tasks through the iterative concatenation of feature maps across layers, ensuring efficient feature reuse and improved gradient flow. *Inception V3*, part of Google's third generation of deep learning architectures, consists of 48 layers and incorporates the Softmax function in its final layer for classification.

ResNet50, or Residual Network, introduces residual layers and skip connections to address the vanishing gradient problem commonly observed in deep neural networks. This architecture enables the training of very deep networks without performance degradation. Finally, *VGG16* is distinguished by its 16 layers, composed predominantly of small 3 × 3 convolutional filters, making it highly effective for image classification and feature extraction.

Data set description

The primary objective of this research was to collect data to identify rice diseases prevalent in Pakistan. The dataset comprises a combination of real-time images captured from rice crops and a selection of images sourced from existing databases. A small number of images for the healthy rice class were obtained from the Kaggle dataset (Riyaz, 2023) and the Plant Village dataset (Hughes and Salathe, 2015), as illustrated in Figure 2.

To enhance model robustness, the dataset underwent pre-processing and augmentation to increase variability. It includes 3,611 high-resolution, full-color images with diverse backgrounds and sizes. Each class is represented by more than 500 images, ensuring balanced coverage of disease categories.

The dataset was divided into training, validation, and testing sets using a 70:20:10 split ratio, resulting in 2,527 training images and 1,084 images for validation and testing, as detailed in Table 2. Examples of diseased leaves, including bacterial leaf blight, brown spot, leaf blast, sheath blight, and healthy rice leaves, are shown in Figure 3 (a), (b), (c), (d), and (e), respectively.

The model demonstrated high performance on both validation and testing sets, indicating that the dataset size was sufficient for effective training and evaluation. The balanced representation of diseases and the implementation of advanced pre-processing techniques contributed to the ability of the model to generalize effectively.

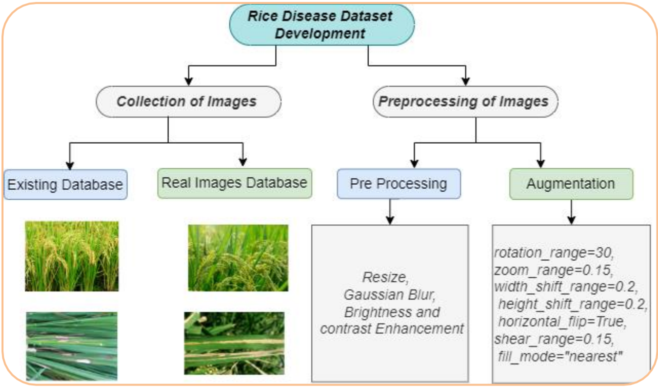

Figure 2. Rice disease dataset development.

Figure 3. Class-wise dataset: (a) Bacterial leaf blight, (b) Brown spot, (c) Healthy rice leaf, (d) Leaf blast, (e) Sheath blight.

Table 2. Class wise distribution of rice disease dataset.

Disease	Total	Training	Validation
Bacterial Leaf Blight	536	375	161
Brown Spot	810	567	243
Healthy Rice Leaf	511	358	153
Leaf Blast	929	650	279
Sheath Blight	825	577	248

Pre-processing of data

Pre-processing is an essential step to enhance specific aspects of images required for processing. It plays a significant role in improving the accuracy and reliability of datasets, which directly impacts the performance of machine learning models trained on them. A well-prepared and cleaned dataset is crucial for various data-driven investigations, such as rice disease classification or other statistical analyses, ensuring precise and meaningful outcomes.

For images downloaded from the internet, pre-processing was necessary to remove unwanted elements and standardize the data. Techniques such as resizing, cropping, sharpening, contrast enhancement, brightness adjustment, and Gaussian blur were applied. After pre-processing, all images were resized to a fixed dimension of 224 × 224 pixels, ensuring uniformity for subsequent model training.

Data augmentation

To expand the dataset size and reduce the risk of overfitting, data augmentation techniques were employed. These methods enhanced the model's generalization capability while diversifying the training data. The applied augmentation techniques included:

1. Horizontal flipping of images,
2. Rotating images by 30 degrees,
3. Applying a height shift range of 0.2,
4. Applying a width shift range of 0.2,
5. Zooming and shearing images by a factor of 0.15.

Methodology for training the proposed model

To improve generalization, the original model was updated by incorporating an additional layer to enhance performance monitoring. The updated architecture, illustrated in Figure 4, comprises 14 convolutional layers, 3 fully connected layers, and 5 max-pooling layers. Key modifications include resizing input images to a fixed dimension of 224 × 224 pixels, ensuring consistent feature extraction across all inputs. The model effectively identifies localized patterns, such as edges and textures, through convolution operations performed with a fixed kernel size of 3 × 3 (Ritharson et al., 2024). Mathematically, the convolution operation for an input image I and kernel K is described in Equation 1 as:

$f(i,j) = \sum_{m=1}^{k} \sum_{n=1}^{k} I(i+m, j+n).K(m,n)$ ------- (1)

Where $f(i,j)$ is the output feature map.

In the convolution process, the kernel traverses the image from the top-left to the bottom-right corner, extracting features along the way. When the stride value is set to 2, the kernel moves two pixels at a time. To improve disease identification, convolution layers are utilized to extract patterns or features from images. The initial convolution layers capture generic features such as edges, while subsequent layers identify domain-specific features.

After each convolution block, a max-pooling layer down-samples the feature maps by retaining the most prominent features, effectively reducing the image dimensions. Convolution layers generate multiple feature maps, which are flattened and mapped in the classification module using a fully connected layer. In this module, the model consists of a feature vector and a dense layer. This feature vector is passed to the next dense layer, which has the same size.

Finally, the softmax activation function connects the neurons of the last dense layer to the output neurons. As described in Equation 2, the softmax function computes the probabilities for each class.

$P(y = i|x) = \frac{e^{zi}}{\sum_{j=1}^{C} e^{zj}}$ ------------------- (2)

Where zi represents the logits for class i, and C is the total number of classes.

The soft-max probability function was used to modify the output layer to include five classes as a result. The sending of data in both directions is necessary for learning to occur. The forward pass utilizes the ReLU activation function to multiply the input neurons by weight values (Zhang et al., 2023). Equation 3 defines the activation function for ReLU.

$f(x) = \max(0, x)$--------- (3)

The ReLU activation function transforms all negative pixel values into positive ones, increasing the model's nonlinearity. During the backward pass, back propagation is used to reduce the loss value. The convolution operator generates gradients at each layer, and the biases and weights are adjusted from the final layer to the first. The model contains 17,074,496 parameters in the convolutional layers. Notably, the model is constructed using previously trained weights through transfer learning, which makes the remaining parameters untrainable. As a result, the model is trained with fewer parameters and at a faster rate. This approach has been shown to enhance classification accuracy for rice disease detection.

Hyper-tuning of parameters

The fine-tuning process of the model typically involves adjusting hyperparameters such as the learning rate, batch size, loss function, and the number of epochs. For the classification model targeting five classes, different values for each hyperparameter within a specified range are considered. The development of an effective model is the result of numerous experiments. The model's accuracy is significantly influenced by variations in the values of these hyperparameters. Table 3 presents the hyperparameters used in the current experiment, which contributed to achieving strong classification accuracy.

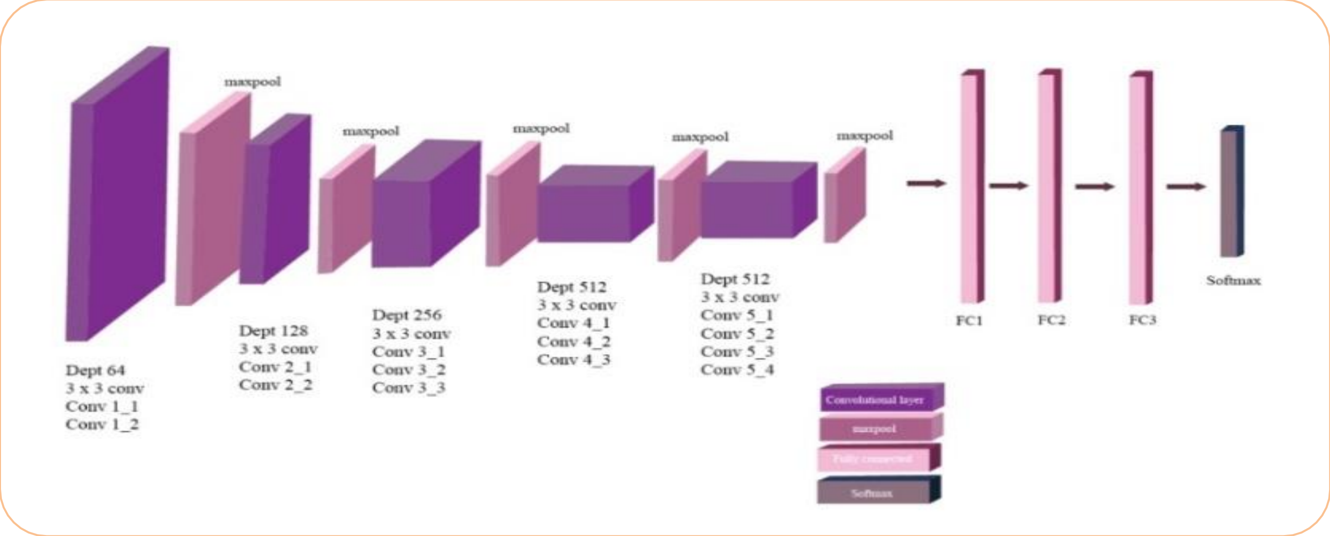

Figure 4: Architecture of proposed model.

Table 3. Parameters used in the training process.

Parameter Name	Parameter Value
Batch size	32
Loss Function	categorical cross-entropy
Optimizer	Adam
Epochs	80
Initial learning rate	$1 e^{-3}$

Experiment setup

The development process began by using Google Colab Notebooks and GPU-enabled computers to create both pre-trained and proposed models. After training the models for 80 epochs, images from various disease categories were used to test their performance. The model's generalization ability was then evaluated by assessing its image identification and classification capabilities using performance metrics.

RESULTS AND DISCUSSION

Performance of state-of-the-art deep learning models

A confusion matrix provides an insightful overview of the classification model's performance by comparing predicted labels with actual labels in a dataset. It illustrates the ratio of correctly predicted positive observations to the total predicted positives (precision) and the ratio of correctly predicted positive observations to all positive observations in the actual class (recall). This detailed analysis offers a clear understanding of the model's strengths and weaknesses.

In machine learning and classification applications, confusion matrices are widely used for an unequivocal evaluation of the model's prediction performance. Moreover, the classification report complements this analysis by including key evaluation metrics such as recall, precision, F1-score, and accuracy.

Table 4 summarizes the effectiveness metrics for the pre-trained models evaluated. The confusion matrix findings for the five classes of the rice diseases dataset are presented in Figure 5(a), (b), (c), and (d), providing a visual representation of the classification results.

The Receiver Operating Characteristic (ROC) curve illustrates the classification performance of different rice disease types, as shown in Figure 6. The x-axis represents the false positive rate, which is the proportion of negative instances incorrectly classified as positive. The y-axis represents the true positive rate, which measures the proportion of actual positive instances correctly identified by the model. The ROC graph evaluates the trade-off between the false positive and true positive rates, providing insights into the model's ability to distinguish between positive and negative classes.

False positive and true positive rates were used to calculate the macro and micro averages for each class, enabling a comprehensive evaluation of the model's performance across multiple categories. Moreover, the graph provides information on how long each model took to train over 80 epochs. Variability in training duration was another key factor considered when selecting the most suitable models.

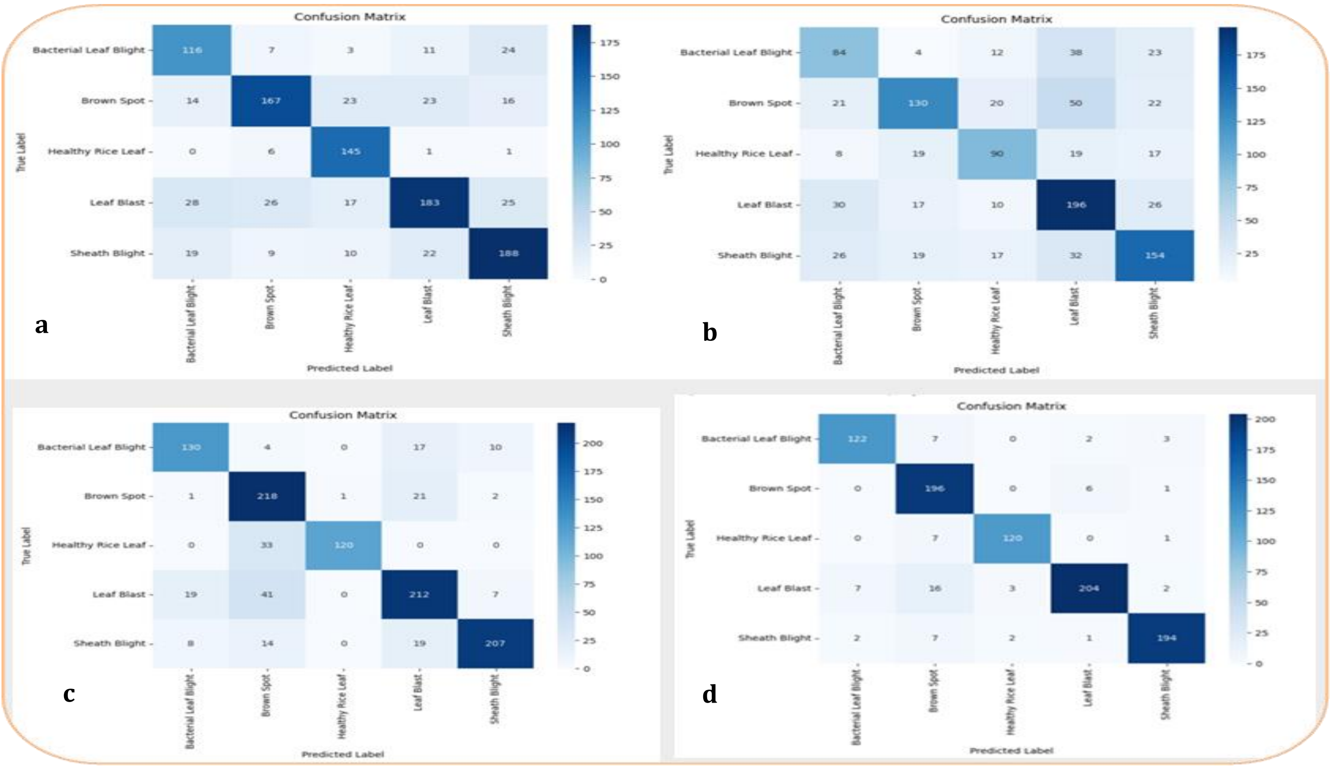

Figure 5. Confusion matrices for classification models: (a) DenseNet121, (b) Inception V3, (c) ResNet50, and (d) VGG16.

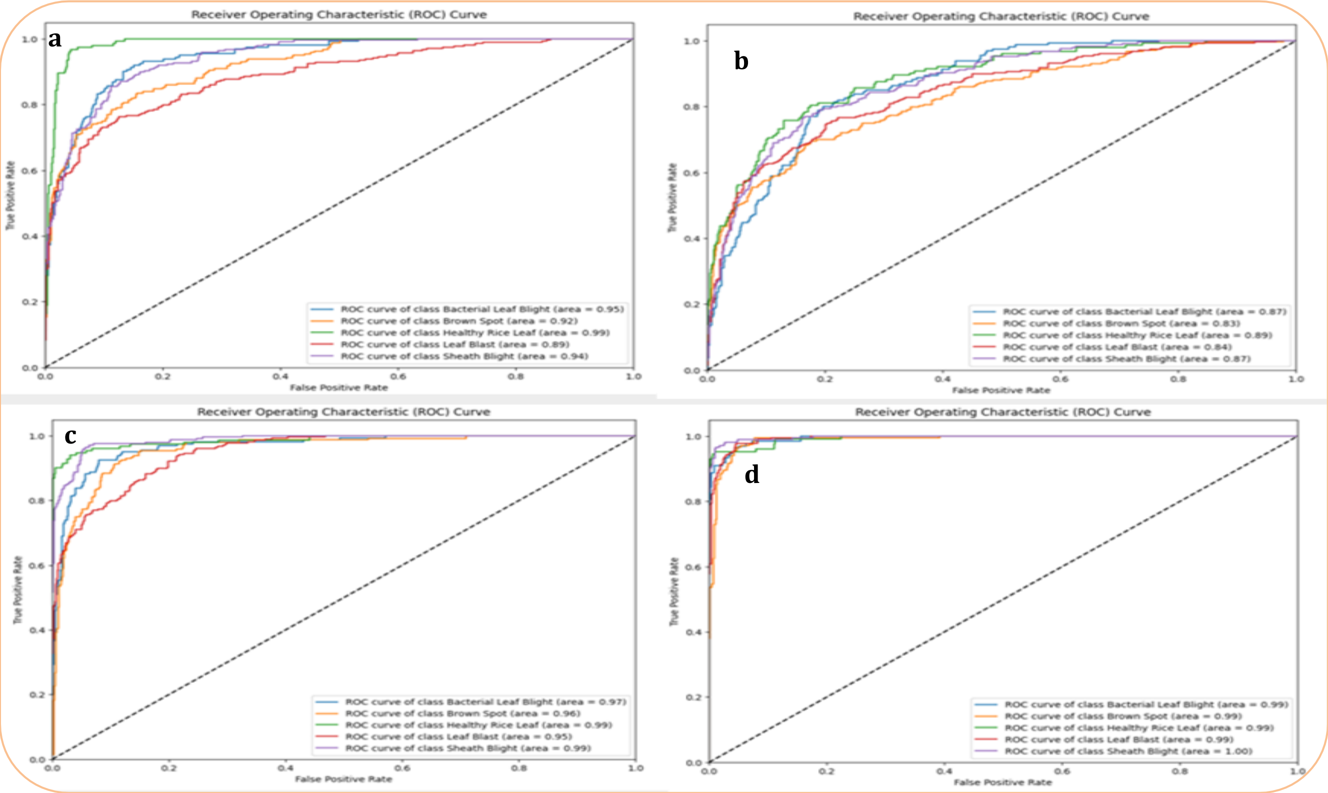

Figure 6. ROC curves for different models: (a) DenseNet121, (b) Inception V3, (c) ResNet50, (d) VGG16.

Table 4. Effectiveness measure analysis of CNN models.

Model Name	Precision	Recall	F1 Score	Accuracy
DenseNet121	0.73	0.75	0.74	74.1%
Inception V3	0.60	0.59	0.59	60.2%
ResNet50	0.84	0.82	0.83	82.1%
VGG 16	0.92	0.93	0.93	93.1%

Proposed model evaluations

The model was successfully trained using images from multiple disease categories over 80 iterations. The objective of the training and testing phases was to train the model, validate its performance, and assess its generalization capability through evaluation metrics. The training loss reflects the model's ability to learn from the training dataset. It is calculated by determining the difference between the target values in the training set and the predicted outputs generated by the model. The primary goal of the training phase is to minimize the loss, ensuring that the model accurately captures the relationship between input data and corresponding target outputs.

In contrast, validation loss measures how well the model performs on new, unseen data. It is determined by calculating the difference between the actual target values in a validation set (or a reserved portion of the training data) and the model's predictions. Validation loss is a critical metric for identifying overfitting or underfitting and assessing whether the model has captured meaningful patterns in the data.

Table 5 presents the accuracy and loss outcomes for both training and validation across various epochs (ranging from 10 to 80). Training accuracy improved progressively, starting at 91.11% after 10 epochs and reaching 98.48% after 80 epochs. Validation accuracy showed a range of 91.25% to 96.32% across different epochs. As the number of epochs increased, training loss steadily decreased, reflecting the model's enhanced learning from the dataset.

The confusion matrix illustrates the performance of a classification model when tested on new data with known actual labels. The performance of the confusion matrix for each class in the rice disease dataset is presented in Table 8. The classification model's performance at various thresholds can be assessed by comparing the true positive rate and false positive rate on the ROC curve, as shown in Figure 7. The comparison results highlight that our customized *VGG-16* model outperforms other models in terms of generalizing transfer learning across different classes of rice diseases, as demonstrated in Figure 8.

Table 5. Training and validation accuracy and loss across epochs.

Epoch	Training Accuracy	Training Loss	Validation Accuracy	Validation Loss
10	0.9211	0.2296	0.9125	0.3230
20	0.9594	0.1403	0.9448	0.1850
30	0.9722	0.0889	0.9632	0.1343
40	0.9777	0.0761	0.9604	0.1608
50	0.9843	0.0521	0.9613	0.1694
60	0.9786	0.0673	0.9687	0.1345
70	0.9865	0.0512	0.9705	0.1267
80	0.9848	0.0484	0.9632	0.2145

Table 8: Performance report of proposed VGG model.

Disease	Precision	Recall	F1 Score	Support
Bacterial Leaf Blight	0.91	0.97	0.94	161
Brown Spot	0.97	0.93	0.95	243
Healthy Rice Leaf	0.99	0.98	0.98	155
Leaf Blast	0.95	0.97	0.96	279
Sheath Blight	0.99	0.98	0.98	248
Accuracy			0.96	

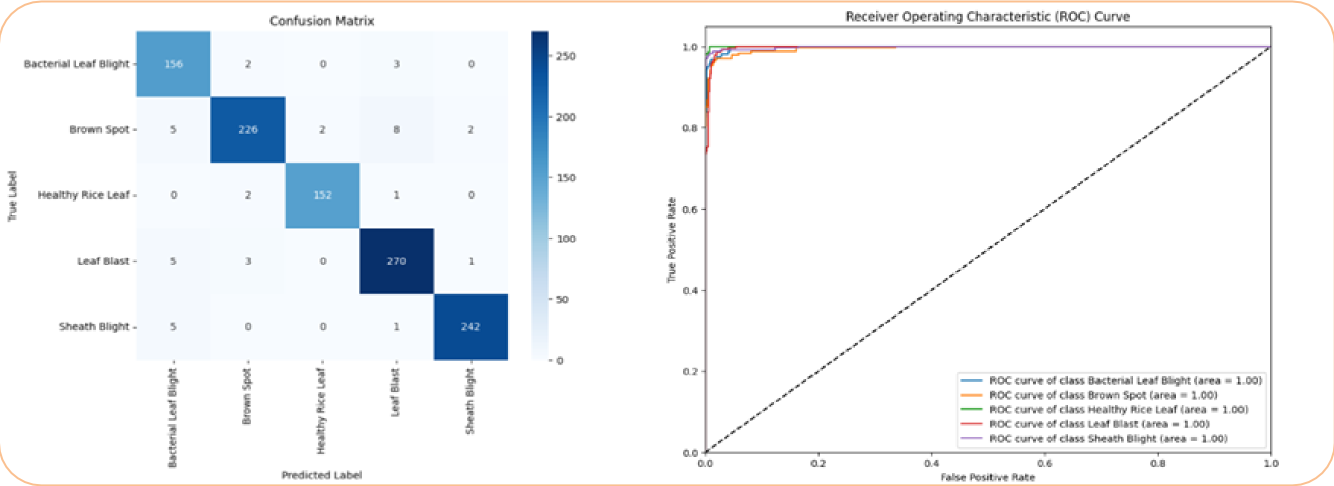

Figure 7. Confusion matrix and roc of proposed VGG model.

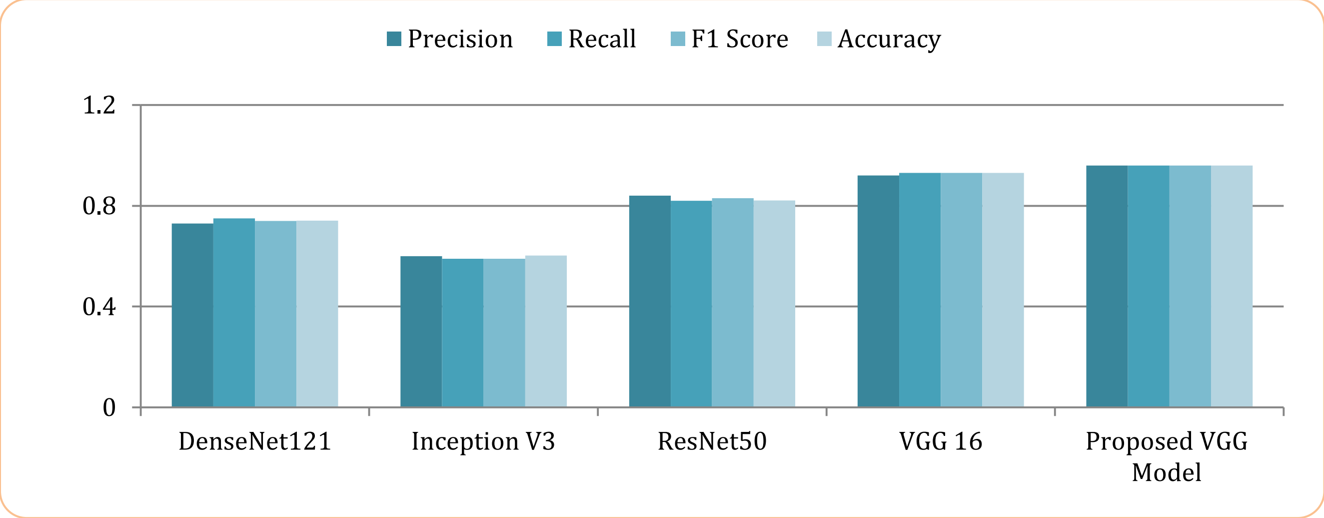

Figure 8. Evaluation of the proposed custom VGG model and pre trained models.

Additionally, both the *VGG-16* and proposed *VGG* models exhibited significant variations during the training phase as the number of epochs increased. During this phase, the *VGG* model experienced fluctuations in validation accuracy. In the ninth epoch, the validation accuracy unexpectedly dropped to 0.57 (57%), while the loss increased to 2.40. However, by the end of the training, the accuracy improved to 93%, as shown in Figures 9(a) and 9(b), and then stabilized at 0.7656 in the subsequent iteration. In contrast, the proposed *VGG* model demonstrated a steady increase in accuracy over time, ultimately achieving a final average accuracy without any sudden spikes.

The proposed model demonstrated superior performance with the incorporation of an additional layer for improved feature extraction. However, certain limitations could affect its performance. If the dataset used for training is small or of poor quality, such as blurry images or incorrect labels, the model may struggle to learn effectively and may fail to identify diseases accurately. Additionally, if the dataset is imbalanced, with more images of one disease than others, the model might become biased towards predicting the rarer diseases. Resizing images to a fixed size could result in the loss of crucial details, particularly when disease signs are very small. Furthermore, since the model uses pre-trained weights, it may not fully adapt to the unique features of rice diseases, especially if these features were not present in the original training data. Enhancing the dataset and testing the model under more diverse conditions could help mitigate these issues.

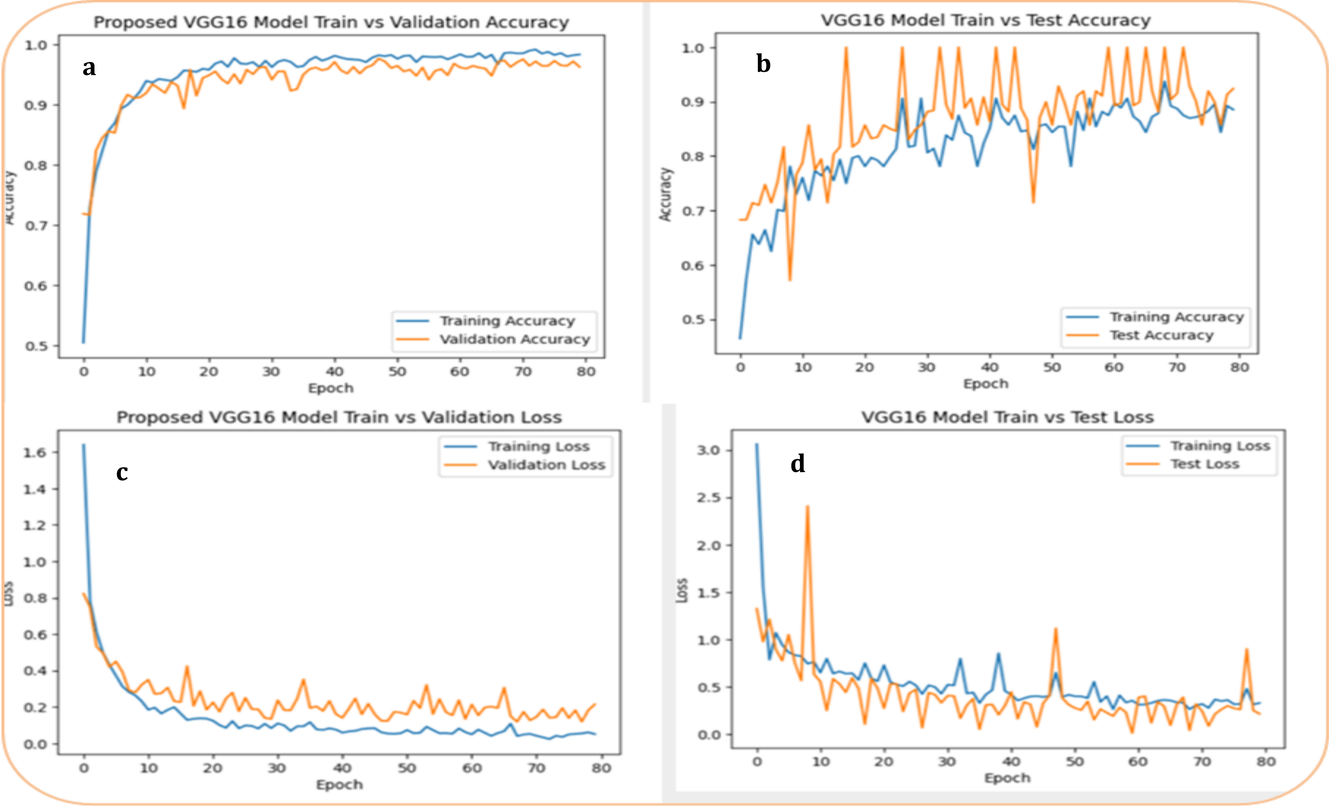

Figure 9: (a)Training, validation Accuracy of Proposed VGG Model (b) Training and validation accuracy of VGG Model (c) Training, validation loss of Proposed VGG Model, and (d) Training and validation accuracy for VGG 16.

CONCLUSION

This study demonstrates that Convolutional Neural Networks (CNNs) and deep learning techniques can effectively detect and classify diseases affecting rice plants at an early stage. The proposed custom *VGG* model proved to be highly effective, achieving a 96% increase in accuracy, along with the highest precision and recall scores. Our method for diagnosing plant diseases is both rapid and reliable, as it successfully identifies and classifies four distinct disease categories in addition to healthy rice plants. Five transfer models were selected and retrained with a focus on real-time deployment, considering factors such as parameter size and model complexity. The customized *VGG* model outperformed all other models in terms of accuracy, recall, and precision. This model's robust performance can be applied to various agricultural scenarios, enabling the classification of crop diseases based on severity.

This research holds significant implications for agriculture by aiding farmers in early disease detection and enabling timely interventions to mitigate crop losses. The findings will have a substantial impact on the development of precision agriculture.

In the future, the custom *VGG* model can be adapted to address multiple crop diseases, leading to more effective and efficient tools for crop disease detection. The adoption of deep learning techniques has the potential to greatly enhance crop production and quality.

AUTHORS' CONTRIBUTIONS

SN and KH designed the study, formulated the experiments, and executed them; SN and KH collected and organized the data, analyzed the results, and wrote the manuscript; SN and AS assisted in writing the manuscript and proofreading the paper.

CONFLICT OF INTEREST

The authors declare that there is no conflict of interest.

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