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Research Article

Innovative Approaches to Rice (*Oryza sativa*) Crop Health: A Comprehensive Analysis of Deep Transfer Learning for Early Disease Detection

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Abstract: In this research, the primary objective is to tackle the pressing issue of identifying and effectively managing diseases in rice plants, a problem that can results in substantial crop losses and pose a severe threat to food security. The study employs Convolutional Neural Networks (CNNs), a type of deep learning model widely used for image analysis, to conduct an extensive investigation using a sizable dataset comprising 5,932 RGB images. These images represent four distinct disease classes in rice plants: Bacterial Leaf Blight (BLB), Blast, Brownspot, and Tungro. To conduct this research, the dataset is split into two subsets: a training set, which comprises 80% of the data, and a testing set, which makes up the remaining 20%. This division allows for a systematic evaluation of the performance of four different CNN architectures: VGGNet, ResNet, MobileNet, and a simpler CNN model. The results of this study consistently show that ResNet and MobileNet outperform the other CNN architectures in terms of their ability to accurately detect diseases in rice plants. These two models consistently achieve remarkable accuracy in identifying these diseases. The research findings not only emphasize the potential of deep learning techniques in addressing the critical issue of rice crop diseases but also highlights the significant role that ResNet and MobileNet play in strengthening crop protection efforts and contributing to global food security.

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1.Introduction

Rice (*Oryza sativa* L.) is the supreme crop of many countries around the globe. It is the largest cultivated and consumed food all over the globe. In comparison to other crops, rice has more nutrients and is affordable to every earning individual. About 70% of the population in Asia has a diet of rice. In 2020 rice production in Assam is 5.1 million tonnes (Sandhya Keelery, 2022). Production of rice at Assam grew at an average rate of 2.73% from 4.73 million tonnes in 2017 to 5.1 million tonnes in 2020 (Pathak et al., 2018). However over time, nematodes, some non-insect pests, and diseases that affect insects have all increased in abundance (Prakash et al., 2014). These biotic stresses caused numerous epidemics to occur throughout the nation. There are several types of rice plants and hence many uncovered diseases are present regarding different rice varieties. Over time, the frequency and extent of the harm have varied (Gowda et al., 2021). Depending on the region, varieties planted, weather circumstances, and production practices, these pests and diseases show concurrent transitions both in their minor and major status (Soren et al., 2020). Sheath rot, early seedling blight, grain discoloration, false smut, bakanae, and narrow brown spots are only a few examples of minor plant ailments that have now developed into serious issues. Among those diseases the most common and destructive diseases are Bacterial Leaf Blight (BLB) (*Xanthomonas oryzae pv. Oryzae*), tungro (*Rice tungro bacilliform virus*), blast (*Magnaporthe grisea*), and brownspot (*Cochliobolus miyabeanus*) which lead to some catastrophic loss of quality and quantity of rice plants yielded in several acres of land. The early identification and accurate diagnosis of these diseases are crucial for implementing timely and effective management strategies, ensuring minimal crop losses, and optimizing yield. Traditionally, agri consultants, agri experts, or farmers themselves would visually inspect the plants to detect any infections since they had the knowledge to do so. The other conventional approach used laboratory testing, which involved measuring soil properties including pH, moisture, and nitrogen. Other frequently used laboratory techniques include microscopic analysis and serological tests. However, these methods have certain drawbacks, such as being time-consuming, requiring staff monitoring, and being ineffective for large farms. Diseases were only discovered when they caused significant crop loss (Patil and Kumar, 2021). Traditionally, experienced professionals visually inspect plant tissue to gauge the severity of plant diseases. The expensive and ineffective evaluation of plant diseases hinders the rapid advancement of modern agriculture (Mutka and Bart, 2015). Automated disease detection models were employed more frequently in precision agriculture, high-throughput crop phenotyping, intelligent greenhouses, and other industries as a result of the expanding uptake of digital cameras and advancements in computer vision (Barman and Choudhury, 2019 and 2022; Barman et al., 2023). Deep learning models were recommended by many studies for image-based identification of diseases of plant (Voulodimos et al., 2018). Deep learning has recently become a potent tool in the field of machine vision and visual analysis, with astounding success in a wide range of fields. Its ability to automatically learn hierarchical representations from large-scale datasets has proven instrumental in solving complex visual recognition tasks. Utilizing previously trained models on a source task to enhance performance on a target task with little labeled data is known as transfer learning, a subset of deep learning. This approach has shown great promise in a wide range of applications, including agriculture and plant pathology. Liang et al. (2019) proposed a rice blast disease recognition using a Deep CNN. They used a dataset of 5808 images and developed a model for rice blast disease classification. Their model produced an accuracy of 95%. Wang et al. (2021) proposed a rice disease detection and classification using an attention-based neural network and bayesian optimization. They used an attention-based depthwise separable neural network with Bayesian optimization to create the model. They used a dataset of 2370 images and their model produced an accuracy of 94.65%. Latif et al. (2022) proposed rice plant diseases using an improved CNN Model. They used an improved CNN model specified as VGG19. They used a dataset with 6 different classes and their model produced an accuracy of 96.08%. The purpose of this study is to assess the efficiency of deep neural networks for the prompt identification of rice diseases such as BLB, tungro, blast, and brown spots. By exploiting the knowledge learned from large-scale image datasets, pre-trained deep neural networks can extract meaningful features from rice disease images, enabling accurate classification and identification. The transfer learning paradigm allows us to leverage the knowledge gained from other related tasks, such as general object recognition or plant disease identification, and adapt it to the specific context of rice diseases.

The primary objectives of this study are twofold.

- First, to evaluate the performance of deep transfer learning models in detecting and classifying common rice diseases.
- Second, to compare their effectiveness against conventional machine learning algorithms. By conducting a comprehensive assessment, we aim to provide valuable insights into the potential of deep transfer learning for early disease identification of rice.

Furthermore, this research will contribute to the development of automated and cost-effective disease monitoring systems that can be deployed in real-world agricultural settings. Early disease detection can facilitate timely interventions, such as targeted pesticide application, disease-resistant crop selection, or site-specific disease management, thereby reducing the risk of yield losses and improving overall crop health. In summary, this paper seeks to demonstrate the potential of deep transfer learning in revolutionizing the early identification and management of rice diseases. By leveraging the power of deep learning, we can pave the way for sustainable and resilient rice production systems, ensuring food security for the growing global population.

2. Material and Methods

The research methods of the current study are presented below.

i. To gather a rice dataset comprising 5932 RGB images and subsequently pre-processing [resizing of images] the dataset for model training and testing.
ii. To develop a CNN-based model capable of detecting common rice leaf diseases accurately, including BLB, blast, brown spot and tungro.
iii. Investigate the performance of different CNN architectures, including transfer learning models such as VGGNet, ResNet, MobileNet.
iv. Finally evaluate the model's accuracy and effectiveness in identifying and classifying the four target rice disease classes.

2.1. About the dataset

The dataset has been collected from a study reported by Sethy et al. (2020). A total of 5932 numbers of RGB images, comprising 4 diseases namely BLB, blast, brownspot, and tungro are considered for this experiment.In this recognition, the total number of images taken for BLB, blast, brownspot,and tungro are 1584, 1440, 1600, and 1308, respectively.

BLB: It is a bacterial disease and one of the most serious diseases of rice. The crop loss due to this disease can be as high as 75%. It thrives in warm, humid environments. Leaf blight can be identified in the initial stage when there are yellow stripes on the leaf, the stripes can be in the middle or parallelly on the leaves eventually leading to the drying of the leaves. A sample image of bacterial leaf blight is shown in the Figure 1.

Blast: Blast can be identified by noticing the rice leaf plants that have eye-shaped spots, initially having a yellow appearance and later leading to a dark brown color. The fungus that causes blast is "*Magnaporthe oryzae*".It can occur when there are blasts pores are present. It occurs in rice plants at all stages of growth. The environment in which disease occurs includes drastic temperature differences in day and night, basically cool temperatures during the daytime. A sample image of the blast is shown in Figure 1.

Brownspot: Brownspot is a fungal disease infecting the leaf sheath, panicle branches, leaves, and spikelets. It is caused by the fungus "*Cochliobolus miyabeanus*". When the leaf is wet for more than 8 – 24 hours only then the infection can occur. This infection mostly occurs during the ripening stages of the crop. The initial stage of the disease is a small circular brown-purple color spot in the leaf. In Figure 1, a sample image of brownspot is depicted.

Tungro: The main cause of this disease is leaf hoppers that transmit the virus from plant to plant. It is the combination of two viruses, one of them is an RNA virus named "*Rice Tungro Spherical Virus*" and the other one is a DNA virus named "*Rice Tungro Bacilliform Virus*". In Figure 1, a sample image of Tungro is depicted.

Figure 1. Sample image of a) BLB, b) blast, c) brownspots, and d) tungro.

2.2. About method

2.2.1. Deep Convolutional Neural Network (DCNN)

Better recognition of images, the process of segmentation, and image retrieval have all been made possible by DCNN's presentation of a functional group of models for better comprehending the information contained in an image. The well-known trained networks of DCNN utilize this dataset after being trained over thousands of thousands of images in the datasets of the CIFAR 100 and Image-Nets, improving the effectiveness of categorization. Our work's main addition is the presentation of detection of object techniques utilizing various trained neural network architectures, where, according to Sharma et al. (2018), modern models perform differently for test photos compared to trained images.

2.2.2. Transfer learning

Transfer learning is a successful technique to develop robust classification networks with little information by adjusting the parameters of a machine learning network that has already been pre-trained on a large dataset, like ImageNet. Even if it was not trained on the dataset of crop leaves, the model can still be triggered by the area of the crop spots, leaves, and backgrounds. There are numerous transfer learning architectures, including ResNet50 (He et al., 2016), Inception-v3 (Szegedy et al., 2016), and VGGNet (Simonyan and Zisserman, 2015) which were used in the area of Agri-informatics. The pre-trained models, such as ResNet and MobileNet, have learned to extract high-level features from images. These features can be highly relevant for detecting diseases in rice plants. Transfer learning allows us to use these well-learned features as a starting point and fine-tune them for the specific task of rice disease recognition.

2.2.3. DCNN-based rice leaf disease recognition model

DCNNs are similar to conventional Artificial Neural Networks (ANN), where neurons are optimized in learning. The proposed DCNN-based model for this experiment has nine layers. The layers are convolution1, pooling1, convolution2, pooling2, convolution3, pooling3, flatten, dense layer1, dense layer2 (Table 1). The first layer of the DCNN is convolution, which considers the input images to perform the convolution operation on the image pixel before sending the results to the pooling layer. In this model, three convolution layers and a few filters have been used. Each filter recognizes specific aspects of the image of the rice leaf disease and is trained spatially, considering its position in the volume it is applied. In Table 1, a description of convolution layers and filters has been given. To make it simple to learn complex relationships in the data, the nonlinear activation function ReLU has been used. For Convo1, Convo2, and Convo3, 16, 32 and 64 filters have been employed, respectively. As pooling lowers variance and computational complexity, there are fewer parameters to learn in this model. The feature map's dimensions are decreased along with the spatial dimensions by downsampling. It also describes the features that may be seen in a section of the convolution's feature map. The results of the very last max pooling layer get flattened into a vector with one dimension and placed into a fully linked dense layer. To identify rice leaf disease, a one-dimensional vector was finally generated by the final max polling layer and provided into the dense layer. Two dense layers with 64 and 4 hidden neurons each were added to the model.

This experiment reported a total of 3 710 308 parameters and among them all are trainable and 0 non-trainable parameters. To learn and tune the network parameters in the convolution, pooling,and dense layers to condense the features into a 1x64 vector, it is required to input the pictures to our model in batches. These characteristics are then transferred to another thick layer to create a vector of 1x5. The images are processed through a series of iterations called epochs and use the collection of validation images to verify the model and its associated parameters.

Table 1. Architecture summary of the DCNN for rice disease dataset classification

Layers	Function	Kernal size	Pool-size	Filter	Output	Parameters
Input					256 x 256	0
Convo1	Convolution	3 x 3		16	16x254x254	448
Pooling	Max Pooling		2,2	16	16x127x127	0
Convo2	Convolution	3x3		32	32x125x125	4640
Pooling 2	Max Pooling		2,2	32	32x62x62	0
Convo3	Convolution	3x3		64	64x60x60	18496
Pooling 3	Max Pooling		2,2	64	64x30x30	0
Flatten	Flatten				57600	0
Dense	Dense				1x64	3686464
Dense_1	Dense				1x4	260

2.2.4 VGG16 (Visual Geometry Group) based rice disease detectionmodel

VGG -16 is 16 layers DCNN which was trained with over 1 million images from the ImgeNet database. The input size of the image for the network is 224x224 (Barman et al., 2020). The VGG 16 contains 5 sets of convolution layers followed by the maxpool layer. In VGG16, there are a total of 14 815 044 parameters; among them, there are 100 356 and 14 714 688 trainable parameters and non-trainable parameters, respectively. In Table 2, a brief description of the different parameters of VGG16 is given.

Table 2. Summary of parameters for VGG16 model training on rice disease dataset

Image		Parameter		Training	
Train set	4746	**Total**	14815044	**Epoch**	10
Validation set	1186	**Trainable**	100356	**Loss**	Categorical cross-entropy
Size	(244,244)	**Non-trainable**	14714688	**Optimizer**	ADAM
				Learning rate	0.0001

2.2.5. Residual Network 50 (ResNet50) based rice disease detection model

He et al. (2016) introduced the Residual Neural Network (ResNet) deep neural network framework. By introducing a novel ”residual” or ”skip connection” concept, was created to overcome the difficulty of training deep neural networks. A special variation of the ResNet architecture called ResNet-50 has 50 layers. ResNet50 is a deeper network compared to earlier versions like ResNet-18 or ResNet-34. It contains 50 layers, including convolutional, pooling, and fully connected layers. ResNet-50 utilizes a specific type of residual block called the bottleneck block. The bottleneck block decreases the number of parameters and computations, which lowers the computational cost of training deeper networks. The training set consists of 4746 images (Table 3). These are the images used to train the ResNet model and adjust its parameters based on the provided labels. The test set contains 1186 images. These images, which are distinct from the training set, are used to assess how well the trained ResNet model performed. The test set aids in evaluating the model’s ability to generalize to new data. In this study, the model has 6 744 164 trainable parameters, which are adjusted based on the training data to improve model performance (Table 3). The model has 18 067 328 non-trainable parameters. The Adam optimizer, a common optimization technique that is well-known for it’s success in training deep neural networks, is utilized in this instance.

Table 3. Summary of parameters for ResNet model training on rice disease dataset

Image		Parameter		Training	
Train set	4746	**Total**	24811492	**Epoch**	10
Test set	1186	**Trainable**	6744164	**Loss**	Categorical Cross Entropy
Shape	(244,244)	**Non-trainable**	18067328	**Optimizer** **Learning rate**	ADAM 0.001

2.2.6. MobileNet based rice disease detection model

The CNNs are used in mobile imaging applications like MobileNet. They are constructed using these compact deep neural networks with depth-wise separable convolutions that can have minimal latency for embedded and mobile devices (Barman et al., 2020). Compact deep neural networks with depth-wise separable convolutions are used in their construction, allowing for minimal latency for embedded and mobile devices (Barman et al., 2020).

In Table 4, a brief description of the different parameters of MobileNet has been given. In this study, the model has 2 228 996 trainable parameters, which are adjusted based on the training data to improve model performance. The model has 34112 non-trainable parameters. The model is trained for 10 epochs like VGG 16 and ResNet 50.

Table 4. Summary of parameters for MobileNet model training on rice disease dataset

Image		Parameter		Training	
Train set	4746	**Total**	2263108	**Epoch**	10
Test Set	1186	**Trainable**	2228996	**Loss**	Categorical cross entropy
Shape	(244,244)	**Non-trainable**	34112	**Optimizer Learning Rate**	ADAM 0.0001

3. Results

Table 5 shows the performance metrics (precision, recall, and F1 score) of different methods (CNN, MobileNet, VGG16, and ResNet 50) for detecting and classifying different rice diseases (Bacterial Leaf Blight, Blast, Brownspot, and Tungro).

Table 5. Comparison of CNN and its transfer learning models for rice disease detection

Methods		Diseases			
		Bacterial Leaf Blight	**Blast**	**Brown Spots**	**Tungro**
CNN	Precision	0.96	0.96	0.99	0.99
	Recall	0.98	0.95	0.97	1.00
	F1 score	0.97	0.95	0.98	0.99
MobileNet	Precision	1.00	0.98	1.00	0.98
	Recall	0.99	1.00	0.99	1.00
	F1 score	1.00	0.99	1.00	0.99
VGG16	Precision	0.98	0.93	0.98	0.99
	Recall	0.94	0.97	0.97	1.00
	F1 score	0.96	0.95	0.98	0.99
ResNet 50	Precision	0.99	0.99	1.00	1.00
	Recall	1.00	1.00	0.99	0.99
	F1 score	1.00	0.99	1.00	1.00

Precision is a measure of the accuracy of the model's positive predictions. It calculates the ratio of true positive predictions to the sum of true positive and false positive predictions. A higher precision indicates that the model has a lower false positive rate. In Table 5, MobileNet achieved high precision scores for most diseases, except for blast where it achieved a precision score of 0.98. This means that MobileNet had a relatively low false positive rate and made fewer incorrect positive predictions for most diseases. Sethy et al., (2020) reported the 0.98 precision in ResNet 50 in their study which is lesser than this study.

Recall, also known as sensitivity, measures the ability of the model to correctly identify positive instances. It calculates the ratio of true positive predictions to the sum of true positive and false negative predictions. A higher recall indicates that the model has a lower false negative rate. In Table 5, MobileNet achieved high recall scores for most diseases, except for brownspot where it achieved a recall score of 0.99. This means that MobileNet correctly identified most positive instances and had a relatively low false negative rate for most diseases.

The F1 score is the harmonic mean of precision and recall. It provides a balance between precision and recall, considering both false positives and false negatives. A higher F1 score indicates a better overall performance of the model. In Table 5, MobileNet achieved high F1 scores for most diseases, except for blast and tungro where it achieved F1 scores of 0.99. This indicates that MobileNet had a good balance between precision and recall for most diseases.

4. Discussion

Overall, based on Table 5, MobileNet appears to be a strong performer for detecting and classifying rice diseases, as it achieved high scores in precision, recall, and F1 scores for most diseases. However, it's worth noting that VGG16 and ResNet 50 also performed well in some metrics and diseases, with generally high scores across the board. The choice of the best method depends on the specific requirements and priorities of the application. Sethy et al. (2020) reported the ResNet 50 as the best model in their study with 98% accuracy and 0.98 F1 score whereas the current study produced 99% accuracy with MobileNet. To compare the results, Table 6 demonstrates the comparative analysis of the different results of the previous study.

Table 6. Comparative analysis of different studies for rice disease detection

Author	Model	No of Rice Disease Class	Accuracy
Sethy et al. (2020)	ResNet 50	04	98%
Deng et al.(2021)	Ensemble Model	06	91%
Upadhyay and Kumar, (2021)	CNN	03	99%
CurrentStudy	MobileNet	04	99%

Table 6, shows a comparative analysis of different studies for rice disease detection, Sethy et al., (2020) used the ResNet 50 model to detect rice diseases. They worked with a dataset consisting of four different rice disease classes. The accuracy achieved by their model was 98%. Deng et al. (2021) employed an Ensemble Model for rice disease detection. Their study involved working with a dataset that consisted of six different rice disease classes. The accuracy achieved by their model was 91%. Upadhyay and Kumar (2021) utilized a CNN for rice disease detection. They worked with a dataset comprising three different rice disease classes. Their model achieved an accuracy of 99%. In this study, we used the MobileNet model for rice disease detection with an accuracy of 99%.

These studies highlight different approaches and models used for rice disease detection, with varying numbers of rice disease classes. The accuracy results suggest that all the models achieved high accuracy in detecting rice diseases, ranging from 91% to 99%. However, MobileNet can be considered one of the best models for rice disease detection. Deep learning models, such as ResNet and MobileNet, excel at automatically extracting intricate features from images. This feature extraction capability allows these models to detect subtle and early visual cues associated with the onset of rice diseases, including changes in leaf color, texture, and structure that may precede visible symptoms and lead to early identification of rice diseases. Again by integrating deep learning models into monitoring systems or deploying them on drones or cameras in the field, it becomes possible to continuously analyze rice plant images in real-time. Early signs of disease development can be detected swiftly, even before the human eye can discern them, enabling timely intervention.

Conclusion

One of the key diagnostic windows for rice diseases lies in the leaves, where distinct diseases manifest with varying impacts. Recognizing the nuanced differences in how these diseases affect the leaves represents a critical aspect of effective disease management. To address this challenge, our study embarked on a comprehensive exploration of various deep-learning algorithms. The overarching objective was clear: to achieve early diagnosis and intervention. Amidst this diverse algorithmic landscape, MobileNet emerged as the standout performer. Its exceptional capabilities in identifying and classifying rice leaf diseases signify a significant stride toward bolstering rice crop health.

Ethical Statement

Ethical approval is not required for this study.

Conflict of Interest

The Authors declare that there are no conflicts of interest.

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