### ORIGINAL CONTRIBUTION



# Classification of Rice Diseases using Convolutional Neural Network Models

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**Abstract** Automatic diagnosis and control of rice plant disease are highly desired by agricultural experts. Many machine learning approaches have been proposed in automating rice disease identification, where deep learning has generated significant outcomes. In the present study, state-of-the-art deep learning models based on transfer learning approach are deployed for the classification of various disease symptoms in rice plant images. The efficiency of the leading pre-trained VGG-16 and GoogleNet convolutional neural network (CNN) models on the heldout dataset is evaluated using a threefold cross-validation method. The trained VGG-16 and GoogleNet CNN models achieved an average classification accuracy of 92.24% and 91.28%, respectively. The experimental results demonstrate the practical usefulness of utilizing the deep learning methodology employing 12,000 labeled images of three different rice diseases with 24 different symptoms. The proposed work finds applications in on-field identification of rice disease symptoms providing actionable information to farmers and policy makers in many aspects of crop handling and management practices.

**Keywords** Rice disease · Image analysis · Deep learning ·

Classifier

Indian rice is very popular among all export destinations because of its flavor and relevance. The enormous global demand for rice has created ideal conditions for rice exports. India surpassed China in rice exports and recorded a 22% growth in 2018. To maintain the quality and integrity of the rice crop, India's rice export quality has been altered from a free to a restricted category [1]. Better agricultural management is necessary to maintain the quality of rice crops. The quality and amount of rice crop are affected as a result of diseases such as viral, bacterial, fungal and shortage of vital minerals. Early detection and classification of rice diseases are essential before they become severe [2]. Rice disease diagnosis necessitates a significant amount of effort and plant disease knowledge, as well as additional pre-treatment time. Rice diseases are often misidentified, resulting in significant losses in yield, time, money and quality. Farmers must constantly monitor the health condition of rice plants. Identification is a major task for a successful crop and automatic field analysis is required to improve this monitoring facility [3].

Identification and classification of rice diseases are made by physical techniques which require the assistance of experts; sometimes it will be prone to error. As a result, the classification of rice diseases is required to assess agricultural products, increase market value and meet quality standards. Significant progress in the field of image processing and machine learning (IPML) has led to a good number of real-world applications in the recent past [4]. Image processing and machine learning techniques are

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Introduction

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employed in the early detection of plant disease. It is always quite challenging to design a computer vision system to recognize and distinguish the images in the real world in real time. This real activity is mainly attributed to the requirement of large computational resources and the development of efficient methodologies. In this study, results of applying IPML techniques for the identification and classification of diseases in rice plants are considered. In this direction, the literature has been carried out to know the state-of-the-art applications of computer technology in the core area of the present work undertaken.

The researchers [5] have developed automated methods for rice disease identification affecting leaves using color image analysis. The approach is based on histogram intersection and K-means clustering methods to analyze different types of rice diseases.

Earlier, the investigators [6] have developed an expert system to identify rice diseases such as leaf blast and leaf brown spot using morphological features. Otsu's method is applied to segment affected leaf from healthy. The classification rate obtained is 79.5% and 68.1% using Bayes' and SVM classifiers, respectively.

The researchers [7] have developed an automated system for classifying rice diseases such as leaf brown spot, blast, sheath rot, bacterial blight, based on color and shape features and rule-based classifier. Fermi energy-based segmentation method is applied to separate infected plants from healthy. Rough set theory (RST) is used to select important color and shape features. It is shown that an average classification rate of 94.21% is obtained.

In the proposed method [8], a color-based recognition system using is used to classify rice diseases such as rice blast, brown spot and leaf blight. The overall classification rate of 100% is achieved using back-propagation neural network (BPNN) classifier.

The researchers [9] have presented grading and classification method for predicting the rice panicle blast level using a hyper-spectral imaging technique. The features derived from the bag of spectra words (BoSW) model are provided as input to the chi-square kernel support vector machine (chiSVM) classifier. The results obtained are 81.41% and 96.40% with six-class grading and two-class grading, respectively.

In the proposed method discussed by the investigators [10], detection of seed-borne rice diseases such as bakanae disease is considered. A genetic algorithm is used to select the essential traits and best model parameters for the SVM classifier. The developed SVM classifier distinguished infected and healthy seedlings with 87.9% classification accuracy.

The deep learning model presented by the researchers [11], the dataset of 500 naturally occurring images of diseased and healthy rice leaves and stems collected in the

experimental rice field is utilized. An accuracy of 95.48% is achieved under tenfold cross-validation strategy using developed CNN model identifying 10 common rice diseases.

The researchers [3] have demonstrated different feature extraction methods and classifiers for paddy leaves disease detection like leaf streak, brown spot, false smut, leaf blast and leaf blight. A hybrid method of grayscale co-occurrence matrix, scale-invariant feature transform and discrete wavelet transform is employed for feature extraction. It is reported that SVM provides better classification accuracy of 98.63% surpassing Naive Bayesian, BPNN and K-nearest neighborhood (KNN) classifiers.

Sethy et al. [12] have discussed several image segmentation, feature extraction, feature selection and classification techniques for the diagnosis of rice plant diseases.

Earlier, the investigators [13] have introduced a deep neural network with Jaya algorithm for recognition and classification of paddy leaf diseases such as bacterial blight, brown spot, sheath rot and blast diseases. The proposed method provides better classification accuracy of 98.9% for the blast affected, 95.78% for the bacterial blight, 92% for the sheath rot, 94% for the brown spot and 90.57% for the normal leaf image surpassing artificial neural network, deep auto-encoder and deep neural network classifiers.

The image recognition [14], outlined deep learning and SVM-based classifiers for the classification of rice leaf diseases. The average classification rate of 96.8% using SVM and deep learning is reported.

The literature review reports that several IPML approaches have been cited in the automation of agricultural processes relating to disease detection. However, the work carried out is focused on generic diseases affecting rice plants. In most of the works cited, disease identification and classification are done on rice plant leaf images. But, plant disease affects various parts of the plants like stem, leaf, etc. In this study, a disease affecting various parts of rice plant like leaf, stem and panicle are considered for identification and classification. Also, varieties of rice diseases identified in the literature are scarce. In the present study, a comprehensive analysis of rice disease symptoms identification and classification is undertaken to aid the farming community. Also, based on previous studies, it is verified that in the existing works, state-of-the-art deep learning techniques are employed to demonstrate the importance of agriculture image processing. This motivated us in deploying a deep learning approach for the present work carried out. The paper is organized into four sections.



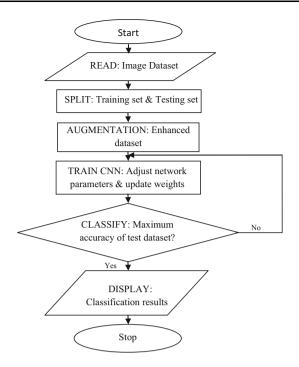


Fig. 1 Schematic flow diagram of the proposed work

# **Proposed Work**

Figure 1 shows the stages involved in the proposed work to automatically identify rice disease symptoms. The work is divided into two stages. In the first stage, the dataset of disease-infected rice images is acquired and labeled in consultation with agricultural experts. The sample images are enhanced using data augmentation techniques. In the second stage, the augmented sample images are provided as input to proposed CNN models for training and classification results are obtained by predicting the trained model on testing images.

### **Image Acquisition**

The images are captured in the paddy field using a NikonD 850 DLSR camera having a resolution of 24 pixels at noontime under natural light conditions. The shutter speed value of 1/60 s at an f/8 aperture and ISO of 1/500 is set for the camera. The object distance of 2.5 m from the disease-infected paddy plant is kept for image acquisition. The camera is tilted at approximately 45° degrees to the object's axis. Whiteboard reflectors are used to control the shadows and highlight contrasts in different lighting conditions.

The experimental dataset of 1200 sample images is acquired from paddy farmlands situated at the University of Agricultural Sciences (UAS), Dharwad, India. The acquired dataset is total with 750 fungal disease-affected images, 250 bacterial disease-affected images and 200 viral

disease-affected images. However, originally acquired field image dataset with 1200 images has been increased to 12,000 labeled images using various image augmentation techniques, to enhance the performance of CNN models and over-fitting problems. Data augmentation using horizontal flip, vertical flip, shear transformation, intensity transformation, random rotation and skewing is done yielding 10 augmented images from every original acquired image. The study considers 7500 sample images (500 samples of each fungal disease symptom), 2500 sample images (500 samples of each bacterial disease symptom) and 2000 sample images (500 samples of each viral disease symptom) for identification and classification purpose. This constitutes 24 different rice disease symptoms of three different plant disease types. The image is resized to  $400 \times 400$  pixels for minimizing the computational time required for further processing and their storage on the medium. In all cases, 24 bits JPEG image format is used. The symptoms of fungal disease, namely, aggregate sheath, blast, crown sheath rot, brown spot, powdery mildew, false smut, eyespot, kernel smut, leaf smut, leaf scald, narrow brown leaf spot, sheath blight, sheath rot, sheath spot, flag leaf sheath are considered. The bacterial disease symptoms, namely, bacterial leaf streak, bacterial blight, footrot, pecky rice (kernel spotting), sheath brown rot are considered. The viral disease symptoms, namely, grassy stunt virus, tungro virus, ragged stunt, yellowing mottle are considered. Some of the disease-infected sample images of rice plants are given in Figs. 2, 3 and 4. Figure 5 shows the classification tree of rice disease symptoms.

#### Classification

A CNN is an artificial neural network (ANN) popularly used for image analysis and classification problems. The CNN can able to detect patterns from the image and make sense of them. In the present work, state-of-the-art pretrained VGG-16 and GoogleNet CNN models are employed as classifiers to classify different disease-affected images of rice plants. Based on experimentation, it is found that VGG-16 and GoogleNet CNN models have better classification accuracy compared to other CNN models in image classification tasks [1]. Figure 6 shows the architecture of the VGG-16 and GoogleNet network layers used in the present work. The VGG-16 and GoogleNet architectures consist of four main neural layers, namely, convolutional layers, pooling layers, fully connected layers, an output layer and several hidden layers. The pretrained VGG-16 and GoogleNet models pass a labeled sample image through the network layers and generate an output of the final class.



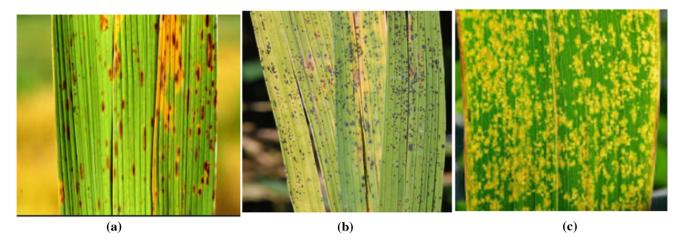


Fig. 2 Fungal disease symptoms: a narrow brown leaf spot, b leaf smut and c eyespot

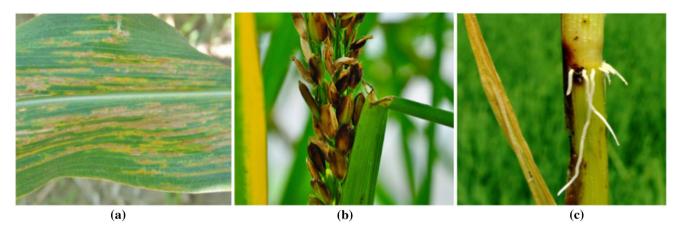
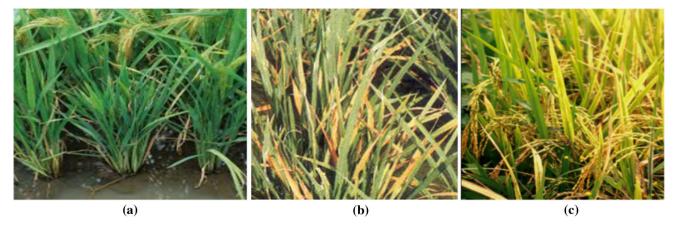


Fig. 3 Bacterial disease symptoms: a bacterial leaf streak, b sheath brown rot and c fruit rot



 $Fig. \ 4 \ \ \mbox{Viral disease symptoms: } a \ \mbox{grassy stunt virus, } b \ \mbox{tungro virus and } c \ \mbox{yellowing mottle}$ 

# VGG-16 Architecture

The VGG-16 (Visual Geometry Group) accepts rice disease-infected color images (R, G, B) of size

 $224 \times 224 \times 3$  pixels [15]. The image is passed through several convolutional layers. The Convolutional filter kernel of image size is  $3 \times 3$  and the convolution is carried out with stride 1. The convolutional layer uses row and



Fig. 5 Rice disease symptoms Paddy/Rice Diseases classification tree Bacterial Viral Fungal 1. Aggregate sheath 1. Grassy stunt virus 1 Bacterial leaf streak 2. Tungro Virus 2. Blast 2. Bacterial blight 3. Brown spot 3. Ragged Stunt 3 Footrot 4 Crown sheath rot 4. Yellowing mottles 4. Pecky rice (Kernel spotting) 5. Powdery mildew 5. Sheath Brown rot 6. Eyespot 7. False smut 8. Kernel smut 9. Leaf smut 10. Leaf scald 11. Narrow brown leaf spot 12. Sheath blight 13. Sheath rot 14. Sheath spot 15. Flag leaf sheath Fungal disease symptoms 0 0 Bacterial disease Viral disease symptoms 0 0 10 0 224 x 224 x 3 VGG16 Input image 0 0 0 0 224 x 224 x 3 GoogleNet 3x3 VGG16-33 **Classification Output** Convolution Max Pooling 3 -Fully Connected layers Output - 41 GoogleNetLayer-143 Output - 144

Fig. 6 Schematic architecture of the VGG-16 and GoogleNet layers

column padding so that the size of the input feature map and the size of the output feature map remains the same. The number of convolutional layers in VGG-16 is 13. It has five max pool layers and the three fully connected networks. First, two fully connected layers have 4096 channels each and fully connected layer has 1000 channels.

### GoogleNet Architecture

The GoogleNet accepts rice disease-infected color images (R, G, B) of size  $224 \times 224 \times 3$  pixels [16]. The GoogleNet architecture is designed with 27 layers deep including convolution layer, maxpool layer, feature concatenation and softmax layer. The basic building block of GoogleNet is the inception module. There are nine identical units repeated in the google lane which are inception units. The inception unit computes the features used in GoogleNet. In the inception module, different features which are computed using convolutional kernel (size:  $1 \times 1, 3 \times 3, 5 \times 5$ ) are stacked together to give a feature map before going to the next layer. The convolution is carried out with stride 1. Then, each of the convolution's feature maps will pass through the combination of convolutions of the current layer.

# Training and Testing CNN Models

4-Fully Connected layers

The proposed VGG-16 and GoogleNet CNN models are trained using the transfer learning approach. The weights are initialized using a pre-trained ImageNet [17] database. There are approximately 1.2 million images and 1000 class groups in the ImageNet dataset, whereas the rice disease enhanced dataset includes 12,000 images and 24 groups. As a result, the dataset is inadequate to train deep neural networks, so ImageNet weights are pre-loaded in all the layers until convergence. The training parameters such as



epoch, mini-batch size and learning rate are adjusted to improve the identification accuracy of VGG-16 and GoogleNet CNN models. A CNN model's learning rate describes how rapidly it adapts to a classification task. The batch size refers to the number of training instances in a particular batch. Iterations are the number of batches required to complete one epoch. The number of times a learning algorithm accesses the entire dataset is measured in epochs. The network is optimized using stochastic gradient descent (SGD) algorithm to minimize the loss function. SGD with momentum constant denoises the gradients and speed up the convergence. Batch normalization is applied to improve overall accuracy and faster learning. ReLU activation function is used for all the hidden layers and softmax function to the output layer. The VGG-16 and GoogleNet CNN models are estimated based on the accuracy of test dataset and cross-entropy loss. The process of transfer learning is shown in Fig. 7.

The classification performance of pre-trained VGG-16 and GoogleNet CNN models is calculated using Expressions (1) and (2). The training parameters values set for implementation of VGG-16 and GoogleNet are listed in Tables 1 and 2.

Classification efficiency (%)

$$= \frac{Sample\ images\ classified\ correctly}{Total\ number\ of\ test\ sample\ images} \times 100 \tag{1}$$

Average classification efficiency (%)

$$= \frac{Sum \, of \, sample \, images \, classified \, correctly}{Total \, number \, of sample \, images} \times 100 \quad (2)$$

Training and Testing CNN Models Using k-fold Cross-Validation

The performance of VGG-16 and GoogleNet CNN models is evaluated by using the k-fold cross-validation method. In this study, k = 3 is chosen, becoming threefold cross-

validation. Based on experimentation, it is observed that for large values (k = 5, 10), the classification results show a decreasing trend in the accuracy. Hence, it is decided to keep the appropriate value for k = 3. The threefold cross-validation process yields a measure of quality for each fold. The dataset has been equally distributed into three subsets as given in Table 3.

The VGG-16 and GoogleNet CNN models are trained and evaluated with each fold (k = 1,2,3) to measure the efficiency of classification as given in Table 4. The model is trained on a training set and evaluated on testing set at each cross-validation cycle. Finally, the accuracy of CNN models is validated by calculating average performance results using Expression (3).

Average 
$$accuracy(\%) = \frac{1}{k} \sum_{i=1}^{k} Accuracy$$
 (3)

for i = 1, 2, 3..., k

Algorithm 1 gives the process of rice disease image samples classification using VGG-16 and GoogleNet CNN models based on transfer learning. Based on the algorithmic steps (3 to 5), the hyper-parameters such as learning rate, number of iterations and the number of images covered in one iteration are tuned to achieve the best classification accuracy. The algorithm outputs weights that are stored in the database for further prediction.

Algorithm.1: Identification and classification of rice disease symptoms.

Input: Rice disease symptoms image dataset(X) and corresponding labels(Y).

CNN parameters (listed in Tables 1 and 2).

Output: CNN weights.

Start.

Step 1: Accept the image dataset.

Step 2: Shuffle and split the image dataset into training set and testing set using a threefold method.

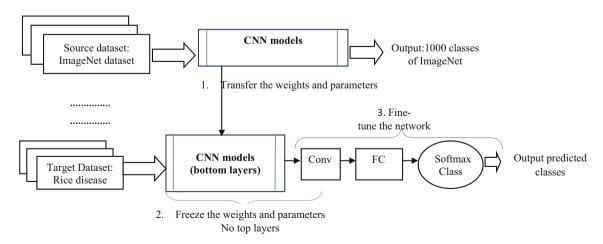


Fig. 7 Transfer learning process



**Table 1** VGG-16 parameters used in experimentation

Parameters	Ideal value
Rate of learning	0.001
Momentum constant	0.9
Number of epochs to train	30
Mini-batch size	64
Number of iterations	125

Table 2 GoogleNet parameters used in experimentation

Parameters	Ideal value
Rate of learning	0.001
Momentum constant	0.9
Number of epochs to train	20
Mini-batch size	100
Number of iterations	80

Table 3 Subset of the image dataset

Set1	Set2	set3
4000 image samples	4000 image samples	4000 image samples

Table 4 Training and testing using threefold validation method

Iteration (fold)	Training	Testing
k = 1	Set = 2,3	Set = 1
k = 2	Set = 1,3	Set = 2
k = 3	Set = 1,2	Set = 3

Step 3: Determine CNN base networks and initialize parameters.

Step 4: Assign network weights  $(w_1, w_2, ..., w_n)$  and Load the pre-trained network.

Step 5: Adjust the network parameters and compute weights.

Step 6: Forward propagation and compute loss (E) using Expression (4).

$$E(W) = -\frac{1}{n} \sum_{x_{i=1}}^{n} \sum_{k=1}^{k} [y_{ik} \log P(x_{i} = k) + (1 - y_{ik}) \log (1 - P(x_{i} = k))]$$

$$(4)$$

where n is the number of training instances in each iteration, w: weight matrices of CNN, i: training samples index, k: classes index,  $P(x_i = k)$ : probability of input  $x_i$  associated with the predicted  $k^{th}$  class.

Step7: Back-propagation and update weights with SGD using Expression (5).

$$W = W_{k-1} - a(\partial E(W)/\partial W) \tag{5}$$

where a is the learning rate, k: classes index.

Step 8: Repeat steps 5 through 7 and update weights for each epoch.

Step 9: Store computed weights in the database.

Step 10: Evaluate the CNN models accuracy using the test dataset.

Stop.

# **Experimental Results**

The algorithms used in the present study are carried out using the deep learning tool of MATLAB 2019b. The configuration of the system includes Nvidia GeForce RTX 2070 GPU with 4 GB RAM, Intel Core i3-7100U processor with 32 GB RAM. The VGG-16 and GoogleNet CNN models with pre-trained weights are trained and tested on three classes of rice disease images.

The classification results achieved using the VGG-16 CNN model, trained and tested on fold k = 1 are presented in Table 5. As observed in Table 5, high classification result is 94.74% with images of crown sheath rot fungal disease symptom and low classification result is 81.42% with images of sheath spot fungal disease symptom. The high classification result is 93.39% with images of footrot bacterial disease symptom and low classification result is 88.43% with black leaf streak bacterial disease symptom images. The high classification result is 95.76% with images of ragged stunt viral disease symptom and low classification result is 89.80% with images of yellowing mottle viral disease symptom.

The classification results achieved using VGG-16 CNN model, trained and tested on fold k=2 are presented in Table 5. As observed in Table 5, high classification result is 96.71% with images of powdery mildew fungal disease symptom and low classification result is 89.20% with images of eyespot fungal disease symptom. The high classification result is 97.07% with images of footrot bacterial disease symptom and low classification result is 91.18% with black leaf streak bacterial disease symptom images. The high classification result is 97.17% with images of yellowing mottle viral disease symptom and low classification result is 91.11% with images of grassy stunt virus viral disease symptom.

The classification results achieved using VGG-16 CNN model, trained and tested on fold k=3 are presented in Table 5. As observed in Table 5, high classification result is 94.73% with images of blast fungal disease symptom and



low classification result is 89.47% with images of leaf smut fungal disease symptom. The high classification result is 96.14% with images of sheath brown rot bacterial disease symptom and low classification result is 91.78% with black leaf streak bacterial disease symptom images. The high classification result is 91.39% with images of grassy stunt virus viral disease symptom and low classification result is 89.57% with images of tungro virus viral disease symptom.

From Table 5, it is seen that the average classification result is 91.36%, 93.35% and 92.01% with images of fungal disease symptoms, bacterial disease symptoms and viral disease symptoms, respectively, using VGG-16 CNN model, trained and tested on fold k = 1,2,3.

The classification results achieved using GoogleNet CNN model, trained and tested on fold k=1 are presented in Table 6. As observed in Table 6, high classification result is 92.63% with images of sheath spot fungal disease symptom and low classification result is 81.12% with images of narrow brown leaf spot fungal disease symptom.

The high classification result is 93.08% with images of pecky rice bacterial disease symptom and low classification result is 88.20% with images of blight bacterial disease symptom. The high classification result is 91.77% with images of yellow mottle viral disease symptom and low classification result is 86.69% with images of tungro virus viral disease symptom.

The classification results achieved using GoogleNet model, trained and tested on fold k=2 are presented in Table 6. As observed in Table 6, high classification result is 96.42% with images of false smut fungal disease symptom and low classification result is 88.13% with images of powdery mildew fungal disease symptom. The high classification result is 92.93% with images of sheath brown rot bacterial symptom and low classification result is 88.58% with images of blight bacterial disease symptom. The high classification result is 95.89% with images of ragged smut viral disease symptom and low classification result is

Table 5 Classification accuracy of rice diseases using threefold validation method with VGG-16

Sl. No	Rice diseases	Rice disease symptoms	k = 1 Classification accuracy (%)	k = 2 Classification accuracy (%)	k = 3 Classification accuracy (%)	Average classification accuracy (%)
1	Fungal	Aggregate sheath	90.87	94.21	93.27	91.36
		Blast	86.74	94.11	94.73	
		Brown Spot	83.77	95.09	91.82	
		Crown Sheath rot	94.74	92.34	93.88	
		Powdery Mildew	86.10	96.71	90.70	
		Eyespot	91.02	89.20	92.24	
		False Smut	86.00	94.20	90.00	
		Kernel Smut	92.62	89.87	92.35	
		Leaf smut	86.23	91.63	89.47	
		Leaf scald	92.34	95.10	91.89	
		Narrow brown leaf spot	93.12	96.59	92.13	
		Sheath blight	91.41	90.42	91.77	
		Sheath rot	91.75	95.05	91.56	
		Sheath spot	81.42	91.92	94.10	
		Flag leaf sheath	83.49	93.72	89.59	
2	Bacterial	Bacterial leaf streak	88.43	91.18	91.78	93.35
		Bacterial blight	89.24	96.12	92.26	
		Footrot	93.39	97.07	95.10	
		Pecky rice	92.42	94.10	94.29	
		Sheath brown rot	92.69	96.14	96.14	
3	Viral	Grassy stunt virus	90.10	91.11	91.39	92.01
		Tungro virus	92.87	92.17	89.57	
		Ragged stunt	95.76	93.41	91.01	
		Yellowing mottle	89.80	97.13	89.88	



89.53% with images of yellowing mottle viral disease symptom.

The classification results achieved using GoogleNet model, trained and tested on fold k=3 are given in Table 6. As observed in Table 6, high classification result is 94.12% with images of powdery mildew fungal disease symptom and low classification result is 87.28% with images of sheath blight fungal disease symptom. The classification result is 95.58% with images of blight bacterial disease symptom and low classification result is 89.83% with black leaf streak bacterial disease symptom images. The high classification result is 94.89% with images of ragged stunt viral disease symptom and low classification result is 90.94% with images of tungro virus viral disease symptom.

From Table 6, it is seen that the average classification result is 91.15%, 91.17% and 91.52% with images of fungal disease symptoms, bacterial disease symptoms and

viral disease symptoms, respectively, using GoogleNet CNN model, trained and tested on fold k = 1,2,3.

Figure 8 shows the confusion matrix obtained for the actual and predicted class generated using the VGG-16 CNN pre-trained model to test the performance of the classifier.

Figure 9 shows the confusion matrix for the actual and predicted class generated using the GoogleNet pre-trained model to test the performance of the classifier.

The performance measures, namely, specificity, sensitivity, precision, negative predictive value, false positive rate, false negative rate, false discovery rate, Matthews correlation coefficient, accuracy, F1 score of each class of rice disease symptom are calculated from the confusion matrix that are listed in Tables 7 and 8.

Table 6 Classification accuracy of rice diseases using threefold validation method with GoogleNet

Sl. No	Rice diseases	Rice disease symptoms	k = 1 Classification accuracy (%)	k = 2 Classification accuracy (%)	k = 3 Classification accuracy (%)	Average classification accuracy (%)
1	Fungal	Aggregate sheath	85.98	93.24	91.34	89.95
		Blast	91.68	89.16	91.93	
		Brown spot	89.26	95.32	88.16	
		Crown sheath rot	83.35	91.55	93.50	
		Powdery mildew	81.28	88.13	94.12	
		Eyespot	88.31	95.72	90.38	
		False smut	86.29	96.42	92.90	
		Kernel smut	83.50	93.75	91.64	
		Leaf smut	85.72	89.89	91.72	
		Leaf scald	83.54	90.44	93.48	
		Narrow brown leaf spot	81.12	91.44	89.17	
		Sheath blight	82.65	93.32	87.28	
		Sheath rot	85.07	92.14	90.59	
		Sheath spot	92.63	95.97	92.03	
		Flag leaf sheath	89.41	94.19	89.08	
	Bacterial	Bacterial leaf streak	92.67	90.83	89.83	91.17
		Bacterial blight	88.20	88.58	95.58	
		Footrot	90.04	90.48	92.48	
		Pecky rice	93.08	89.22	91.22	
		Sheath brown rot	89.45	92.93	92.93	
	Viral	Grassy stunt virus	91.23	90.07	93.07	91.52
		Tungro virus	86.69	92.94	90.94	
		Ragged stunt	89.65	95.89	94.89	
		Yellowing mottle	91.77	89.53	91.53	



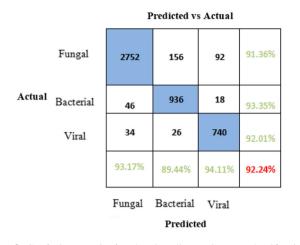


Fig. 8 Confusion matrix for the rice disease images classification using VGG-16

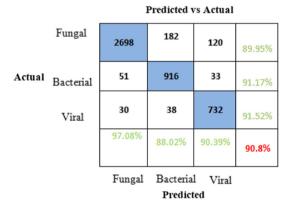


Fig. 9 Confusion matrix for the rice disease images classification using GoogleNet

# **Comparative Study**

The comparative results of the proposed method related to state-of-the-art works published recently (2019–2020) are presented in Table 9. The papers on the identification of diseases affecting rice plants using various image processing and machine learning approaches are reported in the literature. However, in the present study classification of rice disease symptoms is carried out using state-of-theart deep learning models with new dataset and combinations. Most of the published work is focused on fewer of disease categories found on rice plants. In the present study, the dataset includes different types of rice diseases with more varieties of symptoms compared to the previous works undertaken by other researchers. The automatic detection of rice diseases involving parts of the plant such as leaf, stem and chronicle is considered in the proposed work. The experiments conducted in the proposed work have yielded encouraging classification results with the maximum average classification accuracy of 92.24% using VGG-16 CNN model and 91.28% using GoogleNet CNN model. From Table 9, it is observed from the classification results that the proposed VGG-16 and GoogleNet CNN models have given almost similar performances with the results reported in recently published papers. The overall classification performance is acceptable, as the proposed method has higher potential in classifying different types of rice diseases with more varieties of symptoms compared to the previous works undertaken by other researchers.

Table 7 Performance measures obtained using rice diseases classification results with VGG-16

	Sensitivity	Specificity	Precision	Negative predictive Value	False positive Rate	False discovery Rate	False negative Rate	Accuracy	F1 score	Matthews correlation coefficient
Fungal	0.9173	0.9556	0.9718	0.874	0.0444	0.0282	0.0827	0.9317	0.9438	0.8592
Bacterial	0.936	0.9521	0.8372	0.9826	0.0479	0.1628	0.064	0.9488	0.8839	0.8533
Viral	0.925	0.9725	0.8706	0.9848	0.0275	0.1294	0.075	0.9646	0.897	0.8762

Table 8 Performance measures obtained using rice diseases classification results with GoogleNet

	Sensitivity	Specificity	Precision	Negative predictive value	False positive Rate	False discovery rate	False negative rate	Accuracy	F1 score	Matthews correlation coefficient
Fungal	0.8993	0.8254	0.9709	0.5591	0.1746	0.0291	0.1007	0.8894	0.9337	0.6198
Bacterial	0.916	0.9421	0.8063	0.9771	0.0579	0.1937	0.084	0.9367	0.8577	0.8199
Viral	0.915	0.9618	0.8271	0.9826	0.0383	0.1729	0.085	0.954	0.8688	0.8426



Table 9 Comparative results with related work

Author	Observations	Results
[4]	Dataset with five rice diseases such as leaf spot, rice stripe virus, panicle neck blast, Ustilaginoidea virens and grain blast are recognized. Data enhancement is done using reflection deformation and histogram equalization. Multi-scale stacked autoencoder (MSSAE) is developed to recognize various rice diseases	Average accuracy achieved across all disease types is 95.78%
[13]	Dataset with 650 images of rice blast, sheath rot, brown spot, bacterial blight and normal affecting rice plant leaves are recognized. The affected area from normal is segmented using the K-means clustering method. Color and texture are used as features. An optimized deep neural network with Jaya optimization classifier is developed	Average accuracy achieved across all disease types is 94.25%
[18]	Dataset with 500 images of rice stack burn, rice leaf scald, rice leaf smut, rice white tip, rice bacterial leaf streak, etc. is recognized. Pre-trained CNN models are used as classifiers	Average accuracy achieved across all disease types is 98.63%
[1]	Dataset with 6000 images with 11 different stress classes on five different paddy crop varieties is recognized. Pre-trained VGG-16 is used as a classifier	Average accuracy achieved across all disease types is 92.89%
[14]	Dataset with 8911 images of normal, rice blast, rice bacterial spot, rice streak leaf spot and rice sheath blight affecting rice plant leaves are recognized. Color and shape are used as features. SVM and CNN classifiers are developed	Average accuracy achieved across all disease types is 96.8%
[19]	Rice dataset with 2906 positive samples and 2902 negative samples are recognized. Local binary patterns and Haar-wavelet are used as features. CNN with SVM classifier is developed	Average accuracy achieved across all disease samples using CNN combined with SVM is 95.82%
[20]	Different stages of rice blast disease analysis are determined.  Disease-infected color images are converted into Lab color space.  The affected area from normal is segmented using the K-means clustering method. KNN classifier is developed	Average accuracy of the developed algorithm is 94%
[21]	Percentage severity of rice diseases, such as rice blast, brown spot and bacterial blight affecting leaves is estimated. K-means clustering technique is used to separate affected area from normal. Size, color, proximity and centroids are used as features	The percentage of disease-affected area is performed using point feature matching
[22]	The severity of rice blast disease affecting leaves is determined. Four models, namely, Yoshino and Water Accounting Rice Model (WARM), M5Rules and recurrent neural networks (RNN) for predicting rice blast disease are compared	Maximum average accuracy of 88% and 77% is achieved using M5Rules and WARM, respectively
Proposed work	Three major plant diseases affecting rice plants are recognized. The visual-based disease symptoms present on different parts of the rice plant like leaf, stem and panicle are classified. The new dataset is trained and tested using the pre-trained VGG-16 and GoogleNet	Overall average classification accuracies of 92.24% and 91.28% are obtained using VGG-16 and GoogleNet models, respectively

Table 10 Computational complexity of CNN models

Model	GPU memory size (MB)	Elapsed time (minutes)	Epoch	Iteration
VGG-16	43.21	126.47	30	3750
GoogleNet	216.64	273.86	20	1600



### **Computational Complexity**

The training time for the CNN models took a total of 20.8 h to complete. Table 10 presents the trained models' computational complexity in terms of GPU memory size, elapsed training time, iterations and number of epochs. Iteration values and elapsed time are averaged over threefold cross-validation cycles. Memory size represents the size after fine-tuning pre-trained models.

### Conclusion

In the present study, deep learning approach is proposed to automate the identification and classification of diseases affecting different parts of the rice plant. The VGG-16 and GoogleNet CNN models pre-trained on ImageNet are tested for 24 rice disease symptoms images, containing 500 images of each symptom, giving a labeled dataset of 12,000 images, which is more compared to earlier works. The efficiency of the considered models is improved using the threefold cross-validation method. Overall average classification accuracies obtained using VGG-16 and GoogleNet CNN models are 92.24% and 91.28%, respectively. Comparing the results of both the CNN models, the performance of the pre-trained VGG-16 CNN model shows slight improvement than the pre-trained GoogleNet CNN model in the classification of rice diseases. The results drawn are satisfactory and would be of some interest to those working in the area of applying computer technology to farming and agriculture. The proposed method experimental results are at an acceptable level as the study considers more number of dataset compared to the existing works. Since there are no standard databases available for experimentation, the dataset will be useful as the benchmark database for other researchers working on rice disease identification. There is a scope for improving the results with the related state-of-the-art models like DenseNet, Inception-v4, ResNet, AlexNet, etc. as a future scope. Also, the training time of the CNN models can be significantly reduced by optimizing the Matlab code. The dataset can be further enhanced using a deep convolutional generative adversarial network (DCGAN) and efficacy of the developed CNN models can be evaluated. The proposed approach can be applied to a wide range of agriculture/horticulture crops like cereals, commercial crops, fruits, vegetables, etc. Meanwhile, the work carried out can be deployed in hand-held devices to automatically identify plant diseases in real time.

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https://drive.google.com/file/d/1Kk4VKxwhGfBCxRf-crU4BsMKSjgDGhvO/view?usp=sharing.

#### Declarations

Conflict of interest The authors declare that they have no conflict of interest.

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