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Performance analysis of various deep learning models for detecting rice diseases

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ABSTRACT

A major portion of the world's population relies on rice as a staple diet, hence rice is essential to maintaining food security worldwide. Unfortunately, rice crops are susceptible to a number of illnesses that, if detected and treated promptly, can result in significant output losses. Expert visual inspection is a time-consuming and arbitrary part of the conventional procedures for diagnosing diseases in rice. An effective method for automated illness diagnosis in agriculture has evolved in recent years: deep learning, a branch of artificial intelligence. The objective of this research is to compare AlexNet, DCNN, MobileNet, GoogleNet, VGG16, ResNet50 and Xception, these are various deep learning models in order to choose the one that would produce the highest levels of accuracy, precision recall, specificity, and F1-score for detecting rice diseases. In this study we train the model for nine different types of rice diseases named as Rice Blast (Pyricularia oryzae), Rice Sheath Blight (Rhizoctonia Solani), Bacterial Leaf Blight (Xanthomonas oryzae pv. oryzae), Tungro Disease, Rice Grassy Stunt Virus (RGSV), Rice Yellow Mottle Virus (RYMV), Bakanae Disease (Fusarium moniliforme), Brown Spot (Cochliobolus miyabeanus) and Rice Tungro Bacilliform Virus (RTBV) with 30,000 images. For this we used the secondary dataset for analyzing the performance of models. We trained the model for both normalized and non-normalized dataset. After comparing the various models we get the better result from ResNet50 model with accuracy of 97.50%.

Keywords: deep learning; rice disease; CNN; feature extraction; AlexNet; DCNN; MobileNet; GoogleNet; VGG16; ResNet50; Xception

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1. Introduction

A significant majority of the world's population is fed by rice, which is frequently referred to as the "staple of staples" and is an essential component of global agriculture. Nonetheless, a wide range of illnesses continue to pose a threat to the health and productivity of rice crops. In regions that primarily rely on rice as a key food source, notably, these diseases can result in considerable yield and quality decreases, which could jeopardise food security. For efficient disease management of rice illnesses, accurate and prompt diagnosis is crucial. This enables farmers to execute focused control measures and reduce potential losses. Conventional disease diagnosis techniques frequently rely on skilled visual inspection, which can be time-consuming and prone to inaccuracy. There is an increasing chance to enhance the method of identifying rice diseases as a result of the quick development of technology, notably in the agricultural sector. To improve disease detection and diagnosis, a number of techniques are being used, including remote sensing, image analysis, and artificial intelligence.

In this research we train the model for nine different types of rice diseases named as Rice Blast (Pyricularia oryzae), Rice Sheath Blight (Rhizoctonia Solani), Bacterial Leaf Blight (Xanthomonas oryzae pv. oryzae), Tungro Disease, Rice Grassy Stunt Virus (RGSV), Rice Yellow Mottle Virus (RYMV), Bakanae Disease (Fusarium moniliforme), Brown Spot (Cochliobolus miyabeanus) and Rice Tungro Bacilliform Virus (RTBV) with 30,000 images. We used secondary data for processing and trained the different models for these different diseases detection. Three sets of the images—one for training, one for validation, and one for testing—each containing 75%, 10%, and 15% of the total images.

The diseases, which range from fungal blast to bacterial blight, can completely destroy rice harvests, resulting in decreased yields and grain quality. When a plant's defenses are weak, pathogens like Xanthomonas oryzae and Magnaporthe oryzae take advantage, causing symptoms like water-soaked lesions, leaf discoloration, and panicle destruction. Temperature and humidity levels in the environment can hasten the onset of sickness. Researchers and farmers use a range of tactics, such as the cultivation of disease-resistant rice cultivars, crop rotation, and the application of integrated pest management approaches, to counteract these challenges. In order to contain disease outbreaks, monitoring, early discovery, and quick action are essential. Understanding and controlling these diseases is crucial to guaranteeing food security and sustaining agricultural production given the rising worldwide demand for rice. Nematodes, bacteria, viruses, fungi, or other pathogens may cause these illnesses. Among the widespread diseases of rice are listed in **Table 1**:

Table 1. Classification of rice diseases.

Diseases of rice	Description	Image
Rice Blast (Pyricularia oryzae)	Rice blast is one of the worst illnesses to ever affect rice harvests. The fungus Pyricularia oryzae is the cause. The disease manifests as lesions on leaves, stems, panicles, and grains. It can drastically reduce yields if not properly controlled[1,2].	
Rice Sheath Blight (Rhizoctonia Solani)	Sheath blight is caused by the fungus Rhizoctonia Solani. It affects the leaf sheaths and could hasten the degeneration of stems that are close to the soil's surface. The affected plants have white, water-soaked sores on their leaf sheaths[3,4].	
Bacterial Leaf Blight (Xanthomonas oryzae pv. oryzae)[5]	The initial signs of this bacterial infection are water-soaked blisters on the leaves, which later turn yellow and then brown. It may reduce productivity and cause the entire plant to dry out[6,7].	

Table 1. (*Continued*).

Diseases of rice	Description	Image
Tungro Disease	Leafhoppers disperse a virus known as tungro. It affects rice plants by causing slowed growth, yellowing of the leaves, and poor grain quality.	
Rice Grassy Stunt Virus (RGSV)	This viral disease causes plant yellowing and stunting, which ultimately lowers rice yield. It is carried by planthoppers[8].	
Rice Yellow Mottle Virus (RYMV)	This virus causes leaf mottling and yellowing, which hinders photosynthesis and causes grain filling to be poor[9].	
Bakanae Disease (Fusarium moniliforme)	Bakanae, a fungus, kills seedlings, resulting in plants that are elongated, slender, and light green. It might significantly reduce yield.	
Brown Spot (Cochliobolus miyabeanus)	Brown spot is a fungus that affects photosynthesis and reduces yields by causing brown, oval lesions on the leaves[10]	
Rice Tungro Bacilliform Virus (RTBV)	The viral illness RTBV can produce plant yellowing and stunting, which can lower yield	

1.1. Various stages for identifying rice diseases

The development of an automated system that can accurately identify and classify diseases affecting rice plants based on input pictures is required for the diagnosis of rice diseases using deep learning. Many crucial steps in this procedure are often carried out:

a) **Data collection:** Similar to any deep learning study, gathering a huge and diversified set of images of rice illness is crucial. The collection should contain images of both sound and various types of diseased rice plants. It is essential to cover a range of illness types, stages, and severity levels to ensure that the model can generalize effectively.

b) **Data preprocessing:** The captured images need to be preprocessed in order to guarantee consistency and raise the caliber of the data. Preprocessing includes resizing images to a predetermined size, standardizing pixel values, and extending the dataset to boost its size and diversity.

c) **Model architecture selection:** The success of the diagnosis system hinges on choosing the best deep learning architecture. Convolutional neural networks are a popular option for image classification tasks because they have the ability to automatically recognize relevant attributes from images.

d) **Model training:** The dataset has training and validation sets. The deep learning model is taught by adding the disease-related photographs and labels to the training set. Throughout training, the model develops the ability to recognize patterns and features that indicate specific diseases. The validation set prevents over fitting and assists in performance monitoring.

e) **Model evaluation:** A different test dataset is utilized to measure the model's effectiveness and precision following training. The test dataset should consist of unknown data that the model has not encountered during training or validation. An excellent test set accuracy illustrates the model's capacity to recognize rice sickness with accuracy.

f) **Fine-tuning and optimization:** If the model's performance is subpar, its precision can be increased using optimization and fine-tuning techniques. To do this, it may be necessary to adjust hyper parameters, use alternative model architectures, or fine-tune the pre-trained models using relevant data[11].

g) **Deployment:** After the model has an appropriate level of accuracy, it can be utilized as an application or incorporated into agricultural systems. Farmers or agricultural experts can use the technology to automatically detect the presence of diseases by providing photographs of rice plants[12]. See **Figure 1**.

Figure 1. Several phases for detecting pest insects or diseases that affect rice[13].

1.2. Deep learning models

Finding the best deep learning technique for recognizing diseases in rice leaves is the study's main goal. The deep learning models we are looking at for categorization of images include AlexNet, DCNN, MobileNet, GoogleNet, VGG16, ResNet50, and Xception. These models are based on convolution neural networks[14,15].

AlexNet: The AlexNet version reduces the size of the network, reduces overfitting, and increases generalisation by using max-pooling rather than average, overlap pooling filters. The eight-layer AlexNet architecture is composed of three FC layers and five convolutional networks. The remaining three sets with the same activation function employ Conv3-256, Conv3-512, and Conv3-512, respectively[16,17].

DCNN: A method for learning extensive visual highlights is deep-CNN. For deep learning of visual peaks, it uses symmetric skip connections (SSC) between rotating convolutional-deconvolutional layers in a layer-oriented convolutional-deconvolutional technique. Continuous linear and nonlinear capacity make up a deep CNN. Contrary to nonlinear functions, which explain unexpected events, convolution tasks directly express linear functions[18,19]. Convolution layer begins sophisticated component paddy disease depictions after detecting the surrounding properties of paddy crop photographs. The hidden, input, and output layers are each separated into at least three layers in backpropagation neural networks, which employ a multiple-layer feedforward neural network technique[20,21].

MobileNet: In several fields, including object identification, semantic segmentation, and picture classification, MobileNet models have found use, particularly in situations where edge computing or real-time processing are critical. They enable a wide range of applications that need on-device machine learning capabilities because of their effective design, which makes them suited for deployment on gadgets like smartphones, embedded systems, and IoT devices.

GoogleNet: The GoogleNet design gives the network the opportunity to choose from a range of convolutional filter sizes in each block to maximise computational efficiency. The network operates at the same layer thanks to Inception modules. The design contains a total of 27 levels, including 9 stacked inception modules and 22 layered parameters[22]. GoogleNet is constructed on top of the previous layers, with the inception module acting as its base layer. The top layer then applies parallel filtering to the input layer from the layers below it.

VGG16: The CNN architecture known as the Visual Geometry Group (VGG) is intricate and multi-layered. There are 16 and 19 convolutional layers in the VGG-16 and VGG-19, respectively[23]. To boost network depth, these topologies employ incredibly tiny convolutional filters. VGG16 and VGG19 both accept images with three colour channels and a 224 × 224 resolution as input. Convolutional layers with a 3 × 3 receptive field size and maximum pooling layers receive the input.

ResNet-50: This design incorporates the residual block concept to overcome the Resnet50 gradient vanishing/exploding issue. This network uses a technique called skipping connections. Connections are built between them to connect activations in various layers. The block is now finished. To build a ResNet, these remaining blocks are layered. ResNet is a type of artificial neural network that includes “identity connections”, allowing the model to delete one or more layers. The network can be trained using this strategy on a huge number of layers without experiencing performance drawbacks. This has led to ResNet becoming one of the most popular designs for many computer vision issues. An extensive investigation shows that ResNet has the lowest error rate (3.57%) for the top five percentiles of all CNN designs currently in use[24,25].

Xception: A 71-layer deep CNN is called Xception. It is possible to import a pre-trained network that has previously been created using ImageNet and a number of input photos. All of the input photographs are divided into 1000 different categories by the network, including pencils, pens, books, and a lot more. The network has access to a vast library of different feature representations with a variety of input datasets. This pre-trained network requires 299 × 299 pixel input data. A deep convolutional neural network with only convolutional layers is called Xception. The feature extraction building of the Xception architecture consists of 36 convolutional layers[26].

2. Related work

Latif et al.[1] observed that almost half of the world’s population depends on rice, yet diseases that harm rice plants can reduce productivity by 20%–40% annually. Rice prices rise because manual identification necessitates in-depth visual observation and farmer experience. Based on visually distinguishable characteristics of leaves, an automated system using computer vision technology can detect and diagnose five rice illnesses. In order to accurately recognize and diagnose six classes of rice leaves, including healthy ones, this research suggests a modified VGG19-based transfer learning algorithm. The device can identify rice problems in real time when paired with IoT and drone technology.

Fei et al.[9] The study shows how employing ensemble learning techniques can increase the precision of wheat grain yield predictions. Comparing numerous base leaners to simple regression techniques increases the estimate of attributes. The study emphasises the value of phenotyping systems based on UAVs for calculating spectral data from various growth phases. When using a four base learner combination, the results demonstrate strong grain yield prediction results at mid-grain filling stages. For accurate crop breeding, more testing is required.

Using a total of 25,000 photos of stressed and healthy leaves, Jena et al.[12] developed a deep machine vision-based model to detect, categorise, and quantify 8 soybean plant stressors. By using the suggested deep CNN methodology, this method has a detection rate of 94.13%. Vasantha et al.[13] used five different CNN techniques to recognize plant diseases from leaf photos. Agrawal et al.[14] sed the supervised DL model to create an automated wheat disease identification model. A collection of wheat photos with 50k tagged leaf images is used to test it. Four different CNN models are used in the suggested model to identify the seven classes of wheat diseases. According to the findings, the VGG-16 model has a higher detection rate of 97.95%.

Mohapatra et al.[15] used DL techniques to create a model for disease recognition in rice plants. 500 photos of rice plant leaves and stems are used to test it. LeNet-5 and AlexNet CNN models are employed. This study showed that stochastic pooling improves the CNN approach's capacity to generalise while preventing overfitting.

A DenseNet169-MLP model for categorising illnesses of rice plants is presented in the Narmadha et al.[19] Preprocessing, FCM segmentation, and MLP extraction are performed on it. Maximum sensitivity is 96.40%, specificity is 98.27%, precision is 96.82%, accuracy is 97.68%, and F-score is 96.43% according to experimental validation on a benchmark dataset. Hyperparameter tuning methods can be used to make future advancements.

3. Evaluation of the models

The seven network models' performances were contrasted in order to select the top models. Four categories were created from the disease prediction findings for each network model: True Positive (TP), False Positive (FP), True Negative (TN), and False Negative (FN). False positive findings meant that other sorts of diseases were anticipated to be this disease; true positive results meant that the type of disease was correctly predicted. Accuracy, precision, recall, specificity, and F1-score performance indicators were created using these findings. The formula and justifications for each of the many measures utilized in this study are provided in **Table 2**. The fact that this expression stands for True Positive, True Negative, False Positive, and False Negative should be emphasized.

Table 2. Parameters used in models.

Metric	Equation	Measure
Accuracy	$\frac{T_P + T_N}{T_P + T_N + F_P}$	A measure of the ratio of all correct classifications to the total number of the classifications
Precision	$\frac{T_P}{T_P + F_P}$	The ratio of the true positive cases over the total classified positive cases
Recall/sensitivity	$\frac{T_P}{T_P + F_N}$	(Sensitivity) The measure of the proportion of the actual positive cases that were classified correctly
Specificity	$\frac{T_N}{T_N + F_P}$	The measure of the proportion of the actual negative cases that were classified correctly
F1-score	$\frac{2T_P}{2T_P + F_P + F_N}$	The harmonic mean of the precision and recall

3.1. Mean average precision

Mean average precision controls how well the framework can identify items (mAP). For all types of things, it serves as the fundamental unit of measurement. The mean average precision is calculated by dividing the total number of successfully identified photos by the total number of wrongly detected images for each class. The mean average precision is discernible for a number of parameter types. Some of these settings are the minimum batch size, the image scale that matches to the image's short edge, and the maximum pixel size of the scaled input image. For each class of object or class of objects found in the image, the mean average precision is determined. Using the formula below, average precision determines the average precision for recall value for the range of 0 to 1. See Equation 1.

$$P = \frac{No\ of\ true\ detection}{No\ of\ true\ detections + No\ of\ false\ detections} \tag{1}$$

3.2. Data distribution and segmentation

The dataset used for detection of rice diseases containing 30,000 images of nine different diseases such as Rice Blast (Pyricularia oryzae), Rice Sheath Blight (Rhizoctonia Solani), Bacterial Leaf Blight (Xanthomonas oryzae pv. oryzae), Tungro Disease, Rice Grassy Stunt Virus (RGSV), Rice Yellow Mottle Virus (RYMV), Bakanae Disease (Fusarium moniliforme), Brown Spot (Cochliobolus miyabeanus) and Rice Tungro Bacilliform Virus (RTBV) were collected from different resources. 24,068 images of different diseases were collected[27]. And rest of the data collection includes 5932 number images that show four different types of rice leaf diseases: brown spot, bacterial blight, blast, and tungro[28]. We used secondary data for processing and trained the different models for these different diseases detection. Three sets of the images—one for training, one for validation, and one for testing—each containing 75%, 10%, and 15% of the total images.

The input image of a distinct diseased rice leaf is chosen from the dataset folder in the first phase. In order to create a contrast image in natural light conditions and then convert it back to a grayscale image, the contrast of the image must be increased. The RGB to HSV image format colour transformation is then applied to analyse the segmentation of the image. HSV colour models were used to extract those colours (hue, saturation and value). The hue component of the colour space transformation is employed for additional analysis. Next, using image segmentation, the illness spot region is retrieved. Another technique for segmenting images is K-means clustering. Using the k-means clustering technique, the object collection was divided into k groups. The method begins by computing the mean values across all clusters and then determines how far apart each cluster is from the associated mean. At last, allocate the point to the closest cluster.

4. Results and discussion

Initially, experiments were performed with non-normalized data on different CNN models such as AlexNet, DCNN, MobileNet, GoogleNet, VGG16, ResNet50 and Xception using different parameters as shown in **Table 3**. It has been seen that ResNet50 provide the accuracy of 97% for non-normalized dataset. In this we also do the data augmentation to increase the size of dataset and to avoid over fitting problem. For normalized augmented data set ResNet50 achieved 97.50% accuracy as compared to other models.

Table 3. Analysis of different models for non-normalized and normalized data.

Dataset	CNN Model	Accuracy	Precision	Recall/sensitivity	Specificity	F1-score
Non-Normalized	Alex Net	93.0	93.13	93.0	93.24	93.0
	DCNN	89.10	89.0	89.20	88.75	89.15
	Mobile Net	91.80	92.20	92.10	92.24	92.0
	Google Net	94.07	94.10	94.27	92.20	93.19

Table 3. (*Continued*).

Dataset	CNN Model	Accuracy	Precision	Recall/sensitivity	Specificity	F1-score
	VGG16	92.25	93.0	93.0	92.70	93.0
	ResNet50	97.0	97.15	97.0	97.15	97.25
	Xception	96.15	96.10	96.12	96.18	96.27
Normalized Augmented	Alex Net	93.18	93.73	93.07	93.84	93.22
	DCNN	89.80	89.20	89.80	89.07	89.71
	Mobile Net	92.40	92.60	92.40	92.84	92.29
	Google Net	94.87	94.23	94.87	92.42	93.79
	VGG16	93.15	93.39	93.15	93.07	93.20
	ResNet50	97.50	97.52	97.50	97.50	97.50
	Xception	96.52	96.61	96.52	96.58	96.57

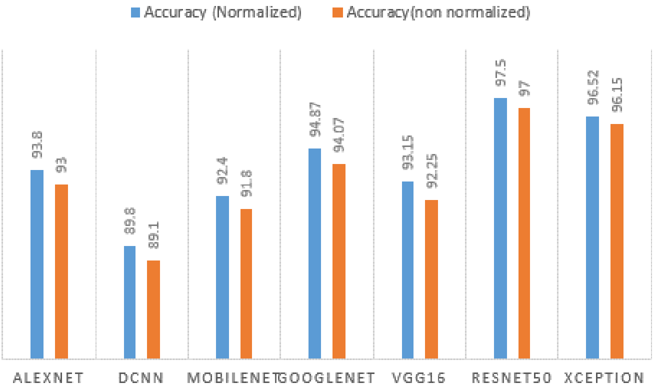

Figure 2. Study of the accuracy for different DL Methods for both normalized and non-normalized data.

The above figure describes the comparison for various models such as AlexNet, DCNN, MobileNet, GoogleNet, VGG16, ResNet50 and Xception, on the basis of accuracy for detecting rice diseases in case of both normalized and non-normalized dataset. From **Figure 2,** it is clear that normalized data provide more accuracy as compared to non-normalized data. ResNet50 model achieved around 97.5% accuracy as compared to other models.

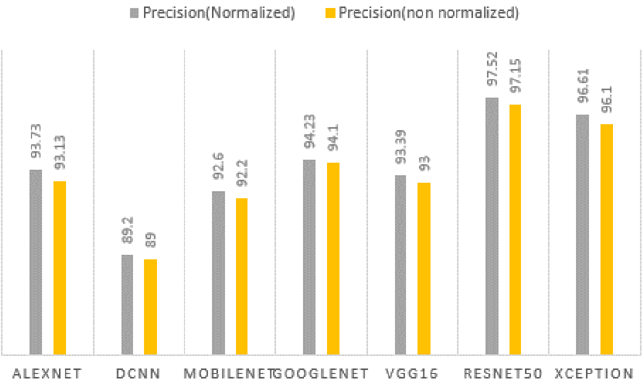

Figure 3. Study of the precision for different DL methods using normalized and non-normalized data.

Figure 3 describe the comparison for various models such as AlexNet, DCNN, MobileNet, GoogleNet, VGG16, ResNet50 and Xception, on the basis of precision for detecting rice diseases for both normalized and non-normalized dataset. From figure it is cleared that normalized data provide more precision in ResNet50 model as compared to non-normalized data with 97.52%.

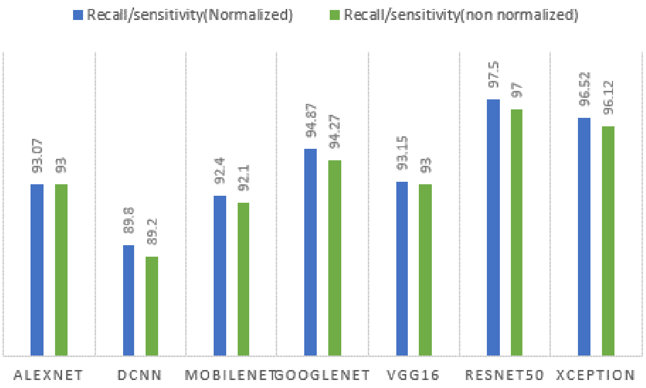

Figure 4. Study of the Recall for different DL Methods using both normalised and non-normalized data.

The above figure describes the comparison for various models on the basis of recall, for detecting rice diseases for both normalized and non-normalized dataset. From **Figure 4,** it is clear that normalized data provide more recall as compared to non-normalized data with 97.5%.

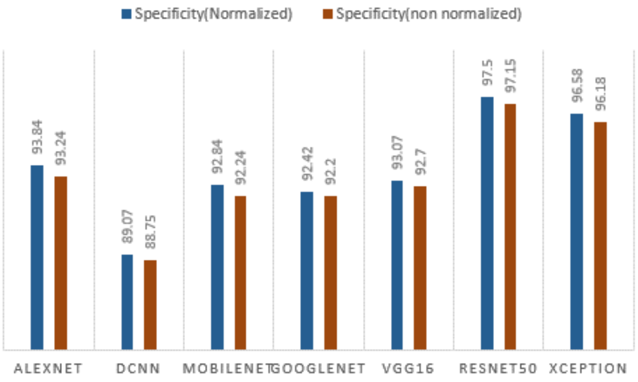

Figure 5. Study of specificity for several DL approaches for both normalized and non-normalized data.

The above figure describes the comparison for various models such as AlexNet, DCNN, MobileNet, GoogleNet, VGG16, ResNet50 and Xception, on the basis of accuracy, precision recall, specificity and F1-score for detecting rice diseases for both normalized and non-normalized dataset. From **Figure 5,** it is clear that normalized data provide more specificity as compared to non-normalized data. For evaluating the model's capability to accurately identify negative instances, it is crucial to examine the specificity of deep learning techniques utilising both normalised and non-normalized data. Because of enhanced convergence, feature balance, and the network's capacity to recognize negative instances, normalised data typically results in better specificity.

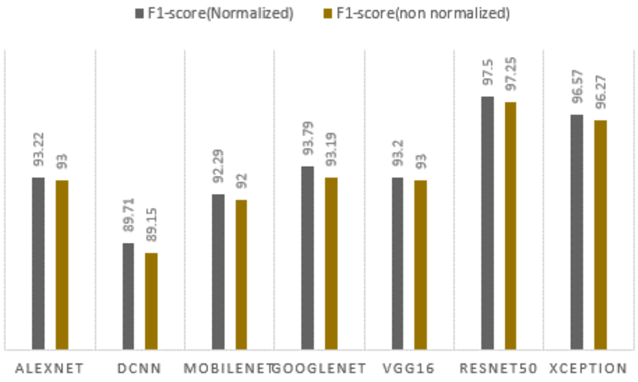

Figure 6. Study of F1-score for several DL approaches for both normalized and non-normalized data.

Study of the F1-score for several DL Approaches using both normalized and non-normalized data including both accuracy and recall when analyzing the F1-score of deep learning approaches on normalized and non-normalized data gives a complete picture of model performance. Because normalized data affects convergence, stability, and the capacity to identify important patterns, it is generally predicted to produce better F1-scores. The precise effect, however, can change depending on the model designs and data properties used. See **Figure 6**.

5. Comparison of the submodels with existing models

Using the same rice dataset, both normalised and non-normalized, we investigated a number of deep learning techniques, including AlexNet, DCNN, MobileNet, GoogleNet, VGG16, ResNet50, and Xception to assess each model's accuracy, precision, recall, specificity, and F1-score. In order to generate better results, the data is normalised using the mean average precision.

It is evident from **Figures 3–6** that ResNet50 achieves greater values when compared to the other models in terms of all evaluated parameters.

6. Conclusion

This paper presents the analysis of various deep learning models named as AlexNet, DCNN, MobileNet, GoogleNet, VGG16, ResNet50, and Xception for detection of nine different rice diseases such as Rice Blast (Pyricularia oryzae), Rice Sheath Blight (Rhizoctonia Solani), Bacterial Leaf Blight (Xanthomonas oryzae pv. oryzae), Tungro Disease, Rice Grassy Stunt Virus (RGSV), Rice Yellow Mottle Virus (RYMV), Bakanae Disease (Fusarium moniliforme), Brown Spot (Cochliobolus miyabeanus) and Rice Tungro Bacilliform Virus (RTBV) at the early stage. For this purpose we used secondary dataset containing 30000 images of different diseases. We compared the various models on the basis of accuracy, precision, recall, specificity, and F1-score. We analysed that ResNet50 model produce 97.50% accuracy and 0.97 F1 score as compared to other models. Among them, GoogleNet and Xception both did well. In the future, we'll expand the horizon to include new diseases and algorithms, which will vastly improve, accelerate, and simplify disease identification.

Author contributions

Conceptualization, SJ and KA; methodology, SJ; Software, SJ; validation, SJ, KA and RK; formal analysis, SJ; investigation, SJ; resources, SJ; data curation, SJ; writing—original draft preparation, SJ; writing—review and editing, SJ; visualization, KA; supervision, RK; project administration, SJ; funding acquisition, KA. All authors have read and agreed to the published version of the manuscript.

Conflict of interest

The authors declare no conflict of interest.

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