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Improving rice disease diagnosis with a deep learning approach using a CNN trained from scratch

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Abstract: Rice is a crucial staple food that sustains millions of people globally; however, its productivity is continuously threatened by various diseases. In recent years, artificial intelligence (AI) and computer vision have emerged as powerful tools for improving the diagnosis and classification of crop diseases, thereby reducing reliance on manual inspection. Despite their success, transfer learning (TL) models based on convolutional neural networks (CNNs) have faced challenges when dealing with limited datasets or closely related image classes. This study aimed to develop and evaluate a CNN model trained from scratch for the classification of rice diseases and to compare its performance with two popular transfer learning models, VGG16 and InceptionV3. A CNN architecture comprising 22 layers was designed and trained using a dataset containing images of eight distinct rice disease classes. The model's performance was compared to that of the transfer learning models under identical experimental conditions, using accuracy and F1-score as key performance metrics. The proposed CNN model demonstrated superior classification performance, achieving an accuracy of 95%, which significantly outperformed InceptionV3 (73%) and VGG16 (71%). Additionally, the CNN model recorded higher F1-scores across all classes (ranging from 0.91 to 0.99) compared to the TL models (ranging from 0.59 to 0.87). The results confirmed that a CNN model trained from scratch could outperform traditional transfer learning models in rice disease classification, particularly when sufficient data was available. These findings highlighted the potential of custom-built CNN architectures in enhancing disease diagnosis accuracy and suggested further improvements with expanded datasets and additional training.

Keywords: Arbitrary-configurations, Convolution neural network, Rice, Transfer-learning model

1. Introduction

Rice is a vital food source for millions globally, with consumption rising from 486.62 million metric tons in 2018-2019 to a projected 507 million metric tons by 2024-2025 (FAO, 2024; Statista, 2024; Shahbandeh, 2021). Despite the rising demand for rice, food security remains a global concern due to declining yields caused by both biotic and abiotic factors, with plant diseases being a major contributor to crop losses. Several rice diseases, including rice blast, sheath blight, and bacterial blight, spread rapidly and continue to threaten agricultural sustainability. Recent reports indicate that rice blast alone can cause annual yield losses ranging from 10% to 30% and, under severe outbreaks, nearly complete crop failure in some regions (Khadka et al., 2025). Globally, plant diseases are estimated to account for 20–40% of crop yield losses, representing economic damage valued in the hundreds of billions of U.S. dollars annually (Gai & Wang, 2024). These escalating impacts highlight the urgent need for effective disease detection and management strategies to safeguard food security.

Traditionally, farmers and agricultural specialists have relied on eye examination for disease identification, which is time-consuming, error-prone, and dependent on expert availability, especially in remote places (John, 2022). To address these issues, researchers investigated automated detection methods based on image processing, machine learning (ML), and computer vision (Zhang et al., 2018). ML allows computers to identify patterns and diagnose diseases by segmenting affected areas and extracting important properties like color and texture. Machine learning (ML) techniques, including support vector machines (SVMs) and pattern recognition, have been utilized for rice disease diagnosis (Rahman *et al*., 2020). However, their performance is heavily reliant on manual feature selection, which demands significant domain expertise (Prajapati et al., 2017). Recent advancements in artificial intelligence (AI) have led to the widespread adoption of deep learning, particularly Convolutional Neural Networks (CNNs), which automatically extract features and enhance classification accuracy. CNN-based models surpass traditional machine learning methods regarding precision, reliance on user input, and real-time disease detection, making them suitable for large-scale agricultural applications (Karthik et al., 2020).

2. Literature review

Several studies have shown that CNNs are effective in detecting rice diseases. For instance, Dey et al. (2022) evaluated four pre-trained CNN models- VGG19, InceptionV3, ResNet50, and VGG16- on a dataset consisting of 2,892 public and field images related to hispa, brown spot, leaf blast, and NPK (Nitrogen, Phosphorus, and Potassium) deficiencies, with VGG19 achieving the highest accuracy at 91.8%. Ghosal et al. (2020) classified rice blast, leaf blight, and brown spot using a CNN-based VGG16 model, attaining an accuracy of 92.46% on 500 field images. Latif *et al*. (2022) employed a modified VGG19 model to diagnose six rice diseases: narrow brown spot, leaf blast, brown spot, bacterial leaf blight, healthy plants, and leaf scald, achieving an accuracy of 96.08%. Other studies investigated alternative CNN architectures for rice disease classification. Swathika *et al*. (2021) trained a proprietary CNN model using 3,081 photos of healthy and diseased rice leaves, with a 70% accuracy. Tejaswini et al. (2022) utilized six CNN models, such as VGG16, VGG19, XCeption, and ResNet50, on a dataset of 1,600 images depicting rice leaves affected by brown-spot, leaf-blast, and hispa. Among them, a five-layer CNN model achieved the highest accuracy, reaching 78.2%.

Previous studies have extensively employed transfer learning (TL) models based on convolutional neural networks (CNNs) for the diagnosis and classification of crop diseases, achieving considerable progress in automating image-based analysis (Kim et al., 2022; Amin et al., 2023). Despite these advances, TL models continue to encounter substantial challenges when applied to domains such as rice disease detection, particularly in distinguishing visually similar disease classes. Common issues reported in prior research include overfitting, exploding gradients, class imbalance, unpredictable model configurations, and data scarcity (Kim et al., 2022). The performance of TL models largely depends on the similarity between the pre-trained features derived from large, generic datasets such as ImageNet and the target dataset. Consequently, when the target domain differs in texture, content, or imaging conditions, TL models may fail to capture essential disease-specific features, leading to reduced classification accuracy and misclassification of closely related infections (Amin et al., 2023).

Moreover, the selection of pre-trained architectures and fine-tuning layers is often guided by convenience or convention rather than by the task's specific visual and structural requirements. This limits the adaptability of TL-based models and their ability to generalize across diverse disease conditions. Training a CNN model from scratch presents an alternative approach, enabling the design of architecture and feature extraction processes that are optimized for the target dataset. Although this approach requires more computational resources and a sufficient volume of labeled images, it offers greater control over model design and reduces dependency on features learned from unrelated datasets.

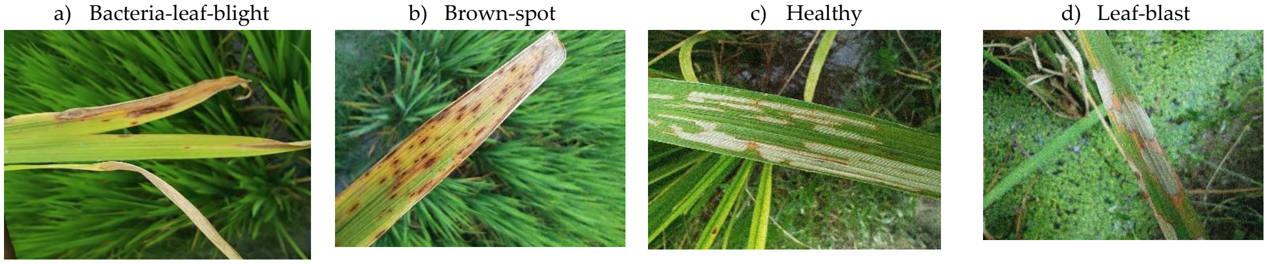
Therefore, this study seeks to solve the problem of limited adaptability and suboptimal performance of TL models in classifying visually similar rice diseases by developing and evaluating a CNN model trained from scratch, specifically designed to enhance accuracy, reliability, and robustness in rice disease detection. The remainder of the study is organized as follows: Section 2 details the material and methods, followed by Section 3, which outlines the experimental setup, Section 4 discusses the results, and Section 5 concludes the paper and presents recommendations.

3. Methodology

3.1. Dataset description

The dataset utilized in this study was sourced from the Mendeley repository, which is accessible to the public at (Mehedi et al., 2023). Figure 1 depicts the eight types of diseases on rice: brown spot, healthy, leaf-blast, leaf-scald, bacterial-leaf-blight, narrow-brown-leaf-spot, rice-hispa, and sheath-blight. Each class contains 500 images, totaling 4,000 images.

a) Bacteria-leaf-blight b) Brown-spot c) Healthy d) Leaf-blast



e) Leaf-scald f) Narrow-brown-leaf-spot g) Rice-hispa h) Shealth-blight

Figure 1: Images used in this study

3.2. Pre-processing methods

To reduce computational costs, the dataset was pre-processed by resizing images from 1600x1200 pixels to 150×150 pixels. This was followed by data augmentation to expand the dataset and assist the models in learning diverse features across multiple dimensions, minimizing the risk of overfitting (Tang *et al*., 2020). Geometric transformations such as scaling, rotation, zooming, and horizontal flipping were employed in the augmentation process. These modifications exposed the models to a wider variety of image variations, enhancing their robustness and generalization.

3.3. Convolution Neural Network

Deep learning heavily relies on CNNs, commonly used in computer vision. Their ability to identify visual patterns in image pixels with minimal pre-processing makes them ideal for image-based detection applications. This section describes the CNN models utilized in this investigation.

VGGNet is an advanced architecture developed for feature extraction from low-resolution images (Simonyan & Zisserman, 2015). The model consists of sixteen convolutional layers, each utilizing a uniform 3×3 filter instead of larger convolutions. Coulibaly *et al*. (2019) found that employing two consecutive 3×3 convolutional layers reduces the number of parameters and enables the use of two Rectified Linear Unit (ReLU) layers instead of one. VGG16, a widely used variation, features 3×3 convolution layers and 2×2 pooling layers.

GoogleNet features an inception module, which includes more layers than typical CNNs. Chen et al. (2021) discovered that replacing fully connected layers at the top of the network with average pooling significantly reduced the parameter count. GoogleNet is optimized for efficiency, minimizing memory and energy usage. This study also covers InceptionV3, an upgraded version of InceptionV1 and InceptionV2 (Szegedy et al., 2016).

3.4. The proposed CNN models

The architecture of the proposed CNN consists of 22 layers in total, as shown in Figure 2. It includes one input layer that accepts images of 150×150 pixels, followed by six convolutional layers that are responsible for feature extraction at various depths. Each convolutional layer is accompanied by six batch normalization layers to stabilize and accelerate the training process. The network also includes three max pooling layers that progressively reduce the spatial dimensions of the feature maps, thereby minimizing computational complexity. To prevent overfitting, two dropout layers are incorporated at different stages of the network. A global average pooling layer is used to aggregate spatial information before the fully connected layers. Finally, the model concludes with two dense layers, one with 128 neurons for feature combination and another output layer with softmax activation for classification across the target classes. The output layer classifies images into eight categories: bacterial-leaf-blight (Blb), brown-spot (Bs), healthy (He), leaf-blast (Lb), leaf-scald (Ls), narrow-brown-leaf spot (Nbls), rice-hispa (Rh), and sheath-blight (Sb). Since some diseases, such as Blb, Lb, and Ls, exhibit visual similarities, the model was trained from scratch to enhance classification accuracy and minimize misclassification.

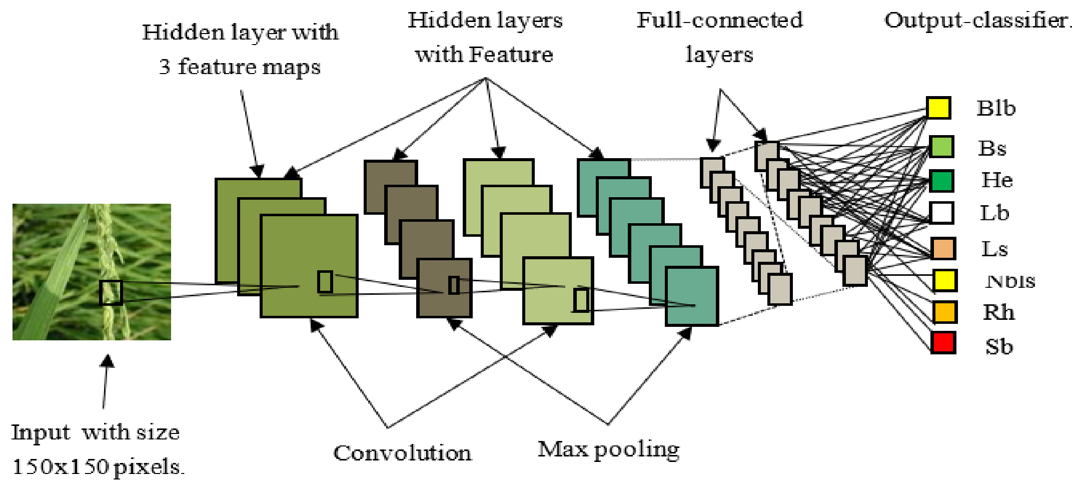


Figure 2: The model architecture of proposed CNN model

3.5. The proposed CNN models

Figure 3 presents the proposed framework and the step-by-step process for model development. Images were pre-processed by resizing from 1600×1200 pixels to 150×150 pixels to enhance computational efficiency. Data augmentation methods like vertical flipping, 90-degree rotations, and a 0.5 zoom range were used to increase generalization and broaden the dataset. After that, the dataset was split into three sets: training (70%), validation (15%) and testing (15%). Three models VGG16, InceptionV3, and the proposed model were trained and validated using the same dataset for comparative analysis. The final 10% of the dataset was used for performance evaluation to identify the most effective model. The Adam optimizer was employed for training, utilizing a dropout rate of 0.1 and a learning rate of 0.001. The models were trained on a system equipped with an NVIDIA GeForce RTX 4080 GPU and 16 GB of RAM.

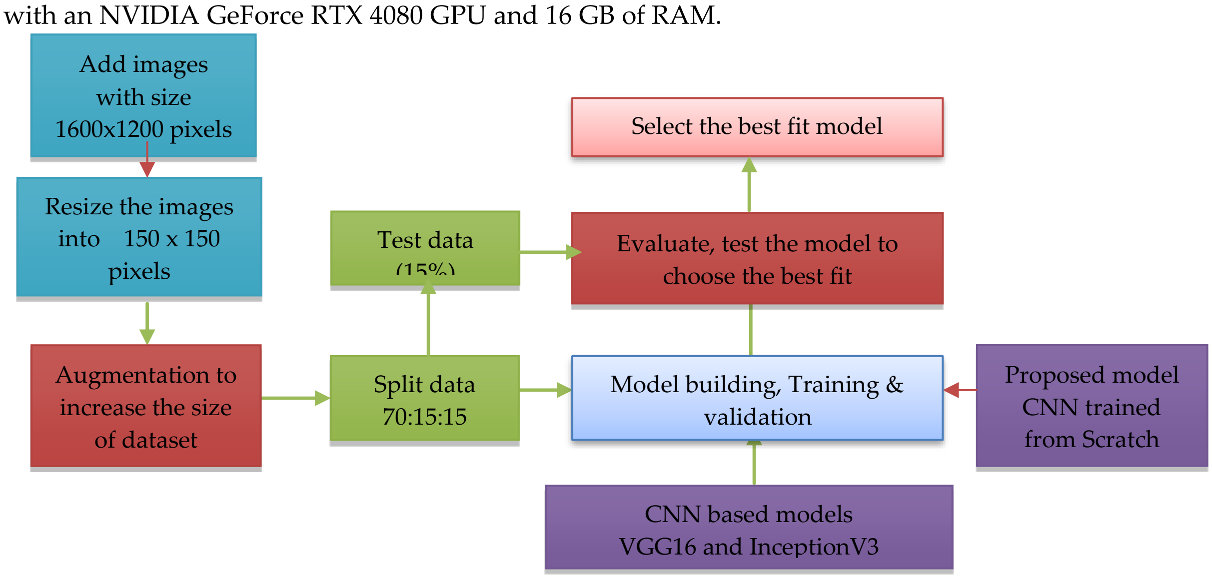


Figure 3: The flowchart showing the summarized steps followed on experimental setup

4. Result and discussion

This section outlines the evaluation parameters, compares the performance of CNN-based models trained using TL versus those trained from scratch, and discusses the contributions and implications of this study.

4.1. Evaluation Parameters

Four parameters, Accuracy (Acc), Precision (Pre), Recall (Rec), and F1-score (Fsc), as shown in Equations 1–4, were used to evaluate the model performance.

$$A_{cc} = \frac{T_{Neg} + T_{Pos}}{T_{Neg} + T_{Pos} + F_{Pos} + F_{Neg}} \quad 1$$

$$P_{re} = \frac{T_{Pos}}{T_{Pos} + F_{Pos}} \quad 2$$

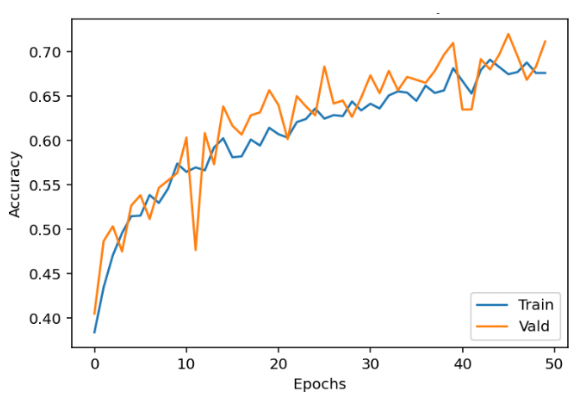
$$R_{ec} = \frac{T_{Pos}}{T_{Pos} + F_{Neg}} \quad 3$$

$$F_{Sc} = 2\left(\frac{P_{re}.R_{ec}}{P_{re} + R_{ec}}\right) \quad 4$$

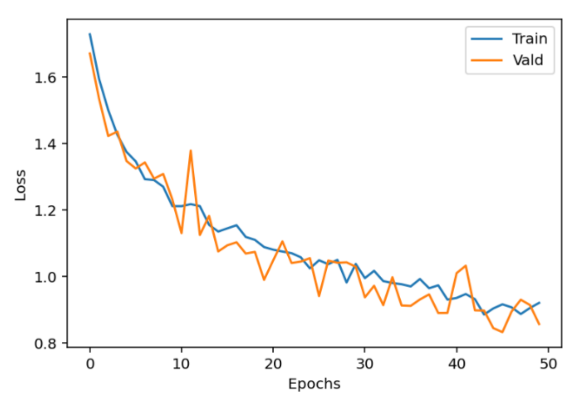
The term "True Negative (T_{Neg})" refers to the accurate prediction of the negative class by the model. A True Positive (T_{Pos}) refers to a situation where the model accurately predicts the positive class. A false negative (F_{Neg}) refers to an incorrect prediction made by the model regarding the negative class. A false positive (F_{Pos}) refers to a situation where a model incorrectly predicts a positive class.

4.2. Model Performance Comparison

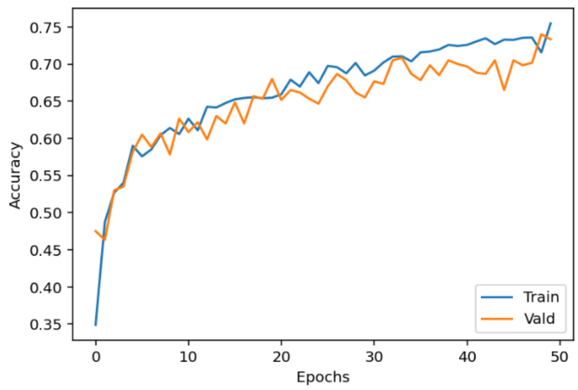
Figure 4(a), (c) and (e) show the training accuracy curves for VGG16, InceptionV3, and the proposed model, while Figure 4(b) (d) and (f) present the corresponding loss curves for VGG16, InceptionV3, and the proposed model. VGG16 achieved 72% accuracy during training and 71% in validation, whereas InceptionV3 reached 74% in training and 73% in validation. The proposed model outperformed both, attaining 96% accuracy in training and 94% in validation. In terms of loss, VGG16 and InceptionV3 had values ranging from 0.6 to 0.9, while the proposed model maintained a lower loss between 0.2 and 0.25 for both training and validation. All models were trained for 50 epochs for direct comparison.



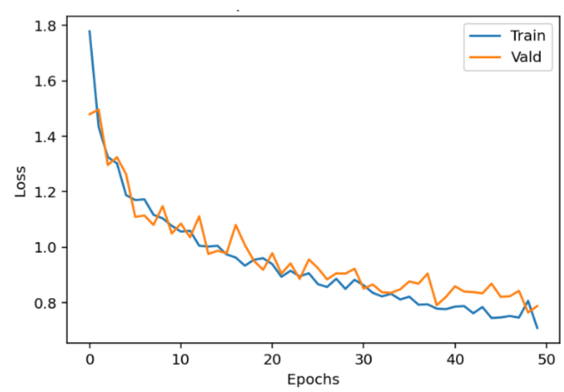
(a) VGG16 Model Training



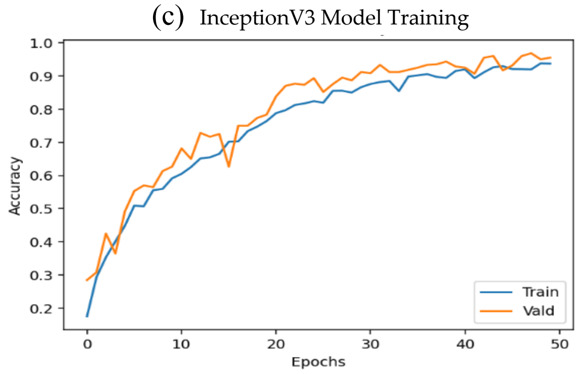
(b) VGG16 Model Loss



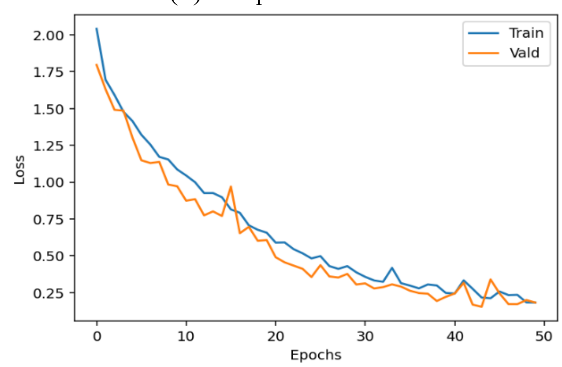
(c) InceptionV3 Model Training



(d) InceptionV3 Model Loss



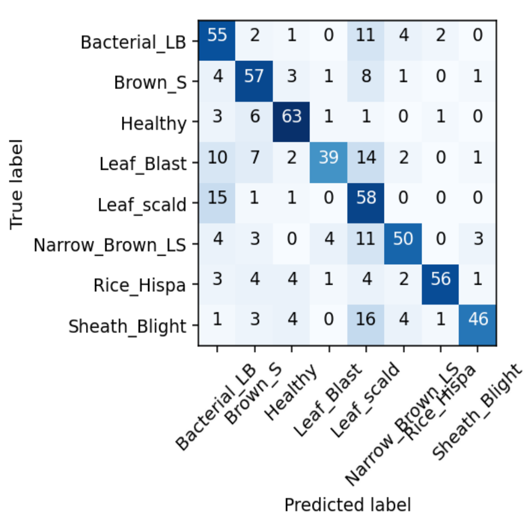
(e) Proposed CNN based Model Training

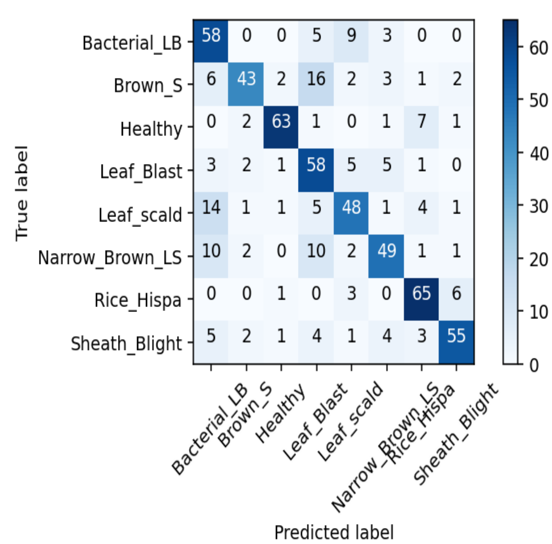


(f) Proposed CNN based Model Loss

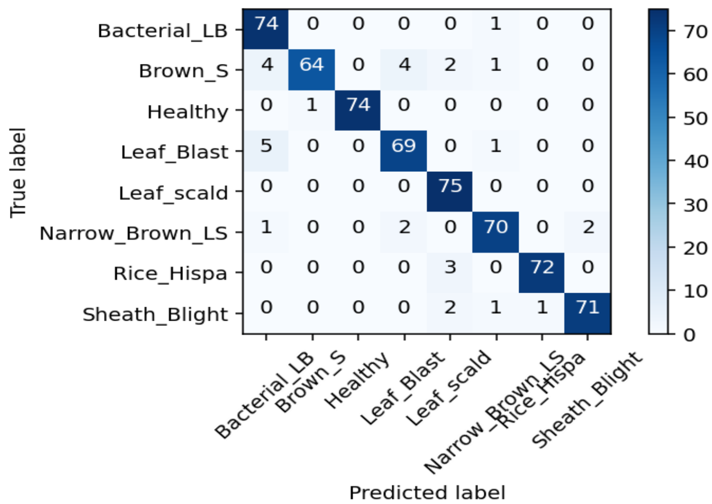
Figure 4: The graphs of training and validation results of the three models, left is accuracy of the model and right depicts the model's Loss.

Figure 5 presents the confusion matrix for VGG16, InceptionV3, and the proposed CNN model. VGG16 performed best in identifying the healthy class, correctly classifying 63 images (84%), while it struggled with leaf-blast, identifying only 39 images (52%) correctly. InceptionV3 showed the highest accuracy for the rice-hispa class, correctly classifying 65 images (86.7%), but had difficulty distinguishing brown-spot, with only 43 images (53.3%) correctly identified. The proposed model achieved outstanding performance in classifying bacterial-leaf-blight, healthy, and leaf-scald, correctly identifying 74 (98.7%), 74 (98.7%), and 75 (100%) images, respectively. However, it performed less effectively in identifying brown-spot, classifying 64 images (85.3%) correctly. Overall, the confusion matrix reveals that VGG16 and InceptionV3 struggled to differentiate bacterial-leaf-blight and leaf-scald. VGG16 misclassified 15 images of leaf-scald as bacterial-leaf-blight, while InceptionV3 misclassified 14 images in the same way.





(a) VGG16 (b) InceptionV3



(c) Proposed model

Figure 5: Confusion matrix of the three experimented models

Table 1 presents the confusion matrix, which assesses the performance of the model using accuracy (Acc), precision (Pre), recall (Rec), and F-score (Fsc) as defined in equations 1-4. The proposed CNN model performed effectively in identifying health-related images, achieving a precision of 1, a recall of 0.99, and an F-score of 0.99. These high scores indicate that the model is very good at correctly predicting and classifying most health images. Additionally, the model correctly diagnosed rice-hispa with an F-score of 0.97, as well as leaf-scald and sheath-bright, both of which had an F-score of 0.96. However, the model had difficulty accurately identifying narrow-brown-leaf-spot, bacterial-leaf-blight, leaf-blast, and brown-spot, which all had lower F-scores ranging from 0.91 to 0.94.

Table 1: Classification report of the proposed CNN model

Classes	Pre	Rec	Fsc	Support
Bacteria-leaf-blight	0.88	0.99	0.93	75
Brown-spot	0.98	0.85	0.91	75
Healthy	1.00	0.99	0.99	75
Leaf-blast	0.92	0.92	0.92	75
Leaf-scald	0.91	1.00	0.96	75
Narrow-brown-leaf-spot	0.95	0.93	0.94	75
Rice-hispa	0.99	0.96	0.97	75
Shealth-blight	0.97	0.95	0.96	75
Acc	**0.95**			**600**

4.3. The Contributions and Implications of the Study

The main objective of this research is to demonstrate that the proposed model, based on CNN, which is trained from the ground up, performs better than two TL models in identifying seven types of rice diseases. The results of the experiments indicate that the model trained from scratch achieves an average accuracy of 95%, meaning it accurately identifies diseases 95% of the time, with only a 5% error rate. In comparison, the InceptionV3 model has an average accuracy of 73%, resulting in a 27% error rate, while the VGG16 model shows an average accuracy of 71%, with a misclassification rate of 29%. The results also highlight that the proposed model excelled in identifying leaf-scald, successfully classifying all images, while the VGG16 model struggled with correctly identifying leaf-blast images.

Despite the suggested model's high performance, it has significant drawbacks. It requires a larger dataset to learn effectively, which increases the risk of overfitting because it relies only on training data to define its weights, ignoring past information from pre-trained models (Sabha *et al*., 2024). Furthermore, training from scratch is computationally hard and time-consuming, making it expensive and resource-heavy (Boulent *et al*., 2019).

The findings have clear implications for precision agriculture, where early and accurate disease detection can minimize crop losses, enhance output forecasts, and boost food security. Training from scratch improves accuracy; however, future optimizations such as data augmentation, hybrid models, or hardware-efficient implementations may facilitate more effective, real-world deployment viable.

5. Conclusion

This study focuses on the usefulness of utilizing a CNN-based model trained from scratch for datasets containing linked images. The suggested model, with a 22-layer architecture, was trained for 50 epochs and compared to two different CNN-based models, VGG16 and InceptionV3. Unlike the suggested model, which was trained from scratch, the top layers of VGG16 and InceptionV3 were fine-tuned while the lower layers remained unchanged. To maintain consistency, each model was trained for 50 epochs.

During testing, the suggested model outperformed the others, with an average accuracy of 95% versus 73% for InceptionV3 and 71% for VGG16. It also achieved higher F1 scores across all classes, ranging from 0.91 to 0.99, compared to VGG16 and InceptionV3, which varied from 0.59 to 0.87. These findings indicate that the suggested model has the potential to perform even better with additional training, as the training graph was still improving at the conclusion of the 50 epochs. Future studies should concentrate on training with more diverse datasets and applying the model to different crops, thereby improving its robustness and generalization.

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