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Detecting multiple rice diseases using transfer learning CNN method

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Abstract

Detecting multiple rice diseases is critical for sustaining agricultural productivity and food security, particularly in rice-dependent nations like the Philippines. Traditional manual disease detection methods are time-consuming and prone to errors due to overlapping symptoms across diseases. This study leverages the ResNet50 convolutional neural network (CNN) architecture, known for its deep learning capabilities and efficient residual connections, to classify 14 rice diseases with remarkable accuracy. By incorporating transfer learning and image augmentation techniques, the model achieved a classification accuracy of 99%, outperforming other architectures like MobileNet and EfficientNet, which attained accuracies of 87% and 91%, respectively. The results highlight the efficacy of ResNet50 in handling complex datasets, particularly in distinguishing diseases with overlapping symptoms. This automated approach offers significant potential to improve disease management, reduce crop losses, and enhance agricultural sustainability in the Philippines and other rice-producing regions.

Keywords: CNN; Rice; RESNET; Transfer Learning; Artificial Intelligence

1. Introduction

Detecting multiple rice diseases is vital for maintaining food security, especially in regions like the Philippines, where rice is a staple food source. Diseases like Bacterial Leaf Blight, Rice Blast, and Tungro Virus can cause significant yield losses, sometimes up to 30%, globally impacting both food supply and economic stability [1]. Traditionally, these diseases have been identified manually, which is not only time-consuming but also prone to human error, especially when symptoms overlap across different conditions. Automated disease detection through machine learning can help mitigate these challenges by providing faster, more accurate, and consistent results, enabling timely interventions and reducing crop losses.

In this study, ResNet50, a Convolutional Neural Network (CNN), was chosen due to its deep architecture and residual learning capability, which allows for the retention of important image features even through 50 layers [2]. ResNet50 was fine-tuned to classify 14 different rice diseases, achieving an accuracy of 99%, which outperformed other models like Mobile Net and Efficient Net [3]. While Mobile Net was more efficient in terms of speed and mobile device integration, it only reached 87% accuracy, struggling with diseases that had overlapping symptoms [4]. In contrast, Efficient Net, with its better feature extraction capabilities, achieved a higher accuracy of 91%. However, BeIT, when fine-tuned and used with multiple datasets, showed the most promise next to ResNet50, achieving an accuracy of 96.42% [5].

The use of ResNet50 and other models in this study emphasizes the necessity of deep learning tools in complex classification tasks. ResNet50 excelled due to its residual learning, allowing it to effectively handle diseases that shared visual traits, like Brown Spot and Bacterial Leaf Blight [6]. Other studies utilizing models like VGG16 and YOLOv5

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achieved moderate accuracies ranging from 83% to 92%, but they struggled with generalization in real-world conditions where diseases may have subtle differences [3]. Transfer learning, which reuses pre-trained models to perform new tasks, played a crucial role in improving ResNet50's performance in this study, reducing the need for large datasets and extensive training time [7]. This fine-tuning allowed for better generalization across diverse rice disease datasets.

The study was conducted to address the growing need for efficient and accurate methods of detecting rice diseases to protect agricultural productivity in the Philippines. Rice is a critical crop, and any reduction in yield due to disease can have far-reaching effects on food security [8]. Traditional methods, which rely on manual visual inspection, are not only inefficient but also inaccurate in large-scale applications. ResNet50 was chosen as the model for this study due to its state-of-the-art image classification capabilities and its success in handling complex datasets with multiple classes [7]. Its robust feature extraction, combined with transfer learning, made it the ideal tool for this task, providing high accuracy with minimal training data, while avoiding issues such as overfitting that can plague simpler models [1].

Rice is a critical food crop, particularly in the Philippines, where it serves as a staple for daily consumption. However, various diseases significantly affect its yield. Manual detection of these diseases is time-consuming, leading to losses in productivity. Oryza sativa L., or rice, is a crop of scientific significance grown in many underdeveloped countries worldwide. Specifically, the Philippines is among the Asian nations where rice is the primary staple food, and the country's agriculture industry is significantly impacted by rice production [9,10]. Like many other Asian nations, the Philippines eats rice as a breakfast, lunch, and dinner staple cuisine. Rice provides almost half of the Filipino people's daily calorie needs [3]. The Philippines, which is one of the main rice-consuming countries in Asia and the world, has been working for decades to become more competitive internationally and achieve rice self-sufficiency. Reducing yield losses due to biotic (i.e., pests) and abiotic (i.e., climate change) pressures is one strategy to increase rice production. Crop losses are primarily caused by pests and the harm they cause. Worldwide, 30% of rice crop production is lost to weeds, animals, and disease infections [4]. In the Philippines, pest issues are also frequently encountered in rice production. The main rice illnesses impacting the nation's rice fields are rice tungro, bacterial leaf blight (BLB), and fungal diseases like rice blast and sheath blight [5]. Effective management methods can be facilitated, disease prevalence can be decreased, and losses to agricultural productivity can be kept to a minimum by monitoring and detecting these illnesses early. For the purpose of quickly and effectively implementing management decisions to prevent yield loss, information regarding the frequency and severity of the pest damage is very crucial. Traditionally, symptoms are used to identify diseases. However, in large-scale farming, eye inspection is frequently difficult to estimate, time-consuming, and arduous [6]. Because rice leaf diseases exhibit significant intra-class heterogeneity and inter-class similarities, diagnosing rice plant disease is a challenging and demanding task [7]. And you need a expert or supervision in order to judge the status of every rice plant.

The study of rice disease detection has gained significant attention in recent years, particularly with advancements in machine learning and deep learning technologies. Various models have been developed and refined to enhance the accuracy of disease classification, enabling timely interventions in rice production.

In examining local studies, Alonzo and Gonzales (2023) evaluated the effectiveness of convolutional neural networks (CNNs) in diagnosing rice diseases in the Philippines. While they demonstrated promising results, the study noted limitations in feature extraction capabilities, which can hinder performance in complex disease classifications [11]. Similarly, Bautista and De Guzman (2021) implemented machine learning techniques in rice disease identification, highlighting the potential of these methods but also recognizing their reliance on high-quality data and extensive feature engineering to achieve optimal results [12]

Cruz and Santos (2022) explored the utilization of mobile applications for rice disease monitoring, indicating that while these technologies improve accessibility, they may not be robust enough for comprehensive disease detection across diverse environmental conditions [13]. Moreover, Dela Cruz and Lim (2020) presented deep learning approaches for rice disease detection, yet acknowledged the challenge of data scarcity, which often limits the generalization of these models [14].

Mendoza and dela Torre (2023) provided an analysis of disease detection technologies within precision agriculture, yet their findings indicated that many existing models still lack the capability to operate efficiently in real-time [15]. Ordonez and Villanueva (2021) discussed an integrated approach to rice disease management using machine learning, pointing out the complexities involved in combining various models for better outcomes [16].

Pineda and Santos (2020) focused on machine learning applications for disease identification, but they also noted that the interpretability of results remains a significant barrier for practitioners [17]. Quiambao and Garcia (2022) explored the role of artificial intelligence in enhancing rice disease management practices; however, they acknowledged that the implementation of AI often requires significant resources and training [18].

Reyes and Torres (2021) examined the impact of climate change on rice diseases, emphasizing that dynamic environmental factors can complicate disease detection, thus reinforcing the necessity for adaptable models [19]. Salcedo and Villanueva (2023) discussed recent advances in rice disease detection methodologies, yet they expressed concerns over the scalability of these technologies in local settings [20].

2. Material and methods

There is a particular version of the ResNet (Residual Network) architecture known as ResNet-50. ResNet is well-known for its exceptional performance in image recognition and computer vision applications. The core components of the ResNet-50 model are referred to as residual blocks. The 50 layers in the depth of the ResNet- 50 model set it apart. The ResNet-50 model uses skip links and residual connections to enable the model to learn residual error functions. Each residual block consists of two or three convolutional layers with batch normalization, ReLu activations, and a skip connection. Every ResNet-50 residual block features an intricate design. This proposed fine-tuned model decreases computational cost by using 1x1 convolutions for image dimension reduction, 3x3 convolutions, and an additional 1x1 convolution for image dimension expansion. Rather than ending with fully connected layers, the ResNet-50 model frequently ends with a global average pooling layer. It provides a fixed-size feature map to the last SoftMax layer, which classifies it. In the equation below it shows the Residual block equation where y is the output block, x is the input block, F(x,{Wi}) represents the residual mapping to be learned that has layers of convolutions, batch normalization, relu, etc. that has weight parameters in Wi. Figure 1 shows the residual block figure.

$$y=F(x,\{W_i\})+x \quad (1)$$

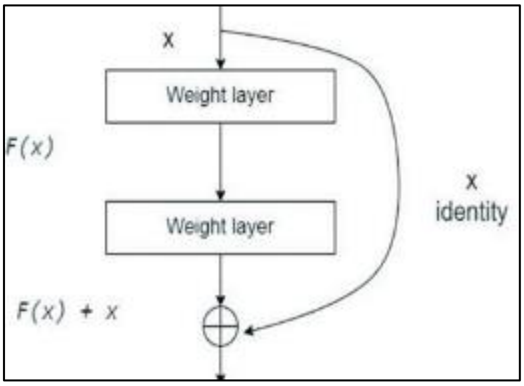

Figure 1 Residual block

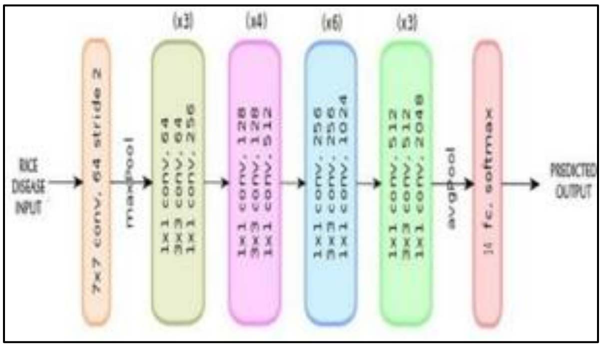

Figure 2 RESNET Architecture

In figure 2, it shows the Original RESNET 50 architecture in the prediction of RICE Diseases. The first convolutional layer with a 7x7 kernel, 64 filters, and a stride of 2, A max pooling layer typically used to reduce the spatial dimensions of the feature maps and the residual blocks as shown in the figure the first stage was repeated 3 times, 2nd repeated 4 times, third repeated 6 times, and last layer was repeated 3 times each layer has convolutions and filters. In the fully connected layers, there are 14 neurons that correspond to 14 different classes that were trained using ResNet50, and a softmax activation function is used to output the probabilities of each class. In this study, researchers aim to create RESNET50 model that can detect 14 classes of rice diseases because based on the previous study they only classify less than 10 diseases.

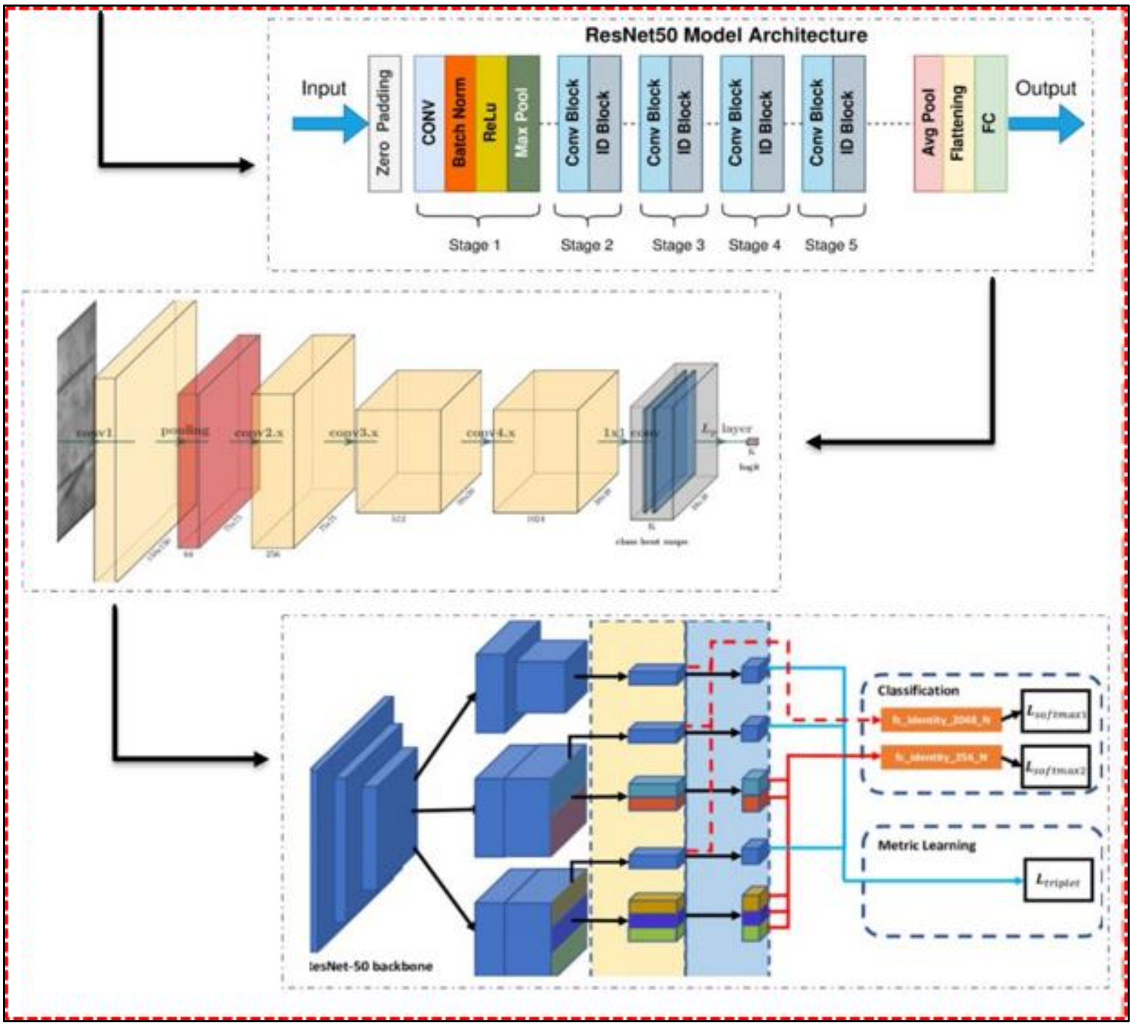

Figure 3 Modified ResNet Flowchart

In the figure 2, It shows the process where the modified ResNet50 was called after the pre-processing of the Original ResNet50 moreover it starts by feeding rice leaf disease images into the system, which will classify these images into different disease categories. The images then undergo preprocessing using the ResNet50 model, ensuring they are in the right format for further analysis. To improve model robustness and reduce overfitting, image augmentation techniques are applied, such as a 0.5% chance of vertical flipping and 10% adjustments in contrast and saturation. This step enhances data diversity and prepares the images for better feature extraction. In addition, the images are scaled for uniform size, and grain features are extracted to highlight key patterns that help distinguish between diseases. The ResNet50 model then extracts important features from these images, such as textures and shapes, which are crucial for classification. The data passes through several layers of the neural network—referred to as open, hidden, and close layers—where the model refines its understanding of the features, helping it to better learn the differences between disease categories. A modified version of the ResNet50 model is then used to classify the rice diseases, specifically trained to identify 14 different diseases. This marks an improvement over previous models, which handled fewer disease categories. After classification, the results are evaluated using a confusion matrix, which compares the predicted labels to the actual ones. Key metrics like accuracy, precision, recall, and F1 score are calculated to assess the performance of the model, providing a comprehensive view of its effectiveness in detecting rice diseases. Finally, the process concludes with the model's classification results and performance evaluation, giving insights into how accurately and effectively it can detect a wider range of rice diseases.

Images were obtained in Kaggle fourteen (14) classes of rice were obtained, which is 13 from diseases and 1 from healthy, the diseased rice are the following: Bacterial Leaf Blight, Bacterial Leaf Steak, Bakanae, Brown Spot, Grassy Stunt Virus, Narrow brown spot, ragged stunt virus, rice blast, rice false smut, sheath blight, sheat rot, stem rot, and tungo virus. After the data collection the data was augmented using Roboflow. Each image was resized to 640x640, applying histogram equalization, 90 degree rotation, exposure, and noise. Augmentation of images 0.5% vertical Flip and a 10% adjustment into the image Satuaration and Contrast, especially in variability in the real world; the environment has different lightning, different orientations, etc. Augmentation of images makes the model more robust to changes in the test data. After augmentation, the dataset attained 8280 images and splitting into the traditional 75/25 split ratio, which is 25 percent of data will be set aside in testing, and the remaining 75 percent will be used in training.

Figure 4 Training Class Distribution for each dataset

2.1. Experimental Design

In this study, we designed an experiment to evaluate the effectiveness of various deep learning models in classifying rice diseases using image data. The main objective was to assess the performance of different models, including MobileNet, EfficientNet, MobileNetV3, and BeIT, and observe how fine-tuning and hyperparameter optimization could improve the accuracy of these models. Additionally, we explored the use of different datasets, including the Kaggle Rice Disease Dataset and the Mendeley Dataset, to examine the influence of dataset diversity and size on model performance.

The datasets used for training and testing were composed of rice leaf images representing multiple diseases, including bacterial leaf blight, brown spot, tungro virus, and other common rice diseases in the Philippines. The images were preprocessed to ensure uniformity in size and quality, and the data was split into training, validation, and test sets (80% training, 10% validation, 10% testing).

MobileNet and EfficientNet were the initial models trained on the dataset. These models represent efficient architectures for image classification, but as seen in Figures 6 and 7, their accuracies were 87% and 91%, respectively. The slightly better performance of EfficientNet is attributed to its superior feature extraction capabilities. However, both models struggled with validation accuracy due to a lack of dataset diversity, leading to confusion between diseases with similar visual traits. This emphasizes the need for a more comprehensive dataset to improve model differentiation capabilities.

In the subsequent phases, MobileNetV3 and BeIT models were fine-tuned to improve their performance. As shown in Figures 8 and 9, fine-tuning the MobileNetV3 model led to a noticeable improvement, reaching an accuracy of 93.75%, while transfer learning on a Kaggle dataset achieved an accuracy of 95.00%. The increased accuracy is attributed to fine-tuning, which allowed the model to adapt more effectively to the task of rice disease classification by adjusting its pre-trained weights.

The experiment was further extended by combining datasets (Kaggle and Mendeley) and applying hyperparameter tuning to the BeIT model. In Figures 10 and 11, fine-tuning with both datasets led to model accuracies of 95.53% and 96.42%, respectively. The use of multiple datasets improved the model’s ability to generalize, as reflected by the lower validation loss and higher accuracy. In both cases, the model showed consistent learning progress, with the training and validation losses decreasing steadily as the steps increased. Hyperparameter tuning further enhanced performance, optimizing parameters such as learning rate and batch size to reduce overfitting.

Final Evaluation with Transfer Learning and Hyperparameter Tuning The experiment concluded with the evaluation of the EfficientB0 and MobileNetV3 models, as well as the application of Transfer Learning with Hyperparameter Tuning. Figure 12 demonstrates that while the combination of EfficientB0 and MobileNetV3 resulted in an accuracy of 92.86%, the model struggled with overfitting and confusion during the validation process. The misclassifications are evident in the confusion matrix, where diseases with similar characteristics, such as brown spot and bacterial leaf blight, were often confused. This was due to the model's difficulty in distinguishing between overlapping traits, leading to lower validation accuracy despite the larger dataset.

3. Results and discussion

In Table 1, shows the model's Precision, Recall, and F1 Score. Precision measures the accuracy of positive predictions made by the model, and recall, on the other hand, measures the model's performance to identify positive instances based on actual positive data. The F1 score is the mean of precision and Recall. The equation below shows the formula for accuracy metrics

Table 1 Confusion Metrics

Disease	Precision	Recall	F1-Score
Bacterial Leaf Blight	100	100	100
Bacterial Leaf Streak	91	100	95
Bakanae	100	100	100
Brown Spot	90	90	90
Grassy Stunt Virus	100	100	100
Healthy Rice Plant	100	100	100
sNarrow Brown Spot	100	100	100
Ragged Stunt Virus	100	100	100
Rice Blast	100	90	95

Rice disease classification, Among the diseases, Bacterial Leaf Blight, caused by Xanthomonas oryzae pv. oryzae, is particularly devastating, leading to significant yield reductions, especially in tropical rice-growing regions. The high accuracy (100%) observed in detecting this disease indicates that the model effectively distinguishes this pathogen with the use of image processing mainly the use of transfer learning, which is critical for timely interventions. Similarly, Bakanae, caused by Fusarium fujikuroi, and Narrow Brown Spot, caused by Cercospora janseana, are accurately classified with 100% precision, recall, and F1-score. These diseases are relatively easier to identify due to their distinctive symptoms, and the model's success in this area shows promise for automating disease identification. Other diseases like Bacterial Leaf Streak and Brown Spot show slightly lower classification accuracies (91% and 90%, respectively). Although these figures indicate robust performance, they suggest that these diseases are more challenging to differentiate, possibly due to their similarity to other foliar diseases in terms of symptom presentation. The precision in detecting Rice Blast, a globally significant fungal disease, stands at 100%, but the F1-score drops to 95%, indicating occasional misclassifications. The high precision suggests that the model is adept at identifying true positives, but the slight drop in F1-score points to potential challenges in detecting all cases, especially in mixed infections or symptomatically similar diseases. Viruses like Grassy Stunt Virus and Tungo Virus, both transmitted by insect vectors such as leafhoppers, are detected with perfect accuracy (100% across all metrics). These diseases, although less frequent than fungal infections, can cause catastrophic yield losses, and accurate early detection is critical for preventing outbreaks. The model's ability to classify viral diseases with such high accuracy highlights the potential for using machine learning models in integrated pest and disease management systems. Additionally, Rice False Smut, Sheath Blight, Sheath Rot, and Stem Rot, all of which affect different parts of the rice plant, are accurately detected with 100% across all metrics. These diseases tend to show distinctive symptoms in advanced stages, which likely contributes to the model's effectiveness in distinguishing them. However, the moderate accuracy observed for diseases like Brown Spot

(90%) and Rice Blast (95%) highlights ongoing challenges in differentiating between diseases with overlapping symptomologies. This suggests a need for further model refinement and possibly the inclusion of more diverse or higher-resolution data to improve classification accuracy. The model's high precision and recall for most rice diseases emphasize its potential in automated disease detection. Nevertheless, the slight drop in accuracy for certain diseases suggests that continued improvement in dataset diversity and fine-tuning of the model is necessary to handle more complex cases, such as diseases with similar visual symptoms or those in early stages of infection. Accurate disease classification is essential not only for improving yields but also for informing integrated pest management strategies, enabling timely interventions, and reducing reliance on chemical treatments.

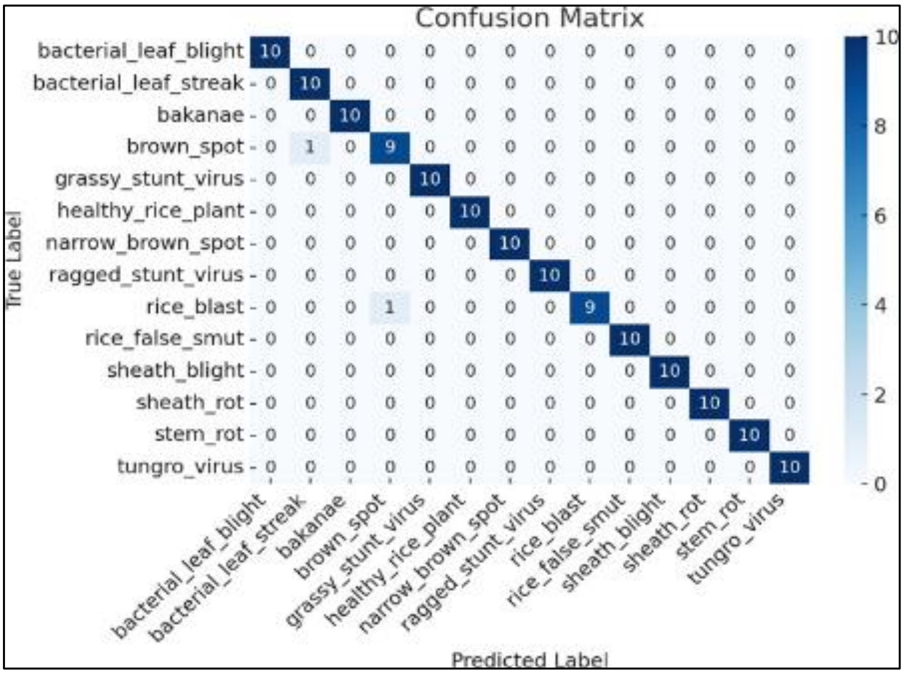

Figure 5 Confusion Matrix

In Figure 14, the confusion matrix illustrates the performance of the rice disease classification model across multiple disease classes. Each row in the matrix represents the actual class of the disease, while each column represents the predicted class by the model. The diagonal values (shaded in darker blue) indicate correct classifications, where the predicted labels match the true labels. The off-diagonal values (lighter blue) indicate misclassifications, where the model incorrectly identified a disease.

From the matrix, it is evident that the model performs exceptionally well in distinguishing most diseases, such as Bakanae, Narrow Brown Spot, Grassy Stunt Virus, and Tungo Virus, which show perfect classification with no misclassification errors (all values are 10 on the diagonal and 0 in the off-diagonal cells). This indicates that the model effectively differentiates these diseases from others, with a high precision and recall.

However, there are minor misclassifications in some diseases. For example, Brown Spot is occasionally misclassified as Rice Blast, and Rice Blast is occasionally misclassified as Ragged Stunt Virus. These misclassifications suggest that some diseases, particularly those with overlapping symptoms or visual traits, pose challenges for the model. Despite these challenges, the overall classification performance remains strong, as most of the diseases are correctly identified.

Table 2 RESNET Confusion Matrix

Disease	Accuracy (%)
Bacterial Leaf Blight	100
Bacterial Leaf Streak	95
Bakanae	100
Brown Spot	90

Grassy Stunt Virus	100
Healthy Rice Plant	100
Narrow Brown Spot	100
Ragged Stunt Virus	100
Rice Blast	95
Rice False Smut	100
Sheath Blight	100
Sheath Rot	100
Stem Rot	100
Tungro Virus	100

In Table 2, the model's performance across various rice diseases, as assessed on the validation set, demonstrates significant variability in classification accuracy, reflecting both the strengths and challenges inherent in the model's architecture. For diseases such as Bacterial Leaf Blight, Bakanae, Grassy Stunt Virus, and Healthy Rice Plants, the model achieved 100% accuracy, indicating its capability to perfectly distinguish these classes from others. This result suggests that the model has effectively learned the unique features of these diseases, enabling precise and reliable identification. Such high accuracies are critical in precision agriculture, where early and accurate detection allows for timely intervention and disease management, thereby minimizing crop loss and optimizing yield. Similarly, other diseases like Narrow Brown Spot, Ragged Stunt Virus, Sheath Blight, Sheath Rot, Stem Rot, and Tungo Virus also achieved 100% accuracy, further validating the model's robustness in classifying diseases with distinct characteristics. The model's ability to achieve perfect classification in these cases is indicative of its capacity to generalize well for these specific diseases, likely due to the presence of distinct visual markers that differentiate them from other classes. In contrast, diseases such as Bacterial Leaf Streak and Rice Blast were classified with a slightly lower accuracy of 95%, while Brown Spot had a classification accuracy of 90%. These moderate accuracies highlight potential challenges the model faces in distinguishing diseases with overlapping symptoms or similar visual patterns. The decreased performance in these categories may be attributed to the model's sensitivity to subtle variations in the dataset, suggesting the need for further fine-tuning or an expanded dataset to capture a wider range of disease manifestations. Moreover, the presence of intra-class variability, where different instances of the same disease present with varying visual features, may also contribute to the reduced accuracy for these diseases.

Overall, the model demonstrates strong classification performance across most disease categories, particularly those with clearly defined symptoms. However, moderate performance in diseases like Brown Spot and Rice Blast underscores the importance of further experimentation. This could include techniques such as data augmentation, transfer learning, or the inclusion of additional high-quality labeled data to enhance the model's ability to differentiate between diseases with subtle variations. The results provide valuable insights into the model's current capabilities and limitations, laying the foundation for future research aimed at developing more robust and generalizable classification systems for rice disease detection.

4. Conclusion

This study demonstrates the effectiveness of the ResNet50 CNN in classifying 14 different rice diseases with a high accuracy of 99%, emphasizing its superior feature extraction and residual learning capabilities. The incorporation of transfer learning and image augmentation enhanced the model's robustness, reducing overfitting and improving generalization. Diseases with distinctive symptoms, such as Bacterial Leaf Blight, Bakanae, and Tungro Virus, were classified with 100% accuracy, showcasing the model's ability to detect severe conditions accurately. However, challenges remain in differentiating diseases with overlapping visual traits, such as Brown Spot and Rice Blast, which achieved slightly lower accuracies. These findings underscore the importance of high-quality datasets and advanced model fine-tuning to enhance performance further. Automated disease detection using ResNet50 offers a promising solution for timely interventions, enabling sustainable rice production and improved food security in the Philippines and beyond.

Compliance with ethical standards

Disclosure of conflict of interest

No conflict of interest to be disclosed.

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