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Enhanced VGG-19 model for rice plant disease detection and classification

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ABSTRACT

Rice is the main staple food and rice farming plays a crucial role in the agriculture sector of Myanmar. It is also an essential pillar in generating foreign income. However, rice diseases seriously reduced the rice production and quality. Early detection of rice diseases is one of the effective ways to reduce the disease spreading and increase yields. Most Myanmar farmers detect rice diseases based on visual judgment and their experience, which leads to delay in taking efficient action. To overcome this challenge, we intend to propose an enhanced rice plant disease classification model that contributes as artificial intelligence (AI) in Myanmar agriculture sector. The proposed model enhances original visual geometry group 19 (VGG-19) by integrating the algorithms: mixture of Gaussians 2 (MOG2), GrabCut, and relevance estimation with linear feature (RELIEF) for classification. It was trained on 6,326 rice plant images of Kaggle and Eastern Shan State and validated using 5-fold nested cross-validation. The training and testing of proposed model are followed as 80:20. The proposed model experimental result is (98.3%) and lowest standard deviation (0.004) across seven classes than the original VGG-19, MobileNet, Efficient Net, and RestNet50 respectively. Future work will expand dataset diversity, enhance early-stage disease prediction, and support mobile diagnostics for real-world agricultural application.

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1. INTRODUCTION

Rice is the heart of Myanmar's economy, food sufficiency and a major source of foreign income. It accounts for over 60% of the country's agricultural gross domestic product (GDP), supports millions of livelihoods, and provides economic stability. Shan State is one of the most important rice-growing regions in Myanmar. However, rice production faces serious threats such as brown spot, leaf smut, sheath rot, stem rot, tungro, and bacterial leaf blight, which reduce yields by up to 30% annually. Rice diseases threaten not only domestic food sufficiency but also rice quality. Moreover, Myanmar farmers in remote areas are experiencing unnecessary losses in rice cultivation due to their inability to identify rice diseases accurately or to connect with agricultural experts. Due to the rare of skilled agricultural professionals, most farmers in Myanmar detect and classify the rice diseases based on visual inspection and their own experience. As a consequence, the farmers delay to control the spread of rice diseases in timely and rice diseases cause severe damage to rice fields. Early rice plant diseases detection and diagnosis can significantly reduce losses. Nowadays, as technology develops, modern technologies such as deep learning, machine learning are being used in the agricultural sector. In Myanmar, there is a need for systems that can easily detect and classify rice diseases automatically to help farmers. According to the United States Department of Agriculture (USDA) rice area estimation, Shan State is the fourth largest rice-growing region in Myanmar [1]. However, automated rice diseases monitoring, detection and classification systems are not yet in utilized in Shan State's farming.

Rice plant disease identification is a key to sustainable crop production and global food production. Early detection of rice plant diseases can significantly improve crop yield and quality. Sari *et al.* [2] investigated the application of ResNet50 deep convolutional neural network (DCNN) for automatic detection of four rice leaf diseases using digital image analysis. The experimental results showed that the 85:15 ratio had the highest accuracy of 81.48%, indicating that ResNet50 provides reliable performance for rice disease classification when appropriate data analysis strategies are used. Vijayan and Chowdhary [3] presented a hybrid optimization framework that combines the whale optimization algorithm (WOA) with adaptive particle swarm optimization (APSO) to enhance image segmentation and feature selection. The selected features were then classified using a convolutional neural network (CNN), resulting in a high classification accuracy of 97.5%. Rodrigo *et al.* [4] presented a lightweight transfer-learning model built on the MobileViTV2_050 architecture with ImageNet-1k pre-trained weights. The model effectively merges the local feature learning capability of CNNs with the global contextual understanding of vision transformers using a separable self-attention mechanism. Its efficiency makes it suitable for deployment in mobile environments. Sobuj *et al.* [5] investigated the effect of incorporating additional feature extraction techniques into the pre-trained EfficientNet-B7 architecture. By integrating histogram of oriented gradients and gradient-weighted class activation mapping (Grad-CAM), their enhanced model achieved an accuracy of 97%. Misba *et al.* [6] introduced a rice leaf disease classification approach based on a CNN enhanced with transfer learning using the visual geometry group (VGG)-16 architecture. Their comparative evaluation demonstrated that the transfer learning–based model achieved 92.46% accuracy, substantially outperforming the CNN trained from scratch, which attained 74% accuracy. Gogoi *et al.* [7] proposed a three-stage CNN framework that enhances classification performance through the use of a parametric rectified linear unit (ReLU) activation function. Trained on 8,883 images across five classes, the model achieved an accuracy of 94%. Akyol [8] presented a rice leaf disease classification method based on hypercolumn deep features extracted at salient interest points. Experimental results indicated that the random forest classifier effectively utilized these features, achieving an accuracy of 93.06%. Kiratiratanapruk *et al.* [9] proposed a rice leaf disease detection approach that integrates CNN-based object detection with an image tiling strategy guided by automatically estimated leaf widths. Using an 18-layer ResNet model evaluated on 4,960 images covering eight disease categories, their method achieved an accuracy of 91.14%. Yakkundimath *et al.* [10] conducted a comparative study of VGG-16 and GoogleNet for rice disease classification using 1,200 images representing fungal, bacterial, and viral infections. The results showed that VGG-16 achieved superior performance, attaining 92.24% accuracy compared to 91.28% for GoogleNet.

Senthil and Khatwal [11] introduced a novel hybrid multi-class support vector machine (MCSVM)-deep neural network (DNN) architecture for accurate rice leaf disease prediction. The MCSVM component focuses on feature optimization after training, while the DNN component enables dynamic updating of features to handle complex and diverse symptoms. It achieved accuracy of 95.2%. Ritharson *et al.* [12] developed a customized VGG-16-based framework that leverages deep learning and transfer learning to classify rice leaf diseases. Their approach successfully recognized nine distinct disease categories and achieved a high classification accuracy of 99.94%. Mahadevan *et al.* [13] introduced a comprehensive rice leaf disease detection framework centered on a deep spectral generative adversarial network (DS-GAN) optimized using an improved artificial plant optimization strategy. The approach improves image quality through an enhanced threshold-based neural network, applies multiscale neural slicing for segmentation, and employs spectral feature selection combined with social spider–based weight optimization to identify the most discriminative features. Li *et al.* [14] developed a DeepLabV3+-based semantic segmentation framework for rice leaf disease analysis, leveraging an encoder–decoder design with atrous convolution and spatial pyramid pooling to enhance segmentation quality. The approach was validated on a dataset comprising four rice leaf disease classes using mean intersection over union (mIoU) and pixel accuracy as evaluation measures. Bi and Wang [15] proposed an attention-enhanced double-branch DCNN for rice disease classification. Their experimental results showed that the proposed model outperformed several well-known CNN architectures, achieving a higher classification accuracy of 98.73% compared with existing methods. Upadhyay and Kumar [16] introduced an efficient rice plant disease detection method using a CNN model and Otsu's global thresholding. Their research focused on three major rice diseases and obtained the achievement a high accuracy of 99.7%. Deng *et al.* [17] proposed ensemble model combining DenseNet-121, SE-ResNet-50, ResNeSt-50, ResNet-50, and ResNeXt-50 for rice disease diagnosis across six disease classes on 3,302 images. Their ensemble approach achieves an overall accuracy of 91%. Shivam and Kumar [18] investigated pre-trained CNN models such as VGG-19, LeNet5, and MobileNet-V2 to identify infected rice plants. They studied two classes (infected leaves and healthy) using 2212 images. Their experiments achieved 77.09%, 76.63%, and 76.92% accuracy for VGG-19, LeNet5, and MobileNet-V2, respectively. Shah *et al*. [19] compared the performance of deep learning models, including Inception v3, VGG-16, VGG-19, CNN, and ResNet50, on 2,000 images for rice disease classification. Their analysis demonstrated that VGG-19 had highest achievement an accuracy of 98.56%. Iqbal *et al*. [20] focused on the early detection of rice diseases using Inception v3 and VGG-19 models. Their research achieved an impressive accuracy of 97.94% with VGG-19. Lwin and Htwe [21] applied AlexNet for rice leaf disease classification and compared with VGG-16. In their analysis, the open dataset got the highest accuracy. Wang *et al*. [22] proposed a lightweight ensemble deep learning model using attention-enhanced EfficientNet with stacked logistic regression for classifying five rice diseases, achieving 96.10% accuracy while outperforming VGG-16, ResNet101, and DenseNet201 with low computational cost.

Peng *et al*. [23] proposed a mutual information–based feature selection method using the minimal-redundancy–maximal-relevance (mRMR) criterion, which enhances classification performance by selecting features that maximize relevance and minimize redundancy. Prity *et al*. [24] proposed a neural network approach for rice leaf disease recognition using feature extraction, dimensionality reduction, and selection with an extreme learning machine classifier on 3,829 images, showing superior performance over direct image-based methods, with Grad-CAM enhancing interpretability. Peng *et al*. [25] introduced RiceDRA-Net, a residual deep learning architecture designed for rice leaf disease recognition. The model was evaluated on both simple and complex background datasets, where it accurately classified four rice leaf disease categories and achieved recognition rates of 99.71% and 97.86%, respectively.

According to our study, most researchers focused on only rice leaves diseases and up to five rice diseases. They applied CNN, the original VGG models or ensemble model to train Kaggle dataset. They utilized the clean images or already segmented images to training model. Some classification models can handle only single background images. They evaluated their models with the specific conditions such as single background images or complex background images. Therefore, our research targets to detect and classify seven classes of rice diseases including healthy class. Our proposed model handles rice diseases not only on leaves but also on whole plant including rice seeds. It modifies the original VGG-19 model that is trained with the combination of Kaggle and own dataset. Our model can manipulate the complex background images by utilization of image segmentation algorithms; mixture of Gaussians 2 (MOG2) and GrabCut. Moreover, in the proposed model, relevance estimation with linear feature (RELIEF) is integrated to the feature selection process that can generate the most relevant features than the features generated from the original VGG-19 model. Therefore, the proposed model offers a robust, reliable and effective solution for rice disease classification and help farmers to protect their crops and increase yields. It also achieved the high accuracy than other previous researches. The proposed system is one of the artificial intelligences (AI) plus agriculture tools to improve the rice production of Eastern Shan State. Moreover, it is also a fulfillment of the gap between the agriculture sector and farmers.

The proposed model is trained by using the combination of two data sources: Kaggle dataset and own dataset. The own dataset is manually collected from Eastern Shan State, Myanmar and validated by the Agricultural Research Department of Kyaing Tong. The images were taken under real-world conditions with different backgrounds and lighting. The dataset consists of six rice diseases of different types and healthy plants. The proposed model can handle both complex background and single background images. The detail information of dataset is described in Table 1.

Table 1. Data distribution in rice plant disease datasets

No	Types of diseases	Number of images	Kaggle dataset	Eastern-Shan State dataset
1	Leaf smut	40	30	10
2	Brown spot	1,610	1,060	550
3	Sheath rot	100	70	30
4	Stem rot	694	400	294
5	Tungro	1,298	1,000	298
6	Bacterial blight	1,584	1,000	584
7	Healthy	1,000	500	500
	Total	6,326	4,060	2,266

The images of six common rice diseases are shown in Figure 1. Brown spot disease, shown in Figure 1(a), is characterized by small to medium circular or oval lesions with dark brown centers and yellowish halos that may coalesce and lead to extensive leaf necrosis. Figure 1(b) shows sheath rot disease affecting the leaf sheath near the panicle, characterized by irregular brown to dark reddish lesions with tissue softening that can hinder normal panicle emergence. Stem rot disease, shown in Figure 1(c), affects the basal stem and lower leaf sheath, presenting dark brown to black lesions, tissue decay, and stem weakening that may cause lodging in severe cases. Figure 1(d) illustrates tungro disease, which is marked by yellow-to-orange leaf discoloration initiating at the leaf tips and margins, as well as stunted growth and decreased tillering. Figure 1(e) shows bacterial leaf blight, characterized by long, linear water-soaked lesions from the leaf margins to the midrib that turn yellowish-white as the disease progresses. Leaf smut disease, shown in Figure 1(f), is identified by narrow, elongated dark brown to black streaks along the leaf veins, which are slightly raised and distinct from circular lesions.

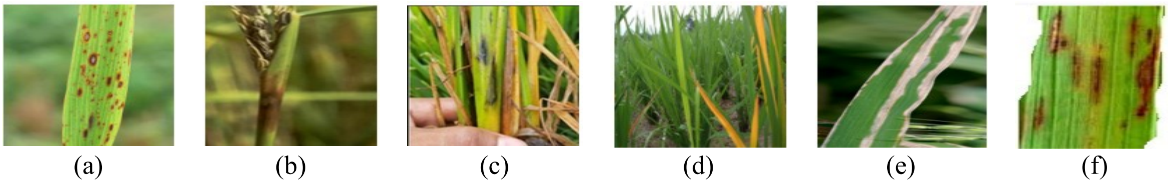

Figure 1. Sample images for different types of rice plant diseases for (a) brown spot, (b) sheath rot, (c) stem rot, (d) tungro, (e) bacterial leaf blight, and (f) leaf smut

2. METHOD

Nowadays, Myanmar's AgriTech sector is improved by using AI technology to improve farming practices, enhance efficiency, and promote sustainability across the food supply chain. It includes many areas like prediction in farming, data analytics, automatic detection and classification for diseases. The proposed model uses a 5-fold nested cross-validation technique, with each fold using 80% of the data for training (approximately 5,060 images) and 20% for testing (approximately 1,266 images), ensuring reliable model evaluation and performance measurement.

This research intends to contribute to the AgriTech sector by implementing the rice diseases classification model which utilizes the deep learning. It supports for improving farming practices and efficiency. The proposed system is based on the original VGG-19 model that includes three steps: preprocessing, feature extraction, and classification. We integrate the image segmentation to preprocessing step and feature selection is added between the feature extraction and classification step. The complete architecture of the proposed system is shown in Figure 2.

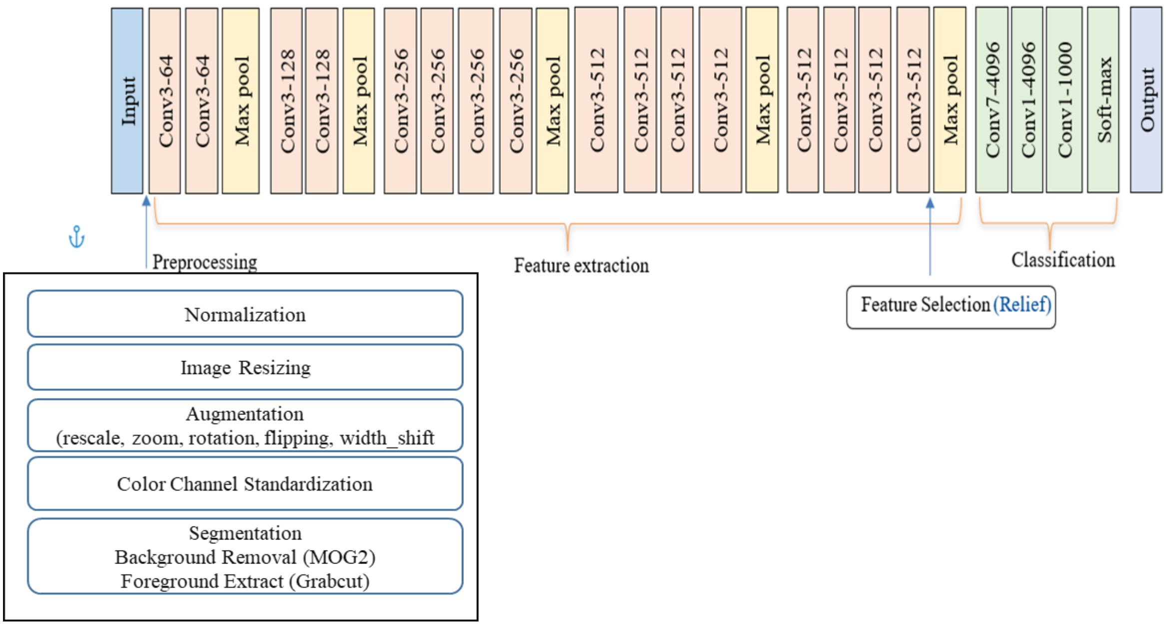

Figure 2. Proposed system for rice plant diseases classification

2.1. Preprocessing

This stage is performed to ensure data quality and upgrade the accuracy of training model. It includes image resizing to transform the same dimensions (224×224) of all input images, normalization, augmentation such as flipping, rescaling, zooming, rotation to improve model generalization, color channel standardization, and transformations to get the compatible format of tensor. The preprocessed images are described in Figure 3. One of the most important steps in the preprocessing of the rice plant disease is removing irrelevant background. However, removing foreground and background processes is not provided in the original VGG-19 model. For image segmentation of the proposed model, MOG2 and GrabCut algorithms are embedded in the preprocessing stage to handle the complex background images, to obtain the meaningful regions or segments, to enable more detailed analysis, to understand the image content and disease regions. They offer the detail analysis of image contents from the images has background noise and foreground noise that confuses the model when standardize the input images. MOG2 is an adaptive background subtraction method that efficiently handles noise, lighting changes, and shadows, making it suitable for images with complex or uncontrolled backgrounds, while GrabCut refines foreground extraction iteratively to remove irrelevant information and produce clean, focused images that enhance the proposed model's performance; the preprocessed outputs are shown in Figure 4.

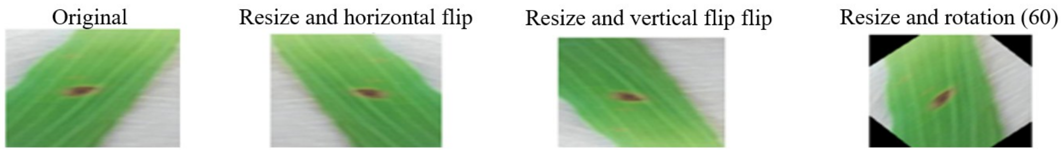

Figure 3. Examples of augmented images

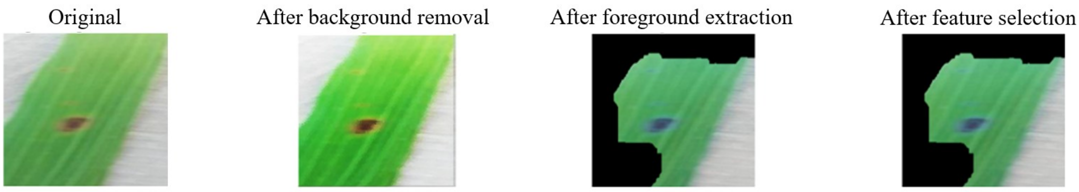

Figure 4. Comparison of resulted images after background removal, foreground extraction, and feature selection process

2.2. Feature extraction

The VGG-19 model, pre-trained on the ImageNet dataset, can be used for feature extraction by extracting features from intermediate layers of the network. This approach allows the model to leverage the learned representations of the model without needing to retrain the entire network. These extracted features serve as high-level image descriptors that improve the classification accuracy of rice plant diseases and reduce computational cost.

2.3. Feature selection

To improve the performance of VGG-19 model and reduce dimensionality, feature selection step is added to the original VGG-19 model because it is not supported in the original VGG-19 model. There are many feature selection algorithms such as mutual information, analysis of variance (ANOVA), least absolute shrinkage and selection operator (LASSO), and RELIEF to find the best set of features that allows one to build optimized the classification model. Table 2 illustrates the number of selected features for each feature selection technique. According to the experimental results of feature selection, the VGG-19 model alone extracts the highest number of features (30,360), while applying feature selection methods reduces the feature count significantly. Among these, VGG-19+LASSO selects the fewest features (24,200), followed closely by VGG-19+RELIEF (25,300), demonstrating their effectiveness in reducing dimensionality. This reduction can lead to more efficient and scalable classification models without substantial loss of information, highlighting the advantage of combining VGG-19 with feature selection techniques.

Table 2. Number of selected features

Combination of model and feature selection method	Number of selected features shape
VGG-19	30,360
VGG-19+principal component analysis (PCA)	28,360
VGG-19+RELIEF	25,300
VGG-19+Mutual	26,800
VGG-19+ANOVA	27,600
VGG-19+LASSO	24,200

Based on the all-experimental results, finally our proposed model utilizes RELIEF algorithm for feature selection. It evaluates each feature by how well it distinguishes between near instances (neighbors) of the same class and different classes. For each instance, it identifies the nearest hit (same class) and nearest miss (different class), updating feature weights to highlight significant features and discard less important ones. It works for noisy and redundant data because it focuses on local differences.

2.4. Classification

The selected features are used to classify the different types of rice plant diseases. The final layers of VGG-19 used the selected features to ensure the accuracy of classification of six rice diseases and healthy plants. This process enhances the generalizability of the model across different environmental conditions and complex backgrounds.

3. RESULTS AND DISCUSSION

To prove the performance of the proposed model, it is tested on the many experiments such as parameter turning, feature extraction, feature selection and model selection to classify the rice diseases. They are tested on Google Colab using the same datasets which is already mentioned. The first experiment shows the training and validation loss of proposed model which affects the accuracy of the model. The best parameters of the proposed model are 10 epochs and a batch size of 32 and the experimental results are shown in Figure 5.

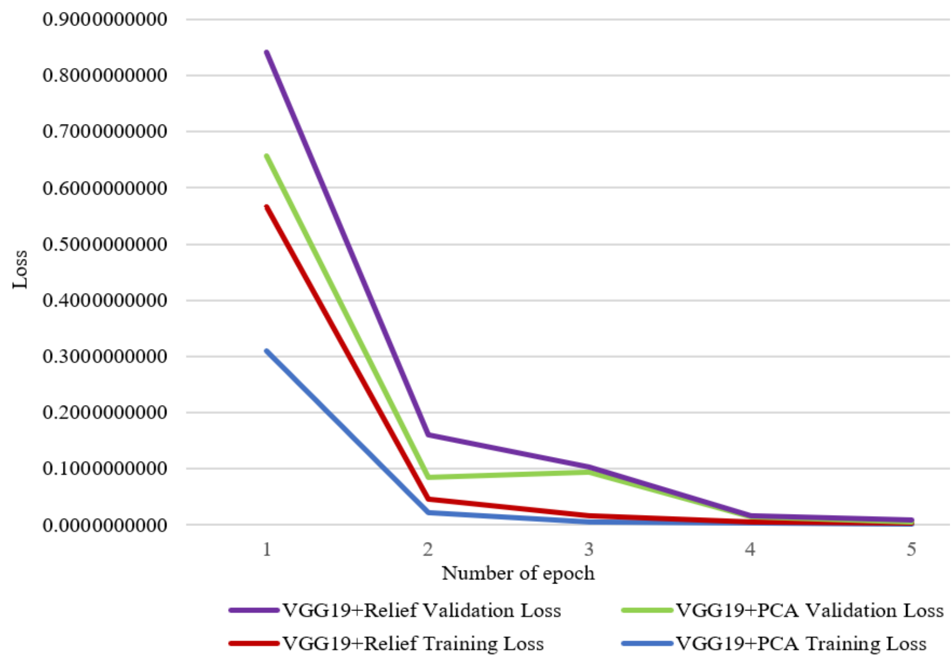

Figure 5. Comparison of the training loss and validation loss of VGG-19 with RELIEF and VGG-19+PCA

The second experiment evaluates the generalization capability of VGG-19 combined with PCA and RELIEF feature selection. The results show that both training and validation losses gradually decline and converge, demonstrating stable learning behavior. The close alignment between the two loss curves indicates effective generalization to unseen data and confirms that the models do not suffer from overfitting. They are shown in Figures 6 and 7. The VGG-19 with RELIEF has smaller gap than VGG-19 with PCA.

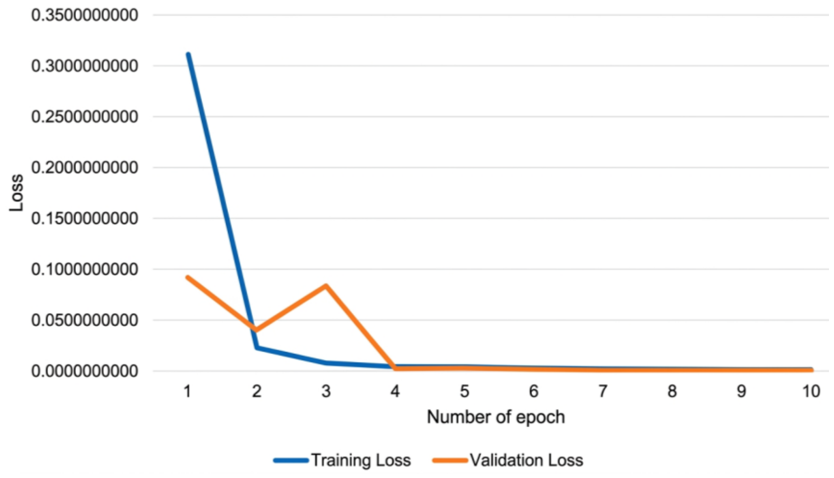

Figure 6. Model generalization of VGG-19 with PCA

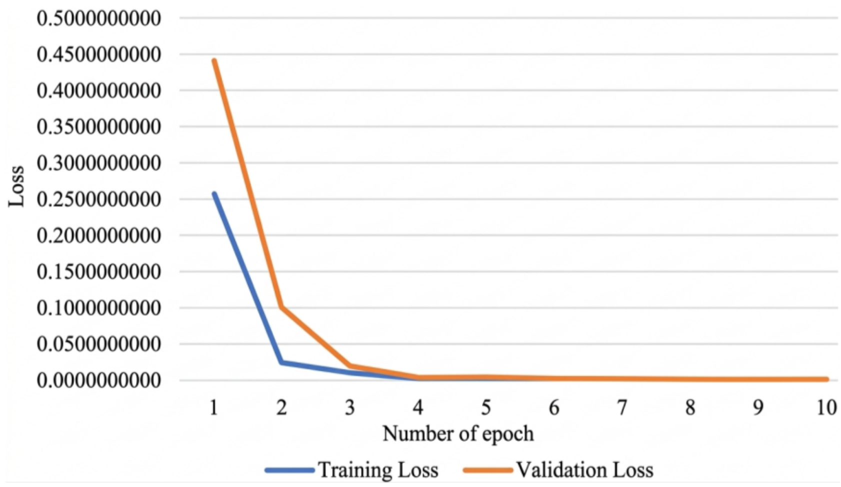

Figure 7. Model generalization of VGG-19+RELIEF

The experimental result of the proposed model is evaluated with nested cross-validation method for each class is described in Table 3. Of the seven test classes, the brown spot and bacterial blight are lower than the other results. The experimental result of the proposed model for each class is described in Table 3. The final experimental result is obtained by comparing with the original VGG-19, integration of VGG-19 with other feature selection methods, MobileNetV3, EfficientNet and RestNet50. The results of these models are shown in Table 4.

Table 3. Experimental result of the proposed model (VGG-19+RELIEF) for each class

Class	Precision	Recall	F1-score
Health	0.995	0.995	0.995
Leaf smut	0.990	0.985	0.988
Sheath rot	0.990	0.985	0.988
Stem rot	0.985	0.985	0.985
Tungro	0.980	0.980	0.980
Bacterial blight	0.970	0.975	0.972
Brown spot	0.975	0.970	0.972
Macro average	0.984	0.982	0.983

The experimental results show that the proposed model (VGG-19+RELIEF) achieved the highest result of 0.983, while EfficientNet attained a comparable result of 0.977. The proposed model is considered superior due to its combination of high result and the lowest standard deviation, indicating stable and reliable performance. These results demonstrate that the proposed approach outperforms the existing model in both feature selection, classification performance, model stability and reliability.

Table 4. Experimental result of the proposed model (VGG-19+RELIEF) and other models

Model	Precision	Recall	F1-score	Standard deviation
MobileNetV3	0.952	0.967	0.956	0.006
EfficientNet	0.976	0.981	0.977	0.005
RestNet50	0.973	0.981	0.976	0.004
VGG-19+RELIEF+MOG2	0.965	0.962	0.964	0.006
VGG-19+RELIEF+GrabCut	0.971	0.969	0.974	0.005
VGG-19+Mutual+MOG2+GrabCut	0.972	0.969	0.984	0.005
VGG-19+ANOVA+MOG2+GrabCut	0.966	0.963	0.971	0.007
VGG-19+LASSO+MOG2+GrabCut	0.980	0.967	0.973	0.007
Proposed model	0.984	0.982	0.983	0.004

4. CONCLUSION

This paper contributes Agri-Tech by offering a robust and cost-effective solution for rice plant disease types, ultimately improving productivity, and ensuring better crop health. We explored the power of deep learning and image processing techniques for rice plant diseases detection and classification. The proposed model based on a DCNN (VGG-19). It is integrated the image segmentation algorithms in preprocessing step and feature selection algorithm after featuring extraction step. It also provides the comprehensive classification and helps early diagnosis. It supports the improvement of crop management and prevention of severe outbreaks. Moreover, it can accurately identify six different types of rice plant diseases. According to the performance analysis, our proposed model is a robust model for rice plant diseases detection and classification and has the highest result of 98.3%. Importantly, the integration of VGG-19 with the RELIEF algorithm achieves the highest classification accuracy, highlighting the effectiveness of the optimal feature selection. Our contribution acts as an assistant for Myanmar farmers and offers a significantly improvement to Myanmar agricultural sector.

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AUTHOR CONTRIBUTIONS STATEMENT

This journal uses the Contributor Roles Taxonomy (CRediT) to recognize individual author contributions, reduce authorship disputes, and facilitate collaboration.

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Khin Mar Soe		✓				✓		✓	✓	✓	✓	✓		
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C : **C**onceptualization
M : **M**ethodology
So : **So**ftware
Va : **Va**lidation
Fo : **Fo**rmal analysis
I : **I**nvestigation
R : **R**esources
D : **D**ata Curation
O : Writing - **O**riginal Draft
E : Writing - Review & **E**diting
Vi : **Vi**sualization
Su : **Su**pervision
P : **P**roject administration
Fu : **Fu**nding acquisition

CONFLICT OF INTEREST STATEMENT

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper. The authors state no conflict of interest.

INFORMED CONSENT

This study does not involve human participants or personal data. Therefore, informed consent was not required for this research.

ETHICAL APPROVAL

This research uses rice leaf image datasets and does not involve human or animal subjects. Therefore, ethical approval from an institutional review board or ethics committee was not required.

DATA AVAILABILITY

The data used in this study were obtained from two sources: a publicly available Kaggle rice leaf disease dataset and an own dataset collected from rice fields in Eastern Shan State, Myanmar. The collected dataset was obtained with permission from the rice field owners and validated by the Agricultural Research Department of Kyaing Tong, Myanmar. The Kaggle dataset is publicly available through the Kaggle repository. The own dataset supporting the findings of this study is available from the corresponding author upon reasonable request due to usage permissions and local data collection restrictions.

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