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Slice Residual U-Net Based Rice Plant Disease Classification Using Convolutional Attentional BiGRU

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Abstract

Rice is one of the highest-produced staples all over the world. The production of rice is frequently threatened by leaf diseases in rice plants, which impacts farmers. This has an impact on economic growth in general. As a result, prompt diagnosis is essential, and appropriate action should be taken to enhance rice yield. The proposed framework in this article introduces a novel deep learning-based method named Convolutional Attentional Bidirectional Gated Recurrent Unit (CAtt_BiGRU) to classify rice leaf diseases. First, pre-processing techniques such as image rescaling and upgraded wiener filtering are applied to the input rice plant leaf images. After pre-processing, slice-based residual U-Net is used to segment the affected regions. The segmented images are then fed to the classification framework. The CAtt_BiGRU model was employed to classify diseases in rice plants. A Convolutional Neural Network (CNN) was employed for feature extraction, and the classification task was carried out by a Bidirectional Gated Recurrent Unit (BiGRU). Our approach surpasses other state-of-the-art methods by achieving an accuracy of 99.64%.

Keywords: Plant Leaf Disease, Image Rescaling, Wiener Filtering, Residual U-Net, Convolutional Neural Network, Bidirectional Gated Recurrent Unit.

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1 Introduction

In certain emerging nations, a significant proportion of the Gross Domestic Product (GDP) is attributed to cultural endeavours. India is a rapidly developing nation, with agriculture serving as the fundamental pillar for its progress (Sharma et al., 2022). In a significant population, rice serves as the primary dietary staple, contributing to around two-thirds of the per capita daily caloric consumption. Achieving specific goals and maintaining economic growth depend on disease-free farming (Nayak & Raghatate, 2024). Plant leaf diseases are a significant contributor to the loss of output. Identifying the diseases in plants is a challenging task (Pushpa et al., 2021). The cultivation of rice plants is significantly impacted by various factors such as strong winds, drought, bad weather conditions, fungal infestations, bacterial infections, and viral infections (Bari et al., 2021). It is imperative to undertake measures aimed at mitigating crop losses resulting from plant diseases (Gladkov & Gladkova, 2021). Timely identification of plant diseases enables farmers to establish protective measures, leading to the cultivation of robust and fruitful food crops (Reddy et al., 2023).

The identification and prevention of illnesses can contribute to enhancing productivity (Patidar et al., 2020; Alborji, 2014). The agricultural sector has substantial difficulties in the area of plant disease diagnosis. Rice plant illnesses are attributed to microorganisms, with fungi being the specific pathogen responsible for the disease (Islam et al., 2021; Praveenraj et al., 2024) The development and spread of plant diseases are also caused by a wide variety of microorganisms. Professionals or farmers with specialized knowledge or training have traditionally been responsible for identifying plant diseases and evaluating crops (Li et al., 2021; Dhanya & Balakrishnan, 2024; Ahad et al., 2023; Adriani et al., 2023). The cost-effectiveness of this technology was compromised due to the requirement of continual monitoring, rendering it unsuitable for bigger fields. Due to the wide range and intricate nature of numerous plant diseases, even seasoned plant pathologists and agronomists struggle to precisely identify specific diseases (Nalini et al., 2021; Shi et al., 2024). It is important to acknowledge that monitoring agricultural areas can be challenging (Kathiresan et al., 2021).

It is more difficult to detect diseases in rice plants early on because plants are more susceptible to a variety of illnesses during their initial development stages (Saeed et al., 2021; Kumar & Yadav, 2024; Sowmyalakshmi et al., 2021). When it comes to disease classification, many machine-learning techniques have been used before. However, the current methodologies cannot reliably forecast diseases and are also characterized by a significant time investment (Assegid & Ketema, 2023). It is vitally important to have preventive measures in the early stages in order to mitigate the transmission of diseases. Early-stage treatment of the disease from the leaves prevents its spread to the stem and food crop, thereby safeguarding against harm (Rani & Singh, 2022; Chinnasamy, 2024). In recent times, deep learning technology has demonstrated various methodologies that aid in identifying early-stage diseases in rice plants. Nevertheless, the current models exhibit several limitations, including issues related to feature dimensionality, increased computing complexity, and diminished accuracy, among others. To tackle these issues, a deep learning-based method is proposed to improve rice plant disease detection (Moupojou et al., 2023).

Motivation: The reviewed studies cover a wide range of geographic areas at both regional and global scales. The geographic breakdown shows that the research has been conducted in various continents and countries mainly in the Asian sub-continent (Ganesan & Chinnappan, 2022; Rao & Menon, 2024; Fernández-Urrutia et al., 2023) Rice is a significant agricultural commodity that is widely cultivated throughout Asia. Farmers frequently encounter a multitude of challenges when it comes to farming paddy crops. The occurrence of agricultural damage can be because of multi-factors, including weather changes, illnesses, and pests (Dubey & Choubey, 2024). The current state of farmers' interest in paddy cultivation has undergone a decline. Manually identifying leaf disease often requires more time and incurs higher costs. Previous studies have presented a range of machine learning methodologies aimed at identifying plant leaf diseases. However, these processes exhibit lower accuracy, a high rate of mistakes, and require a significant amount of time. With the advent of deep learning approaches, early identification of disease and accurate classification is possible. Inspired by this, the present study offers an innovative deep-learning method aimed at classifying many forms of leaf diseases in rice plants. The contributions of the proposed work are given as,

- To propose a unique deep learning technique for the effective classification of rice plant leaf diseases.
- To separate the affected regions from the leaf image using slice-based residual U-Net.
- To use the Convolutional Attentional BiGRU (Catt_BiGRU) model for classification, while CNN pulls out features, and BiGRU organizes the diseases into groups.
- To evaluate and analyze the performance of the proposed technique based on the performance metrics.

Some of the existing studies that works in the plant disease detection field using varied schemes are discussed as follows,

Leaves of rice plants can be infected by a variety of diseases, including bacterial blight, tungro disease, brown spot, and blast (Das & Kapoor, 2024; Rumy et al., 2021). There are three main types of leaf images: those showing early blight, healthy leaves, and late blight diseases. Included in the dataset used for this investigation are 1,503 photos of potato leaves and 5,932 images of rice leaves. Finally, the performance of the developed model is compared with other machine learning methods such as SVM, K-NN, Random Forest, and decision tree. The simulation results prove the strength of the developed model in plant disease detection however the utilized CNN model demands more training data due to its inefficiency.

Lei & Ibrahim, (2024) presented a deep convolutional neural network method that eliminated noise in the collected images and binarized using a model called Otsu's thresholding during the pre-processing phase. Leaf smut, fungal brown spot, and bacterial blight are the three principal diseases that are the focus of this investigation. Here, the technique depends on completely connected CNN and is trained to utilize 4000 sample images for diseased leaves and 4000 healthy leaf samples for identifying 3 diseases. The experimental results have shown that the developed model attained superior performance as compared with various existing techniques employed for rice plant disease detection. But, the model faced vanishing gradient issues and hence it impacted the training process (Islam et al., 2021).

Daniya and Vigneswari (Wang et al., 2024) employed a hybrid optimization approach to classify plant diseases. In this context, the pre-processing stage involves the utilization of a region of interest extraction technique. Deep fuzzy clustering is employed to segment the regions that have been impacted (Yu et al., 2023). In this study, various characteristics are retrieved, including statistical features, CNN features, entropy, local gator XOR pattern (LGXP), and local optimum oriented pattern (LOOP). The Rider-Henry Gas Solubility Optimization (RHGSO) technique is used to train a deep neuro-fuzzy structure is the next step after the initial classification phase. Then, a deep residual structure is used for the second stage of classification. The simulation results prove that the developed model has obtained above 90% of classification performance in each metric. However, the complexity of the utilized model is enhanced and is not suitable for unseen or new data in this plant disease classification task (Latif et al., 2022).

Research by Karunanidhi et al. on Oryza sativa plant was centered around accurately identifying leaf diseases. In this study, deep learning models, specifically ResNet-152 and Enhanced Hybrid Neural Network (CoAtNet), were suggested (Sharma et al., 2022). The collection of both healthy and sick images is sourced from the Villupuram district, located in the state of Tamil Nadu. A total of 3071 images were gathered from farmers' fields that were exposed to suitable sunlight conditions. This study used a methodology that identified various diseases. The experimental analysis shows that this model has attained above 96% of accuracy rate but the performance may be limited while utilizing a large amount of data. Also, computational complexity is the major drawback of this model (Vasantha et al., 2021)

Jiang et al. employed a dense network as a benchmark model, incorporating the squeeze excitation and channel attention mechanism to enhance important properties while suppressing undesirable ones (Upadhyay & Kumar, 2022). Next, separable convolutions that are based on depth are introduced and replace specific convolutions in densenets to enhance parameter utilization. The utilization of the Adabound technique, in conjunction with adaptive optimization, results in a reduction in the time required for parameter change. Here, nine kinds of rice disease datasets are utilized, and the results are compared with existing classification techniques. The accuracy achieved is 97% with a reduced recognition speed of 3.71s. However, the presence of larger parameters leads to higher computational resources, which affect the model's stability (Jiang et al., 2023).

Problem Statement

The cultivation of rice plants has posed a significant difficulty for farmers worldwide. Bacterial blight, leaf spot, and brown spot are among the diseases that can infect rice plant leaves. Monitoring plant health has been the subject of several recent scientific developments. However, their ability to reliably classify damaged leaves is inefficient. Additionally, the current mechanisms exhibit a significant mistake rate. The effectiveness of machine learning procedures is somewhat lower when compared to deep learning processes. Therefore, it is imperative to develop a more effective system for the said purpose. Most of the studies use the dataset in Plant Village extensively, we have considered the dataset from (Daniya & Vigneshwari, 2023; Karunanithi et al., 2022)

The remaining part of the paper is organized as follows: The details of the proposed methodology is laid out in Section 2, Section 3 presents the results and discussion, Section 4 provides a detailed discussion of achieved performance and Section 5 contains the Conclusion and Future scope.

2 Proposed Methodology

It is a big challenge to diagnose rice plant infections at an early stage. Although many strategies have been suggested to solve this issue but, the current models exhibit several limitations, including issues related to feature dimensionality, increased computing complexity, and diminished accuracy, among others. To overcome these challenges, a novel deep learning approach has been proposed to enhance the identification of diseases in rice plants. As an initial step, it is important to De-noise the excessive noise in the raw input images. If not done this will negatively impact the performance of the system. The workflow of the proposed study is depicted in Figure 1.

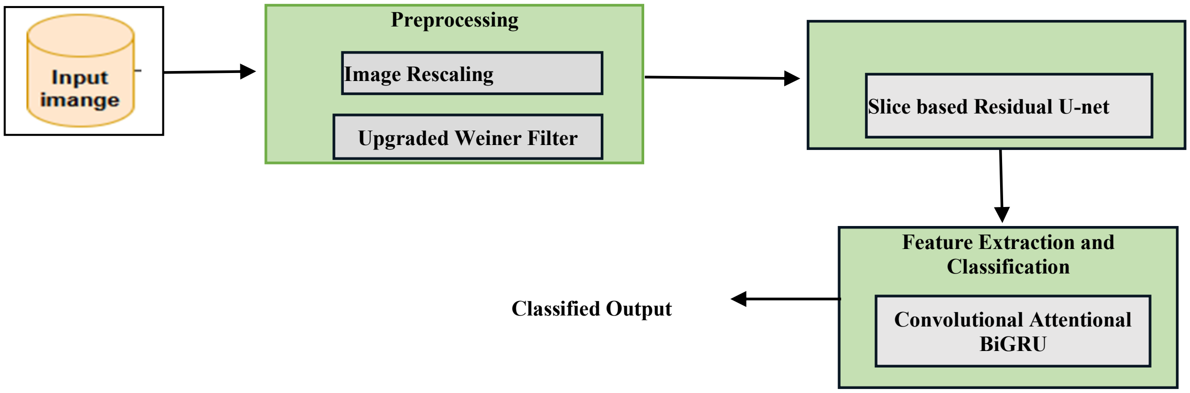


Figure 1: Workflow of the Proposed Study

The present study incorporates pre-processing techniques such as image rescaling and improved Wiener filtering (Up_WFT). The images are then segmented using a slice-based residual U-Net model (S_RU-Net). The output is then passed into a composite framework known as convolutional attentional BiGRU (CAtt_BiGRU). While BiGRU handles the classification problem, this framework makes use of a CNN to extract features. As a result, numerous diseases affecting the rice plant are appropriately classified.

2.1 Pre-Processing

The following are some of the preprocessing carried out on the images from the raw dataset.

2.1.1 Image Rescaling

This image-rescaling approach reduces the varying sizes of the input images to a uniform scale. The input images are downsized to a scale of 256x256. One notable benefit of this approach is the enhancement of storage capacity, resulting in a reduction in computational time.

2.1.2 Upgraded Wiener Filtering

Wiener filtering is used to De-Noise the images. For a particular pixel location (k_1, k_2), the enhanced wiener filter is given by equation (1)

$$EWF[Z(k_1,k_2)] = \mu + \frac{\sigma^2 - \sigma_k^2}{\sigma^2}(Z(k_1,k_2) - \mu) \quad (1)$$

Here, Z represents the input image, μ gives the mean, σ_k represents the variance of the noise, and variance σ^2 are locally determined from the set of $(M \times N)$ local neighbourhoods of every pixel in equation (2) & (3).

$$\mu = \frac{1}{NM} \sum_{k_1,k_2 \in A} Z(k_1,k_2) \quad (2)$$

$$\sigma^2 = \frac{1}{NM} \sum_{k_1,k_2 \in A} Z^2(k_1,k_2) - \mu^2 \quad (3)$$

Here, the d-index, which is the ratio of the mean's variance is used to measure the list of observed occurrences that are dispersed or clustered.

$$I = \frac{\sigma^2}{\mu} \quad (4)$$

$$EWF[Z(k_1,k_2)] = \mu + I - \sigma_m^2 (Z(k_1,k_2) - \mu) \quad (5)$$

A d-index is used to obtain estimates other than variance in order to enhance the performance. Equation (4) & (5) can be rewritten as follows,

$$EWF[(Z(k_1,k_2))] = \mu + (Z(k_1,k_2) - \mu) - \frac{\sigma^2}{I}(Z(k_1 k_2) - \mu) \quad (6)$$

$$= Z(k_1,k_2) - \frac{\sigma^2}{I}(Z(k_1 k_2) - \mu) \quad (7)$$

$$= Z(k_1,k_2) - \mu\left(\frac{\sigma_m^2}{\sigma^2}(Z(k_1,k_2) - \nu)\right) \quad (8)$$

If $\frac{\sigma_m^2}{\sigma^2}(Z(k_1,k_2))$ is multiplied by the mean, an approximation of noise is attained in equation (6)-(8). The input images are shown in Figure 2 (a)-(c) and the resultant pre-processed images are shown in Figure 3(a)-(c).

Input images

(a)Input image1 (b)Input image2 (c) Input image3

Figure 2 (a) -(c): Input Images from Dataset

Pre-Processed Images

(a) Pre-Processed Image 1 (b) Pre-Processed Image 2 (c) Pre-Processed Image 3

Figure 3 (a)-(c): Pre-Processed Output Images

2.2 Segmentation using Slice based Residual U-net Model (S_RU-Net)

The segmentation stage takes the pre-processed images and uses them to divide the disease-affected regions into smaller ones so that they may be more easily categorized. In the suggested approach, slice-based residual U-Net is used for segmentation. Figure 4 depicts the design of the slice-based residual U-Net model.

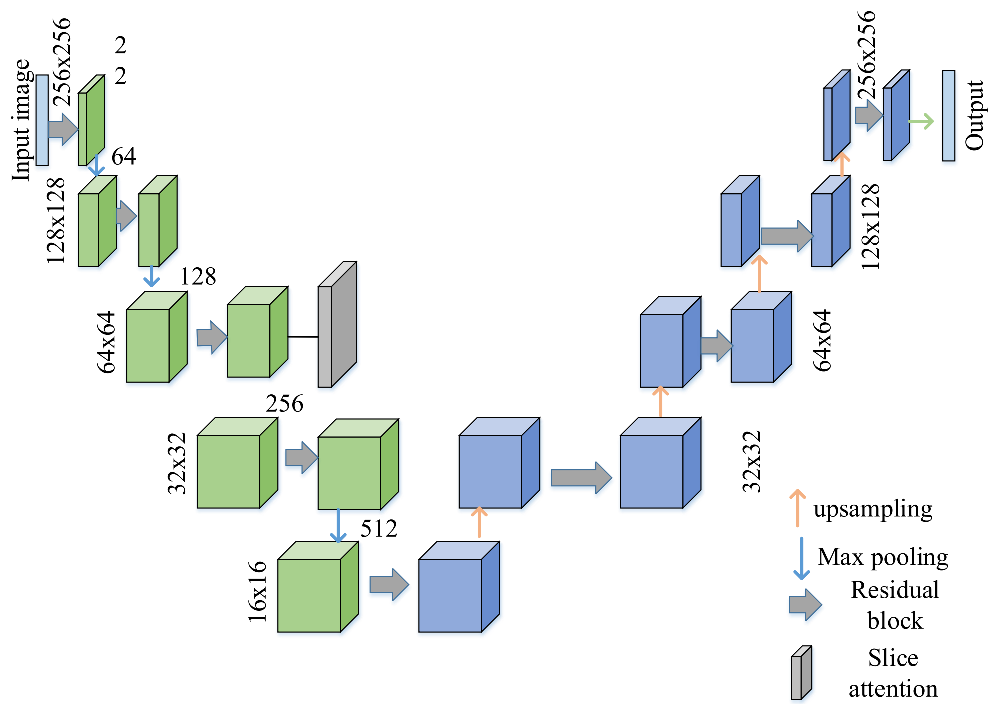


Figure 4: Structure of Slice based Residual U-Net Model

Here, instead of using the construction blocks of the U-net model, we use specific residual blocks along the encoding and decoding paths. The components of each residual block include convolution, batch normalization, and the ReLU activation function. Here, the top layer makes use of 16 feature maps, while the bottom layer makes use of 512 feature maps following a two-fold increase. Every convolution process employs a 3x3 filter size. ReLU is employed to introduce non-linearity into the model, whereas batch normalization serves the dual purpose of regularizing the model and reducing the internal co-variant shift. After the first ReLU activation function, a dropout operation with a rate of 0.5 is done to each residual block to mitigate over-fitting. Next, the output and input are merged (identity short-cut). Afterward, the spatial dimension is sampled downwards from one layer to the next using a 2x2 max-pooling with a stride of 2.

The convolution layer receives the input before the max-pooling procedure. Here, the input is passed through several convolutions with filter sizes comparable to the input filter size in the convolution layer. In the first two units, dilated convolution is performed using dilation rates of (1, 2, 3) due to a significant semantic gap between the encoder and decoder features. The faster dilation rates are followed by slower dilation rates of (3, 2, 1) for the gathering of local features after the accumulation of many in formation. For these latter two levels, the semantic gap between decoder and encoder traits shrinks. The decoding process of a pipeline involves combining the output of each convolution module with the relevant high-level feature.

Feature maps go through bilinear interpolation and upsampling throughout the decoding process. Both the slice attention unit and the residual units are shown in the input. In the last layer, a sigmoid activation operation and a convolution operation are performed to produce the final segmented lesion.

Residual Layers

Although using deeper networks results in better performance, training such a deep network is challenging. In particular, a shortage of training data makes it challenging to use deeper networks. Therefore, the network's depth can be increased, or a pre-trained network can be used in conjunction with fine-tuning. The vanishing gradient problem that arises when network depth is increased can be fixed by sending the data forward through several levels.

Residual blocks are employed as a substitute for basic U-Net units, avoiding the need for deeper networks. In the U-Net architecture, the remaining blocks help with feature propagation by integrating features through skip connections. The utilization of identity shortcut mapping is employed to propagate low fine information, hence improving network performance without entering into deeper layers. Each residual layer is represented as (equation (9) & (10)):

$$b_1 = k(a_i) + G(a, V_i) \quad (9)$$

$$a_{i+1} = g(b_i) \quad (10)$$

Here, a_i and a_{i+1} refers to the input as well as output of the i^{th} residual unit, $G(.)$ specifies the residual function, and $g(a_i)$ refers to an identity mapping function.

Slice Attention Gate Module

The collection consists of a substantial quantity of mass shapes and sizes. The mass is quite diminutive in comparison to the surrounding area. Therefore, deep networks produce subpar categorization outcomes. Hence, the residual U-Net architecture incorporates a slice attention Gate module, which is in Figure 4.

In the Figure 4, a_i denotes the feature map of i^{th} layer output and f_i indicates the signal vector of the gate, which determines the focus region of each pixel and is obtained from the coarser scale. By lowering the noise in unrelated property responses, the β_i coefficient provides distinct activations related to the target task. Finally, element-wise multiplication of β_i a_i and maps yields the attention gate's output in Equation (11).

$$G_{out} = \beta_i \times a_i \quad (11)$$

Multiplicative attention modules typically have faster calculation ability and use minimal memory. The suggested work utilizes the multiplicative attention module, which is provided by

$$\beta_i = \sigma_2\left(\delta^T\left(\sigma_1\left(\delta_a^T f_i + y_f\right)\right) + y_\delta\right) \quad (12)$$

Here, σ_1 refers to the ReLu function: $\sigma_1(l) = \max(0, l)$, σ_2 is written as the sigmoid function, $\sigma_2(l) = 1/(1+e^{-l})$ δ refers to the linear transformation that uses $1 \times 1 \times 1$ a dimensional convolutional operator. y_δ and y_f refers to biased terms (Equation (12)). Every weight of the attention gate module is randomly initialized based on the principle of back-propagation. The segmented images are displayed in Figure 5, demonstrating the efficient segmentation of illness-affected areas utilizing slice based residual U-net.

Figure 5: Output Segmented Images

2.3 Classification Using Convolutional Attentional BiGRU (CAtt_BiGRU)

The segmented images are subsequently utilized within the categorization framework. The extraction of significant features will be carried out by the CNN, while the classification task will be performed by the Bidirectional Gated Recurrent Unit. This research makes use of CNN's built-in convolution and pooling layers. The architecture of the proposed convolutional attentional BiGRU model is depicted in Figure 6.

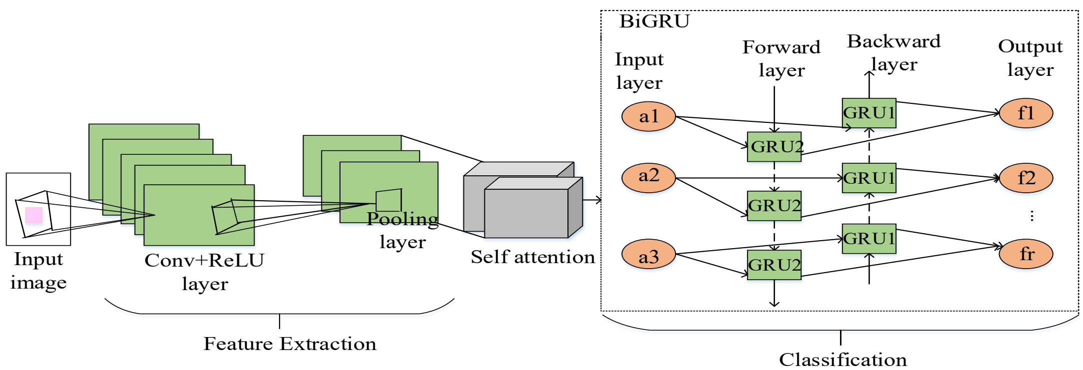


Figure 6: Architecture of Convolutional Attentional BiGRU Model

Convolution Layer

In a CNN, the convolution layer serves as the intermediary component. Images typically exhibit a state of immobility. This phenomenon indicates that the creation of a certain component of the image is analogous to that of any other part. Consequently, a characteristic acquired in one area will exhibit an identical pattern in another area. A small subset is extracted from a larger image and subsequently applied to each individual subset inside the larger image. When a point is traversed, it undergoes convolution to a singular position. A small portion of an image that moves over a larger image is known as a filter, sometimes known as a kernel. The configuration of the filters is contingent upon the chosen backpropagation mechanism.

Pooling Layer

The term “pooling layer” pertains to the process of downsampling an image. The function utilizes a limited portion of the convolution output as its input and applies subsampling techniques to generate a singular output. The Max pooling technique is used here. Pooling reduces the number of parameters that need to be computed while ensuring that the design remains unaffected by changes in size, shape, and scale.

BiGRU

The reset gate determines how the incoming input data is integrated with the previous memory, as shown in the following equation (13), and the Gated Recurrent Unit (GRU) gets to the gate state using the prior hidden state f_{r-1} and the current input a_r.

$$t_r = \sigma(v_t \bullet [f_{r-1}, a_r]) \quad (13)$$

Equation (14) represents the update gate, which finds the amount of existing memory saved to the current time step.

$$h_r - \sigma(v_h \bullet \lfloor f_{(r-1)}, a_r \rfloor) \quad (14)$$

In this case, σ stands for the sigmoid function, which transforms the data into 0–1 values that can be used as gating signals to regulate the data flow in all directions. v_t and v_h refers to the weights for the reset gate as well as the update gate correspondingly. Equation (15) shows that after receiving the gated signal, the current inputs a_r are combined and triggered using the tanh function to achieve the movement of the hidden state $f_r^{'}$ at the time r.

$$f_r^{'} = \tanh(v \bullet [t_r \otimes f_{r-1}, a_r]) \quad (15)$$

The size $v \bullet [t_r \otimes f_{r-1}, a_r]$ identifies the degree of integration present in input a_r and the information history. An improved $v \bullet [t_r \otimes f_{r-1}, a_r]$ rating indicates a greater desire to retain information and a higher level of integration.

The present hidden state is expressed in the following equation (16)

$$f_r = (1 - h_r) g_{r-1} + h_r \otimes f_r^{'} \quad (16)$$

The size of h_r is positively associated with the data that has to be recollected in intervals [0, 1], $(1 - h_r) f_{r-1}$ represents the forgetting hidden state of the previous moment, $h_r \otimes f_{'r}$ indicates the selective memory for the hidden state, f_r represents forgotten previous information present in f_{r-1} and the present new information is added in $f_r^{'}$.

Two sets of GRU make up BiGRU; one set uses forward unset features and the other uses backward unset features. This makes use of contextual global features for the neural network.

Self-Attention

The self-attention blocks are utilized within the residual blocks, which perform both feature transformation and feature aggregation. In this case, two processing streams get the feature tensor as input, which stands for channel dimensionality D. The left stream computes the attention weights β by calculating the δ (through mappings ϕ and γ) and a consequent mapping ς. The input characteristics are transformed, and the processing dimensionality is decreased by applying a linear transformation α to the right stream. A Hadamard product is used to combine the two streams' outputs. A final linear layer is used to process the integrated features, increasing the dimensionality to C. After that, they are subjected to element-wise non-linearity and normalization. Therefore, self-attention primarily concentrates on the pertinent elements that contribute to enhancing accuracy. As a result, the leaf disease of rice plants is being appropriately classified using the suggested framework. Figure 7 shows the images that have been classified by the proposed CAtt_BiGRU model.

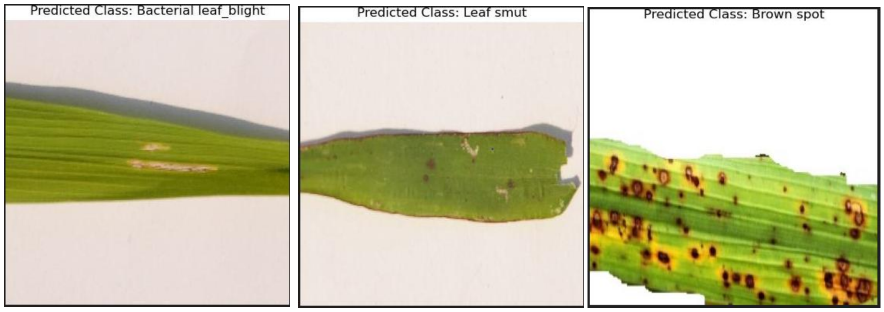


Figure 7: Classified Images

Figure 7 illustrates the classified images. Image 1 is classified as Bacterial Blight disease, image 2 is classified as leaf smut disease, and image 3 is classified as Brown spot disease. Thus, the input images are effectively classified using the proposed CAtt_BiGRU model.

3 Results and Discussion

The Rice Leaf Disease Dataset (https://www.kaggle.com/bahribahri/riceleaf) is utilized for analysing the proposed model in classification task. The utilized dataset is gathered from kaggle repository which involves four directories. Four categories of rice leaves like healthy, brown spot, bacterial leaf blight, and leaf smut are present in the data set. Each classes includes 4000 number of files and hence the total of 16,000 files are presented. In this dataset, the rice leaf images are presented in JPG file format with different sizes. For simulation, the above dataset is split into 70:30 for training and testing purpose. The proposed study collects the dataset images and performs pre-processing, segmentation and classification process. This model's performance is evaluated using different measures that are outlined. Also, the results are compared with four existing techniques, namely BiGRU, DenseNet, CNN, and ResNet.

Accuracy: The concept of accuracy refers to the degree of proximity between the observed value and the reference value. It is expressed in the following equation (17)

$$Accuracy = \frac{tp + tn}{tp + tn + fp + fn} \quad (17)$$

tn denotes the True Negative, fp represents the False Positive, tp denotes the True Positive, and fn specifies the False Negative.

Precision: is typically defined as the ratio of true positives to the sum of true positives and false positives. It is represented mathematically in Equation (18).

$$Precision = \frac{tp}{tp + fp} \quad (18)$$

Recall: also known as sensitivity or true positive rate, is the ratio of correctly identified positive results to the total number of true positives and false negatives. The equation (19) contains the following information.

$$Recall = \frac{tp}{tp + fn} \quad (19)$$

F1 score: A statistical indicator of accuracy that is unaffected by negative numbers is the F1 Score (equation (20)).

$$F - score = 2\frac{\text{Re}\,call \times \text{Pr}\,ecision}{\text{Re}\,call + \text{Pr}\,ecision} \quad (20)$$

Mean Square Error (MSE): A statistical tool called the MSE is used to calculate the difference amongst the projected and actual values. If there are no errors, the MSE will be zero. It is expressed mathematically as in equation (21).

$$\text{MSE} = \frac{1}{p}\sum_{i=1}^{p}\left(P_i - \hat{P}_i\right)^2 \quad (21)$$

Here, Pi, denotes the observed values, $\hat{P}_i$ denotes the predicted values, and p denotes the total number of observations.

Root Mean Square Error (RMSE): RMSE stands for the square root of the mean squared difference between the values that were predicted and those that were measured in Equation (22).

$$\text{RMSE} = \sqrt{\frac{1}{p}\sum_{i=1}^{p}\left(P_i - \hat{P}_i\right)^2} \quad (22)$$

Mean Absolute Error (MAE): The average of all the absolute mistakes is called the mean absolute error. In math terms, it can be written as the following equation (23).

$$\text{MAE} = \sum_{i=1}^{p}\left|P_i - \hat{P}_i\right| \quad (23)$$

3.1 Performance Comparison Analysis

To show that the suggested technique works, the results it gets are compared to those of other methods already in usage.

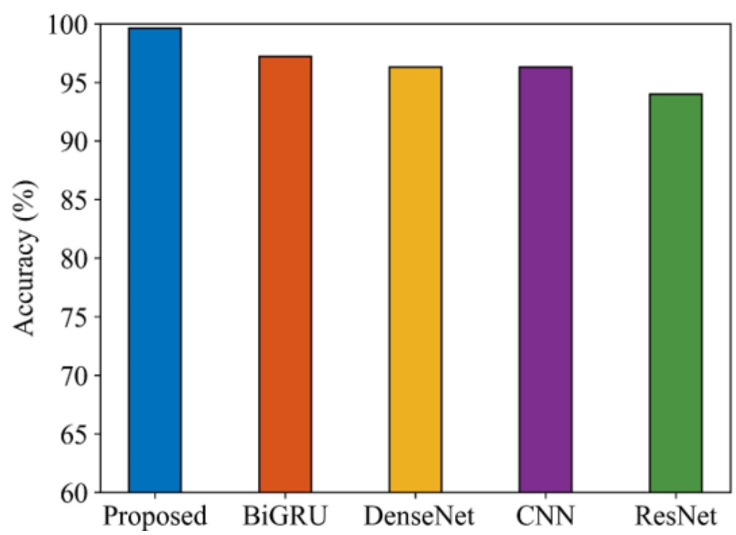


Figure 8: Accuracy Comparison Analysis

Figure 8 shows the accuracy comparison analysis of proposed and existing methods. It has been seen that the suggested method works 99.64% of the time, which is better than the current methods. The existing approaches, such as BiGRU, DenseNet, CNN, and ResNet, achieve accuracy of 97.22%, 96.30%, 96.30%, and 93.98% respectively.

Figure 9 depicts the precision comparison analysis of proposed and existing methods. The suggested method outperforms the other methods with an accuracy of 99.39%. The other methods reach a degree of accuracy of 90.83%, 94.56%, 94.49%, and 94.95%. This proves that the suggested method outperforms the current standards for disease categorization in rice leaves.

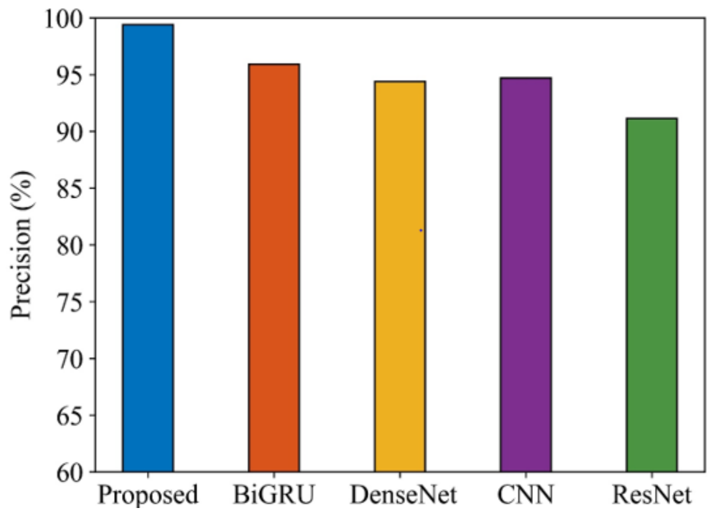


Figure 9: Precision Comparison Analysis

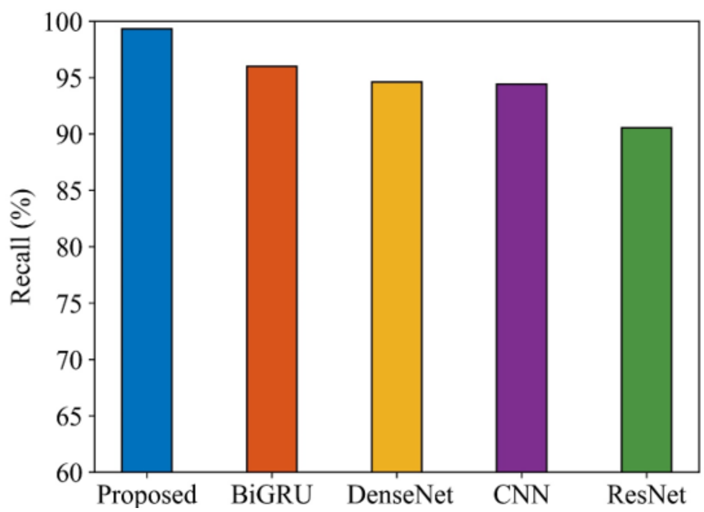


Figure 10: Recall Comparison Analysis

The recall comparison analysis is shown in Figure 10. A recall of 99.31% is attained by the suggested method. However, the existing approaches achieve a recall of 95.99%, 94.6%, 94.42%, and 90.54%, respectively. Thus, the proposed technique effectively classifies the types of rice leaf diseases. However, the existing approaches fail to achieve better efficiency.

Figure 11 indicates the F1-score performance analysis of both proposed and existing methods. Outperforming the current methods, the suggested method attains an F1 Score of 99.25%. It is clear from the graph that the existing approaches achieve an F1 Score of 95.95%, 94.49%, 94.56%, and 90.83%, respectively. Hence the attention mechanism employed in the proposed approach focuses on the most significant features for classification.

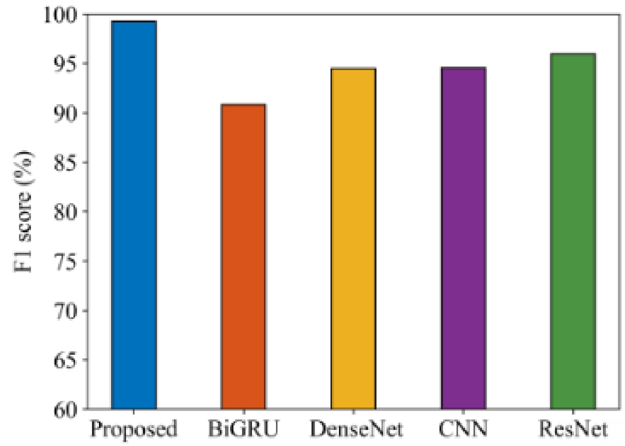


Figure 11: F1 Score Comparison Analysis

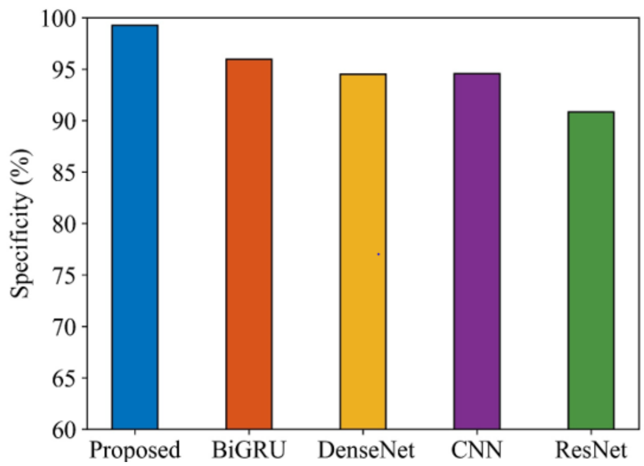


Figure 12: Specificity Comparison Analysis

Figure 12 represents the specificity comparison of proposed with other existing techniques. The proposed technique achieves a specificity of 99.67%. However, the existing mechanisms achieve a specificity of 97.88%, 97.21%, 97.15%, and 95.37%, respectively. This demonstrates the efficacy of the suggested method for classification tasks.

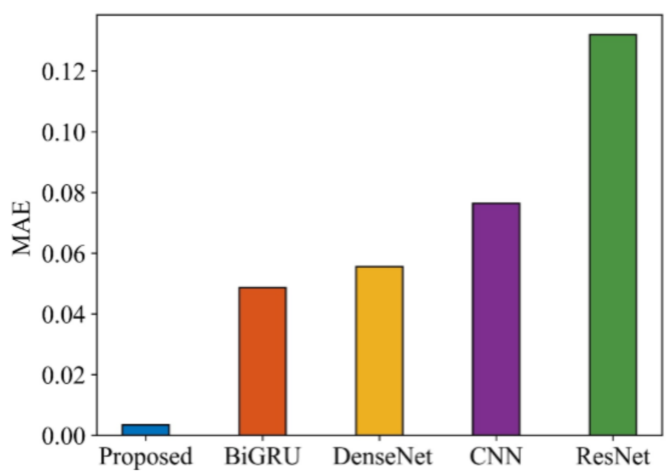


Figure 13: MAE Comparison Analysis

Figure 13 compares the MAE of proposed with other existing methods. The proposed technique shows a very low MAE, which is 0.0034, lower than the existing approaches. The existing approaches incur an MAE of 0.0486, 0.0555, 0.0763, and 0.1319.

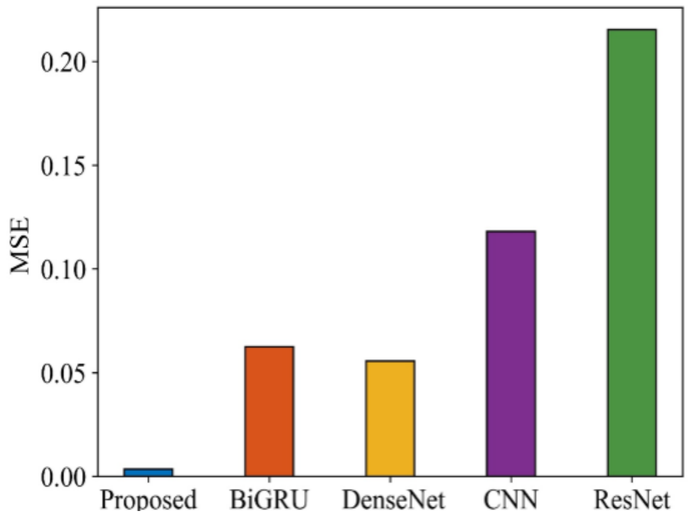


Figure 14: MSE Comparison Analysis

Figure 14 displays the mean squared error (MSE) comparison between the proposed and existing methods. The suggested method outperforms the current mechanisms in terms of both MAE and MSE, both of which are extremely low. The existing systems have an MSE of 0.0625, 0.0555, 0.1180, and 0.2152, respectively.

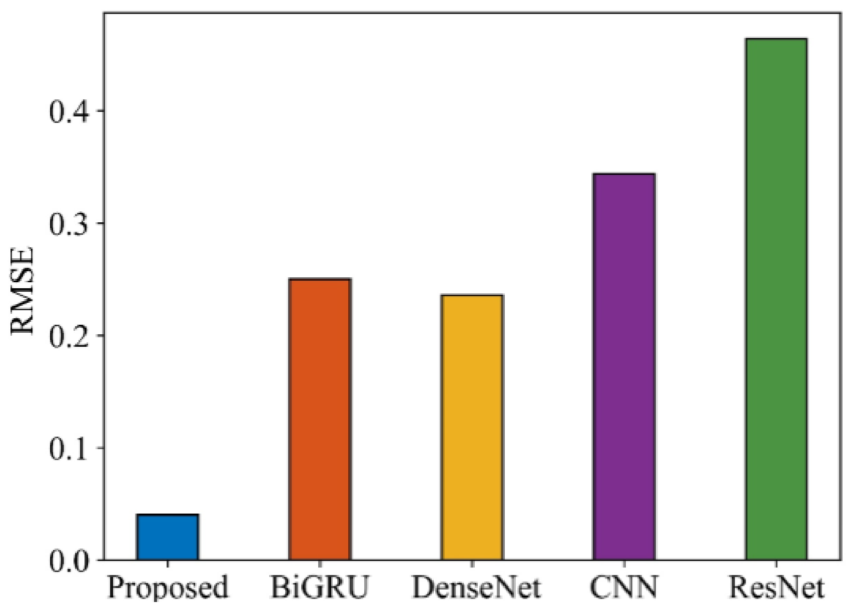
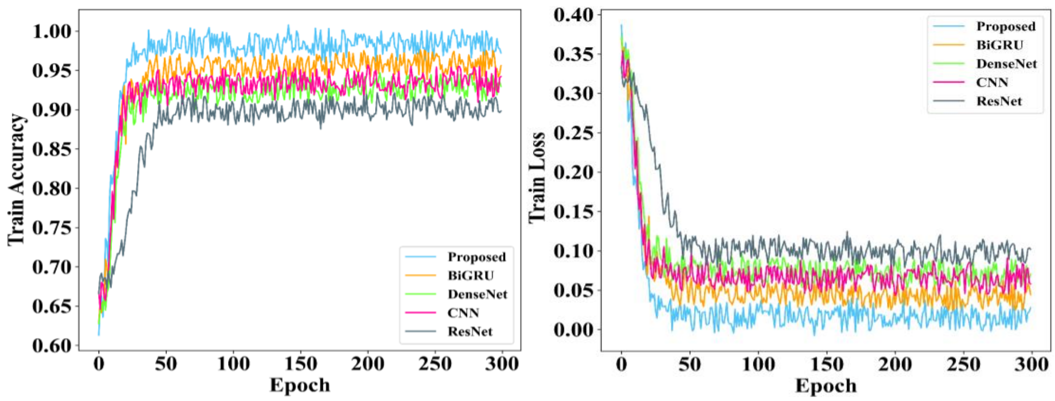


Figure 15: RMSE Comparison Analysis

Figure 15 shows the RMSE of proposed method in comparison with other existing methods. It is observed that the RMSE of the proposed technique is 0.0403. The other existing systems achieve an RMSE of 0.25, 0.2357, 0.3435, and 0.4639. All the above measures indicate that the suggested method clearly performs better. Table 1 shows the performance metrics comparison.

Table 1: Performance Metrics Comparison

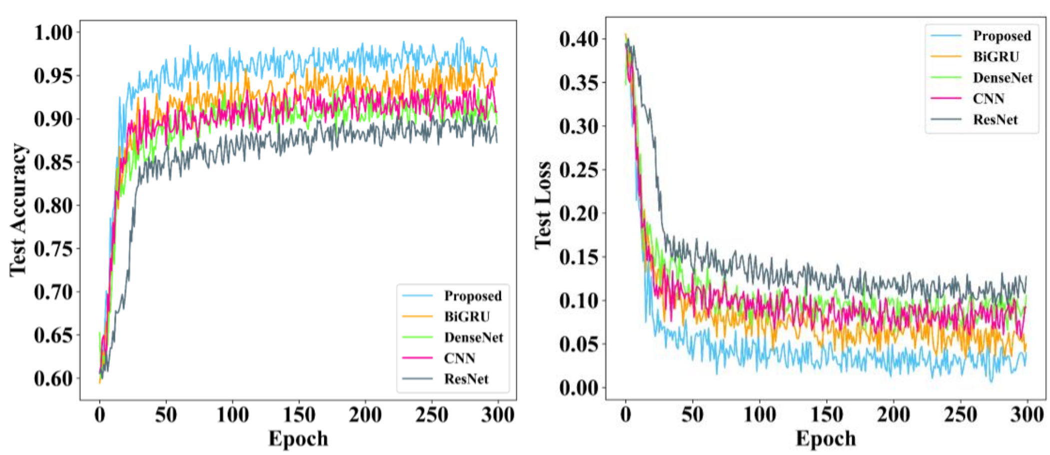
Performance Metrics	Techniques				
	Proposed	**BiGRU**	**DenseNet**	**CNN**	**ResNet**
Accuracy	0.9964	0.9722	0.963	0.963	0.9398
Recall	0.9931	0.9599	0.946	0.9442	0.9054
Precision	0.9939	0.9591	0.9438	0.9469	0.9113
F1_score	0.9925	0.9595	0.9449	0.9456	0.9083
RMSE	0.0403	0.25	0.2357	0.3435	0.4639
MAE	0.0034	0.0486	0.0555	0.0763	0.1319
Specificity	0.9967	0.9788	0.9721	0.9715	0.9537
MSE	0.0034	0.0625	0.0555	0.1180	0.2152



(a) (b)

Figure 16 (a)-(b): Analysis of Training Accuracy and Loss

Figure 16 (a) shows the training accuracy curves, and here, the training accuracy increases with an increase in epoch values and attains a peak at the 50th epoch. The training accuracy will then remain a constant throughout the training period. Figure 16(b) shows the training loss curves of proposed and existing methods. The training loss decreases with an increase in epoch, and at the 50th epoch, the loss reaches a minimum and, after that, remains constant throughout the entire training period.



(a) (b)

Figure 17 (a) - (b): Analysis of Testing Accuracy and Loss

Figure 17 (a) shows the testing accuracy curves, and here, the testing accuracy increases with an increase in epoch values and reaches a peak at the 50th epoch. After that, the testing accuracy attains a constant value. Figure 17(b) shows the testing loss curves of proposed and existing methods. The testing loss declines with the rise in the epoch, once the loss reaches a minimum, it continues to remains constant throughout the entire testing period.

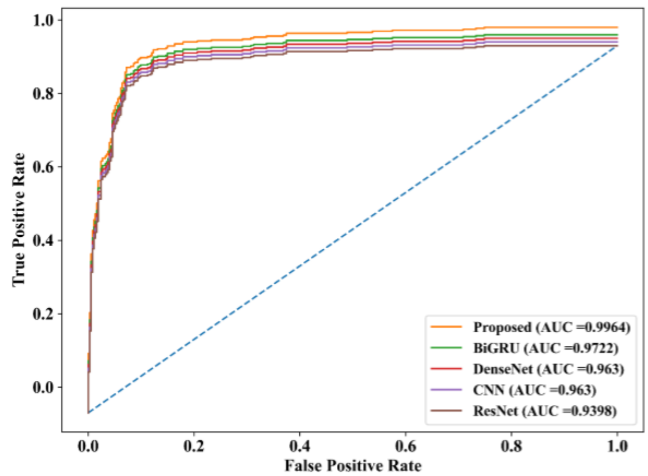


Figure 18: RoC Curve Comparison

Figure 18 illustrates the ROC curve comparison of proposed and existing methods. The RoC of the suggested method is getting close to one, as seen in the graph confirming the outperformance of the proposed method.

4 Discussion

The proposed rice plant disease classification system named as CAtt_BiGRU model was compared with existing models based on various performance metrics as briefed in the previous section. The existing models considered for comparison have taken images of the plant leaves to find the type of disease. From table 2 it is clear that the proposed deep learning methods achieves better performance. The proposed method processes a huge set of images without any manual feature extraction process. The common challenge faced by existing methods is handling large datasets. Due to human intervention, most models have difficulty extracting the relevant features; however, the suggested approach extracted it automatically. The proposed model outperformed the existing methods because of noise removal by an upgraded wiener filtering process, followed by segmentation and classification. Also, the proposed CAtt_BiGRU model incorporates the benefits of both CNN and BiGRU networks. By adopting convolutional layers, the proposed model can captures essential features information like edges, textures and shapes. Such features are highly beneficial for categorizing the diseased and non-diseased images. Also, the utilization of BiGRU blocks performs temporal and sequential learning process which assist to improve the classification performance. On the other hand, the incorporation of attention mechanism in the proposed model allows to focus on the most essential regions of the given images and allocates weights to make precise outcomes.

Thus, the great efficacy of proposed model aids to gain improved classification performance as compared with existing methods. The attained superior results clearly shows that the proposed model have addressed all the issues faced by the existing studies.

This proposed model requires reduced computational resources and provides the diagnosed results within 2.68s. Thus, it justifies the strength of proposed rice disease detection model.

Table 2: Comparison of the Results

Author	Method	Dataset	Parameters measured
Sharma et al., (2022)	CNN	RICE dataset	Accuracy-99.58%, Precision-99.63%, Recall-99.6%, F-score-99.69%
Upadhyay & Kumar, (2022)	Deep CNN	Rice leaf dataset	Accuracy-99.7%
Daniya & Vigneshwari, (2023)	Optimization Enabled Deep Learning method	Combination of Rice plant dataset and Rice disease dataset	Accuracy-93%, recall-94.59%, specificity-83.83%, f-score-91.42%
Karunanithi, et al. (2022)	CoAtNet	Rice disease dataset	Accuracy-96.56%
Jiang et al., (2023)	Dense Net	Rice disease dataset	Accuracy-99.4%
Proposed method	Slice Residual U-Net based Rice Plant Disease Classification Using Convolutional Attentional BiGRU	Rice leaf disease dataset	Accuracy- 99.64%, precision-99.39%, Recall- 99.31%, F1 score- 99.25%, Specificity-99.67%, MAE-0.0034, MSE-0.004 and RMSE- 0.0403

5 Conclusion and Future Scope

A novel deep learning-based classification network called Convolutional Attentional BiGRU is proposed. which effectively classifies the diseases in rice plants. The input images are pre-processed using image rescaling and upgraded wiener filtering, and the classification accuracy is improved. The disease affected portions are effectively segmented using slice based residual U-Net model to ensure misprediction is avoided. The segmented regions are fed to the classification framework. Using the convolutional neural network, important features are extracted, and thus, feature dimensionality issues are solved. Finally, using the Bidirectional Gated Recurrent Unit, the types of rice leaf disease are efficiently classified. The proposed model's performance is contrasted with that of four currently used methods: CNN, BiGRU, DenseNet, and ResNet. With the suggested method, the following results are obtained: 99.64% accuracy, 99.39% precision, 99.31% recall, 99.25% F1 score, 99.67% specificity, 0.0034 MAE, 0.004 MSE, and 0.0403 RMSE. However, the proposed study has evaluated the results by using only one dataset. This can be considered in the future by utilizing different dataset to further prove the strength of developed model. The proposed study can be expanded in the future by employing meta-heuristic optimization techniques to optimize the model's hyper-parameters. Also, the proposed work failed to implement the proposed model in real-world scenarios and so that it will be addressed in the future by analysing the model’s efficiency using real-time samples.

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E-search Involving Human and /or Animals – Not Applicable

Informed Consent – Not Applicable

Note: On behalf of all authors, the corresponding author states that there is no conflict of interest.

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