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A Multi-ViTs-Based Approach for Automatic Rice Leaf Disease Classification

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Abstract

Rice, an important food crop, is often faced with widespread and highly contagious diseases that have posed significant threats to agricultural development. However, traditional rice disease identification methods, which rely on the subjective visual examination of experts, hinder timely disease prevention. The advancements in computer vision and deep learning techniques have been key in improving crop disease diagnosis and recognition. This paper suggests a new approach for classifying rice leaf diseases, first via enhancing the input rice plant image through the conversion and extraction techniques. Secondly, by employing the multiple Vision Transformers (ViTs) method, which adopts and dedicates one ViT per type of disease, thereby improving the accuracy and robustness of the disease's classification in rice plants. The implementation and evaluation of the proposed methodology on 5932 rice plant images demonstrate superior performance in identifying four common kinds of rice leaf diseases, namely bacterial blight, blast, brown spot, and tungro. The precision, recall, and F1-score are significantly improved to become 98%, 98.25%, and 98.125%, respectively. The findings of this work enrich the domain of agricultural technology by introducing an innovative approach to enhance disease management in rice cultivation, which aims to foster robust crop yields to mitigate losses associated with plant diseases.

Keywords: Rice leaf diseases, deep learning, vision transformers, decision fusion.

نهج قائم على محولات الرؤية المتعددة للكشف التلقائي عن أمراض أوراق الأرز

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الخلاصة

غالبًا ما يواجه الأرز، وهو محصول غذائي مهم، أمراضًا واسعة الانتشار ومعدية للغاية تشكل تهديدات كبيرة للتنمية الزراعية. ومع ذلك، فإن الطرق التقليدية لتحديد مرض الأرز، والتي تعتمد على الفحص البصري الشخصي للخبراء، تعيق الوقاية من المرض في الوقت المناسب. لقد كان التقدم في رؤية الحاسوب وتقنيات التعلم العميق أمرًا أساسيًا في تحسين تشخيص أمراض المحاصيل والتعرف عليها. تقترح هذه المقالة نهجًا جديدًا لتصنيف أمراض أوراق الأرز من خلال تحسين صورة نبات الأرز المدخلات واستعمال محولات الرؤية

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المتعددة .(ViTs) يعتمد نظام ViTs المتعدد المقترح على ViT واحد لكل نوع من الأمراض وبالتالي تحسين دقة وقوة اكتشاف الأمراض في نباتات الأرز. يُظهر تنفيذ وتقييم المنهجية المقترحة على 5932 صورة لمصنع الأرز أداءً فائقًا في تحديد أربعة أنواع شائعة من أمراض أوراق الأرز وهي اللفحة البكتيرية والانفجار والبقعة البنية والتونغرو. تم تحسين الدقة والاستدعاء وكذلك درجة F1 بشكل ملحوظ لتصبح 98% و98.25% و98.125% على التوالي. تعمل نتائج هذا العمل على إثراء مجال التقنية الزراعية من خلال تقديم نهج مبتكر لتعزيز إدارة الأمراض في زراعة الأرز ويهدف إلى تعزيز غلات المحاصيل القوية للتخفيف من الخسائر المرتبطة بالأمراض النباتية.

1. Introduction

There is always a threat of wide-spreading and contagious diseases, which is common in rice farming. This problem has been a major stumbling block to developing agricultural practices [1]. Detecting the presence of diseases in rice plants at an early stage is very important for maintaining high quality and yield. Deformation, decay, and leaf discoloration are among the physiological and morphological variations that indicate disease presence [2]. However, the conventional way of diagnosing rice diseases using visual inspection by experts is one of the barriers to timely control of these diseases. It is necessary to develop new methods for accurately diagnosing and categorizing rice diseases in order to improve yields and protect against pests and pathogens.

In smart agriculture and computer vision, artificial intelligence (AI) is greatly significant for plant disease identification and pathology [3]. Therefore, the main focus is on creating machine and deep learning architectures that can deal with various challenges in this area. For instance, supervised learning methods are commonly employed in crop detection, yield forecasting, and disease diagnosis [4]. By using different images of rice plants to generate any relevant patterns connected with diseases, classical machine learning algorithms can be trained. However, these models usually rely on the quality and representativeness of manually designed features. With deep learning and particularly the Convolutional Neural Networks (CNNs), disease detection was revolutionized automatically by learning hierarchical features from raw data [5]. Furthermore, deep learning techniques possess the ability to identify features that conventional machine learning methods might overlook. The utilization of deep learning models that acquire hierarchical features has substantially enhanced the accuracy of rice disease diagnosis [6].

In recent times, the domain of computer vision has observed the emergence of a noteworthy innovation referred to as the Vision Transformer (ViT). Based on the success of transformers in natural language processing, ViT uses similar architecture, but this time for visual data. It allows to capture global dependencies found in images, thereby making it appropriate for disease detection on rice plants. ViT performs exceptionally well in understanding long-range dependencies alongside contextual information from pictures, enabling it to identify latent patterns showing different ailments [7]. The key contributions of this work can be outlined as follows:

- Introducing a method with Multi-Vision Transformers (Multi-ViTs) designed for the automated identification of four different diseases affecting rice leaves.
- Enhancing the input images via a sequence of preprocessing techniques.

The rest of this paper is presented as follows: Section 2 offers a brief review of the related work. Section 3 outlines the methodology. Section 4 provides the performance evaluation and results. Section 5 elucidates the principal conclusions of this study.

2. Related works

Given the multitude of structures for machine learning algorithms, Ahmed et al. [8] compared four various models, including K-Nearest Neighbor (KNN), J48, Naive Bayes, and logistic regression, to detect three rice leaf disease types. The decision tree exhibited the highest accuracy of 97% on the tested data. Islam et al. [9] utilized the decomposition of the rice image into sub-bands up to 2 levels, performed using a discrete wavelet transform (DWT). Then the features were extracted from these sub-bands, and the classification was carried out to implement the ensemble of linear classifiers with the adoption of the random subspace technique that achieved a classification accuracy rating of 95%. Shrivastava et al. [10] used Support Vector Machine (SVM) to classify the rice leaf diseases into four classes using AlexNet as a feature extractor, and it had a 91.37% accuracy rate. Additionally, SVM was also employed in [11] based on different color spaces of a rice plant image for better performance that obtained 94.65% accuracy. Meanwhile, Saha et al. [12] used textural and statistical features fed into the random frost predictor to identify the prevalent occurrences of rice leaf disease categories, achieving an accuracy of 92.77%.

Deep learning techniques such as the CNNs prove their superiority compared to traditional machine learning approaches. Consequently, Ghosal et al. [13] utilized the well-known VGG-16 pretrained network and fine-tuned it to get a performance accuracy of 92.46%. Furthermore, Temniranrat et al. [14] developed a system called LINE Bot for identifying five types of rice diseases. Their proposed method utilized images taken from paddy fields and incorporated deep learning techniques, including You Only Look Once (YOLOv3), achieving a true positive rate of 95.6%. The development of a lightweight CNN architecture for automated detection of rice leaf smut and rice leaf blight is proposed in [15], and to address the issue of data scarcity, a practical variance modeling mechanism and a custom filter development mechanism were employed, assisted through a reference protocol for filter suppression, and reached an F1-score of 94%. Similarly, Narmadha et al. [16] extracted the features of the rice plant images from three rice disease classes using a pre-trained DenseNet. Subsequently, these features were fed into a Multilayer Perceptron (MLP) classifier, resulting in an achieved F1-score of 96.43%.

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Bhuyan et al. [17] performed a stacked parallel CNN that incorporates squeeze and excitation (SE) component SE_SPnet to predict the disease of rice leaf in an efficient way that achieved 98.5% as an F1-score. In the same context, Wang et al. [18] leveraged the MobileNet architecture and tuned it based on a Bayesian optimization approach, which achieved an accuracy of 94.65% in classifying four rice leaf diseases. Furthermore, Patil et al. [19] collected 3200 samples from various rice health categories using sensors and a camera.

The MLP was used to extract the numerical features from the sensor-collected data. Subsequently, visual features were extracted from the captured rice images. These features were fused through a concatenation layer followed by a dense layer, yielding an F1-score of 95.5% as a singular output for diagnosing various rice diseases. Zeng et al. [20] introduced the Candy algorithm as an image enhancement technique and presented a neural network using the Inception-V4 backbone and a coordinate attention mechanism to improve feature capture, resulting in an average rice disease classification accuracy of 95.57%.

As deep learning has progressed, researchers have increasingly turned to ViT as a pivotal model in various applications due to its unique architecture that leverages self-attention. Borhan et al. [21] found that while attention blocks improve prediction accuracy, they also slow it down. Therefore, they suggested a combination of CNN and ViT for rice disease detection that reached an average F1-score of 97%. In the same context, Patilet et al. [22] developed a rice transformer that integrates inputs from farm sensors and field images, then extracts the features using an attention mechanism. These features were then processed through a cross-attention module to enhance the detection of rice disease, attaining an accuracy of 97.38%.

3. Materials and methodology

In this section, the details concerning the dataset and the proposed methodology are expounded upon through the utilization of appropriate subheadings.

3.1 Dataset

To implement Vision Transformer (ViT) models for the detection of rice leaf diseases, this study utilized the Rice Leaf Disease Image Samples dataset available on Mendeley [23], consisting of 5932 images depicting various rice leaf diseases such as bacterial blight, blast, brown spot, and tungro, as detailed in Table 1. Each affected rice leaf manifests distinct disease symptoms and characteristics, delineated as follows: Bacterial Blight: It is caused by Xanthomonas oryzae; this affliction manifests through lesions initiating at the leaf tip and extending several inches towards the leaf base. It stands as a formidable threat, causing substantial losses in rice production [24, 25].

- Blast: It is caused by Magnaporthe oryzae; this fungal disease manifests with initial symptoms of elliptical or spindle-shaped white to grey-green spots, featuring dark red to brownish borders. Some spots may exhibit a diamond shape with broad centers and pointed ends [26].
- Brown Spot: A fungal infection causes this disease, resulting in sizable spots on leaves that can lead to leaf death. In the early stages, small dark brown to purple lesions appear, developing into circular to oval shapes with a light brown to gray center, surrounded by a reddish-brown margin due to fungal toxin production [27].
- Tungro: is a viral infection in rice plants transmitted by the green leafhopper. It causes stunting, yellowing of leaves, and reduces grain yield [28].

Table 1: The four rice leaf diseases described in the utilized dataset

Disease Class	Bacterial Blight	Blast	Brown Spot	Tungro
# Images	1584	1440	1600	1308
Sample				

3.2 Vision Transformer (ViT)

The Vision Transformer (ViT) is a neural network architecture that was originally designed for natural language processing (NLP) [29]. It has demonstrated efficient results in diverse applications in the computer vision area involving plant disease classification. The ViT consists of self-attention blocks and MLP networks. It also includes a linear projection and positional embedding mechanism to process the input images. Fig. 1 illustrates the structure of a ViT. The input image is partitioned into nonoverlapping patches of a fixed size. Then, the patches are flattened, and a linear projection is utilized to perform positional embedding. The primary goal of positional embedding is to preserve the spatial information of patches in the original image. The resulting vector is subsequently transmitted to the transformer block. A standard transformer block has two fundamental elements: multi-head self-attention (MHA) and a MLP. Each component is prefaced by a normalization layer and concludes with a residual connection. Self-attention within MHA is individually applied to each patch [29] [30]. In MHA, the input vector undergoes a transformation into three distinct vectors: Q, K, and V, referring to query, key, and value, respectively. The computations are expressed as Q = XWQ, K = XWK, and V = X WV, where WQ, WK, and WV denote the respective weight matrices. A score matrix is generated by taking the dot product of Q and K, reflecting the saliency of the embedded patch. Subsequently, the activation function known as SoftMax is employed on the score matrix. This output is then multiplied with V to produce the self-attention result, as depicted in Equation 1, where dk signifies the dimension of the vector K. By leveraging the power of self-attention mechanisms, the ViT model can capture meaningful relationships between different patches of an image and make accurate predictions [30].

$$Self\_Attention(Q,K,V) = SoftMax\frac{QK^T}{\sqrt{d_k}} \times V \tag{1}$$

Then the computation of the MHA block output is determined as:

$$MHAout = (MHA(norm(x_{in})) + x_{in} \tag{2}$$

The transformer block subsequently incorporates the MLP after the MHA layer. The output of the transformer block can be calculated as follows:

$$ViTout = MLP(norm(MHAout)) + MHAout \tag{3}$$

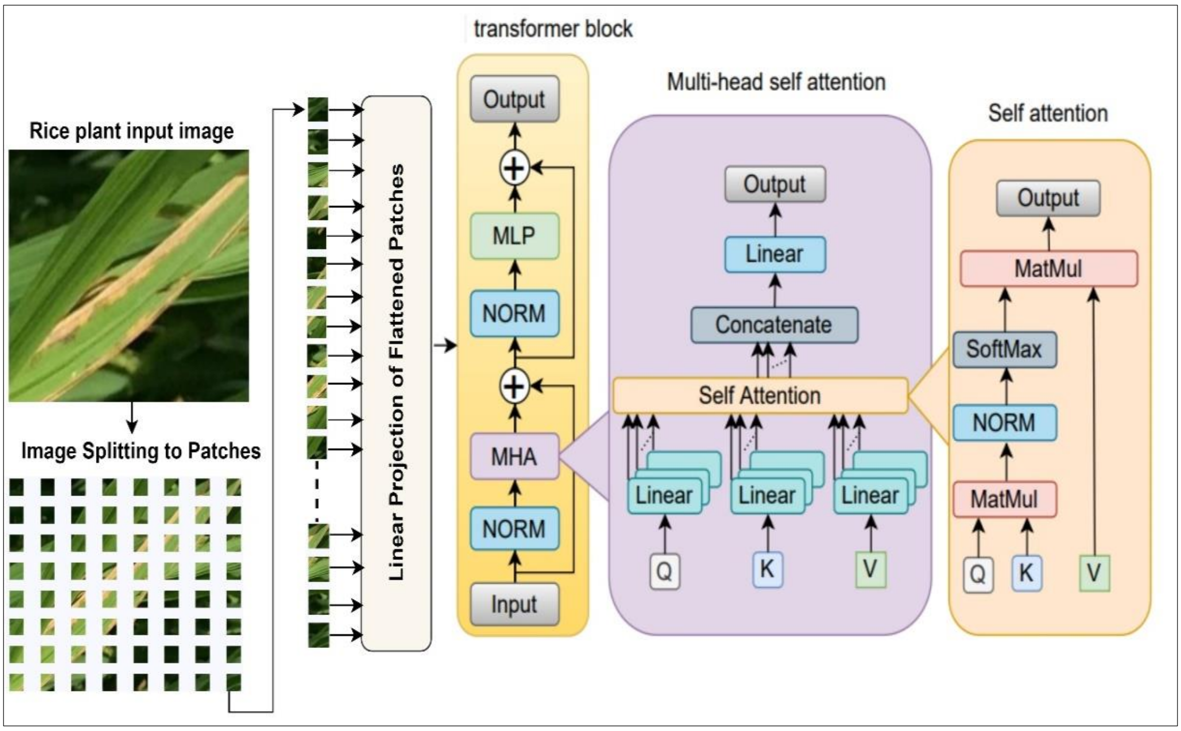

Figure 1: The general workflow of the ViT

3.3 *Preprocessing*

Before training the ViT models, the images need to be preprocessed. This first step is critical in the whole process of recognizing rice diseases, which leads to more accurate and precise identification of the specific disease. Initially, the original images were resized to the dimension of 128×128 pixels to maintain consistent input size for efficient processing and computational simplicity. Then, the dataset was divided into 80% for training (including 20% for validation) and 20% for testing per disease class, as shown in Table 2. Furthermore, it is critical to implement data augmentation techniques as a way of preprocessing in order to improve the variety of training data obtained by flipping, cropping, rotating, and color jittering the training data samples, as shown in Fig. 2. After that, the HVS (Hue Value Saturation) conversion technique was employed, followed by extracting the saturation part, converting it into a binary image, and finally adding it to the resized image. This procedure aims to isolate and remove background, thereby emphasizing what is present at the forefront. Fig. 3 shows the implemented preprocessing steps.

Table 2:Dataset sampling detail

Class	Total	Train	Test
Bacterial Blight	1584	1268	316
Blast	1440	1152	288
Brown Spot	1600	1280	320
Tungro	1308	1047	261

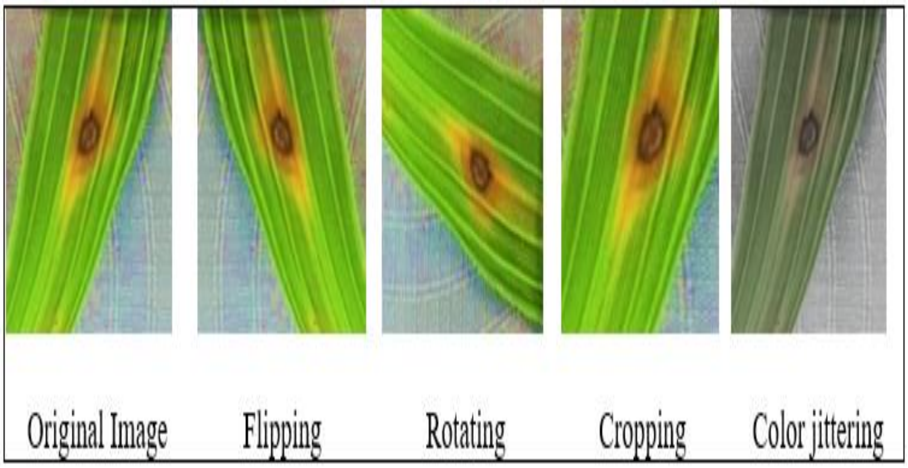

Figure 2: Data augmentation samples

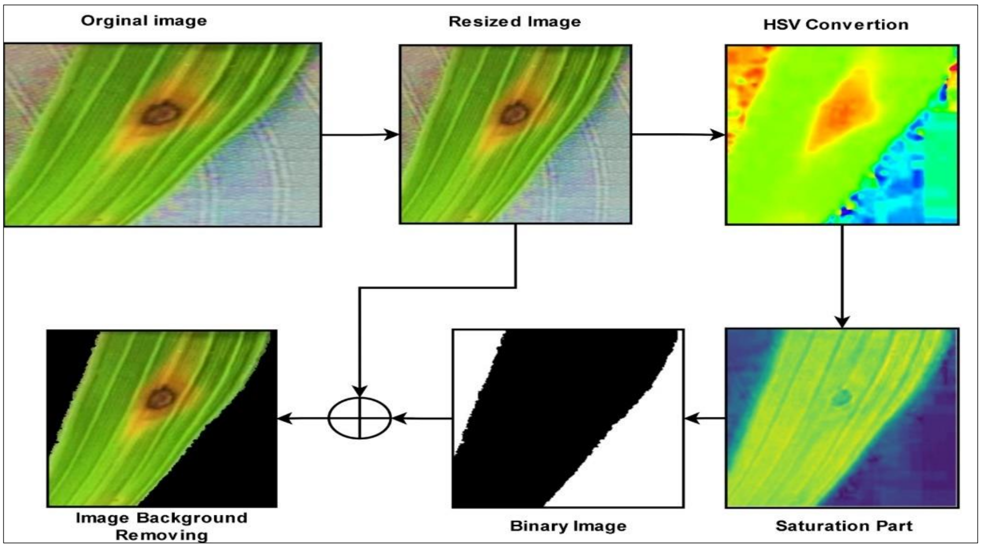

Figure 3: The pre-processing steps on the data samples

3.4 The proposed method

This work approaches the classification of rice leaf diseases by applying multi-ViTs. The method uses a separate ViT for each disease class to enhance accuracy and robustness in rice plant disease detection. A multi-ViTs method was proposed, designed, implemented, and evaluated, showing better results in terms of the identification and classification of four common sorts of rice leaf diseases. This study advances agricultural technology by providing an enhanced method for managing rice crop diseases. Algorithm 1 shows the pseudocode for the proposed methodology, while Fig. 4 depicts the main steps that were involved in it. Moreover, the suggested approach carefully chose the hyperparameters to enhance the model performance. The learning rate is set at 0.001 to handle optimization step size. The image size is standardized at 128×128 pixels, ensuring a consistent and manageable input dimension. A total of 64 patches are utilized, each with a size of 16×16 pixels, contributing to the granularity of the input representation. The Adam optimizer is employed to facilitate efficient parameter updates and convergence during the training process.

Algorithm 1: The pseudocode of the proposed methodology

```
Input: Dataset of images with corresponding labels for rice leaf diseases
Output: The classes of the rice leaf diseases
•   start
o   Training Phase
for each rice leaf disease class do
    1: Split an image into patches
        patches=SplitImageIntoPatches(images_for_disease_class)
    2: Flatten the patches
        flattened_patches = FlattenPatches(patches)
    3: Produce lower-dimensional linear embeddings
        embeddings = LinearTransform(flattened_patches)
    4: Add positional embeddings
        embeddings_with_position= AddPositionalEmbeddings(embeddings)
    5: Feed the sequence as an input to a standard transformer encoder
        transformer_output = TransformerEncoder(embeddings_with_position)
    6: Train the model with image labels
        trained_model =TrainModel(transformer_output, labels_for_disease_class)
end for
o   Testing Phase
    tested_image = LoadTestImage()
    for each trained_model do
    1: Split an image into patches
        patches = SplitImageIntoPatches(tested_image)
    2: Flatten the patches
        flattened_patches = FlattenPatches(patches)
    3: Produce lower-dimensional linear embeddings
        embeddings = LinearTransform(flattened_patches)
    4: Add positional embeddings
        embeddings_with_position = AddPositionalEmbeddings(embeddings)
    5: Feed the sequence as an input to a standard transformer encoder
        transformer_output = TransformerEncoder(embeddings_with_position)
    6: Each transformer provides a binary decision on the determined class of disease
        binary_decision = MakeBinaryDecision(trained_model, transformer_output)
    7: Store the binary decision for fusion
        binary_decisions_for_fusion = AppendToDecisionsList(binary_decision)
end for
8: Fuse the output of the four TiVs to get the final accurate decision
    final_decision = FuseBinaryDecisions(binary_decisions_for_fusion)
9: Output: The final accurate decision on the determined class of disease
•   End
```

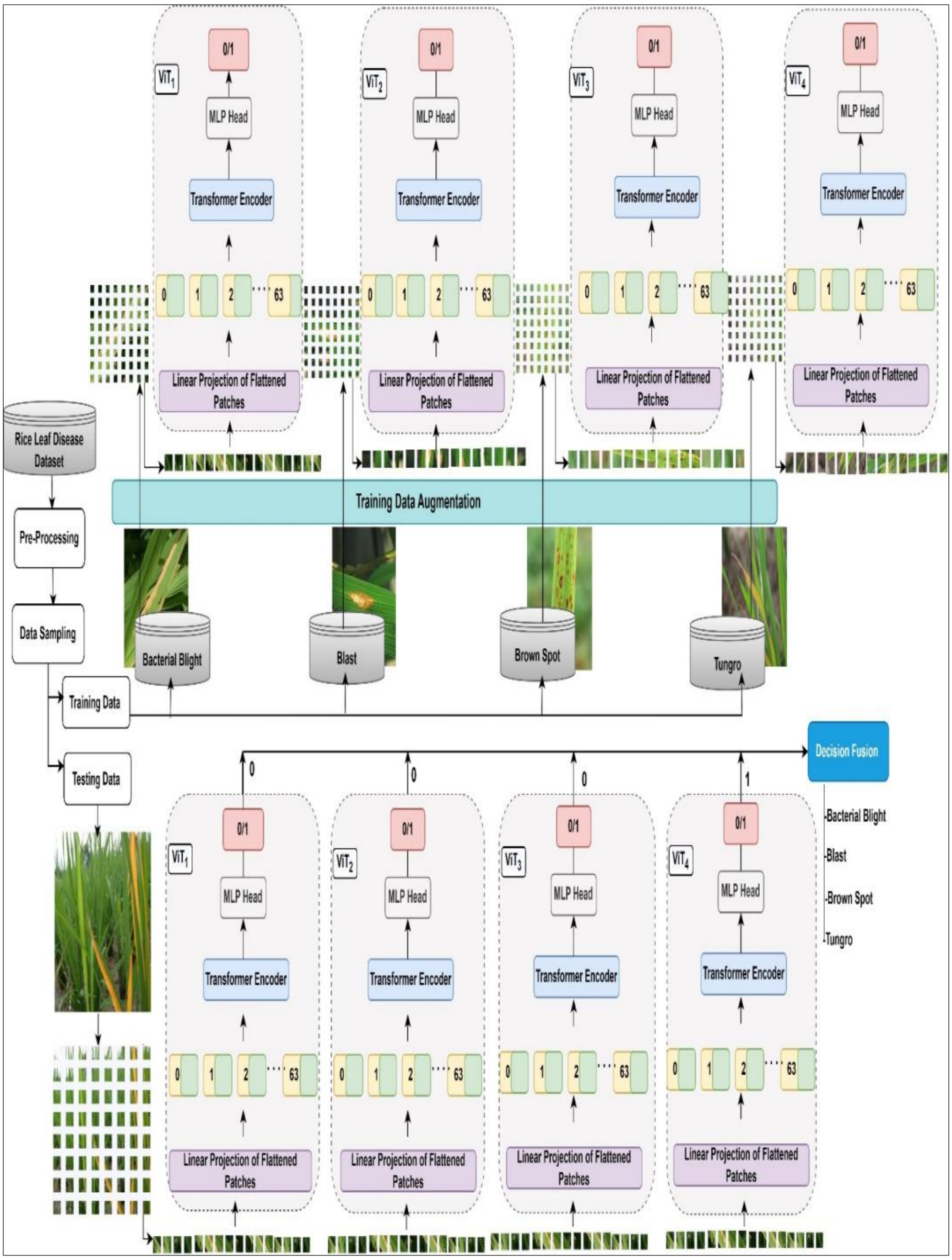

Figure 4: The general framework of the proposed methodology

4. Result and discussion

4.1 Performance Evaluation Metrics

The evaluation of the proposed methodology involves standard classification performance metrics, including precision, recall, and F1-score. The term TP refers to the count of true positives, which represents instances that were correctly identified. The count of false negatives (FN) indicates instances that were not correctly detected. FP represents the count of false positives, indicating instances incorrectly identified as positive when they are actually negative. The precision is defined as the proportion of true positive (TP) samples out of all samples predicted to be positive, and this can be expressed as [31, 32]:

$$Precision = \frac{TP}{TP+FP} \tag{4}$$

The percentage of positive samples correctly predicted as positive is referred to as recall, and this can be formulated as follows:

$$Recall = \frac{TP}{TP+FN} \tag{5}$$

F1-score is the harmonic mean of precision and recall and gives a balanced evaluation of the classifier's performance as:

$$F1 - Score\ = 2 \times \frac{(precision * recall)}{(precision + recall)} \tag{6}$$

4.2 The Performance of the proposed Methodology

To evaluate the performance of the proposed methodology, the Rice Leaf Disease Image Samples dataset was utilized. According to Fig. 5, the confusion matrices show how the four types of rice diseases were grouped in both Uni-ViT and Multi-ViT settings. Meanwhile, Table 3 presents the precision, recall, and F1-score for both uni and multi ViTs. In the uni-ViT model, commendable precision and recall ranged from 97% to 98%, resulting in a consistently high F1-score average of 97.25%. The multi-ViTs model was used to increase precision and recall across different disease classes, ranging from 98% to 99%, resulting in an improved average F1-score of approximately 98.25%. The results clearly show that the use of multi-ViT configurations significantly enhances classification overall performance, demonstrating its superiority over the uni-ViT model. These outcomes suggest that using separate ViT models for each disease category enhances the overall performance measures when compared to other conventional or single ViT alternatives. Therefore, employing individual ViT models specifically designed for identifying specific disease patterns could potentially result in improved performance. As a result, a more nuanced feature extraction and representation, as well as integrating the ViTs model into the identification of rice leaf diseases, can enable accurate and effective classification of diverse types of rice leaf maladies.

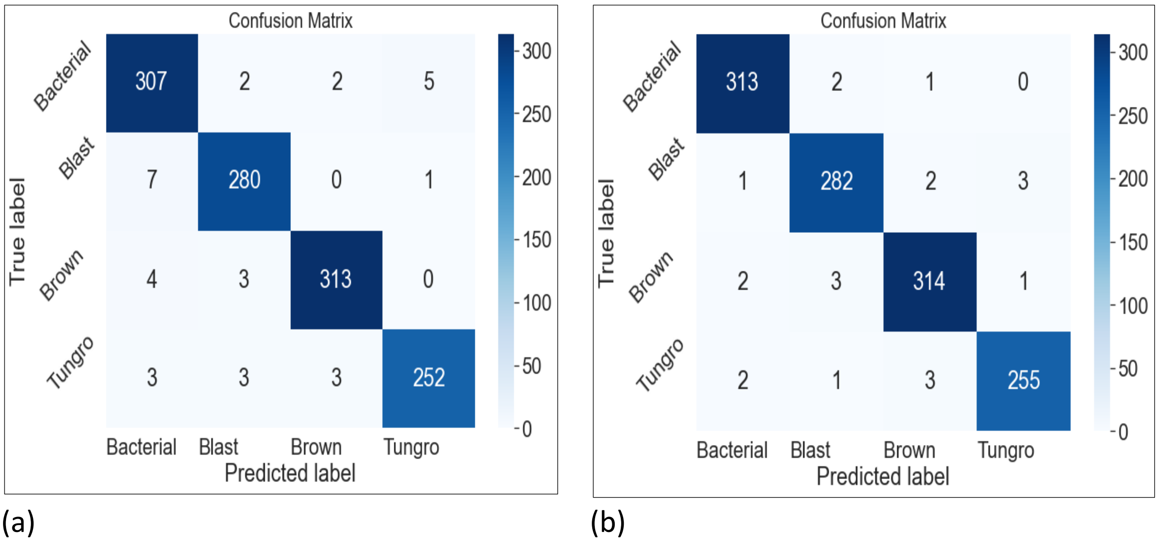

Figure 5: The confusion matrix of a) Uni-ViT b) Multi-ViTs

Table 3: The results of the Proposed Methodology

Proposed Model	Disease Class	Precision (%)	Recall (%)	Fl-score (%)
Uni-ViT	Bacterial Blight	98	98	98
	Blast	98	97	97
	Brown Spot	97	97	97
	Tungro	97	98	97
	Average	**97.5**	**9.75**	**97.25**
Multi ViT	Bacterial Blight	98	99	99
	Blast	98	98	98
	Brown Spot	98	98	98
	Tungro	98	98	98
	Average	**98**	**98.25**	**98.125**

4.3. Performance comparison with state-of-the-art

This study undertakes a comparison with state-of-the-art methods, aiming to elucidate the strengths and potential advancements of the proposed methodology in comparison to established benchmarks. The proposed methodology, particularly the multi-ViTs configuration, demonstrates competitive performance compared to existing state-of-the-art methods, emphasizing their potential advancements in rice disease classification as shown in Table 4. This finding is pivotal in advancing agricultural technology by offering reliable tools for early detection and management of rice leaf diseases, thereby promoting healthy crop yield and reducing losses due to plant diseases.

Table 4: Performance comparison with state-of-the-art

Method	#Class	Precision (%)	Recall (%)	Fl-score (%)
Lightweight CNN[15]	2	95	93	94
DenseNet169-MLP[16]	3	96.82	98.27	96.43
MLP+CNN[19]	4	95.5	95.5	95.5
ICAI-V4 [20]	4	96.11	95.55	95.81
The proposed Uni-ViT	4	97.5	97.5	97.25
The proposed multi-ViT	4	**98**	**98.25**	**98.12**

5. Conclusions

In this study, the proposed multi-ViTs method for classifying rice leaf diseases has demonstrated significant improvements in the performance accuracy and robustness compared to the state-of-the-art. It attained heightened precision, recall, and F1-score across four prevalent rice ailments: bacterial blight, blast, brown spot, and tungro. The adoption of multi-ViTs has arisen as a viable contender to CNNs in visual recognition duties, presenting superior computational effectiveness and precision. The suggested approach's effectiveness can be attributed to the unique focus mechanism embedded within each ViT, tailored for discerning specific disease patterns. This ensures a more intricate extraction and portrayal of features. This research enhances the field of agricultural technology by presenting an advanced approach to mitigate diseases in rice cultivation, foster optimal crop productivity, and minimize losses attributed to plant ailments.

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