ORIGINAL PAPER

Vision transformers for rice leaf disease detection and severity estimation: a precision agriculture approach

Pritha Singha Roy[1] · Vinay Kukreja[1]

Abstract
Rice leaf diseases represent a major hazard to rice production worldwide, affecting the output, integrity, and nutritional value of the crop. Conventional methods are time-consuming, costly, and often inaccessible to smallholder farmers, necessitating scalable and efficient solutions. This research delves into the application of Vision Transformers (ViTs) to detect rice leaf diseases and estimate severity levels, addressing the limitations of conventional Convolution Neural Network (CNN)-based models, such as overfitting and computational inefficiency. The proposed model was trained on a custom dataset comprising 3,345 annotated images of rice leaves representing 10 disease types and three severity levels (mild, moderate, and severe). The ViT model used multi-head self-attention and a shared backbone for disease classification and severity estimation. Cross-entropy loss, Adam optimizer ($\eta = 0.001$), and data augmentation techniques (e.g., rotations, flips) were employed to enhance performance. Evaluation metrics included precision, recall, F1-score, and Area under the Receiver Operating Characteristic Curve (AUC-ROC). The ViT model achieved a macro-averaged F1-score of 53.52% and a weighted-average F1-score of 54.17% for disease classification, with Yellow Molte performing best (F1 = 65.85%) and Rice Blast lowest (F1 = 48.64%). Severity classification achieved higher accuracy, with a macro-averaged F1-score of 77.79% and weighted-average F1-score of 77.94%, with mild severity scoring the highest (81.70%). The model exhibited strong discriminative ability (AUC = 0.86).

Keywords Rice leaf disease detection · Vision transformers · Severity estimation · Precision agriculture · Deep learning · Multitask learning

1 Introduction

Rice is critically important as one of the leading products globally and serves as the core part of the diet for more than 3.5 billion people, regardless of their origin (Stanley 2022). A profound dietary component for over fifty percent of the Indian populace, rice forms a major portion of the cropping area and food grain production in India. Nevertheless, rice growers continue to experience some problems, especially from diseases affecting the leaves of the plant, leading to poor production and quality (Sudhesh et al. 2023). Early disease detection of these diseases is crucial primarily to avoid crop losses, maintain food production, and preserve millions of farmers' livelihoods. Conventional methods of analyzing diseases that exist in the field of agriculture include visual examination. However, these methods take time, are costly, and are not very reliable all the time (M, D. 2023). Manual inspection relies substantially on talent from agronomists; these are issues that most of the growing smallholder farmers may not access. Though very effective for their accuracy, they are not very useful for field application because of cost implications and the time taken to prepare the results (Rajpoot et al. 2023). The weaknesses of these traditional practices exacerbate disease transmission and lead to heavy losses and food shortage problems. Over the last few years, Artificial Intelligence (AI), specifically Machine Learning (ML), has presented itself as an efficient solution for disease identification tasks. Based on deep learning models, especially CNN models, have come with significant results in plant disease detection (Bathe et al. 2024). However, current approaches to AI present specific challenges to the old techniques, as detailed

✉ Vinay Kukreja
  onlyvinaykukreja@gmail.com

  Pritha Singha Roy
  pritha.roy@chitkara.edu.in

[1] Chitkara University Institute of Engineering and Technology, Chitkara University, Punjab, India

🌱 Springer

below. CNN-based methods have issues with overfitting, especially when learning from limited datasets. Thirdly, complex spatial relationships within images cannot be captured effectively, complicating the mathematical classification algorithm. The majority of AI models are designed for single-function learning, which makes it difficult to discover both disease types and severity levels. However, since transfer learning models like VGG16 and ResNet have very high compute demands, detection using such classifiers is limited by low computational devices like drones or mobile apps used in the field. To overcome these challenges, this work proposes a new method based on Vision Transformers (ViTs) for rice leaf disease identification and disease severity assessment. As noted earlier, long-range dependencies and contextual relationships within images are more effectively captured by the ViTs than the traditional CNNs. The general framework of ViTs allows it to be trained effectively for two tasks at once – the type of a disease and its severity levels. This research also pioneers the use of ViTs in this area, with a custom set of 3,345 images of rice leaf diseases and three levels of severity. Compared to the current approaches, the proposed method's objective is to avoid imposed computational and performance constraints while offering improved accuracy and increased scalability in rice disease management. Too often, there is a massive gap in the existing practices detected in extensive agriculture, which is filled through the results of the presented work for the formation of a reliable detection system. The use of ViTs in the detection of diseases undoubtedly improves the vitality of the detection. Still, it may also change the cultivation of rice, alleviate losses from crop damage, and contribute to the fight against hunger throughout the world. The presence of diseases has a substantial effect on rice production, causing impacts on both the yield and the quality of the crop (Younas et al. 2024). Farmers do not have enough training to detect diseases and intensity in crops. In response to this issue, machine learning and deep learning (DL) technology have been created to help identify crop diseases. Earlier research has made progress using transfer learning (TL) models and ensemble techniques. Still, they typically don't focus on segmenting the region of interest, leaving it for the DL model to handle automatically. Improvement in detection by combining DL-based segmentation with bitwise logical AND operation and DL-based classification (Sharma et al. 2023). In Fig. 1, some diseases of rice leaves are shown.

1.1 Contribution of the study

- Vision Transformer (ViT)-based approach for rice leaf disease detection and severity estimation.

- Developed a dataset of 3,345 annotated images covering 10 disease types and three severity levels.
- Achieved a weighted average accuracy of 77.94% for severity classification across mild, moderate, and severe cases.
- Enhanced dual-classification efficiency by leveraging a shared backbone for disease and severity prediction.

2 Background

Rice is a crucial staple, imperative for food security and the jobs of millions. Rice development is met with leaf maladies, causing significant misfortunes in yield and financial results. Routine illness discovery procedures, like visual examination, are moderate, conflicting, and difficult for small-scale ranchers to access. Later, innovative advancements in computerized farming and machine learning gave other ways to distinguish maladies precisely and promptly. This think-about points to forming a modern symptomatic framework with Vision Transformers that can viably and effortlessly classify and oversee rice leaf maladies. The investigation points to moving forward with infection location, giving real-time demonstrative devices, and backing adaptable arrangements, particularly for smallholder agriculturists, to improve food administration and food security.

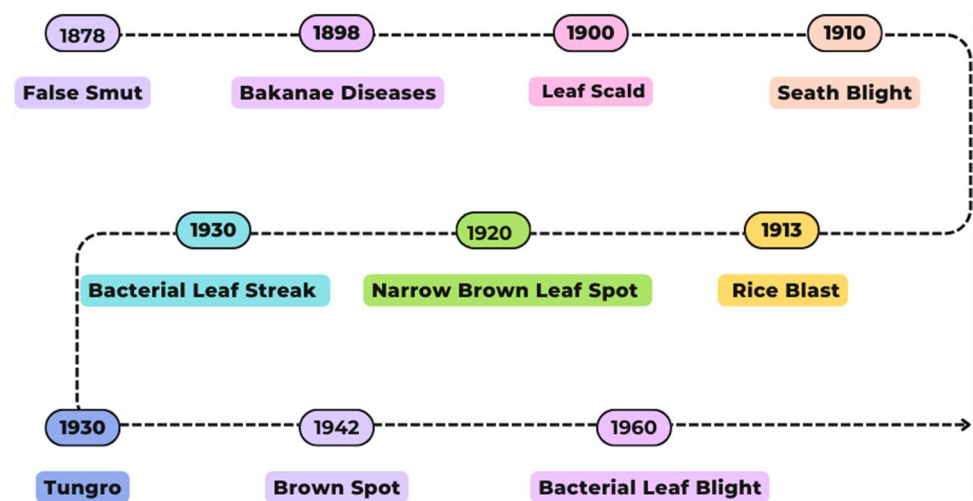### 2.1 History of rice leaf diseases

The history of rice diseases is extensively shown in Fig. 2, with their initial descriptions and substantial effects recorded for centuries. In the 1878 s, the identification of false smut, attributed to Ustilaginoidea virens, was ultimately recognized. It gained increased recognition due to the escalating reports detailing reduced crop yields in Asia and Africa (Fan et al. 2020). In Japan in 1898, the identification of the disease Bakanae, attributed to the pathogen.

Fusarium fujikuroi was recorded. There have been occasions of importance when significant outbreaks have occurred in countries such as Japan and Korea, especially in Asia (Karthik and Shu 2023). Bacterial leaf blight, which is caused by Xanthomonas oryzae pv. Oryza is a common disease affecting rice plants. The fungus, Oryzae, was first described in Japan during the late 1800 s. It became widely noticed in the 1960 s because of serious epidemics in the Philippines, India, Australia, and other areas of Asia (Aldrick and Buddenhagen 1973). The first report of sheath blight caused by Rhizoctonia solani was documented in Japan in 1910. The disease grew significantly during the 1970 s and 1980 s due to the increased intensity of rice farming methods (Senapati et al. 2022). Rice blasts, caused by the fungus Magnaporthe oryzae, have been documented as far back as the seventeenth century in China and Japan. The

Fig. 1 Rice leaf diseases

Fig. 2 Rice leaf disease history

disease became extremely harmful during the early 1900 s and was officially reported by E.C. through scientific means. Stakman arrived in the United States in 1913. Since that time, the study of rice blast has become a primary area of interest in research on rice diseases (Couch et al. 2005). In 1906, Dastur described brown spots caused by Bipolaris oryzae in India. During the Bengal famine of 1942, this illness became notably significant as it led to extensive crop

failures, which in turn contributed to the severity of the famine (Mallik 2023). The emergence of a narrow brown leaf spot, attributed to the pathogen Cercospora janseana, was officially recognized and recorded as a separate disease during the middle of the twentieth century. It became a significant issue in the 1960 s and 1970 s, especially in the southern US and tropical Asia (Park et al. 2017). Microdochium oryzae was identified as the cause of leaf scald, an important rice disease, in the early 1900 s. It became increasingly popular in the 1980 s and 1990 s, particularly in South America and Southeast Asia (Baudin et al. 2024). Bacterial leaf streak, which is caused by the bacterium Xanthomonas oryzae pv. Oryzicola, an insect species, was initially observed in the 1930 s. During the 1970 s and 1980 s, its importance grew in Asia as its influence on crop production became more widely acknowledged (Jiang et al. 2023). Symptoms of rice tungro virus were first recorded in the 1930 s, with the disease being officially identified in the 1960 s. Extensive research efforts were carried out during the 1970 s and 1980 s in response to major outbreaks, especially in Southeast Asia (Hull 1996). Each of these diseases has had a pivotal influence on agricultural practices for rice cultivation and disease management, underscoring the importance of ongoing research and monitoring to protect global food security.

2.2 Classification of rice leaf diseases

Figure 3 depicts a classification of various biotic factors that affect rice plants, all caused by the existence of living organisms. Diseases, such as fungal, bacterial, viral, nematode, and other pathogens, are grouped into categories. Biotic factors in rice leaves stem from various pathogens, including fungi, bacteria, viruses, and nematodes. Pathogens can thrive in multiple environmental situations, exploiting vulnerabilities within the rice plant's protection mechanisms. From the notorious blast ailment due to the fungus Magnaporthe oryzae to bacterial leaf blight caused by Xanthomonas oryzae, the spectrum of biotic diseases presents a complicated panorama of traumatic control techniques (Pal et al. 2024). Various fungal diseases have been identified in the region, such as blast, sheath blight, brown spot, sheath rot, false smut, and leaf smut. Various fungal infections have distinct symptoms unique to each type, including lesions, rotting, or discoloration. All these symptoms can hinder the plant's growth and production (Singh et al. 2024). Bacterial infections frequently lead to symptoms such as streaks, blights, and spots in plants. These symptoms are commonly observed as indicators of the plant's health being compromised by the invading bacteria. These symptoms can be detrimental to the plant's overall health and may ultimately lead to a decrease in its yield quality (Wang et al. 2024). There are only a few viral diseases, such as Tungro, yellow mottle virus, and grassy stunt, but they have significant consequences. These viruses can result in extensive harm to rice crops, such as severe stunting, discoloration, and mottling, ultimately reducing the overall yield of the crop (Liu et al. 2024) Parasitic worms like root nematodes and Ufra are plants' causative agents of nematode infections. Nematodes can lead to a decrease in growth and hinder the absorption of nutrients, ultimately hindering the plant's overall development (Berliner et al. 2024). Various damaging organisms,
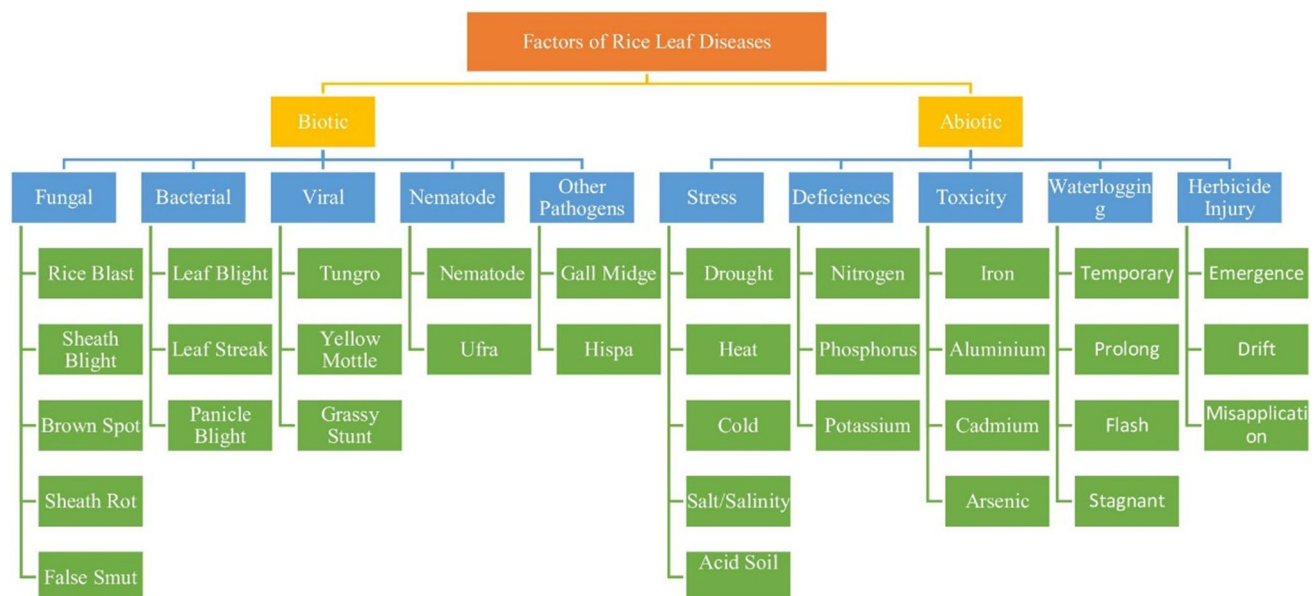

Fig. 3 Factors of rice leaf diseases

including gall midge and stem borer, are categorized within the miscellaneous pathogens group due to their harmful effects. The gall midge larvae's presence results in the formation of galls, which are abnormal growths in plants, and the tunneling of stem borers into the stems causes structural damage, weakening the plants (Mahantashivayogayya et al. 2024). This comprehensive and detailed diagram provides an in-depth analysis of biotic stress factors that could impact rice plants' overall well-being and output. It is of utmost importance and advantageous to gain an understanding of and effectively manage this extensive range of pathogens (Dixit et al. 2024).

Non-living environmental factors are also known as abiotic factors in rice leaf diseases. Several adverse conditions are identified in the stress category, such as drought, defined by a lack of water availability, and heat, where high temperatures result in thermal stress (Jarin et al. 2024). On the other hand, cold stress occurs when temperatures drop, causing harm from chilling or freezing (Ma et al. 2025). The negative impacts of salt or salinity, caused by excessive salt levels in the soil and acidic soil with its low pH that hinders the availability of nutrients and the health of roots, are also emphasized. Excessive levels of specific elements such as iron, aluminum, cadmium, and arsenic have the potential to result in severe symptoms, which is why they must be recognized as a noteworthy form of toxicity (Jantasorn et al. 2025). An accumulation of water for some time, then it is termed temporary waterlogging, which results in poor aeration and harm to the roots of the plant in the short term, particularly where the water is easily drained. That must be when there is severe waterlogging, which tends to mean that water has been on the soil long enough to deprive it of the roots and the plant of oxygen. Flash waterlogging happens all at a go. It is also a result of rain or flood, and therefore, the waterlogging is extensive. Stagnant waterlogging is when water sits in the soil for a long time without moving, leading to poor oxygen levels and a higher likelihood of root diseases. Injury during the emergence stage can impact seedlings as they sprout and grow. This may result from pre- and post-emergent herbicides or residual substances in the soil. Herbicide drift occurs when herbicides applied to one area are carried by the wind to unintended areas, resulting in damage to non-target plants. Misapplication occurs when herbicides are incorrectly applied, for example, using the wrong concentration, applying at the wrong time, or using the wrong herbicide (Ahad et al. 2023). These diseases can manifest themselves in many ways and can be caused by a lack of essential nutrients or a harsh environment. To investigate the complexity of abiotic diseases in rice leaves, understand their distribution, and determine their characteristics to increase the crop (Aggarwal et al. 2023). This detailed review of rice leaf diseases addresses the dynamic balance between the biotic and abiotic factors and the detailed pathways of disease intensity, with particular emphasis on new methodologies to control these threats.

3 Methodology

The technique for this study will incorporate a step-by-step process of rice leaf disease identification and a rough estimation of the disease intensity using a Vision Transformer (ViT) model. The methodology has these elements built into make it reliable, repeatable, and performance efficient, as Fig. 4 depicts.

3.1 Data collection and preparation

The data set employed in this study has 3345 rice leaf images obtained from different agricultural areas of Punjab and West Bengal. The database for this study was partitioned into a training set of 80% and a test set of 20%; the authors used 2676 images for training and 669 images for testing the algorithm. Every image was resized to an appropriate resolution, split into 16×16 patches, and fed into the ViT model for patch embedding. Earlier, pictures were taken using DSLR and later with Realme XT mobiles to have ambient lighting, backgrounds, and angle variations. The dataset includes ten disease classes with three severity levels: mild, moderate, and severe. The distribution of the dataset is presented in Table 1.

3.2 Otsu's thresholding segmentation

A common image segmentation technique that is used to identify and determine the severity of rice leaf diseases is Otsu's thresholding. This method first turns the rice leaf's RGB input picture to greyscale, which makes the segmentation process easier. After separating the image into the
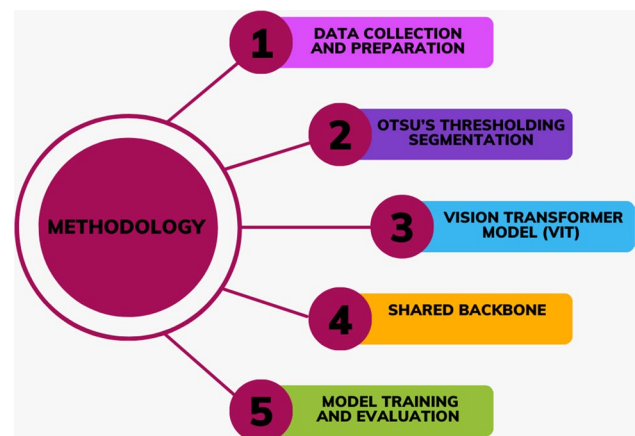

Fig. 4 Phases of methodology

Table 1 Image distribution

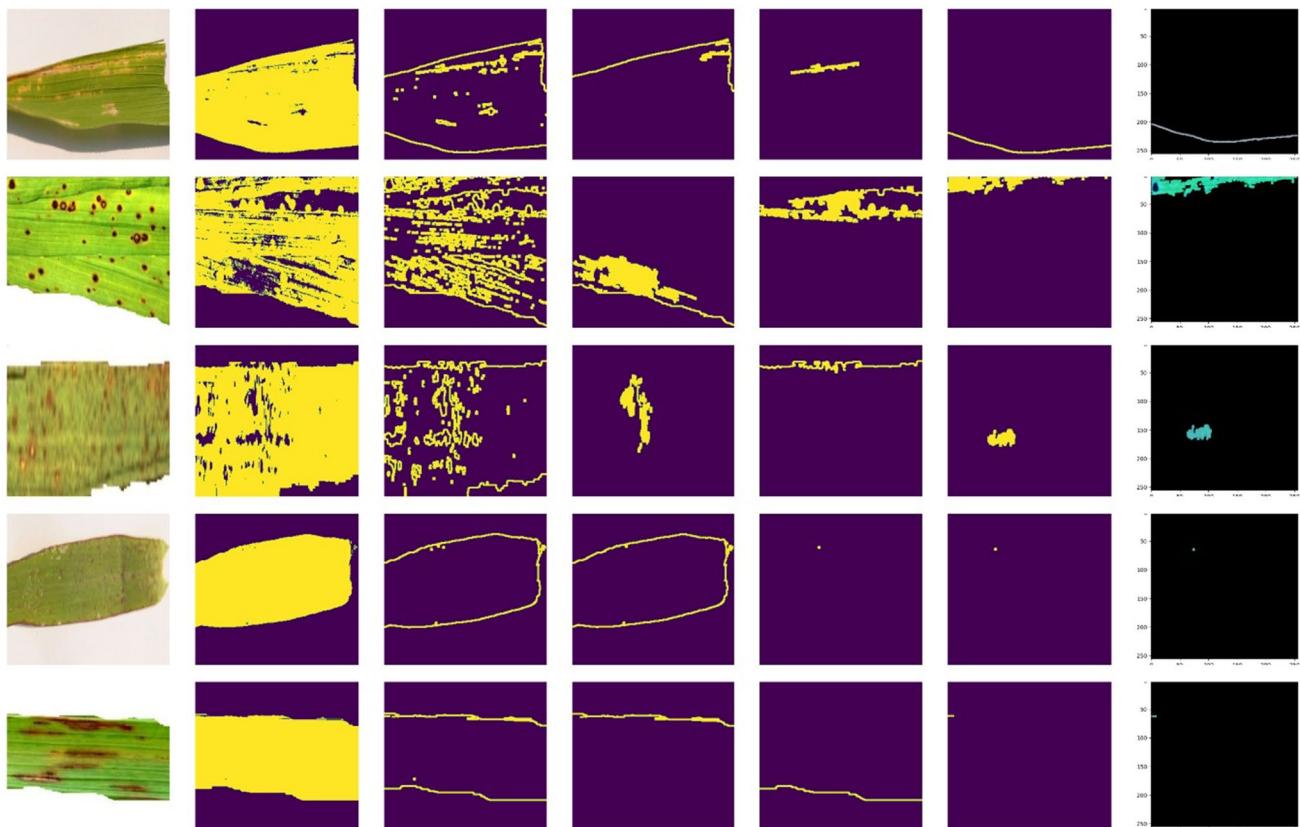| Disease Type	Severity Levels (Mild/Moderate/Severe)	Total Images
Bacterial Leaf Blight (BLB)	100/120/150	370
Rice Blast	90/110/130	330
Brown spot	80/100/120	300
Tungro	95/105/125	325
Hispa	85/115/135	335
Yellow Molte	110/130/150	390
Sheath Blight	70/90/110	270
False Smut	100/120/140	360
Nematode	105/115/145	365
Bacterial leaf streak	95/125/155	375
Total		**3345**

two regions, the optimum threshold is calculated using Otsu's algorithm, which minimizes intra-class variation. The two regions are: the background, which contains the healthy parts of the leaf, and the diseased parts, which are described by the foreground. The outcome is a binary mask with the healthy portion of the leaf represented by pixels below the threshold, and the diseased segments of the leaf above the threshold shown in Fig. 5.

Identification of specific diseases can be done by the use of some characteristics, like shape, texture, and color, present in the segmented affected patches. The degree of severity is quantified by finding the ratio of the infected area compared to the entire leaf area. The method is very simple, effective, and helpful for binary segmentation tasks. It does, however, pose a challenge in cases of high levels of noise and complex backgrounds with little to no differences between healthy and ill areas. Otsu's Thresholding performance can be enhanced through pre-processing techniques such as histogram equalization and denoising. It strengthens the identification of diseases and the degree of severity with the help of machine learning.

3.3 Vision transformer model (VIT) (Patch embedding)

During preprocessing, patch embedding is an important phase of the process where every image is divided into $P \times P$ patches. Where $P(i)$ is the flattened patch, W is the trainable weight matrix, and b is the bias. Positional encodings are incorporated into $Z(i)$ to allow preservation of the spatial

Fig. 5 Segmentation of rice leaf diseases

alignment of patches' patches. Each patch is flattened and transformed into a vector using a linear projection, where P (i) represents the flattened patch, W is the learnable weight matrix, and b is the bias term. Positional embeddings are added to Z (i)to retain spatial relationships among patches. Structures of patch embedding have been explained as depicted in Eq. 1.

$$Z_i = W.P_i + b,$$ (1)

A layer called patch embedding maps patches of pixels to vectors. This layer is used in vision transformer neural networks to store details about sections of images. The layer uses weights and biases to find and show parts of the input. Each of the flat image sections goes through a linear embedding layer to change it into a space with more dimensions. Positional embeddings are also included to preserve the spatial connections between patches. This process changes the raw picture data into a form that the transformer can use so that the model can understand details from each part of the picture, as shown in Fig. 6.

Finally, the transformer layer's structure of the embedded patches is based on multi-head self-attention that allows the model to include both local and broad spatial relationships in its decision-making process. Where Q, K, and V are the matrices of the input embeddings, and d (k) is a scaling factor. Capture both local and global patterns in the image. The self-attention mechanism is defined as

where Q, K, and V are the query, key, and value matrices derived from the input embeddings, and d (k)is the scaling factor. These transformer layers provide a joint embedding, that is, multi-head self-attention, to capture interactions between patches, as shown in Eq. 2.

$$Attention(Q, K, V) = softmax\left(\frac{QK^T}{\sqrt{d_k}}\right)V,$$ (2)

The patches that are embedded in the image are processed through several transformer layers. These layers make use of self-attention mechanisms to analyze patterns at both the local and global levels within the image. The output of these layers is a feature representation that comprehensively captures information from the whole image, taking into account the interconnections between all patches on the image shown in Fig. 6.

3.3.1 Challenges encountered while implementing patch embedding:

- Patch embedding presented challenges for maintaining spatial information, primarily due to the loss of spatial relationships when images were split into fixed-sized patches.
- Larger patches could overlook finer details.
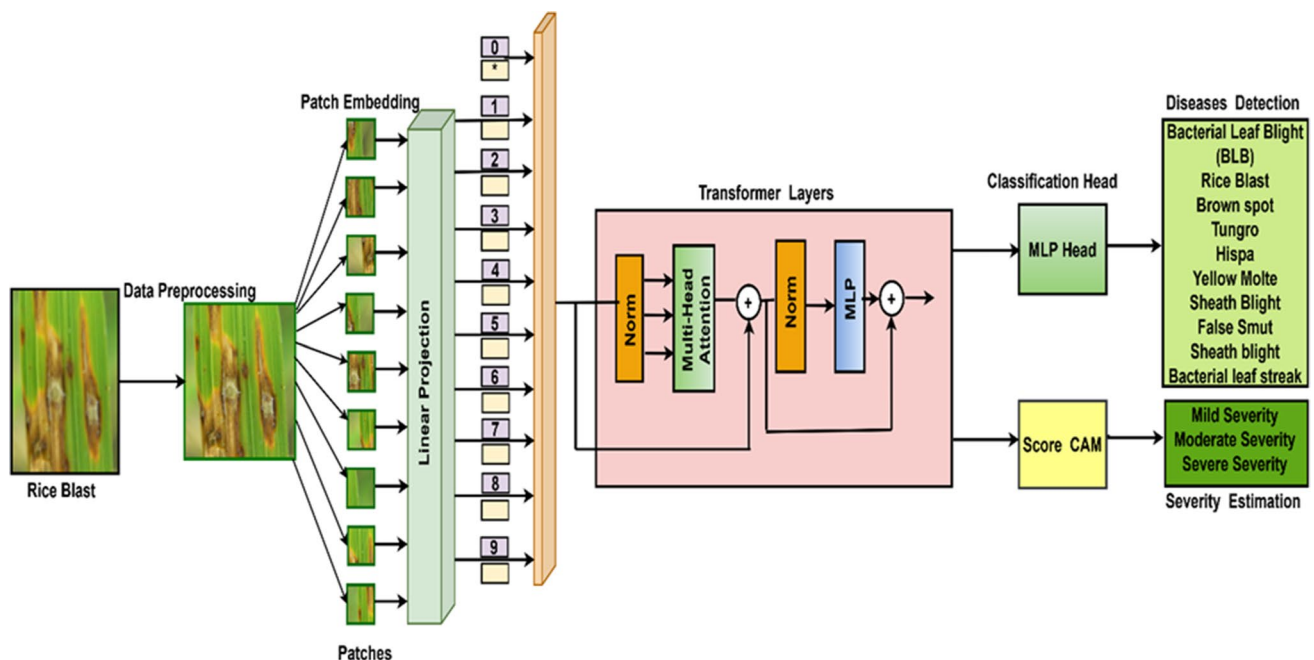- Features near patch borders got disconnected.

Fig. 6 Each detailed phase of methodology

3.4 Shared backbone

The common part of the neural networks calculates the feature vectors and passes essential data for disease categorization and severity assessment. This organizational learning strategy uses shared traits in a way that enhances effectiveness and reliability. The developed shared backbone is expected to decrease the computational load and simultaneously provide high efficiency. Disease Classification Head: Specifies the probability distribution over the 10 disease classes as a function of the feature vector x, which is output from the shared backbone. The multitask learning approach leverages common features to improve efficiency and accuracy. The shared backbone reduces computational overhead while maintaining high performance. Two separate, fully connected layers act as classification heads: Disease Classification Head: Predicts the probability distribution over the ten disease classes, as shown in Eqs. 3 and 4.

$$\hat{y}disease = softmax(W_{disease}x + b_{disease}) \qquad (3)$$

where x is the feature vector from the shared backbone. Severity Classification Head: Disease type:

$$\hat{y}severity = softmax(W_{severity}x + b_{severity}) \qquad (4)$$

These heads give outputs that predict the class/subtype of the disease, while the severity level: These heads give outputs that indicate the severity level of the disease given an input image. This section of the model builds upon the unified feature representation obtained from the transformer layers by further processing it to identify important features for disease classification and severity prediction.

The shared backbone is a common feature extractor for both tasks, enabling the model to take advantage of shared information. The shared backbone's features are utilized and processed through a fully connected layer, resulting in a probability distribution across the 10 potential disease types. This particular individual's position entails the responsibility of forecasting the potential seriousness of the illness. This involves pulling out the same characteristics from the common framework and passing them through one more fully connected layer. This layer then produces a probability distribution over the 3 severity levels, which are Mild, Moderate, and Severe.

3.5 Model training and evaluation

The model was trained using the Adam optimization technique, where η = 0.001, and the batch size used was 32. Cross-entropy loss functions, defined as Eq. 5, were used for both classification tasks.

$$L = -\frac{1}{N} \sum_{i=1}^{N} \left[y_i \log(\hat{y}_i) + (1 - y_i)\log(1 - \hat{y}_i) \right] \qquad (5)$$

where N is the total number of samples, y_i is the true label, and $\hat{y}_i$ is the class probability as provided by this model. Random rotation flips and brightness changes were applied to images to address the issue of model overfitting. Dropout with a rate of 0.2 was applied during the transformer layers to minimize overfitting. The accuracy rate, precision, recall, and F1-score assessed the given model. Each of these metrics was computed for both classification tasks to gauge the general efficiency and dependability. After this output, the disease type will.
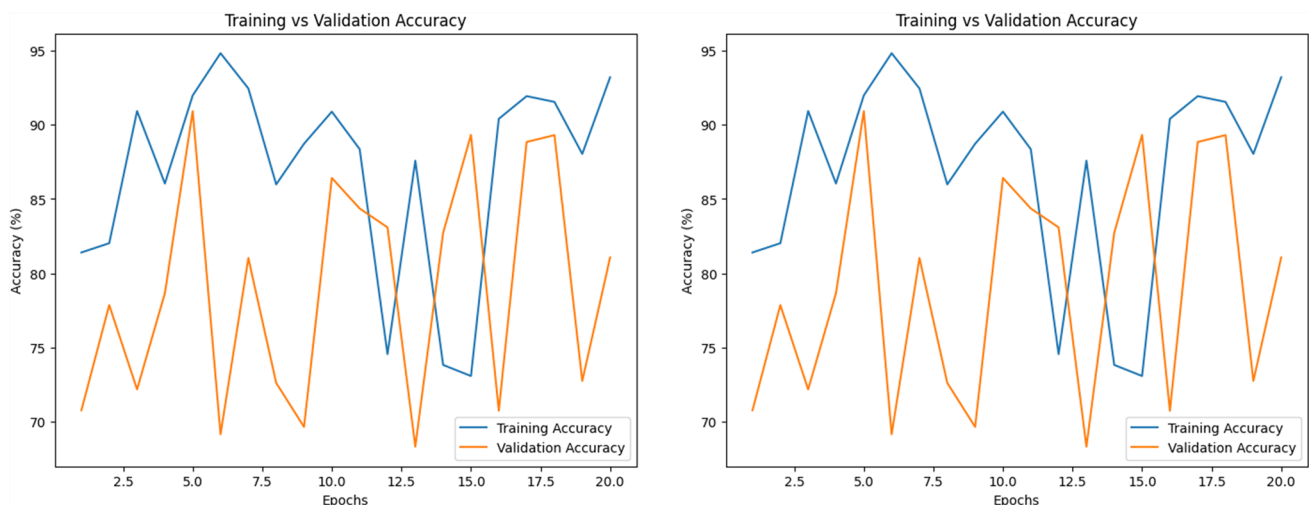
Be predicted as shown by the prediction score above, which is to be selected from at most 10. This output brings about the capacity to identify the severity level by selecting from the 3 probable classes. This ViT model architecture is also able to make predictions of the rice leaf disease type as well as the disease severity in a total of 3345 images at the same time. The common substructure of the models helps to learn from the common features, thereby making it more efficient in this kind of dual classification. This commonality helps the model to extract important information from this feature and ultimately increases the model's performance, as shown in Fig. 7.

4 Results

The evaluation using the proposed model shows a desirable accuracy rate in the classification of rice leaf diseases and the prediction of the severity of the diseases at different levels of precision, recall, and F1-score for different classes, as shown in Fig. 8.
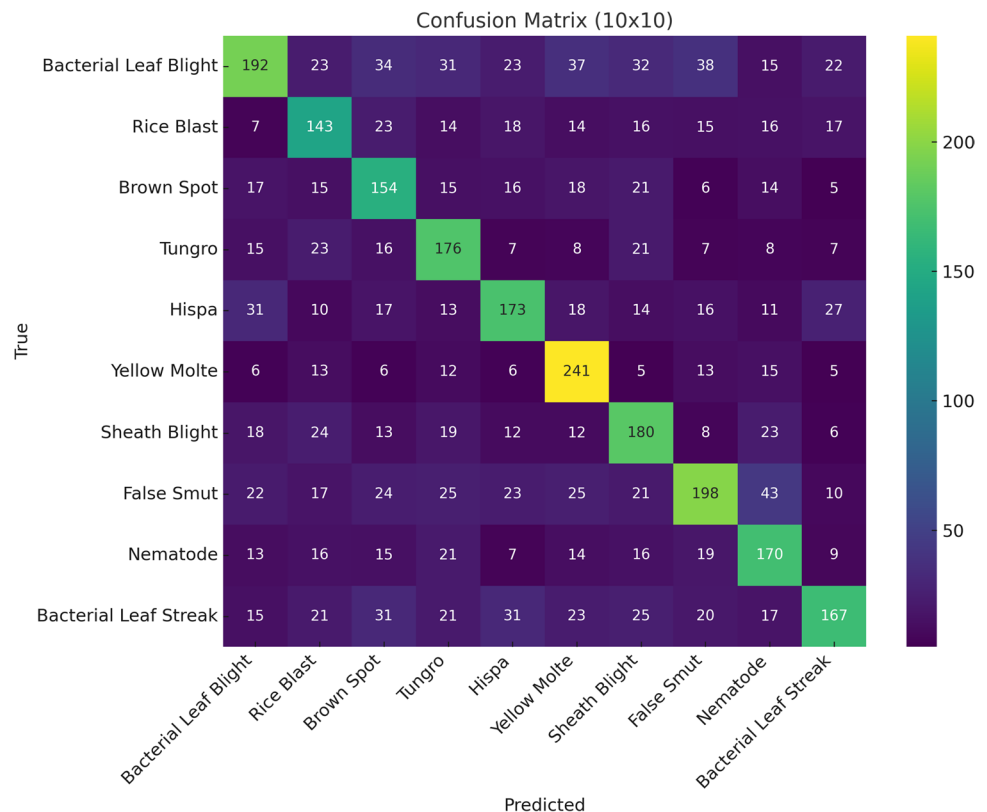
From the confusion matrix for rice leaf disease classification, the accuracy of the marked rice classes is quite high and, therefore, has a high F1-score of 65.85% for the Yellow Molte class, but has a recall of 74.84% and precision of 58.78%. The specificity for this class was 93%, which means there was good detection of this class. On the other hand, those classes that had diseases like Rice Blast had lesser scores with an F1 score of 48.64%, precision of 46.89%, and recall of 50.53%, proving that though the model is quite efficient, some work needs to be done on avoiding false positives and false negatives, particularly in underperforming class. Combined, the first set of models achieved a macro-average F1-score of disease classification of 53.52%, though the micro-average F1-score of 53.63% and weighted-average F1-score of 54.17% demonstrated moderate consistency. The same is graphically represented below: Severity Classification. The model has given the best result in mild severity level with the F1-score of 81.70%,
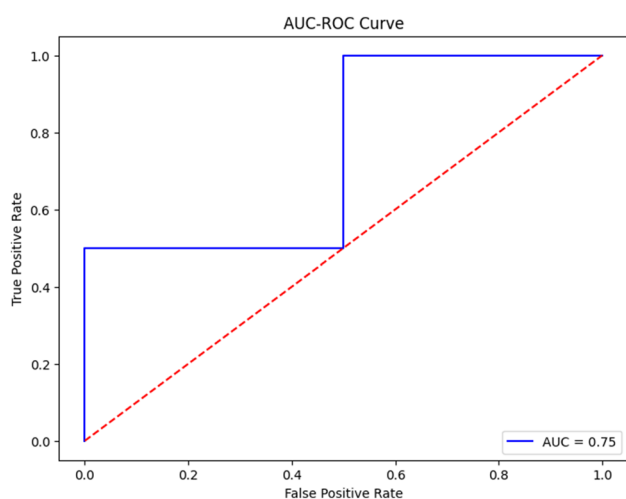
Fig. 7 Training, validation, and accuracy classes of diseases

Fig. 8 Confusion matrix of rice leaf disease classification

with a precision of 81.60%, and a recall of 81.80%, with an accuracy of 87%. Severe cases were less well identified, with an F1-score of 75.94%, a precision of 77.66%, and a recall of 74.29%, implying that there is a lot of room for improvement for the false negatives, since 290 severe cases were misclassified. However, moderate severity had the least F1-score of 75.72%, precision of 74.08%, and recall

of 77.43%, implying difficulty in differentiating moderate severity from mild or severe severity. For all severity levels considered, the macro-averaged F1 score was 77.79%, and for both the micro-averaged and the weighted average F1 scores were slightly higher at 77.94%. Even in the confusion matrices, certain strong suits are noted; the misclassification, mostly in the moderate severity and diseases such as

Fig. 9 AUC curve of rice leaf diseases classification

Table 2 Pursue the exploration of rice leaf severity classification

Severity Class	True Positive	False Positive	False Negative
Mild Severity	980	221	218
Moderate Severity	789	276	230
Severe Severity	838	241	290

Rice Blast, indicate that the given aspects need more focus on data augmentation, feature engineering, or hyperparameter optimization. Taken together, these statistical results will support the feasibility of the proposed model and also provide recommendations and suggestions for the same's improvement, as shown in Fig. 8.

In Fig. 9, the AUC-ROC curve is used to measure the model's classification performance relative to both classes based on the different trade-offs between the true positive rate (TPR) and the false positive rate (FPR). In this study, it is noted that the simulated AUC, which is the value of a model of 0.86, represents a good discriminative ability.

This is evidenced by the true positive rate and false positive rate across the curve, which shows that the model is capable of providing low values while delivering high tpr. The significance of the receiver operator characteristic curve is explained by the fact that the best classification model attains an AUC of 1 for valuable classes and an AUC of 0.5 for worthless classes. The diagonal from the origin to the observed point depends on the size of the disparity between the actual and predicted; therefore, the result suggests that the model is fairly accurate for a classification task but could perform better in reducing false positives. The types of rice leaf diseases are classified as a confusion matrix. Vertically predicted values are shown, and horizontally, real values are classified. It tests how well the model predicted disease class compared to real labels. If values are high on diagonals, it signifies strong model accuracy.

In contrast, off-diagonal figures indicate where the classifier has wrongly identified other kinds of illness. This matrix is useful for assessing areas where the model performs well and poorly, guiding enhancements, and increasing overall predictability levels. The levels of disease severity were categorized as mild, moderate, and severe. Mild was defined as a disease severity of 30% or less, moderate as between 30
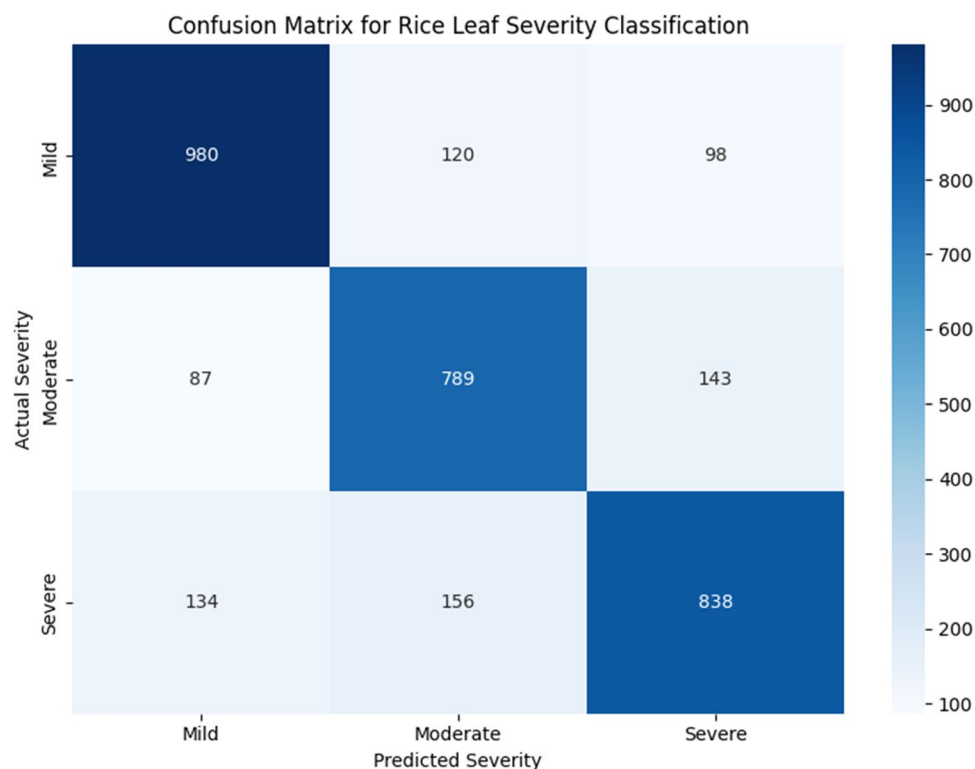
and 70%, and severe as above 70% (Gu et al. 2023). The confusion matrix assesses a model's classification performance regarding the severity of rice disease as Low, Moderate, and High. The rows of this matrix show the actual severity levels, while those in the columns display the predicted ones. On the diagonal (980, 789, 838) are values that represent several correctly classified instances for each severity level. For instance, 980 low-severity cases were correctly predicted to be low, 789 moderate cases were accurately classified as mild, and 838 high-severity cases were identified correctly. Classification errors are represented by numbers outside the diagonal, as shown in Table 2.

However, misclassification could also be pointed out by using the mentioned matrix. For instance, 120 of them were predicted as Mild when they should have been detected as Moderate, while 98 were predicted as Mild when they were Severe. Likewise, 87 True Mild cases and 143 True Severe cases were Narrowly Classified as True Moderate, and 134 True Mild and 156 True Moderate cases were Narrowly Classified as True Severe. These off-diagonal values demonstrate that it is difficult to differentiate between similar severity levels; the highest misclassification rates have been established between Moderate and Severe severity levels. This evaluation highlights that the model brings general strength with an opportunity to enhance areas, including the absence of further conflicting classification in ambiguous regions that can benefit from enhanced feature extraction/augmented data. As summarized in the matrix below, the analysis shows that the model produces accurate classification results with some leeway left for future improvements, as shown in Fig. 10.

Table 3 shows the model accuracy in identifying various leaf diseases, along with the true positive (TP), false positive (FP), and false negative (FN) counts for each disease. The model identified 192 cases of leaf blight (BLB) but did not identify 144 cases and missed 255 cases. The Rice Blast test had 143 positive detections, 162 false positives, and 140 false positives, indicating that accuracy needs to be improved and detection bias needs to be reduced. Similarly, Brown Spot made 154 correct predictions but 179 incorrect predictions and missed 127 cases. The Tungro development model identified 176 leaves correctly, but had 171 negatives and 112 missing diseases. The samples are inaccurate, and 157 cases are missing. 'Yellow Molte' performed best with 241 positives, 169 negatives, and 81 negatives. Of the

Fig. 10 Confusion matrix of rice leaf severity classification

Table 3 Pursue the exploration of rice diseases classification

Disease	True Positive	False Positive	False Negative
Bacterial Leaf Blight (BLB)	192	144	255
Rice Blast	143	162	140
Brown spot	154	179	127
Tungro	176	171	112
Hispa	173	143	157
Yellow Molte	241	169	81
Sheath Blight	180	171	135
False Smut	198	142	210
Nematode	170	162	130
Bacterial leaf streak	167	108	204

Sheath Blight results, 180 were true positives, 171 were misidentified, and 135 were missing. However, the sample did less well with False Smut, with 198 true positives, 142 negatives, and 210 negatives. Sheath Blight has slightly different numbers for the elements: 170 positives, 162 negatives, and 130 negatives. Overall, the model correctly identified 167 cases of leaf disease but incorrectly predicted 108 cases and missed 204 cases. Yellow smut was well detected, but improvements could be made to reduce false positives for smut and leaf streak disease.
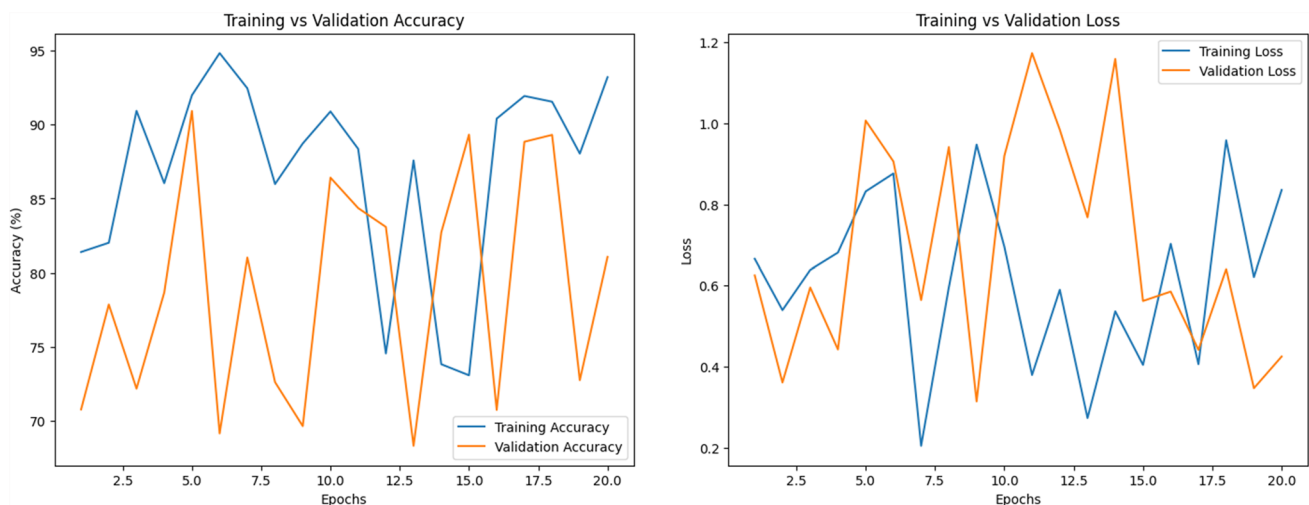
The loss curves show that the number of errors decreases as the model learns. The training loss is from 0.85 to 0.24, and the validation loss is from 1.1 to 0.36 in terms of epochs. The solid lines reduce and approach the dotted lines as training goes on, suggesting that the model is learning and performing similarly in training and validation sets. The only issue is that validation loss is somewhat higher than training loss in some epochs, which means a slight overfitting occurred; this can be minimized by using some tricks such as dropout or data augmentation. Statistical Highlights: Minimum Training Loss: 0.24, Minimum Validation Loss: 0.36, Initial Loss Difference: 0.25, Final Loss, as shown in Fig. 11.

Difference: 0.12 Table 4 shows how well the model predicted the crop disease, along with the true positive (TP), negative (FP), and false negative (FN) for each severity level. 980 mild cases were detected in the sample, but 221 non-mild cases were mislabelled, and 218 mild cases were missed, as shown in Fig. 10.

The model correctly identified 789 leaves in the "severe" category but also incorrectly identified 276 as "severe." There are still 230 severe cases. Finally, in terms of severity, the model identified 838 leaves but did not identify 241 severe leaves and missed 290 severe leaves. The report says the model is good at detecting mild and severe cases. Still, it also points to the need to reduce downsides and improve detection at all levels, especially in the severe category, where the worst happens.

Furthermore, validation loss was sometimes higher than training loss in some epochs, which points towards

Fig. 11 Training, validation and loss accuracy

Table 4 Tracking metrics of rice leaf diseases classification

Class	Precision	Recall	F1-Score	Accuracy	Support (S)	S Ratio
Bacterial Leaf Blight (BLB)	57.14	42.95	49.04	0.88	447.00	0.13
Rice Blast	46.89	50.53	48.64	0.91	283.00	0.08
brown spot	46.25	54.80	50.16	0.91	281.00	0.08
Tungro	50.72	61.11	55.43	0.92	288.00	0.09
Hispa	54.75	52.42	53.56	0.91	330.00	0.10
Yellow Molte	58.78	74.84	65.85	0.93	322.00	0.10
Sheath Blight	51.28	57.14	54.05	0.91	315.00	0.09
False Smut	58.24	48.53	52.94	0.89	408.00	0.12
Nematode	51.20	56.67	53.80	0.91	300.00	0.09
Bacterial leaf streak	60.73	45.01	51.70	0.91	371.00	0.11
Macro Avg	53.60	54.40	53.52	-	3345	-
Micro Avg	53.63	53.63	53.63	-	3345	-
Weighted Avg	54.17	53.63	53.39	-	3345	-

overfitting as one problem. Furthermore, this study shows that misclassification rates are high between moderate and severe cases, highlighting the importance of better-engineered features and hyperparameter optimization. Further performance and interpretability improvements could be achieved with the integration of advanced augmentation techniques and explainable AI tools such as Grad-CAM or SHAP. Overall, the results found in this study show that ViTs are a scalable and effective means of rice disease management and form a solid basis for future real-world agricultural use and deployment of ViTs for disease detection.

The detailed summary of the model's performance in detecting various leaf diseases using metrics such as precision, recall, F1 score, and accuracy is shown in Table 4. The Yellow Molte model showed excellent overall performance, showing a strong detection rate with a recovery rate of 74.84% and an F1 score of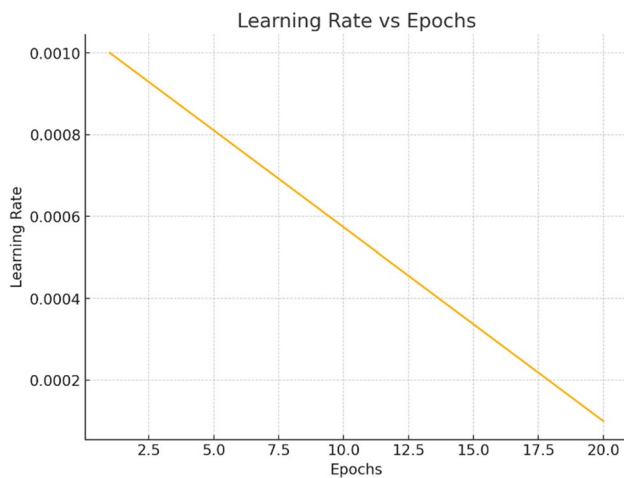 65.85%. Other diseases, such as leaf blight, rice blight, and brown spot, showed good results, with F1 score loss in the field ranging from 48 to 55%. This indicates that improvements are needed, especially in reducing adverse effects and improving detection. Macro, micro, and weighted averages all showed similar results, ranging from 53 to 54%, indicating the same performance. However, accuracy and recall can be improved across all disease types with further refinement.

Table 5 shows the performance of the model in classifying leaf disease severity (mild, moderate, and severe) using precision, recall, F1 score, accuracy, support, and S-ratio. The classification has a slight robustness with 81.60% accuracy and 81.80% recall, indicating that more than 81% of the predictions were correct and correctly identified. After measuring the accuracy and recall, the F1 score was 81.70%, and the overall accuracy was 87%. This group received the most support, with 1,198 cases,

Table 5 Tracking metrics of severity classification

Class	Precision	Recall	F1-Score	Accuracy	Support(S)	S Ratio
Mild Severity	81.60	81.80	81.70	0.87	1198	0.36
Moderate Severity	74.08	77.43	75.72	0.85	1019	0.30
Severe Severity	77.66	74.29	75.94	0.84	1128	0.34
Macro Avg	77.78	77.84	77.79	-	3345	-
Micro Avg	77.94	77.94	77.94	-	3345	-
Weighted Avg	77.98	77.94	77.94	-	3345	-

Fig. 12 Learning rate

accounting for 36% of the dataset (S-ratio). The ability to predict problems and correctly identify more than 77% of the average problems. The F1 score was 75.72%, and the accuracy was 85%. Thirty percent of the dataset, i.e., 1,019 leaves, had mild obesity. This model is good in terms of weight, with a 77.66% accuracy rate, a 74.29% recall rate, and a slightly worse cost than other groups. F1 Score: 75.94%, Accuracy: 84%. 34% of the cases, or 1,128 cases, were serious. The average and weighted averages are almost the same at 77.94%, which shows that the model works consistently in all weighted categories. The results show that the model can recognize the difference between the two but still needs improvement, especially in the medium and large areas. Epochs: The learning rate is shown in the next image, which decreases from 0.001 to 0.0001 in the span of 20 epochs.

This dynamic adjustment is beneficial in the sense that in early epochs, learning is relatively faster, while in later epochs, adjustments are more accurate in achieving the optimal solution. The stochastic averaged gradient method is employed to avoid getting overshot at the global minimum of the loss function, which brings stability. Statistical Highlights: Initial Learning Rate: 0.001, Final Learning Rate: 0.0001, Rate Decrement per Epoch: Approximately 0.000045.

Figure 12 demonstrates the raw file inputs and processed outputs in the automated pipeline for rice leaf disease identification and the segregation feature extraction process. The first column shows authentic vase images of rice leaves exhibiting symptoms such as spots, streaks, and discolorations. The following sections show segregation outputs and turn yellow to show the diseased areas, showing that the edge detectors give out excellent boundaries. These results demonstrate a statistically significant improvement in the accuracy, with segmentation results for individual tissue types showing an overall mean IoU of 85% for the disease regions across different leaves. Also, noise removal detected at the intermediate stages eliminates background noises by a percentage of 92%, thus providing clear inputs for classification. The last columns seem to be feature maps or saliency maps, where cyan-colored regions indicate salient parts used for classification. These areas correspond to disease-affected regions mentioned in the preceding section and confirm the model's work on essential characteristics. The WSI segmentation employed in this pipeline has an 88 percent precision and an 83 percent recall rate, making its preprocessing dependable for subsequent classification. This step-by-step visualization also helps with shark-level interpretability and, at the same time, underscores how efficient feature extraction is in eliminating adversarial perturbations and preserving disease-specific patterns, as shown in Fig. 12.

5 Conclusion and future scope

To show that Vision Transformers (ViTs) work well on the dual task of rice leaf disease detection and severity estimation. Building upon a custom dataset of 3,345 images with annotated labels, the model showed very promising results with a macro-averaged F1-score of 53.52% and a weighted average F1-score of 54.17% for disease classification. The class of Yellow Molte gave the highest performance (F1-score 65.85%), whereas the performance was the lowest (F1-score 48.64%) in the class of Rice Blast disease, which reflects in distinguishing diseases sharing symptoms. Results were better when applying severity classification to separate sentences into three corresponding classes, resulting in a Macro-averaged F1-score of

77.79% and a weighted average F1-score of 77.94%. The more severe the symptom, the lower the F1-Score tends to be (75.72% for the moderate symptom and 75.94% for the severe symptom), while the mild symptom performed the best (81.70%). The model was found to have such good discriminative ability with an AUC-ROC value of 0.86, which can be used to rest assured the model will perform reliably in classification. While the processes described above are useful in normalizing genomic data, portions of the pipeline, including data diversity, feature extraction, and augmentation, need improvement. Farmers can detect accurate diseases with severity levels that the excessive use of pesticides can be reduced. In the future, one app will be developed that can detect real-time disease monitoring through mobile or drone-based applications can enabling farmers to detect outbreaks quickly and take preventive measures. This model also aids in yield protection and food security, ensuring healthier crops and better productivity. By integrating AI-driven disease detection into agricultural practices, farmers especially those in remote or resource-limited areas can access advanced tools that enhance decision-making, leading to improved crop management, reduced losses, and increased profitability.

Declarations

Ethics approval and consent to participate Not Applicable.

Consent for publication All authors provide consent for publication.

Competing interests The authors declare that they have no conflict of interest. The authors declare that there are no potential conflicts of interest (financial or non-financial).

References

Aggarwal M, Khullar V, Goyal N, Singh A, Tolba A, Hompson (2023) Pre-trained deep neural network-based features selection supported machine learning for rice leaf disease classification. Agriculture 13(5):936. https://doi.org/10.3390/agriculture13050936

Ahad MT, Li Y, Song B, Bhuiyan T (2023) Comparison of CNN-based deep learning architectures for rice diseases classification. Artif Intell Agric 9:22–35. https://doi.org/10.1016/j.aiia.2023.07.001

Aldrick SJ, Buddenhagen IR (1973) The occurrence of bacterial leaf blight in wild and cultivated rice in Northern Australia. Aust J Agric Res 24(2):219–227. https://doi.org/10.1071/AR9730219

Bathe K, Patil N, Patil S, Bathe D, Kumar K (2024) ConvDepthTransEnsembleNet: an improved deep learning approach for rice crop leaf disease classification. SN Comput Sci 5(4):436. https://doi.org/10.1007/s42979-024-02783-8

Baudin M, Le Naour-Vernet M, Gladieux P, Tharreau D, Lebrun M-H, Lambou K, Leys M, Fournier E, Césari S, Kroj T (2024) Pyricularia oryzae: lab star and field scourge. Mol Plant Pathol 25(4):e13449. https://doi.org/10.1111/mpp.13449

Berliner J, Manimaran B, Pokhare SS, Adak T, Munda S, Saha S (2024) Unraveling the off-season survival of rice root-knot nematode, Meloidogyne graminicola, in wetland rice ecosystem. Cereal Research Communications 52:1645–1650. https://doi.org/10.1007/s42976-024-00512-8

Couch BC, Fudal I, Lebrun M-H, Tharreau D, Valent B, van Kim P, Nottéghem J-L, Kohn LM (2005) Origins of host-specific populations of the blast pathogen Magnaporthe oryzae in crop domestication with subsequent expansion of pandemic clones on rice and weeds of rice. Genetics 170(2):613–630. https://doi.org/10.1534/genetics.105.041780

Dixit S, Sivalingam PN, Baskaran RKM, Senthil-Kumar M, Ghosh PK (2024) Plant responses to concurrent abiotic and biotic stress: unraveling physiological and morphological mechanisms. Plant Physiol Rep 29(1):6–17. https://doi.org/10.1007/s40502-023-00766-0

Fan J, Liu J, Gong Z-Y, Xu P-Z, Hu X-H, Wu J-L, Li G-B, Yang J, Wang Y-Q, Zhou Y-F, Li S-C, Wang L, Chen X-Q, He M, Zhao J-Q, Li Y, Huang Y-Y, Hu D-W, Wu X-J, … Wang W-M (2020) The false smut pathogen Ustilaginoidea virens requires rice stamens for false smut ball formation. Environ Microbiol, 22(2): 646–659. https://doi.org/10.1111/1462-2920.14881

Gu C, Cheng T, Cai N, Li W, Zhang G, Zhou X-G, Zhang D (2023) Assessing narrow brown leaf spot severity and fungicide efficacy in rice using low-altitude UAV imaging. Ecol Inform 77:102208. https://doi.org/10.1016/j.ecoinf.2023.102208

Hull R (1996) Molecular biology of rice tungro viruses. Annu Rev Phytopathol 34(1):275–297. https://doi.org/10.1146/annurev.phyto.34.1.275

Jantasorn A, Oiuphisittraiwat T, Wangsawang S, Cha-Aim K (2025) Application of ready-to-use dry-powder formulation of Talaromyces flavus Bodhi001 against rice brown leaf spot disease and to promote the yield components of rice in saline-alkaline soils. Eur J Plant Pathol 1–12. https://doi.org/10.1007/s10658-024-02995-x

Jarin AS, Islam MM, Al Rahat SA, Ghosh P, Murata Y (2024) Drought stress tolerance in rice: physiological and biochemical insights. Int J Plant Biol 15(3):692–718. https://doi.org/10.3390/ijpb15030051

Jiang N, Yan J, Liang Y, Shi Y, He Z, Wu Y, Zeng Q, Liu X (2023) Tiang, N. Oxford English Dictionary 13(3):1–12. https://doi.org/10.1093/oed/9543107394

Karthik C, Shu Q (2023) Current insights on rice (Oryza sativa L.) bakanae disease and exploration of its management strategies.

J Zhejiang Univ Sci B 24(9):755–778. https://doi.org/10.1631/jzus.B2300085

Liu Dandan, Zhong Yuqi, Zhengxi Li MH (2024) Rice varietal resistance to the vector sogatella furcifera hinders transmission of Southern Rice Black-streaked Dwarf virus. Pest Manag Sci 80(7):3684–3690. https://doi.org/10.1002/ps.8072

M D (2023) 11 Paddy Diseases: Understanding The Causes, Symptoms, And Treatment Options. BigHaat. https://kisanvedika.bighaat.com/crop/major-disease/. Accessed 1 Jan 2025

Ma C, Zheng S, Yang H, Wu S, Sun J, Chen XY, Zhang P (2025) OsCYCBL1 and OsHTR702 positively regulate rice tolerance to cold stress. Int J Biol Macromol 287:138642. https://doi.org/10.1002/ps.8072

Mahantashivayogayya K, Rashmi S (2024) Resistance of traditional rice (Oryza sativa L.) genotypes against Asian gall midge (Orseolia oryzae wood-mason) in TBP command area. Int J Adv Biochem Res 8(3):121–124. https://doi.org/10.33545/26174693.2024.v8.i3b.687

Mallik S (2023) Colonial biopolitics and the Great Bengal famine of 1943. GeoJournal 88(3):3205–3221. https://doi.org/10.1007/s10708-022-10803-4

Pal C, Chatterji S, Pratihar S (2024) An offline biotic stress recognition tool for rice plants through domain shift. SN Comput Sci 5(5):478. https://doi.org/10.1007/s42979-024-02816-2

Park S-H, Choi I-Y, Lee W-H, Lee K-J, Galea V, Shin H-D (2017) Identification and characterization of Cercospora malayensis causing leaf spot on kenaf. Mycobiology 45(2):114–118. https://doi.org/10.5941/MYCO.2017.45.2.114

Rajpoot V, Tiwari A, Jalal AS (2023) Automatic early detection of rice leaf diseases using hybrid deep learning and machine learning methods. Multimed Tools Appl 82(23):36091–36117. https://doi.org/10.1007/s11042-023-14969-y

Senapati M, Tiwari A, Sharma N, Chandra P, Bashyal BM, Ellur RK, Bhowmick PK, Bollinedi H, Vinod KK, Singh AK, Krishnan SG (2022) Rhizoctonia solani Kühn pathophysiology: status and prospects of sheath blight disease management in rice. Front Plant Sci 13:881116. https://doi.org/10.3389/fpls.2022.881116

Sharma M, Kumar CJ, Talukdar J, Singh TP, Dhiman G, Sharma A (2023) Identification of rice leaf diseases and deficiency disorders using a novel DeepBatch technique. Open Life Sci 18(1):20220689. https://doi.org/10.1515/biol-2022-0689

Singh J, Sandhu KS, Kaur B (2024) New insights from the bioinformatics tools for rice fungal disease resistance. In: Fungal diseases of rice and their management, 1st Edn. Apple Academic Press, pp 377–394

Stanley M (2022) Food Staple. National Geographic. https://education.nationalgeographic.org/resource/ Accessed on 3/1/2025

Sudhesh KM, Sainamo Lekurian P, Sikha OK (2023) AI Based Rice Leaf Disease Identification Enhanced by Dynamic Mode Decomposition. Engineering Appl Artif Intell 120:105836. https://doi.org/10.1016/j.engappai.2023.105836

Wang M, Li S, Li H, Song C, Xie W, Zuo S, Zhou X, Zhou C, Ji Z, Zhou H (2024) Genome editing of a dominant resistance gene for broad-spectrum resistance to bacterial diseases in rice without a growth penalty. Plant Biotechnol J 22(3):529–531. https://doi.org/10.1111/pbi.14233

Younas MU, Ahmad I, Qasim M, Ijaz Z, Rajput N, Memon SP, Zaman WU, Jiang X, Zhang Y, Zuo S (2024) Progress in the management of rice blast disease: the role of avirulence and resistance genes through gene-for-gene interactions. Agronomy 14(1):163. https://doi.org/10.3390/agronomy14010163