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Deep Vision Transformer with Tasmanian Devil Optimization for Multiclass Paddy Disease Detection and Classification for Precision Agriculture

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ABSTRACT Rice is the daily consumed crop all over the country and other parts of the world. Rice is cultivated in most of the states. Nevertheless, rice plant diseases deteriorate the quantity and quality of the crop. Rice plants are affected by various conditions, for example: sheath blight, foot rot, and so on, producing a loss in the farming yield. Therefore, earlier disease recognition in crops is important. Performing intelligent Farming is a hot zone of investigation to prevent more harm to crops. The extensive growth of Deep Learning (DL) makes it probable to attain the objective of disease recognition in crops. In this manuscript, we introduce a new Deep Vision Transformer with Tasmanian Devil Optimization for Multiclass Paddy Disease Detection and Classification (DViTTDO-MPDDC) technique for Precision Agriculture. The major intention of the DViTTDO-MPDDC technique focuses on the automatic classification and recognition of paddy plant diseases. To accomplish this, the DViTTDO-MPDDC technique uses the wiener filter (WF) technique for the noise removal process. Besides, the vision transformer (ViT) technique is used for feature extraction purposes. Additionally, the attention mechanism-based convolutional neural network with bidirectional long short-term memory (AM-CNN-BiLSTM) technique is used for the paddy disease detection process with 95.71% accuracy. Eventually, the TDO algorithm is exploited for the hyperparameter fine-tuning of the AM-CNN-BiLSTM model. To demonstrate the good classification outcome of the DViTTDO-MPDDC algorithm, a wide variety of models occurs on the benchmark database. The extensive comparable findings ensured the betterment of the DViTTDO-MPDDC method over the current methods.

INDEX TERMS Paddy Disease Detection, Tasmanian Devil Optimization, Wiener Filter, Deep Learning, Vision Transformer.

I. INTRODUCTION

In the 21st century, paddy is still the major grain in human food bases the standard source of energy, and a significant percentage of proteins consumed by almost three billion people [1]. Many times farmers have to confront different issues in paddy cultivation like diseases, Destruction of cultivable land, better population, pests, and changes in climate, etc. Because of these different issues, nowadays agriculturalists are becoming uninterested in paddy farming [2]. This study has concentrated only on the diseases and pests to the several difficulties of rice cultivation. There are three important types of paddy diseases miscellaneous, fungal, and bacterial diseases. These contain subcategories like bacterial blight, brown spot, bacterial leaf streak, bronzing, leaf smut, leaf burn, panicle disease, etc [3]. Bacterial Leaf Curse (BLB) and brown spots were current natural illnesses in rice. However, the advanced technologies for diseases and pests were still delimited [4]. Usually, the physical identification of paddy disease is the unassisted eye observation of experts that browns over additional time, expensive on massive farms. It is difficult to measure and sometimes it delivers an error when differentiating the type of the disease [5]. Due to the unawareness of suitable supervision to resolve paddy plant leaf disease, paddy productivity is reduced as delayed. To overwhelm this, proper and fast identification processes were needed for the paddy leaf disease diagnosis. This study primarily concentrated on the five most widespread paddy leaf illnesses healthy leaf, Brown spot, leaf smut, leaf blast, and bacterial blight [6]. Different novel methods were targeted for the improvement of disease and the recognition of pests, which aid in extending the quality and quantity of the crops for the farmers and the individuals doing farming [7]. In farming, an Artificial Intelligence (AI) method has a huge possibility to offer information concerning the soil quality, while implanting, whereas to sprig pesticide; there is a greatest possibility of pest infection [8]. AI techniques are utilized worldwide that aid farmers in enhancing the efficacy of crop health monitoring. They could be utilized for disease management around each crop. AI approaches that are utilized for generating and emerging smart machines have been utilized for crop management with greater precision than humans can do. Farmers are implementing the methods of AI and Machine Learning (ML) to enhance the efficacy of crop management that embraces recognition and preserving the crops from different pests insects and diseases [9]. ML, satellite imaging, data analysis, AI, and computer vision are developing technologies and the safest environment for the formation of an ecosystem essential for intelligent farming [10]. These technologies are an addition to attaining a higher average crop yield and great price controls for farmers.

This manuscript introduces a new Deep Vision Transformer with Tasmanian Devil Optimization for Multiclass Paddy Disease Detection and Classification (DViTTDO-MPDDC) technique for Precision Agriculture. To accomplish this, the DViTTDO-MPDDC technique uses the wiener filter (WF) technique for the noise removal process. Besides, the vision transformer (ViT) technique is used for feature extraction purposes. Additionally, the attention mechanism-based convolutional neural network with bidirectional long short-term memory (AM-CNN-BiLSTM) technique is used for the paddy disease detection process. Eventually, the TDO algorithm is exploited for the hyperparameter tuning of the AM-CNN-BiLSTM model. To demonstrate the good classification outcome of the DViTTDO-MPDDC algorithm, a wide variety of models occurs on the benchmark database. The extensive comparable findings ensured the betterment of the DViTTDO-MPDDC method over the current methods.

II. RELATED WORKS

Venkatraman [11] presents a new hybrid deep learning (DL) classification intended by prolonging the Excitation -and-Squeeze system structure with a Swish ReLU activation function and the channel attention mechanism. The channel attention mechanism in our presented technique determines the utmost significant channels of the feature needed for identification in the feature selection (FS) and extraction. The problem of the declining ReLU can be alleviated by using the activation function of the Swish ReLU, and the blocks of the Excitation-and-Squeeze to enhance the cross-channel interaction and data propagation. Vidivelli et al. [12] present a structure for the rice leaf disease classification by utilizing our presented Fractal and Local Binary Pattern features, which are extracted from digital images of unhealthy leaves. To attain the objective of accurate and efficient disease recognition, recent technologies were used like machine learning (ML) and image processing methods. Our presented method utilizes an Adaboost ensemble classifier for identification that has been displayed to be efficient in various applications. Sahasranamam et al. [13] proposed the AI features of the ResNet50 structure to offer a new technique for paddy illness recognition. Farmers confront various issues in rising paddy as its yield can be influenced by different factors such as varying weather pests, biodiversity, disease, and environment. Conventional techniques integrated with intelligent farming, advanced, technology, and tools were required for bulk food productivity. Now a method utilizing a ResNet50, Convolutional Neural Network (CNN) that classifies illness in paddy leaf.

Nagarajan [14] presents a cutting-edge hybrid DL method intended to tackle the crucial needs for precise and well-timed classification and identification of paddy leaf diseases. Conventional techniques frequently deficit the accuracy and efficacy needed for effectual disease recognition, requiring the improvement of more advanced techniques. Our presented method optimizes the feature extraction abilities of hierarchical relationship and the EfficientNetB0 that taking the capabilities of CapsNet, resultant in greater illness identification performance. Dubey and Choubey [15] propose an automated leaf disease recognition utilizing the DL method. Initially, the taken paddy leaf images were transformed into an RGB color method the median filter can be utilized to reduce the noise existing in the green band. Later, the color and texture features were extracted from the green band. Afterward, the feature extraction and significant features were chosen by utilizing an integration of machine learning (ML) and the optimizer method. Now, primarily, the features were chosen by utilizing the adaptive rain optimization algorithm (ARO) and a SVM-recursive feature elimination (SVM-RFE). At that time, the usual features were chosen. The chosen features were specified to the adaptive bi-long short-term memory (ABi-LSTM) classification to identify an image as Bacterial Leaf Blight disease, normal or Tungro image, or Blast disease.

Bharanidharan [16] proposed to execute an improved lemurs optimizer method as a filter-based feature transformation method for improving the precision of identifying different paddy diseases over ML methods by processing the current paddy leaves images. The novel lemur's optimizer can be modified over the stimulation of Sine Cosine Optimization for emerging the presented improved lemur's optimizer method. Salamai et al. [17] propose lesion-aware visual transformers for precise and consistent recognition of paddy leaf illnesses by classifying discriminative features of the lesion. A new multi-scale contextual feature extraction system can be proposed to aid in taking a contextual global and local illness representing features at various channels and scales. Next, a weak supervised Paddy Lesion Localization (PLL) unit has been proposed to find the individual lesions in paddy leaves, which offers the method of discriminating leaf areas that could direct the decision of the last classification. A feature fine-tuning unit can be proposed to enable modeling the relations in the local and global latent spaces, thus enhancing the spatial transformations among the paddy leave visual semantics.

III. PROPOSED METHOD

In this manuscript, we have introduced a novel DViTTDO-MPDDC method for precision agriculture. The major intention of the DViTTDO-MPDDC technique focuses on the automatic classification and recognition of paddy plant diseases. To accomplish this, the DViTTDO-MPDDC technique has image preprocessing, feature extractor, classification, and parameter tuning process. FIGURE 1 depicts the entire flow of the DViTTDO-MPDDC technique. Initially, the DViTTDO-MPDDC technique uses the WF technique for the noise removal process. The WF is an effective tool in image pre-processing for paddy diagnosis of disease, intended to minimize noise and improve the clearness of the image [18]. It works by approximating the original image with statistical information of either the image or the noise, making it best for blurred or noisy paddy field images. Using the WF, particulars like leaf textures or diseased spots become more distinct, aiding in the accurate identification of disease features. This improves the performance of ML algorithms applied for the classification of diseases. Generally, it aids improve image quality, resulting in more precise paddy disease detection outcomes.

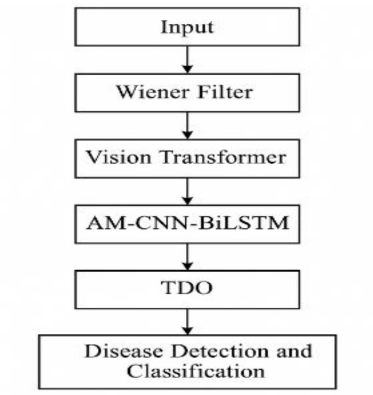

FIGURE 1. **Overall flow of DViTTDO-MPDDC technique**

Besides, the ViT technique is used for feature extraction purposes. The ViT depicts a new improvement in the computer vision (CV) framework, using a transformer-based algorithm usually applied in natural language processing (NLP) for inspired tasks. By using the Multi-Head Self Attention method, the ViT determines an outstanding ability for feature learning. Consequently, it has developed as a very encouraging method for increasing the implementation of a kind of CV task, as shown in Eq. (1) [18].

$$Attention\,(Q, K, V) = softmax\left(\frac{QK^T}{\sqrt{d}k}\right)V \quad (1)$$

whereas V, K, and Q are "Values" "Keys", "Queries" and respectively. To organize the image for input within ViT, a preprocessing stage is essential. It includes separating the image toward a sequence of patches, with a patch dimension $(16, 16)$ and strides of $(16, 16)$ which are identified by the user. These patches are further compressed into vectors and pass over a dense layer with linear activation to allow qualified embeds. A location encoder is afterward included in every encoding patch that can be required to avoid the meaning loss that may result from the arbitrary patch structure. To allow classification, this ViT algorithm embeds a token of CLS as well as the location-encoding patches. The inputs are further accepted through the converter encoding system that includes a sequence of Dense layers and Multi-Head Self Attention. For the identification of images, just the result of the CLS sign patch is needed, for the convertor will pool the feature vector of the classification. At last, it includes passing the vector over the function of softmax to gain the likelihood of prediction. The ViT has represented robust implementation in terms of larger training of the dataset, owing to its capability to efficiently take and remove common features from the data, which might aid prevent problems related to overfitting. Therefore, ViT is recognized as a suggested technique to improve classification precision in dataset challenges.

Moreover, the AM-CNN-BiLSTM model is utilized for the paddy disease detection process. CNN is extensively applied in the sequence data [20]. It is separated into 3 layers: the Fully Connected (FC), the convolutional, and the pooling layers. These pooling and convolution layers represent a majority of the CNN. Every data layer feature is removed over the convolutional kernel to gain a correlation; networking parameters were decreased over the pooling layer, hence decreasing the model complexities and computation load; and data features were incorporated and output on the layer of the FC. The particular CNN layer calculations are shown in the following Eq. (2), (3), (4) [3]. xxx:

$$C_i = R(X_{i-1} * W_c + b_1) \quad (2)$$

$$P_i = R(C_i) + b_2, \quad (3)$$

$$H_i = \sigma(P_i \times W_H + b_3), \quad (4)$$

Here, C_i represent layer output, i, from the convolutional layer; P_i denotes pooled layer output; R signifies activation function of $Relu$; σ stands for activation function of Sigmoid; H_i symbolizes FC layer output result; W_c and W_H characterize the weight matrix; b_1, b_2 and b_3 are offsetting terms; $*$ represent convolutional operation.
Initial methods for time sequence handling applied Recurrent Neural Networks (RNN). Nevertheless, in training a longer sequence, RNN is associated with the problem of explosion and gradient disappearance. in such cases of defects, investigators have suggested LSTM (a special RNN) over 3 gated elements within LSTM; in sequence, there are gates of input, forget, and output to solve these issues.

The forget gate designates that the information of the preceding node can be selected forgotten, the input gate selects inputs the necessary information to the following state, and the output gate defines which information is output as the present state. The next is the Eq. (5), (6), (7), (8), (9), (10) [2], [1] for diverse cells in LSTM:

$$i_t = \sigma(W_3 \times x_t + W_7 \times h_{t-1} + b_4), \quad (5)$$

$$f_t = \sigma(W_4 \times x_l + W_8 \times h_{t-1} + b_5), \quad (6)$$

$$o_t = \sigma(W_5 \times x_t + W_9 \times h_{t-1} + b_6), \quad (7)$$

$$\tilde{c}_l = \tanh(W_6 \times x_l + W_{10} \times h_{t-1} + b_7), \quad (8)$$

$$c_l = f_t \otimes c_{l-1} + i_l \otimes \tilde{c}_l, \quad (9)$$

$$h_t = o_t \otimes \tanh(c_l), \quad (10)$$

Here, i_t denotes input gate, f_t represents the gate of forgetting, o_t signifies output gate, x_i is the input vector at present; σ stands for the activation function of sigmoid; tanh refers to the activation function of hyperbolic tangent; W_3, W_4, W_5, W_6 represents weights of input layer to various gating methods; b_4, b_5, b_6, b_7 are terms of offset; W_7, W_8, W_9, W_{10} denotes weights of hidden layers (HL) for various gating methods; c_t signifies a component that maintains information at present; c_{t-1} symbolizes an element that maintains information at the preceding time; c_t stands for the new value of storage unit; $\otimes$ characterizes the multiplication of vector components.

The LSTM-NN only takes into consideration the correlation among the forward input sequences individually, whereas Bi-LSTM is made up of forward and backward LSTM units, permitting it to gain the upcoming sequenced information concurrently, compute the forward and backward (before and after-the-current-moment) information, and attain the outcome of linear superposition. Data are fixed from 2 directions for solving the problem of explosion and gradient disappearance. To increase the accuracy of the model the Bi-LSTM system has been accepted in this article. Now, w_{fx} and w_{fx} represents weightings from the input layer to every node; w_{fh} and W_{gh} denotes weights from the HL to every node. The output, h_{Bt}, then the Bi-LSTM layer is formulated below Eq. (11) [21]:

$$h_{Bt} = BiLSTM(H_{c,\,t-1}H_{c,t}), \tag{11}$$

Here, $H_{c,t}$ symbolize the CNN layer output at present, and $H_{c,t-1}$ stands for the CNN layer output at the preceding time.
Attention Mechanism (AM) was created from the analysis of human vision that can be frequently applied in AI, ML, and other domains. The theory is to allocate various weights to the input data and acquire the preferred data through weighting and employing a parameters model. The AM can expertly select local and global relationships, concentrate on additional vital information, and allocate significance to information at various times. Hence, afterward, the AM is presented within the CNN layer, enhancement and recalibration of data features is understood by stimulating and squeezing channels of the feature to improve important features and overwhelm irrelevant features, avoiding unimportant information in impression outcomes, and lastly achieving the determination of enhancing the method. The particular computation of the Attention layer can be shown below Eq. (12), (13), (14) [21]:

$$e_t = \tanh(W \times h_t + b), \tag{12}$$

$$a_t = \frac{\exp(e_t \times v)}{\sum_{i=1}^{t} \exp(e_t \times v)'}, \tag{13}$$

$$s_t = \sum_{i=1}^{i} a_t \times h_t{}', \tag{14}$$

whereas e_t represents a distribution of status value; W and b signify weight and biased terms of Attention; v refers to Attention value; a_t symbolize weight coefficients. The weighted amount of e_t and a_t provides the output s_t. FIGURE 2 depicts the architecture of AM-CNN-BiLSTM.

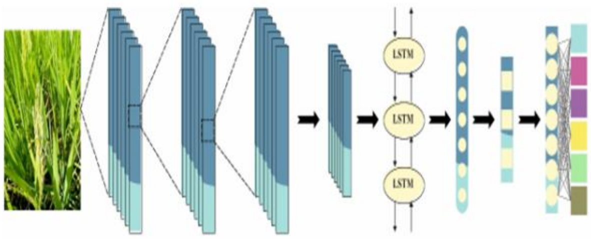

FIGURE 2. Structure of AM-CNN-BiLSTM

At last, the TDO method is exploited for the hyperparameter fine-tuning of the AM-CNN-BiLSTM system. It provides the mathematical design and modeling of a metaheuristics method named the TDO algorithm [21]. The carnivorous is the TD that the Dasyuridae family serves on the marsupial wild animal. TDs were carpetbagger mammals that, but able to hunt prey, would consume on carrion whether or not it was presented. The TD utilizes various eating methods. The TD consumes on carrion within the initial approach. It feeds and hunts on prey by attacking it during the next method. The design of TDO includes modeling this TD process of feeding. The natural behavior of Tasmanian demons is pretended, and an optimization has been defined throughout the feeding. An optimum solution can be obtained depending on the process of optimization for an optimizer problem. These mechanisms correspond to food access in the habits and lives of the TD. The arithmetical models of TD methods to reach food resources are provided for the growth of an operative to gain an optimal solution to optimizing challenges.

TDO Population members, who are hunters of problem-solving space, propose candidate values for problem variables depending on their location within the searching space. Based on the limitation difficulties, the initial population was generated at random agents. The element counts are equivalent to the problem variable numbers in which the vector is each population member. The subsequent Eq. (15) [6] states the TDO members set.

$$Y = \begin{bmatrix} Y_1 \\ \vdots \\ Y_j \\ \vdots \\ Y_M \end{bmatrix}_{M\times N} = \begin{bmatrix} y_{1,1} & \cdots & y_{1,k} & \cdots & y_{1,n} \\ \vdots & \ddots & \vdots & \ddots & \vdots \\ y_{j,1} & \cdots & y_{j,k} & \cdots & y_{j,n} \\ \vdots & \ddots & \vdots & \ddots & \vdots \\ y_{M,1} & \cdots & y_{M,k} & \cdots & y_{M,n} \end{bmatrix} \tag{15}$$

The 3[rd] candidate solution is Y_j using the TD population Y. For $k\ th$ variable, the candidate value is, $y_{j,k}$ and the TD searching count is M in the specified challenges depending on the variable counts is n. According to the variables of an objective function, each candidate solution computes the problem of the target function. The succeeding Eq. (16) [21] defines the objective function.

$$G = \begin{bmatrix} G_1 \\ \vdots \\ G_j \\ \vdots \\ G_M \end{bmatrix}_{M\times 1} = \begin{bmatrix} G(Y) \\ \vdots \\ G(Y_J) \\ \vdots \\ G(Y_M) \end{bmatrix}_{M\times 1} \tag{16}$$

The value of the objective function vectors is G, along with jth candidate solution offers the value of an objective function is G_j. The objective carrion chooses the ith population member for the jthTD. The following exploration Eq. (17) [21] pretends the randomly selected form.

$$CA_j = Y_i, j = 1,2,\dots,M, i \in \{1,2,\dots,M|i \neq j\} \tag{17}$$

The jth TD with the nominated carrion is CA_j. During this search space, estimate the original position based on the nominated carrion for the TD. Eq. (18) [21], Eq. (19) [21] upgrades the novel agent position.

$$y_{j_i k}^{new,R_1} = \begin{cases} y_{j,k} + s \cdot (d_{j,k} - I \cdot y_{j,k})_) G d_j < G_j \\ y_{j,k} + s \cdot (d_{j,k} - y_{j,k}), else \end{cases} \tag{18}$$

$$Y_j = \begin{cases} Y_j^{new\cdot R_1}, G_j^{new\cdot R_1} < G_j \\ Y_j, else \end{cases} \tag{19}$$

According to the primary approach, the jth TD with its original status is $y_{j,k}^{new,R_1}$. The objective value represents random range s, which drops into an interval of 0 to 1, and the interval of 1 or 2 for the randomly generated numbers I.
The prey position accepts the location of other population members whereas upgrading the jth TD. The following Eq. (20) [21] states the prey selection procedure.

$$p_j = Y_i, j = 1,2, M, i \in \{, 2, M | i \neq j\} \quad (20)$$

The jth TD with the chosen prey is p_j. After it improves the objective function values, the earlier location is substituted, and the original location for the TD is designed using Eq. (21) [6], (22)[21].

$$y_{j,k}^{new,R_2} = \begin{cases} y_{j,k} + s \cdot (q_{j_ik} - I \cdot y_{j,k})_) Gq_j < G_j \\ y_{j,k} + s \cdot (y_{j,k} - q_{j,k}), else \end{cases} \quad (21)$$

$$Y_j = \begin{cases} Y_j^{new \cdot R_2}, G_j^{new \cdot R_2} < G_j \\ Y_j, else \end{cases} \quad (22)$$

The jth with its original status is $y_{j,k}^{new,R_2}$. The chosen prey objective function is Gq_j. The TD receives the recently designed location and whether it distributes a better value for such a target function in comparison with the location of the previous one. The TD location updating process is mimicked in the Eq. (23), (24), (25)[21] in the following.

$$S = 0.01 \left(1 - \frac{1}{T_{\max}}\right) \quad (23)$$

$$y_{j,k}^{new} = y_{j,k} + (2s - 1) \cdot S \cdot y_{j,k} \quad (24)$$

$$Y_j = \begin{cases} Y_j^{new}, G_j^{new} < G_j \\ Y_j, else \end{cases} \quad (25)$$

The TDO method develops a Fitness Function (FF) to get enhanced classifier execution. It identifies a positive integer to indicate the greater execution of the candidate solutions. In this work, the reduction of the classification rate of error can be examined as the FF, as specified in Eq. (26) [21].

$$fitness(x_i) = ClassifierErrorRate(x_i)$$

$$= \frac{no.of\ misclassified\ samples}{Total\ no.of\ samples} * 100 \quad (26)$$

IV. RESULT ANALYSIS

The simulation study of the DViTTDO-MPDDC algorithm is executed using a benchmark database from the Kaggle repository [22]. The database holds 3000 images under 10 classes each class contains 300 images are demonstrated in TABLE I. FIGURE 3 illustrates the sample images.

TABLE 1
Details on database

Class	Labels	No. of Images
bacterial_leaf_blight	C1	300
bacterial_leaf_streak	C2	300
bacterial_panicle_blight	C3	300
blast	C4	300
brown_spot	C5	300
dead_heart	C6	300
downy_mildew	C7	300
hispa	C8	300
normal	C9	300
tungro	C10	300
Total Number of Images		3000

Each image in the collection is annotated based on the disease or condition it signifies, facilitating efficient training and assessment of machine learning models. The allocation of photos among the 10 classes guarantees a balanced dataset, essential for creating precise and resilient models. The dataset's range of plant illnesses and conditions makes it a suitable baseline for assessing the proposed algorithm's ability to effectively identify and categorize plant health concerns. The next part will offer a detailed analysis of the simulation research findings, including performance measures and comparisons to current methodologies.

FIGURE 3. Sample images

In TABLE 2. Gives the details of paddy disease recognition results of the DViTTDO-MPDDC approach. with 70%TRAPS and 30%TESPS are depicted. The TABLE values implied that the DViTTDO-MPDDC algorithm has identified 10 distinct classes. With 70%TRAPS, the DViTTDO-MPDDC model offers an average $accu_y$ of 97.51%, $prec_n$ of 87.66%, $sens_y$ of 87.52%, $spec_y$ of 98.62%, and $F1_{score}$ of 87.52%, respectively. Followed by, with 30%TESPS, the DViTTDO-MPDDC algorithm provides average $accu_y$ of 97.42%, $prec_n$ of 87.11%, $sens_y$ of 87.15%, $spec_y$ of 98.57%, and $F1_{score}$ of 87.07%, correspondingly. Although the overall accuracy is comparable to the TRAPS configuration, certain classes such as C1 (96.44%) and C5 (96.89%) show slightly lower performance, particularly in terms of precision and recall. This suggests that using a smaller portion of the dataset for training may impact the model's ability to generalize across all classes.

TABLE 2
Paddy disease recognition outcome of dvittdo-mpddc approach under 70%traps and 30%tesps

Class Labels	$Accu_y$	$Prec_n$	$Sens_y$	$Spec_y$	$F1_{Score}$
TRAPS (70%)					
C1	97.57	87.13	87.56	98.63	87.34
C2	97.33	84.26	89.22	98.21	86.67
C3	97.90	89.85	88.06	98.95	88.94
C4	96.90	87.44	82.27	98.62	84.78
C5	97.62	89.71	86.32	98.89	87.98
C6	97.14	85.50	84.65	98.47	85.07
C7	97.43	89.37	85.25	98.83	87.26
C8	98.10	88.64	92.86	98.68	90.70
C9	97.67	85.16	95.20	97.97	89.90
C10	97.48	89.53	83.82	98.95	86.58
Average	97.51	87.66	87.52	98.62	87.52
TESPS (30%)					
C1	96.44	87.64	78.79	98.63	82.98
C2	97.11	83.65	90.62	97.89	87.00
C3	96.78	86.46	83.84	98.38	85.13
C4	97.44	84.34	87.50	98.41	85.89

C5	96.89	82.61	86.36	98.03	84.44
C6	97.44	90.32	85.71	98.88	87.96
C7	97.89	89.02	87.95	98.90	88.48
C8	98.89	93.48	95.56	99.26	94.51
C9	97.67	85.71	84.51	98.79	85.11
C10	97.67	87.88	90.62	98.51	89.23
Average	97.42	87.11	87.15	98.57	87.07

In the TRAPS (70%) setup, the DViTTDO-MPDDC algorithm outperforms all disease classes, with an average accuracy of 97.51%. This high degree of accuracy implies that the model is good in classifying photos into the appropriate illness categories. Precision and recall levels are often balanced, indicating that the model can correctly recognize and categorize both positive and negative examples. For example, Class C8 (Hispa) has an F1 score of 90.70%, indicating that the model can not only properly identify the majority of Hispa cases, but also avoid incorrectly categorizing healthy plants or other illnesses as Hispa. However, in other courses, performance is significantly lower. Class C4 (Blast), for example, has an F1 score of 84.78%, suggesting that the model can differentiate this condition with high accuracy (96.90%) but may sometimes misclassify certain occurrences owing to visual similarities with other diseases. Class C9 (Normal) obtains a high sensitivity of 95.20%, indicating that the model excels at properly recognizing healthy plants, which is critical for discriminating between sick and non-diseased plants. Overall, the TRAPS setup performs well with high specificity, guaranteeing that the model avoids false positives and accurately identifies plant diseases in reality. In the TESPS (30%) setup, where only 30% of the dataset is utilized for training, the model's performance suffers marginally, with an average accuracy of 97.42%. This decrease in accuracy indicates that a smaller training set reduces the model's capacity to learn the characteristics of plant diseases efficiently, resulting in significantly less robust generalization. While accuracy remains good, several courses show more severe reductions in performance than TRAPS. For example, Class C1 (Bacterial Leaf Blight) has a precision of 87.64% and an F1 score of 82.98%, indicating that the model has difficulty in reliably detecting this illness while attaining a reasonably high accuracy of 96.44%.

FIGURE 4. $Accu_y$ the curve of the DViTTDO-MPDDC approach

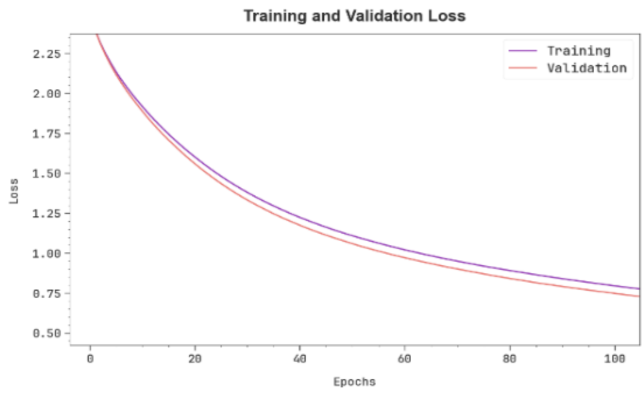

FIGURE 5. Loss curve of the DViTTDO-MPDDC approach

In FIGURE 4, the TRA $accu_y$ (TRAAC) and validation $accu_y$ (VLAAC) findings of the DViTTDO-MPDDC algorithm are shown. The rate of $accu_y$ are estimated for 0-100 epoch counts. The FIGURE underlined that the rate of TRAAC and VLAAC displays a growing trend that reported the capability of the DViTTDO-MPDDC method with greater execution over various iterations. Moreover, the TRAAC and VLAAC remain closer over the epochs, which shows lower minimum overfitting and displays improved execution of the DViTTDO-MPDDC technique, promising constant prediction on unseen samples. In FIGURE 5, the TRA loss (TRALS) and VLA loss (VLALS) graph of the DViTTDO-MPDDC technique is exhibited. The rate of loss is estimated for 0-100 epoch counts. It is denoted that the rate of TRALS and VLALS demonstrate a reducing trend, which informed the capability of the DViTTDO-MPDDC methodology in balancing a trade-off between generalization and data fitting. The constant reduction in the rate of loss moreover promises the superior performances of the DViTTDO-MPDDC technique and fine-tuning the prediction outcomes over time.

To exhibit the efficiency of the DViTTDO-MPDDC model, a comprehensive comparison study is made in TABLE 3 [23, 24]. In FIGURE 6, a comparative $sens_y$ and $spec_y$ values of the DViTTDO-MPDDC method are offered. The findings show that the ANN, AlexNet, and LR techniques have displayed the worst rate of $sens_y$ and $spec_y$. Simultaneously, the DT and Deep NN methods have achieved slightly enhanced $sens_y$ and $spec_y$. Meanwhile, the VGG-16 and AI-FMPLDDC approaches have displayed closer values of $sens_y$ and $spec_y$. Nevertheless, the DViTTDO-MPDDC system outcomes in enhanced execution with $sens_y$ and $spec_y$ of 87.52% and 98.62%, correspondingly.

TABLE 3
Comparative outcome of dvittdo-mpddc technique with existing techniques

Methods	$Sens_y$	$Spec_y$	$Prec_n$	$Accu_y$	$F1_{Score}$
DViTTDO-MPDDC	87.52	98.62	87.66	97.51	87.52
AI-FMPLDDC	87.25	97.13	84.31	96.17	86.22
VGG-16 Model	86.80	93.20	80.20	92.90	85.90
Deep NN Model	73.50	89.40	74.90	90.00	81.50

Logistic regression	68.00	87.20	67.60	86.00	77.00
ANN Algorithm	63.30	81.60	60.90	80.00	68.30
AlexNet Model	65.00	78.00	72.00	70.00	65.00
Decision Tree	86.70	83.20	82.70	91.10	86.17

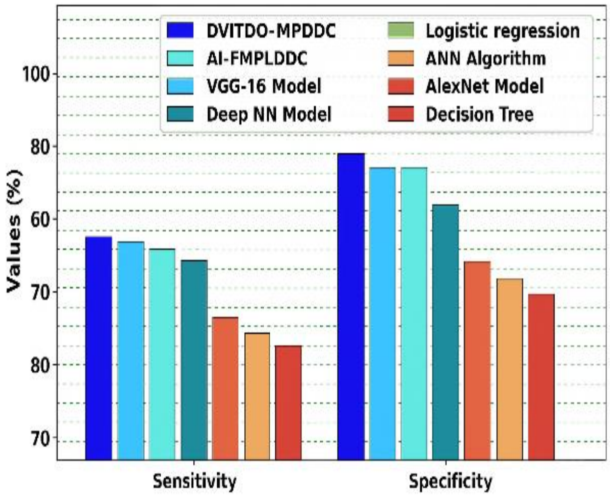

FIGURE 6. $Sens_y$ and $spec_y$ outcome of DViTTDO-MPDDC technique with existing approaches

In this study, we propose a novel deep learning framework titled Deep Vision Transformer with Tasmanian Devil Optimization (DVITDO-MPDDC) for the efficient detection and classification of multiclass paddy leaf diseases, aimed at enhancing precision agriculture. The core architecture leverages Vision Transformers (ViTs), known for their superior ability to capture global image features through self-attention mechanisms, making them particularly effective in plant pathology tasks involving complex patterns. To further enhance classification accuracy and training efficiency, the Tasmanian Devil Optimization (TDO) algorithm is integrated. TDO is a nature-inspired metaheuristic technique that fine-tunes the transformer's hyperparameters, optimizing the model's convergence and generalization abilities.

The identification and categorisation of paddy diseases are essential for precision agriculture, since they aid in averting substantial crop losses and safeguarding food security. Recent breakthroughs in deep learning and machine learning have facilitated the creation of automated systems capable of accurately recognising several paddy illnesses. These systems use several models and methodologies to improve the accuracy and efficacy of disease detection, therefore facilitating sustainable agriculture operations. This document examines several techniques and methodology used in the detection and classification of multiclass paddy diseases [25].

Deep Learning Models: DenseNet attained an accuracy of 95.7% in identifying eleven rice illnesses, while RegNet, using transfer learning, obtained an accuracy of 96.8%. These models exhibit efficiency owing to their very low parameter counts, making them appropriate for practical applications. CNN Variants: CNN models, such as MobileNetV2, have shown exceptional accuracy in illness categorisation, with MobileNetV2 attaining an accuracy of 98.05% on the PaddyDoctor dataset. These models are proficient at analysing photos to categorise illnesses according to visual symptoms. The Random Forest Classifier attained an accuracy of 97.62% in the categorisation of four varieties of paddy leaf diseases, illustrating its proficiency in multiclass classification problems. Collective and Composite Methodologies Ensemble Stacking: Employing pre-trained models such as ResNet50, InceptionV3, and MobileNetV2, an ensemble stacking methodology attained a notable accuracy of 96.09%. This approach minimises false positives and negatives, hence improving early illness identification. A hybrid model integrating CNN and SVM was used to identify illness severity levels, with an accuracy rate of 98.43%. This method effectively identifies both the kind and severity of illnesses [26] Sophisticated Methods. The Deformable Transformer Attention Mechanism effectively tackles difficulties in intricate situations, including significant overlap and morphological anomalies, attaining an accuracy of 100% and an F1-score of 94.3%. It illustrates the capability of transformer-based models in enhancing detection accuracy [27,28].

Despite the substantial improvements in accuracy and efficiency of paddy disease detection afforded by these sophisticated models and methodologies, issues persist regarding scalability and practical implementation. Considerations such as dataset variety, computing resources, and model interpretability are essential for the efficient deployment of these systems in diverse agricultural contexts. Furthermore, the integration of these technologies with mobile apps and IoT devices might enhance precision agriculture by offering real-time disease monitoring and management options. The identification and categorisation of paddy diseases are essential for precision agriculture, since they aid in mitigating substantial crop losses and safeguarding food security [29]. Recent breakthroughs in deep learning and machine learning have facilitated the creation of automated systems capable of accurately recognising several paddy illnesses. These systems use several models and methodologies to improve the accuracy and efficacy of disease detection, therefore facilitating sustainable agriculture operations. The following sections examine several techniques and procedures used in the detection and classification of multiclass paddy diseases [30].

V. CONCLUSION

In this manuscript, we have introduced a novel DViTTDO-MPDDC methods for precision agriculture. The major intention of the DViTTDO-MPDDC technique focuses on the automatic classification and recognition of paddy plant illnesses. This study seeks to provide a complete multi-class dataset of rice illnesses, including eleven distinct rice diseases and one healthy leaf category, therefore resolving the shortcomings of prior studies. To accomplish this, the DViTTDO-MPDDC technique uses the WF technique for the noise removal process. Besides, the ViT technique is used for purposes of feature extraction. Additionally, the AM-CNN-BiLSTM model is applied for the process of paddy disease detection with 97.51% accuracy. Eventually, the TDO algorithm is exploited for the hyperparameter tuning of the AM-CNN-BiLSTM model.To demonstrate the good classification outcome of the DViTTDO-MPDDC algorithm, a wide variety of models occurs on the benchmark database. The extensive comparable findings ensured the betterment of the DViTTDO-MPDDC method over the current methods. Future research may concentrate on augmenting the multi-class rice disease dataset to include a wider array of rice illnesses beyond the eleven already recognised, hence improving the relevance of detection techniques for agricultural workers confronting various disease concerns.

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