A novel approach to detect tomato leaf disease using vision transformer

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ABSTRACT

Tomatoes are one of the most widely consumed vegetables across the world. However, tomatoes are prone to diseases. Recognizing and classifying tomato leaf diseases is crucial task. Various deep learning (DL) methods have been developed by several researchers, but they have some complex issues like noise in images, high computational complexity, poor accuracy, and limited feature selection. The main goal of this research is to present novel DL based tomato leaf disease classification framework with neural network based gated vision transformer (G-ViT) model assisted attention mechanism. The proposed framework uses dilated convolution with bidirectional long short-term memory (Bi-DLSTM) used for efficient feature extraction to enhance the classification. An effective chaotic spider wasp optimization (CSWO) is used for feature selection. Further, novel attention based gated vision transformer (A-GVT) is used to classify tomato leaf diseases which integrates strengths of attention mechanism and G-ViT models. Further, to improve the generalizability of classification model, its parameters are tuned with black widow optimization (BWO) algorithm. The experimental findings shows that proposed framework outperformed previous studies on tomato leaf disease identification and classification models in terms of accuracy, precision, recall, F1-score, specificity, mean absolute error (MAE), and root mean square error (RMSE) with 99.7%, 98.29%, 98.22%, 98.25%, 99.19%, 0.03, and 0.25 respectively. The proposed study can pave a way for new agricultural revolution.

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1. INTRODUCTION

Agriculture aids the nation's development. The economy of the nation mainly depends on agriculture [1]. The role of agriculture has expanded with the acceptance of technologies like green energy such as biofuels. Furthermore, agriculture is the source of raw materials in making chemicals and medicines [2]. According to the report of food and agricultural organization (FAO) of the United States, the rate of hunger is gradually increasing since 2014 [3]. Plants provide food for all living beings and life is not possible without plants. Although plants are essential for life, their production is affected by several diseases [4]. Tomato is a kind of fruit or vegetable, which is widely cultivated in India. There are many types of tomato diseases and pests in the whole growth of tomato life cycle [5].

Tomatoes are rich in nutrients highly consumed by humans [6]. Tomatoes can grow in any type of soil if it has an adequate drainage [7]. The demand of the tomato is high due to its pharmacological properties such as reducing hypertension, gingival bleeding, and hepatitis [8]. These plants are more susceptible to diseases and causes financial loss in agricultural sector [9]. Hence, identifying the plant diseases are important to lighten up the yield losses [10].

Traditional diagnostic methods are expensive, time consuming and labor-intensive. Visual analysis and chemical testing are the most used traditional methods for tomato leaf disease diagnosis [11]. Farmers mainly use traditional methods of identifying diseases by sharing samples with experts to identify the disease. Experts mostly do naked eye observations for disease identification, and this leads to more complications in terms of disease identification [12]. According to statistical data, more than 20 tomato diseases affects the tomato crop production across the globe [13]. With the development of computers and internet of things (IoT) technologies, the agricultural disease diagnosis has enhanced [14].

Some of the plant diseases can be diagnosed by examining the nucleus. Hence, cell segmentation is an important aspect of tomato plant disease identification [15]. Deep learning (DL) techniques are commonly used for segmentation and classification of disease diagnosis [16]. DL with convolutional neural networks (CNN) enhances the diagnosis and classification of tomato leaf diseases. CNN extracts the features and ensure reliability, authenticity and validation of the model [17]. CNN has several architectures and most of them have large number of deep layers with large number of parameters [18].

In recent times, several studies were established to analyze the diseases of tomato leaves. DL methods are the most general method used for detection of tomato leaf diseases automatically. Nevertheless, many of the DL architectures has some complications like computational complexity, updating the parameters and so on which leads to classification complexity. To deal with these limitations the proposed study introduces a novel classification approach for tomato leaf disease recognition with attention based gated vision transformer (A-GVT). Major contributions of the proposed research are listed as follows: i) to extract the features of tomato leaf diseases a dilated convolutional bidirectional long short-term memory (Bi-DLSTM) network is employed; ii) to increase the accuracy of classification and to select the optimal features a chaotic spider wasp optimization (CSWO) is utilized; iii) to accurately classify the tomato leaf diseases, an attention based gated vision transfer model is deployed; and iv) to reduce the tomato disease classification complexity, parameters of these models are tuned using Blackwidow optimization algorithm. Remaining part of this article is organized in the subsequent order: the following section presents several literature reviews based on the classification of tomato leaves. In section 2, proposed methodology is explained. Section 3 evaluates experimental findings and section 4 summarizes the whole research as conclusion.

The various existing studies associated with disease diagnosis of tomato leaves are surveyed in this part. Computer vision methodology utilizes a capsule neural network named CapsNet is developed by Abouelmagd *et al.* [19] to overcome the relative spatial and orientation relationships in datasets. Pre-processing and data augmentation methods are utilized to overcome the overfitting issues. A standard dataset named plant disease images of tomato from Kaggle is used and consists of almost 70,800 images. The dataset contains 10 labeled classes which undergoes training and testing. Classification metrics like accuracy, recall, F1-score and precision are evaluated for performance measurement. CapsNet attained 96.39% accuracy with the rate of loss at 0.221. This approach failed to consider the unmanned aerial vehicle (UAV) to gather plant leaf images.

To reduce the tomato plant losses, a transfer learning based CNN on tomato leaf disease diagnosis is presented by Saeed *et al.* [20]. The tomato leaf disease classification is carried out by two models which are pretrained–Inception-V3, Inception-ResNet-V2, and these models were trained under PlantVillage datasets and real-time captured images of total 5,225 images. This study analyses only two types of leaf diseases of tomato–early blight of tomato and yellow leaf curl virus. This approach consists of data collection, image pre-processing, augmentation, model with training (80%), validation (10%), and testing (10%) of datasets. Then transferred to learning models for classification and evaluation of diseases. The approach proposed in the study attained 99.22% accuracy.

To avoid the loss in the agriculturally based economy Ashok *et al.* [21] presented a DL-based image processing technique for tomato leaf disease diagnosis. The technique is established based on segmentation, open-source algorithms and clustering for the accurate prediction of tomato leaf diseases. The images are collected directly from plants and these images undergoes pre-processing, extraction of features, segmentation and categorization using CNN. This study analyzes only Phoma rot, leaf miner and target spot tomato leaf diseases. The presented study's performance is evaluated using metric accuracy and an accuracy of 98.12% is achieved. A CNN based tomato leaf disease detection is developed by Agarwal *et al.* [22] to increase the productivity of tomatoes. The images of tomato diseases are collected from a public repository–PlantVillage and consists of the following classes: healthy, bacterial spot, late blight, early blight, leaf mold, two-spotted spider mite, septoria leaf spot, target spot, yellow leaf curl virus, and septoria leaf spot. The CNN model for categorization consists of three layers of convolution with one max pooling layer and two fully connected layers. The main limitation of the study is that a small number of images were trained.

A DL based agro deep mobile application is developed by Paymode *et al.* [23] to detect the tomato leaf diseases in early stages. The model training took place with PlantVillage dataset. The dataset consists of a total of 12,000 images with ten classes. These images were fed into augmentation process to increase the performance and to reduce over fitting. The CNN model consists of input layers, hidden layers, pooling layers with fully connected layers. The performance evaluation of this classification model obtained an accuracy of 97%. In addition to that, the segmentation performance parameters used were F1-score, precision, recall, G-means, and sensitivity.

A deep convolutional neural network (DCNN) integrated with attention mechanism is developed by Zhao *et al.* [24] for the accurate prediction of variety of tomato diseases. PlantVillage dataset consists of 4,585 images with 10 classes utilized. After the data augmentation process 22,925 images were obtained and 80%-20% train-test split was used. The performance of the model was evaluated using some metrics like accuracy, recall, precision, F1-score and obtained the highest values of 96.81%, 96.77%, 96.81%, and 96.79% respectively.

To improve the performance of tomato leaf disease diagnosis and to reduce the impact on crop production, Zhou *et al*. [25] presented a reconstructed deep residual dense network (RRDN). The dataset of AI CHALLENGER 2018 for tomato leaf disease is taken in this study and with 13,185 images categorized into 9 classes. The dataset was divided into training, test, and validation with a ratio of 6:2:2. The RRDN model improves the denoising issues in the images. This paper highlights the training and testing accuracy of RRDN models with advanced methods. On comparing with those traditional approaches, RRDN attained highest accuracy of 95% in tomato leaf disease identification.

Tomato leaf disease detection using the three-machine learning (ML) methods like CNN, k-nearest neighbor (KNN), and support vector machine (SVM) was developed by Lekha *et al*. [26]. The images used in this paper were taken from PlantVillage image dataset with a total of 16,102 images with all 10 classes. 80% of the images underwent training and 20% of images were fed into validation. Training and testing accuracy are evaluated with 40 epochs on CNN model. Evaluating the accuracy of these ML models, CNN attained the highest accuracy of 79.14% compared with SVM (68.22%) and KNN (74.56%).

Target identification algorithm improved the detection of tomato leaf disease, and has some limitations such as diversity of complex backgrounds, generalization ability and reduced accuracy. Hence to overcome these shortcomings, Wang *et al*. [27] presented a target detection model based on improved YOLO-v5. The images used in these experiments were collected from internet sources, image synthesis and Kaggle, containing a total of 4,578 images. The dataset consists of four classes like leaf mold, early blight, healthy leaves and late blight. Target detection with global attention mechanism (TDGA) was developed based on YOLO-v5. This TDGA model attained 91.40% of accuracy which was much better than the original YOLO-v5 model.

To identify the leaf diseases accurately, early CNN based AlexNet and VGG-16 are utilized by Shanthi *et al*. [28]. The PlantVillage dataset collected from Kaggle consists of the following classes: healthy leaves, Bacterial spot, early blight, yellow leaf curl, leaf mold, and septoria leaf spot leaves. The dataset images undergo train, test and validation phase in the ration of 8:1:1. The images are pre-processed, normalized and augmented for better performance. This study highlighted the accuracy performance for each class and the model attained an accuracy of 91.2%.

A DL-based CNN model was developed by Ibañez and Muñoz [29] to monitor and classify the tomato leaf diseases using a publicly available dataset of 11,000 images. The dataset is accomplished with 2,500 images gathered from the Mexican fields. For feature selection, the CNN model consists of kernel size of 3×3 with four convolutional layers. After that, the classification model comprised of global average pooling layer, SoftMax activation for dense layer. To analyze the performance of the model classification metrics is observed. The highest accuracy of 99.6% is attained by customized CNN model.

A DL based DenseNet architecture was implemented by Yulita *et al.* [30] to detect the tomato leaf diseases and it was implemented in a mobile application. The image data for tomato leaf disease was downloaded from Kaggle with 10,000 images. The image data was fed to pre-processing and data augmentation was used for obtaining quality image and to avoid overfitting. Then classification was carried out by DenseNet architecture with 10 dense units. After that the mobile application's primary goal was to detect the tomato leaf diseases for Indonesian farmers. The effectiveness of the model was assessed based on classification metric.

A DCNN approach was established by Lingwal *et al.* [31] to detect tomato plant leaf diseases. The data was collected from the public repository, namely, PlantVillage dataset. The image data was divided into training, validation and testing in a ratio of 70:10:20. The efficiency of the DenseNet, Inception-V3, ResNet, VGG-16, and base CNN was evaluated for metric performances. The validation and training accuracy of all these models were evaluated for performance analysis. Among all these methods VGG-16 performed better with 90.84% accuracy.

Tomato leaf disease detection for agro based industries was developed by Roy *et al.* [32] based on novel PCA DeepNet. The tomato image data was gathered from public repository dataset consisting of 18,128 images of tomato leaves. The image data was split into 7:3 ratio for training and validation. This dataset underwent data engineering, feature selection and classification. The PCA DeepNet model attained an accuracy of 99.6%, recall of 98.49%, precision of 98.5%, and F1-measure of 98.5%.

To overcome the complex background of the image, Peng *et al.* [33] established a Dense Inception MobileNet-V2 parallel convolutional block attention network for the diagnosis of tomato leaf disease. The study utilized the tomato leaf disease dataset of 1,256 images with five leaf diseases and the number of images were expanded to 8,190 images using image enhancement. Classification metric was evaluated for the analysis of performance. The accuracy attained by this model was 94.44%. Data augmentation was not managed properly, which is the limitation of this model.

A tomato leaf disease detection in early stages is quite necessary to detect the tomato leaf diseases. Hence Gaashani *et al.* [34] developed a tomato leaf disease classification model based on transfer learning and feature integration. The study used a dataset which was gathered from a publicly available dataset named PlantVillage and used 1,152 images for further processes. This model was evaluated by three popular traditional ML classifiers: SVM, random forest, and multinomial logistic regression, and multinomial logistic regression outperformed with an average accuracy of 97%. The major issue is that the high accuracy in a particular data set may lead to over fitting.

The tomato disease classification is carried out by fine-tuned residual neural network models. Kanda *et al*. [35] developed an intelligent based DL method for recognizing the common diseases in tomatoes. The tomato leaf disease dataset consisted of 18,160 images and divided into training and validation phase and attained best solution in the ratio of 8:2. The classification approach was carried out by a transfer learning model followed by a CNN with several layers. This study conducted an experimental evaluation based on various train and validation ratio, different batch sizes. Confusion matrix was evaluated for performance validation.

An explainable driven DL framework for tomato leaf disease classification was performed with transfer learning based EfficientNet-B5 model which was demonstrated by Bhandari *et al.* [36]. The study used the tomato leaf disease dataset from Kaggle. The dataset images were divided into 90:10 for training-testing split and furthermore, the 10% images from training were also considered for validation phase. Initially the dataset images were augmented to avoid overfitting, then the images were fed into EfficientNet-B5 to increase efficiency and accuracy. Then for statistical analysis explainable artificial intelligence (XAI) technique was utilized. All classification metrics were evaluated for the performance evaluation.

An automatic segmentation (AS) based tomato leaf disease classification was performed [37] to avoid overfitting issues in the DL approaches. The tomato PlantVillage dataset with 18,161 images were utilized to augment the images. The modified UNet model was utilized to segment the input images. Then the optimization with hyperparameters based on artificial rabbit algorithm (HPOARA) is demonstrated to classify tomato leaf diseases as healthy or unhealthy. Classification metric was validated for the performance evaluation. Various meta-heuristic approaches were analyzed to increase classification accuracy.

A combination of CNN, convolutional block attention module (CBAM) and SVM were utilized to classify and identify the tomato leaf disease by Altalak *et al.* [38]. Tomato leaf disease dataset images were pre-processed and augmented for further classification process. Images were zoomed, flipped horizontally and vertically, rotated, shifted in width and height and then used for the augmentation. CNN based ResNet-50 was utilized for feature extraction. After that the base ResNet-50 model was fed into CBAM and SVM classification model. The model was trained with 50 epochs and attained 97.2% of classification accuracy.

Tomato leaf disease identification plays a vital role in agricultural sector. So, it is necessary to identify the diseases which affects the production of tomatoes. Several researchers have developed numerous methods to identify and classify diseases. On analyzing the various studies, insufficient data segmentation, limited number of training and testing epochs, absence of meta-heuristic approaches, high computational complexity, limited feature extraction and inefficiency of pre-processing methods are considered as the main limitations of existing approaches. In view of these limitations the suggested methodology proposed a novel tomato leaf disease classification framework and is explained in detail in the following section.

To deal with these limitations the proposed study introduces a novel classification approach for leaf disease detection of tomatoes based on A-GVT model. The following is an overview about the novel contributions of the proposed research. First, to extract the features of the tomato leaf diseases a Bi-DLSTM network is employed. Second, to increase the accuracy of classification and to select the optimal features a CSWO is utilized. Third, to accurately classify the tomato leaf diseases, an attention based gated vision transfer model is deployed. Fourth, to reduce the tomato disease classification complexity, parameters are tuned using the black widow optimization (BWO) algorithm.

Tomato leaf disease identification plays a vital role in agricultural sector. It is necessary to identify the diseases which affects the production of tomatoes. So, several researchers have developed numerous researches in the name of tomato leaf disease detection, identification and classification. On analyzing various previous studies, insufficient data segmentation, limited number of training and testing epochs, absence of meta-heuristic approaches, high computational complexity, limited feature extraction, and inefficiency of pre-processing methods are considered as the main limitations of existing approaches. In view of these limitations the suggested methodology proposed a novel tomato leaf disease classification framework is developed and is explained in detail in the following section.

2. METHOD

Tomatoes are universal crop with high nutritional values; however, it is prone to various diseases, and precise identification of those diseases are still a challenging task. Hence, this presented research utilized a novel and effective tomato leaf disease classification using DL architecture. This research finds the experts of agriculture sector for analyzing the tomato leaf diseases. Overall workflow of the suggested tomato leaf disease classification framework is pictured in Figure 1.

This research begins with data acquisition, which is collected from PlantVillage–a public repository and pre-processing of images to improve the quality of data. The pre-processed images are segmented using residual attention UNet++ to identify various parts of diseased portions. Secondly, the features are selected and extracted from the images that are segmented, and a chaotic spider wasp optimizer algorithm (CSOA) is considered to select the optimal features. Then the classification of diseases of tomato leaves is carried out using A-GVT to categorize the types of diseases. In addition to that, optimization is used to refine the parameters for enhanced performance of classification model.

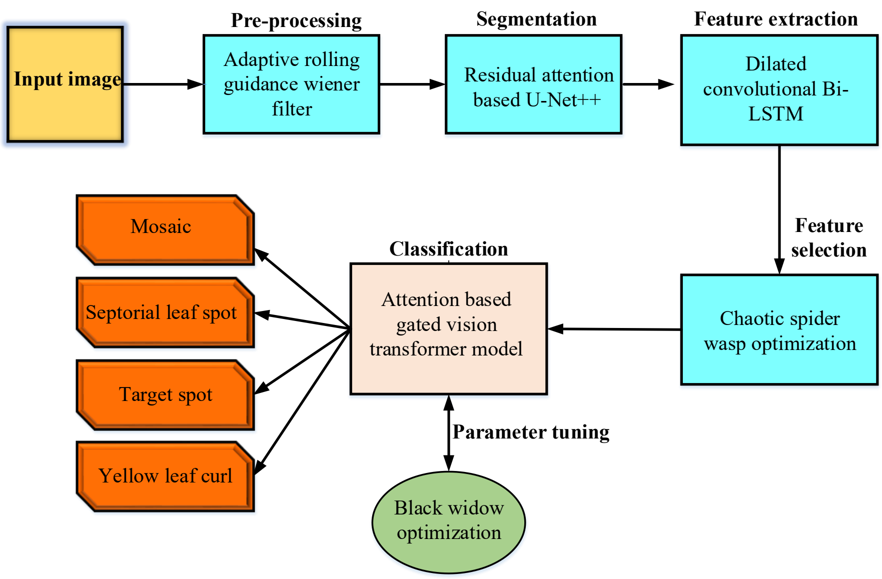

Figure 1. Overall workflow of proposed tomato leaf disease classification method

2.1. Pre-processing

The pre-processing was performed to remove the noise and to recover the edges by adaptive rolling guidance wiener filtering technique (ARGWF) [39]. In rolling guidance wiener filter, the guided filtering is used for edge recovery process. The guided filter improves the removal of small structures, enhance the structure and edges of the input images. For small structural removal the wiener filtering is used to smooth the input images, and the filtered image is represented as (1).

$$G = Wienerfilter(i, r, \eta, M) \quad (1)$$

Where G denotes the smoothed image, i represents input image, filter radius is represented as$r$, regularization parameter is denoted as η, and M is computed for the size of every local path with the box filter. Then the recovery of edge is done by guided filter, and it is an iterative process. The edge recovery process is represented as (2).

$$H^{n+1} = Guidedfilter(H^n, i, \sigma_s, \lambda_r^2) \quad (2)$$

Here, guided filtering operation is denoted $Guidedfilter(.)$, $H^n$is the image which is smoothed for the n^{th} iteration, λ_r^2 and σ_s are the regularization parameter and standard deviation respectively. In general, ARGWF is simply written as (3).

$$I = ARGWF(i, \sigma_s, \lambda_r, N) \tag{3}$$

Here, the filtering output is represented as I and N denotes the iteration number. The ARGWF smooth the input images, and the filtered images edges are mainly blurred to focus on large-scale edge details in the successive edge recovery process.

2.2. Segmentation

The segmentation of the pre-processed images are done by residual attention based UNet++ [40] model to significantly identify the diseased parts of the tomato plant. Residual attention based UNet++ is the combination of residual network, attention mechanism and UNet++. The integration of these networks brings some benefits including UNet++ improvises the semantic gap between the encoder and decoder networks and feature maps, residual unit addresses the degradation problem and eases the training network, and the attention mechanism suppress the irrelevant segmentation background area and also increases the weight of the target area. The UNet++ connects the encoder and decoder network through revised skip pathways. The encoder networks feature map is mapped to the decoder network with the help of dense convolutional blocks. The skip pathway is formulated in (4).

$$y^{p,q} = \begin{cases} P\{y^{p-1,q}\}, \\ P\left\{\left[\int \begin{matrix} q-1 \\ k=0 \end{matrix} A_g(y^{i,k}), U(y^{p+1,q-1})\right]\right\} \end{cases}, \begin{matrix} q = 0 \\ q > 0 \end{matrix} \tag{4}$$

Where $y^{p,q}$ represents the output of the node $Y^{p,q}$, p indicates the layer (down sampling) according to the encoder sub network, the convolutional layer of the block (dense) along with skip pathways and are denoted as q, a convolutional operation followed by rectified linear unit (ReLU) activation function is represented as $P\{.\}$, A_g and [] represents the attention gate and concatenation layer respectively. $U\{.\}$ represents the up-sampling operations.

2.3. Feature extraction

After segmentation, segmented images go through feature extraction process. For efficient tomato leaf disease identification, an effective feature extraction is necessary. For that purpose, the proposed approach utilizes Bi-DLSTM model. Compared to traditional feature extraction approaches including long short-term memory (LSTM) and CNNs, the proposed approach offers a hybridized approach which integrates the benefits of both bidirectional long short-term memory (Bi-LSTM) model and dilated convolutions. The architecture of Bi-DLSTM is visualized in Figure 2.

While using recurrent neural networks (RNN) for extracting long features, maintaining mid- and short-term memory is quite challenging. To overcome this issue and to enhance the extraction capability a new dilated LSTM has been introduced and it has one dilated recurrent layer with fixed dilations. Although a standard LSTM solves the vanishing gradient descent problem, it has some limitations while learning long-term dependencies. The main issue in standard LSTM is the change of cell state, when new functions are added to the inputs. These issues are addressed by using the dilations and skipping connections in the dilated LSTM. A recurrent skip connection with dilations increases exponentially in a multi-layered learning model implementation is utilized for the dilated LSTM implementation. The complex data are learned on different layers of dilated LSTM. The dilated recurrent skip connection in the LSTM cell can be represented as in (5).

$$r_t^{(l)} = LSTM\left(i_t^{(l)}, r_{t-d^l}^{(l)}\right) \tag{5}$$

Here, $r_t^{(l)}$ represents the cell in layer $l$at a time t, $d^{(l)}$ represents the length of skip of layer l and the LSTM input layer l at time t is denoted as $i_t^{(l)}$. The dilation of the l-th layer $d^{(l)}$ is calculated as in (6).

$$d^{(l)} = P^{(l-1)}, l = 1,2, \dots \dots L \tag{6}$$

Where P and L implies the dilations at different layers. The combination of dilated recurrent layers brings out some benefits via which different layers concentrate on different resolutions and enables the network to learn more long-term dependencies. Not only that, but it also reduces the path between different time steps.

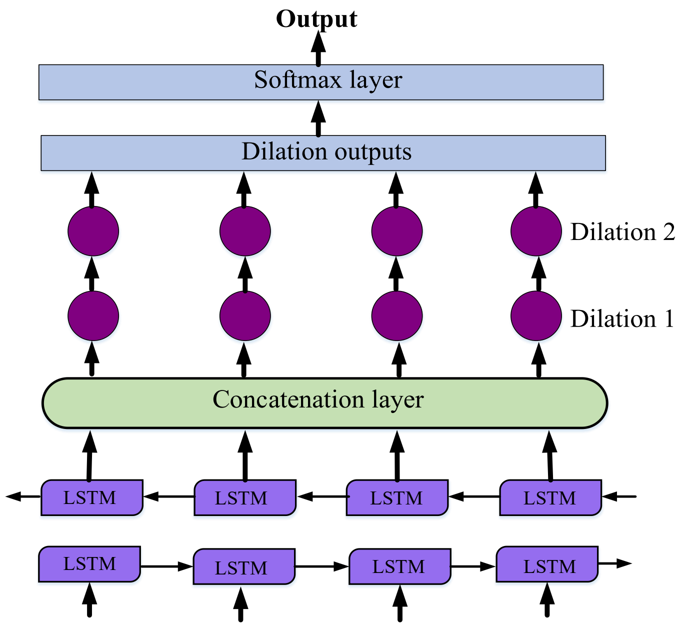

Figure 2. Architecture of Bi-DLSTM

2.4. Feature selection

It is a process of selecting efficient and optimal features from the extracted features. In this proposed approach, feature selection is done by CSWO algorithm. It is an improved version of spider wasp optimizer (SWO) [41] which is a meta-heuristic approach used to address the continuous optimization issues. The feature selection based CSWO algorithm is categorized into several activities like initialization, fitness evaluation, spider movement, wasp movement, and chaotic mapping.

2.4.1. Initialization of parameters

Initialization of parameters randomly generates population of spiders and wasps within the search space and the size of the search space is defined as $No.of spiders/wasps(p/q) * \left(No.of features(N)\right)$. The wasp and spider population are described as (7) and (8).

$$W = \begin{bmatrix} W_{1,1} & \cdots & W_{1,n/2} & \cdots & W_{1,n} \\ \vdots & \ddots & \vdots & / & \vdots \\ W_{q/2,1} & & W_{q/2,n/2} & & W_{q/2,n} \\ \vdots & / & \vdots & \ddots & \vdots \\ W_{q,1} & \cdots & W_{q,n/2} & \cdots & W_{q,n} \end{bmatrix}_{q\times n} \tag{7}$$

$$S = \begin{bmatrix} S_{1,1} & \cdots & S_{1,n/2} & \cdots & S_{1,n} \\ \vdots & \ddots & \vdots & / & \vdots \\ S_{p/2,1} & & S_{p/2,n/2} & & S_{p/2,n} \\ \vdots & / & \vdots & \ddots & \vdots \\ S_{p,1} & \cdots & S_{p,n/2} & \cdots & S_{p,n} \end{bmatrix}_{p\times n} \tag{8}$$

2.4.2. Fitness evaluation

The fitness of each subset of features (each row of wasps and spiders), is calculated by passing each subset into the fitness function. The results are stored as wasp fitness and spider fitness. After that, the new populations spider sorted and wasp sorted are created, which stores the subset of features for the spider and wasp populations in ascending order of error or fitness value. Spider top and wasp top are the newly defined populations to store those populations for the current iteration respectively. The four fitness functions such as decision tree (DT), naïve Bayes (NB), KNN, and linear discriminant analysis (LDA) used in this method are passed into SWO function for the results. The calculation of fitness F_x for each selected subset of features then be computed by (9) and (10).

$$F_x = \sum_{x=1}^{n_x} \frac{Error_x^o}{n_x} \tag{9}$$

$$Error_x^o = [y_x^{'o} \neq y_x^o] \tag{10}$$

Where the difference between the original and predicted results are denoted by $Error \rightleftarrows_x^o$ and n_x is used to represent the total number instances.

2.4.3. Spider movement

The spider movement or cross over function is performed by concatenating some features from the spider top (T_S) and wasp top (T_W) population which are depicted as in (11) and (12).

$$FeatS_q = T_S\left[Re\,m\left(q, \frac{N_S}{2}\right)\right]\left[: \frac{N_{feat}}{2}\right] \tag{11}$$

$$FeatW_q = T_W\left[Re\,m\left(q, \frac{N_W}{2}\right)\right]\left[\frac{N_{feat}}{2} :\right] \tag{12}$$

Here $FeatS_q$ and $FeatW_q$ are the features selected from T_S and T_W for the iteration q. N_{feat} represents the total number of features available, N_S and N_W denotes the number of spiders and wasps respectively. To retrieve the original number of features, spider, and wasp features are concatenated and a new subset is formed from where features for each iteration is applied to a new population named New_S.

2.4.4. Wasp movement

The wasp movement or mutation is performed by randomly changing the selection of certain features in the wasp top population. The newly formed features are stored in a new population named New_W. The mutated value for the new population is calculated as in (13).

$$Mut_p^W = T_W\left[Re\,m\left(q, \frac{N_W}{2}\right)\right][p] \times [Rand(0,1)] \tag{13}$$

Here Mut_p^W represents the mutated value for the feature for $p$number of iteration and $Rand(a, b)$ returns an integer with the bounds of a and b. Then the initial spider and wasp populations are concatenated with the new population and all the fitness features are compared to the best global fitness value for all iterations. The global fitness and the features are updated only when the local fitness value exceeds a global fitness value. The entire process will be repeated until the maximum number of iterations is achieved. Then only the final variables are returned to the global best fitness and global best features.

2.4.5. Chaotic improvement

For optimal feature extraction, the model is improved with an optimization algorithm. The algorithm is updated with Chebyshev chaotic map [42], which improves the efficiency of the algorithm and perform well on feature extraction process. The updated chaotic map representation is described as in (14).

$$p_{q+1} = cos\left(q\, cos^{-1}(p_q)\right) \tag{14}$$

The presented feature selection algorithm combines the strength of both SWO and chaotic mapping. This Chebyshev chaotic mapping enhances the search capability of SWO which helps to find better features that helps the model for accurate classification. In summary, the presented feature selection algorithm effectively captures the most relevant features for tomato leaf disease classification.

2.5. Classification

After the extraction of features and selection of optimal features, classification of tomato leaf diseases is carried out by A-GVT model. The classification model categorizes the features based on the types of diseases. The architecture of A-GVT is depicted as Figure 3.

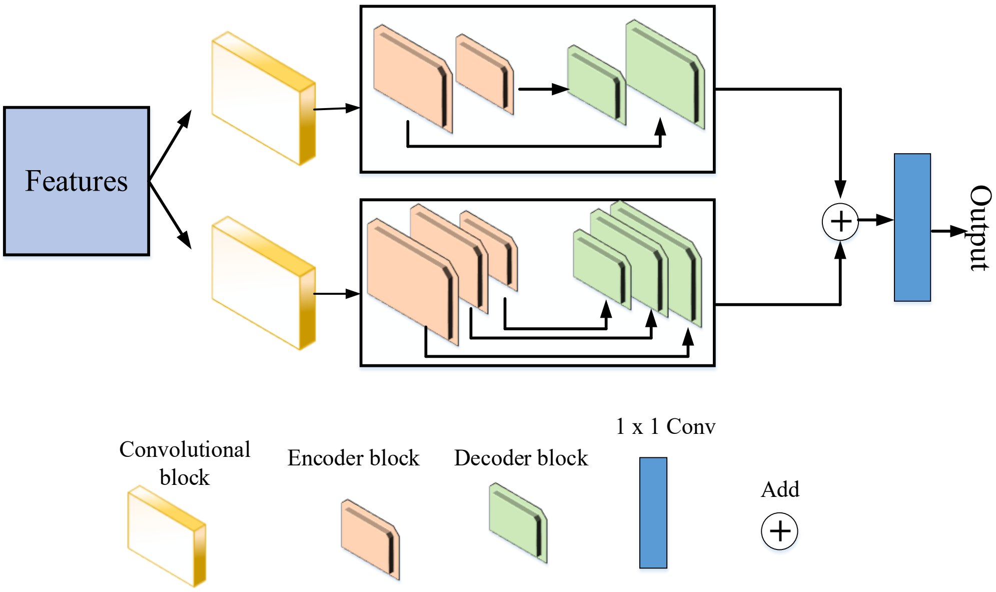

Figure 3. Architecture of A-GVTs

To overcome the computational complexity of affinities, self-attention [43] is decomposed into two self-attention modules. The first module employs the height axis of feature map, and the second module works on width axis. The self-attention layer is calculated with the help of projected input, and it is expressed as in (15).

$$x_{pq} = \sum_{h=1}^{H} \sum_{w=1}^{W} soft\,max\left(q_{pq}^{T} k_{hw}\right) v_{hw} \quad (15)$$

Here queries are represented as q, the keys are denoted as k and the values are described as v. W and H are the width and height of the feature maps. The self-attention mechanism gathers local information from the feature map. Calculating these affinities is computationally expensive and self-attention layer does not utilize positional information. It is useful in vision transformer (ViT) model to detect the structure of the object. The axial attention and positional embedding are combined to utilize it for all the queries, keys and values. The self-attention mechanism with transformer model and positional encodings for any input feature map can be written as in (16).

$$x_{pq} = \sum_{w=1}^{W} soft\,max\left(q_{pq}^{T} k_{pw} + q_{pq}^{T} r_{pw}^{q} + k_{pw}^{T} r_{pw}^{k}\right)\left(v_{pw} + r_{pw}^{v}\right) \quad (16)$$

Where r^q, r^k, r^v all these modules belong to a width wise attention model. In (16) describes the attention along with width axis, similarly attention with height axis is also expressed. On combining these two self-attention models, a new computationally efficient single self-attention model is formed. The self-attention layer with positional encoding can calculate non-local context by using computational efficiency. The proposed approach utilizes small scale datasets. To solve the issue of accurate positional bias, and to control the positional bias, a modified attention block is developed which can be employed in the encoding of non-local context. Architecture of gated attention mechanism is illustrated in Figure 4.

The self-attention model is updated with G-ViT model applied on the width axis is expressed as in (17).

$$x_{ij} = \sum_{w=1}^{W} soft\,max\left(q_{pq}^{T} k_{pw} + G_{Q} q_{pq}^{T} r_{pw}^{q} + G_{K} k_{pw}^{T} r_{pw}^{k}\right)\left(G_{V1} v_{pw} + G_{V2} r_{pw}^{v}\right) \quad (17)$$

Where the self-attention formula follows with gated mechanism. G_Q, G_K, G_{V1}, G_{V2} are parameters, and they together create gated mechanism which influence the positional encoding with non-local context. The gated mechanism will assign an accurate positional encoding a high weight compared with inaccurate learning models. The proposed A-GVT uses gated self-attention layer as the basic building block of the classification model.

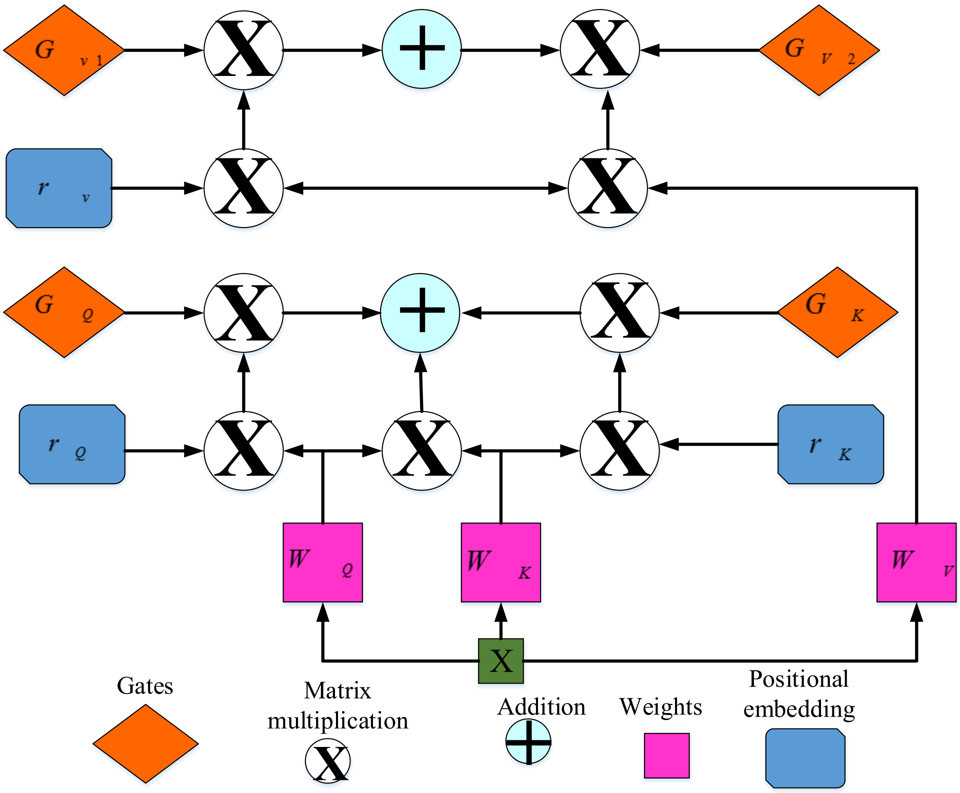

Figure 4. Architecture of gated attention layer

2.6. Black widow optimization algorithm

The BWO is a meta-heuristic algorithm developed to solve complex numerical optimization problems. The BWO deliver fast convergence, avoid optimal local solutions and balance the exploration and exploitation phase. Hence, BWO is a good method to solve optimization problems and to tune the parameters. The optimization algorithm initializes random weights and uses mutation to select random features from the extracted images. After that the obtained features are stored as new features and attains optimal weights. A summary of BWO optimization is expressed as follows.

i) Initialization: the number of widows with size N represents its population, and each widow can be constituted as an array as $widow = (y_1, y_2, \dots \dots, y_{Nv})$, where N_v is the dimension of the optimization problem. The fitness of the widow is calculated by evaluating the fitness function of each widow in the array. The fitness can be represented as $fitness = f(y_1, y_2, \dots \dots, y_{Nv})$.

ii) Procreate: in this the parents and offspring are combined; the evaluation of crossover result is stored and represented as in (18).

$$x_1 = \alpha \times y_1 + (1 - \alpha) \times y_2 \text{ and } x_2 = \alpha \times y_2 + (1 - \alpha) \times y_1 \tag{18}$$

iii) Cannibalism: after cannibalism, a new population is assessed and stored in a variable pop2.

iv) Mutation: random selection of features from the population is mutated and forms a new population and is stored in a variable named pop3. Then the pop3 is sorted to return best widow threshold values. After all this, the parameters are tuned based on the best weights. The algorithm of BWO is described as Algorithm 1.

```
Algorithm 1: The BWO algorithm
Initialize: maximum no. of iterations, procreating rate, cannibalism rate, mutation rate.
while Stop condition not met do
  for i=1 to nr do
    select 2 solutions as parents from pop1 randomly.
    Create D children
    On the basis of rate of cannibalism, kill a few children
```

```
    The remaining solutions should be saved into pop2
  end for
  Based on the rate of mutation, compute the no. of children mutated
  for i-1 to nr do
    Find a solution from pop1
    Randomly mutate one chromosome of the solution and create new solution
    Store the new solution into pop2
  end for
  Now, pop=pop2 + pop3
  Return the solution which is best
  Return the solution which is best from pop
end while
```

3. RESULTS AND DISCUSSION

This section covers experimental procedure with dataset details and parameter description. Along with this the performance metrics is validated to prove the efficiency of the presented approach. Further this section discusses the performance of proposed approach with previous models. In addition to that, visual analysis of suggested approach is illustrated for better visualization.

3.1. Dataset description

In this study, the data is captured from PlantVillage dataset, a publicly available repository. The images comprise of four types of diseased classes tomato mosaic virus, tomato target spot, tomato septoria leaf spot, and tomato yellow leaf curl virus. These four classes are used in this presented approach. Some of the original sample images of these four classes are depicted as Figure 5.

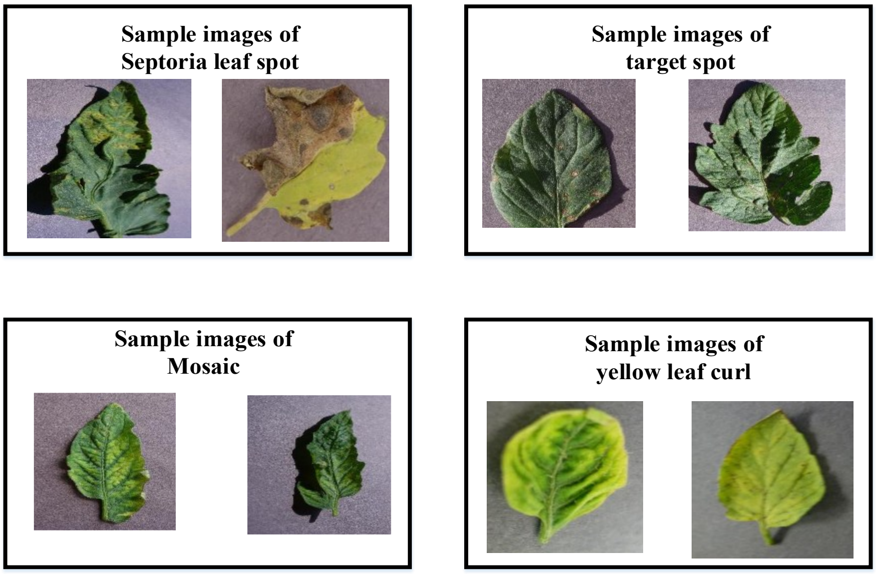

Figure 5. Sample images of tomato leaf disease classes

3.2. Parameter tuning

The parameter tuning is done by BWO optimization to increase the performance of the model during the classification phase. In the presented method, the transformer_units, transformer_layers, dropout_rate, and GRU_units are mainly tuned to enrich the classification process. Some other parameters also updated in this model and an overview of parameter tuning is described in Table 1.

3.3. Performance metrics

The presented approach analyzes some performance metrics including accuracy, precision, recall, F1-score, specificity, mean absolute error (MAE), and root mean square error (RMSE) for validating the efficacy. Moreover, training and testing accuracy and loss, receiver operating characteristic (ROC) curve also validated. These metrics are commonly used for classification approaches. Mathematical representation of these metrics is represented in Table 2. Here, p, q, u, and v represent the true positive, true negative, false positive, and false negative respectively.

Table 1. Parameter tuning details

Parameter	Value
Shape_input	(none, 1037)
Patch_size	1
Number of patches	(Shape_input [0] // patch_size)*(Shape_input[1] // patch_size)
Projection of dimension	64
Number of heads	4
Units of transformer	[projection of dimension*2, projection of dimension]
Transformer_layers	8
Rate of dropout	0.1
GRU_units	64
Batch_size	32
Epochs	300
Loss	Categorical cross entropy
Optimizer	BWO (custom optimizer)

Table 2. Performance metrics description

Performance metrics	Formula
Accuracy (%)	$\frac{p+q}{p+q+u+v}$
Precision (%)	$\frac{p}{p+u}$
Recall (%)	$\frac{p}{p+v}$
F1-score (%)	$2\times \frac{precision*recall}{precision+recall}$
Specificity (%)	$y=\frac{q}{q+u}$
RMSE	$RMSE = \sqrt{\frac{\sum_{i=1}^{n}(x_i - x_p)^2}{n}}$
MAE	$MAE = \frac{\sum_{i=1}^{n}\lvert y_i - x_i\rvert}{n}$

3.4. Performance analysis

The tomato leaf disease identification and categorization's performance are carried out by A-GVT model to accurately identify the type of disease. The classification performance metrics is compared with some of the previous approaches such as DCNN, DenseNet, ViT, and Efficient-Net B3 to prove the efficacy of the model done in this study. Figure 6 describes the performance analysis of proposed approach in terms of accuracy (Figure 6(a)), precision (Figure 6(b)), recall (Figure 6(c)), F1-score (Figure 6(d)), specificity (Figure 6(e)), MAE (Figure 6(f)), RMSE (Figure 6(g)), and ROC (Figure 6(h)) curve with existing approaches.

From the analysis, it is clear that the current approach outperformed well on existing models' performances. The accuracy of the presented approach is 99.7% which is attained due to the CSWO. Generally, precision and recall values are increased when large amounts of data are present or by the usage of better optimizer for tuning the parameters. Here, the precision and recall of proposed method is 98.29% and 98.22% respectively. This is due to the custom optimizer named black widow optimizer which is used to update the parameters.

As already known, that increase in precision and recall increases the F1-score value. 98.25% is the F1-score value attained in this presented approach. The specificity attained here is 99.19%, which ensures that the classification model correctly identified the diseased classes. The MAE and RMSE of the proposed model are 0.03 and 0.25 respectively. If the error rate is low, the model performs well, here the proposed approach utilizes some pre-processing techniques and uses more data on training phase to improve the error rate. The ROC curve of proposed with existing approaches is analyzed and the proposed approach have a high true positive rate (TPR) hence, the ROC value reaches near to 1 which indicates higher performance. All these aforementioned metrics' better performances are due to the effective architecture of the proposed model. The performance comparison of different models is described as Table 3.

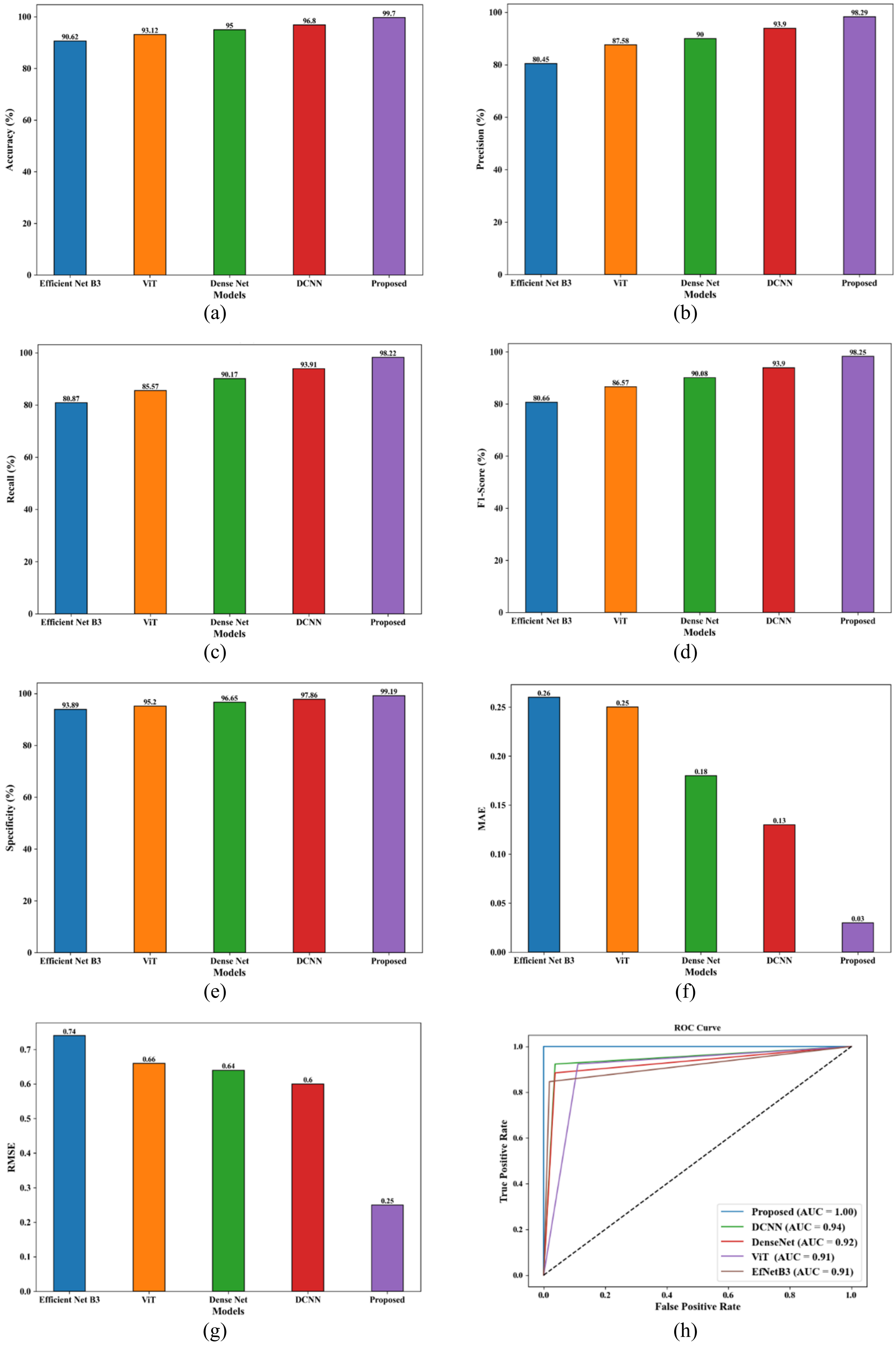

Figure 6. Performance analysis of proposed with previous methods in terms of (a) accuracy, (b) precision, (c) recall, (d) F1-score, (e) specificity, (f) MAE, (g) RMSE, and (h) ROC

Table 3. Performance comparison of current approach with previous approaches

Approaches	Accuracy (%)	Precision (%)	Recall (%)	F1-Score (%)	Specificity (%)	MAE	RMSE
DCNN	96.8	93.9	93.91	93.90	97.86	0.13	0.60
DenseNet	95	90	90.17	90.08	96.65	0.18	0.64
ViT	93.12	87.58	85.57	86.57	95.20	0.25	0.66
EfficientNet-B3	90.62	80.45	80.87	80.66	93.89	0.26	0.74
Proposed	99.7	98.29	98.22	98.25	99.19	0.03	0.25

The training and testing accuracy of proposed approach is depicted in Figure 7 and the loss of training and testing is depicted in Figure 8. The proposed method attained a high training and testing accuracy which is evidenced in Figure 7. These accuracies are increased with increase in the number of epochs. Here, 300 epochs were used to train and test the model. Efficient feature selection using an optimization algorithm and the better classification architecture leads to an increased training and testing accuracy. Furthermore, the training loss and testing loss is reduced by improving the batch size and adjusting the rate of learning with the highest number of epochs. In general, lowest amount of loss indicates better classification performances.

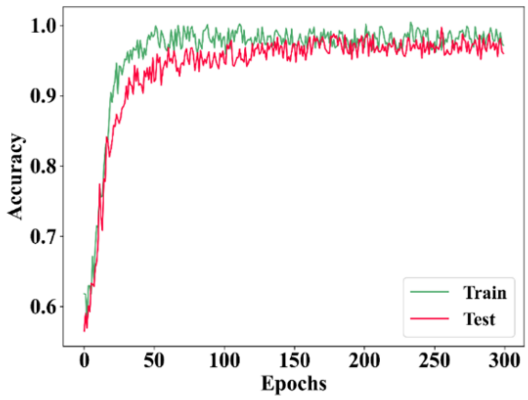

Figure 7. Training and testing accuracy of proposed method

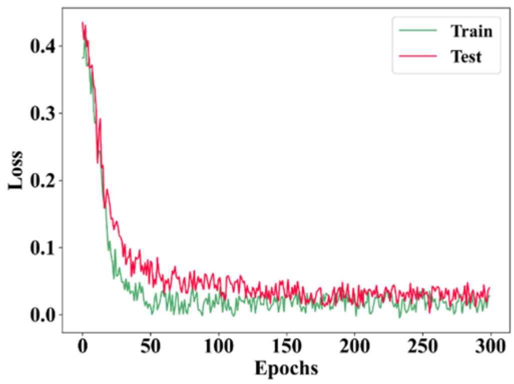

Figure 8. Training and testing loss of proposed approach

3.5. Visual analysis

Proposed method's efficiency was validated with widely used performance metrics which shows the effectiveness of the classification model. This study is based on image data, so this section visualized the research outcomes which consists of pre-processing, segmentation, and categorization of the tomato leaf disease images with different diseased classes. This visualized result helps the experts for further research on tomato leaf disease identification or categorization with these pre-processing and segmentation methods. Figure 9 describes the pre-processing, segmentation and classification outcomes of various diseased classes.

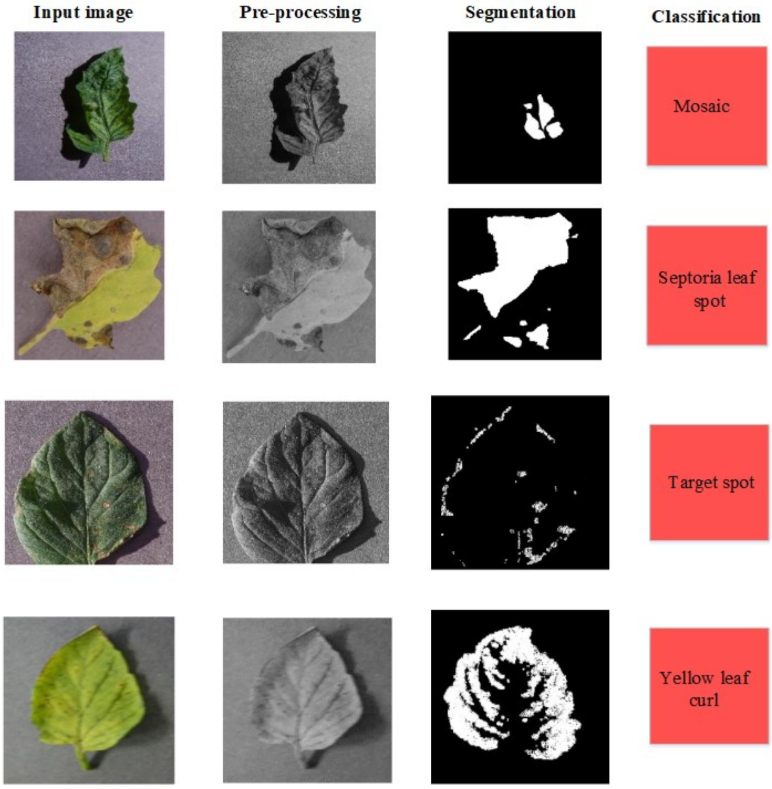

Figure 9. Classification output of proposed approach

3.6. Discussion

In this research, tomato disease classification meant to automatically identify and categorize the diseased classes from the input images. This research utilized PlantVillage dataset with four types of diseased classes. This research pipeline includes data acquisition, pre-processing, segmentation, feature extraction, feature selection, and classification and fine tuning. To provide accurate classification, this research utilized PlantVillage dataset with four disease classes including mosaic, septoria leaf spot, target spot, and yellow leaf spot. The presented A-GVT classification model identifies the diseases among these four classes. The input data are pre-processed and segmented using ARGW filter and residual attention-based U-Net++ model. Further to extract the features from segmented mask image, an integrated approach named Bi-DLSTM is developed. As it combines dilated convolutions and Bi-LSTM model which helps to analyze long range dependencies and provide efficiency in computation. This combined feature extraction provides better flexibility and scalability. However, feature extraction reduces the amount of image features, this research employed feature selection for identifying intrinsic characteristics or informations which was relevant to the model for classification. So, CSWO is employed as feature selector which accurately performs the specific task. Further, novel A-GVT model precisely categorize the diseased classes as it combines the strengths of both ViT model and attention mechanism. In addition to this, BWO is employed to optimize the parameters of A-GVT model for providing better computation and improved accuracy. By integrating these advancements, the presented tomato leaf disease classification effectively outperformed all the existing approaches.

Different tomato leaf disease classification and identification frameworks have been developed by various researchers. However, they possess better performances but comes along with some limitations. For instance, Zhao *et al.* [24] developed a CNN based model for detecting tomato leaf diseases and these CNN uses traditional models for the recognition of tomato diseases. Traditional models failed to analyze the parameter tuning and optimum solution for the model. But the proposed model utilizes efficient integrated DL approach which has increased the classification accuracy. An efficient feature extraction method is implemented in the proposed approach, but most of the existing ones such as, Lekha *et al.* [26] failed to implement the feature extraction process which reduces the optimal feature selection. Classification accuracy is increased when training is done with a greater number of epochs. But in Altalak *et al.* [38], the accuracy is less as compared to the proposed approach. This is because of the high number of training approaches; the presented model trains the dataset images with 300 epochs while [38] used only 50 epochs for training. Some meta-heuristic approaches were utilized to improve the performance of the model, Khan *et al*. [37] used traditional method for optimization which reduces the classification accuracy compared with proposed approach. The suggested approach implemented two optimization algorithms for optimal feature selection and parameter tuning, which lead to increased performance. Compared with some of the existing studies, the proposed approach attained highest accuracy of 99.7% and better scalability in disease classification. The comparative analysis with existing approaches is described in Table 4.

Table 4. Comparative analysis of accuracy with state-of-the-art methods

Author and references	Methods used	Accuracy (%)
Abouelmagd *et al.* [19]	CapsNet	96.39
Ashok *et al.* [21]	CNN	98.12
Basavaiah *et al.* [44]	DT classifier	90
Basavaiah *et al.* [44]	Random forest classifier	94
Proposed	A-GVT	99.7

4. CONCLUSION

In this paper, an effective A-GVT model is demonstrated for the identification and classification of tomato leaf diseases. The methodology focused on identifying the most common diseases such as yellow leaf curl, septoria leaf spot, target spot, and mosaic diseases that affects the tomato plant leaves. The main pros of the proposed approach are that computational complexity is reduced and enhances the categorization accuracy on comparing with traditional existing methods. Comparing the relative performance of the presented model it reveals that the classification model A-GVT with BWO attains better performance like 99.7% accuracy, 98.29% precision, 98.25% F1-score, recall of 98.22%, and 99.19% of specificity. The experimental findings proved that the proposed approach delivers better classification accuracy, scalability and robustness. In future, the proposed model will explore with the new integrated and advanced model with a greater number of diseased classes with some other crops for providing better generalizability and it will be improved to identify the severity of tomato leaf diseases. Furthermore, an XAI technique namely Shapley additive explanations (SHAP) and local interpretable model-agnostic explanations (LIME) approaches can be used for better feature interpretability.

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AUTHOR CONTRIBUTIONS STATEMENT

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

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Jaswinder Singh	✓	✓				✓		✓		✓		✓	✓	

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

CONFLICT OF INTEREST STATEMENT

Authors state no conflict of interest.

DATA AVAILABILITY

Data in this study is taken from public repository, PlantVillage. Data availability is not applicable to this paper as no new data were created or analyzed in this study.

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