



Research article

Deep transfer learning with gravitational search algorithm for enhanced plant disease classification

Mehdhar S.A.M. Al-Gaashani^{a,*}, Nagwan Abdel Samee^b, Reem Alkanhel^b, Ghada Atteia^b, Hanaa A. Abdallah^b, Asadulla Ashurov^c, Mohammed Saleh Ali Muthanna^d

^a School of Resources and Environment, University of Electronic Science and Technology of China, 4 1st Ring Rd East 2 Section, Chenghua District, Chengdu, 610056, Sichuan, China

^b Department of Information Technology, College of Computer and Information Sciences, Princess Nourah Bint Abdulrahman University, P.O. Box 84428, Riyadh, 11671, Saudi Arabia

^c School of Communication and Information Engineering, Chongqing University of Posts and Telecommunications, Chongqing, 400065, China

^d Institute of Computer Technologies and Information Security, Southern Federal University, 344006, Taganrog, Russia

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ABSTRACT

Plant diseases annually cause damage and loss of much of the crop, if not its complete destruction, and this constitutes a significant challenge for farm owners, governments, and consumers alike. Therefore, identifying and classifying diseases at an early stage is very important in order to sustain local and global food security. In this research, we designed a new method to identify plant diseases by combining transfer learning and Gravitational Search Algorithm (GSA). Two state-of-the-art pretrained models have been adopted for extracting features in this study, which are MobileNetV2 and ResNe50V2. Multilayer feature extraction is applied in this study to ensure representations of plant leaves from different levels of abstraction for precise classification. These features are then concatenated and passed to GSA for optimizing them. Finally, optimized features are passed to Multinomial Logistic Regression (MLR) for final classification. This integration is essential for categorizing 18 different types of infected and healthy leaf samples. The performance of our approach is strengthened by a comparative analysis that incorporates features optimized by the Genetic Algorithm (GA). Additionally, the MLR algorithm is contrasted with K-Nearest Neighbors (KNN). The empirical findings indicate that our model, which has been refined using GSA, achieves very high levels of precision. Specifically, the average precision for MLR is 99.2%, while for KNN it is 98.6%. The resulting results significantly exceed those achieved with GA-optimized features, thereby highlighting the superiority of our suggested strategy. One important result of our study is that we were able to decrease the number of features by more than 50%. This reduction greatly reduces the processing requirements without sacrificing the quality of the diagnosis. This work presents a robust and efficient approach to the early detection of plant diseases. The work demonstrates the utilization of sophisticated computational methods in agriculture, enabling the development of novel data-driven strategies for plant health management, therefore enhancing worldwide food security.

* Corresponding author.

E-mail addresses: mr.mehdhar@uestc.edu.cn, mr.mehdhar@gmail.com (M.S.A.M. Al-Gaashani), nmabdelsamee@pnu.edu.sa (N.A. Samee), rialkanhal@pnu.edu.sa (R. Alkanhel), geatteiaallah@pnu.edu.sa (G. Atteia), haabdullah@pnu.edu.sa (H.A. Abdallah), asadullahashur@gmail.com (A. Ashurov), muthanna@sfedu.ru (M.S. Ali Muthanna).

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1. Introduction

Globally, the incidence of plant disease epidemics is on the rise, posing a threat to food security in susceptible regions [1]. Data from the United Nations Food and Agriculture Organization survey data, pests and diseases destroy between 20% and 40% of worldwide crop yields each year [2]. Hence, plant disease detection and recognition at an early stage is essential, as it not only increases the pace of food production but also protects farmers from costly pesticides. Nonetheless, plant leaf diseases are usually classified by trained experts through a costly, inefficient process and inefficient visual examination by skilled professionals. Farmers must acquire precision technology that enables them to prevent and mitigate losses caused by various plant diseases [3]. With this modern technology, agriculturalists have the potential to automate the process of identifying plant ailments, therefore saving time and cost, especially in regions where the visual examination is challenging to perform, such as extensive farmland [4]. Computer Vision (CV) technology is one of the most advanced technologies that have been utilized for plant disease recognition in the last decade [5,6]. K-nearest neighbors algorithm (k-NN), artificial neural networks, random forests, and Support Vector Machines (SVM) are some of the computer vision-based technologies used for the automated detection and classification of crop diseases [7]. These approaches mainly rely on handcrafted features such as the Spatial Gray Level Dependence Matrix (SGLDM), Color Coherence Vector (CCV), Gray Level Co-occurrence Matrix (GLCM), Color Co-occurrence Matrix (CCM), Colour histogram, color moments, and Local Binary Patterns (LBP) [8,9]. These approaches depend heavily on the custom-built features we give. Handcrafted features are often unstable, making the usage of large amounts of data difficult and time-consuming. In general, discrimination is restricted [10].

On the other hand, Convolutional Neural Networks (CNNs, or ConvNet) have demonstrated exceptional outcomes as feature extractors and classifiers in recent years [11]. As a pivotal branch of machine learning, CNNs excel in distilling deep, high-level information from a single image and adeptly handle various data formats, including images, signals, and videos. Their widespread application across diverse fields underscores the significant strides made in deep learning, enhancing both image classification and detection technologies universally [12]. A straightforward CNN model consists of numerous hidden layers, including a convolutional layer, a pooling layer, an activation layer, a normalization layer, a fully connected layer, and a SoftMax layer. Studies showed that employing CNN features outperforms handcrafted features in terms of performance [13]. Various CNN models have been proposed in recent years, including MobileNetV2, GoogleNet, AlexNet, DenseNet, and ResNet. These models, however, are computationally demanding, requiring extensive training, significant computational power, and vast datasets.

In contrast, Transfer Learning (TL) techniques can substantially reduce training time, enhance neural network performance, and obviate the need for massive data quantities [14]. A remarkable approach to harnessing the advantages of both CNNs and traditional classifiers involves integrating CNN models with shallow classifiers such as SVM and XGBoost. In this configuration, CNN models serve as feature extractors, while shallow classifiers assume the role of classification components [15]. Nonetheless, deep features are often redundant, which may decelerate the training process. Moreover, the redundancy of features usually leads to poor performance. For that reason, the selection of optimal features is essential. Within the field of machine learning, it's imperative to diminish the high-dimensional data. Many features aren't practical for obtaining the desired learning result in many data sets with a massive number of features and a small number of observations, such as bioinformatics data. The small number of observations can lead to the learning algorithm overfitting to the noise. Reduced features can save storage and computation time while improving interpretability [16]. Feature selection can be classified into three categories based on distinct search strategies: filter methods, wrapper methods, and embedding methods [17].

In this study, we propose a novel hybrid classification method for crop disease image detection designed to address the limitations of existing approaches and improve the efficiency of plant disease recognition. Our method leverages the advantages of both CNNs and traditional classifiers by integrating pre-trained models, MobileNetV2 and ResNet50V2, with TL techniques [18,19]. We extract and fuse features from different layers of pre-trained models (MobileNetV2 and ResNet50V2), followed by the application of a gravitational search algorithm for optimal feature selection. The proposed method reduces resource requirements while achieving accuracy comparable to state-of-the-art approaches [20]. Our hybrid method, evaluated on a diverse database of diseased plant leaf images, achieves accuracy comparable to state-of-the-art approaches while requiring fewer resources. Furthermore, we provide a thorough evaluation and comparison of our results with established baseline models and prevailing techniques in the literature. This research is poised to make a substantial impact on the way plant diseases are detected and managed, especially in extensive farmlands and regions where manual, visual examination is challenging. Farmers, agricultural scientists, and agro-based industries stand to benefit most from our work as the automatic identification of plant diseases can lead to timely interventions, thereby saving costs, preventing crop losses, and increasing food production efficiency. Furthermore, the reduced resource requirement makes this method a highly scalable solution suitable for deployment in varied environments, even those with limited computational resources. The primary contributions of our study, adding novelty and significance to the existing body of literature, include.

- Effective application of TL technique on pre-trained MobileNetV2 and ResNet50V2 networks, with layers reused for our classification challenge.
- Development of a multi-level feature extraction method that enhances the model's ability to classify plant leaf diseases.
- Incorporating a gravitational search algorithm to determine the optimal feature set for final recognition from the fused features, a first in the context of plant disease detection, marking a novel approach in the realm of plant disease identification.
- Significant reduction in resource requirements while delivering accuracy comparable to state-of-the-art approaches, setting a new benchmark for efficiency in plant disease detection techniques.

- Thorough evaluation and comparison of our results with established baseline models and existing techniques in the literature contribute to an enriched understanding of the evolving field of automated plant disease detection.

2. Literature review

Several artificial intelligence-based strategies for automatic crop disease image recognition have been reported in the literature. These approaches can be classified into three categories: conventional machine learning methods, deep learning models, and hybrid approaches.

2.1. Conventional machine learning methods

Conventional machine learning methods are a subsection of Artificial Intelligence (AI) that primarily relies on handcrafted features. Scale-invariant feature transform (SIFT) [21], Histograms of Optical Flow (HOF), and the Histogram of Oriented Gradients (HOG) [22] are examples of handcrafted features. Handcrafted features are derived from the image data using various algorithms, such as the Histogram of Oriented Gradients (HOG) and the Histogram of Optical Flow (HOF). Traditional machine learning algorithms such as SVM, Random Forest (RF), and MLR frequently employ these features for disease recognition. For instance, the authors of [23] proposed a novel image-processing methodology based on candidate hot-spot detection and statistical inference approaches to address wheat disease diagnosis in field settings. Color and texture features have been extracted and fed to shallow classifiers RF and naive bayes. The system was tested on wheat photos with three illnesses (rust, septoria, and tan spot). This method achieved an average accuracy of 78% [24]. proposed a method for identifying and diagnosing the four most prevalent alfalfa leaf diseases. Cropping images resulted in the creation of sub-images with one or more lesions. SVM, regression tree, LDA, logistic regression analysis, and naive bayes classifiers were trained using color, shape, and texture, and PCA was utilized to reduce the dimension of the features. SVM surpassed all other classifiers, with a recognition accuracy rate of 97.64% on the training set and 94.74% on the testing set. Particle Swarm Optimization (PSO) was proposed to segment sunflower leaf lesions [25]. They utilized numerous pre-processing techniques for their dataset, including median filtering, segmentation via thresholding, image scaling, PSO, and RGB to HSI conversion. Subsequently, using color and texture characteristics, an MDC classifier was trained to classify six sunflower leaf diseases. This methodology registered an average accuracy of 98%. The authors of [26] used 300 images from the PlantVillage dataset to derive color and texture features. These features were then inputted into the Multiclass SVM algorithm, which is used to identify potato leaf disease. They achieved an average accuracy of 93.7%. These techniques are expensive and time-consuming since they rely on handcrafted features.

2.2. Deep learning methods

There are many deep learning methods mentioned in the literature for plant disease detection. For example, in Ref. [27], five submodels: ResNet-50, ResNeXt-50, DenseNet-121, ResNeSt50, and SE-ResNet-50, are tuned and tested using the TL approach. Ensemble learning was then implemented, combining multiple submodels into one, resulting in an accuracy of over 98% and an F1 score of 0.95. A large dataset of 33,026 images was used to train and test the proposed method. The authors of [28] proposed models that incorporate attention mechanisms to enhance feature extraction and classification accuracy. They achieved this by devising a self-service network (SANET) that builds upon the ResNet50 architecture. Notably, SANET incorporates a kernel attention mechanism, which enables precise classification of rice diseases through the utilization of artificial intelligence techniques. Their model achieved a test set accuracy of 98.71%, outperforming some of the existing methods. The authors of [29] proposed a nine-layer deep convolutional neural network to classify 38 different healthy and unhealthy crop species based on leaf images and achieved an average accuracy of 96.46% in the final experiment. Wang et al. [30] developed a CNN-based method to identify four stages of black rot disease severity in apple trees. They tested the developed method on the PlantVillage dataset and achieved an average accuracy of 90.4%. In Ref. [31], the authors proposed a customized CNN model for tomato disease classification. Their model is comprised of 3 convolution and max pooling layers with a varying number of filters in each layer. They obtained an average accuracy of 91.2%. In Ref. [32], the authors proposed a few-shot learning (FSL) technique that combines three training topologies for classifying plant infections (a Siamese network with two subnets, and contrastive loss, a baseline fine-tuning Inception V3 network, and a Siamese network with three subnets and triplet loss). Using the PlantVillage dataset, the suggested model was trained and verified. They reported an average precision greater than 90% and a decrease of 89.1% in training data.

2.3. Hybrid methods

Many studies in the literature tried to take advantage of both DL and ML for plant disease detection [33]. They used deep learning for feature extraction and traditional machine learning algorithms for classification. For instance, the authors in Ref. [15] proposed a hybrid method based on TL and feature concatenation for identifying tomato leaf disease. They extracted features from two state-of-the-art pre-trained models and then concatenated them to create a single vector. Subsequently, they reduced the combined features. Finally, the authors fed these features to shallow classifiers: SVM, Random Forest (RF), and Multinomial Logistic Regression (MLR) for final classification. They achieved an average accuracy of 96%. In Ref. [34], the authors proposed a hybrid method using shallow CNN for extracting features PCA to reduce the dimensions. SVM and RF are utilized to identify different diseases in corn, apples, and grapes. They obtained an f1-score of 94%.

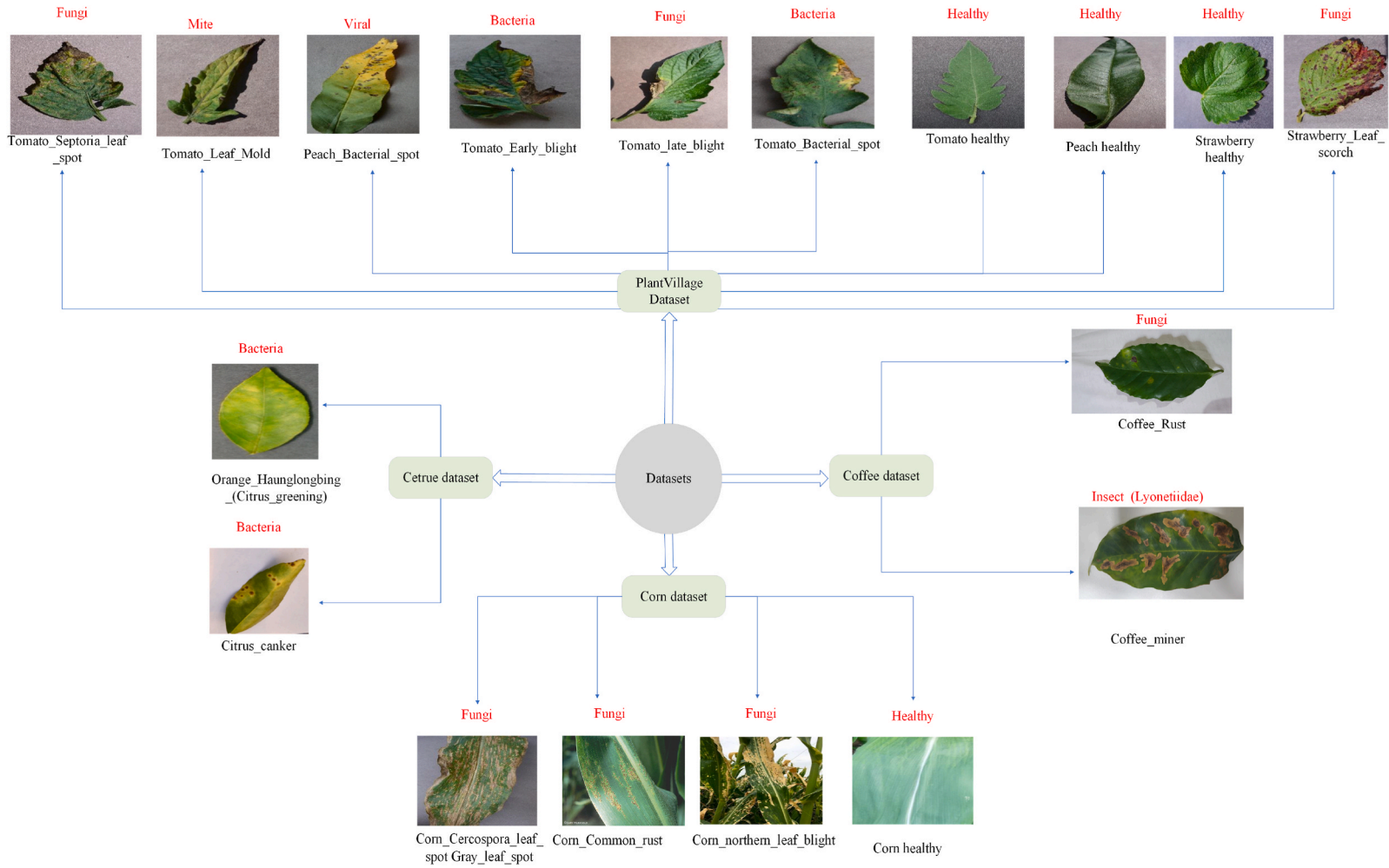


Fig. 1. Some samples from the dataset.

3. Materials and methodology

This section outlines the suggested deep learning and machine learning-based algorithms. Several deep learning and machine learning models are available, but MobileNetV2, ResNet50V2, and MLR were utilized for this study due to their established capacity for detection and classification in several scientific fields.

3.1. Dataset description

The authors have compiled a dataset comprising 18 classes of plant leaves, including four healthy leaf types and 14 types affected by various diseases. The dataset is an amalgamation of images from multiple sources, including PlantVillage [35], coffee dataset [36], citrus dataset [37], and corn dataset [38]. Two additional classes were derived from the coffee dataset and two from the citrus dataset. Four more classes were obtained from the corn dataset. Since the images in the dataset have different resolutions, they were resized to 224 x 224 pixels to match the input layer dimensions of the deep learning models, MobileNetV2 and ResNet50V2.

To improve the performance, the authors applied data normalization and augmentation techniques. The pixel values of the image dataset were normalized between 0 and 1, which can significantly accelerate the model training process. Data augmentation methods, such as random rotation (0°, 90°, 180°, and 270°), flipping (0.2), shearing (0.2), zooming, and fill mode set to constant with a gray pixel value, were employed to increase the dataset size. In Fig. 1, some samples from the datasets used in this study are shown.

3.2. MobileNetV2

MobileNet is a streamlined deep CNN model tailored for mobile and embedded devices. It leverages an innovative technique known as Depthwise Separable Convolutions (DWSC) to dramatically minimize the requisite parameters for network training. In addition to having fewer parameters and less computing complexity than conventional convolution, DWSC considerably improves predictive performance. Two components comprise the depth-wise separable convolutional: the depthwise convolutional and the pointwise convolutional. For a feature map of $D_F \cdot D_F \cdot M$ in size, the kernel size is $D_k \cdot D_k \cdot P$, where M is the input channel, and P indicates the number of convolution kernels. A computing cost of DWSC (O_{DSC}) is expressed by Equation (1):

$$O_{DSC} = M \cdot P \cdot D_F \cdot D_F + D_k \cdot D_k \cdot M \cdot D_F \cdot D_F \quad (1)$$

The computational cost of standard convolutions (SC) in the identical case can be estimated with Equation (2):

$$O_{SC} = D_k \cdot D_k \cdot M \cdot P \cdot D_F \cdot D_F \quad (2)$$

The relative reduction in computational expense by using DWSC, compared to SC, is quantified by a factor Z, which is defined in Equation (3). This factor highlights the efficiency gains offered by DWSC:

$$Z = \frac{D_k \cdot D_k \cdot M \cdot D_F \cdot D_F + M \cdot P \cdot D_F \cdot D_F}{D_k \cdot D_k \cdot M \cdot P \cdot D_F \cdot D_F} = \frac{1}{P} + \frac{1}{D^2} \quad (3)$$

MobileNetV2 closely resembles its predecessor, MobileNet, with the exception that it makes utilization of inverted residual blocks with bottlenecking capabilities. In this study, the authors Utilized the pre-trained MobileNetV2 network as one of the feature extractors methods for our proposed method.

3.3. ResNet50V2

ResNet [39] has been designed to tackle image identification tasks more precisely by increasing the number of layers and avoiding vanishing gradient problems. ResNet offers numerous architectures based on layers, including ResNet50 and ResNet101. ResNet50V2 is an improved variant of ResNet50 that outperforms ResNet50 and ResNet101 on the ImageNet dataset. In ResNet50V2, the propagation concept of the block-to-block links was modified. ResNet50V2 performs admirably on the ImageNet dataset.

In this study, we have used the TL technique of ResNet50V2, and we have extracted features from the last and intermediate layers. The central concept of ResNet is the introduction of an "identity shortcut link" that bypasses one or more levels.

3.4. Transfer learning (TL)

Transfer learning is a powerful concept in machine learning that allows the knowledge of a learning model on huge data to be transferred to another model for a task from the same domain or an approach to the domain. Developing deep neural network models for image classification from scratch is a costly and time-consuming task. In addition, since deep learning models rely heavily on massive datasets, training with a small dataset is exceptionally challenging [40]. TL reduces the need for extensive data and computation when developing models for specific problems. In this work, the TL of state-of-the-art pre-trained models was utilized by the authors to address these constraints. These models may be used for prediction, feature extraction, and fine-tuning. The authors applied the Lightweight models MobileNetV2 and ResNet50V2 as static feature extractors. The fundamental precept is to employ these pre-trained models, minus their terminal classification layer, for feature extraction, which is then fused, followed by feature selection using GSA, and then supplied to a shallow classifier for the final classification. The general architecture of the TL concept is illustrated in Fig. 2.

3.5. The gravitational search algorithm (GSA)

GSA is a meta-heuristic inspired by physics that is used to tackle optimization problems. It is derived from Newtonian gravity theory in physics. The search agents are modeled as a collection of Newtonian-based objects that interact with one another. The particles' gravitational attraction can attract other agents. Fig. 3 illustrates that the masses will gravitate toward the heaviest option because it provides the optimal solution in the state search space.

Considering P masses (search agents) in a search space of p dimensions. As seen in Equation (4), the value of the i_{th} solution (mass) is denoted by the vector X_i .

$$X_i = (x_i^1, \dots, x_i^d, \dots, x_i^p), i = 1, 2, \dots, P \tag{4}$$

Where $i = 1, 2, 3, 4 \dots p$ and x_i^d is the location of the particle i in dimension d_{th} .

As detailed in Equation (5), the force $F_{ij}(t)$ that agent j exerts on agent i at time t is calculated as follows:

$$F_{ij}(t) = G(t) \frac{M_j(t) \times M_i(t)}{R^2} (X_j(t) - X_i(t)) \tag{5}$$

where $M_j(t)$ is the active gravitational mass related to agent j , $M_i(t)$ is the passive gravitational mass related to agent i , $G(t)$ is gravitational constant at time t , and R^2 represents the distance between particles j and i .

The cumulative impact of these forces from multiple agents leads to a total force acting on particle i in a given dimension d , as described in Equation (6). This total force, $F_i^d(t)$, accounts for the influences from the K best agents and is determined by:

$$F_i^d(t) = \sum_{j \in K_{\text{best}}, j \neq i} \text{rand}_j F_{ij}^d(t) \tag{6}$$

where rand_j is a random number in the interval $[0, 1]$, and K_{best} is the set of first K agents with the best fitness value and biggest mass.

Acceleration:

Based on the principles of motion, the acceleration of the i_{th} particle may be computed as the sum of the gravitational forces exerted by all other particles divided by the mass of particle i . This can be mathematically formed as shown in Equation (7):

$$a_i(t) = \frac{\sum_{j=1, j \neq i}^N (q \times F_{ij}(t))}{M_i(t)} \tag{7}$$

In which q is a random variable between 0 and 1, $F_{ij}(t)$ represents the gravitational force exerted by particle j on particle i at a certain iteration t . $M_i(t)$ is the inertial mass of agent i .

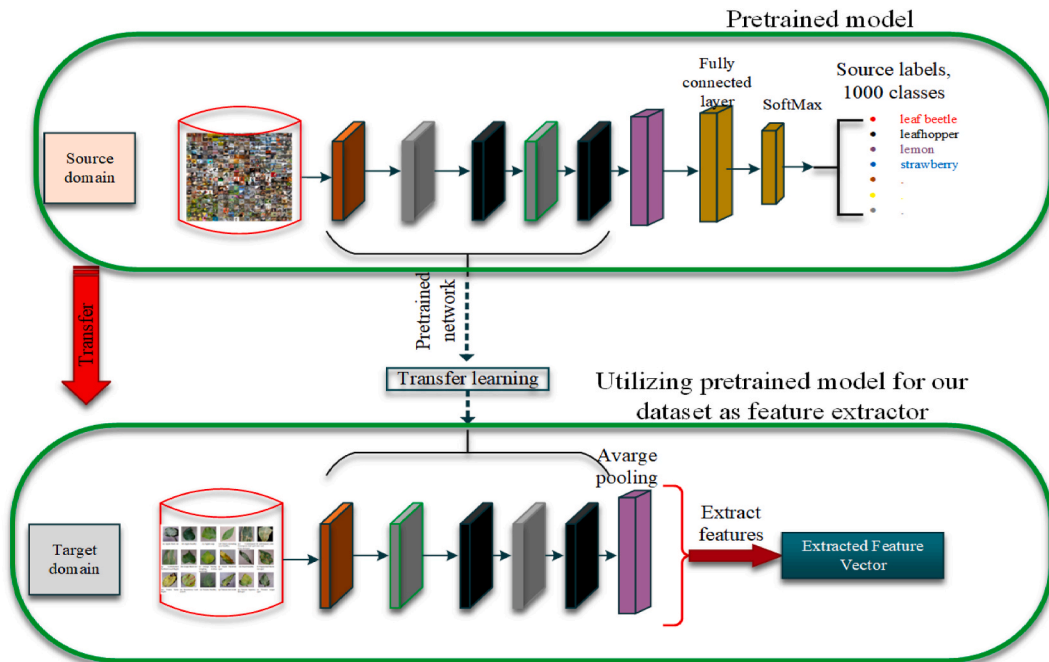


Fig. 2. Illustration of TL method.

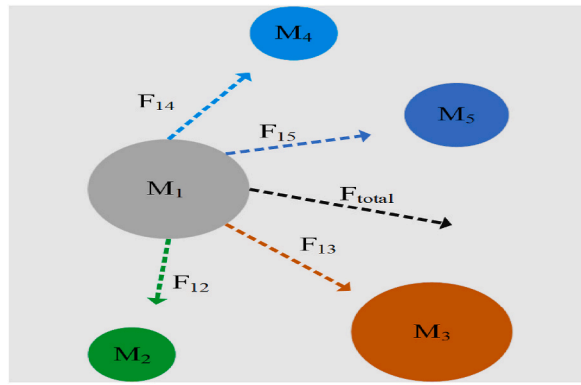


Fig. 3. The interaction of agents in GSA.

Velocity: The velocity $v_i(t+1)$ is updated using Equation (8):

$$v_i(t+1) = r \times v_i(t) + a_i(t) \tag{8}$$

The updated position of search agent X_i at iteration $t + 1$ is given by Equation (9):

$$X_i(t+1) = X_i(t) + V_i(t+1). \tag{9}$$

where $X_i(t+1)$ is the agent at the $(t + 1)^{th}$ iteration, $X_i(t)$ is the position of the t^{th} iteration and $V_i(t+1)$ is the velocity at the $(t + 1)^{th}$ iteration.

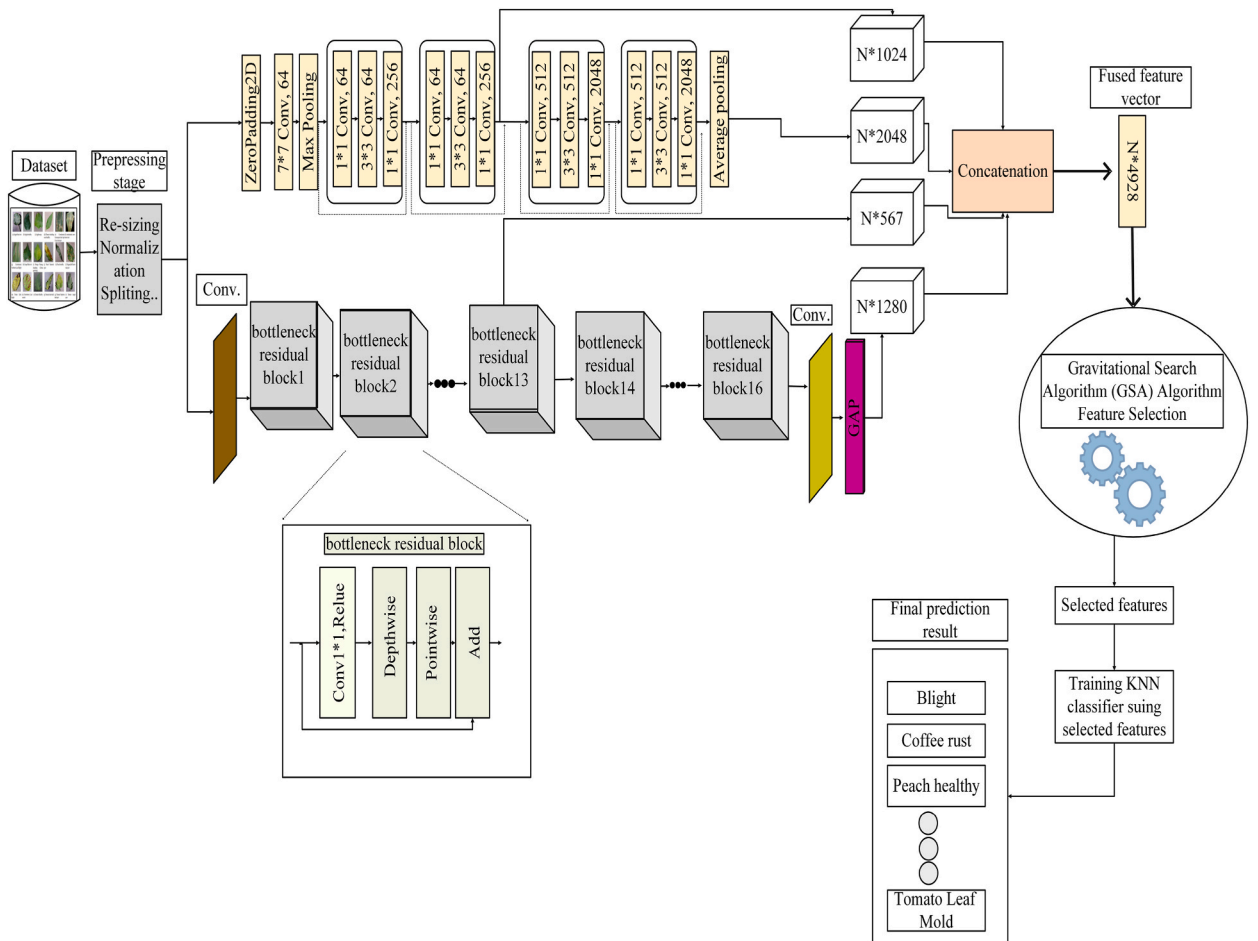


Fig. 4. The architecture of the proposed framework.

With the help of the previous equations, the M_i mass is calculated as explained in Equation (10):

$$M_i(t) = \frac{m_i(t)}{\sum_{j=1}^N m - j(t)} \quad (10)$$

In which the $m_i(t)$ is determined by Equation (11):

$$m_i(t) = \frac{fit_i - \text{worst}(t)}{\text{best}(t) - \text{worst}(t)} \quad (11)$$

where the cost function is represented as fit_i , $\text{worst}(t)$ and $\text{best}(t)$ are indicate masses with worst and best (solution fitness value of the cost function, respectively.

In this work, the wrapper FS model is employed to assess the quality of each subset of features, and two learning algorithms from different families (KNN and MLR) are utilized for all tests, as shown in Fig. 4. The effectiveness of the classifier was assessed based on its accuracy.

4. Results and discussion

In this study, the performance of the proposed methodology was appraised using six metrics: F1-score, Sensitivity, Accuracy, Precision, and Area Under the Curve (AUC), confusion matrix. Accuracy, recall, precision, and F1-score may be calculated quantitatively using true positive (TP), false negative (FN), true negative (TN), and false positive (FP) as shown in Equation (12) through (15):

$$F1 - score = 2 \times \frac{\text{Precision} \times \text{Sensitivity}}{\text{Precision} + \text{Sensitivity}} \quad (12)$$

$$\text{Sensitivity} = \frac{TP}{TP + FN} \quad (13)$$

$$\text{Precision} = \frac{TP}{TP + FP} \quad (14)$$

$$\text{Accuracy} = \frac{TP + TN}{TP + FN + FP + TN} \quad (15)$$

Where TN represents a true negative, FN stands for a false negative, FP corresponds to a False Positive, and TP represents a true positive. In the realm of binary classification, the Receiver Operating Characteristics (ROC) curve is extensively utilized for the appraisal of a classifier's output. Nevertheless, by adapting the One vs. All method, we have extrapolated it to address multiclass classification issues. In addition, Figs. 10 and 11 depict the confusion matrices and ROC curves of the MLR algorithm based on the GSA features of the proposed model, respectively.

4.1. Feature extraction stage

The features are extracted from the last and intermediate layers, as shown in Fig. 5. Using MobileNetV2, the features are extracted

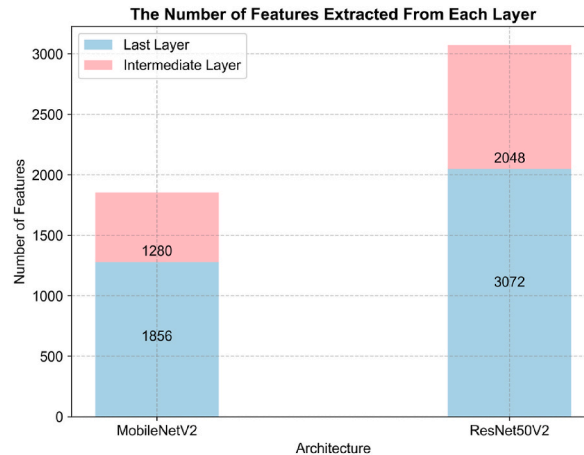


Fig. 5. The number of features extracted from each layer.

from the last global average pooling layer, and we have obtained a feature vector of dimension $N \times 1280$, taking 35.23 seconds for feature extraction.

Furthermore, we have added the global average pooling layer after the `block_11_expand_relu` layer, and we obtained $N \times 576$ feature vector, taking 23.96 seconds for the feature extraction phase. Using ResNet50V2, the features are extracted from the last global average pooling layer, and we have obtained a feature vector of dimension $N \times 2048$, taking 89.74 seconds for feature extraction. Moreover, we added the global average pooling layer after the `conv4_block3_3_conv` layer and obtained the $N \times 1026$ feature vector, taking 67.22 seconds for the feature extraction phase. These feature vectors are concatenated together, and we obtained a feature vector of $N \times 4928$. Fig. 7 presents the feature extraction time for each layer, along with the training and testing times for the MLR classifier applied to the feature vectors extracted from each individual layer and the fused feature vector.

4.2. Feature selection and classification stage

The proposed model was evaluated on the collected dataset that contains 18 leaf images of infected and healthy leaves. Using the GSA method, our suggested model attained the maximum accuracy upon this selected feature vector. F1-score, the precision, and recall for MLR based on different multi-level features for each class, are shown in Table 2. Our proposed model consisted of three main stages. In the first stage, we trained the MobileNetV2 and ResNet50V2 pre-trained models using the TL approach. Then we removed the classification part of the pre-trained models and utilized them as feature extractors for training traditional machine learning algorithms. We obtained four feature vectors $N \times 1280$, $N \times 576$, $N \times 2048$, and $N \times 1026$ for the last layer of MobileNetV2, the intermediate layer of MobileNetV2, the terminal layer of ResNet50V2, and the intermediate layer of ResNet50V2 as depicted in Fig. 4. In the second stage, the extracted features undergo dimensionality reduction via the application of the GSA algorithm as an FS technique. KNN and

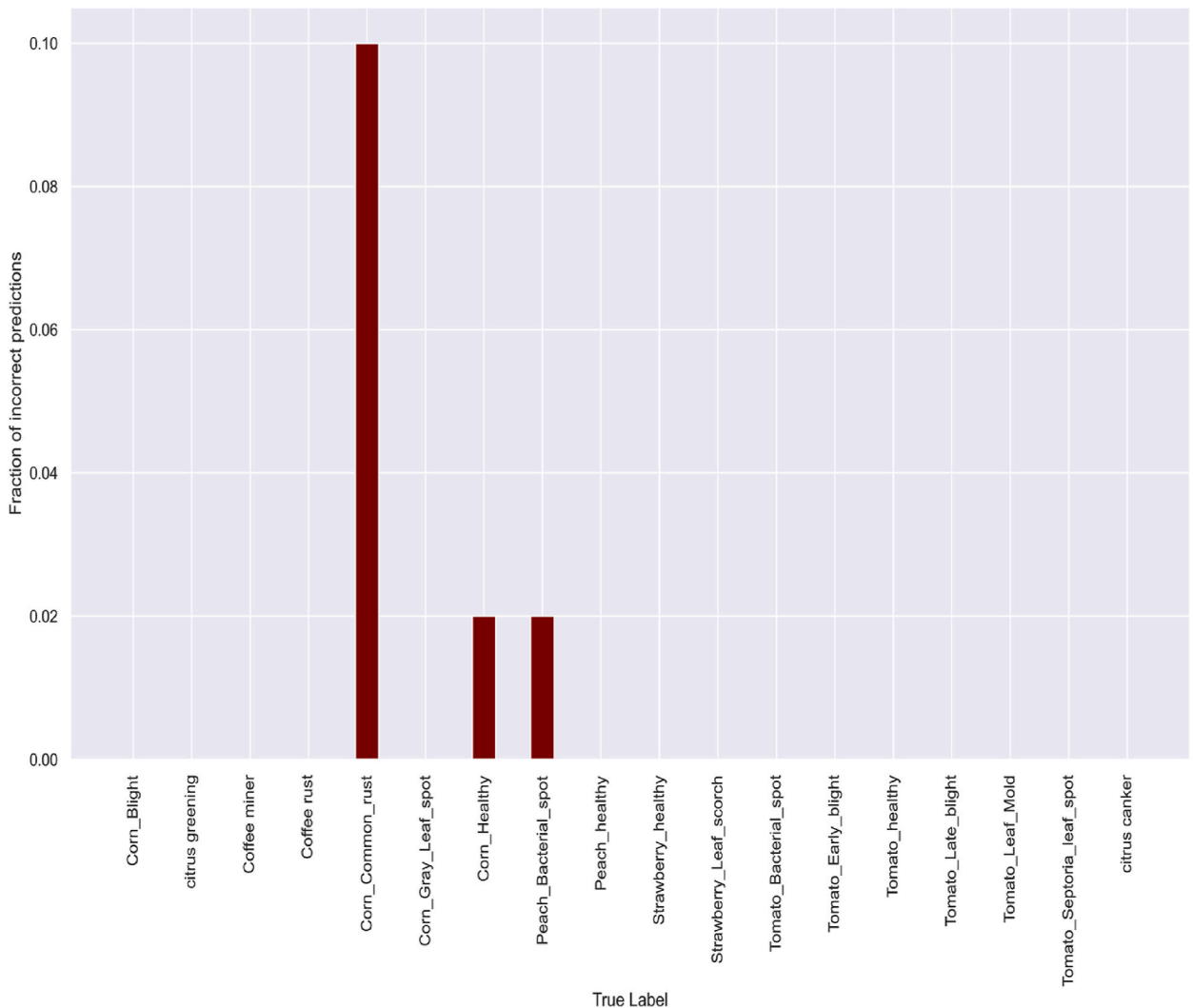


Fig. 6. Fractional of correct prediction of GSA + MLR approach.

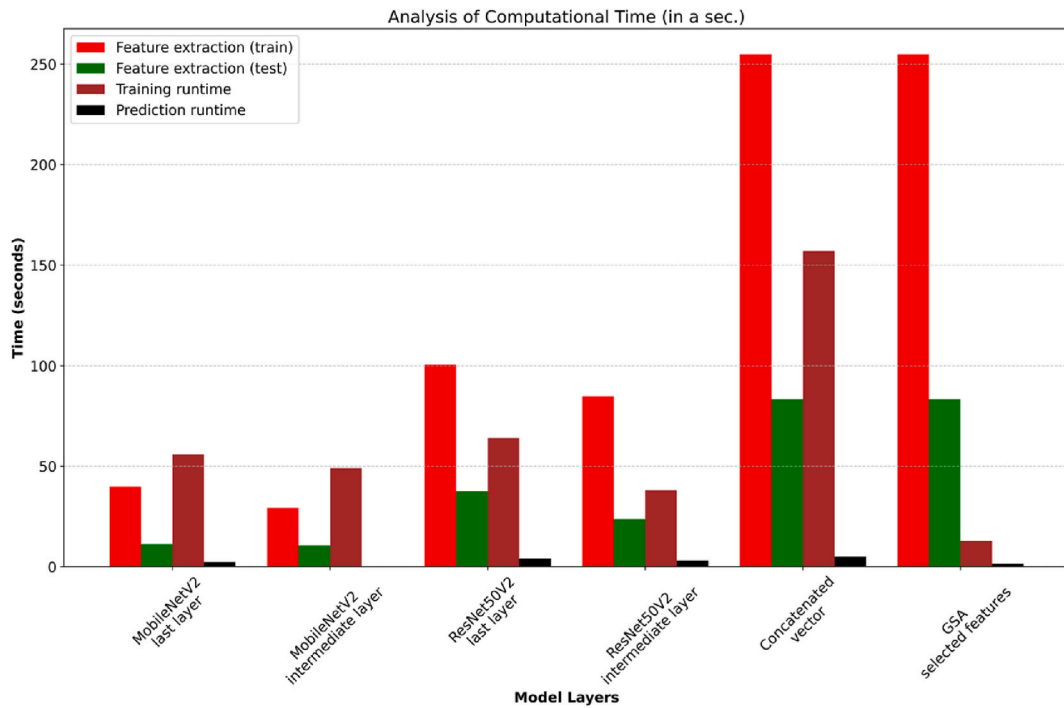


Fig. 7. Analysis of computational time (in a sec.).

MLR have been utilized as evaluators for the GSA algorithm. Table 1 shows KNN and MLR's accuracy before and after applying the GSA method, which is 97.5% and 98.1% for KNN and MLR, respectively, before using GSA and 98.6% and 99.2% for KNN and MLR, respectively for GSA-based selected features.

Moreover, we have compared the features of GSA to GA features, as shown in Table 1. As shown in Fig. 9 and Table 1, the GSA features showed the best performance for KNN and MLR, and it has reduced the features by an average of 50.04%. The KNN classifier obtained the best performance on the fused features from the intermediate and last layers with GSA, which is 98.6%. In addition, the features extracted from individual layers for MobileNetV2 and ReseNetV250 models have been tested to prove that the fused features provide more discriminative features for the classification algorithm, as can be seen in Fig. 8. Table 2 displays each class's precision, recall, and f1-score when using GSA features with the MLR algorithm as an evaluator. Fig. 9 displays a performance comparison of MLR and KNN on fused features with GSA and GA. The best result obtained in this study is when we utilized GSA with MLR, so we further demonstrate the effectiveness of the MLR + GSA approach by the fraction of correct predictions, as shown in Fig. 6. Furthermore, Fig. 10 depicts the confusion matrix of MLR with GSA. Moreover, the receiver operating characteristic (ROC) of MLR with the GSA approach is shown in Fig. 11.

4.3. Discussion and comparisons with state-of-the-art methods

As can be seen from Fig. 4, the proposed framework encompasses three essential stages: feature extraction, selection, and classification. MobileNetV2 and ResNet50V2 networks have been exploited as feature extractor models. For classification purposes, these models extracted salient features from new data. Furthermore, TL enables the network to acquire the ideal weight settings, which allows for the extraction of more pertinent information. The models' lowest layers extracted lower-level features, including blobs, corners, curves, and edges. The top layers efficaciously extrapolated high-level features imbued with more discriminative information, pivotal for classification tasks [41]. To overcome this problem, a method of multi-level feature extraction is proposed. The extracted features are concatenated to generate one vector feature that contains more discriminative features from the top and intermediate layers. Fig. 5 illustrates the number of features extracted from each layer in the ResNet50V2 and MobileNetV2 models. It is evident that

Table 1
The comparison of GSA and GA algorithms.

Approach	Number of the original features	Number of selected features	Accuracy before FS	Accuracy after FS
KNN + GSA	N*4928	2456	97.5	98.6
KNN + GA	N*4928	2426	97.5	97.9
MLR + GSA	N*4928	2479	98.1	99.2
MLR + GA	N*4928	2466	98.1	98.7

Table 2
F1-score, recall and precision for various disease classes of GSA + MLR approach.

The disease	Precision (%)	Recall (%)	F1-score (%)
Blight	93	100	96
Citrus greening	100	100	100
Coffee miner	100	100	100
Coffee rust	100	100	100
Common_rust	100	90	95
Gray_Leaf_spot	98	100	99
Corn_Healthy	98	98	98
Peach_Bacterial_spot	100	98	99
Peach_healthy	100	100	100
Strawberry_healthy	100	100	100
Strawberry_Leaf_scorch	100	100	100
Tomato_Bacterial_spot	100	100	100
Tomato_Early_blight	100	100	100
Tomato_healthy	98	100	99
Tomato_Late_blight	100	100	100
Tomato_Leaf_Mold	100	100	100
Tomato Septoria leaf spot	100	100	100
Citrus canker	100	100	100

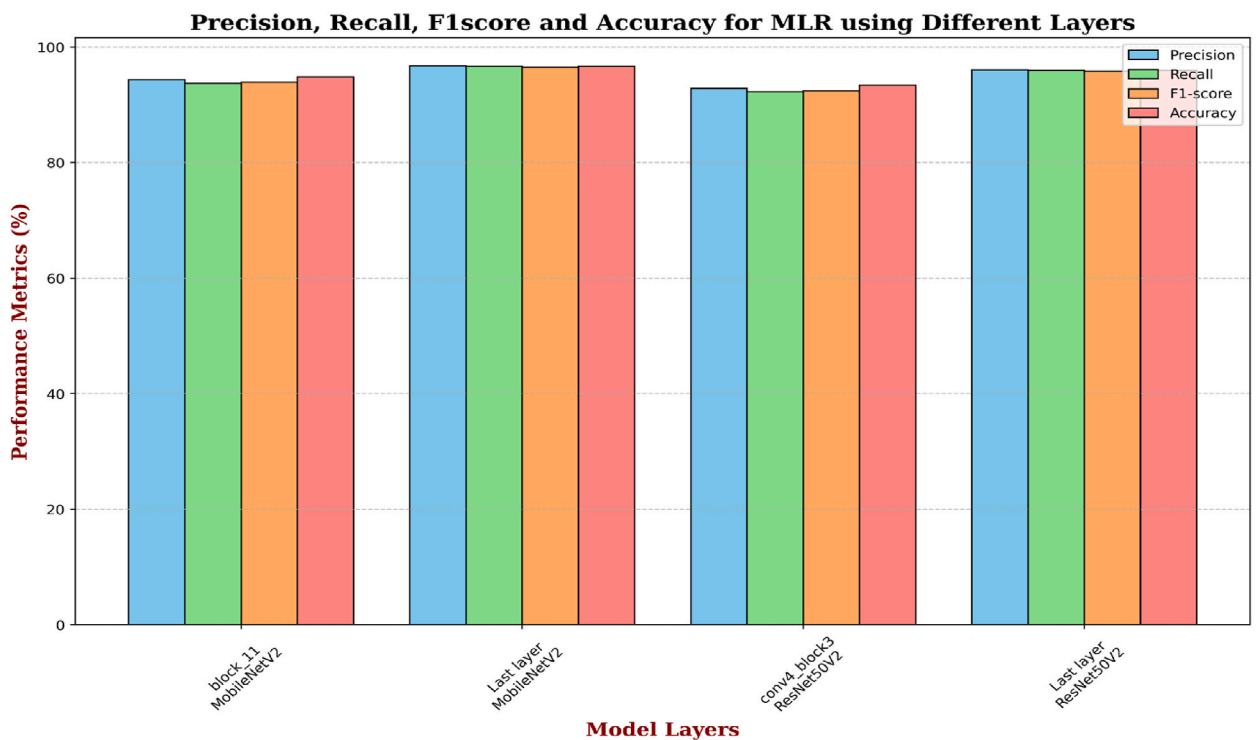


Fig. 8. Precision recall f1score and accuracy for MLR using different layers.

the last layer of ResNet50V2 contributes the most to the combined feature vector, accounting for an average of 41.6% of the total features. Data redundancy (highly correlated features) diminishes classification accuracy and construction time. We utilized GSA for feature selection to minimize the dimensions of these features. The accuracy of KNN and MLR has been compared before and after using the GSA algorithm, as illustrated in Table 1. In addition, the authors compared GSA to GA and reported that GSA performed better for both classifiers (KNN and MLR) for classifying plant diseases.

4.3.1. Classification performance comparison with other approaches on PlantVillage's classes

Table 3 presents a comparison of our method's disease detection results with those from other studies, specifically from Refs. [6, 15], and [42]. The diseases analyzed include Peach Bacterial spot, Peach healthy, Strawberry healthy, Strawberry Leaf scorch, Tomato Bacterial spot, Tomato Early blight, Tomato healthy, Tomato Late blight, Tomato Leaf Mold, and Tomato Septoria leaf spot. Our method, based on the MLR model, exhibits a superior exemplary level of efficacy with an average accuracy of 99.8%. This outperforms

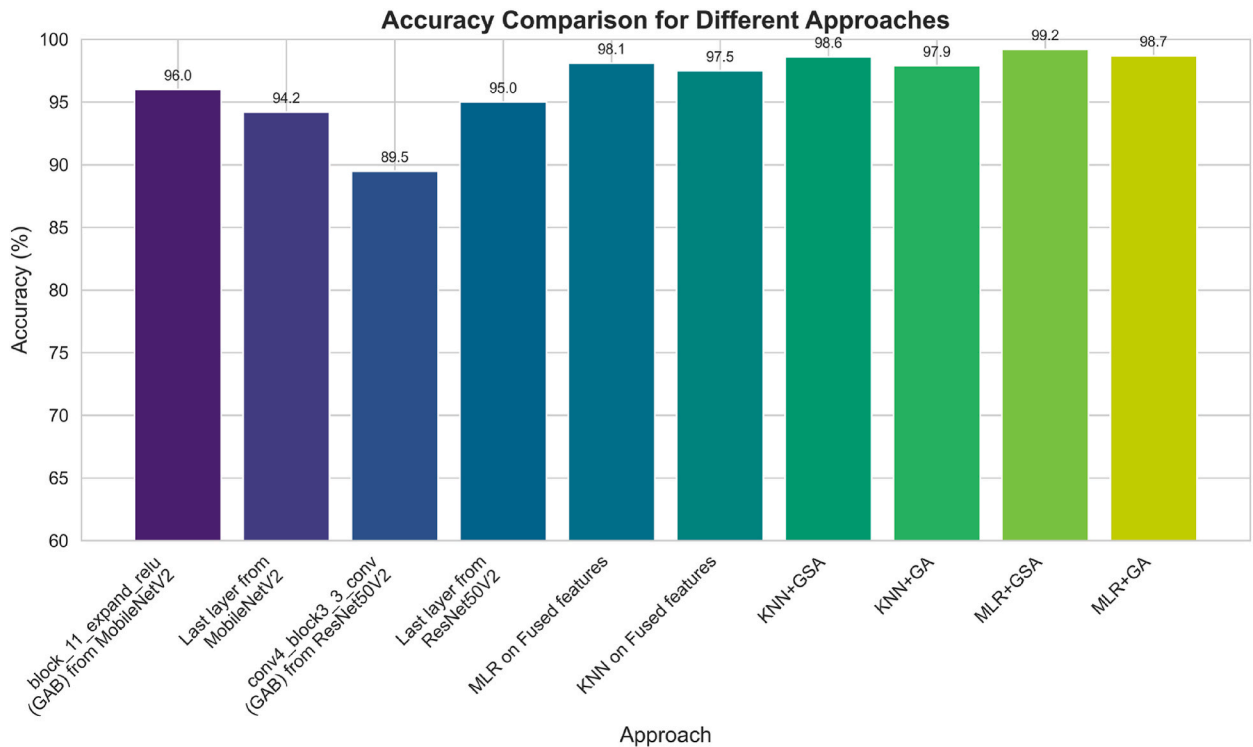


Fig. 9. Performance comparison of the proposed approaches.

the results from the study [15] with an average of 83.4% and the study [6] with averages of 98.02% and 96.621% for Meta learner (XGBoost) and Majority voting, respectively. Our method also shows better performance compared to the EfficientNetB5 (99.91%) and EfficientNetB4 (99.96%) models of the study [42].

While our method demonstrates impressive results for most diseases, there is an inconclusive result for Tomato healthy class with a 98% accuracy compared to the 100% achieved by EfficientNetB4. This discrepancy could result from differences in the dataset or training methodology. Additional experiments and testing on a larger dataset or with different MLR model configurations may help clarify this result and further improve performance. Our method displays remarkable and consistent performance in detecting plant diseases compared to other studies and models. However, some inconclusive results warrant further investigation and experimentation to better understand and improve our method.

4.3.2. Classification performance comparison with other approaches on coffee's classes

The performance of multiple models in identifying two different coffee diseases, Coffee miner and Coffee rust, is compared in Table 4. Five investigations from 2022 to 2021 are compared with our technique, which employs several models, including ResNet50, SVM, MobileNetV2, and EfficientNetB4. With 100% accuracy for both diseases, our approach performs remarkably well in identifying both Coffee miner and Coffee rust. Our technique routinely performs better than the other research. The closest rival is study [43], which uses ResNet50 and achieves an average accuracy of 96.45% for coffee miner and 98.9% for coffee rust. The accuracy of the subsequent experiments varies, with study [44] employing MobileNetV2 displaying the lower average performance at 95.5%, and with the study [45] employing SVM displaying the lowest average performance at 95.5%.

Although our method performs well, it is crucial to take into account the likelihood of overfitting or other circumstances that may have contributed to flawless outcomes. To confirm the robustness of our strategy, additional testing and validation using alternative datasets or maybe including data augmentation techniques may be required. Our approach regularly performs better than the other research in identifying the diseases of coffee miner and Coffee rust. To validate the findings and correct any potential overfitting or dataset-related concerns, additional trials should be run.

4.3.3. Classification performance comparison with other approaches on corn's classes

Table 5 provides a comparison of our method against three other studies from 2019 to 2020, focusing on the detection of corn pathologies, specifically Corn leaf Blight, Common rust, Gray Leaf spot, and Corn_healthy. The studies employ different models: author-defined CNN, VGGNet + inception, and modified LeNet, while our method utilizes MLR. Our method demonstrates a superior overall average accuracy of 97.15%, which is notably higher than the average accuracies of studies [45] (92.85%) [43], (84.25%), and [46] (95.5725%). In particular, our method shows perfect accuracy for Common rust and impressive results for Corn leaf Blight, Gray Leaf spot, and Corn healthy detection, with 92.6%, 98%, and 98% accuracy, respectively.

Confusion Matrix for MLR+GSA

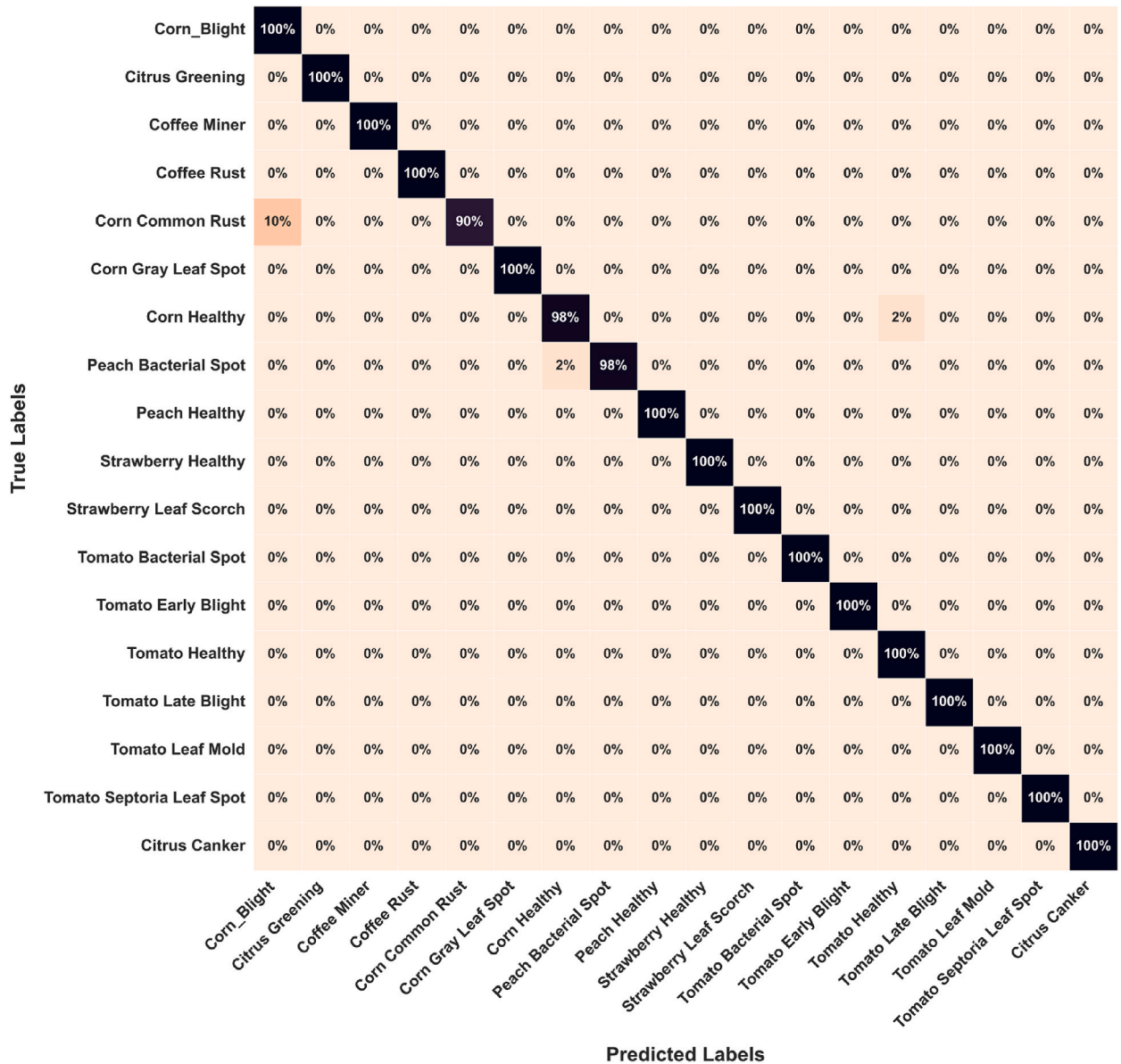


Fig. 10. Confusion matrix for GSA + MLR approach.

However, it is essential to note that study [45] exhibits higher accuracy for Corn leaf Blight (99.9%) compared to our method, and study [46] shows marginally better results for corn healthy (99.7%). Meanwhile, the study [43] consistently presents lower accuracy across all diseases, which may indicate a limitation in the model or dataset. While our method outperforms other studies in most categories, some inconclusive results may be due to differences in the datasets, preprocessing techniques, or model architectures. To better understand these discrepancies, additional experiments could be performed. These may include testing different model architectures, using larger or more diverse datasets, and implementing.

Advanced preprocessing techniques or data augmentation. Our method demonstrates a strong performance in detecting corn diseases compared to other studies. However, further experiments are needed to clarify the inconclusive results and to ensure an exhaustive comprehension of the strengths and limitations of the of the varied models.

4.3.4. Classification performance comparison with other approaches on citrus's classes

Table 6 illustrates a juxtaposed evaluation of diverse models utilized for the identification of two distinct categories of citrus ailments, namely citrus greening and citrus canker. The method utilized through the employment of MLR is subjected to comparison

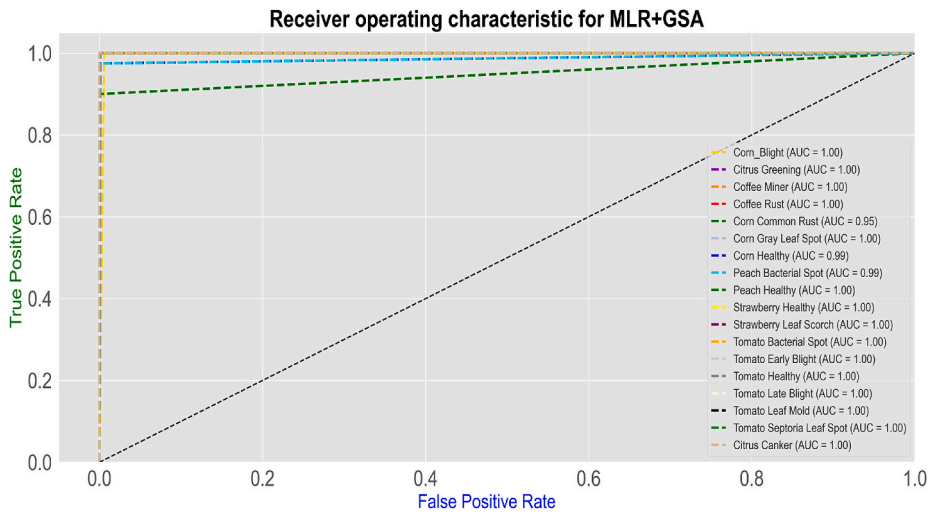


Fig. 11. ROC for GSA + MLR approach.

Table 3
Classification Performance Comparison with other approaches on PlantVillage’s classes.

Study Class	Our method	[15]	[6]	[6]	[42]	[42]
Year	2023	2022	2022	2022	2021	2021
Model	MLR	MLR	Meta learner (XGBoost)	Majority voting	EfficientNetB5	EfficientNetB4
Peach_Bacterial_spot	100%	–	100%	98.3%	99.74%	100%
Peach_healthy	100%	–	100%	100%	99.84%	100%
Strawberry_healthy	100%	–	100%	100%	100%	100%
Strawberry_Leaf_scorch	100%	–	100%	98.36%	100%	100%
Tomato_Bacterial_spot	100%	75%	98.4%	95.16%	99.85%	99.9%
Tomato_Early_blight	100%	–	94.9%	91.23%	99.90%	99.9%
Tomato_healthy	98%	86%	98.2%	96.4%	99.95%	100%
Tomato_Late_blight	100%	71%	98.3%	95.16%	99.79%	99.9%
Tomato_Leaf_Mold	100%	96%	92.1%	93.4%	100%	99.9%
Tomato_Septoria_leaf_spot	100%	89%	98.3%	98.2%	100%	100%
Average	99.8%	83.4%	98.02%	96.62%	99.91%	99.96

Table 4
Classification Performance Comparison with other approaches on coffee’s classes.

Study Class	Our method	[43]	[45]	[44]	[44]	[44]
Year	2023	2022	2022	2022	2022	2022
Model	MLR	ResNet50	SVM	MobileNetV2	EfficientNetB4	ResNet50
Coffee miner	100%	94%	95%	93.2%	92.8%	91%
Coffee rust	100%	98.9%	96%	100%	98.8%	100%

Table 5
Classification Performance Comparison with other approaches on corn’s classes.

Class Study	Our method	[45]	[45]	[46]
Year	2023	2019	2020	2019
Model	MLR	Author-defined CNN	VGGNet + inception	modified LeNet
Corn leaf Blight	92.6%	99.9%	80.75%	98.14%
Common_rust	100%	87%	93.50%	99.87%
Gray_Leaf_spot	98%	91%	84.75%	84.58%
Corn_Healthy	98%	93.5%	78.00%	99.70%
Average	97.15%	92.85%	84.25%	95.57%

Table 6
Classification Performance Comparison with other approaches on citrus's classes.

Study Class	Our method	[49]	[48]	[47]	[47]	[47]
Year	2023	2022	2018	2022	2022	2022
Model	MLR	ResNet50	SVM	ResNet50	MobileNetV2	CNN-based
citrus greening	100%	90%	99.5%	95%	95%	100%
citrus canker	100%	100%	94.3%	90.9%	90.7%	95.5%
Average	100%	95%	96.9%	92.95%	92.85%	97.75%

with five other studies that were conducted between 2018 and 2022. These studies employed distinct models such as ResNet50, SVM, MobileNetV2, and CNN-based methods. The method employed exhibits exceptional performance, attaining a perfect accuracy rate of 100% for both citrus greening and citrus canker. By contrast, the other research exhibits different levels of precision. The utilization of a CNN-based model in the investigation of [47] has yielded outcomes that are the most proximate to the actual values. Specifically, the model has achieved a 100% accuracy rate for citrus greening and a 95.5% accuracy rate for citrus canker, resulting in an average accuracy rate of 97.75%. The remaining studies demonstrate lower mean accuracies, with a range of 92.85% in the study [47] utilizing MobileNetV2 to 96.9% in the study [48] employing SVM.

Although our approach exhibits superior performance compared to other investigations, it may be necessary to conduct additional research to eliminate the possibility of overfitting or other extraneous variables that could have influenced the outcomes. Further experimentation utilizing varied datasets or incorporating data augmentation methodologies may serve to validate the dependability and applicability of our approach. Our approach exhibits a consistent superiority over other investigations in the identification of citrus greening and citrus canker ailments.

Further experimentation and validation are necessary to verify these findings and mitigate potential concerns regarding overfitting or limitations of the dataset.

While the study presents a promising framework for the automatic classification of plant diseases using a multi-level feature extraction strategy, there are limitations that require further investigation. These include expanding the dataset to include a broader range of plant diseases and species, standardizing image resolutions, evaluating the performance with other pre-trained models designed specifically for plant disease identification, investigating alternative feature selection techniques, evaluating the method's performance with additional machine learning classifiers, and investigating the practical implementation of the proposed method in actual agricultural settings. Future research can refine the proposed framework and increase its potential for effective and efficient plant disease identification and management by addressing these limitations.

5. Conclusions

In this study, we introduced a novel framework for the automatic classification of plant leaf diseases, significantly addressing an ongoing challenge in global agricultural production. We utilized state-of-the-art pre-trained models, MobileNetV2 and ResNet50V2, to extract features from the average pooling layer of the intermediate and final layers. These features were then optimized using the Gravitational Search Algorithm (GSA), which is a unique aspect of our approach. Our evaluation demonstrated that our method outperforms existing models in plant disease recognition, with the MLR classifier based on GSA-optimized features achieving the highest testing performance with an average accuracy of 99.2%. Notably, our proposed method also achieved a substantial reduction in the number of features by 50.04 percent, significantly minimizing the computational cost. This research has made a noteworthy contribution to the field of automatic plant disease detection. By enhancing the accuracy and efficiency of disease classification, we offer a more effective and cost-friendly solution for the agriculture sector. Moving forward, we plan to explore fine-tuning approaches with new pre-trained models, possibly incorporating data augmentation techniques. Additionally, we will investigate the fusion of classifiers' outputs using an ensemble approach based on fine-tuned and scratch-based features derived from deep neural networks. Our work sets the foundation for future research aimed at further improving the detection and classification of plant diseases.

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Data availability statement

In this study, we utilized datasets that are publicly available for download, eliminating the necessity to establish a dedicated storage database. Interested readers can access these datasets directly from their respective official websites, following the provided guidelines to suit their research needs.

CRediT authorship contribution statement

Mehdhar S.A.M. Al-Gaashani: Writing – original draft, Software, Methodology, Conceptualization, Investigation. **Nagwan Abdel Samee:** Writing – review & editing, Formal analysis. **Reem Alkanhel:** Resources, Funding acquisition, Project administration. **Ghada Atteia:** Writing – review & editing, Visualization, Validation. **Hanaa A. Abdallah:** Formal analysis, Conceptualization. **Asadulla Ashurov:** Software, Data curation. **Mohammed Saleh Ali Muthanna:** Formal analysis, Conceptualization.

Declaration of competing interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

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