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An Efficient Hybrid CNN Classification Model for Tomato Crop Disease

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Abstract: Tomato plants are vulnerable to a broad number of diseases, each of which has the potential to cause significant damage. Diseases that affect crops substantially negatively impact the quantity and quality of agricultural products. Regarding quality crop maintenance, the importance of a timely and accurate diagnosis cannot be overstated. Deep learning (DL) strategies are now a critical research field for crop disease diagnoses. One independent system that can diagnose plant illnesses based on their outward manifestations is an example of an intelligent agriculture solution that could address these problems. This work proposes a robust hybrid convolutional neural network (CNN) diagnostic tool for various disorders that may affect tomato leaf tissue. A CNN and an inception module are the two components that make up this hybrid technique. The dataset employed for this study consists of nine distinct categories of tomato diseases and one healthy category sourced from PlantVillage. The findings are promising on the test set, with 99.17% accuracy, 99.23% recall, 99.13% precision, 99.56% AUC, and 99.17% F1-score, respectively. The proposed methodology offers a solution that boasts high performance for the diagnostics of tomato crops in the actual agricultural setting.

Keywords: hybrid CNN classification model; tomato crop disease; deep convolutional neural network; smart agriculture

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1. Introduction

Each year, around 177 million tons of tomatoes are produced worldwide, which are among the essential crops. Tomatoes can improve health and lower the risk of diseases like cancer, osteoporosis, and heart disease. Regular tomato consumers are less at risk of cancers such as prostate, stomach, lung, breast, oral, colorectal, cervical, esophageal, pancreatic, and many other forms [1,2]. Since healthy plants are particularly susceptible to illnesses, which have devastating consequences on the agricultural economy, protection from disease is necessary to ensure the quantity and quality of crops.

The primary cause for the reduction in worldwide tomato production is tomato disease, according to research conducted by the Food and Agriculture Organization of the United Nations (FAO) [3,4]. Most tomato infections, however, begin inside the leaves and gradually extend to the entire plant. It is crucial to note that early monitoring is necessary for selecting the most effective strategy and preventing disease progression. Experts frequently identify and detect diseases through straightforward manual [5,6]. Therefore, to detect crop disease early on, deep learning and machine learning techniques have emerged as the main directions for future research. Timely disease management will increase the survival rate of crops, flowers, and vegetables, including fruits and grass [7,8].

The conventional, professional diagnosis of diseases that affect tomato leaves is both expensive and prone to subjectivity [9,10]. The detection of agricultural diseases is presently making substantial use of machine learning, computer vision, and deep learning due to the fast rise of computer technology. The development of open-source hardware has increased in recent years, which has stimulated the architecture and deployment of low-cost agricultural monitoring devices that are equipped with artificial intelligence (AI) and image-processing algorithms. The commonality of disease features, which makes it difficult to discern between different disease types, contributes to the poor accuracy of sickness detection in natural environments that are very complex [11,12].

Today, convolutional neural networks (CNNs) are more capable than standard feature extraction methods. CNN is a deep learning network that performs at a high level and employs an end-to-end architecture and abandons the complicated procedures of image preprocessing and feature extraction, simplifying the identification process compared with its learning model counterparts. Deep learning has gained significant dominance in several application areas in recent years. This new subject of deep learning is rapidly expanding and has been applied to the majority of classic application domains as well as some new application areas that provide more excellent prospects. In the fields of medical imaging, machine translation, speech identification, computer vision, image processing, medical information processing, art, natural language processing, robotics and control, bioinformatics, and cyber security, among others, deep learning outperforms conventional machine learning techniques [13–15].

This article presents a practical hybrid classification approach using image data to identify ten different diseases that have the potential to damage tomato plants. The model's CNN architecture combines VGG [16] blocks and the inception [17] module. The proposed model obtains a high classification accuracy rate on a large dataset compared to other already developed approaches. In this way, image-based tomato disease identification enables agricultural domain specialists to detect damaged crops as early as feasible to avoid production loss problems.

The main contributions of the proposed work can be summarized as follows:

- A hybrid-enhanced CNN model is proposed for tomato disease identification. An inception block was added to the VGG16 model in order to take use of the capabilities of simultaneous multiscale feature extraction. The hybrid CNN model has powerful feature extraction qualities and uses these capabilities.
- The effectiveness of the proposed hybrid CNN model was analyzed through rigorous high-level simulations. The results obtained from the developed hybrid CNN model were compared against the most recent and state-of-the-art models.

The remaining sections are organized as follows: Section 2 examines the newest disease categorization strategies for tomato crops. Section 3 then explains the architecture of the proposed approach, while Section 4 analyzes the findings and compares the acquired classification accuracy with current classification methods. Section 5 concludes the work provided in this article and provides an outlook for the future.

2. Related Work

A significant amount of research has been carried out in order to find the most effective solution to the problem of crop disease identification. This has been accomplished by establishing methods that assist in the identification of crops in an agricultural context. This section covers research that has been vetted by experts, and it focuses on tomato plant disease and CNN methodology.

Rangarajan et al. [18] classified six distinct illnesses and a healthy tomato variety using AlexNet and VGG16. Performance was examined by adjusting the number of pictures, weight and bias learning rates, and batch sizes. They found that AlexNet provides more precision with less execution time than VGG16. Using 13,262 images, the classification rate for VGG16 was 97.29%, while for AlexNet, it was 97.49%. A modified CNN model was developed by Agarwal et al. [19] by altering the structure and architecture of the VGG16 network. They compared this model against three different kinds of deep learning models (VGG16, InceptionV3, and MobileNet) using ten different classes of tomato. The custom CNN model was trained using 1400 images of tomato leaves from 10 different classes, and then it was verified with 300 images from each class. Each category in the testing set comprised a total of 100 images. The custom CNN model achieved an accuracy rate of 98.40%.

Agarwal et al. [20] developed a CNN-based disease identification model for tomato crops. In the proposed CNN-based architecture, there were three convolution layers, followed by a max-pooling layer and a configurable number of filter layers. The leaf data for tomatoes were taken from the dataset provided by PlantVillage. Within the collection, one class only contained healthy images, and nine classes were dedicated to various illnesses. The model's average testing accuracy was 91.20%. Support vector machine (SVM), convolutional attention module (CBAM), CNN, and two phases of transfer learning were used in a hybrid system that was described in [21]. This system was designed to categorize ten illnesses that can be found in tomato leaf tissue. The leaf images for tomatoes come from the dataset maintained by PlantVillage. The accuracy of the testing performed on the classification model was 97.20%.

Mim et al. [22] designed a customized CNN architecture for the detection of diseases that affect tomato leaves. This dataset consists of 6000 images and includes 5 distinct diseases that may affect tomato leaves and a healthy condition. The accuracy of classification achieved by the custom CNN model was 96.55%. In [23], a restructured residual dense network was presented to diagnose tomato leaf diseases. This model takes the best aspects of dense and deep residual networks and integrates them into a single solution. As a result, the number of training process parameters decreases, increasing the computation accuracy. Additionally, the flow of information and gradients was improved. The results of experiments indicated that this model had an accuracy of 95.00%.

Ouhami et al. [24] used transfer learning in three CNN models. These models included DensNet121, DensNet161, and VGG16. There were a total of six categories in the dataset, with three categories representing harm caused by insects and three classes representing symptoms produced by cryptogamic pathogens. The accuracy of DensNet161 was 95.65%, whereas the accuracy of DensNet121 was 94.93%, and that of VGG16 was 90.58%. The authors of [25] developed a CNN architecture to efficiently detect and categorize the tomato illnesses utilizing 3000 unique tomato leaf images that were afflicted by 9 distinct diseases and 1 healthy leaf class. The prediction accuracy of the categorization model was 98.49%.

Brahimi et al. [26] categorized nine different illnesses in tomato variety using AlexNet and GoogleNet. Employing 14,828 tomato images, the accuracy rate for GoogleNet was 99.185%, and a precision rate of 98.529%, a recall rate of 98.532%, and an F1-score of 98.518% were observed. In [27], the authors compared the VGGNet, LeNet, ResNet50, and Xception models for tomato leaf disease detection. All the networks were trained using 14,903 images and included 10 distinct diseases. The VGGNet model revealed a test accuracy of 99.25%. The authors of [28] compared four CNN models (Xception, NasNetMobile, MobileNetV2, and MobileNetV3) for ten tomato leaf disease detection categories. They used 18,215 tomato images from the Plantvillage dataset and increased the whole dataset 6 times, so the augmented set consisted of 109,290 images. The Xception model reached an accuracy of 100.00%, but from the confusion matrix, the 100% identification results were achieved in one of the ten tomato categories in the test data set.

In [29], the authors compared the InceptionV3, GoogleNet, AlexNet, ResNet50, and ResNet18 models for ten distinct diseases of tomato detection. All networks were trained to utilize 18,160 images from the Plantvillage dataset. The GoogleNet model reached an accuracy of 99.39%, but from the confusion matrix, the 100% identification results were achieved in three of the ten tomato categories in the test data set.

In Table 1, a detailed comparison of the categorization systems listed above is included, as well as an analysis of each system in terms of the algorithm used and the accuracy gained. In our work, the initial collection included 18,160 images of tomato leaves, and by augmenting the data only in the training dataset, it became 76,995 images. None of the previous works include such a large number of tomato leaf images, and unlike previous studies, we achieved 100% identification results in six of the ten tomato categories in the test dataset, based on the results of our experiments.

Table 1. A comparison of the several tomato crop methods.

Reference	Algorithm	Accuracy (%)
[18]	VGG16	97.29
	AlexNet	97.49
[19]	Modified VGG16	98.40
[20]	CNN model	91.20
[21]	CNN-SVM-CBAM	97.20
[22]	CNN model	96.55
[23]	Restructured residual dense network	95.00
[24]	DensNet161	95.65
	DensNet121	94.93
	VGG16	90.58
[25]	CNN model	98.49
[26]	GoogleNet	99.18
	AlexNet	98.66
[27]	VGGNet	99.25
	LeNet	96.27
	ResNet50	98.65
	Xception	98.13
[28]	Xception	100.00
	NasNetMobile	84.00
	MobileNetV2	75.00
	MobileNetV3	98.00
[29]	InceptionV3	98.65
	GoogleNet	99.39
	AlexNet	98.93
	ResNet50	99.15
	ResNet18	99.06

Thus, in this study, a hybrid CNN classification strategy was developed for the diagnosis of tomato diseases based on image evidence from a large dataset. The primary goal of our proposed architecture was to enhance the accuracy of tomato leaf identification and minimize the number of incorrect classifications. The hybrid CNN architecture was trained and tested using image data containing ten different kinds of tomato diseases. The classification accuracy of the model was 99.17%. The suggested method may assist professionals working in the agricultural sector in terms of improved screening since it has a high accuracy rate.

3. Proposed System

3.1. Dataset Description

The collection PlantVillage comprises 18,160 images of tomato leaves that are available to the public and represent 9 illnesses and 1 healthy condition [30]. Each of the ten types of tomatoes is represented by a single leaf in each image. Every image was shot against a plain neutral background to seem reasonably uniform. In addition, every leaf was positioned such that it would be centered on each image. No trimming or preprocessing was performed on the images; thus, they may contain display borders in the background that were irrelevant. The dataset was provided in the JPEG file format, and the resolution was 256 pixels on each side. A sample of nine different illnesses that might affect tomato leaves is shown in Figure 1, along with a healthy leaf.

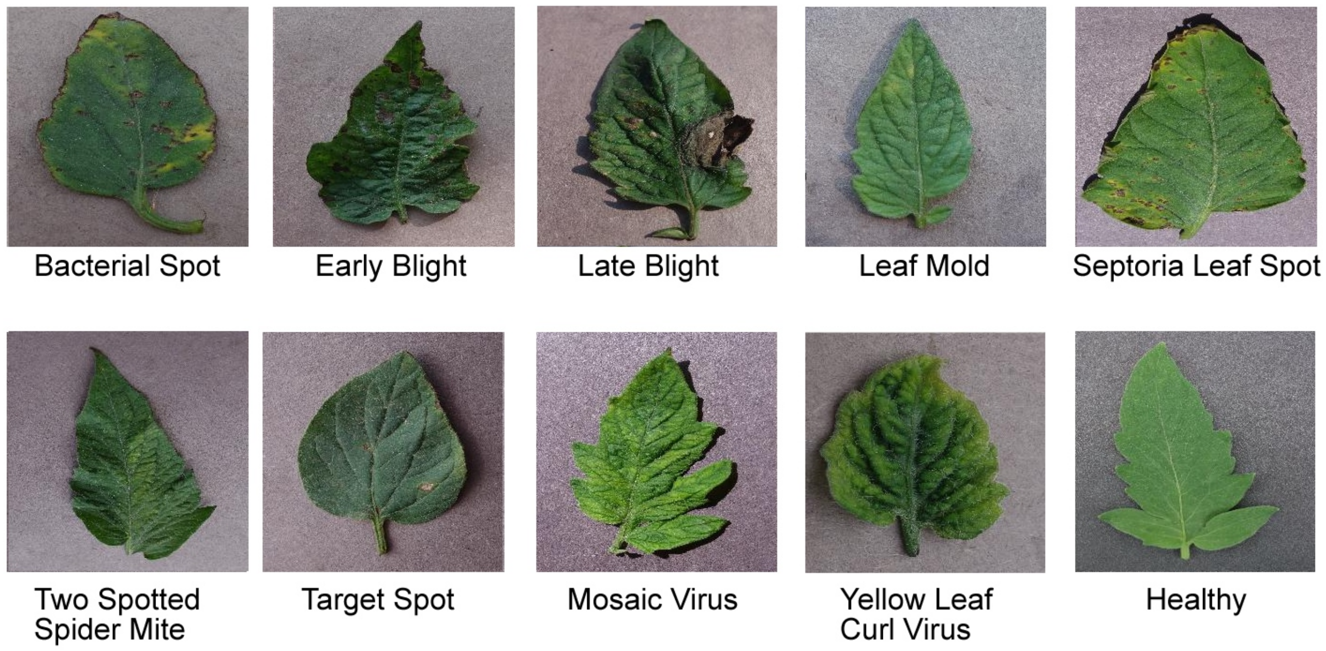


Figure 1. Sample images of the tomato plant from the PlantVillage collection (nine diseases and one healthy).

3.2. Data Augmentation

In order for DL algorithms to handily train and improve their performance, they need a large volume of data. Data augmentation is the method of increasing the size of a dataset by generating new training data from the current training data. By augmenting the data, we can create a larger and more diverse dataset, which can improve the model's generalization ability and help it perform better on new data. Therefore, the model can train more efficiently and produce more accurate predictions if the dataset has a vast quantity of varied and well-labeled data. Conversely, the model's poor performance is caused by having a small dataset. In addition to improving model performance, data augmentation can also help to reduce overfitting, which is a common problem in DL [31,32].

In this work, we improved the data quality using techniques such as vertical flipping, height shift, zoom, horizontal flipping, random rotation, shearing transformation, and width shift, with the ranges shown in Table 2. Figure 2 illustrates a number of different applications of data enhancement applied to the training dataset.

Table 2. Tomato details of data augmentation in the training set.

Parameter	Value
Random rotation	[+12, −12]
Width shift	[0.6, 1.1]
Zoom	[0.5, 0.9]
Fill mode	Nearest
Horizontal flip	True
Height shift	0.15
Shearing transformation	0.25
Vertical flip	True

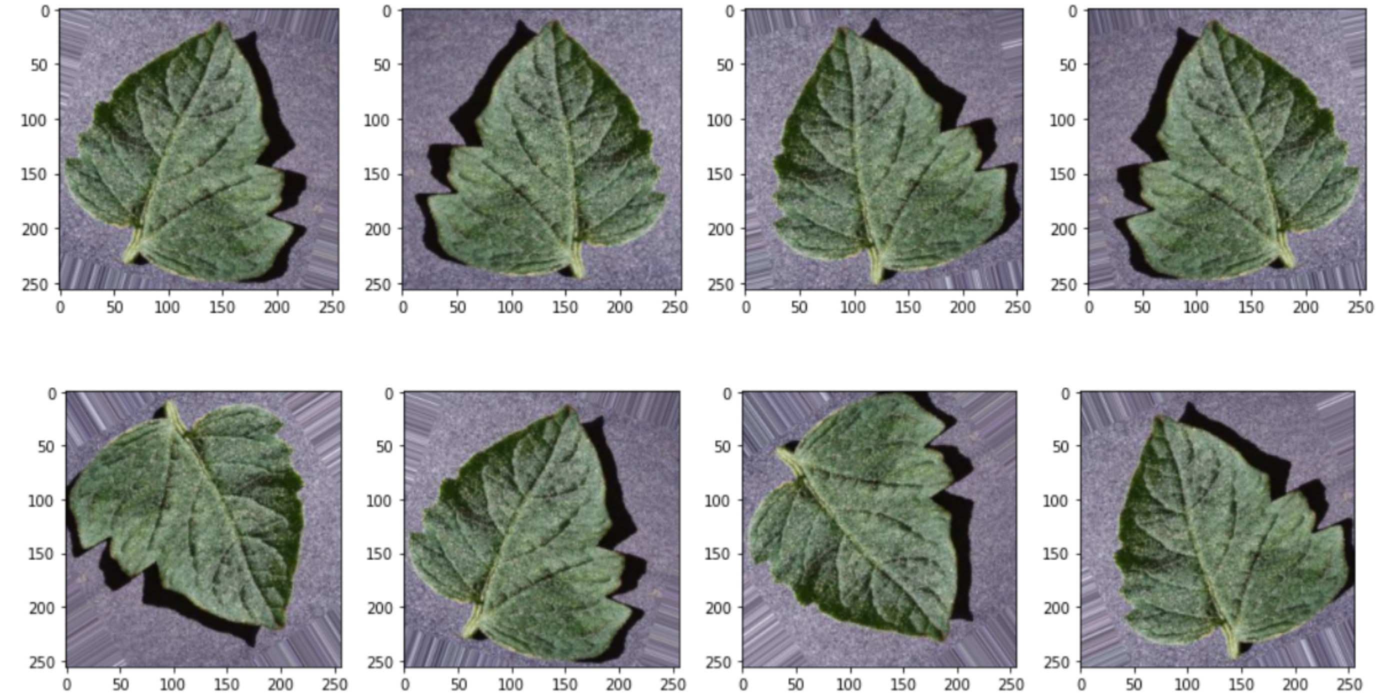


Figure 2. An augmented sample in the training dataset using classical geometric transformations.

3.3. Split Dataset

In deep learning, the ratio of a dataset's training, validation, and test sets is determined by the size and nature of the dataset. A typical split ratio is 90/10, in which 90% of the data are used for training/validation and 10% for testing. Out of the 90% of data used for training/validation, 80% were used for training and 10% for validation. This ratio is frequently employed when the dataset is relatively large, and there are sufficient data to effectively train the model while still leaving sufficient data for validation and testing. Thus, the larger the number of input images used during the training process, the better the learning of the model [33].

A training dataset is a collection of data utilized to train a CNN. The model is trained on a large volume of labeled data, which are then used to train the model to make predictions on new, unused data in order to improve the model's predictive accuracy. It is essential to employ a high-quality, diverse dataset representative of the data that the model will encounter in the real world, as the quality of the training dataset is crucial to the model's performance.

A validation dataset is a collection of data used to evaluate the performance of a CNN during training. The model is evaluated on a validation dataset to determine how well it can generalize to new, unused data. The training dataset is larger than the validation dataset. It is utilized to tune the model's hyperparameters, learning rate, and the number of hidden layers to enhance its performance on the validation dataset. Using a validation dataset, the model can be trained to optimize its performance on new data instead of merely memorizing the training dataset.

A testing dataset is a collection of data used to evaluate a CNN after training. The testing dataset is distinct from the training and validation datasets and is used to evaluate the model's performance on new, unused data. The testing dataset provides an objective evaluation of the performance of the model. It is used to compare the performance of various models or variants of the same model.

The training dataset was the only one to which post-split data augmentation techniques were applied. After augmentation, the size of the training images was expanded 5 times. Thus, the original collection comprised 18,160 images of tomato leaves and, with data augmentation, it became 76,995 images. An overview of the tomato dataset is shown in Table 3.

Table 3. Tomato datasets (training, validation, and testing).

Categories	Number of Original Images	Training Images	Training Images after Augmentation	Validation Images	Test Images
Early Blight	1000	810	4050	90	100
Target Spot	1404	1138	5688	126	140
Mosaic Virus	373	302	1508	34	38
Septoria Leaf Spot	1771	1434	7169	159	178
Late Blight	1909	1547	7736	172	190
Healthy	1591	1288	6440	143	160
Spider Mites	1676	1357	6786	151	168
Bacterial Spot	2127	1724	8618	192	212
Leaf Mold	952	770	3852	86	96
Yellow Leaf Curl Virus	5357	4340	21,699	482	535
Total Images	18,160	14,709	73,544	1634	1817

3.4. Hybrid CNN Model for Tomato Crop Disease

In order to differentiate between the ten unique illnesses that might affect tomatoes, we developed a hybrid CNN model that is both effective and practical. Combining the VGG blocks with the inception module resulted in the most advanced state-of-the-art CNN model. Growing the scale of a deep neural network is the quickest and easiest way to enhance the performance of these kinds of systems.

The VGG provides powerful and accurate classification capabilities. The dimensions of the input image were 224 × 224 × 3. The first VGG block had 64 filters and outputted a feature map of size 224 × 224 × 64, and the output shape was 112 × 112 × 64. The second VGG block had 128 filters and outputted a feature map of size 112 × 112 × 128, and the output shape was 56 × 56 × 28. The third VGG block had 256 filters and outputted a feature map of size 56 × 56 × 256, and the output shape was 28 × 28 × 256. The fourth VGG block had 512 filters and outputted a feature map of size 28 × 28 × 512, and the output shape was 14 × 14 × 512. The fifth VGG block had 512 filters and outputted a feature map of size 14 × 14 × 512, and the output shape was 7 × 7 × 512.

In addition, the inception module has shown its usefulness for implementation in GoogleNet and has been proven to accomplish remarkable and unachievable outcomes. Inception modules have four parallel convolutional and pooling layers that are designed to capture various spatial scales. These layers are designed to work in conjunction with one another. As a result of this, we were able to improve the capacity of the newly developed hybrid network to extract features by including an inception module into the conventional VGGNet.

The hybrid CNN model for tomato crop disease includes the following components: 13 convolutional layers for feature extraction, each with a size of 3 × 3; 5 max-pooling layers, each with a size of 2 × 2; an inception module; a global average pooling layer (GAP); and the softmax activation function for classification. After each convolutional layer, there was a ReLU layer, which acted as an activation function for the model. The mathematical computation of the ReLU activation function is shown in Equation (1). The final layer contained one feature map for each matched category of the classification job that was constructed using global average pooling.

$$\mathrm{ReLU}(z) = \begin{cases} 0, & \text{if } z < 0 \\ z, & \text{if } z \geq 0 \end{cases} \tag{1}$$

One advantage of using global average pooling is that it is better suited to the convolution structure that exists between feature maps and categories. Finally, the softmax function was used while dealing with multiclass classification issues and trying to forecast output images. Equation (2) depicts the mathematical computation of the softmax activation function, where z_i represents input data, and k is the number of categories.

$$\text{Softmax}(z_i) = \frac{e^{z_i}}{\sum_{y=1}^{k} e^{z_y}} \tag{2}$$

The inception module diagram is shown in Figure 3, and the hybrid network diagram is presented in Figure 4.

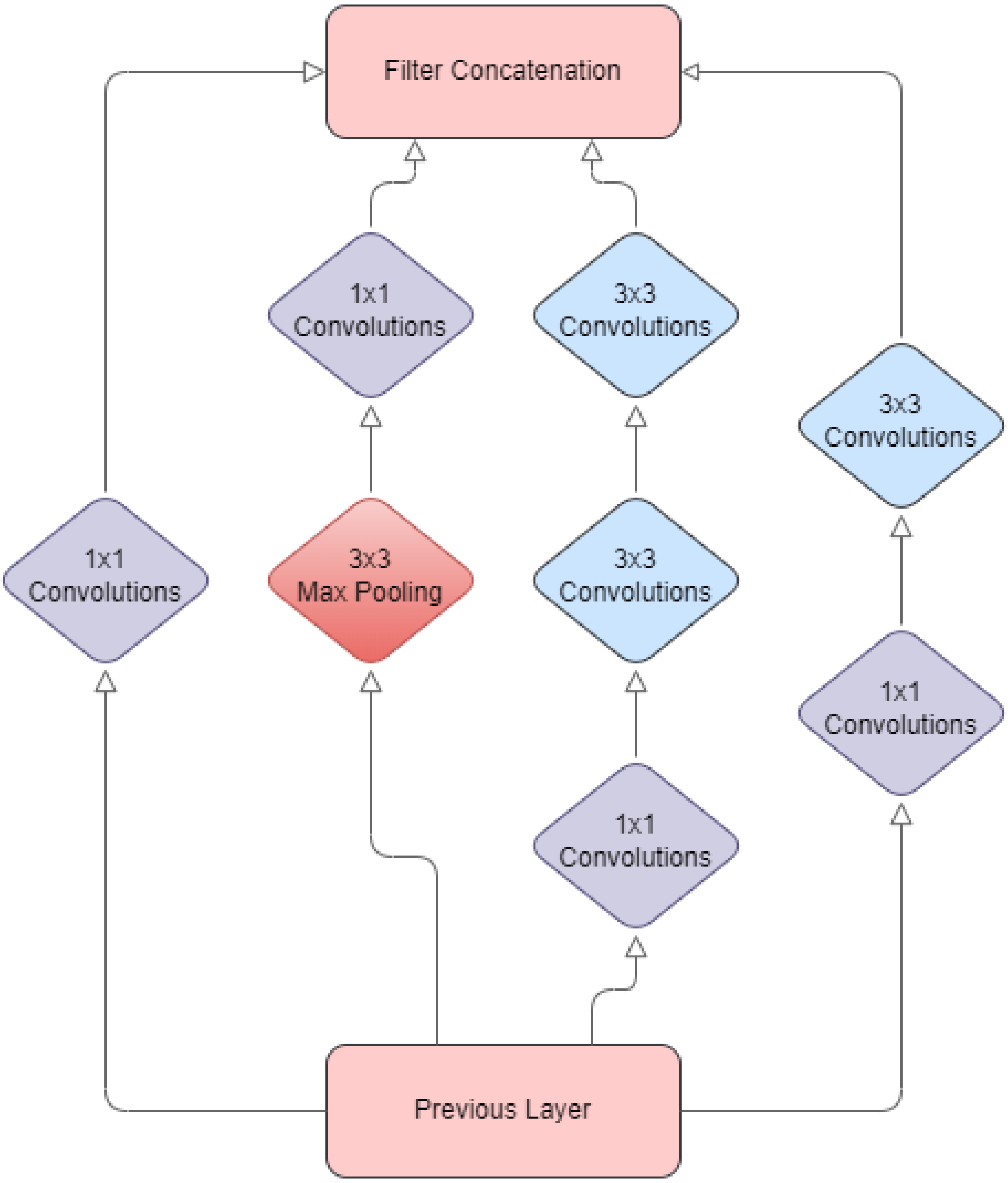


Figure 3. Inception module diagram.

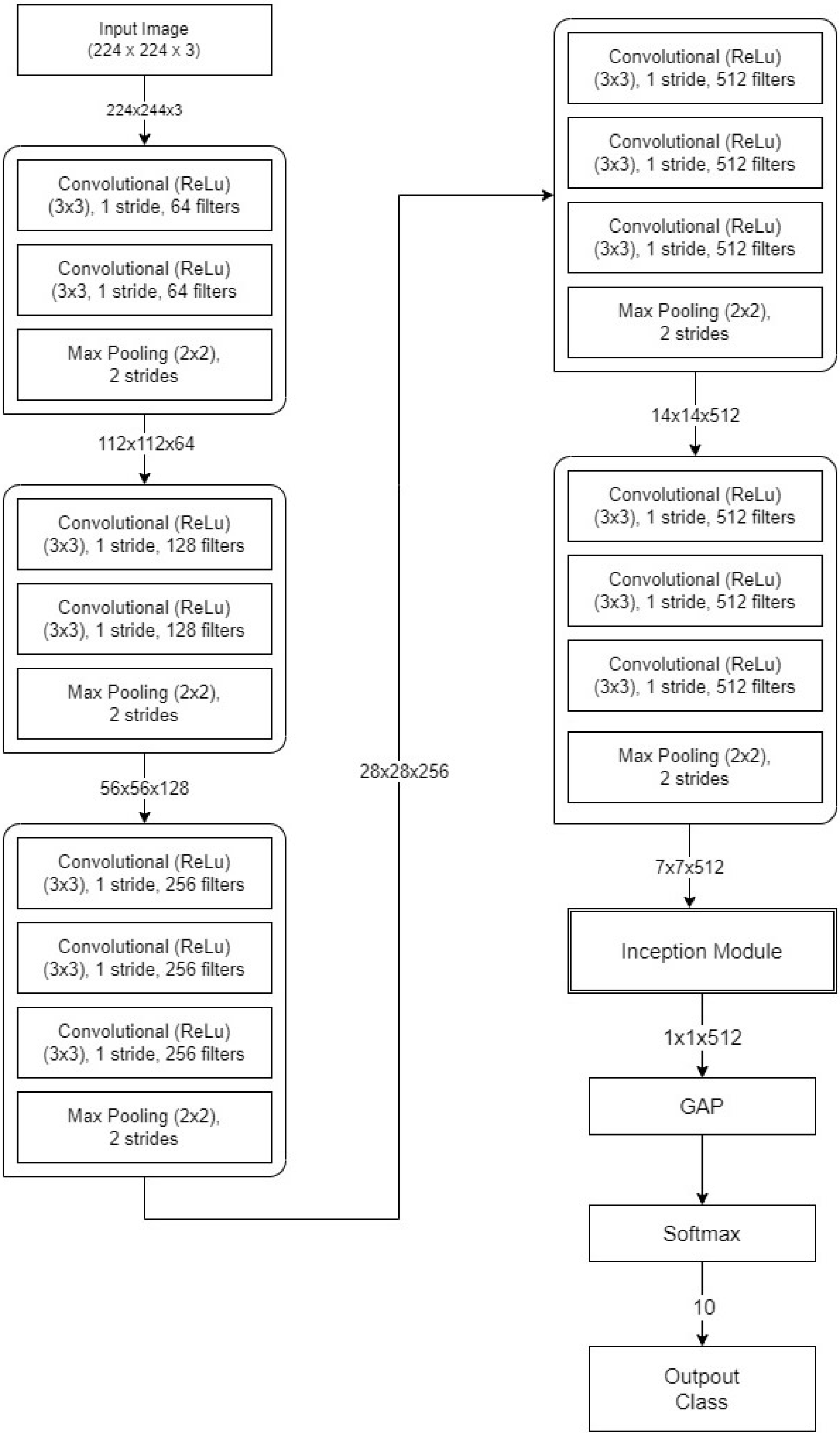


Figure 4. Hybrid CNN model diagram with five VGG blocks, inception module, GAP, and softmax activation function for classification.

3.5. Implementation Specification

All the experiments were conducted using a GPU (NVIDIA GTX 1070 with 8GB RAM). Python 3, the Keras package, CUDA, Matplotlib, and CuDNN were the primary libraries used in the process of implementing the hybrid CNN model, as well as all of the models that were compared. The values of the training settings were set to enable the model to effectively generalize new data, thus producing accurate forecasts based on test data. All CNN models were optimized using an Adam [34] optimizer with the learning rate set at 0.0001, and the epoch was set at 30. The categorical cross-entropy was used to compute the loss function of all of the models. Table 4 outlines the particular training settings in all of the models.

Adam is an established algorithm for optimization. It is an extension of the gradient descent optimization algorithm, a popular optimization strategy used while training DL models. It is also computationally effective, which is one of the reasons it is such a popular option; identification tasks have been performed with its assistance on several occasions.

The batch size is used to establish the total number of samples that pass through the model before the parameters of the model may be updated. A batch size of 16 necessitates more updates to the model's parameters, but each update will be based on a smaller sample of the data. This resulted in better stable estimations of the loss function and gradients.

Cross-entropy is a loss function, and it is well suited for identification assignments. When training a classifier, the objective is to achieve the lowest possible error between the predicted and the actual class probabilities. Because it pushes the model to be more cautious in its predictions, cross-entropy is a good option because it helps the model achieve better accuracy overall.

The number of epochs is a hyperparameter that specifies the total number of times the model is trained using the whole training dataset. The performance of the model was significantly affected by using 30 epochs.

During the training process, the learning rate is a hyperparameter that affects the size of the step at which the optimizer updates the model parameters. It is common practice to use a learning rate of 0.0001 to guarantee that the model can train efficiently and converge to a satisfactory solution.

Table 4. Training settings for all models.

Parameter	Value
Optimizer	Adam
Batch size	16
Loss function	Cross-entropy
Epochs	30
Learning rate	0.0001

3.6. Performance Metrics

The performance of the developed model was analyzed using the following metrics: accuracy, precision, recall, receiver operating characteristic curve (ROC), and F1-score [35]. The four evaluation metrics were calculated using Equations (3)–(6), where tp, fn, fp, tn represent the number of true positives, false negatives, false positives, and true negatives. Finally, the ROC is called the area under the curve (AUC). It indicates how well the model can differentiate between different types of data. When the AUC is higher, the model can better differentiate between the category who have the disease and those who do not.

$$\text{Accuracy} = \frac{tp + tn}{tp + fn + fp + tn} \times 100\% \tag{3}$$

$$\text{Precision} = \frac{tp}{tp + fp} \times 100\% \tag{4}$$

$$\text{Recall} = \frac{tp}{tp + fn} \times 100\% \tag{5}$$

$$\text{F1-score} = \frac{2 \times (\text{ Precision } \times \text{ Recall })}{(\text{ Precision } + \text{ Recall })} \times 100\% \tag{6}$$

4. Results

The primary goal of our proposed architecture was to enhance tomato leaf detection accuracy and decrease erroneous classifications. To evaluate the performance of the hybrid CNN model, we compared the accuracy/loss performance, recall, F1-score, precision, overall accuracy, and AUC.

4.1. Training Loss and Accuracy

To evaluate the performance of the hybrid CNN model, we compared the Inception-ResNet, and ResNet152 accuracy performance and loss performance. The network was trained by considering the parameters listed in Table 4. The hybrid CNN model achieved a training accuracy of 99.83%, a validation accuracy of 99.17%, a loss of 0.1853, and a validation loss of 0.1834. The InceptionResNet model demonstrated a training accuracy of 99.69%, a validation accuracy of 98.40%, a loss of 0.2103, and a validation loss of 0.2305. Finally, the ResNet152 model showed a training accuracy of 99.45%, a validation accuracy of 97.30%, a loss of 0.2348, and a validation loss of 0.9730. Figures 5 and 6 show the change in training accuracy and loss for the three convolutional models for 30 epochs.

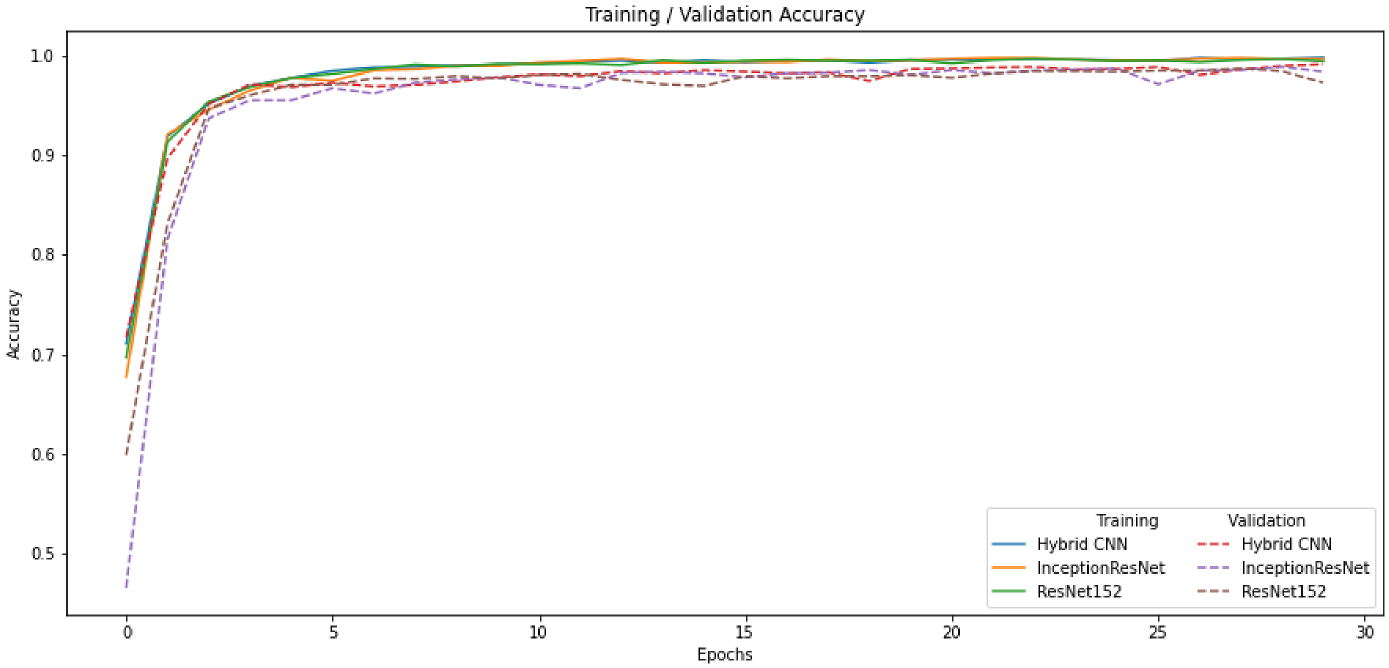


Figure 5. Comparative training accuracy of all models.

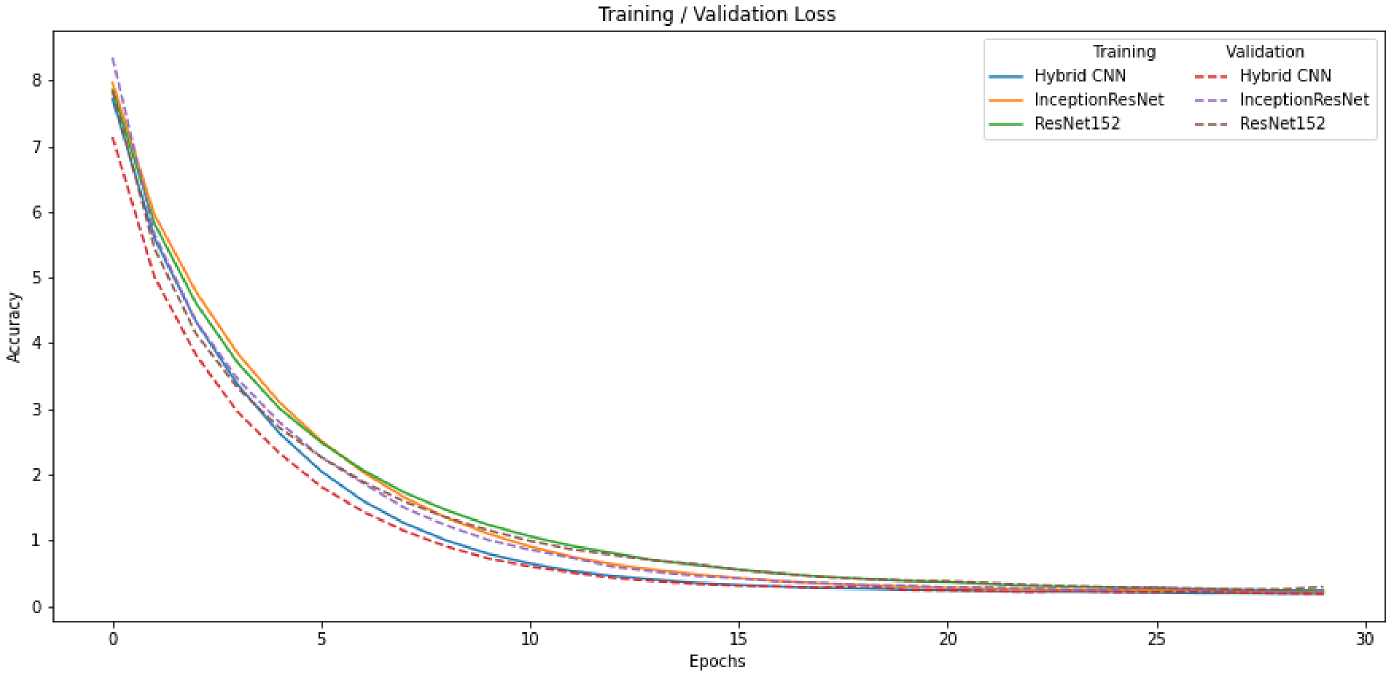


Figure 6. Comparative loss function on the training dataset of all models.

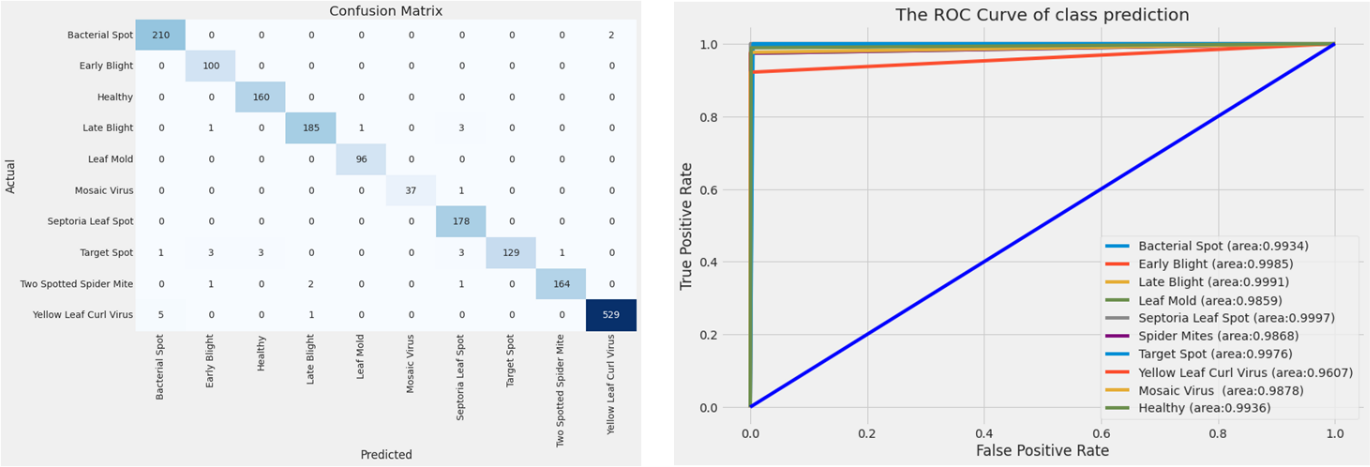
4.2. Evaluation of Models on the Test Dataset

Table 5 presents the performance measurement results in the test set to compare the various models. In addition, the results of applying each model to the various tomato crop disease scenarios included in the test set are summarized in Table 6 below.

Table 5. Performance metrics of three models.

Performance Metrics (%)	InceptionResNet	ResNet152	Hybrid CNN
Training accuracy	99.69	99.45	99.83
Testing accuracy	98.40	97.30	99.17
Precision	98.27	97.19	99.13
Recall	98.24	97.09	99.23
F1-score	98.23	96.95	99.17
AUC	99.03	98.39	99.56

Compared with the ResNet152 and InceptionResNet models, the suggested hybrid CNN model in this study revealed superior average testing accuracy, with an accuracy of 99.17%, under the same experimental settings as those of ResNet152 and InceptionResNet. At the same time, the rate of convergence in the presented model was the fastest among all the models. In addition, the model was stable, and the variance in loss performance had a limited range. The results in Table 6 reveal that the addition of the inception module yielded much better outcomes for the model. In Figures 7–9, we present the confusion matrix and ROC curve plots for the three models.

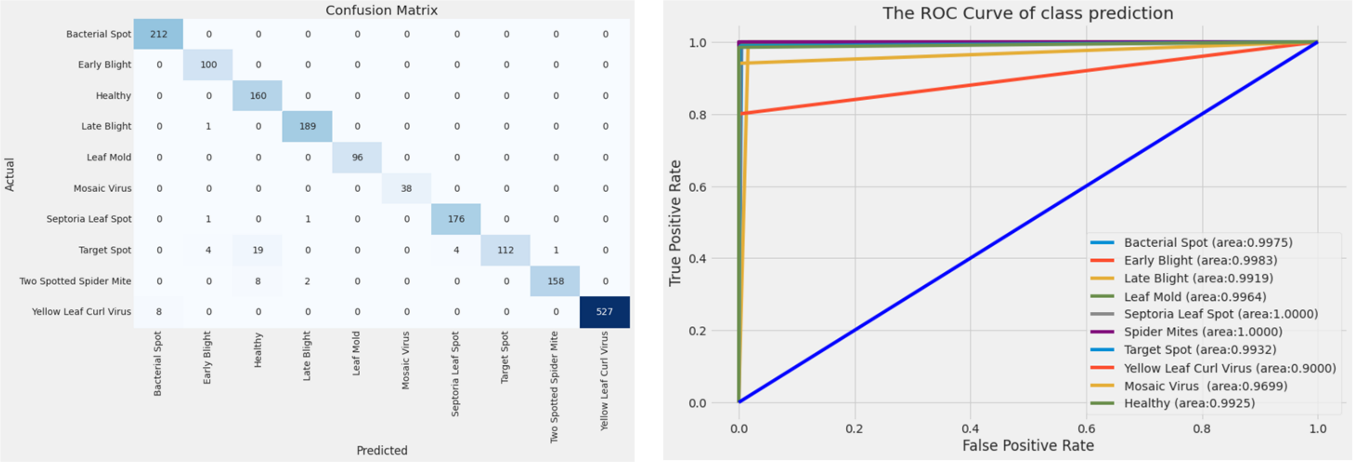


Confusion Matrix

Actual \ Predicted	Bacterial Spot	Early Blight	Healthy	Late Blight	Leaf Mold	Mosaic Virus	Septoria Leaf Spot	Target Spot	Two Spotted Spider Mite	Yellow Leaf Curl Virus
Bacterial Spot	210	0	0	0	0	0	0	0	0	2
Early Blight	0	100	0	0	0	0	0	0	0	0
Healthy	0	0	160	0	0	0	0	0	0	0
Late Blight	0	1	0	185	1	0	3	0	0	0
Leaf Mold	0	0	0	0	96	0	0	0	0	0
Mosaic Virus	0	0	0	0	0	37	1	0	0	0
Septoria Leaf Spot	0	0	0	0	0	0	178	0	0	0
Target Spot	1	3	3	0	0	0	3	129	1	0
Two Spotted Spider Mite	0	1	0	2	0	0	1	0	164	0
Yellow Leaf Curl Virus	5	0	0	1	0	0	0	0	0	529

Actual
Predicted
The ROC Curve of class prediction
True Positive Rate
False Positive Rate
0.0
0.2
0.4
0.6
0.8
1.0
Bacterial Spot (area:0.9934)
Early Blight (area:0.9985)
Late Blight (area:0.9991)
Leaf Mold (area:0.9859)
Septoria Leaf Spot (area:0.9997)
Spider Mites (area:0.9868)
Target Spot (area:0.9976)
Yellow Leaf Curl Virus (area:0.9607)
Mosaic Virus (area:0.9878)
Healthy (area:0.9936)

Figure 7. Confusion matrix and ROC curve of InceptionResNet model on the tomato test data.

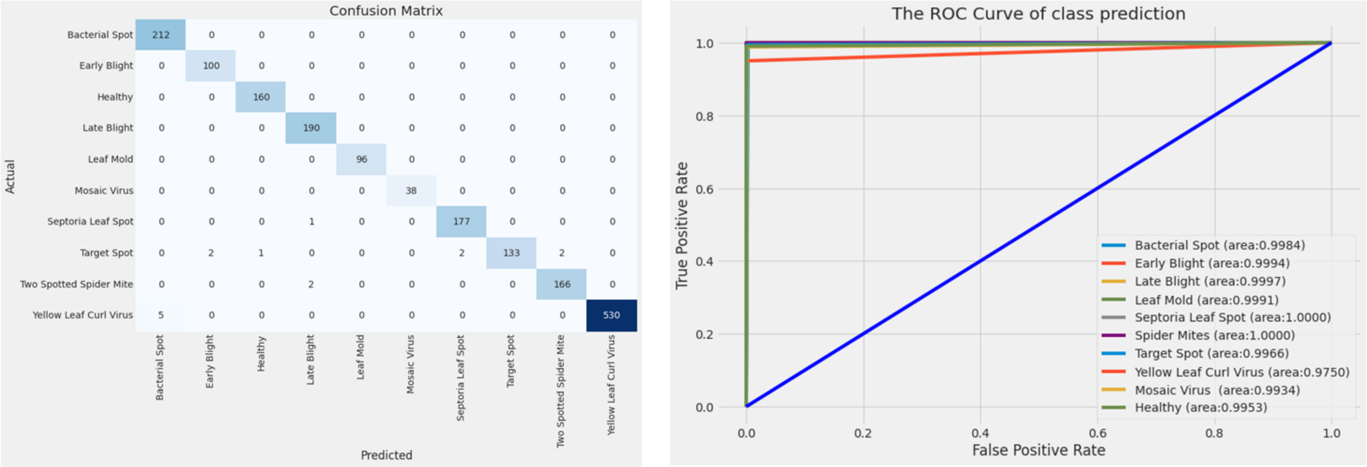


Confusion Matrix

Actual \ Predicted	Bacterial Spot	Early Blight	Healthy	Late Blight	Leaf Mold	Mosaic Virus	Septoria Leaf Spot	Target Spot	Two Spotted Spider Mite	Yellow Leaf Curl Virus
Bacterial Spot	212	0	0	0	0	0	0	0	0	0
Early Blight	0	100	0	0	0	0	0	0	0	0
Healthy	0	0	160	0	0	0	0	0	0	0
Late Blight	0	1	0	189	0	0	0	0	0	0
Leaf Mold	0	0	0	0	96	0	0	0	0	0
Mosaic Virus	0	0	0	0	0	38	0	0	0	0
Septoria Leaf Spot	0	1	0	1	0	0	176	0	0	0
Target Spot	0	4	19	0	0	0	4	112	1	0
Two Spotted Spider Mite	0	0	8	2	0	0	0	0	158	0
Yellow Leaf Curl Virus	8	0	0	0	0	0	0	0	0	527

Actual
Predicted
The ROC Curve of class prediction
True Positive Rate
False Positive Rate
0.0
0.2
0.4
0.6
0.8
1.0
Bacterial Spot (area:0.9975)
Early Blight (area:0.9983)
Late Blight (area:0.9919)
Leaf Mold (area:0.9964)
Septoria Leaf Spot (area:1.0000)
Spider Mites (area:1.0000)
Target Spot (area:0.9932)
Yellow Leaf Curl Virus (area:0.9000)
Mosaic Virus (area:0.9699)
Healthy (area:0.9925)

Figure 8. Confusion matrix and ROC curve of ResNet152 model on the tomato test data.



Confusion Matrix

Actual \ Predicted	Bacterial Spot	Early Blight	Healthy	Late Blight	Leaf Mold	Mosaic Virus	Septoria Leaf Spot	Target Spot	Two Spotted Spider Mite	Yellow Leaf Curl Virus
Bacterial Spot	212	0	0	0	0	0	0	0	0	0
Early Blight	0	100	0	0	0	0	0	0	0	0
Healthy	0	0	160	0	0	0	0	0	0	0
Late Blight	0	0	0	190	0	0	0	0	0	0
Leaf Mold	0	0	0	0	96	0	0	0	0	0
Mosaic Virus	0	0	0	0	0	38	0	0	0	0
Septoria Leaf Spot	0	0	0	1	0	0	177	0	0	0
Target Spot	0	2	1	0	0	0	2	133	2	0
Two Spotted Spider Mite	0	0	0	2	0	0	0	0	166	0
Yellow Leaf Curl Virus	5	0	0	0	0	0	0	0	0	530

Actual
Predicted
The ROC Curve of class prediction
True Positive Rate
False Positive Rate
0.0
0.2
0.4
0.6
0.8
1.0
Bacterial Spot (area:0.9984)
Early Blight (area:0.9994)
Late Blight (area:0.9997)
Leaf Mold (area:0.9991)
Septoria Leaf Spot (area:1.0000)
Spider Mites (area:1.0000)
Target Spot (area:0.9966)
Yellow Leaf Curl Virus (area:0.9750)
Mosaic Virus (area:0.9934)
Healthy (area:0.9953)

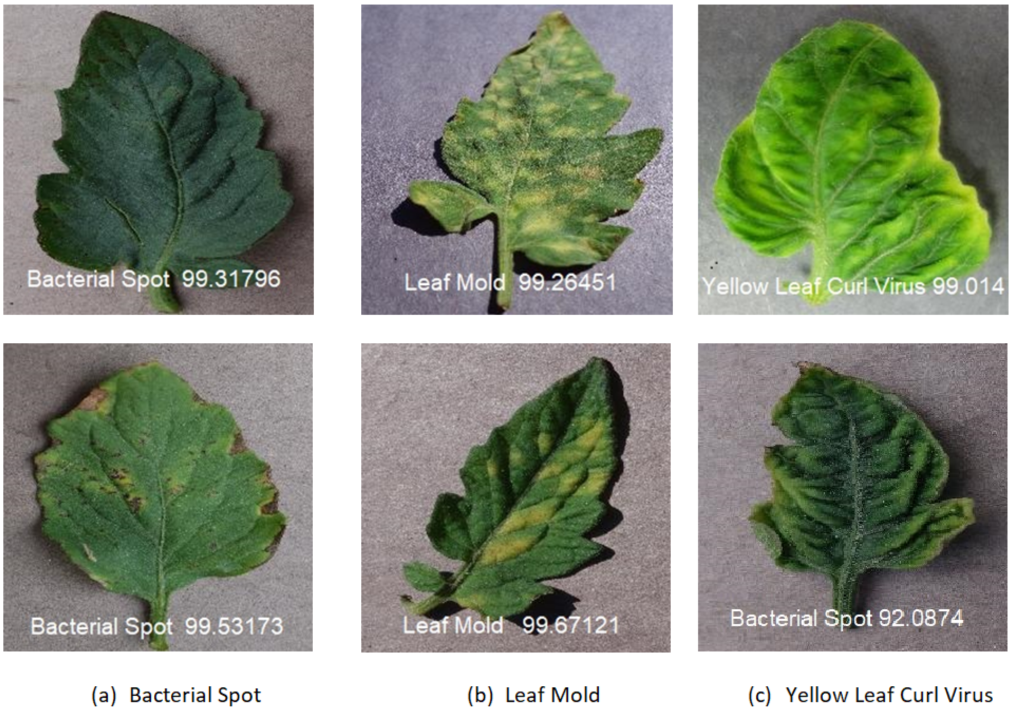
Figure 9. Confusion matrix and ROC curve of proposed hybrid CNN model on the tomato test data.

Table 6. Performance evaluation of three models.

Model	Categories	Precision	Recall	F1-Score
InceptionResNet	Bacterial Spot	0.9722	0.9906	0.9813
	Healthy	0.9816	1.0000	0.9907
	Mosaic Virus	1.0000	0.9737	0.9867
	Two Spotted Spider Mites	0.9939	0.9762	0.9850
	Late Blight	0.9840	0.9737	0.9788
	Early Blight	0.9524	1.0000	0.9756
	Septoria Leaf Spot	0.9570	1.0000	0.9780
	Leaf Mold	0.9897	1.0000	0.9948
	Yellow Leaf Curl Virus	0.9962	0.9888	0.9925
	Target Spot	1.0000	0.9214	0.9591
ResNet152	Bacterial Spot	0.9636	1.0000	0.9815
	Healthy	0.8556	1.0000	0.9222
	Mosaic Virus	1.0000	1.0000	1.0000
	Two Spotted Spider Mites	0.9937	0.9405	0.9664
	Late Blight	0.9844	0.9947	0.9895
	Early Blight	0.9434	1.0000	0.9709
	Septoria Leaf Spot	0.9778	0.9888	0.9832
	Leaf Mold	1.0000	1.0000	1.0000
	Yellow Leaf Curl Virus	1.0000	0.9850	0.9925
	Target Spot	1.0000	0.8000	0.8889
Hybrid CNN	Bacterial Spot	0.9770	1.0000	0.9883
	Healthy	0.9938	1.0000	0.9969
	Mosaic Virus	1.0000	1.0000	1.0000
	Two Spotted Spider Mites	0.9881	0.9881	0.9881
	Late Blight	0.9845	1.0000	0.9922
	Early Blight	0.9804	1.0000	0.9901
	Septoria Leaf Spot	0.9888	0.9944	0.9916
	Leaf Mold	1.0000	1.0000	1.0000
	Yellow Leaf Curl Virus	1.0000	0.9907	0.9953
	Target Spot	1.0000	0.9500	0.9744

It can be seen from Figure 9 that the proposed hybrid CNN model showed identification results that were 100% accurate in six out of ten categories. This is because the diseases that fall into these categories have unique symptoms and characteristics compared with the other categories.

As shown in Figure 10, the identified categories for most of the tomato plant images corresponded to their actual kinds. For instance, the proper disease for the image in Figure 10a was accurately diagnosed as a "bacterial spot" with a probability greater than 99.30%. Similarly, the proposed method correctly identified each sample in Figure 10b. On the other hand, inconsistent lighting conditions, such as shadowing in the images, affected the feature extraction. Thus, they could lead to inaccurate classifications of tomato diseases, as shown in Figure 10c. According to the results, it can be concluded that the suggested hybrid network is beneficial in improving the accuracy of tomato leaf identification.



(a) Bacterial Spot (b) Leaf Mold (c) Yellow Leaf Curl Virus

Figure 10. The examples of identification results of tomato plant diseases on the test data.

5. Conclusions and Future Work

Tomato plants are vulnerable to a broad number of diseases, each of which, if allowed to develop further, has the potential to cause significant damage to the plant if it is permitted to continue. It is impossible to exaggerate how important it is to arrive at a diagnosis as promptly and correctly as is humanly feasible. The objective of this work was to propose a hybrid deep convolutional neural network as a diagnostic tool for a variety of diseases that may impact tomato leaf tissue. This hybrid diagnostic instrument revealed an accuracy of 99.17%, a recall of 99.23%, a precision of 99.13%, and an F1-score of 99.17%. We believe the presented approach provides a potential solution that will be of significant value to the field of agriculture. Consequently, future work that further builds this hybrid network will facilitate the improvement in the efficiency of the categorization model, thus leading to further overall improvement.

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Abbreviations

The following abbreviations are used in this manuscript:

AI	Artificial Intelligence
AUC	Area Under the Curve
CBAM	Convolutional Attention Module
CNN	Convolutional Neural Network
DL	Deep learning
FAO	Food and Agriculture Organization of the United Nations
MDPI	Multidisciplinary Digital Publishing Institute
ROC	Receiver Operating Characteristic Curve
SVM	Support Vector Machine
VGG	Visual Geometry Group

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