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Modifiye-InceptionResNetV2 Mimarisi Kullanarak Domates Yaprak Koşullarının Etkili Tespiti

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ÖZ

Domates yapraklarını etkileyen hastalıkların zamanında tespit edilmesi ve tedavi edilmesi, bitki üretkenliğini, operasyonel verimliliği ve genel kaliteyi artırmak için esastır. Domates bitkileri çeşitli hastalıklara oldukça duyarlıdır ve çiftçilerin bu hastalıkları yanlış teşhis etmeleri, yetersiz tedavi stratejilerine yol açarak hem bitkilere hem de tarım ekosistemine zarar verebilir. Domates mahsullerinin kalitesinin sağlanması, zamanında ve doğru teşhise büyük ölçüde bağlıdır. Günümüzde derin öğrenme teknikleri, domates bitkilerinde hastalıkları sınıflandırmak gibi çeşitli uygulamalarda önemli başarılar göstermiştir. Bu çalışma, Modifiye-InceptionResNetV2 modeli adlı bir derin öğrenme mimarisi kullanarak domates yaprak koşullarını daha hassas bir şekilde tespit etmek için bir yaklaşım sunmaktadır; bu model, InceptionResNetV2 transfer öğrenme modeline dayanmaktadır. Önerilen mimari, temel model içindeki sınıflandırma bloğunu güçlendirmeye odaklanarak domates yapraklarının durumunu daha doğru bir şekilde tanımlama performansı elde etmeyi amaçlamaktadır. Ayrıca, sınıflandırma doğruluğunu artırmak için çeşitli ön işleme adımları ve artırma teknikleri kullanılmaktadır. Bilinen bir kamu veritabanı olan on sınıflı bir veri seti kullanılarak yapılan deneysel analiz, sırasıyla etkileyici eğitim, doğrulama ve test doğruluk oranlarına ulaşmaktadır: %99,74, %99,79 ve %99,20. Önerilen model, çiftçiler için önemli bir araç olarak hizmet edebilir; domates hastalıklarının etkili bir şekilde tespit edilmesine ve önlenmesine yardımcı olarak bitki hastalıklarının hızlı ve basit erken teşhisini sağlar. Deneysel sonuçlar, domates yaprak hastalığı sınıflandırmasında önceki çalışmalara üstünlüğünü ortaya koymaktadır.

Efficient Detection of Tomato Leaf Conditions using Modified-InceptionResNetV2 Architecture

Research Article

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ABSTRACT

Timely identification and treatment of diseases affecting tomato leaves are essential for enhancing plant productivity, operational efficiency, and overall quality. Tomato plants are highly vulnerable to a diverse range of diseases, and farmers' misdiagnosing of these ailments can lead to insufficient treatment strategies, causing harm to both the plants and the agroecosystem. Ensuring the quality of tomato crops relies significantly on prompt and accurate diagnoses. In contemporary times, deep learning techniques have demonstrated remarkable success across various applications, including classifying diseases in tomato plants. This study presents an approach for detecting tomato leaf conditions more precisely using a deep-learning architecture, namely the Modified-InceptionResNetV2 model, based on the InceptionResNetV2 transfer learning model. Our proposed architecture focuses on strengthening the classification block within the base model to achieve more accurate performance in identifying the condition of tomato leaves. Additionally, several preprocessing steps and augmentation techniques are employed to improve classification accuracy. Experimental analysis using a well-known, publicly available ten-class dataset achieves impressive training, validation, and testing accuracy rates of 99.74%, 99.79%, and 99.20%, respectively. The proposed model could serve as a vital tool for farmers, aiding in the efficient detection and prevention of tomato diseases and enabling rapid and simple early detection of plant diseases. Experimental results showcase its superiority over previous studies in tomato leaf disease classification.

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1. Introduction

Plants are crucial in sustaining human life by providing nourishment and shielding from harmful rays. They are indispensable for terrestrial ecosystems and safeguarding the ozone layer, which protects against UV radiation. The tomato, known for its nutritional richness, is extensively cultivated and consumed globally (Erika et al., 2020). Each year, approximately 160 million tons of tomatoes are consumed worldwide, making them a vital source of income for farming households and contributing significantly to poverty alleviation efforts (Bhandari et al., 2023). Tomato cultivation and production significantly influence the agricultural economy because nutrient richness positions them as highly esteemed crops globally (Trivedi et al., 2021). Tomatoes, renowned for their nutritional value, boast medicinal characteristics that offer protection against health-related problems, including high blood pressure, gum bleeding, and hepatitis. The surge in tomato demand has primarily stemmed from their medicinal and culinary uses. Small-scale farmers, contributing over 80% of agricultural output, encounter significant crop losses, with diseases and pests causing nearly half of the damage (Bhandari et al., 2023). It is crucial to recognize and comprehend parasite insects and illnesses that affect field crops in order to limit the detrimental impacts they have on tomato farming. Consequently, diagnostic research pertaining to field agricultural diseases is of the utmost relevance.

Plant diseases have been detected using machine-learning techniques since their inception (Reza et al., 2017; Panchal et al., 2019; Deepa et al., 2021). For plant health conditions identification, Chakraborty et al. (2021) employed an image-segmentation technique to isolate disease lesions from the leaves of apples. They then utilized support vector machines (SVM) to accurately identify the disease, taking into account the color and striping features of the lesions. Qin et al. (2016) developed a classification model to identify alfalfa leaf diseases utilizing a naïve Bayes approach combined with linear discriminant analysis. They extracted various features, including color, shape, and stripes, from lesions on the leaves. Chuanqi Xie and Yong He(2016) used an analysis of the textural features of tomato images to obtain an early detection accuracy of 88.46% for tomato blight. Rahman et al. (2023) describe a strategy of image processing based on autonomous detection and provide treatments for tomato leaf diseases. The suggested technique calculates 13 distinct statistical characteristics from tomato leaves using the grey-level co-occurrence matrix method. The acquired characteristics are sorted into various illnesses using the support vector machine (SVM). The results of the experiment indicate that the proposed method provides accurate annotations: one hundred percent for healthy leaves, ninety-five percent for early-blight conditions, ninety percent for septoria-leaf spots, and eighty-five percent for late-blight conditions. Despite the existence of numerous machine learning algorithms, image preprocessing and feature extraction, both intricate processes, are typically required prior to image recognition. However, convolutional neural networks (CNN) can bypass these steps by automatically identifying images and extracting discriminant features.

These days, deep learning techniques, especially CNNs, have made important strides in computer vision, automatically identifying and extracting distinctive characteristics while reducing reliance on manually crafted features, thereby enhancing classification accuracy. For instance, Zhong et al.(2021) utilized convolutional techniques to tune the parameters of dual-channel neural networks VGG16 and ResNet for the detection of maize leaf diseases, achieving a classification performance of 93.33%. However, this method requires further enhancements for better identification rates, high-resolution images, and complex model parameters. Paul et al. (2023a) suggested a lightweight custom CNN model and used TL-based models (VGG16 and VGG19)in order to detect tomato leaf conditions. The suggested model, leveraging data augmentation approaches, outperformed all other models in terms of accuracy and recall, achieving a remarkable 95.00%. Gulzar et al. (2023) developed an enhanced model using MobileNetV2, achieving 99% accuracy across 40 distinct fruits. Bouni et al. (2023) presented a deep CNN) and transfer learning that was used to identify tomato leaf disease. DenseNet, VGG-16, AlexNet, and ResNet make up CNN's backbone. The comparative performance of these networks is evaluated employing the Adam and RmsProp optimization techniques, revealing that the DenseNet pretrained model, when utilizing the RmsProp optimizer, yields the most notable performance, achieving an exceptional accuracy of 99.90%. Aggarwal et al. (2023) introduced a stacked ensemble technique to enhance F1 scores, which involved aggregating predictions from three pre-trained models: ResNet152, VGG16, and DenseNet169. Their findings suggest that assembling multiple weak CNNs outperforms single models in terms of prediction accuracy. Another study employing CNN and transfer learning successfully classified 14 common seeds (Gulzar et al., 2020), showcasing the advancements in deep learning technology. Agarwal et al. (2020) suggested a CNN architecture to classify tomato leaf illnesses. Adam and the SGD optimizer have been used to implement the suggested CNN model. The outcomes demonstrate that, when used with the SGD optimizer, the CNN model obtains an accuracy of 0.9966) and a loss value of 0.0044. Zhang et al. (2023) introduced M-AORANet, which accurately identifies tomato leaf diseases by extracting fine multi-scale attributes and locating lesions on tomato leaves, achieving a recognition accuracy of 96.47% from 7493 photos. Sun et al. (2017) improved the AlexNet architecture by minimizing convolutional kernel size and parameters, while Deng et al. (2023) presented a CNN architecture for detecting the tomato leaf conditions utilizing an online dataset and additional images from the country's fields. The proposed model effectively identifies and categorizes diseases found on tomato leaves, achieving an accuracy exceeding 99% in both the training and test datasets. These diverse strategies offer valuable insights for further research and development.

This study presents a tomato leaf disease detection approach employing a novel deep learning architecture, namely Modified-InceptionResNetV2. Exploiting the architecture of pre-trained models, we load the weights of the pre-trained model to use it for feature extraction. Afterward, the results of the model are combined to aid in identifying and categorizing leaf pictures. To enhance the effectiveness of our approach, we incorporate various preprocessing phases and augmentation techniques. These steps contribute to improved experimental outcomes, enabling the precise detection of tomato leaf conditions. The following sections of this paper are structured as outlined below: In Section 2, we detail our overall methodology, encompassing a thorough discussion of data description, preprocessing with augmentation techniques, and the proposed model architecture. Section 3 delves into a comprehensive analysis of the experimental results, accompanied by an in-depth discussion. Finally, Section 4 summarizes the key findings and delineates future plans.

2. Methodology

A tomato leaf condition detection approach is presented in this study. Firstly, a well-known publicly available tomato leaf dataset (comprising ten classes) is collected for analysis. Next, data preprocessing and augmentation techniques are implemented, aiding in enhancing diversity and robustness. The entire dataset is then split into three subsets to train the model, validate its performance, and test its effectiveness on unseen data with the proposed architecture. Finally, various performance evaluation metrics are calculated to compare overall performance and assess the effectiveness of our proposed model. The overall working procedure of the proposed approach is illustrated in Figure 1.

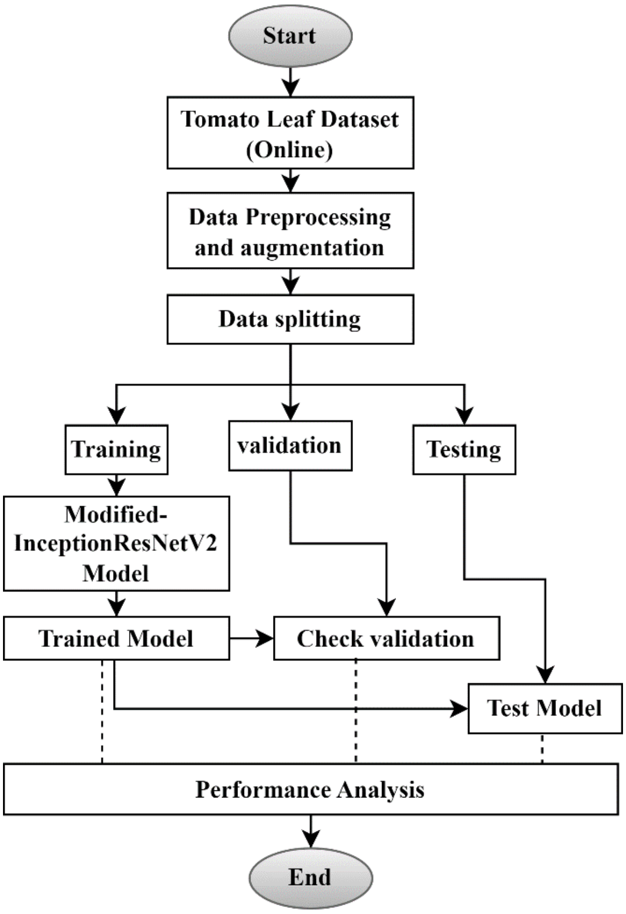


Figure 1. The working flow of the tomato leaf condition detection approach.

2.1. Data Description

In this experimental analysis, we leveraged the Kaggle dataset(Tomato leaf disease detection by Kaustubh, 2024), a widely acknowledged and extensively utilized public resource renowned for its comprehensive collection of 11.000 images. These meticulously curated and evenly distributed images span a diverse array of tomato leaf disease manifestations, encompassing ten distinct categories. Each category comprises precisely 1100 images, ensuring a balanced representation across the dataset. The inclusion of such a vast and diverse set of images provides researchers and practitioners with a rich source of data to explore and analyze the complexities of tomato plant health. To provide visual context, representative images from each class are depicted in Figure 2, offering insights into the visual characteristics associated with different disease states.

2.2. Data Preprocessing and Augmentation

After the dataset acquisition, a meticulous data preprocessing pipeline is implemented to optimize the performance of both the InceptionResNetV2 and modified InceptionResNetV2 models in the task of tomato leaf disease detection. The dataset is initially split into three subsets: a training set (9000 images), a validation set (1000 images), and an unseen testing set (1000 images). This partitioning strategy facilitates effective model training, validation, and evaluation of previously unseen data. To ensure a consistent input format for the models, all images are resized to dimensions of 224x224 pixels, with three color channels (RGB). Pixel values undergo normalization via the preprocessing function from TensorFlow's Keras applications, specifically the Xception model. This step is pivotal for facilitating effective learning by rescaling pixel values to fall within the range of -1 to +1. Augmentation techniques, such as horizontal and vertical flips, brightness adjustments, 90-degree rotations, and zooming, are applied using the ImageDataGenerator class from TensorFlow to enhance the diversity and robustness of the training set. These techniques introduce variability into the training data, promoting model generalization. The training set generator is configured to produce batches of images and corresponding categorical labels during the training phase. The validation set generator is also set up to facilitate model evaluation during the validation phase. Careful consideration is given to determining the number of steps per epoch during training and validation based on the size of the respective datasets and the batch size. This configuration ensures that the models iterate through the entire dataset during each epoch, contributing to comprehensive learning and evaluation.

(a) Bacterial spot (b) Early blight (c) Healthy (d) Late blight (e) Leaf Mold

(f) Mosaic Virus (g) Septoria LeafSpot (h) Spider Mites (i) Target Spot (j)YellowLeafCurlVirus

Figure 2. Visualization of each class of tomato leaf images (random selection)

2.3. Proposed Model Description

In this experimental analysis, a pretrained Inception-ResNet-v2 model (Szegedy et al., 2016) is employed, which serves as a fusion of the Inception and ResNet architectures. This model is considered a pinnacle in deep neural network design, undergoes modifications for performance improvement, and its application is explored in the crucial task of tomato leaf image classification. The inceptionResNetv2 architecture is composed of 164 deep residual layers. The overarching structure is composed of multiple blocks, encompassing Input, Stem, ten instances of InceptionResNet_A, Reduction_A, 20 instances of InceptionResNet_B, Reduction_B, 10 instances of InceptionResNet_C, Average Pooling layers, Dropout layers, and SoftMax layer. It's important to highlight that the Inception-ResNet blocks incorporate a range of scale factors, enabling the adjustment of outputs within distinct ranges for each block. The network is designed to take RGB images with dimensions of 224 (height) x 224 (width) x 3 (depth) as input. With its numerous blocks and carefully designed layers, this comprehensive architecture is tailored for tomato leaf image classification, showcasing the model's versatility and effectiveness in complex visual recognition tasks. This adaptability is embedded in its architecture, with key components outlined as follows:

Inception Blocks: The Inception block is the core building block of the model, utilizing parallel convolutional operations to capture features at different scales. The outcome of the section is attained through the integration of results from each concurrent branch. The output of an Inception block can be represented as follows:

$$Inception\ Block\ (Output) = Branch\ (1), Branch(2), \ldots, Branch\ (n) \tag{1}$$

Residual Connections: Residual connections facilitate the flow of information through skip connections, addressing the vanishing gradient problem and aiding the training process of deep neural networks. The residual connection can be formulated as follows:

$$Residual\ (Output) = Input + Convolution(Input) \tag{2}$$

Stem Architecture: The stem architecture efficiently processes input images, typically utilizing convolutional and pooling layers for low-level feature extraction. The stem architecture output can be expressed as:

$$Stem\ (Output) = Convolution(Input) \tag{3}$$

Fully Connected Layers: These layers process flatten feature maps to produce final predictions. The representation of the output from the fully connected layer is as follows:

$$Output = \ Fully\ Connected\ (Flatten(Feature\ Maps)) \tag{4}$$

Training Dynamics: The model is trained using backpropagation and gradient descent, with the addition of residual connections aiding the training of deep networks. The gradient update equation can be expressed as:

$$Weights \ \leftarrow \ Weights \ - \alpha \cdot \frac{\partial\ Loss}{\partial\ Weights} \tag{5}$$

Model Parameters: Inception-ResNet-v2 achieves parameter efficiency by judiciously combining inception blocks and residual connections. The total number of parameters in the model can be computed as:

$$Total\ Parameters = \sum_{layers} \ Parameters\ in\ Layer \tag{6}$$

This study modifies the pre-trained Inception-ResNet-V2 model to enhance its performance for more precise tomato leaf disease detection. The illustration of the modified InceptionResNetV2 model is shown in Figure 3.Initially, the InceptionResNetV2 model with ImageNet pretrained weights is employed, excluding the final fully connected layer and setting the layers of the base model to trainable. Feature extraction is performed up to the last convolutional layer, a critical point in the hierarchy of the InceptionResNetV2 architecture.

The extracted features are then flattened, creating a one-dimensional array of values—essential for preparing the feature maps for further processing in the subsequent dense layers. Three dense layers with LeakyReLU activation functions (1024, 512, and 320 units) are introduced to enhance the classification block. LeakyReLU's small negative slope during the negative part of the activation prevents the issue of "dead neurons" and facilitates the learning of intricate patterns and features. This hierarchical structure enables the model to capture representations at different levels of abstraction. Dropout layers (with rates of 0.6, 0.3, and 0.2, respectively) are strategically placed after each dense layer. Dropout is a regularization technique that helps to prevent overfitting problems during training by introducing redundancy.

By randomly deactivating a portion of neurons in each iteration, dropout compels the network to depend on alternative pathways, thereby averting excessive reliance on specific features. This, in turn, promotes improved generalization, reduces overfitting, and enhances the robustness of the learned features. The final dense layer, equipped with SoftMax activation, produces output probabilities for the classification into 10 classes corresponding to different tomato leaf categories. The model is compiled using categorical crossentropy loss, which is suitable for multi-class classification tasks. With a learning rate set to 0.0001, the Adam optimizer facilitates efficient weight updates during training. The metric used for model evaluation is accuracy, measuring the model's ability to classify instances across all classes correctly.

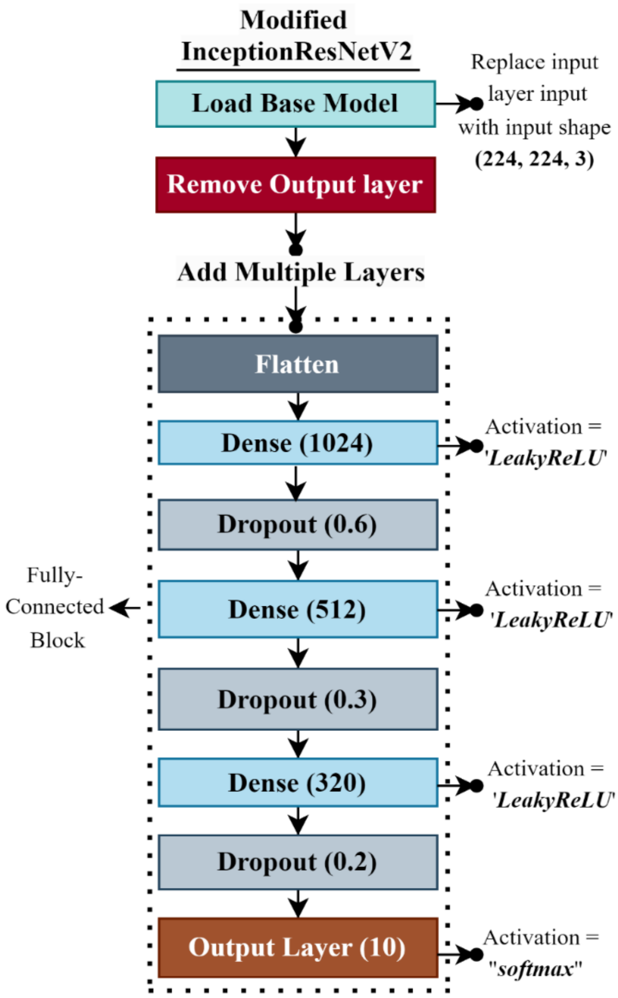


Figure 3. The architecture of the proposed modified InceptionResNetV2 model.

2.4. Performance Evaluation

In this investigation, accuracy (ACC), precision (P), recall (R), and F1 score are selected as evaluation metrics to gauge the efficacy of deep learning algorithms comprehensively (Paul et al., 2023b). Assessment indexes, including false negative rate (FN), false positive rate (FP), true negative rate (TN), and true positive rate (TP), are employed to construct these metrics. The derivation of these indicators is outlined as follows:

$$ACC = \frac{(TP + TN)}{(TP + TN + FP + FN)} \tag{7}$$

$$P = \frac{TP}{(TP + FP)} \tag{8}$$

$$R = \frac{TP}{(TP + FN)} \tag{9}$$

$$F1 = \frac{2 * (P * R)}{(P + R)} \tag{10}$$

2.5. Computing Environment

This experiment investigates tomato leaf disease identification through a deep learning approach, with implementation conducted on the Kaggle platform. Kaggle provides a standardized computing environment (GPU: Tesla P100-PCIE-16GB, RAM: 32GB), fostering collaborative research and reproducibility. This analysis utilizes a variety of libraries, including TensorFlow for numerical computation and machine learning, Keras for building the architecture of neural networks, NumPy for calculating mathematical operations and data analysis, Matplotlib for managing graphs, and additional libraries related to experimentation.

3. Result and Discussion

The experimental outcomes of tomato leaf disease detection using the proposed deep learning method are presented in this section, highlighting the model's robustness and adaptability in addressing diverse conditions. For this purpose, a novel deep learning architecture (modified InceptionResNetV2) is proposed and constructed based on the pretrained InceptionResNetV2 model. Initially, the tomato leaf dataset is divided into three subsets: the training set (consisting of 9000 images) for model training, the validation set (comprising 1000 images) for assessing the model's validity, and the testing set (with 1000 images) for evaluating the model's effectiveness. The implementation details for both models are consistently maintained to ensure a fair comparison, involving the utilization of identical hyperparameters, adherence to the same training procedures, and evaluation based on standardized metrics. Finally, the performance of the proposed model is compared with that of some recently popular models mentioned in the literature. Various evaluation metrics, including accuracy, precision, recall, and F1-score, are calculated to assess the model's performance.

In evaluating the testing performance of the InceptionResNetV2 model across a diverse range of plant disease classes, Table 1 provides a comprehensive analysis of precision, recall, and F1-score metrics, accompanied by corresponding support values. Notably, disease classes such as 'healthy' showcase exemplary accuracy metrics, boasting a precision of 0.9798, a recall of 0.9700, and an F1-Score of 0.9749. Similarly, ‘mosaic virus’ and ‘Yellow Leaf Curl Viru’ demonstrate robust performance, exhibiting high precision values (0.9773 and 0.9681, respectively) along with balanced recall and F1-scores, underscoring the model's efficacy in accurately identifying these diseases. However, a meticulous examination unveils areas that warrant improvement. While achieving a commendable recall of 0.9200, the ‘Early blight’ class presents a lower precision of 0.7188 and an F1-Score of 0.8070. This indicates a propensity for the model to generate false positives in identifying 'Early blight,' highlighting the need for refinement to enhance precision. Additionally, providing insight into the overall performance of the InceptionResNetV2 model, the training accuracy stands at 0.9223, while the validation accuracy is 0.8875. The model exhibits a commendable final testing accuracy of 0.8970.

Table 1. Testing performance of the InceptionResNetV2 model.

Disease	Precision	Recall	F1-Score
Bacterial spot	0.9158	0.8700	0.8923
Early blight	0.7188	0.9200	0.8070
Late blight	0.9318	0.8200	0.8723
Leaf Mold	0.7833	0.9400	0.8545
Septoria leaf spot	0.8681	0.7900	0.8272
Spider mites	0.8448	0.9800	0.9074
Target Spot	0.9259	0.7500	0.8287
YellowLeafCurl Virus	0.9681	0.9100	0.9381
Mosaic virus	0.9773	0.8600	0.9149
Healthy	0.9798	0.9700	0.9749
Average	**0.8914**	**0.881**	**0.8817**

Table 2 presents the testing performance metrics of our enhanced InceptionResNetV2 model across diverse plant disease classes, emphasizing exceptional precision, recall, and F1-score values, complemented by corresponding support values.

Table 2. Testing performance of the modifiedInceptionResNetV2 model.

Disease	Precision	Recall	F1-Score
Bacterial spot	1.0000	0.9800	0.9899
Early blight	0.9897	0.9600	0.9746
Late blight	0.9706	0.9900	0.9802
Leaf Mold	0.9901	1.0000	0.9950
Septoria leaf spot	0.9901	1.0000	0.9950
Spider mites	1.0000	1.0000	1.0000
Target Spot	1.0000	0.9900	0.9950
YellowLeafCurl Virus	0.9804	1.0000	0.9901
Mosaic virus	1.0000	1.0000	1.0000
Healthy	1.0000	1.0000	1.0000
Average	**0.9921**	**0.992**	**0.9920**

The model demonstrates exceptional accuracy, particularly in categories like 'Spider mites, 'Two-spotted mites,' 'mosaic virus,' and 'healthy.' Precision, recall, and F1-score all attain a perfect value of 1.0000 in these classes, showcasing the model's precise identification of these diseases with no misclassifications. Even in challenging scenarios like 'Bacterial spot' and 'Yellow Leaf Curl Virus,' the model maintains high precision values of 1.0000 and 0.9804, respectively, showcasing its robust performance in accurate disease identification, particularly when precision is crucial. A comparative analysis between the modified InceptionResNetV2 model (Table 2) and the baseline model (Table 1) reveals consistent outperformance across all disease classes regarding precision, recall, and F1-score. This improvement underscores the success of the introduced modifications, resulting in heightened accuracy and reliability in plant disease identification. Examining the comprehensive performance metrics of the modified InceptionResNetV2 model unveils notable outcomes: the training accuracy achieves an impressive 99.74%, the validation accuracy holds steady at 99.79%, and the testing accuracy reaches 99.20%. Comparing these values to the baseline model's performance (final training accuracy: 92.23%, final validation accuracy: 88.75%, final testing accuracy: 89.70%), there is a substantial improvement across the board. The training accuracy shows an increase of approximately 7.51%, the validation accuracy increases by around 11.04%, and the testing accuracy improves by about 9.21%. These percentage improvements underscore the significant advancements in enhancing the model's performance through the proposed modifications. In conclusion, the presented results highlight the success of the modifications made to the InceptionResNetV2 model, leading to superior performance compared to the baseline and establishing the modified model as a robust and reliable choice for plant disease identification.

Figure 4 illustrates the performance analysis and visualization of the InceptionResNetV2 model during the training and validation phases. This model is trained with a batch size of 64 for 50 epochs, employing the categorical crossentropy loss function and being optimized with Adam (learning rate: 0.0001). This figure provides insights into the model's dynamic behaviour across epochs, presenting key metrics and trends contributing to a nuanced understanding of its training and validation performance. Figure 5 illustrates the performance analysis and visualization of the modified InceptionResNetV2 model during both the training and validation phases. Employing the same hyperparameters, this curve showcases the model's ability to achieve superior performance compared to the base model.

3.1. Confusion Matrix

Figures 6 and 7 present the confusion matrices obtained while evaluating the InceptionResNetV2 and the proposed modified-InceptionResNetV2 models. The confusion matrix's diagonal entries show the instances when the model accurately predicted the class (true positives and true negatives). On the other hand, the off-diagonal elements correspond to misclassifications, indicating cases where the model's predictions did not align with the actual classes (false positives and false negatives). The confusion matrix is computed for both models using an unseen testing set. In the confusion matrix presented in

Figure 6, it is clear that 881 images are accurately predicted, while the InceptionResNetV2 model misclassifies a total of 119 images. Conversely, modifying the InceptionResNetV2 model shown in Figure 7 achieves successful predictions for 992 out of 1000 testing images, with only 8 misclassified. This comparison highlights the enhanced performance of the modified-InceptionResNetV2 model, demonstrating a significant reduction in misclassifications compared to the original InceptionResNetV2. The modified model's ability to accurately predict a higher proportion of testing images positions it as a noteworthy improvement, suggesting a cutting-edge performance in plant disease identification.

3.2. Comparative Analysis

After analyzing the performance of the proposed approach, we also compare it with some recent related studies to assess the effectiveness and applicability of our proposed architecture, as shown in Table 3. Most of the studies on tomato leaf disease detection achieve impressive performance. In the studies conducted by (Deng et al., 2023) and (Tang et al., 2023), the MC-UNet and PLPNet models were employed, achieving accuracy rates of 91.32% and 94.5%, respectively. Kumar et al. (Kumar et al., 2023) focused on classifying tomato leaf diseases, introducing an approach that utilized the CMNV2 method and achieved an impressive accuracy of 99.28%. Notably, their study was limited to images from two distinct classes. In study (Saeed et al., 2023), the Inception ResNet V2 model was applied, resulting in an accuracy of 99.22%, but the analysis was confined to three classes.

On the other hand, in this experimental analysis, we utilize a dataset containing ten classes of tomato leaves to identify the crops' conditions precisely. Here, we introduce an architecture, Modified-InceptionResNetV2, which plays a key role in achieving state-of-the-art performance compared to the recent related studies mentioned in this literature.

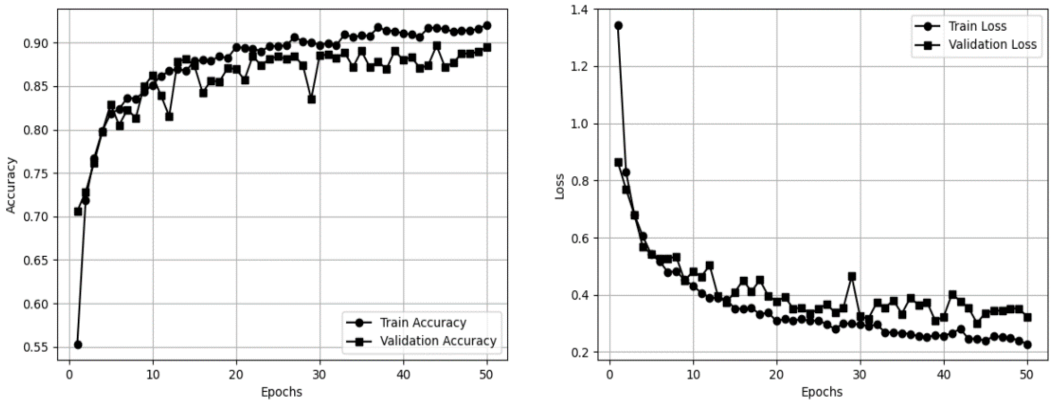


Figure 4. Performance analysis and visualization of the InceptionResNetV2 model during the training and validation phases.

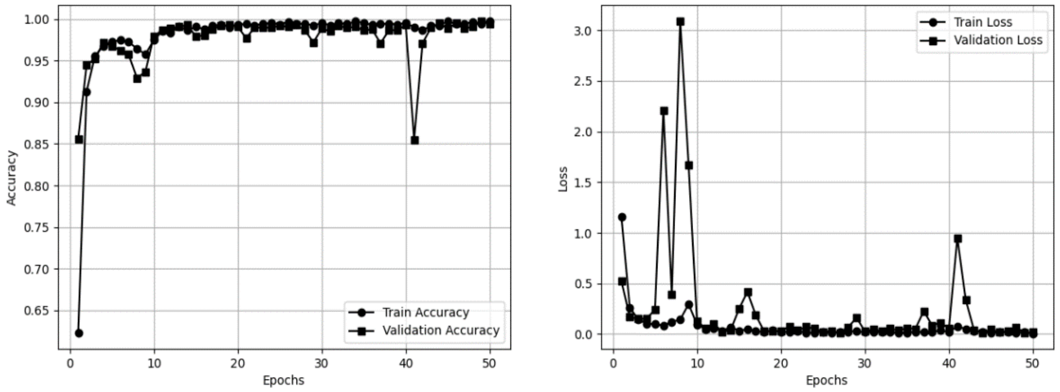
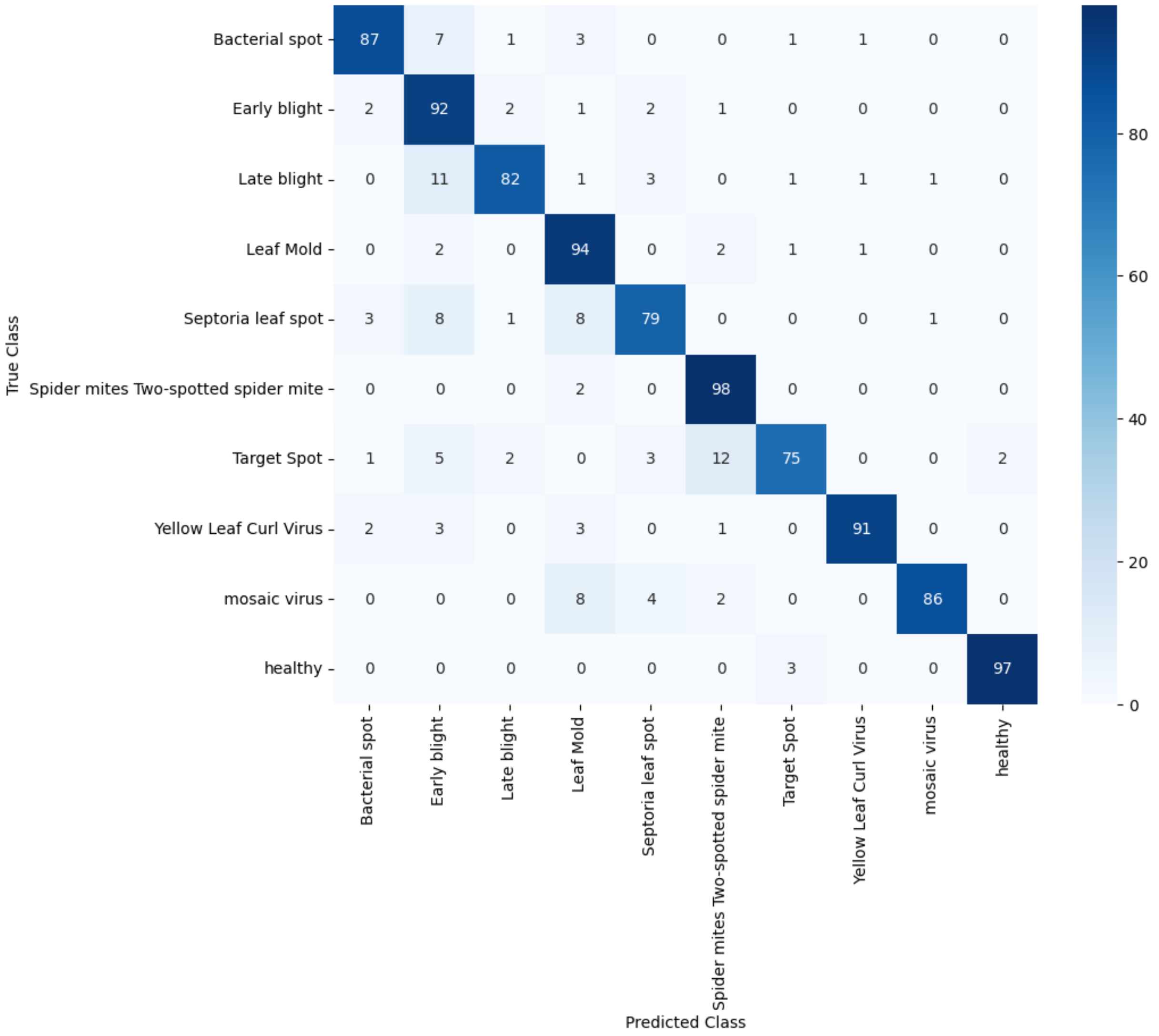
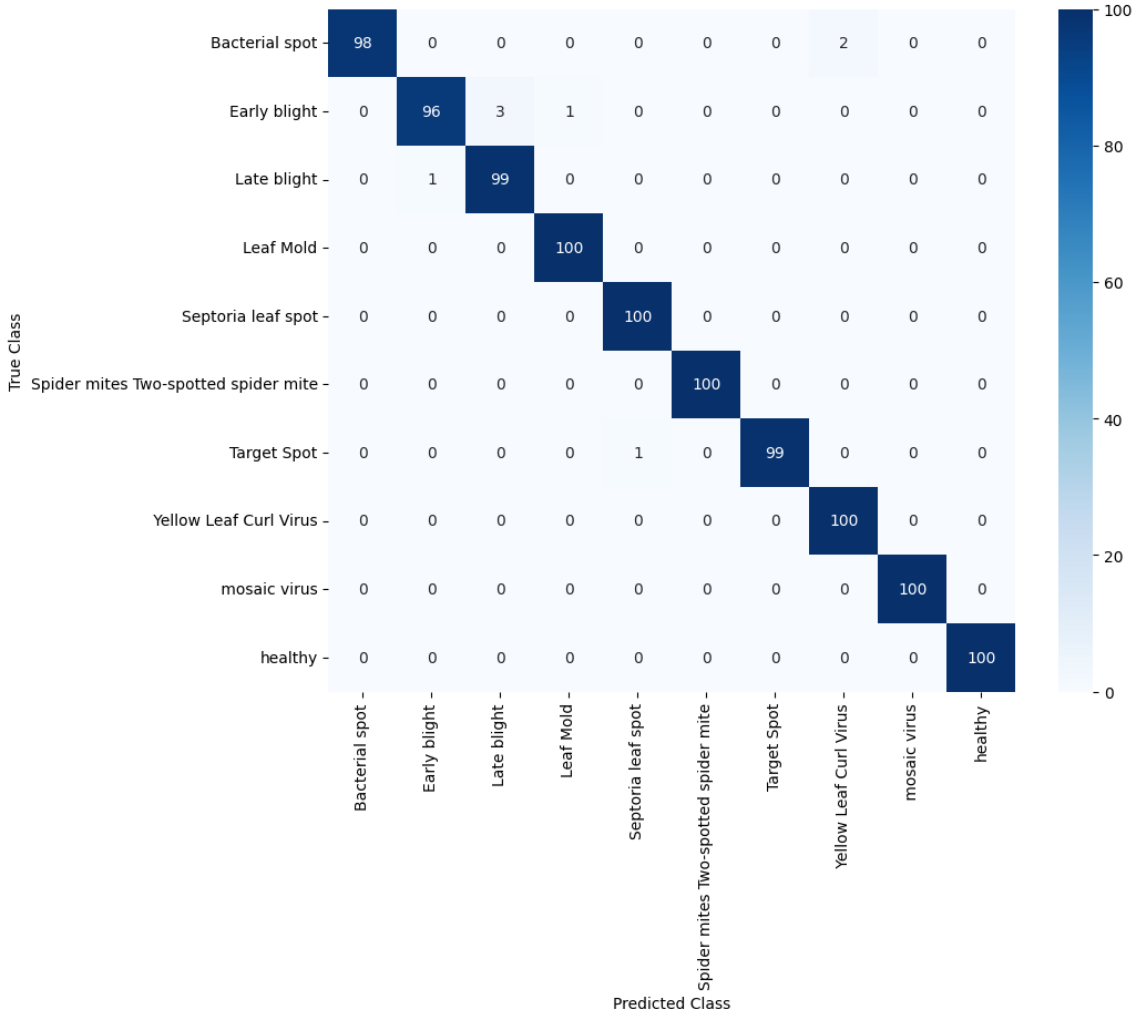


Figure 5. Performance analysis and visualization of the modified-InceptionResNetV2 model during the training and validation phases.



	Bacterial spot	Early blight	Late blight	Leaf Mold	Septoria leaf spot	Spider mites Two-spotted spider mite	Target Spot	Yellow Leaf Curl Virus	mosaic virus	healthy
Bacterial spot	87	7	1	3	0	0	1	1	0	0
Early blight	2	92	2	1	2	1	0	0	0	0
Late blight	0	11	82	1	3	0	1	1	1	0
Leaf Mold	0	2	0	94	0	2	1	1	0	0
Septoria leaf spot	3	8	1	8	79	0	0	0	1	0
Spider mites Two-spotted spider mite	0	0	0	2	0	98	0	0	0	0
Target Spot	1	5	2	0	3	12	75	0	0	2
Yellow Leaf Curl Virus	2	3	0	3	0	1	0	91	0	0
mosaic virus	0	0	0	8	4	2	0	0	86	0
healthy	0	0	0	0	0	0	3	0	0	97

Figure 6. Confusion Matrix for InceptionResNetV2 Model.



	Bacterial spot	Early blight	Late blight	Leaf Mold	Septoria leaf spot	Spider mites Two-spotted spider mite	Target Spot	Yellow Leaf Curl Virus	mosaic virus	healthy
Bacterial spot	98	0	0	0	0	0	0	2	0	0
Early blight	0	96	3	1	0	0	0	0	0	0
Late blight	0	1	99	0	0	0	0	0	0	0
Leaf Mold	0	0	0	100	0	0	0	0	0	0
Septoria leaf spot	0	0	0	0	100	0	0	0	0	0
Spider mites Two-spotted spider mite	0	0	0	0	0	100	0	0	0	0
Target Spot	0	0	0	0	1	0	99	0	0	0
Yellow Leaf Curl Virus	0	0	0	0	0	0	0	100	0	0
mosaic virus	0	0	0	0	0	0	0	0	100	0
healthy	0	0	0	0	0	0	0	0	0	100

Figure 7. Confusion Matrix for the Proposed Architecture (Modified-InceptionResNetV2).

Table 3. Performance comparison of our proposed method with some recent studies.

References	Dataset	Class	Image contains	Model	Accuracy
(Parvez et al., 2023)	PlantVillage	3	6926	CNN	0.9839
(Hossain et al., 2023)	Kaggle	10	20000	MaxViT	97%
(Huang et al., 2023)	PlantVillage	8	1654	FC-SNDPN	Training:99.83 Testing: 97.59
(Deng et al., 2023)	PlantVillage	4	6,372	MC-UNet	91.32%
(Tang et al., 2023)	Self-built	5	13,597	PLPNet	94.5%
(Kumar et al., 2023)	Kaggle	2	6980	CMNV2	**99.28%**

(Peng et al., 2023)	Own Collected	5	1256	DIMPCNET	94.44%
(Saeed et al., 2023)	PlantVillage	3	5225	Inception ResNet V2	99.22%
Proposed Method	Kaggle	10	11000	Modified-InceptionResNetV2	Training: 99.74% Validation: 99.79% Testing: 99.20%

4. Conclusion

This study focuses on the precise classification of ten different types of tomato leaf diseases using deep learning techniques and evaluates its effectiveness compared to recent similar studies. This research investigates the application of InceptionResNetV2, modifying the model to propose Modified-InceptionResNetV2 for enhanced performance in classifying a ten-class tomato leaf condition Kaggle dataset. Besides, data preprocessing and augmentation techniques are applied to improve model robustness. Both models are trained and tested under the same hyperparameters and environment for fair comparison. Experimental results demonstrate the superior performance of the proposed method, with accuracies of 99.74% in training, 99.79% in validation, and 99.20% in testing. The classification report for each class of images, incorporating precision, recall, and F1-score metrics, confirms the high performance of the proposed model. These findings suggest the potential of the proposed approach as an automated tool for early detection of tomato leaf diseases, thereby enhancing production yields. Furthermore, the study hints at broader applications beyond tomato diseases, indicating possibilities for integrating additional methodologies such as segmentation, feature extraction, ranking-oriented classification, and object detection to achieve even better results.

Statement of Conflict of Interest

There is no conflict.

Author’s Contributions

The author confirms sole responsibility for the following: study conception and design, data collection, analysis and interpretation of results, and manuscript preparation.

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