Improvement Classification Approach in Tomato Leaf Disease using Modified Visual Geometry Group (VGG)-InceptionV3

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***Abstract*—This paper presents a new method for optimizing tomato leaf disease classification using Modified Visual Geometry Group (VGG)-InceptionV3. Improved performance of VGG-16 model as a base model with InceptionV3 block reduced the number of convolution layers of VGG-16 from 16 to 10 layers, and added an InceptionV3 block that was improved by adding convolution layer from 3 to 4 layers to increase the accuracy of tomato leaf disease classification and reduce the number of parameters and computation time of the model. The experiments were performed on tomato leaves from the PlantVillage dataset of 10 classes, consisting of nine classes of diseased leaves and one class of healthy leaves. The results showed that the proposed method was able to reduce the number of parameters and computation time with and accuracy of tomato leaf disease classification was 99.27%. Additionally, the proposed approach was compared with state-of-the-art Convolutional Neural Network (CNN) models such as VGG16, InceptionV3, DenseNet121, MobileNetV2, and RestNet50. Comparative results showed that the proposed method had the highest accuracy in the tomato leaf disease classification and required a smaller number of parameters and computational time.**

Keywords*—*Modified VGG-InceptionV3; InceptionV3; VGG-16; tomato leaf disease classification

I. Introduction

The rapidly changing climate will have a detrimental effect on agricultural crops. If farmers do not deal with such impacts in time, the result could be widespread damage, causing the production to not meet the standards and market demands. Therefore, there are many researchers from various fields of knowledge trying to develop new research and technology to help solve problems for farmers to be able to recognize and solve plant diseases quickly and accurately. One of the popular technologies for plant disease identification is image processing. Computer image classification is becoming increasingly popular and applied to a wide variety of applications. Developing a computer that can see images like humans and training computers to learn images, be able to analyze and recognize images, and be able to classify images like humans. Computer image processing can be applied to machine learning to allow computers to process large numbers of images accurately and quickly. Detecting and identifying plant diseases requires computer-aided image classification because machine learning can classify images accurately and quickly.

Computer vision is a part of Artificial Intelligence technology that seeks to train computer algorithms to automatically analyze, classify and detect images using neural networks and deep learning. It can detect and recognize images in both still images, video images, as well as real-time images. Computer vision technology is widely used in current research such as medical imaging diagnosis [1], [2], [3], [4] sign language classification [5] facial emotion recognition [6], and includes the detection and identification of various plant diseases such as the identification of corn leaf disease [7], pepper bell [8], rice diseases [9], mango leaf disease [10] etc. In addition, research on real-time plant disease detection and identification [11], [12], [13] was developed by developing a model that can be used on resource-constrained mobile devices. It can be used more easily and conveniently to including the development to use on mobile devices and work without an internet connection [14]. Currently developing or improving the model of the Convolutional Neural Network (CNN) focuses on reducing the number of parameters and computational costs of the model. Because the previous CNN model was a large, multi-layered deep network, and the huge number of parameters used for computation also required a lot of machine resources, it was not suitable for use on mobile devices with resource constraints. A lightweight Convolutional Neural Network is a small CNN model developed to support deployment on mobile or resource-constrained devices. Lightweight CNN reduces the number of model layers and the number of compute parameters of the model to reduce computation time but to still have better performance. Describe lightweight CNN models [15] such as MobileNet, MobileNetV2, SqueezeNet, ShuffleNet, and PeleeNet. These models use a smaller number of parameters and computation time and can perform faster while providing cost-effectiveness. The accuracy is still high compared to the base and state-of-the-art CNN model.

A lightweight CNN model is presented in this paper. The aim is to optimize tomato leaf disease classification with lightweight models that can reduce the number of model parameters and reduce computational time for the model to be deployed on mobile devices. However, the accuracy of disease classification was still high. We present Modified VGG-InceptiopV3. By using the base model of VGG-16 from the original VGG-16 which has a total of 16 layers and approximately 138.4 million parameters. This is considered a large network, so it takes a long time to process and requires a lot of computing costs, in this work the number of layers has been reduced from 16 to 10 layers and the InceptionV3 block has been improved by adding a convolution layer for getting the input image from 3 to 4 convolution layers to make the model wider and faster in parallel, which can reduce the number of parameters and computation time and resizing the convolution filter size from 3 x 3 to 1 x 3 and 3 x 1, then add an modified InceptionV3 block to the VGG model. The proposed model was implemented for the disease classification of tomato leaves from the PlantVillage dataset of 10 classes for nine classes of diseased leaves and one class of healthy leaves. The proposed method used 1,767,652 parameters and compared the accuracy of tomato leaf disease classification and compared the results with state-of-the-art CNN models such as VGG16, InceptionV3, DenseNet121, MobileNetV2, and ResNet50. The proposed method uses the least parameters but had the highest accuracy.

The remainder of this paper is as follows: “Related Work” is presented in the second part, “Proposed Methods” is presented in the third part, presents the, “Results and Discussion” is presented in the fourth part, and the “Conclusion” is presented in the fifth part.

II. RELATED WORK

This section presents articles related to tomato leaf disease classification using the CNN model and various improvements to CNN models. The research without the CNN model for disease classification of tomato leaves required manual extraction of tomato leaf features [16] such as color features, shape features, texture features, etc. But using the CNN model, the image features are extracted automatically.

Zhou and Zhou et al. [17] presents a hybrid deep learning model for tomato leaf disease identification by improving residual dense network to Restructure Deep Residual Dense Network. The develop model would combines deep residual networks and dense networks. Original residual dense blocks extract image features through dense-connected convolution layers, where RDBs are directly connected to all subsequent layers, where input images are aggregated into Res-Dense-Block (RDB) batch normalized and are then added after convolution in the RDB. A LeakyReLU activity function was added. Then, in the residual layer, concatenate tensor combines an improved RDB block with the input layer. Experiments were performed on a tomato leaf dataset from the AI CHALLENGER dataset of 13,185 images. The results showed that the proposed method was 95% accurate in tomato leaf disease classification and had the highest accuracy compared to other CNN models such as Deep CNN, ResNet50, and DenseNet121 with 93.21%, 88.49%, 91.96% accurate, respectively.

Djimeli - Tsajio and Thierry et al. [18] presents an automated method for the detection and identification of tomato leaf disease using a neural network. The model of the proposed method uses transfer learning from ResNet101 and ResNet152 models to extract the features of tomato leaf images. The disease of tomato leaves was then classified by Multi-Layer Perceptron (MLP). Transfer learning from pre-trained ResNet101 and ResNet152 models to achieve shape features, color features, and other features. Features are separated into multiple levels, giving different feature vector sizes. ResNet101 and ResNet152 were then adjusted and combined image features based on the variance and mean deviation of features, mean of two features, and concatenation of two features. Then, use the MLP to classify the features vector that is assigned several 400 neurons in the hidden layer and 10 in the output layer. The results showed that the classification from the features vector with the combination of features from ResNet101 and ResNet152 models had an accuracy of 98.3% with the highest accuracy being 98.9%.

Thangaraj and Anandamurugan et al. [19] presented a model to identify tomato leaf disease using a Modified-Xception model deep neural network. The proposed method uses transfer learning for transfer learning weights and parameters. The process of the model is divided into two parts: feature extraction and classification. The feature extraction process consists of convolution layers and pooling layers using the Rectified linear unit (ReLu) activation function, using max-pooling to reduce the size of the feature map obtained from the convolution layers. The classification process uses Global Average Pooling (GAP) instead of the fully connected layer in the original networks. GAP calculates the mean value of each feature map and sends it to the output layer. In the output layer, use the Softmax function for tomato leaf disease classification. After replacing the output layer with GAP, fine-tuning was used to update the weights obtained from training the model with the tomato leaf dataset. The model training process was compared using various optimizers such as Adaptive Moment Estimation (Adam), Stochastic Gradient Descent (SGD), and Root-Mean-Square Propagation (RMSprop), and experiment with tomato leaf datasets from the PlantVillage dataset. The results showed that using Adam and RMSprop optimizers had better accuracy than SGD optimizer. The Adam optimizer had the highest accuracy of 99.55%, followed by RMSprop of 99.01%, SGD of 81.77%, respectively.

Kaur and Harnal et al. [20] presented a Modified InceptionResNet-V2 (MIR-V2) model to identify tomato leaf disease. Improved from the basic model, the InceptionResNet-V2 (IR-V2) model, which is a collaboration of InceptionV1 and ResNetV2, is used to transfer learning from the InceptionResNet-V2 model to increase the accuracy of tomato leaf disease identification and improve the model with four different InceptionResNet-V2 types. Changing the internal Maxpool layer of InceptionResNet-V2 as follows: 1) 3 - Max pool layer InceptionResNet - V2 (3MPL - IR - V2), 2) 3 - Max pool layer with skip connection (3MPL - SC), 3) 2 - Max pool - layer InceptionResNet - V2 (2MPL - IR - V2) and 4) 2 - Max pool layer with skip connection (2MPL - SC). Then, experiment with the tomato leaf dataset and determine the accuracy of the modified MIR-V2 model and basic IR-V2 to obtain the highest accuracy in disease identification of tomato leaves. The results showed that the 2MPL-SC modification of the Maxpool layer of InceptionResNet-V2 with the highest accuracy was 98.92% compared to the remaining three improvements.

Moussafir and Chaibi et al. [21] presents a model to optimize tomato leaf disease identification using a CNN model in combination with a genetic algorithm. In the first step, tomato leaf disease identification results were compared from the 10 classes PlantVillage dataset. Experiment with CNN models such as VGG16, ResNet50, EfcientNetB0, EfcientNetB1, EfcientNetB2, EfcientNetB3, and EfcientNetB4 using transfer learning and fine-tuning techniques. Two of the models with the highest accuracy in tomato leaf disease classification were obtained. The two most accurate models are then adapted to the genetic algorithm. The genetic algorithm selects the weights generated during the CNN learning process to create a new weight matrix and then considers it the weighted average. The CNN model for disease identification of tomato leaves showed that the two most accurate models, ResNet50 and EfcientNetB0, had 96.6% and 95.6% accuracy. When a genetic algorithm was used to create a new weight matrix from the ResNet50 and EfcientNetB0 models, the accuracy of tomato leaf disease identification was increased to 98.1%.

Thakur and Sheorey et al. [22] presents a model for the identification of plant disease with leaf imagery. Convolutional Neural Network named 'VGG-ICNN'. The presented model is a collaboration of VGG-16 and GoogleNet InceptionV7 block models, aiming to reduce the size of the network while maintaining high data classification performance. The proposed model consists of two convolutions (Conv) layers using filter size 64, followed by a max-pooling layer, followed by two convolutions (Conv) layers using filter size 128, and followed by the max-pooling layer like the base model of VGG-16. Three Inceptionv7 blocks were then added to the end of the VGG-16 max-pooling layer. The InceptionV7 block uses a filter size of 1024. The Global Average Pooling (GAP) layer is used instead of the flattening layer to reduce the number of parameters for model training followed by a fully connected layer using the SoftMax activation function for data classification. The proposed model can reduce the number of parameters to approximately six million parameters, which is comparable to lightweight CNN models. The model was evaluated by experimenting with five datasets, including small datasets and large datasets: PlantVillage dataset, Embrapa dataset, Apple dataset, Maize dataset, and Rice dataset. The results showed that the proposed method when experimented with all five datasets, the PlantVillage dataset had the highest accuracy of 99.16%, followed by the Rice dataset, Apple dataset, Embrapa dataset, and Maize dataset with 96.67%, 94.24%, 93.66%, and 91.36% respectively.

Tuncer, A. [23] presents a new model for the detection and identification of plant leaf diseases. The proposed method is a hybrid deep neural network with Inception architecture and depthwise separable convolutions intended to reduce the number of parameters and computational costs but still has high data classification efficiency. The Inception architecture can extract image features in parallel and can combine features, while depthwise separable convolution separates the features to independently convoluted the spatial convolution of the input image and combine them as output from the convolution layer. The proposed model replaced 1×1 and 3×3, 1×1, and 5×5 convolutions with 3×3 depthwise and 1×1 pointwise convolution, and 5×5 depthwise and 1×1 pointwise convolution in the Inception block. The model consists of two blocks of Modified Inception architecture, four depthwise separable convolution layers, and four pooling layers, followed by a fully connected layer and Softmax classifier. Experiment with the PlantVillage dataset of 30 classes. The results showed that the proposed method was able to achieve a plant disease classification accuracy of 99.27% and a 75% reduction in the number of parameters from the base CNN model. Like Hassan, M.S. et al. [24] convolution layer was replaced with a depth separable convolution to reduce the number of parameters and computational costs of the model.

Lee and Lin et al. [25] presents CNN architecture for potato leaf disease detection. The proposed model consists of one convolution layer with filter size 64, two convolution layers with filter size 128, three convolution layers with filter size 256, after the convolution layer, followed by a Pooling layer and a Dropout layer. There is a filter size equal to the convolution layer and finally, the Fully Connected layer that uses the Softmax function. In the experimental process to prevent overfitting, the number of cycles in the training model was increased to maintain the model's accuracy. The model presented was experimented with the potato leaf dataset from the PlantVillage dataset and compared the performance of the models presented with the VGG-16 and VGG-19 models. The results showed that the proposed method had the highest accuracy of 99.53%, followed by VGG-16 and VGG-19 with an accuracy of 98.15% and 48.55%, respectively, and the proposed method could reduce the number of parameters used by approximately 99.39%.

Jiang and Chen et al. [13] presents a model for real-time detection of apple leaf disease, the INAR-SSD model, developed the VGGNet model in combination with Inception in the process of extracting image features. Then use the Rainbow concatenation method to improve the integration of feature maps. Pooling and deconvolution will work together to create a feature map between layers. The proposed model adds two layers of Inception modules to the VGG-16 model network to improve the feature extraction capabilities of multi-scale images. Thus, the proposed model can detect diseases of various sizes on the same plant leaf. The model architecture consists of the first seven layers retaining the VGG-16 architecture, then the eighth and ninth layers are replaced by two modules of Inception, while the tenth to thirteenth layers retains the VGG-16 architecture. The Fully Connected layers were replaced by three convolutions: 1x1, and the last layer was followed by the Softmax layer. The experiment was performed with a dataset of apple leaves obtained from laboratories and field photographs. The results showed that the proposed method has an accuracy of 97.14% in apple leaf disease identification and provides the highest accuracy compared to other CNN models such as AlexNet, GoogLeNet, InceptionV3, ResNet-101, ResNet-50, ResNet-34, ResNet-18, and VGGNet-16, it shows that the INAR-SSD model has a detection efficiency of 78.80% mAP and a detection speed of 23.13 FPS.

Nagi and Tripathy [26] presents a model for grape leaf disease identification using a lightweight CNN that reduces the number of parameters for calculation but still maintains high accuracy for grape leaf disease identification. The model presented is developed on the basis of the VGG-16 model which has a total of 16 layers, thus presenting the model by reducing the number of layers of VGG-16 to 6 layers and adjusting the filter size of the convolution layer. The model consists of an input layer that receives input image size 128 x 128 pixels, the first convolution layer using filter size 128, followed by a Maxpooling 2x2 layer, and next, one convolution layer using filter size 64, Maxpooling 2x2, then followed by Flatten and Fully connected layer and in the output layer use Softmax function. An Adam optimizer was used to experiment with grape leaves from the PlantVillage dataset of 3,423 images. The results showed that the proposed method had the highest accuracy in disease identification of grape leaves 98.4%, compared to MobileNet, VGG-16, and AlexNet accuracy values are 98.1%, 96.6%, and 95.7% respectively. Furthermore, the proposed method can reduce the number of parameters to approximately two million parameters.

According to the research article, reducing the number of layers of the VGG-16 model can reduce the number of model parameters and computation time. But it still has higher classification efficiency, and using the Inception block can extract parallel image features, thereby reducing run time and obtaining full image features. With the use of CNN models, the disease of tomato leaves can be identified more accurately.

III. Proposed Methods

In this section, we present the workflow of the proposed method. It contains a detailed dataset used for the experiment and describes in detail the VGG-16 model, the InceptionV3 model, as well as the Modified VGG-Inception which is a new model for disease identification of tomato leaves.

A. *Dataset*

In this experiment, we used the tomato leaf dataset from the Plant Village dataset [27], accessible from www. kaggle.com. This public dataset for image processing and computer vision contains 38 classes of diseased and healthy plant leaves, 14 different plants. In this work, we selected a dataset of nine classes of diseased tomato leaves and one class of healthy tomato leaves for a total of ten classes including Bacterial spot, Early blight, Late blight, Leaf Mold, Mosaic virus, Septoria leaf spot, Spider mites, Target spot, Yellow leaf curl virus, and Healthy as shown in Fig. 1 The image has an RGB color model with dimensions of 256 x 256 pixels, so it resizes the image to 224 x 224 pixels and removes the image's background before training the model. A total of 18,159 tomato leaf images were included, detailed in Table I, and the dataset was divided into three folders: training 70%, validation 20%, and test 10%.

B. *VGG-16*

VGG-16, developed by Simonyan, K. et al. [28] from Visual Geometry Group, Department of Engineering Science, University of Oxford, won the ImageNet Large-Scale Visual Recognition Challenge (ILSVRC) 2014. The VGG-16 consists of an input layer, a convolution layer, and an output layer, totaling 16 layers. The input layer receives image data size 224 x 224 pixels and is an RGB color image, thus having 3 color channels. The convolution layer consists of 13 Conv2D layers using filter size 64 of 2 Conv2D, 128 of 2 Conv2D, 256 of 3 Conv2D, and 512 of 6 Conv2D using kernel size 3 x 3 all layers of the network, after Conv2D followed by a Maxpooling layer of 5 layers, size 2 x 2 strides equal to 2 all layers of the network and followed by 3 Fully Connected (FC) layers, 2 of which Fully Connected use 4096 classes and the last layer uses 1000 classes, while the output layer uses SoftMax as the activation function. The architecture of the VGG-16 model is shown in Fig. 2. The basis of the VGG-16 model is approximately 138.4 million parameters.

C. *InceptionV3*

InceptionV3 was developed by Szegedy, C. et al. [29] in 2015 and received first-place certification in the ImageNet Large-Scale Visual Recognition Challenge (ILSVRC) 2015. InceptionV3 is the 3rd edition of Inception. Its purpose is to increase the efficiency of image classification but to reduce the computational cost, parameters, and calculation time. The first architecture of Inception is shown in Fig. 3 using the principle of extracting features of parallel images, different filters size, resulting in feature maps of different sizes. This contains a convolutional layer 1x1, convolution layer 1x1, followed by a layer convolution layer 5x5, convolution layer 1x1, followed by a layer convolution layer 3x3 and the Maxpooling layer, followed by the convolution layer 1x1. And later InceptionV3 adjusted the architecture as shown in Fig. 4. InceptionV3 adjusts the filter size to be smaller. Base Inception used convolution layer 5 x 5, change to convolution layers 3x3 two layers. The architecture of InceptionV3 consists of layers convolution layer 1x1, convolution layer 1x1, followed by two convolution layers 3x3, convolution layer 1x1, followed by a convolution layer 3x3, and the Max pooling layer, followed by the convolution layer 1x1. Which the replacement Convolutional layer 5x5 to two convolutional layers 3x3, the number of parameters has been reduced from (5x5) = 25 to (3x3) + (3x3) = 18 parameters.

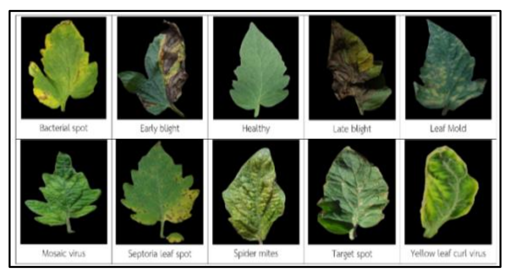

Fig. 1. Sample of tomato leaves from the PlantVillage dataset.

TABLE I. Describes the Number of Classes and Images of the Dataset

Class	Number of Images	Class	Number of Images
Bacterial spot	2,127	Mosaic virus	373
Early blight	1,000	Septoria leaf spot	1,771
Healthy	1,591	Spider mites	1,676
Late blight	1,908	Target spot	1,404
Leaf Mold	952	Yellow leaf curl virus	5,357
Total number of images			**18,159**

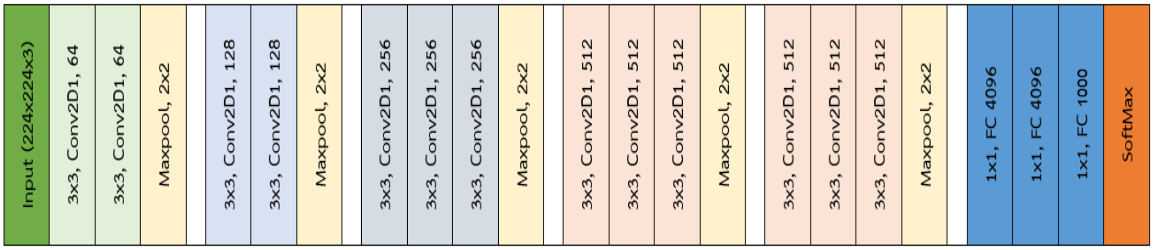

Fig. 2. Base architecture of the VGG-16 model.

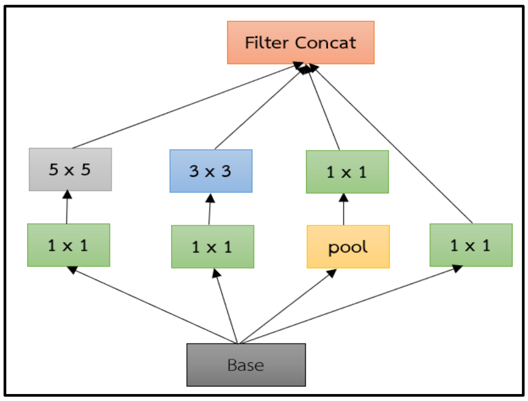

Fig. 3. Base inception architecture.

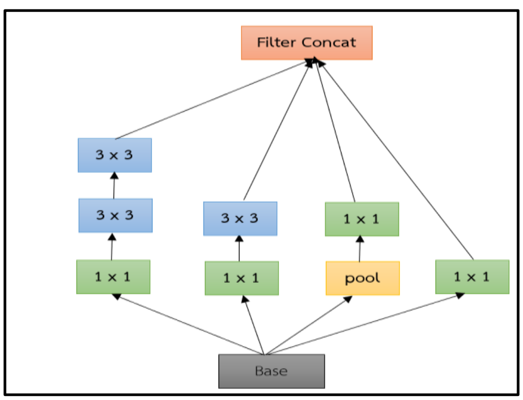

Fig. 4. Base inceptionV3 architecture.

D. The Proposed Modified InceptionV3

The advantage of the InceptionV3 architecture is that the feature extraction of parallel images is distributed simultaneously, providing feature maps of different sizes and reducing the number of parameters and computation time. Therefore, in this work, the architecture of InceptionV3 has been improved by increasing the network width by having the number of layers. The convolution layer has been increased from three layers to four layers, as shown in Fig. 5. The optimized InceptionV3 architecture consists of layers. Convolution layer 1x1, convolution layer 1x1, followed by convolution layer 1x3, and convolution layer 3x1, convolution layer 1x1, followed by convolution layer 1x3 and convolution layer 3x1, convolution layer 1x1, followed by convolution layer 1x3 and convolution layer 3x1, and the Maxpooling layer, followed by the convolution layer 1x1. Extract features in parallel across the four convolution layers and reduces the number of features with the Maxpooling layer which is the replacement of convolution layer 3x3 with convolution layer 1x3 followed by convolution layer 3x1 as convolution separation to be smaller and can reduce computational times.

E. The Proposed Modified VGG-Inception

In this work, we present an improvement on tomato leaf disease classification methods using Modified VGG-Inception. The proposed method was developed using VGG-16 as the base model in combination with the improved InceptionV3 block. The objective was to increase the accuracy of tomato leaf disease classification and reduce computation costs in terms of the number of parameters and processing time. The architecture of the proposed model is shown in Fig. 6. Reduced the number of layers of the VGG-16 model from 16 to 10 layers, and then added a block of modified InceptionV3 between the fourth and fifth layers of the VGG model. The proposed model consists of an input layer that receives image input as a 224 x 224 pixel, RGB color image. Then the first and second layers of the convolution layer use filter size 64, and next, the third and fourth layers use filter size 128, just like the base model of VGG-16. The next layer adds a block of Modified InceptionV3. The fifth to the seventh layer, the convolution layer uses a filter size of 256, followed by Maxpooling 2x2 and BatchNormalization at all layers using a kernel size 3x3 for all of the networks as with the base VGG-16 model. Then the eighth to the tenth layer is followed by a Fully Connected layer with 10 classes in the tomato leaf disease classification using the SoftMax function. Configure the parameters for the experiments of the presented model as in Table II.

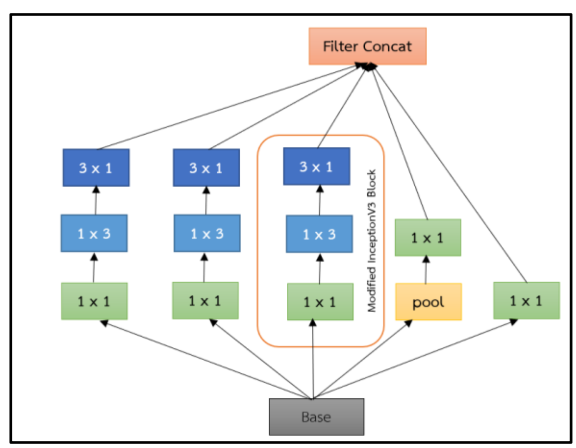

Fig. 5. Modified inceptionV3 architecture.

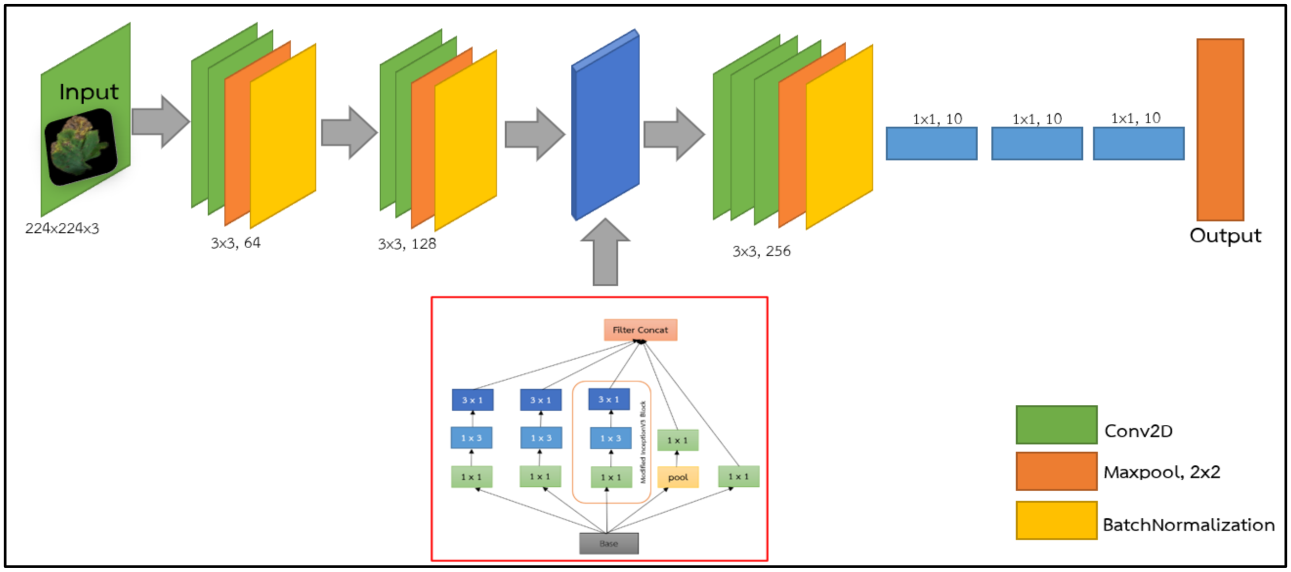

Fig. 6. The proposed modified VGG-InceptionV3 architecture.

TABLE II. CONFIGURING PARAMETERS FOR EXPERIMENTS

Name of the Parameter		Parameter
1.	Optimizer	Adam optimizer
2.	Learning rate	0.001
3.	Batch size	64
4.	Epochs	50
5.	Training data	70%
6.	Validation data	20%
7.	Testing data	10%

IV. RESULTS AND DISCUSSION

This research presents a Modified VGG-InceptionV3 model aiming to improve the limitations of VGG-16, which is a large network and requires high computational costs to a lightweight network by reducing the number of parameters and computational costs, but the model still delivers high disease classification accuracy of tomato leaves and allows this lightweight model to be used on mobile devices or low-resource devices. The presented models were evaluated using the PlantVillage dataset of 18,159 tomato leaf images, nine classes of diseased leaves, and one class of healthy leaves. The image processing procedure resizes the image to 224 x 224 pixels and removes the background of the image. The dataset is divided into a training set of 70%, a validation set of 20%, and a testing set of 10%. Experiment using Adam as an optimizer, set the learning rate to 0.001, batch size to 64, and experiment with 50 epochs.

The proposed model is an improvement based on the VGG-16 model by reducing the number of VGG-16 layers from 16 to 10 layers and improving the InceptionV3 block by increasing the number of convolution layers from 3 layers to 4 layers for a more fully distributed extraction of image features and resized the kernel size of the convolution layer in the InceptionV3 block from 3x3 to 1x3 and 3x1 instead to reduce the number of model parameters. The number of parameters of the Modified InceptionV3 block is shown in Table III. This can reduce the number of parameters by 58.42% from the base InceptionV3 block.

In the process of reducing the number of layers of the base model VGG-16, we experimented with adding a Modified InceptionV3 block to the VGG-16 network and then tried reducing the number of layers of the VGG-16 model layer by layer. The results of the experiment found that by reducing the number of layers of the VGG model, the number of layers with the highest accuracy of tomato leaves classification was obtained using the ten-layer VGG model, as shown in Table IV. In addition, as the number of VGG-16 layers is reduced, the number of parameters and processing time of the model are also reduced.

The results of the experiment showed that the use of the improved InceptionV3 block in combination with the base model VGG-16 reduced the number of model parameters from approximately 138.4 million to approximately 14.7 million. When reducing the number of layers of the VGG-16 model layer by layer until there are ten layers remaining, the highest accuracy for tomato leaf disease classification was 99.27%, and the number of parameters was reduced from approximately 14.7 million to 1,767,652 parameters, with an F1 score of 99.07%. But when reducing the number of layers of the VGG-16 model to nine and eight layers, there was a decrease in the number of model parameters but a decrease in accuracy. The proposed method has accuracy in classifying tomato leaf diseases according to the Confusion Matrix as shown in Fig. 7.

TABLE III. COMPARES THE NUMBER OF PARAMETERS OF THE INCEPTIONV3 BLOCK AND MODIFIED INCEPTIONV3 BLOCK

Base InceptionV3 Architecture			**Modified InceptionV3**		
Layers	***Filter size***	***Parameters***	***Layers***	***Filter size***	***Parameters***
Conv2D1_1	1x1, 32	4,128	Conv2D1_1	1x1, 32	4128
Conv2D1_2	3x3, 32	9,248	Conv2D1_2	1x3, 16	1552
Conv2D1_3	3x3, 32	9,248	Conv2D1_3	3x1, 16	784
Conv2D2_1	1x1, 32	4,128	Conv2D2_1	1x1, 32	4128
Conv2D2_2	3x3, 32	9,248	Conv2D2_2	1x3, 16	1552
MaxPooling	3x3	-	Conv2D2_3	3x1, 16	784
Conv2D2	1x1, 32	4,128	Conv2D3_1	1x1, 16	2064
Conv2D3	1x1, 32	4,128	Conv2D3_2	1x3, 32	1568
			Conv2D3_3	3x1, 32	3104
			MaxPooling	3x3	-
			Conv2D4	1x1, 16	2064
			Conv2D5	1x1, 32	4128
Total Parameters		**44,256**	**Total Parameters**		**25,856**

TABLE IV. COMPARE THE ACCURACY OF VGG-16 WITH THE MODIFIED INCEPTIONV3 BLOCK

Number of Layers (VGG-16 Model)	**Accuracy (%)**	**Loss**	**Times**	**Parameter**	**F1 Score**
16	94.70	0.2325	728s	14,715,108	92.44
15	97.70	0.0698	676s	12,355,300	97.07
14	99.12	0.0341	643s	9,995,492	98.85
13	98.86	0.0417	563s	7,648,996	98.41
12	91.44	0.2992	517s	5,289,188	89.32
11	97.10	0.0964	412s	2,929,380	96.10
10	**99.27**	**0.0267**	**386s**	**1,767,652**	**99.07**
9	98.69	0.0471	379s	1,177,572	98.32
8	97.75	0.0236	290s	1,029,988	97.20

class		0	1	2	3	4	5	6	7	8	9	Accuracy (%)
Bacterial spot	0	460	0	0	0	0	0	0	0	0	0	100
Early blight	1	0	231	2	0	0	0	2	0	0	0	98.30
Late blight	2	0	5	407	1	2	0	0	0	1	0	97.84
Leaf Mold	3	0	0	0	223	1	1	0	0	0	0	99.11
Septoria leaf spot	4	1	2	0	0	385	0	0	1	0	0	98.97
Spider mites	5	0	0	0	0	0	364	0	2	4	0	98.38
Target spot	6	0	0	0	0	0	1	313	0	1	0	99.37
Yellow leaf curl virus	7	0	0	0	0	0	0	0	1106	0	0	100
Healthy	8	0	0	0	0	0	0	0	0	353	0	100
Mosaic virus	9	0	0	1	0	0	0	0	1	0	90	97.83

Fig. 7. Confusion matrix.

TABLE V. COMPARING ACCURACY BETWEEN THE PROPOSED MODEL AND STATE-OF-THE-ART CNN

Model	**Accuracy (%)**	**Loss**	**Times**	**Parameter**
ResNet50	57.31	1.3035	699s	23,608,202
VGG16	86.19	0.4178	875s	14,719,818
Inception-V3	94.22	0.2311	196s	21,823,274
DenseNet121	94.42	0.1644	416s	7,047,754
MobileNetV2	98.59	0.0759	117s	2,270,794
Proposed Model	**99.27**	**0.0267**	**386s**	**1,767,652**

The class that can be classified with the highest accuracy is Bacterial spot, Yellow leaf curl virus, and Healthy with 100% accuracy, followed by Target spot and Leaf Mold with 99.37% and 99.11% accuracy respectively. The least accurate was Mosaic virus and Late blight with 97.83% and 97.84% accuracy respectively. Because of the diseased leaves of the Late blight class, the leaves are almost burnt brown to the extent that they resemble those in the Early blight class, so the model classified the leaves from the Late blight class as the Early blight class and mosaic virus disease, the leaves are pale green to almost yellow, similar to those with the Yellow Leaf Curl Virus class and Late blight class. In addition, to evaluate the effectiveness of the proposed model, we compared tomato leaf disease classifications using the methods presented against state-of-the-art Convolution Neural Network models including VGG-16, Inception-V3, DenseNet121, MobileNetV2, and ResNet50, shown in Table V. Comparative results showed that the proposed models had the highest accuracy in tomato leaf disease classification, followed by MobileNetV2, DenseNet121, Inception-V3, VGG-16, and ResNet50 with 98.59%, 94.42%, 94.22%, 94.22%, 86.19%, and 57.31% accurate, respectively. The proposed model uses fewer parameters than MobileNetV2, a lightweight model suitable for use on mobile devices. Although the proposed method takes longer to process, when comparing accuracy and loss values, the proposed method still gives better results.

V. CONCLUSION

This paper presents a new approach to improving the accuracy of tomato leaf disease classification. Improvement of the Modified VGG-InceptionV3 model based on the VGG-16 model in combination with the InceptionV3 block, reducing the number of layers of the VGG-16 model from 16 to 10 layers and improving the InceptionV3 block by adding the convolution layer from 3 layers to 4 layers. Tomato leaf disease was classified with the model presented by using the tomato leaf disease dataset from the PlantVillage dataset, with a disease identification accuracy of 99.27%. The proposed method can reduce the number of model parameters to 1,767,652 parameters, which is considered a lightweight but still highly accurate model for classifying tomato leaf disease. Compared with state-of-the-art CNN models such as VGG16, Inception-V3, DenseNet121, MobileNetV2, and ResNet50, the proposed method has the highest accuracy in tomato leaf disease classification. Therefore, in the future, the proposed model can be developed for use on small mobile devices and possibly classify more diverse plant leaf diseases to assess the effectiveness of the model.

REFERENCES

[1] S., Deepak, and P. M., Ameer, "Automated categorization of brain tumor from MRI using CNN features and SVM", *Journal of Ambient Intelligence and Humanized Computing 12*, pp. 8357–8369, 2021.

[2] R., Sivanandan and J., Jayakumari, "A new CNN architecture for efficient classification of ultrasound breast tumor images with activation map clustering based prediction validation", *Medical & Biological Engineering & Computing 59*, pp. 957–968, 2021.

[3] H., Che, L.G., Brown, D.J., Foran, J.L., Nosher and l., Hacihaliloglu, "Liver disease classification from ultrasound using multi-scale CNN", *International Journal of Computer Assisted Radiology and Surgery 16*, pp. 1537–1548, 2021.

[4] A.M., Ibraheem, K.H., Rahouma, and H.F.A., Hamed, "3PCNNB-Net: Three parallel CNN branches for breast cancer classification through Histopathological images", *Journal of Medical and Biological Engineering 41*, pp. 494–503, 2021.

[5] A.A., Barbhuiya, R.K.,Karsh and R., Jain, "CNN based feature extraction and classification for sign language", *Multimedia Tools and Applications 80*, pp. 3051–3069, 2021.

[6] R.Z., Cabada, H.R., Rangel, M.L.B., Estrada, ans H.M.C., Lopez, "Hyperparameter optimization in CNN for learning-centered emotion recognition for intelligent tutoring systems", *Soft Computing 24*, pp. 7593–7602, 2020.

[7] J., He, T., Liu, L., Li, Y., Hu and G., Zhou, "MFaster R-CNN for maize leaf diseases detection based on machine vision", *Arabian Journal for Science and Engineering*, 2022. https://doi.org/10.1007/s13369-022-06851-0.

[8] H., Mustafa, M., Umer, U., Hafeez, A., Hameed, A., Sohaib, S., Ullah and H.A., Madni, "Pepper bell leaf disease detection and classification using optimized convolutional neural network", *Multimedia Tools and Applications*, 2022. https://doi.org/10.1007/s11042-022-13737-8.

[9] R., Yakkundimath, G., Saunshi, B., Anami and S., Palaiah, "Classification of rice diseases using Convolutional Neural Network models", *J. Inst. Eng. India Ser. B 103*, pp. 1047–1059, 2022.

[10] M. Prabu and B.J., Chelliah, "Mango leaf disease identification and classification using a CNN architecture optimized by crossover-based levy flight distribution algorithm", *Neural Computing and Applications 34*, pp. 7311–7324, 2022.

[11] J., Liu and X., Wang, "Early recognition of tomato gray leaf spot disease based on MobileNetv2-YOLOv3 model", *Plant Methods 16:83*, 2020. https://doi.org/10.1186/s13007-020-00624-2.

[12] X., Wang, J., Liu and X., Zhu, "Early real-time detection algorithm of tomato diseases and pests in the natural environment", *Plant Methods 17:43*, 2021. https://doi.org/10.1186/s13007-021-00745-2.

[13] P., Jiang, Y., Chen, B., Liu, D., He, and C., Liang, "Real-time detection of apple leaf diseases using deep learning approach based on improved Convolutional Neural Networks", *IEEE Access*, vol. 7, pp. 59069-59080, 2019.

[14] A., Shelke and N., Mehendale, "A CNN-based android application for plant leaf classification at remote locations", *Neural Comput & Applic*, 2022. https://doi.org/10.1007/s00521-022-07740-1.

[15] B., Abdelmalek, K., Ahmed, and T.M., Amine, "A survey on lightweight CNN-based object detection algorithms for platforms with limited computational resources", *International Journal of Informatics and Applied Mathematics*, Vol. 2, No. 2, pp. 28-44.

[16] J., Basavaiah and A.A., Anthony, "Tomato leaf disease classification using multiple feature extraction techniques", *Wireless Personal Communications 115*, pp. 633–651, 2020.

[17] C., Zhou, S., Zhou, J., Xing and J., Song, "Tomato leaf disease identification by Restructured Deep Residual Dense Network", *IEEE Access*, vol. 9, pp. 28822-28831, 2019.

[18] A.B., Djimeli-Tsajio, N., Thierry, L.T., Jean-Pierre, T.F., Kapche and P., Nagabhushan, "Improved detection and identification approach in tomato leaf disease using transformation and combination of transfer learning features", *Journal of Plant Diseases and Protection 129*, pp. 665–674, 2022.

[19] R., Thangaraj, S., Anandamurugan and V.K., Kaliappan, "Automated tomato leaf disease classification using transfer learning-based deep convolution neural network", *Journal of Plant Diseases and Protection 128*, pp. 73–86, 2021.

[20] P., Kaur, S., Harnal, V., Gautam, M.P., Singh and S.P., Singh, "A novel transfer deep learning method for detection and classification of plant leaf disease", *Journal of Ambient Intelligence and Humanized Computing*, 2022. https://doi.org/10.1007/s12652-022-04331-9.

[21] M., Moussafr, H., Chaibi, R., Saadane · A., Chehri, A.E., Rharras and G., Jeon, "Design of efficient techniques for tomato leaf disease detection using genetic algorithm-based and deep neural networks", *Plant Soil*, 2022. https://doi.org/10.1007/s11104-022-05513-2.

[22] P.S., Thakur, T., Sheorey and A., Ojha, "VGG-ICNN: A lightweight CNN model for crop disease identification", *Multimedia Tools and Applications*, 2022. https://doi.org/10.1007/s11042-022-13144-z.

[23] A., Tuncer, "Cost-optimized hybrid convolutional neural networks for detection of plant leaf diseases", *Journal of Ambient Intelligence and Humanized Computing 12*, pp. 8625–8636, 2021.

[24] S.M., Hassan, A.K., Maji, M., Jasinski, Z., Leonowicz and E., Jasinska, "Identification of plant-leaf diseases using CNN and transfer-learning approach", *Electronics 10(12)*, 1388, 2021. https://doi.org/10.3390/electronics10121388.

[25] T.Y., Lee, I.A., Lin, J.Y., Yu, J., Yang and Y.C., Chang, "High efficiency disease detection for potato leaf with Convolutional Neural Network", *SN Computer Science 2:297*, 2021. https://doi.org/10.1007/s42979-021-00691-9.

[26] R., Nagi and S.S., Tripathy, "Deep Convolutional Neural Network based disease identification in grapevine leaf images", *Multimedia Tools and Applications 81*, pp. 24995–25006, 2022.

[27] D.P., Hughes and M., Salathe, "An open access repository of images on plant health to enable the development of mobile disease diagnostics", arXiv:1511.08060, 2015.

[28] K., Simonyan and A., Zisserman, "Very Deep Convolutional Neural Networks for large-scale image recognition", *Published as a conference paper at ICLR 2015*, pp. 1 - 14, 2015.

[29] C., Szegedy, V., Vanhoucke, S., Ioffe, J., Shlens, and Z., Wojna, "Rethinking the Inception architecture for Computer Vision", arXiv:1512.00567v3.