

# IDENTIFICATION SYSTEM OF TOMATO LEAF DISEASES BASED ON OPTIMIZED MobileNetV2

## 基于改进 MobileNetV2 的番茄叶部病害识别

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### ABSTRACT

Crop diseases have an important impact on the safe production of food. Therefore, the automated identification of pre-crop diseases is very important for farmers to increase production and income. In this paper, a tomato leaf disease identification method based on the optimized MobileNetV2 model is proposed. A dataset of 20,400 tomato disease images was created based on tomato disease images taken from the greenhouse and obtained from the PlantVillage database. The optimized MobileNetV2 model was trained with the dataset to obtain a classification model for tomato leaf diseases. The average recognition accuracy of the model is 98.3% and the recall rate is 94.9%, which is 1.2% and 3.9% higher than the original model, respectively, after experimental validation. The average prediction speed of the model for a single image is about 76 ms, which is 2.94% better than the original model. To verify the performance of the optimized MobileNetV2 model, it was compared with the Xception, Inception, and VGG16 feature extraction network models using migration learning, respectively. The experimental results show that the average recognition accuracy of the model is 0.4 to 2.4 percentage points higher than that of the Xception, Inception, and VGG16 models. It can provide technical support for the identification of tomato diseases, and is also important for plant growth monitoring under precision agriculture.

### 摘要

农作物病害威胁粮食的安全生产。因此，农作物前期病害的自动化识别对农民增产增收十分重要。本文提出了一种基于优化 MobileNetV2 模型的番茄叶部病害识别方法。基于从温室拍摄及 PlantVillage 数据库获取的番茄病害图像，创建了一个包含 20400 张番茄病害图像数据集。用数据集对优化的 MobileNetV2 模型进行训练，获得了番茄叶部病害的分类模型。经试验验证，该模型的平均识别准确率为 98.3%，召回率为 94.9%，比原模型分别提高了 1.2% 和 3.9%。该模型对单张图片的平均预测速度约为 76ms，比原模型提高了 2.94%。为验证优化的 MobileNetV2 模型的性能，分别与使用迁移学习的 Xception、Inception、VGG16 特征提取网络模型进行了比较。试验结果表明，该模型的平均识别准确率比 Xception、Inception、VGG16 模型高出了 0.4~2.4 个百分点。可为番茄病害的识别提供技术支持，同时对精准农业下的植物生长监控具有重要意义。

### INTRODUCTION

The healthy and stable development of the tomato industry is of great significance to the development of the national economy and the increase in income of farmers. However, in recent years, due to changes in cultivation systems and inadequate plant protection measures, the variety and extent of tomato diseases have been increasing (Xiong Y. *et al.*, 2020). There are five common diseases of tomatoes, including late blight, grey mould, powdery mildew, spotted blight and yellowing varroa virus. Efficient identification and control of tomato leaf diseases can significantly reduce the damage caused by the disease and contribute to increased tomato yields (Liu J. *et al.*, 2020). How to accurately and effectively identify crop diseases is an important area of research. A great deal of work has been done in the field of disease identification (Xiao M.H. *et al.*, 2020), which can effectively identify the type and severity of crop diseases.

With the rapid development of computer vision and artificial intelligence, deep learning technology is becoming more and more important in the field of image recognition (Too E. *et al.*, 2019). Convolutional Neural Networks (CNN) have a strong self-learning capability and are typical of deep learning techniques.

CNN can learn a large amount of knowledge through abstract analysis of data to achieve fast and accurate classification (Jiang P. et al., 2019). Compared with traditional neural networks, CNN has a strong ability to adapt and generalize. CNN reduces the number of parameters by sharing weights, thus significantly reducing the computational effort. The research method used in this study is the CNN.

In recent years, deep learning technology has been gradually applied in agriculture, which has led to further improvements in the accuracy and efficiency of crop disease identification (Hu W. et al., 2020). Zhao et al. used a deep learning approach to extract cotton foliar disease characteristics such as wilt, brown spot, and horn spot. The average test accuracy of the trained model on the test set was 93.5% (Zhao L. et al., 2021). Venkatesh et al. proposed a fine-tuned MobileNet convolutional neural network model based on deep learning and used for the classification of strawberries and cherries. The average recognition accuracy of the model is 98.60% and the loss rate is about 0.38% after experimental testing (Venkatesh N. et al., 2021). Zeng et al. proposed a method for citrus disease detection based on GANs data enhancement and Inception\_v3 model. Zeng trains InceptionV3 model with 14056 images. The test accuracy of the model reached 92.6%, which is 20% higher than the model trained on the original image dataset (Zeng, Q. et al., 2020). Lv et al. designed a novel feature extraction model called DMS-Robust AlexNet based on AlexNet model. New model combines the advantages of multi-scale convolution and dilated convolution to improve feature extraction. The training accuracy of the model is 98.8% (Lv M. et al., 2020). An Xception-based method for medicinal plant identification was proposed by Roopashree et al. The average recognition accuracy of the method on the DeepHerb dataset was 97.5% (Roopashree, S. et al., 2021). Zhang et al. proposed an improved maize leaf disease diagnosis model based on GoogLeNet. The improved GoogLeNet model has significantly less number of parameters than the VGG and AlexNet models. After experimental testing, the improved GoogLeNet model achieved an average recognition accuracy of 98.9% (Zhang H. et al., 2018). Wang et al. proposed a Dense-MobileNet network-based image classification method for image classification of animals. The average recognition accuracy of the model was 96% after experimental testing (Wang W. et al., 2020).

Research on crop foliar disease identification has focused on machine learning and deep learning. However, the methods that have been applied to crop disease identification rarely balance accuracy and efficiency (Liu B. et al., 2020). In view of the above, a lightweight convolutional neural network-based method for tomato leaf disease identification is proposed in this paper.

## MATERIALS AND METHODS

### IMAGE ACQUISITION

The images used in the experiment were partially collected from a tomato greenhouse in Huai Gang, Shan County, Shandong Province (34°48'22"N, 116°59'13"E). The collection time is February 3 and February 4, 2021 from 8:00-11:00 am and 14:00-17:00 pm. The tomato variety is West Pink 3. The image acquisition device is Redmi note7. A total of 3000 images of tomato leaves were collected, including late blight, leaf mold, powdery mildew, blotch, yellowing varroa virus and healthy images. The image resolution is 3000 x 4000 pixels and the format is jpg. To enrich the experimental data, some tomato leaf images were selected from the PlantVillage database (Hassan S. et al., 2021). Some of the images are shown in Fig. 1.

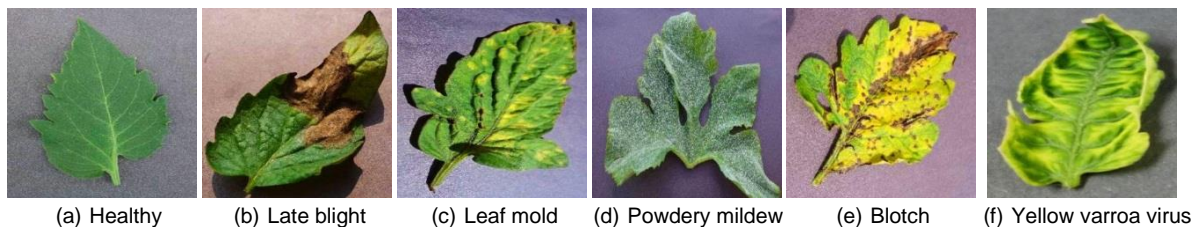


Fig. 1 - Example of tomato leaf image

### AUGMENT DATA

To reduce the experiment running time, the original image was resized to 500 × 500 pixels by Python programming. A random selection of 2400 images from tomato leaf images was used as the test set. To better extract tomato leaf features and avoid overfitting in training, image expansion is performed on the dataset (Chen X. et al., 2020). In this case, the original image is flipped 180 degrees. The image brightness is transformed to between 0.8 and 1.2 of the original image brightness.

Gaussian noise with a variance of 0.02 is added to the image. Transform the chromaticity of the image to 120% of the original image chromaticity of the tomato leaves. A total of 18,000 images were augmented. The dataset contains a total of six categories of tomato leaf late blight, leaf mold, powdery mildew, blotch disease, yellow varroa virus and healthy images. The number of images included in the dataset is shown in Table 1.

Table 1

The number of images included in the dataset

Disease	Original dataset	Augmented dataset	Training dataset	Validation dataset	Test dataset
Late blight	1200	1800	2200	400	400
Leaf mold	1200	1800	2200	400	400
Powdery mildew	1200	1800	2200	400	400
Blotch	1200	1800	2200	400	400
Yellow varroa virus	1200	1800	2200	400	400
Healthy	1200	1800	2200	400	400

**OPTIMIZED MOBILENET**

MobileNetV2 network is a lightweight neural network proposed by Google for embedded devices such as cell phones. Its core idea is depthwise separable convolution (*Bi C. et al., 2020*). Using depth wise separable convolution can reduce the parameters of the model and realize the light weight of the model. The MobilenetV2 model uses the bottleneck residual block structure (*Chen J. et al., 2020*). The structure of bottleneck residual block is shown in Fig 2. Boosting is performed using 1x1 convolution before the 3x3 network structure. Dimensionality reduction is performed using 1x1 convolution after 3x3 network structure. Dilation first, then compression, is better than convolving directly with a 3x3 network.

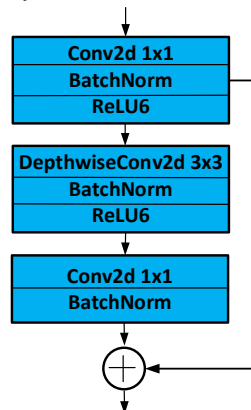


Fig. 2 - The structure of bottleneck design

1) **BNECK BLOCK**

Although bottleneck residual block as the main structure of MobileNetV2 model is beneficial for model accuracy, this design may lead to information loss and gradient confusion. Short connections in the inverse residual block can affect the gradient back propagation (*Sun J. et al., 2020*). To address the limitations of the bottleneck residual block module, the size and number of convolutional kernels were fine-tuned and a new Bneck block structure was proposed. The Bneck block structure introduces deep convolution, which can reduce the computational effort of the model. To ensure short connections for high-dimensional features, the position of the 3x3 convolution was adjusted, as shown in Fig. 3. The Bneck block structure first up-dimensions the input feature map using a 3x3 convolution, then extracts features from the feature map using a 1x1 convolution kernel, and finally down-dimensions the feature map using a 3x3 convolution. When stride=1, a shortcut branch exists to connect the input to the output, as shown in Fig. 3(a). When stride=2, there is no shortcut branch, as shown in Fig. 3(b).

The Bneck block structure does not construct short connections between bottleneck layers, but between higher dimensional features, as shown in Fig. 3(b). Wider short connections help to pass more information from the input tensor to the output tensor and thus have more gradients to pass back. The linear bottleneck layer helps to avoid zeroing of features, which in turn leads to information loss. Therefore, an activation function is not added after the 3x3 convolution used for dimensionality reduction. The H-swish activation function is added after the 1x1 convolution and the first 3x3 convolution.

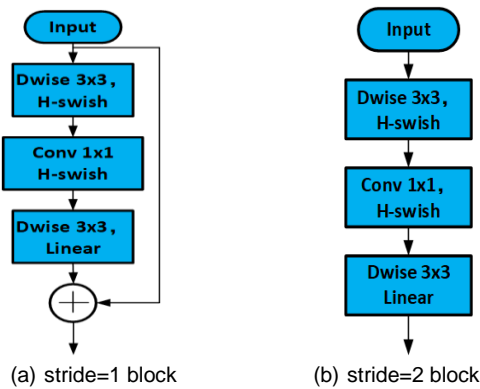


Fig. 3 - The structure of Bneck design

To further improve the model recognition accuracy, the output of the optimized MobileNetV2 network is batch normalized. A dropout layer with a p-value of 0.5 is added after batch normalization to keep some of the network nodes from working in order to prevent the model from overfitting. A global average pooling layer was added behind the dropout layer to replace the fully connected layer, significantly reducing the model parameters. Finally, a Softmax classifier is added for the classification of images. The newly generated network consists of two main parts. The first part is the pre-training module, which is used to extract image features. The second part is an extension layer that extracts high-dimensional features for image classification.

## 2) ACTIVATION FUNCTION

The main role of the activation function in neural networks is to enhance the nonlinear modelling capability of the network (Zhang S. *et al.*, 2019). It is only after adding the nonlinear activation function that the deep neural network has the ability to learn nonlinear mapping in layers. The original MobileNetV2 model uses the *ReLU* activation function. The *ReLU* activation function can be expressed by Equation (1).

$$ReLU(x) = \max(0, x) \quad (1)$$

From Equation (1), it can be seen that *ReLU* saturates when  $x$  is less than zero, while when  $x$  is greater than zero, there is no saturation problem. Therefore, *ReLU* is able to keep the gradient from decaying when  $x$  is greater than zero, thus alleviating the gradient disappearance problem. However, as the training progresses, some of the inputs fall into the hard saturation zone, resulting in the corresponding weights not being updated. Similar to sigmoid, the mean value of the output of *ReLU* is greater than zero.

To further improve the recognition accuracy of the model, the *h-swish* function is chosen to replace the *ReLU* activation function of the original MobileNetV2 model. The *h-swish* function can be represented by Equation (2).

$$h-swish[x] = x \frac{ReLU(6(x+3))}{6} \quad (2)$$

The activation function *h-swish* is unbounded, lower bounded, smooth, and non-monotonic. From Equation (2), it can be seen that the value of the *h-swish* function can be taken to be negative. The *h-swish* function has a wider range of values and stronger convergence performance than the *ReLU* function.

## 3) LOSS FUNCTION

The loss function is an important tool to measure the gap between the network output and the target (Liu B. *et al.*, 2020). The cross-entropy loss function can better solve the problem of too slow update of the loss function weights. Therefore, this paper uses the cross-entropy loss function in the loss layer. The cross-entropy loss function can be represented by Equation (3).

$$loss = - \left[ \frac{1}{n} \sum_x [y \ln a + (1-y) \ln(1-a)] \right] \quad (3)$$

Where,  $x$  is the number of samples,  $y$  is the actual number of labels,  $a$  is the predicted output, and  $n$  is the total number of samples.

## 4) OPTIMIZER FUNCTION

The parameter update of the Adam optimizer is not affected by the scaling transformation of the gradient (Yuan Y. *et al.*, 2021). Its parameters are well interpreted and usually require only minor adjustments. Adam

Optimizer is able to automatically adjust the learning rate. Therefore, the Adam optimizer was chosen. The initial learning rate of the model is set to 0.001.

5) THE OVERALL STRUCTURE OF THE OPTIMIZED MOBILENETV2

The optimized MobileNetV2 model contains 7 Bneck blocks, 2 convolutional layers, 2 global average pooling layers, 1 dropout layer, and 1 fully connected layer. The model uses a linear bottleneck and inverted residuals structure to optimize the network, reducing the model by about 2 million parameters. The parameters of the model are shown in Table 2. The technical route for tomato foliar disease identification is shown in Fig. 4.

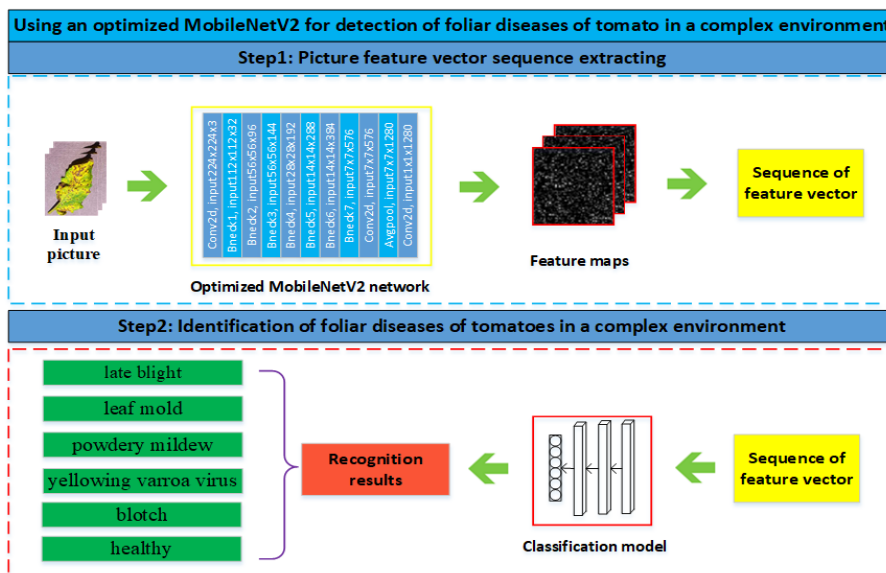


Fig. 4 - Technical route of identification of foliar diseases of tomatoes

Table 2

Relevant parameters of the MobileNetV2 model

Operator	Input	Output	<i>t</i>	<i>c</i>	<i>n</i>	<i>s</i>
conv2d 3x3	224x224x3	112x112x32		32	1	2
Bneck	112x112x32	56x56x96	2	16	1	2
Bneck	56x56x96	56x56x144	6	24	1	1
Bneck	56x56x144	28x28x192	6	32	3	2
Bneck	28x28x192	14x14x288	6	64	3	2
Bneck	14x14x288	14x14x384	6	96	4	1
Bneck	14x14x384	7x7x576	6	160	4	2
Bneck	7x7x576	7x7x960	6	320	2	1
conv2d	7x7x960	7x7x1280		1280	1	1
Avgpool	7x7x1280	1x1x1280			1	
conv2d	1x1x1280	1x1x1280		k	1	
Avgpool/dropout	1x1x1280	1x1x1280				
Dense	1x1x1280	1x1x6				

In the table, *t* represents the expansion multiplier, *c* represents the number of output channels, *n* represents the number of repetitions, and *s* represents the stride size.

EXPERIMENT AND ANALYSIS

TRAINING DETAILS

1) EXPERIMENTAL PLATFORM

The experimental platform is shown in Table 3.

Table 3

Experimental platform

Equipment	Specifications
System	Windows10
Language	Python3.8
Framework	Cuda10.0 Tensorflow2.3.0
CPU	Inter Xeon E5-2609 v4@1.70GHz
RAM	32G
GPU	NVIDIA GeForce GTX 1080(8G)

2) BATCH SIZE AND EPOCHS

In this paper, the tomato leaf dataset contains a total of 20,400 images from six categories. 2400 images were randomly selected as the test set. The training set and validation set are divided in a ratio of 4:1.

3) DIVISION OF THE DATA SET

The values of the batch size were set to 6, 12, and 24. The experimental comparison shows that the model is most stable when the value of batch size is 6. When epochs exceed 40, the loss convergence is no longer significant, so the number of training rounds of the model was set to 40.

EVALUATION INDICATORS

There are various evaluation indicators for disease identification models. Different evaluation metrics are selected to evaluate the model performance from different perspectives (Shi C. et al., 2020). In this paper, the accuracy, precision, recall and specificity are chosen as evaluation metrics. The calculated expression is as follows.

$$accuracy = \frac{TP + TN}{TP + TN + FP + FN} \tag{4}$$

$$precision = \frac{TP}{TP + FP} \tag{5}$$

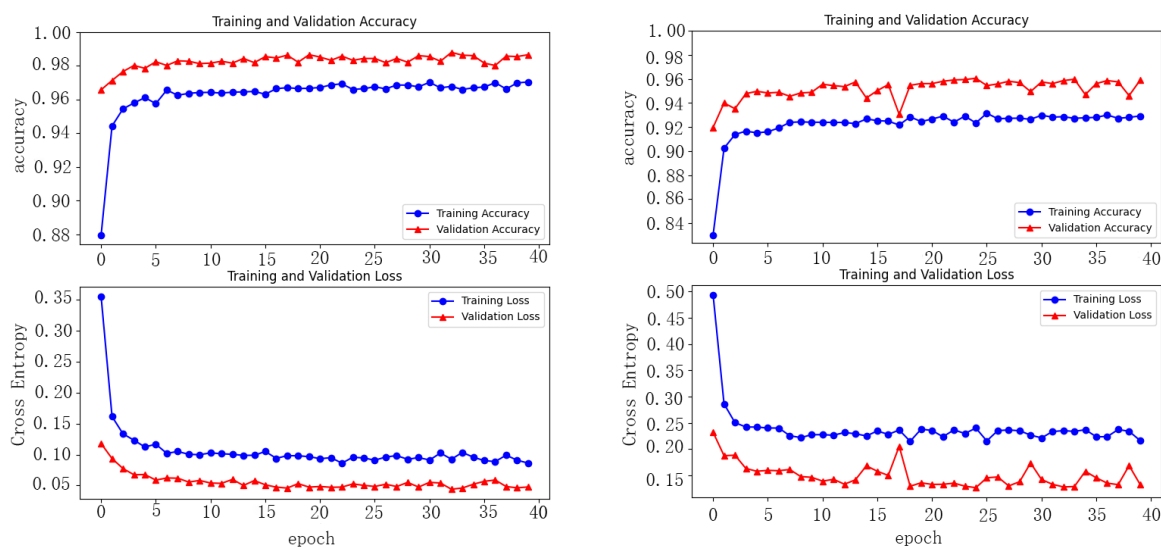
$$recall = \frac{TP}{TP + FN} \tag{6}$$

$$specificity = \frac{TN}{TN + FP} \tag{7}$$

Here, *TP* and *FN* represent the number of correct and incorrect predictions for positive samples, respectively. *TN* and *FP* represent the number of negative samples correctly predicted and incorrectly predicted, respectively.

RESULTS AND ANALYSIS

The master model chosen for this study is the optimized MobileNetV2. The network models of the control group were InceptionV3, Xception and VGG16, respectively. Different models were trained separately with the same data set in the same experimental setting. Each model was iterated 40 times. The training model was saved once every 5 iterations. The optimal model was selected by comparing the performance of each model. The training results of the model are shown in Fig. 5.



(a) Optimized MobileNetV2, above is the accuracy and below depicts the loss of the model

(b) Inception, above is the accuracy and below depicts the loss of the model

Fig. 5 - Comparison of the highest recognition accuracy and loss value of each model

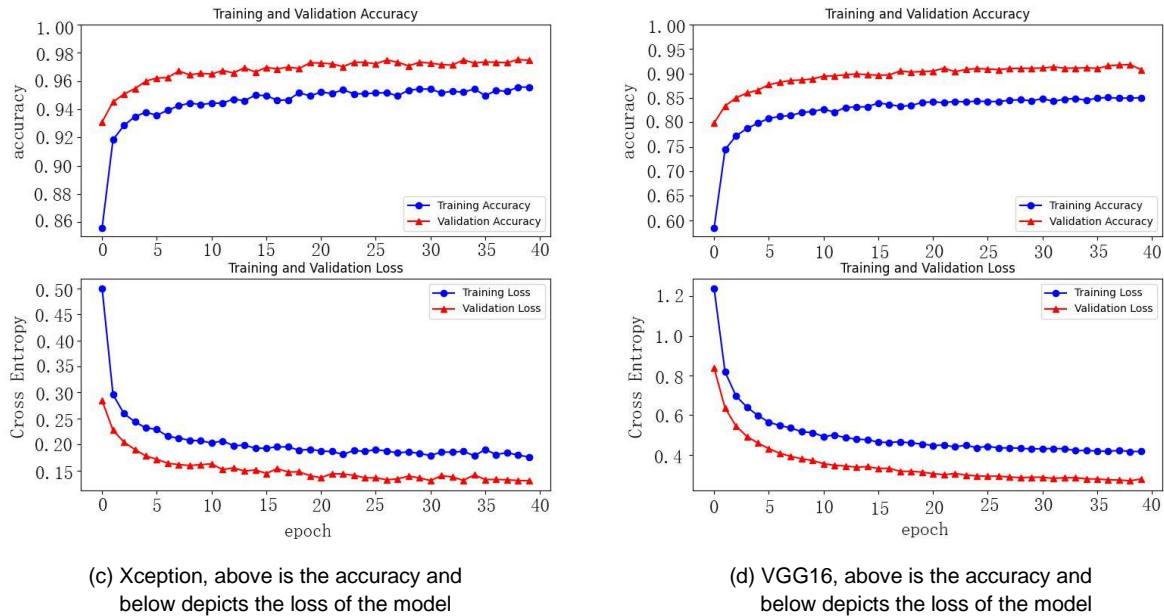


Fig. 5 - Comparison of the highest recognition accuracy and loss value of each model

As can be seen from Fig. 5, the optimized MobileNetV2 model proposed in this paper achieved high training accuracy and low loss values in tomato disease classification. The training accuracy and loss values of the model on the training set are 96.31% and 0.1071, respectively. The training accuracy and loss values of the MobileNetV2 model on the validation set are 98.27% and 0.0562, respectively. In terms of model convergence, the MobileNetV2 model converges the fastest and basically converges in about 10 iterations. Compared with Inception, Xception and VGG16, the optimized MobileNetV2 model can train the optimal model in the shortest time. The VGG16 model converges the slowest and basically tends to converge after about 30 iterations. By comparing the accuracy and loss curves of each model, it can be found that the loss of the model on the training set is slightly higher than that on the validation set, and the accuracy on the training set is slightly lower than that on the validation set.

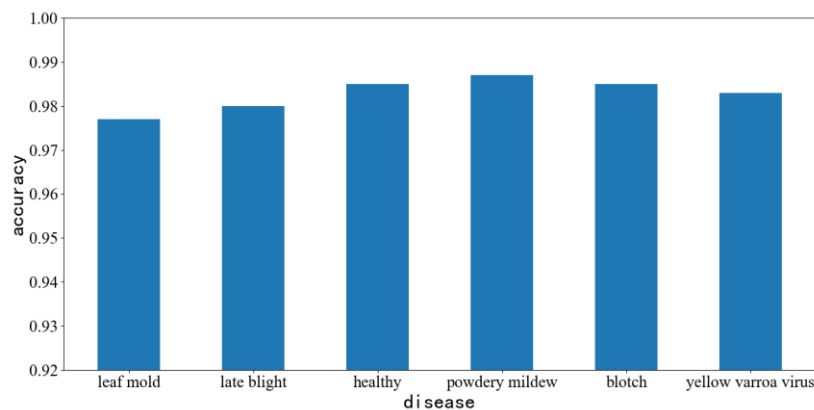


Fig. 6 - Recognition accuracy of the proposed algorithm for different behaviours

Fig. 6 shows the test categories and the corresponding accuracies for optimizing MobileNetV2 on the test set. As can be seen from Fig. 6, tomato powdery mildew was identified with the highest accuracy of 98.7%. The lowest identification accuracy of 97.7% was obtained for tomato leaf blight. The identification accuracy of all six types of tomato leaf diseases was above 97%. Fig. 7 shows the recall, precision and specificity of the optimized MobileNetV2 for the identification of different tomato foliar diseases. As can be seen from Fig. 7, the optimized MobileNetV2 model has the highest recognition accuracy and recall rate for tomato downy mildew, mainly because tomato downy mildew is distinctly different from other diseases.

The lowest accuracy and recall was for tomato leaf mold, mainly because the disease characteristics of tomato leaf mold and late blight are similar, and tomato leaf mold is easily misdiagnosed as late blight.

Especially in the early stages of the disease, the two diseases are extremely similar and difficult to distinguish. The recall and precision of the model for six tomato diseases identification were between 92% and 97%, while the specificity was above 98%. The average recall, precision and specificity of the model for six tomato diseases identification were 95%, 94.9% and 98.9%, respectively. After experimental testing, the average prediction speed of the model for a single image is about 76 ms. The experimental results show that the proposed optimized MobileNetV2 model can consistently identify leaf diseases of tomato.

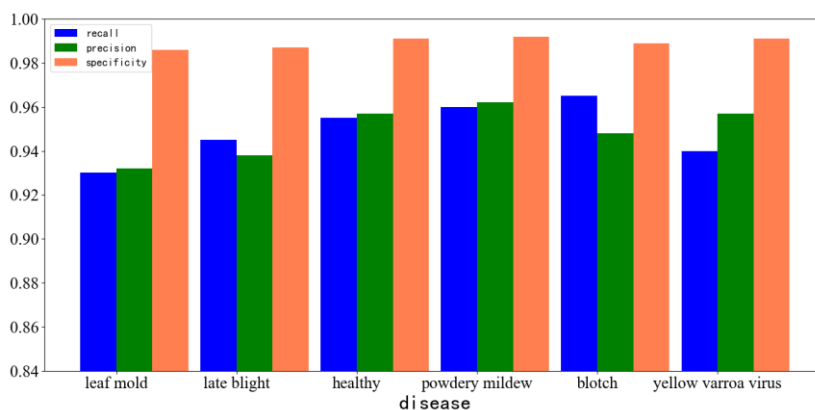


Fig. 7 - The recall, precision and specificity of different disease by proposed algorithm

In this paper, networks such as Inception, VGG16, and Xception are used as control groups to extract image features. The recognition results of different feature extraction networks are compared to verify the effectiveness of the performance of the optimized MobileNetV2 model. The classification models trained by different feature extraction networks were tested with a test set. The test results are shown in Fig. 8.

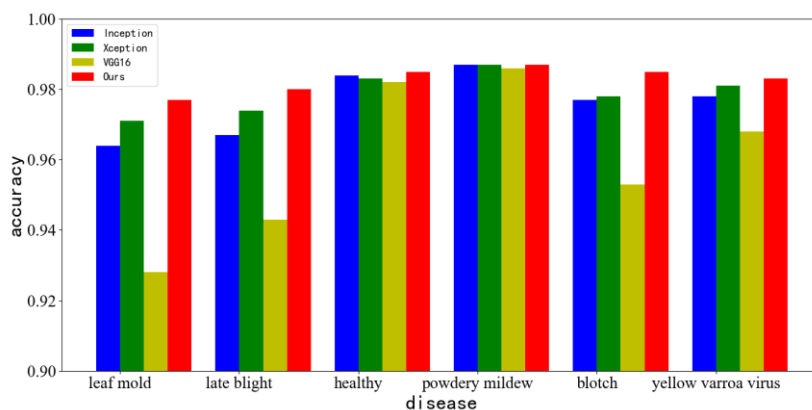


Fig. 8 - Diseases recognition result based on different feature extraction networks

As seen in Fig. 8, the average recognition accuracy of Inception, Xception, and VGG16 models on the test set for the six diseases was 97.6%, 97.9%, and 96%, respectively. The optimized MobileNetV2 model has an average recognition accuracy of 98.3%, which is 2.4%, 0.7% and 0.4% higher than the VGG16, Xception and Inception models, respectively. The test results showed that the VGG16 model had the lowest specificity of 97.4%. The optimized MobileNetV2 model has the highest specificity of 98.9%, which is 1.5% higher than the VGG16 model. The recall rates of the Inception, Xception, and VGG16 models were 92.9%, 93.8%, and 88.6%, respectively. However, the optimized MobileNetV2 model had the highest average recall rate of 94.9% for the six diseases. The optimized MobileNetV2 model has an average recognition accuracy and recall rate of over 90% for six diseases on the test set, which indicates that the model better balances the two evaluation metrics of model accuracy and recall rate.

Fig. 9 shows the results of our method and the MobileNetV2 model for tomato disease identification. According to the analysis of the experimental results, although the recognition accuracy of the MobileNetV2-based recognition method for tomato downy mildew was close to that of our method, the optimized



MobileNetV2 model was significantly more accurate than the MobileNetV2 model for the remaining five diseases.

The average recognition accuracy of the optimized MobileNetV2 model is 98.3%, which is 1.2% higher than the original model. The average recall of this model is 94.9%, which is 3.9% higher than the original model. The average prediction speed of the optimized MobileNetV2 model for a single image is about 76 ms, which is 2.94% better than the original model. Our proposed method has a better classification recognition effect than the original model.

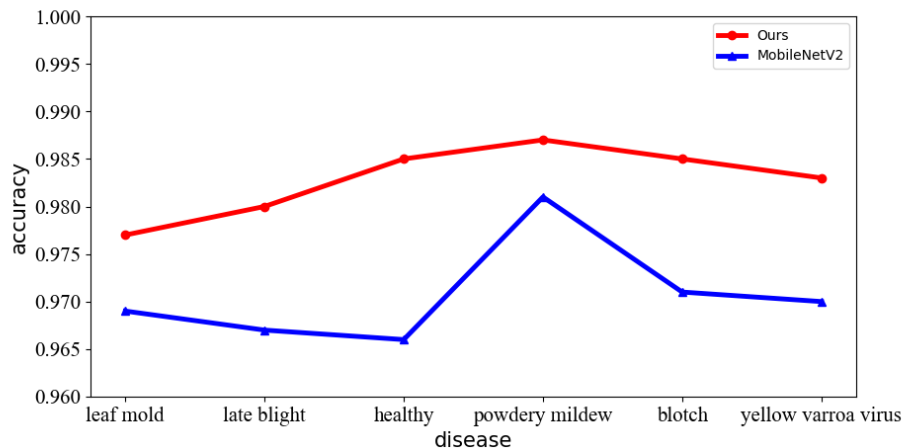


Fig. 9 - Diseases recognition result of our method and MobileNetV2

## CONCLUSIONS

In this paper, it was proposed to apply lightweight convolutional neural networks to identify six different leaf diseases of tomato based on deep learning techniques. Based on the MobileNetV2 model, the model has been improved to further adapt to the needs of miniaturization and fast computation of the network model. A new Bneck block structure is proposed for the improvement of MobileNetV2 model. The output of the model was normalized and followed by the addition of a Dropout layer. Replacing the fully connected layer with a global average pooling layer substantially reduces the model parameters. The optimized MobileNetV2 model has an average recognition accuracy of 98.3% and a recall rate of 94.9%, which are 1.2% and 3.9% higher than the original model, respectively. The average prediction speed of the model for a single image is about 76 ms, which is 2.94% better than the original model. Comparison tests with Inception, Xception, and VGG16 models show that the improved MobileNetV2 model has higher average recognition accuracy and recall, and better balances recognition accuracy, recall, and memory requirements consumed for running. The model is minimally affected by factors such as light intensity, weather changes, indicating that the model has good robustness. The optimized MobileNetV2 model can provide a technical reference for the identification of tomato leaf diseases and is important for the remote diagnosis of plant diseases under precision agriculture.

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