FINE-GRAINED TOMATO DISEASE RECOGNITION BASED ON DEEP CONVOLUTIONAL NETWORK

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基于深度卷积网络的细粒度番茄病害识别

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ABSTRACT

Early diagnosis and accurate identification of fine-grained tomato diseases can control the spread of diseases and insect infections, thus ensuring the healthy development of the tomato industry. In this paper, four lightweight models of Tiny-AlexNet and Mid-AlexNet based on AlexNet and Tiny-VGG16 and Mid-VGG16 based on VGG16 were proposed for 5 kinds of early and late leaf diseases such as tomato powdery mildew. The computation speed of the model is accelerated by reducing the number of neurons in the fully connected layer. In order to avoid degradation in network training, data extension technology is introduced to prevent model overfitting. Among them, the Mid-VGG16 model is significantly better than accurate in early disease recognition, thus verifying the effectiveness of the lightweight model. The proposed model not only improves the accuracy, but also reduces the test time. The results were tested across 20 655 data sets on early and advanced disease. Compared with the trad.itional model, the average prediction accuracy of the proposed model is improved by about 0.15%, and the detection time is significantly reduced by about 50%. The improved model has strong robustness and high stability. The model can be used to accurately identify early diseases and facilitate real-time detection and prevention of tomato diseases.

摘要

细粒度番茄病的早期诊断和准确识别可以控制病虫害感染的传播,从而确保番茄产业的健康发展。本文针对番茄白 粉病等5种早期和晚期叶子病,提出了基于AlexNet的Tiny-AlexNet、Mid-AlexNet和基于VGG16的Tiny-VGG16、Mid-VGG16 4种轻量级模型。通过减少全连接层中神经元的数量,加快了模型的计算速度。为了避免网络训练中的退化, 引入了数据扩展技术,防止了模型的过拟合。其中Mid-VGG16模型在早期疾病识别方面的准确率明显优于晚期,从而 验证了轻量级模型的有效性。提出的模型在确保准确精度提高的同时,测试时间的消耗也大大减少。实验结果通过 20 655 张关于早期和晚期疾病的数据集测试,与传统模型相比,提出的模型的平均预测准确率提高了约0.15%,检测 时间得到了约50%的显著降低。经过改进的模型具有较强的鲁棒性和高稳定性。模型可用来准确识别早期疾病,进而 便于番茄疾病的实时检测与防治。

INTRODUCTION

Tomato is a widely used crop in a nutritious world with a unique taste and health effect, an important in agricultural production and trade around the world (*Suryawati et al., 2018*). However, diseases in tomato leaves cause major production and economic losses, as well as reductions in both the quality and quantity of the agricultural output. The preventive measure by detecting earlier phase of the tomato diseases is one of the critical tasks in an overall crop disease management to avoid a greater loss (*Batool et al., 2020*). A disease may have different symptoms in different periods of the same species of tomato. The diseases affecting tomato leaves mainly include tomato powdery mildew, early blight, leaf mold, spot blight, and yellow leaf curl (*Foysal et al., 2019*). How to quickly and accurately identify tomato diseases, so as to take effective prevention and control measures, is of great significance to ensure crop production and improve farmers' income. Recently, several researchers have reported that Deep Learning is a better approach to achieve high accuracy in plant disease identification (*Agarwal et al., 2019*). *Mokhtar et al. (2015*) have demonstrated the use of support vector machines (SVM) algorithm with different kernel functions for detecting 2 types of diseases, and obtained an accuracy of 90% in average and 92% based on the quadratic kernel function. *Amanda et al. (2017)* used migration learning of convolutional neural networks (CNN) for the identification of brown leaf spot (BLS), red

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mite damage (RMD), green mite damage (GMD), cassava brown streak disease (CBSD), and cassava mosaic disease (CMD). *Fuentes et al. (2018)* studied a tomato pest diagnosis system based on deep neural network, with refinement filter bank. This system can solve the problem of low accuracy due to the false positives generated by the bounding box generator, and class unbalances that appear especially on datasets with limited data. A simplified CNN model is proposed comprising of 8 hidden layers. The proposed light weight model performs better than the traditional machine learning approaches as well as the pre-trained models and achieves an accuracy of 98.4% (*Ale et al., 2019*). *Kr et al. (2020)* exploited the features learned by the CNN at various processing hierarchy using the attention mechanism and achieved an overall accuracy of 98% on the validation sets in the 5-fold cross-validation.

Fang et al. (2020) use the multiple-size convolutional checking model based on the traditional residual network model, and reduce the parameters of the network. Compared with the Mobile Net model, although the model size is slightly larger, it has higher accuracy, better performance and is more stable. *Verma et al. (2020)* have implemented three well known CNN models, namely, AlexNet, SqueezeNet and Inception V3, for evaluating disease severity in Tomato Late Blight disease separated into three stages (early, middle and end) of disease severity.

The above studies stayed only on the variant deep convolutional networks for coarse-grained tomato disease classification, and did not focus on the disease occurrence period. In actual production, the early and late images of the same disease show different characteristics. If the disease can be early recognized and the prevention measures can be taken, the loss will be greatly reduced. Therefore, effectively extracting early and late tomato disease characteristics by deep convolutional networks remains to be solved.

This paper studies the recognition of fine-grained tomato disease. The Tiny-AlexNet model and Mid-AlexNet model are proposed through the change of the number of nodes in the sixth and seventh fully connected layers of the AlexNet model. The lightweight models are obtained such as the Tiny-VGG16 and Mid-VGG16 model while ensuring accuracy by modifying the first and second fully connected layers in VGG16. Samples of 5 types of diseases with different severity levels were divided into early and later levels for training and testing. The proposed models improve an average prediction accuracy compared to the traditional model. While ensuring the accuracy improvement, the testing time consumption has also been greatly reduced. It provides technical support for the intelligent diagnosis system of fine-grained tomato diseases.

MATERIALS AND METHODS

<u>Datasets</u>

Data Description

The data set used in the model in this paper comes from the crop disease data set of the 2018 Global Al Challenge. First of all, this paper screens the pictures related to tomatoes to construct the tomato disease data set. The filtered data set contains 7659 pictures. All pictures in the data set are taken under natural light conditions and have different resolutions. Each picture contains only one tomato leaf, and the leaf occupies the main position of the picture. The data set includes 5 types of diseases including tomato powdery mildew, early blight, leaf mold, spot blight, and yellow leaf curl. For the samples of each type of disease, this paper is further divided into two levels, early and late. The first and third rows in Figure 1 represent the early and late leaves of the corresponding disease category. The distinction between early and late stages of each disease is based on the following:

(1) Symptoms of powdery mildew in the early and late stages: small green spots or white mold spots appear on the early leaves, scattered in different areas of the leaves. The late fading green dots adhere to each other into irregular white powder spots of varying sizes and white flocs on the surface.

(2) Early blight early and late symptoms: small black spots appear in the early leaf infection and slowly expand into concentric round spots, and yellow or light green halos appear around the round spots. At the late stage, brown to dark brown irregular round or oval lesions appeared on the branches of the stem, accompanied by gray-black mold.

(3) Symptoms of early and late leaf mold disease: Oval or irregular light yellow spots appear on the surface of early leaves. Late disease spots develop into gray or black-purple irregular mold layers. In severe cases, leaves often appear withered and curled.

(4) Symptoms of spot blight in the early and late stages: water-stained spots appear on the surface of early leaves, and fish-eye-like spots appear as the disease worsens, with many black spots scattered around them. In the late stage, brown spots cover the whole leave, and the leaves are gradually withered.

(5) Early and late symptoms of yellow flower curly leaf disease: The early leaves become smaller and show fold clusters, the leaves are slightly yellow and the edges are rolled up, and the leaves are thick, brittle

and hard. The symptoms worsen in the late stage, the leaves are obviously yellow and the edges are curled seriously, and the leaves are obviously thickened.

After the above operations, 10 types of disease classification labels in different periods are finally generated, including 319 early powdery mildew, 966 late powdery mildew, 251 early early blight, 442 late early blight, 325 early leaf frost disease, and 336 late leaf frost disease, 421 cases of early spot blight, 807 cases of late spot blight, 1338 cases of early yellow flower curl and 2454 cases of late yellow flower curl disease. It is not difficult to find that the unbalanced distribution of the number of samples in each category may lead to deviations in different categories when training the model. Compared with the sample balanced data set, the data set constructed in this paper can further detect the training stability of the model.

Data Preprocess

In order to obtain valid input to the model, this paper further processes the data set as follows:

1) In order to reduce the amount of calculations and increase the speed of model calculations, this paper adjusts the image size to 224x224 (width 224 pixels, height 224 pixels), and fills in the part that is less than the pixel size, and the area is pixel compressed. After this step, the data of different categories are shown in the first and third rows in Figure 1.

2) To enrich the data set, avoid overfitting of model training, and improve the generalization ability of the model, this paper performs random rotation angle (the maximum rotation angle is 30 degrees), random horizontal or vertical translation (the maximum translation distance is 0.1 × image width or height), random zoom, random horizontal flipping and other operations on 7659 pictures respectively, by introducing slight disturbances. To achieve data expansion, the pixel missing parts appearing after the data enhancement operation are filled by adjacent pixels. After part of the data is processed in this step, the enhanced result is shown in the second and fourth rows of Figure 1.



Fig. 1 - Part of Dataset and Preprocess

After the above two steps of processing, the final data set size is expanded to 20,655 sheets. This paper randomly divides it into training set, validation set and test set according to the ratio of 8:1:1. The training set size is 16,525 sheets, the verification set size is 2065 sheets, and the test set size is 2065 sheets.

Disease identification Model

Tiny-AlexNet model and Mid-AlexNet model

According to the structural characteristics of each part of CNN, in the traditional AlexNet network structure, there are more neurons in the fully connected layer (*Krizhevsky et al., 2012*), which brings greater problems to the operation; to reduce the amount of model calculations and reduce the memory usage, the fully connected layer of the AlexNet model was improves. In the AlexNet model, the fully connected layer integrates and normalizes the highly abstracted features after multiple convolutions, classifies and outputs the classification probability of each object according to the object characteristics, and the subsequent classifier can be based on the fully connected layer. In other words, the fully connected layer maps the features learned by the network to the label space of the sample, especially the fully connected layer connected to the last convolutional layer. When the number of neurons is too large, it results in the occurrence of over-fitting phenomenon, the slowing down of convergence speed. Therefore, the change of the number of neurons in the fully connected layer affects the recognition speed and accuracy of the model.

According to the structural characteristics of the fully connected layer, the number of nodes are changed in the sixth and seventh fully connected layers of the model and the value of the classifier label in the eighth fully connected layer on the basis of the AlexNet model, that is, to change m, n in Figure 2. The value of o to achieve the optimization of the AlexNet model is shown in Figure 2.



Fig. 2 - Schematic Diagram of AlexNet Convolutional Neural Network

The optimized model is still composed of a convolutional layer and a fully connected layer. By replacing the original fully connected layer of AlexNet twice. Two different models named Tiny-AlexNet (which set m=512, n=512) and Mid-AlexNet (which set m=1024, n=1024) are proposed. The improvements of Tiny-AlexNet and Mid-AlexNet models are based on the AlexNet model. The number of classifiers in the sixth and seventh fully connected layers and the eighth fully connected layer are changed and migrated to mobile devices for real-time pest infestation. It is shown in Table 1 for the number of convolutions used in each layer.

Tiny-VGG16 and Mid-VGG16 models

Compared with AlexNet, the improvement of VGG16 (*Simonyan et al., 2014*) lies in the use of several consecutive 3x3 convolution kernels instead of the larger ones in AlexNet (11x11, 7x7, 5x5). For a given receptive field, the effect of using a stacked small convolution kernel is better than directly using a larger convolution kernel (using three 3x3 convolution kernels instead of 7x7 convolution kernels, and two 3x3 convolution kernels instead of 5* 5 convolution kernels), because multiple non-linear layers can increase the depth of the network to ensure that more complex patterns are learned at a lower cost. Its network structure is shown in Figure 3.



Fig. 3 - Schematic Diagram of VGG16 Convolutional Neural Network

It is shown in Table 1 for the number of convolutions used in each layer about six models.

Table 1

Architecture of ConvNet										
Tiny AlexNet	Mid AlexNet	AlexNet	Tiny VGG16	Mid VGG16	VGG16					
Input(224×224 RGB Images)										
	Conv(3,96)		Conv(3,64)×2							
	MaxPool		MaxPool							
	Conv(96,256)		Conv(64,128)×2							
	MaxPool		MaxPool							
	Conv(256,384)		Conv(128,256)×3							
	Conv(384,384)		MaxPool							
	Conv(384,256)		Conv(256,512)×3							
			MaxPool							
	MaxPool		Conv(512,512)×3							
			MaxPool							
FCL(512,512)	FCL(1024,1024)	FCL(4096,4096)	FCL(512,512)	FCL(1024,1024)	FCL(4096,4096)					
FCL(512,512)	FCL(1024,1024)	FCL(4096,4096)	FCL(512,512)	FCL(1024,1024)	FCL(4096,4096)					
FCL(512,10)	FCL(1024,10)	FCL(4096,10)	FCL(512,10)	FCL(1024,10)	FCL(4096,10)					

The number of convolutions used in each layer about six models

VGG16 consumes more computing resources, and uses more parameters, which brings more memory usage. Most of the parameters are from the first fully connected layer. In order to obtain a lightweight model while ensuring accuracy, this paper modified the first and second fully connected layers in VGG16 to construct Tiny-VGG16 respectively (the number of hidden nodes in the first fully connected layer is 512, and in the second fully connected layer the number of hidden nodes is 512) and the Mid-VGG16 model (the number of hidden nodes in the first fully connected layer is 1024, and the number of hidden nodes in the second fully connected layer is 1024).

EXPERIMENT

Experimental Setup and Evaluation Indicators

Experimental Setup

The experiment is performed on an Ubuntu workstation equipped with an Intel(R) Core(TM) i9-9900 CPU@3.60GHZ, accelerated by RTX2080Ti GPU 11G memory.

The experiment divides the data set into three parts: training set, validation set and test set. The training set size is 16,525, the validation set size is 2065, and the test set size is 2065. In order to avoid memory overflow, a batch training method is adopted to compare the Tiny-AlexNet, Mid-AlexNet, and AlexNet models with Tiny-VGG16, Mid-VGG16, and VGG16 on the test set 32 pictures are trained for each batch. This paper sets the number of iteration rounds to 100, and uses categorical_crossentropy in keras as the cost function. In order to solve the problem of gradient disappearance and explosion in the back propagation process, Batch Normalization is introduced to standardize the input of the hidden layer of the network. In addition, in order to prevent over-fitting, the EarlyStopping mechanism in keras is introduced. This paper sets the training to stop when the loss of the verification set no longer decreases in the last 10 iterations. In order to improve the efficiency of tuning, this paper adopts Adaptive Moment Estimation, Adam optimization model (*Kingma et al., 2014*), and its initial learning rate is set to 0.001. In order to automatically modify the learning rate, the ReduceLROnPlateau of keras is introduced. This paper sets the learning rate to 0.9 times the current learning rate when the loss function value of the verification set does not decrease in the process of 5 iterations. In order to save the optimal model parameters, after each iteration is completed, it is determined

whether to save the current model by observing whether the loss function value of the verification set decreases. Finally, the saved model structure and parameters are used to predict the disease picture category of the test set.

Evaluation Indicators

In this paper, the average accuracy evaluation index recognized in the field of image classification is used to evaluate the classification results of the model. Its definition is shown in formula (1):

$$AA = \frac{1}{n_c} \sum_{i=1}^{n_c} \frac{n_{ii}}{n_i}$$
(1)

Where n_c represents the total number of sample categories, this paper takes 10; *i* is the category label, and this paper takes 1~10; n_i represents the total number of samples with category *I*; n_{ii} represents the total number of samples whose category *i* is correctly predicted as the *i*-th category.

Study for Different Models

Classification Accuracy

Different models use the same experimental parameters. Table 1 shows the prediction accuracy of each disease category in the test set on different models, and the last line represents the accuracy on the entire test set.

Table 2 shows that:

The Tiny-AlexNet, Mid-AlexNet model proposed in this paper achieves better classification accuracy than the AlexNet models for all 5 early and late tomato diseases. Compared with AlexNet model, The Tiny-AlexNet model classification accuracy improved by 0.11%, the Mid-AlexNet model classification accuracy improved by 0.20%. The Tiny-VGG16, Mid-VGG16 models also achieve better classification accuracy than the VGG16 model. Compared with VGG16 model, the Mid-VGG16 model classification accuracy improved by 0.17%. Although the Tiny-VGG16 model classification accuracy declined, it is only 0.47 percentage points below the VGG16 model.

The accuracy advantage of the Mid-VGG16 model is significantly higher than the others. It achieves optimal classification performance in all early disease categories except early leaf frost disease. Moreover, although the best effect is not achieved in early leaf frost disease, competitive classification accuracy is also obtained, being only 0.18 percentage points lower than the optimal model. In addition, the Mid-VGG16 model has a good recognition ability and obtains the best average accuracy of 97.08%. It can provide a real-time scientific basis for tomato early disease prevention.

Cleasification accuracy of each model

Table 2

Classification accuracy of each model										
	Tiny- AlexNet	Mid- AlexNet	AlexNet	Tiny- VGG16	Mid- VGG16	VGG16				
Early powdery mildew	97.64	97.46	97.64	97.37	97.82	97.55				
Late powdery mildew	97.64	97.46	97.55	97.19	97.82	97.55				
Early Early blight	98.82	98.55	98.64	99	98.91	98.82				
Late Early blight	98.64	98.28	98.09	98.82	99	98.55				
Early leaf frost disease	98.09	98.55	98.28	97.91	98.37	98.55				
Late leaf frost disease	97.73	98.46	97.64	98	98.28	98				
Early spot blight	98.19	97.82	98.19	98.28	98.55	97.91				
Late spot blight	98.37	97.46	97.82	98.46	98.28	98.09				
Early yellow flower curly leaf	91.83	91.92	91.29	89.75	91.92	92.2				
Late yellow flower curly leaf	91.65	91.74	91.47	89.66	91.83	91.92				
Average	96.86	96.77	96.66	96.44	97.08	96.91				

Note: Each row represents the prediction accuracy of different models on the specified row category, each column represents the classification accuracy of the specified column model in different categories, and the bold data represents the best accuracy rate of the corresponding column model in the specified row category label.

Model Stability

In order to further observe the stability of different models during the training process, Figure 5 shows the accuracy and loss function changes of each model with the training epochs on the test set during 100 rounds of iteration.

As shown in Figure 4, the two classical convolutional neural networks and the four proposed models begin to converge after a certain number of epochs and finally achieve their optimal recognition performance. On the whole, the training processes of every model are basically stable after 20 epochs. The results indicate that the reduction in the number of nodes does not only affect the recognition accuracy of the model, but also improve it and ensure the model stability.



Fig. 4 - Verification of Set Accuracy and Loss Function for Each Model Iterative Process

Model Prediction Confusion Matrix

In order to further observe the specific performance of each model on the prediction set, Figure 5 shows the confusion matrixes of Tiny-AlexNet, Mid-AlexNet, AlexNet, Tiny-VGG16, Mid-VGG16, and VGG16 on the test set.



Fig. 5 – Six model Test Set Confusion Matrix

Note: Line numbers 1 to 10 indicate early powdery mildew, later powdery mildew, early early blight, later early blight, early leaf frost disease, later leaf frost disease, early spot blight, later spot blight, early yellow flower curl leaf disease, and in the case of later yellow flower curl leaf disease, the column numbers 1 to 10 are consistent with the row number category corresponding to the corresponding number

The fraction of accurately predicted images for 10 types of leaf disease is presented in detail. Each column in the figure represents the predicted category, the value of which represents the number percentage predicted for that category; each row represents the true category of the data, and the percentage number represents the value of data instances that actually belong to the category; the value of the intersection of rows and columns represents the predicted data as the number of corresponding row categories, and the value of the diagonal line is the percentage of the results of the correct prediction. Figure 6 shows the prediction results of the modified model is not inferior to the standard model in the same category and can also be provided a reference for fine-grained tomato disease identification.

Model Testing Time

In computational theory, the simplest computational resources are computation time, the number of parameters necessary to solve a problem, and memory space *(Liu et al., 2017)*. Six models were trained with batch size 32 in the experiment. Figure 6 shows the testing time of six models.



The Tiny-AlexNet model has the minimum testing time among all the CNN-based models. All AlexNetbased models have smaller testing times than the VGG16-based models, because it takes less memory space for the AlexNet model than for the VGG16 model. The proposed models based on AlexNet and VGG16, not only have a shorter testing time, but also acquire the best accuracy of tomato leaf diseases identified. It meets the needs of real production and provides a real-time guarantee for the mobile defense of leaf diseases.

CONCLUSIONS

In this paper, four lightweight CNN models have been proposed for the classification of 10 types of finegrained tomato diseases in different periods. For the experimental purpose, data set has been taken from the 2018 Global AI Challenger data set and applying the data augmentation techniques is used to balance the samples in each class. For the performance evaluation purpose traditional models have also been executed. The performance of the proposed models is compared on various evaluation metrics such as confusion matrix, accuracy, loss, testing time etc.

The experimental results show that the efficiency of the proposed models is better than that of the traditional models. The testing time of the lightweight models is significantly reduced while improving recognition accuracy of tomato leaf disease. It is conducive to the real-time prevention and control of the disease.

In addition, the recognition accuracy of early diseases is higher than that of late diseases, which shows that the proposed model can be used to identify early diseases accurately and facilitate the early detection of tomato diseases to take prevention and control measures.

Although the sample distribution of the original data set is destroyed by data amplification, the proposed models can avoid the occurrence of overfitting while improving validation accuracy without excessive jitter. It is shown that the models have vast robustness and high stability.

At present, the model introduces a large number of simulation data through data expansion, and cannot fully identify multiple diseases on the same leaf, which is limited to the leaf images with simple background and single disease. In the future, the dataset of tomato disease should be further enriched to fully extract the disease symptoms with the multi-scale and multi-dimensional characteristics. An end-to-end recognition model will be established to further improve the recognition accuracy and practicability of the model.

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