Recognition of Kiwi Leaf Diseases Based on Deep Learning

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Abstract

In order to improve the performance of kiwi leaf disease recognition model,a new model based on convolutional neural network is proposed. Firstly, the leaf disease dataset was built which included four kiwi leaf disease,i.g. brown spot, ulcer, mosaic and anthracnose, amount to 7310. Secondly, the data set is pre-processed to add the model data. Last, a 9-layer convolutional neural network model was designed based on AlexNet. At the same time, we use the transfer learning method which adopt the knowledge learned from VGG16,VGG19, InceptionV3, and InceptionV4 on the ImageNet image dataset to the task of kiwi leaf disease classification and recognition. The experimental results show that the transfer learning training model has better classification performance and higher convergence speed, data expansion helps to increase the diversity of the data and avoid overfitting, using the VGG19 convolutional neural network pretrained model. The classification accuracy rate of transfer learning and data augmentation is up to 96.73%.

Keywords

Training model, Time-consuming , Neural network, Leaf disease classification.

1. Introduction

As the kiwi industry continues to grow in China, the possibility of large-scale diseases also increases.Although the use of chemical pesticides can control plant diseases, due to the wide variety of diseases, misdiagnosis is prone to occur only by artificial visual observation and empirical judgment. For different kiwi diseases, a large number of pesticide spraying methods are used, which will cause damage to kiwi [1-2]. The key to treating kiwi disease is to quickly and accurately diagnose the type of disease, and the automatic identification of crop diseases can prevent gaining time, minimize economic losses, and avoid pesticide abuse. Therefore, the study of plant diseases based on deep learning methods has important theoretical and practical significance.With the continuous development of computer technology and the rise of smart agriculture and agricultural informatics, many researchers at home and abroad have begun to use computer technology, digital image processing technology, and pattern recognition technology to study plant disease identification [3-7].In recent years, a large number of scholars at home and abroad have begun to carry out plant disease identification and diagnosis research based on computer vision technology [8-13].Using machine learning to analyze and identify diseases is expected to become an effective method for crop disease diagnosis, and deep learning-based image recognition technology has the advantages of high accuracy and strong robustness. Compared with machine learning-based classifier classification accuracy, Higher [14-15].Guo Xiaoqing based on improved Multi-Scale AlexNet tomato leaf disease image recognition, introduced multi-scale receptive field extraction features, the average recognition accuracy reached 92.7%, and reached 89.2% recognition accuracy on the self-sampling set[16].Lueta et al. Proposed a field-based automatic wheat disease diagnosis system based on a weakly supervised deep learning framework. In the field, only image annotation was used for image training to achieve the unity of wheat disease identification and disease area location. [17]. Wei Liran et al. Based on the kernel function support vector machine for multi-class detection and recognition rate of plant leaf diseases up to 89.5% [18]. Qin Feng used the convolutional neural network to extract the features of the lesion image, and established a recognition support vector machine model for the four common alfalfa leaf diseases. The training set recognition accuracy rate was 94.91%, and the test set recognition accuracy rate was 87.48% [19] . Xie Zeqi et al. Based on the environmental information and color characteristics of crop leaf disease level recognition algorithm for leaf diseases with a complex background recognition accuracy of 92.7% [20], Yu Xiuli et al combined the texture features and shape features of wheat leaf lesions, using The support vector machine algorithm has realized the accurate identification of wheat powdery mildew, stripe rust and leaf rust, and the comprehensive recognition rate based on shape features can reach 99.33% [21]. Jia Min used BP neural network and support vector machine classification model to classify and identify three different types of kiwi leaf diseases, and the average recognition rate of the three diseases was about 89% [22].

In the above literature, the support vector machine (SVM) method is mostly used, but the training and parameter optimization of the SVM takes a lot of time, and there are problems such as overfitting and complicated processes. The BP neural network method has similar problems. In order to improve the accuracy of kiwi leaf disease recognition, this study proposes two recognition methods based on convolutional neural networks. Based on the same image preprocessing method, the experimental results are selected by analyzing and comparing the models. Optimal recognition model. TensorFlow framework is used to implement model training, model testing and model result output. Using deep learning to analyze and identify four kinds of kiwi leaf diseases, it can achieve a high recognition accuracy rate, which provides a good reference value for common disease recognition and diagnosis of kiwi leaves. It also provides a feasible solution for the identification of other plant leaf diseases.

2. Materials and methods

2.1 Experimental data acquisition

In this study, four kinds of kiwi leaf diseases, such as brown spot disease, ulcer disease, mosaic disease, and anthracnose disease, which are more common in the Shaanxi region and have more severe leaf disease, were used as experimental research objects. The images of kiwi disease leaves were collected by using a combination of web crawler and field shooting. According to the needs of this experiment, a comparative analysis was performed based on the crop disease and insect atlas. Based on the images obtained by the two image acquisition methods, 189 kiwi leaf anthracnose, 208 brown spot disease, 184 ulcer disease, and 150 mosaic disease were screened. As shown in Figure 1. First make 10 copies of each image with a uniform size of 256 * 256 pixels, and then perform the following affine transformation on the image: arbitrary scaling between 80% and 120%, translation between -20% and + 20%, rotation- Between 45 and +45 degrees, with a shear transformation of -16 and +16 degrees, (rectangular to parallelogram), using the nearest neighbor difference or bilinear difference, full white and black, see Fig.1. Using digital image processing methods to simulate the same image at different angles and different backgrounds can greatly increase the size of the data set and improve the classification recognition rate.

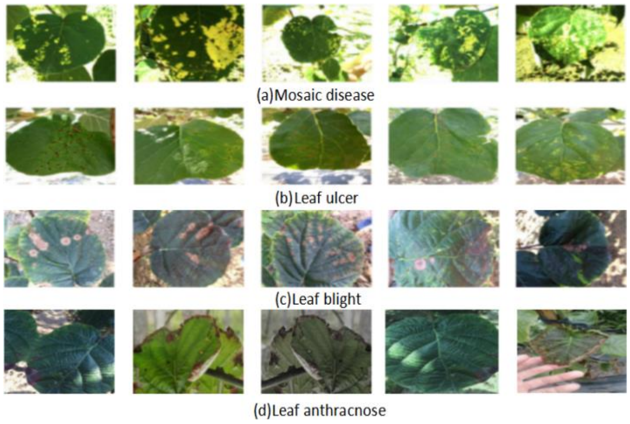
(a)Mosaic disease
(b)Leaf ulcer
(c)Leaf blight
(d)Leaf anthracnose

Fig.1 Leaf disease map

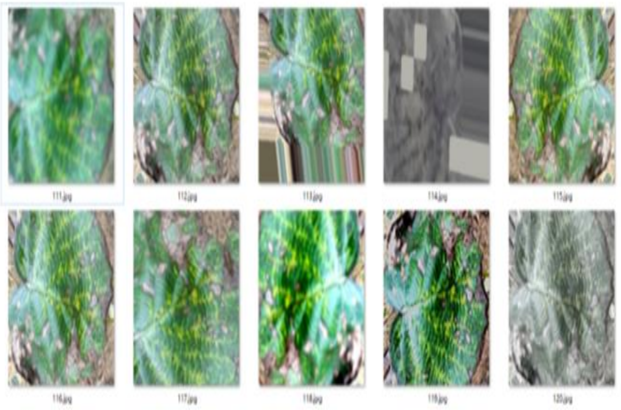

Fig. 2 Data preprocessing diagram

2.2 Data Set

The data set is the basis for building the recognition model, and it is also the basic data set for the test model. Based on the image pre-processing, this study builds a data set for model training and testing. The data set includes 7310 pieces of 256×256 color pictures, see Table.1. The training set accounts for 80% and the test set accounts for 20%.

Table 1 Data set size

leaf disease image dataset	Total sample	Number of training sets	Number of validation sets
Anthracnose	1890	1640	250
Brown spot	2080	1820	260
Leaf ulcer	1840	1590	250
Mosaic	1500	1250	250

3. Identification of kiwi leaf diseases based on CNN model

3.1 Convolutional neural network model design

AlexNet was designed by Hinton and his student AlexKrizhevsky [23]. It consists of 5 convolutional layers and 3 fully connected layers. Compared with LeNet, its main features are: using ReLU as the activation function, and using Dropout during training to immediately ignore certain neurons to prevent overfitting. The maximum pooling is used in all convolutional neural networks to avoid the blurring effect of average pooling. Propose LRN layer and use CUDA to accelerate the training of deep convolutional networks. Data enhancement, randomly extracting 224 * 224 size areas from 256 * 256 images. In this study, referring to the conv-> pool-> ReLU model of the AlexNet convolutional neural network, the design of the convolutional neural network, see Fig.3.

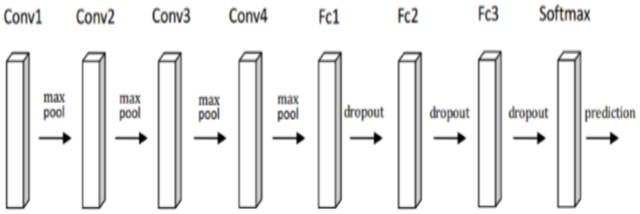

Fig.3 CNN Network Structure

The network consists of four convolutional layers and three fully connected layers. The maximum pooling operation and ReLU function activation must be performed between each convolutional layer. It differs from AlexNet in that it does not use the LRN layer because many researchers It was found that LRN played a small role. At the same time, the way data is augmented is different. In this study, the data augmentation dataset was used for training using the autonomous scheme, and the data diversity was stronger than the original data augmentation method of AlexNet.

3.2 Training methods

The batch training method is used to divide the training set and test set into multiple batches. Each batch trains 64 pictures, that is, batch size is set to 64, and the accuracy is verified with 1010 pictures. The verification is set to 1010 (verification Machine sample number). Iterate through all the pictures in a training set as an epoch, and iterate a total of 10,000 times. The Adam optimization algorithm was used to optimize the model, and the initial learning rate was set to 0.0001.

3.3 Experimental results and analysis

The model layer convolution layer uses different sizes of convolution kernels to make the receptive fields different, and the ability to extract image features is also different. As can be seen from Table 3, the effect of using the size $5 \times 5 * 2 + 3 \times 3 * 2$ is better than $7 \times 7 * 2 + 5 \times 5 * 2$, and the effect of using $5 \times 5 * 4$ is slightly weaker, but in general, the size of the convolution kernel size for model recognition accuracy Less affected. Pooling usually uses two types, maximum pooling and average pooling. The middle layer uses maximum pooling to extract features that are most conducive to distinguishing between different leaf diseases and discards redundant features. Models 1, 2, 5 and 3, 4, and 6, see Table.2. use maximum pooling and average pooling, respectively. The results show that global average pooling is more effective than global maximum pooling. This shows that the use of global maximum pooling can easily cause the loss of extracted deep feature information, thereby reducing the recognition accuracy, while global average pooling averages all the values of the entire feature map, making full use of all the information of each feature map. Conducive to extracting key features.

Table 2. CNN Model Training Results

Number	Convolution kernel size	Global pooling type	Accuracy
1	5×5*2+3×3*2	Max pooling	76.97%
2	7×7*2+5×5*2	Max pooling	76.63%
3	5×5*2+3×3*2	Average pooling	79.01%
4	7×7*2+5×5*2	Average pooling	77.87%
5	5×5*4	Max pooling	72.54%
6	5×5*4	Average pooling	73.79%

4. Identification of kiwi leaf diseases based on transfer learning model

Due to the unsatisfactory recognition results of the improved model experiments based on the AelxNet model, this study looks for new recognition directions. In most cases, retraining a convolutional neural network from scratch requires a lot of data, but in reality often it is not possible to obtain enough data. For this study, there is currently no open source large kiwi disease leaf image library on the Internet, and the kiwi disease leaf images we have collected are also very limited, which is not enough to support retraining a deep convolutional neural network from scratch. Need to find methods to solve the problem of small disease data sets.

4.1 Selection of network model

4.1.1 VGGNet Convolutional Neural Network

The hidden layer of VGG-16 is composed of 13 convolutional layers, 3 fully connected layers, and 5 pooling layers [24]. see Fig.4. The VGG model uses a deeper network structure, a smaller convolution kernel, and a pooled sampling domain, which enables it to control the number of parameters while obtaining more image features, avoiding excessive calculations and overly complex structures. The network architecture of VGG19 and VGG16 is roughly the same, except that three more convolutional layers are added to enable more detailed feature extraction.

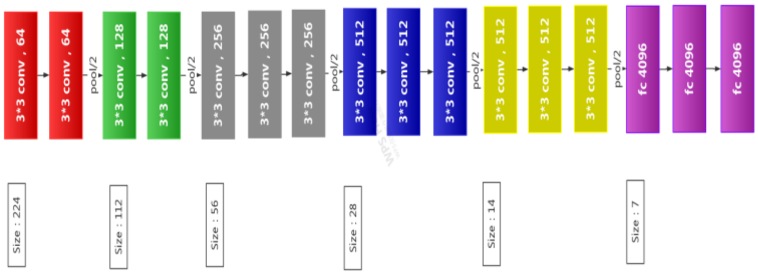

Fig. 4 VGG16 Network Structure

4.1.2 GoogleNet Convolutional Neural Network.

GoogLeNet is the first large-scale convolutional neural network formed by stacking with the Inception module. Unlike ordinary convolutional networks, Google Inception Net controls the amount of calculations and parameters while achieving good classification performance, removes the last fully connected layer and uses the global average pooling layer, uses the Inception Module to improve parameter utilization, see Fig.5. using different sizes of convolution kernels to increase diversity and introducing auxiliary classifiers, the nxn convolution kernels are changed to 1xn and nx1 convolution kernels to save parameters, speed up operations, reduce overfitting, increase A layer of non-linear extended model expression ability.

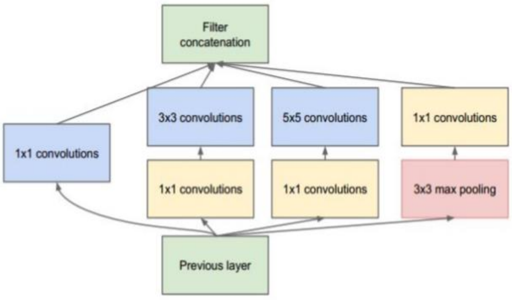

Fig. 5 InceptionV3 Module Structure Diagram

4.2 Training methods

For all models, the learning rate drop type is set to fixed, the optimizer selects rmsprop, the weight attenuation is set to $4*10^{-5}$, the batch size is set to 32, and the learning rate is divided into 10^{-4}, $5*10^{-4}$, and 10^{-3} According to the above network structure, it is divided into loading all layers of pre-trained parameters and retraining all layer parameters on the kiwi leaf disease image data set to build a model and loading all layers of pre-trained parameters and training only the final output on the kiwi leaf disease image data set Layer parameters are modeled in two cases.

4.3 Experimental results and analysis

From Table 3, we can know that different pre-training models, fine-tuning the same layer parameters, training loss changes and verification accuracy at the same learning rate, can be obtained on the kiwi leaf disease data set established in this study, VGG19 and VGG16 training The model is better than the InceptionV3 and InceptionV4 models. The classification effect of the four models on this problem is vgg19, vgg16, InceptionV3, and InceptionV4 from high to low. The best-performing Vgg19 model can achieve a verification accuracy of 96.727%, indicating that the model has better recognition performance. see Table.3, we can see that the same pre-training model, training the same number of layers, changes in training loss under different learning rates, and verifying the accuracy rate. For example, for InceptionV3, training the same number of layers, and its training loss changes under different learning rates as the picture shows. The same pre-training model under the same number of training layers, the larger the learning rate, the faster the training loss decreases and the fluctuation is relatively small. With the same pre-training model, the training loss for training all parameters is less than training only the output layer parameters. The same conclusions can be drawn for the remaining four models.

Table 3 Migration Model Test Results

Id	Pre-trained model	Training position	Learning rate	Training loss	Verification accuracy
1	InceptionV3	All	0.0001	0.4196	94.545%
2			0.0005	0.2604	96.091%
3			0.001	0.2547	96.636%
4		Logits \AuxLogits	0.0001	0.9905	84.091%
5			0.0005	0.83	85.545%
6			0.001	0.7712	85.727%
7	InceptionV4	All	0.0001	0.6782	95.636%
8			0.0005	0.4559	94.636%
9			0.001	0.4146	94.818%
10		Logits \AuxLogits	0.0001	1.2947	71.818%
11			0.0005	1.2747	79.182%
12			0.001	1.2442	79.000%

13	VGG16	All	0.0001	0.0488	96.364%
14			0.0005	0.1711	96.724%
15			0.001	0.0502	96.091%
16		Fc8	0.0001	0.4377	86.818%
17			0.0005	0.3316	86.545%
18			0.001	0.2287	86.000%
19	VGG19	All	0.0001	0.0533	96.636%
20			0.0005	0.0531	95.636%
21			0.001	0.0526	96.727%
22		Fc8	0.0001	0.9647	87.636%
23			0.0005	0.5459	84.636%
24			0.001	0.7608	88.000%

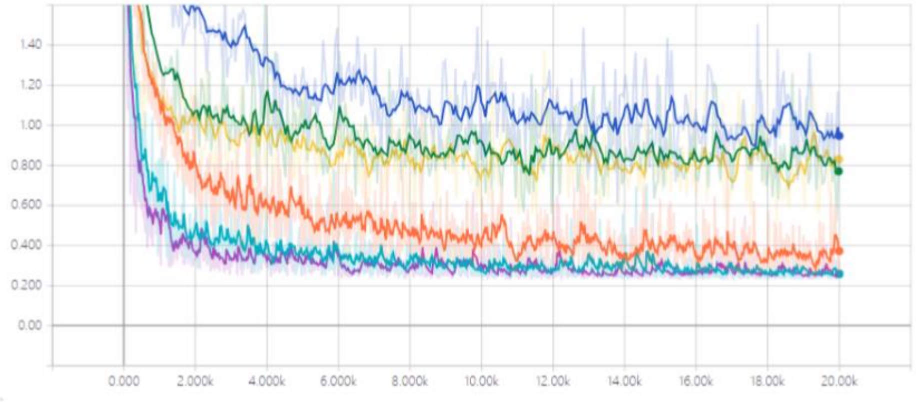

Fig. 6 Comparison on Loss of Different Parameters on Inception V3

5. Conclusion

In this study, four common kiwi diseases: anthracnose, brown spot disease, mosaic disease, and ulcer disease were taken as research objects. The kiwi leaf disease recognition based on transfer learning was studied. Various network models pre-trained using ImageNet were suitable for migration. When it come to the diagnosis of plant leaf diseases, the Vgg19 model with the best effect can reach a verification accuracy of 96.727%. At the same time, a diagnosis model of kiwi leaf disease was established, but the CNN model established in this study is not as effective as the model of transfer learning training and needs to be improved. The study found that in the transfer learning, the same pre-trained model under the same number of training layers, the larger the learning rate, the faster the training loss decreases and the fluctuation is relatively small, under the same learning rate, the training loss of all training parameters is less than the training output only Layer parameters. Global average pooling is better than global maximum pooling.

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