

Original Research Paper

Automatic Diagnosis of Soybean Leaf Disease by Transfer Learning

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Abstract: Soybean diseases and insect pests are important factors that affect the output and quality of soybeans, thus it is necessary to do correct inspection and diagnosis of them. For this reason, based on improved transfer learning, this study proposed a classification method for soybean leaf diseases. Firstly, leaves were segmented from the whole image after removing the complicated background images. Secondly, the data-augmented method was applied to amplify the separated leaf disease image dataset to reduce overfitting. At last, the automatically fine-tuning convolutional neural network (Autotun) was adopted to classify the soybean leaf diseases. The verification accuracy of the proposed method is 94.23, 93.51 and 94.91% on VGG-16, ResNet-34 and DenseNet-121 networks respectively. Compared with the traditional fine-tuning method of transfer learning, the results show that this method is better than the traditional transfer learning method.

Keywords: Transfer Learning, Deep Convolutional Neural Network, Classification Recognition, Soybean Diseases

Introduction

Soybeans, the primary source of edible oils, are one of the leading seed soybean plants in the world today. Soybean oil accounts for 25% of the global edible oil. At the same time, it accounts for 60% of the global livestock feed, which is the main component in poultry and fish formula fodders (Agarwal *et al.*, 2013). Besides, with the comprehensive soybean nutrition and abundant content, it is contributed to preventing heart disease and diabetes. Nowadays, China is the 4th soybean producing country in the world, next only to the USA, Brazil, and Argentina. Dating back to the agricultural era of China, the Chinese began to cultivate and plant soybeans. Also, the northeast is the leading soybean planting area in China. Different prevalent diseases and insect pests will take place every year. More severely, it will result in more than 30% of the output loss (Zhou *et al.*, 2021). The insufficient soybean plant protection procedure, the increase of fungus virus pathogen categories, and poor cultivation methods are causes for increasing the damage degree of soybean plant diseases and insect pests. This thesis studied the categories of the soybean leaf diseases, which can be divided into multiple types, including anthracnose, bacterial blight, bacterial leaf spot, soybean mosaic virus, copper poison disease, charcoal rot, frogeye, leaf blight, wind blight, downy mildew, powdery mildew, rust disease and tan disease (Ohki *et al.*, 2021).

At present, recognition of soybean leaf diseases is based on human eye recognition, which will be influenced by a subjective explanation of crop disease professionals, resulting in misjudgment (Barbedo, 2016). Moreover, for most small and medium-sized farmers, it is difficult for them to contact professionals, leading to some delays in finding out the reasons for the leaf disease symptoms and preventive solutions. This severely affects the quality and output of soybeans. As a result, an automatic and reliable computer-assisted system is needed to solve the efficiency issue of soybean leaf disease detection and recognition. At present, establishing accurate technology to identify soybean leaf diseases is the key to preventing soybean leaf diseases and insect pests. Detecting the plant diseases by using the technology of image processing is a difficult task (Sardogan *et al.*, 2018; Rastogi *et al.*, 2015; Prasad *et al.*, 2016; Khirade and Patil, 2015) Martinelli *et al.* (2015) have proposed various technologies of plant pest identification and detection and summarized the traditional detection technology and innovative detection technology from many aspects (Martinelli *et al.*, 2015; Sankaran *et al.*, 2010).

In current days, the traditional detection technologies get involved in molecules, serology, and DNA while the innovative detection technologies include volatile organic compounds, spectrum technology Convolutional Neural Networks (CNN), etc. Shrivastava and Hooda (2014) put forward the digital picture processing

technique to detect and classify the tan disease and frogeye. In detail, the recognition accuracy rate of the tan disease and frogeye respectively reached 70 and 80%. However, the above-mentioned methods have shown some limitations. Firstly, the research only considered two kinds of soybean diseases and insect pests. Secondly, the recognition accuracy rate in the current research field was not enough. Based on salient regions, (Gui *et al.*, 2015) came up with a method to detect soybean leaf disease and insect pests, extracting disease areas from soybean leaf disease images. However, such a method failed to detect the soybean disease types and the recognition accuracy rate. Kaur *et al.* (2018) studied and designed a semi-automatic soybean disease and insect pest recognition system based on the K-means algorithm, and identified 3 diseases including downy mildew, frogeye, and leaf blight. The average maximum accuracy rate reached 90%, which could not satisfy the high recognition accuracy rate in today's research fields. Araujo and Peixoto (2019) put forward a digital picture processing technology combined with the color moments, Local Binary Pattern (LBP), and Bag-of-Visual-words (BoVw) and recognized 8 kinds of leaf diseases, including bacterial blight, rust disease, copper poison disease, soybean mosaic virus, target leaf spot, downy mildew, powdery mildew, and tan disease, showing the classification accuracy rate of 75.8%.

For this reason, the follow-up study can pay much attention to analyzing how to improve the recognition accuracy rate while identifying multiple types of soybean leaf diseases. As a modern image processing and data analysis method, deep learning is equipped with a good image analysis effect and huge development potential. With the successful application of deep learning in each field, it has been gradually applied in the agricultural field (Kamilaris and Prenafeta-Boldú, 2018). In the past several years, deep learning has gained extremely excellent performance, especially for the Deep Neural Network (DNN) (Learning, 2020). In the image recognition field, CNN is rapidly developing, which can extract key features from lots of input images. Soybean leaf diseases could be easily and accurately classified through CNN, however, which needs lots of calculation resources and time, as well as huge datasets or plenty of input images. To solve the above shortcomings of a convolutional neural network, transfer learning, a widely used technology, uses a deep neural network pre-trained on a large-scale data set to solve the specific model training task with limited data (Sufian *et al.*, 2020). This research regards autotun (Basha *et al.*, 2021) as the skeleton and put forward a soybean disease recognition system, which is composed of two modules, including the image processing module and classification module.

The purpose of the image processing module is to

extract the leaf region from the leaf image with a complex background, that is, to remove the background from the whole image. The classification module uses autotun to fine-tune pre-trained CNN on the soybean leaf disease datasets, thus the classification model trained in the original datasets will show excellent performance on the target dataset. In other words, more complicated features can be learned from the soybean leaf disease datasets to improve the leaf disease recognition accuracy rate. The results of the recognition system proposed in this research were compared with the traditional fine-tuning methods of transfer learning. Such methods and the method in this research have used the same dataset. The experimental and comparative analysis indicated that the method proposed in this research showed excellent performance, namely, relatively unapparent and more detailed leaf structure features could be successfully learned while getting a higher classification accuracy rate in the validation set.

Materials and Methods

Experimental Materials

The soybean leaf disease image data used in this research were gained from the digi pathos plant dataset images provided by Embrapa, including 459 images and 11 types, which could be subdivided into bacterial leaf spot, southern blight, target leaf spot, rust disease, powdery mildew, downy mildew, copper poison disease, grey speck disease, soybean mosaic virus, healthy and unknown diseases. During the model training process, 80% of images were used for training while 20% of images were applied for validation. Table 1 shows each leaf disease's image quantity in the training stage and validation stage in the original dataset. Figure 1 shows the sample image of soybean diseases.

Due to the small dataset in this research, transfer learning can be trained under the small-scale dataset. Also, the data-augmented technology can be applied to amplify the dataset to reduce overfitting and under fitting. In the computer vision field, each dataset of image classification issues needs to use a specific data-augmented strategy to gain the best classification effect. This research applied a high-efficient automatic data-augmented method based on the search algorithm: Auto augment (Hataya *et al.*, 2020). The data augment in the image recognition field generally applies equalization, flip horizontal, cutting, and rotation. Auto augments in this research define the search space. The data-augmented scheme is composed of multiple strategies while each strategy includes two different image processing methods (the equalization, flip horizontal, cutting, and rotation), as well as the use sequence and probability for each image processing method. In this research, the genetic algorithm (Guan *et al.*, 2020) was chosen as the search algorithm to find out the best data-augmented scheme in the search space.

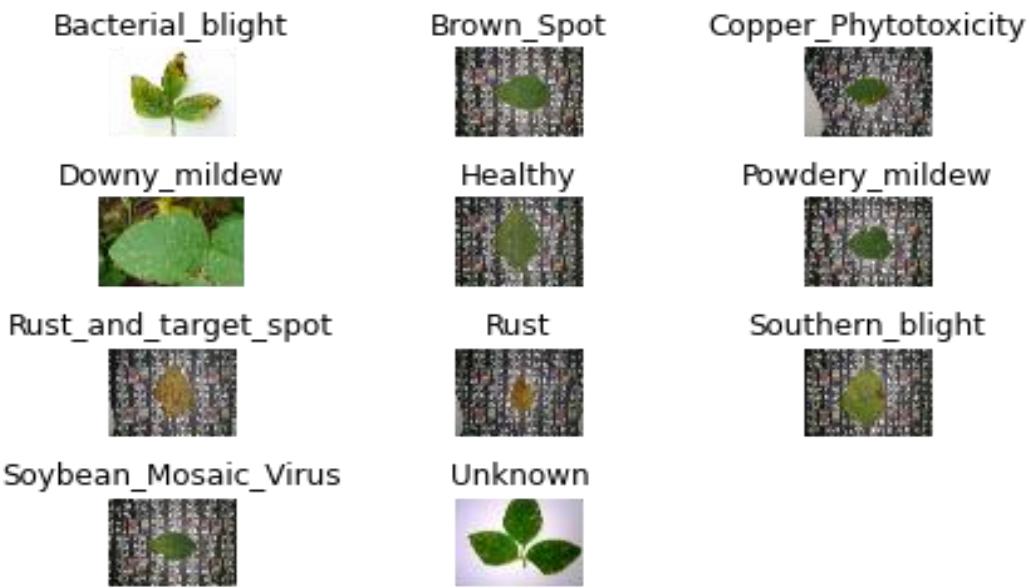


Fig. 1: Soybean leaf disease sample figure including healthy and unknown

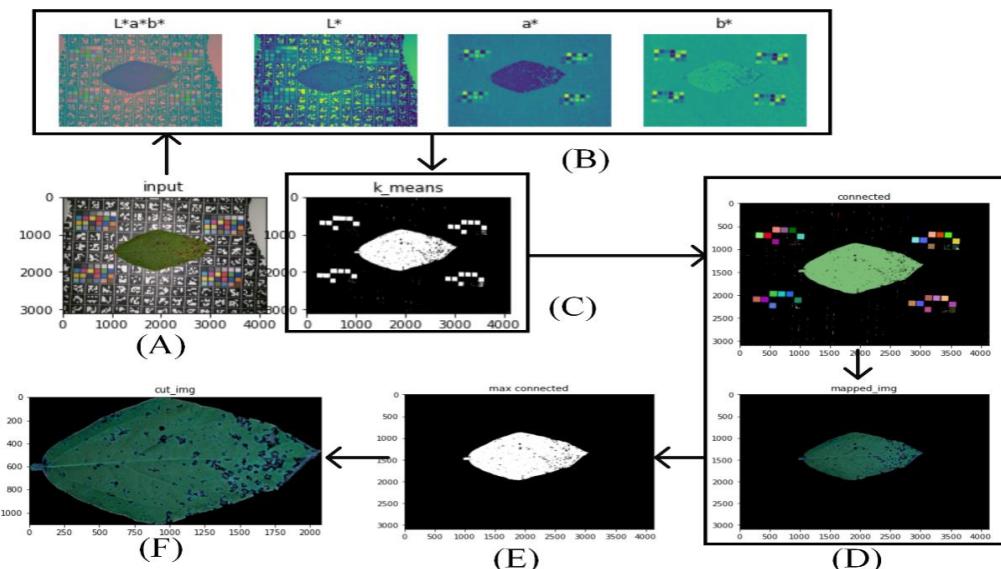


Fig. 2: The image processing module: Leaves in the entire image can be separated clearly

Table 1: The image quantity in the training stage and verification stage

No.	Disease (healthy) types	Training sets	Validation sets	Total
1	Bacterial blight	44	12	56
2	Southern blight	49	13	62
3	Target spot	26	6	32
4	Rust	52	13	65
5	Healthy	7	2	9
6	Powdery mildew	61	16	77
7	Downy mildew	40	11	51
8	Copper phytotoxicity	18	5	23
9	Brown spot	16	5	21
10	Soybean mosaic virus	17	5	22
11	Unknown	32	9	41
	Total	362	97	459

The Image Processing Module

By observing the sample image in Fig. 1, it can be found that the area of the blade is much smaller than that of the background. The leaves in the whole image are segmented before the image is input into the classifier, then the classifier can accurately extract the features related to leaf disease for accurate leaf disease recognition. The image processing module is composed of four submodules and its composition structure and output image are shown in Fig. 2.

The first submodule converts the RGB color space image into L*a*b* color space, which is the 3D real space. L represents luminance, a stands for the component from

green to red and b is the component from blue to yellow. Among them, the output of the b channel component is the input of the second submodule, as shown in Fig. 2(B). The second submodule applies K-means (Sinaga and Yang, 2020) clustering algorithm to cut b channel components' images into two clusters ($k = 2$). One cluster corresponds to the leaf area (the interesting area) while another cluster corresponds to the background area excluding leaves. In detail, white (the pixel 255) is used to represent the foreground (the leaf area) while black (the pixel 0) is applied to represent the background. In this research, L and A channels did not get excellent output in the image segmentation, thus components of L and A channels did not participate in the K-means cluster. However, after the soybean leaves are segmented by the K-means clustering algorithm, there are still some non-leaf areas in the image background area, which means the K-means clustering algorithm divides some areas into prospects in the background, as shown in Fig. 2(C). Beyond that, the third submodule applies K-means clustering output images as the images after improved input segmentation. The main purpose of the third submodule is to find out and cut out the maximum connected domain, that is, the soybean leaf area. The image includes a plurality of connected domains, the image region composed of foreground pixels with the same pixel value and in adjacent positions in the image, which includes leaf regions and other connected domains that are not needed or irrelevant but are divided into the foreground. In this research, the connected domain label algorithm (Perri *et al.*, 2020) was adopted to gain the number of connected domains in the input images and different connected domains are marked with different colors, as shown in Fig. 2(D). Besides, the maximum connected domain or a pair of binary images can be extracted from the marked connected domains. Pixel 1 with data normalization represents the leaf area while pixel 0 means the background area. At last, binary images are mapped to the original input RGB images, gaining the RGB images with the leaf areas which are used as the input of the 4th submodule. The mapping algorithm converts the normalized binary images into the three-channel images and then multiplies the original input RGB images.

The 4th submodule converts the binary processing of input images into the single-channel, as shown in Fig. 2(E). Two lists are set up to do the simple iterative algorithm. The horizontal list conducts traversal on the x-axis of input images while the vertical list conducts traversal on the y-axis of input images. Coordinate points with the pixels of 254 are added to the list. The minimum of the horizontal list is the left boundary while the maximum is the right boundary. The minimum of the vertical list is the bottom boundary while the maximum is the top boundary. The leaf area images are cut on the corresponding interval, as shown in Fig. 2(F).

The above-mentioned image processing module is applied to all images of the dataset but only leaves the leaf area, removing the irrelevant background. With a tiny

minority, this module will cut the leaf area into the background while the background area will be cut into the foreground. The sum of pixels after cutting and clipping all image leaf areas is not the same, thus the image size is reset as 224*224*3 as a whole.

Autotun Methods

In recent years, deep learning has made remarkable achievements in target detection, computer vision, natural language processing, automatic speech recognition, and semantic analysis (Fan, 2020). Compared with the shallow algorithm model of traditional machine learning, deep learning shows remarkable superiority in feature extraction and modeling. At present, CNN is one of the primary forms of deep learning, featured with the local connection, weight sharing, pooling operation, and multi-layer structure. It is suitable for the image classification field. Models with excellent performance include VGG-16 (Simonyan and Zisserman, 2014), ResNet-34 (He *et al.*, 2016), Inception (Szegedy *et al.*, 2015), dense net (Huang *et al.*, 2017), and Exception (Chollet, 2017). They generally need lots of training data and calculation resources to gain excellent performance. However, it is a pity that the new research field does not have sufficient data to support such models. Facing the above-mentioned challenges, transfer learning is a common solution and can provide favorable performance in small-scale datasets. Transfer learning uses CNN advantages and conducts fine-tuning on the pre-trained CNN in the source tasks on the target dataset to satisfy the demands of target tasks (Pio *et al.*, 2021). However, in actual applications, relative to the source dataset, the target dataset has a limited scale so the model overestimates the overfitting caused by the feature capacity of target tasks. Based on the improved transfer learning, Bayesian optimization was carried out to fine-tune the pre-trained CNN and fit the soybean disease classification task in this research. This section focuses on discussing the experimental method. Figure 3 shows the improved strategies for the training of CNN and traditional transfer learning in this research.

Autotun method was applied in this research so that hyper-parameter search space will not be limited to the last fixed layer or several layers. This method firstly removes the pre-trained CNN softmax layer and uses a new softmax layer for replacement. The number of nerve cells is equal to the category of the target dataset. Also, Bayesian optimization is used to automatically adjust the CNN layer. The layer in front of CNN represents the general original features, such as the margin and spot. These features are common to most tasks. The exclusive features of target tasks can be extracted from several last layers. As a result, this method could adjust the CNN layers from right to left (from the last layer to the initial layer). As shown in Fig. 3(C), the locking symbol means to freeze this layer while the unblocking symbol refers to conducting fine-tuning on this layer. The specific steps of using Bayesian optimization to adjust CNN automatically are stated in Table 2.

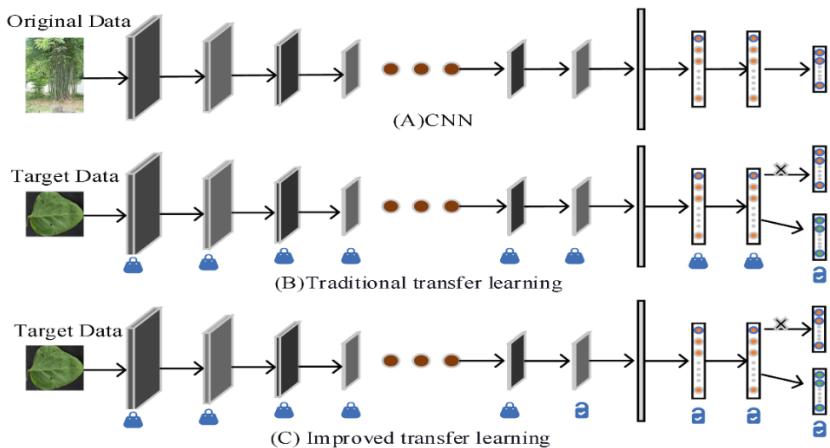


Fig. 3: Improved transfer learning. Generally, transfer learning removes the last layer (softmax) of the pre-trained CNN and adds a new softmax layer to adapt to the target task. Then, it conducts training on the target dataset of the last layers or the last several layers. The number of the selected training layers is judged by the target dataset size and the similarity with the source dataset. The pre-trained CNN model is designed for the source dataset, showing the poor performance on the target dataset

Table 2: Bayesian optimization algorithm

No.	Algorithm: Bayesian optimization for automatic adjustment of CNN
1	Input: Original CNN, hyper-parameter search space S, training set, verification set, and epochs (pre-trained CNN's epochs quantity)
2	Output: The improved CNN network for the target dataset
3	1: Procedure: Autotun
4	2: It is assumed that GP is used as the prior distribution of the target function F
5	3: At the initial point m_0 , $n = m_0$, the target function F is calculated. m_0 in this experiment is initialized as 10
6	4: while $k \in n + 1, \dots, N$ do //Traversal hyper-parameter search space
7	5: Prior is used to update the posteriori distribution of the target function F
8	6: The next sample point x_k of the gathering function's maximum is selected
9	7: Calculation of $y_k = F(x_k)$
10	8: Return x_k //Return the point with the best structure

Table 3: Relevant hyper-parameter search space in the CNN layer

No.	Network layer type	Relevant parameter types	Parameter values
1	Convolutional layer	Filter size Step size The number of filters	{1,2,3,5} 1 {64,128,256,512}
2	Maximum pooling layer	Filter size Step size	{2,3} 1
3	Average pooling layer	Filter size Step size	{2,3} 1
4	Fully connected layer or dense layer	The number of fully connected layer nerve cells	{1,2,3} {64,128,256,512,1024}
5	Dropout	Dropout factor	[0,1] interval is 0.1

In this study, the hyper-parameter search space involved in different CNN layers was discussed. This research applied VGG-16, ResNet-34, and DenseNet-121. Such networks could be gained by pre-training in the ImageNet (Deng *et al.*, 2009) dataset. Autotun applied in this research conducted fine-tuning on the soybean leaf disease dataset to gain better performance. Hyper-parameter search space of fine-tuning is illustrated in Table 2, which involves 6 operations of the convolutional layer and pooling layer. The fully-connected hyper-parameter includes the number of layers and nerve cells. Dropout is adopted on the fully-

connected layer and dense layer. Dropout is a mainstream regularization with the factor to be adjusted in the range of [0, 1]. The offset is 0.1, namely the Dropout factor value should be {0, 0.1, 0.2, 0.3, 0.4, 0.5, 0.6, 0.7, 0.8, 0.9, 1}.

In the process of the experiment, the connectivity of pre-trained CNN was not modified to make the model suitable for the soybean leaf disease dataset. Two operators including 1*1 convolution and upper sampling operation were used in the research to respectively solve the unmatched issue of tensors in deep and spatial dimensions.

Bayesian Optimization

On the target dataset, the pre-trained CNN conducts the automatic fine-tuning and it is regarded as a black box optimization issue. In other words, target functions are not directly accessed. In this thesis, Bayesian optimization was applied to do fine-tuning for CNN. F was set up as the target function with the mathematical form as (1):

$$F : R^d \rightarrow R \quad (1)$$

Bayesian optimization can be expressed by formula (2):

$$x^* = \arg \max_{x \in S} F(x) \quad (2)$$

where, is used as the input. In formula (2), S represents the hyper-parameter search space, as shown in Table 3. Any point in search space is used to solve the value consumption calculation resource of the target function F, which can be gained by conducting fine-tuning (re-training) for the original CNN layer on the target dataset. x^* represents the optimal estimation of relevant hyper-parameter in the CNN layer after fine-tuning.

Bayesian optimization is composed of the agent model and gathering function (Pelikan, 2005). The agent model is a Bayesian statistical model and uses Gaussian Process (GP) regression to establish the approximation of the target function F. It is assumed that GP is used as the prior distribution of the target function F. The gathering function uses the EI function to find out the global maximum of the target function F.

Results and Discussion

This research was applied for the classification and identification of bacterial leaf spot, southern blight, target leaf spot, rust disease, powdery mildew, downy mildew, copper poison disease, grey speck disease, and soybean mosaic virus.

The image processing module output of the soybean leaf disease recognition system used in this research is illustrated in Fig. 2. The experimental results indicated that such a method was effective for the background segmentation of soybean leaf disease images. The interesting areas or leaf areas can be separated from the complicated background. The features of the infected disease and insect pest parts were reserved in the separated leaf images, thus the output images of the image processing module will be suitable for the classification

module to do feature extraction.

After gaining the leaf images without the complicated background, auto augment technology can be used for data augment. 80% of images could be used as the training set at random while 20% of images could be selected as the validation set to verify the accuracy rate of the classifier. The accuracy rate can be defined as formula (3):

$$\text{accuracy}(x) = \frac{T_{px}}{T_{px} + T_{nx}} \quad (3)$$

where, x represents the leaf disease type. T_{px} and T_{nx} respectively represent the times of success and failure to identify the leaf disease x in the entire system or the average classification accuracy rate of each leaf disease in the entire system.

Influence of Bayesian Optimization on Experimental Results

The classifier autotun used in this research can fit the soybean leaf dataset's CNN structure through algorithm 1 learning to improve the training transfer learning. As shown in Table 3, the optimal configuration of different layer structures and related super parameters were obtained after automatically fine-tuning CNN by the Bayesian optimization algorithm. In the soybean leaf disease dataset, the VGG-16 network (pre-training on ImageNet dataset) was conducted fine-tuning in this research to gain a 92.55% of validation accuracy rate in the experiment, overlapping a fully connected layer with 1024 nerve cells. In detail, the Dropout factor with the originally connected layer is 0.6, overlapping the maximum pooling layer. The filter size is 3*3 to do fine-tuning for the ResNet-34 network. The dropout factor including the originally connected layer is 0.3. The filter size of the last two convolutional layers is 3*3, respectively including 512 and 256 pieces. Through fine-tuning on the DenseNet-121 network, 92.29% of the validation accuracy rate was gained in the experiment, overlapping a new fully-connected layer with 1024 nerve cells. The Dropout factor with the originally connected layer is 0.4. The filter size of the last two convolutional layers respectively reaches 5*5 and 2*2, including 512 and 128 pieces. The fully-connected layer and parameters listed exclude the fully connected layer of output because of the number of nerve cells in the output category. Table 4 indicates that 3 CNN structures obtained by Bayesian optimization could gain excellent performance on the soybean leaf disease dataset.

Table 4: Optimal hyper-parameter configuration

No.	CNN types	Fully connected layer			Convolutional layer			Maximum pooling		
		Layers	Cells	Dropout	Layers	Filter size	Filters	Layers	Filter size	Accuracy
1	VGG-16	1	1024	0.6	-	-	-	1	3*3	92.55
2	ResNet-34	1	256	0.3	2	{3*3,3*3}	{512,256}	-	-	90.16
3	DenseNet-121	1	1024	0.4	2	{5*5,2*2}	{512,128}	-	-	91.29

Table 5: Classification performance comparison

No	CNN types	Transfer learning types	Fine-tune layers	Trained parameters(million)	Validation accuracy
1	VGG-16	Autotun	3	0.82	94.23%
		Traditional fine-tune	3	1.33	85.52%
2	ResNet-34	Autotun	2	0.66	93.51%
		Traditional fine-tune	2	0.54	87.13%
3	DenseNet-121	Autotun	4	1.50	94.91%
		Traditional fine-tune	4	0.80	87.74%

Influence of Autotun Method on Experimental Results

Table 5 shows the accuracy rate from the traditional fine-tuning method of transfer learning and autotun in the research in VGG-16, ResNet-34, and DenseNet-121 structures for the soybean leaf disease dataset. To prove the autotun improvement on transfer learning, the layers of the traditional fine-tuning method remain consistent with the layers gained by automatic fine-tuning of autotun. The findings indicated that compared with the traditional fine-tuning method of transfer learning, the autotun method used in this research significantly improved the performance (validation set's accuracy rate) or the number of trained parameters was relatively reduced). For the pre-trained VGG-16 model, the traditional fine-tuning gained 85.52% of the validation accuracy rate on the soybean leaf disease dataset, requiring 1.33 million parameters relating to three layers. The autotun method used in this research conducted automatic fine-tuning for the pre-trained VGG-16 model, gaining 94.23% of the validation accuracy rate on the soybean leaf disease dataset. Compared with the traditional fine-tuning method, the trained parameters only used 823000 which was reduced by 38%. The autotun method used in this research could conduct fine-tuning for the pre-trained ResNet-34 and DenseNet-121 model on the soybean leaf disease dataset, finding that the trained parameters were slightly higher than the traditional fine-tuning method of transfer learning because the extra fully-connected layer was considered in the parameter search space. Such a method respectively gained 93.51 and 94.91% of the validation accuracy rate on the soybean leaf disease dataset while the traditional fine-tuning method respectively gained 87.13 and 87.74% of the validation accuracy rate. Through comparison, it could be proven that the extra fully-connected layer could improve the performance of the validation data.

In addition to the comparative analysis between Table 3 and Table 4, the same source data set (ImageNet dataset) and target data set (the soybean leaf disease dataset) were used during the fine-tuning of vgg-16, resnet-34, and densenet-121 networks by autotun method and traditional fine-tuning method. At the same time, the number of fine-tuning layers in the traditional fine-tuning method remained the same as the layers gained by automatic fine-tuning from the autotun method. The analysis of these trainable parameters and verification accuracy obtained from the control experiment shows that the autotun

method used in this study has excellent performance on the soybean leaf disease data set and possesses good generalization ability on convolutional neural networks with different structures.

Conclusion

The quality and quantity of soybeans can be affected by diseases and insect pests. In this research, the identification method for 9 kinds of leaf diseases including bacterial leaf spot, southern blight, target leaf spot, rust disease, powdery mildew, downy mildew, copper poison disease, and soybean mosaic virus, as well as healthy leaves and unknown leaf diseases was proposed while the traditional transfer learning method was improved to identify soybean leaf diseases.

In this research, the image segmentation method was applied to remove the complicated background and cut it into the leaf areas with the auto augment technology to augment data and reduce overfitting. Relevant findings indicated that the current research method of conducting background segmentation for soybean leaf disease images was effective. The interesting areas or leaf areas could be separated from the complicated background. The characteristics of disease symptoms were reserved in the segmented leaf image. The autotun method used in this research improved transfer learning. On the soybean leaf disease dataset, VGG-16, ResNet-34, and DenseNet-121 network models (ImageNet pre-training) were conducted automatic fine-tuning. The validation accuracy rates of VGG-16, ResNet-34, and DenseNet-121 networks obtained through the methods used in this study reached 94.23, 93.51 and 94.91% respectively, showing better performance and fewer trained parameters than the traditional fine-tuning method of transfer learning. Other existing soybean leaf disease databases would be considered to train and test the generalization ability on different data sets of the autotun method, in further research.

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Author's Contributions

Xiao Yu and Qi Gong: Designed and performed the experiments, and work. Designed the experiments and revised the manuscript.

Cong Chen: Participated to collect the materials related to the experiment.

Lina Lu: Designed and performed the experiments, and work.

Ethics

The authors declare their responsibility for any ethical issues that may arise after the publication of this manuscript.

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