Identification of Cucumber Leaf Diseases Based on Transfer Learning

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IDENTIFICATION OF CUCUMBER LEAF DISEASES BASED ON TRANSFER LEARNING

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ABSTRAC In this paper, a recognition framework of cucumber leaf diseases based on depth learning is proposed. In the feature extraction stage, the framework uses migration learning to train VGG19 and Inception V3 models, uses parallel maximization fusion method for information fusion, and uses whale optimization algorithm for feature optimization. In the final classification process, supervised learning algorithm is used to classify the selected best features. The experiment was carried out on a self-made dataset, which was composed of five cucumber diseases. The accuracy of the algorithm was 96.5%, and the time consumed was 45.28s.

Key Words： Transfer learning; Whale optimization algorithm; Disease identification

0 Introduction

Cucumber leaf segmentation and recognition is a challenging task due to scale change, shape, contrast, color and other factors. Researchers have proposed many methods to effectively detect cucumber diseases.In this paper, in order to improve the accuracy of cucumber disease identification, different depth CNN model features are connected to obtain better accuracy. By selecting stable features for classification, a variety of optimization techniques are used to obtain better results. Based on this, a new improved framework for cucumber leaf disease identification was proposed. In this work, the following major contributions have been made:(1) According to the prepared cucumber leaf disease data set, fine tune VGG19 and Inception V3. The last fully connected layer was removed from the two models and a new layer was added, including five classes.(2) A parallel maximum correlation method is proposed to fuse deep learning features in vectors.(3) A whale optimization algorithm for selecting the best features is implemented(4) Calculate the results of each step separately and compare them with the latest technology.

1 Methods

The method consists of three stages: In the first stage, the depth CNN model of pre training is implemented using transfer learning for depth feature extraction; Secondly, the features extracted from depth are fused; In the final stage, the whale optimization algorithm is used to optimize the extracted features and perform classification. ES-KNN classifier (Ensemble of Subset of K-Nearest Neighbours) is used to achieve competitive performance with low computing cost. The specific process of this method is shown in the figure:

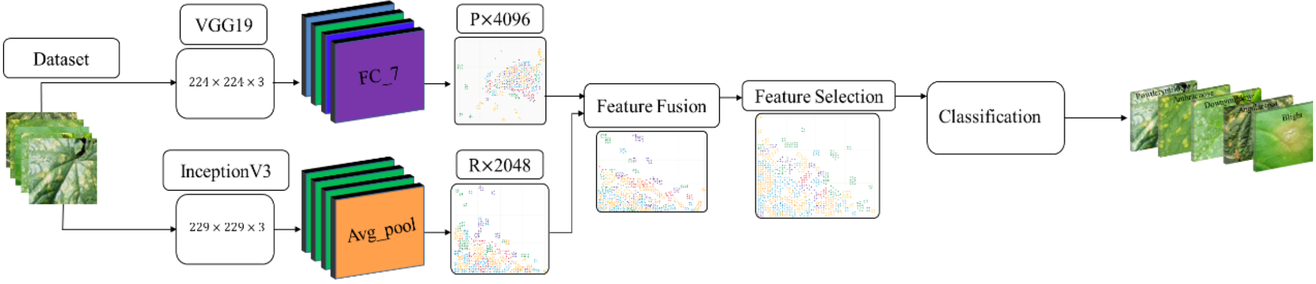

Fig 1: Identification method of cucumber diseases in this project

1.1 Depth feature extraction

CNN model mainly consists of convolution layer, pool layer, full connection (FC) layer and a ReLU activation function. In our proposed method, two pre trained depth CNN models, VGG19 and Inception V3, are used for feature extraction. Pre trained depth CNN models Inception V3 and VGG19 are used for feature extraction. We use cucumber dataset to extract deep features, and use 70:30 for training and testing. We preprocess the image of the input layer, and adjust the image size according to the size of the input layer. In the VGG19 model, the first convolution layer is used as the input layer, and the FC layer is activated and features are extracted to obtain 1 × 4096. ψ^{l1} represents the feature vector extracted using VGG19. The structure for feature extraction is shown in Figure 2

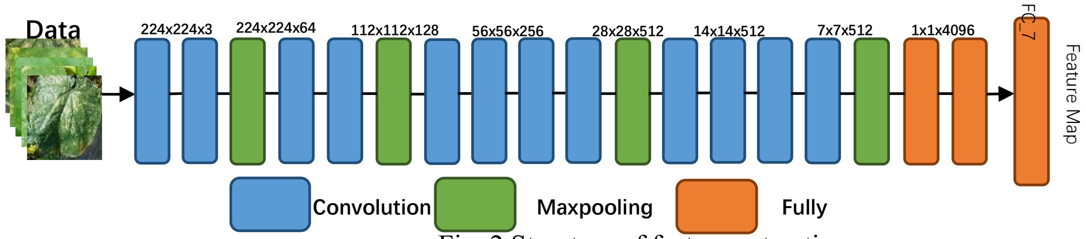

Fig. 2 Structure of feature extraction

At the same time, Inception V3 is also used for feature extraction. The convolution layer is used as input, and the average pool is used for feature extraction by performing activation. By activating the average pool layer, 1×2048 size feature map, used for feature vector ψ^{l2} represents. In the training and testing stages, the features extracted from Inception V3 and VGG19 are connected. The detailed architecture of Inception V3 is shown in Figure 3. By modifying the deep learning model, we use sigmoid as the training function. Other parameters are as follows: Epoch 200; Iterations per epoch 30; Minimum batch size 64; The learning rate is 0.0001;

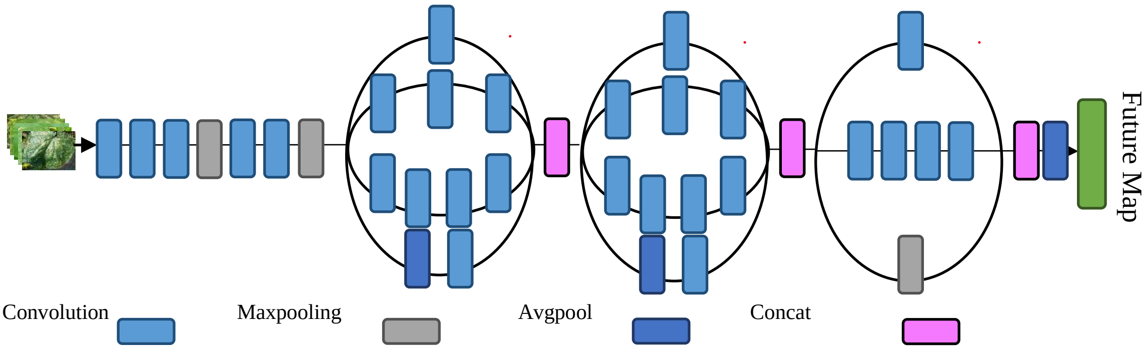

Figure 3 Pre training Inception V3 architecture for feature extraction using transfer learning

1.2 Feature fusion

Feature fusion is a hot research field in the field of pattern recognition [4]. Target classification needs a strong and dense feature space, and feature fusion is the method to solve this problem. Feature fusion plays an important role in obtaining accurate results, but it will seriously affect the calculation cost. A new feature fusion method, parallel maximum covariance (PMC), is proposed. The fusion process balances the size of the feature space to obtain a single feature vector. Suppose we have two $\psi^{l1}$and ψ^{l2}The depth CNN feature space represented, whose dimension is $p{\times}q$ and $p{\times}r$ Where p represents the image in the feature map, and q represents the feature vector p extracted by VGG19 × 4096. The dimension of Inception V3 feature map is expressed as r × 2048。 We add the average filled value to balance the length of the two feature maps. Assume that a represents the mode field ψ_1 .The column vectors m and b represent the pattern field ψ_2. The row vector projection using time series can be as follows:

$$y_1 = \psi_1^T \psi^{(l1)} \tag{1}$$

$$y_1 = \psi_1^T \psi^{(l2)} \tag{2}$$

The maximum covariance is:

$$c = Cov[y_1, y_2] \tag{3}$$

$$c = Cov[\psi_1^T \psi^{(l1)}, \psi_1^T \psi^{(l2)}] \tag{4}$$

$$c = \frac{1}{n-1} Cov[\psi_1^T \psi^{(l1)}, \psi_1^T \psi^{(l2)}] \tag{5}$$

$$c = \psi_1 (C_{\psi_1 \psi_2}) \psi_2 \tag{6}$$

$$C_{\psi_1 \psi_2} = \frac{1}{n-1} (\psi^{(l1)} \psi^{(l2)T}) \tag{7}$$

ψ_1 and $\psi_2$is used for covariance between $C_{\psi_1\psi_2}$ indicates that it has i and j characteristics respectivelyψ_i and ψ_j. The final fused feature map has the maximum covariance $C_{\psi_1\psi_2}$。 The fusion process creates opportunities to add redundant features. In our fusion method, we get the final N × 6145 dimensional fusion feature vector.

1.3 Feature optimization

The use of feature optimization techniques improves the performance of machine algorithms by deleting irrelevant and redundant features. In the detection of crop diseases, different algorithms are used to optimize the data in order to better diagnose diseases. For the classification of crop diseases, the whole optimization algorithm (WOA) [5] is used for feature optimization. In nature, humpback whales usually live in groups. In the process of predation, humpback whales will surround their prey in groups, and constantly spit out bubbles in the process of spiral movement, thus forming a spiral "bubble net", which will force the prey closer and closer until it can be swallowed in one bite.

2 Results and discussion

2.1 Experimental environment

The cucumber disease identification method has been implemented on an extended cucumber dataset. The data set contains images of different colors and directions, and is captured under different lighting conditions. Augmentation was performed to increase dataset size and eliminate category imbalance. A total of five diseases were considered, including angular spot (71 images), powdery mildew (43 images), downy mildew (104 images), fusarium wilt (54 images) and anthrax (67 images). All images are in RGB (red, green, blue) format, and the original image size is 256

× two hundred and fifty-six × 3。 After the amplification process, the number of images of each type reached 500. Sample images from the cucumber leaf dataset are presented in Figure 4. The proposed training and testing methods were performed using the 70:30 method and ten fold cross validation. The simulation of the proposed method is performed on a desktop computer equipped with an Intel i7 eighth generation computer processing unit (CPU), 16GB RAM, and an 8GB graphics card. Different classifiers were used to classify cucumber diseases, and robust classifiers with high accuracy were selected. Different evaluation methods (such as accuracy, false negative class rate (FNR) and calculation time) are used to evaluate the performance of this method.

Fig. 4 Sample image in cucumber leaf image dataset

	Angularspot	Anthracnose	Downymildew	Blight	Powderymildew			
Angularspot	92%	8%					92%	8%
Anthracnose	5%	94%	1%		<1%		94%	6%
Downymildew	1%	2%	97%		<1%		97%	3%
Blight			1%	98%	1%		98%	2%
Powderymildew	2%	1%	1%	1%	95%		95%	5%

Fig. 5 Cucumber disease identification confusion matrix

2.2 experimental result

This section presents the experimental results of this method. Table 1 shows the results of depth feature fusion. The depth features are extracted using the pre trained depth CNN model and parallel connection is performed. Multiple classifiers are applied to the fused feature space to perform recognition. ES-KNN achieves the highest accuracy of 95.2% with a false negative class rate (FNR) of 4.8%. Other classifiers such as F-KNN C-SVM, Q-SVM, ESD, MG-SVM, W-KNN and EB Tree achieve the accuracy of 94.6, 95.6, 94.9, 64.2, 93.3, 87.1 and 89.4 respectively. The fusion of depth features improves the recognition accuracy to some extent, but also increases the calculation time.

Table 1 Cucumber disease identification results based on depth feature fusion

Method	Accuracy(%)	FNR(%)	Time(s)
ES-KNN	95.2	4.8	250.63
F-KNN	94.6	5.4	58.365
C-SVM	95.6	4.6	175.36
Q-SVM	94.9	5.1	159.73
ESD	64.2	35.8	956.46
MG-SVM	93.3	6.7	204.98
W-KNN	87.1	12.9	59.113
EB-Tree	89.4	10.6	83.476

Table 2 Cucumber disease identification based on feature optimization method

Method	Accuracy(%)	FNR(%)	Time(s)
ES-KNN	96.5	3.5	45.28
F-KNN	94.2	5.8	11.46
C-SVM	93.8	6.2	32.508
Q-SVM	93.6	6.4	29.505
ESD	93.1	6.9	175.86
MG-SVM	93	7	38.444
W-KNN	86.5	13.5	11.278
EB-Tree	88.2	11.8	27.444

The proposed feature optimization method improves the performance of pattern recognition by reducing the computation time. WOA is used to optimize the fused feature vector to select the best feature, which will affect the model accuracy and calculation time. Table 2 shows the robustness and computability of the method. Different classifiers are used to classify the optimized feature space, and the best classifier is selected based on accuracy and calculation time. The results show that ES-KNN achieves the highest accuracy of 96.5% at 3.5% FNR. The function of ES-KNN classifier is also verified by the confusion matrix shown in Figure 5. The accuracy of W-KNN was the lowest, 86.5%. The recognition accuracy of other classifiers such as F-KNN C-SVM, Q-SVM, ESD, MGSVM and EB Tree was 94.2%, 93.8%, 93.6%, 93.1%, 93% and 88.2% respectively.

3 **Results and discussion**

Compared with the existing cucumber disease identification methods, this method has achieved a competitive performance in terms of accuracy and computing time. For a comprehensive comparison with the existing methods, see Table 3. Lin et al. [7] proposed a semantic segmentation based method to identify powdery mildew by implementing a deep CNN model on the segmented image, and achieved an average accuracy of 96.8% on a single type of powdery mildew. The feature selection method proposed by Zhang et al. [8] identifies three cucumber diseases, with an accuracy rate of 96%. Zhang et al. [9] proposed a global expansion CNN model for identifying cucumber diseases. This method can effectively identify six different diseases of cucumber, and the accuracy rate is 94.65%. Ma et al. [10] proposed a recognition method of cucumber anthracnose, powdery mildew, leaf spot and downy mildew based on deep CNN model. The accuracy of this method is 93.4%. The proposed method of deep feature fusion and feature selection for cucumber diseases has a recognition accuracy of 96.5% for five cucumber diseases, namely, angular leaf spot, powdery mildew, downy mildew, fusarium wilt and anthrax. Compared with the prior art, the proposed method achieves the accuracy of all five diseases in less computing time

Table 3 Comparison between the proposed method and existing technology

Author	Classes	Method	Accuracy(%)
Lin et al.[7]	1	Semantic segmentation and CNN	96.8
Zhang et al.[8]	3	EfficientNet with ranger optimizer	96
Zhang et al.[9]	6	Global pooling dilated CNN	94.65
Ma et al.[10]	4	Deep CNN	93.4
Proposed	5	Deep feature fusion with WOA optimization	**96.5 （45.28s）**

3. 1 Conclusion

In order to effectively identify cucumber diseases, a deep learning method including feature fusion was proposed. WOA is used to optimize the proposed depth feature fusion method. The method of depth feature fusion and selection includes two stages. In the first stage, the pre trained depth CNN model (VGG19 and Inception V3) is used to extract depth features. The extracted depth features are fused, and different classifiers are used for recognition. The results show that the accuracy of ES-KNN algorithm is 95.2%, and the calculation time is 250.63 s. Feature selection is used to reduce computation time and improve recognition accuracy. The machine learning algorithm is used to classify the optimized features using WOA. Table 2 shows that ES-KNN achieves 96.5% accuracy and requires 45.28 seconds of calculation time. The results show that the proposed method has strong robustness and low cost for cucumber disease identification.

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