Research on Rice Disease Identification Model Based on Migration Learning in VGG Network

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Abstract

Purpose: Aiming at the problems of slow speed, over-fitting and unsatisfactory recognition of traditional recognition models, VGG16 convolutional neural network is applied to rice disease identification, and the knowledge learned by VGG16 model is transferred to rice disease identification by means of migration learning method to construct the recognition model.

Method: The classifier uses linear discriminant analysis by setting different learning rates to fine tune the network parameters. Using image processing technology to expand the disease image set, according to the disease characteristics, the sample is divided into 10 types of diseases such as rice blast, sheath blight, rice smut and bacterial blight, and 90% of each sample is randomly selected as the training set. 10% of the samples were used as test sets, and the samples were trained using the 10-fold cross-validation method. During the simulation training, the other two methods were compared and analyzed.

Result: The experimental results show that the accuracy, balance F score and prediction speed of the disease recognition model using parameter trimming and linear discriminant classifier are higher than the other two recognition models. The average correct rate is 97.19%, the equilibrium F score is 96.75%, and the prediction speed is 175 samples per second; from the performance analysis of the model, the accuracy rate did not show large fluctuations. After 100 trainings, the training and prediction accuracy rate reached 96%, the loss rate showed a gradient downward trend, and the change was relatively stable; The 10 types of disease samples were predicted, and the average accuracy was 97.08%, the recovery rate was 96.22%, and the F1-score value was 96.75%.

Conclusion: The method has the characteristics of high accuracy, strong generalization ability, good robustness and small loss rate. This provides reference and reference for plant disease identification research.

1. Introduction

Rice is the world's main food crop. More than half of the world's population mainly feeds on rice, and rice diseases seriously affect the yield and quality of rice. Rice diseases have the characteristics of various types, large occurrence areas, strong epidemics, and heavy damage. The losses caused by diseases and insect pests are huge every year. Therefore, if the rice diseases are diagnosed quickly and accurately and effective control measures are taken, it will help improve the yield and quality of rice.

With the development of computational intelligence and machine learning technology, image
recognition technology has achieved breakthrough research results, and is widely used in facial recognition, motion detection, fingerprint recognition, license plate recognition, disease classification and other related fields. In particular, the successful application of deep learning algorithms in the field of image recognition has effectively improved the accuracy and speed of image recognition. Since deep learning does not rely on image specific features for image recognition, it makes intelligent interaction more natural and opens up the way for the application of image recognition technology.

In recent years, many researchers have applied deep learning algorithms in the identification of plant diseases, such as alfalfa leaf, apple, grape, corn, winter jujube, strawberry, tomato and other diseases [1-9], and achieved good results. Because there are many factors for the development of rice diseases and insect pests, and the disease diagnosis is more complicated, there are few related literatures on the application of deep learning algorithms to rice disease identification. Lu Yang [10] et al. proposed a technique based on deep convolutional neural network (CNNs) to apply to rice disease identification. Experiments show that it can effectively identify 10 common rice diseases with an accuracy of 95.48%. Huang Shuangping [11] and others used the deep convolutional neural network GoogLeNet model to detect rice ear blast, and used Inception basic modules to repeatedly stack to build a main body network, with the highest recognition accuracy rate of 92.0%. The convolutional neural network recognition model established by Qiu Jing [12] has an average recognition rate of 96.03%.

Transfer learning is an important branch in the field of machine learning. Its goal is to complete the transfer of knowledge between related fields. It has the functions of accelerating the learning speed, improving the robustness of the model and generalization ability, so it is popularized and applied to image classification [13], recognition [14], anomaly detection [15] and other fields. It has also been popularized and applied to disease recognition technology. For example, Long Mansheng [16] used the AlexNet network architecture to establish a disease recognition model for Camellia oleifera, and used migration learning to optimize AlexNet. The classification accuracy rate was 96.53%. There was no over-fitting phenomenon and convergence speed and classification performance are both high. In particular, the proposal of VGGNet [17] provides a concise and practical model for image classification [18] and target detection [19].

This research attempts to use the VGGNet network architecture to establish a disease recognition model, optimize the model using migration learning and linear discriminant classifiers, and identify 10 rice diseases, aiming to provide a wider range of practical solutions for intelligent identification of plant diseases reference.

2. Materials and methods

2.1. Experimental data

The rice disease images used in this research are partly downloaded from the Internet by means of web crawlers, and partly taken by Canon 800D digital cameras. In order to ensure that the images searched on the Internet are accurate and reliable, the images are processed as follows: use the python scripting language to delete duplicate images by comparing the name, size and date of the images; delete the images with smaller resolution and size less than 500 pixels; data The image size of the set is uniformly adjusted to 256×256; in order to highlight the disease characteristics, the data set is preprocessed; the rice disease expert classifies all the sample sets. In the end, a total of 1000 available original images were obtained, including rice blast, sheath blight, rice smut, bacterial leaf blight, flax spot, bacterial brown spot, bacterial stripe disease, sheath rot, and narrow stripe there are 10 diseases of spot disease and red blight, each with 100 images. In order to reduce the over-fitting of the image set during the training phase, image enhancement techniques such as translation, rotation, cutting, flipping and perspective transformation are used to operate on the original image. Each type of sample set is expanded to 500, and the total sample set is 5000. Make labels for the sample set, and use 0, 1,…, 9 to represent the corresponding category labels. A sample of the disease is shown in Figure 1. The sample set was imported into the computer in jpeg format to construct a rice disease database.
2.2. Experimental method

2.2.1. Disease recognition model structure
Because the choice of network architecture and classifier has a great influence on the effect and efficiency of image classification, the construction of deep convolution recognition model and the selection of classification algorithm are particularly important. This rice disease recognition model adopts the convolutional neural network VGG16, and its main principle: the convolution layer realizes the extraction of disease feature data, the use of linear filters to filter the rice disease image, the relu activation function to extract the disease features, and the pooling layer Extract important features of disease images, reduce network complexity, and avoid over-fitting. The fully connected layer uses classification functions to calculate probabilities to achieve image classification and recognition. The VGG16 network architecture consists of 13 convolutional layers, 5 pooling layers and 3 fully connected layers. Since the disease recognition model is designed to identify 10 diseases in rice, the number of neurons in the output layer of the last fully connected layer is 10. The model architecture is shown in Figure 2.

2.2.2. Classifier design
The classifier of this study uses a linear recognition classifier. The core idea is that when classifying the predicted samples of rice diseases, first project the predicted samples of the diseases to extract
sample features, and calculate the Gaussian distribution probability density function of each category, with the largest probability is the category of the prediction sample to achieve the purpose of prediction classification.

Rice disease classification is a multi-classification problem, assuming a data set $D=\{(x_1,y_1),(x_2,y_2),\ldots,(x_m,y_m)\}$, $x_i$ represents a set of observation values in the feature vector of the rice sample set, which is an $n$-dimensional vector, $y_i$ indicates the disease category of the rice sample $x_i$, which is the sample label, $y_i\in\{0,1,\ldots,9\}$.

Using linear discriminant analysis to classify rice diseases is a multi-class projection to low-dimensional space. Assuming that the low-dimensional space vector dimension is $k$, the corresponding vector is $(w_1,w_2,\ldots,w_k)$. The matrix composed of vectors is $W$.

LDA the optimization goal is: $\max J(W) = \prod_{i=1}^{d} \frac{w_i^T S_{hb} w_i}{w_i^T S_{ib} w_i}$ \hspace{1cm} (1)

Where $S_b$ is the inter-class scattering matrix, $S_b = \sum_{j=0}^{9} N_j (\mu_j - \bar{x}) (\mu_j - \bar{x})^T$, $\bar{x}$ is the mean of all samples, $\mu_j (j = 0,1,\ldots,9)$ is the mean of the $j$-th sample, $N_j (j = 0,1,\ldots,9)$ is the number of samples of type $j$.

$S_w$ is the intra-class scattering matrix. $S_w = \sum_{j=0}^{9} \sum_{k=1}^{n_j} (x_j^k - \mu_j) (x_j^k - \mu_j)^T$, $x_j^k$ is the $k$th sample of the $j$th disease.

Solving the maximum value of equation (1) can be transformed into the eigenvalue of the matrix: $S_w^{-1} S_b W = \lambda W$ \hspace{1cm} (2)

Equation (2) The eigenvector corresponding to the largest $k$ eigenvalues is the matrix $W$.

2.2.3. Learning rate design

This research will use the differential learning rate to fine-tune the network parameters. The concept of differential learning rate divides the network architecture into different functional learning layers. During training, different learning rates are set for different functional learning layers to achieve the desired result. The disease recognition model is divided into a migration layer and a fully connected layer. The migration layer is used to identify general features such as image edges, shapes, colors, and the fully connected layer is used to identify advanced features of disease images. The learning rate of the migration layer is set to a higher learning rate to achieve extract all the features of the disease image, set the learning rate of the fully connected layer to a lower learning rate to achieve network fine-tuning, thereby improving model classification accuracy and reducing classification error rate, achieving network migration learning, and increasing network prediction speed.

3. Experimental design and result analysis

3.1. Experimental designs

Model training and testing are carried out in the Keras deep learning open source framework, and Python is selected as the programming language. Windows 7 operating system, Intel(R) Core(TM) CPU, main frequency 2.20 GHz, memory 8GB.

In order to prevent over-fitting, improve the robustness and generalization ability of the model, and obtain a reliable and stable classification and recognition model, this study uses 10-fold cross validation for simulation experiments. The original sample set is divided into two image subsets: training set and test set. The training set accounts for 90% and the test set accounts for 10%. That is, 450 images of each type of disease are in the training set and 50 in the test set. Image training uses a 10-fold cross-testing method. Each training set is used for feature extraction and input to the
corresponding classifier. The test set is input to the trained disease model to classify disease images. The cross-testing principle diagram is shown in Figure 3.

![Cross-validation schematic of disease model](image)

**Fig.3 Cross-validation schematic of disease model**

### 3.2. Model comparison experiment

The disease recognition model constructed in this study was compared and analyzed with the other two models.

**Model A:** Using the VGG16 network architecture, the first 13 layers are the transfer learning layer, the learning rate of the transfer layer is set to 0.001, and the learning rate of the 3-layer fully connected layer is set to 0.2, so as to achieve fine-tuning of the network, and the classifier is a linear discriminant analysis.

**Model B:** Using VGG16 network architecture, the advanced feature extraction layer is the 15th layer of the disease recognition model, the 16th layer is the image classification layer, the number of neurons is 10, and the classifier is linear discriminant analysis.

**Model C:** Using migration learning to fine-tune network parameters, using the VGG16 network architecture, the first 13 layers are the migration learning layer, the learning rate of the migration layer is set to 0.001, and the learning rate of the fully connected layer is set to 0.2, so as to achieve fine-tuning of the network. The classifier is softmax function.

**Experiment 1:** Comparison experiment on the accuracy of disease classification and recognition of three different models

The disease data were simulated and trained for three different models, and the experimental designs were all tenfold crossover test methods. The following indicators are used to evaluate the effectiveness of the model.

\[
accuracy = \frac{TP + TN}{TP + TN + FN + FN} \quad (3)
\]

\[
recall = \frac{TP}{TP + FN} \quad (4)
\]
Among them: accuracy: accuracy rate; recall: recall rate; precision: precision rate; F1 is the balanced F score, the harmonic mean of precision rate and recall rate; TP (true positive): true positive; TN (true negative): true negative; FP (false positive): false positive; FN (false negative): false negative.

Input the training set to the three recognition models, and after obtaining stable network parameters, input the samples of the test set to the trained network model, and perform 100 experiments to obtain the average value of the model evaluation indicators. The classification and recognition results are as follows Table 1 shows:

| Model | Accuracy (%) | Recall (%) | Precision (%) | F1 (%) |
|-------|--------------|------------|---------------|--------|
| A     | 97.19        | 97.28      | 96.22         | 96.75  |
| B     | 95.67        | 96.53      | 93.54         | 95.01  |
| C     | 96.24        | 96.82      | 94.72         | 95.76  |

It can be seen from Table 1 that Model A has the best disease classification and recognition effect, with an accuracy rate of 97.19, and high recall, precision and balanced F score, indicating that the prediction performance of Model A is good, and is better than the other two models. Among them, model B has the lowest accuracy.

Experiment 2: Comparative analysis of model complexity
In order to study the impact of the complexity of the disease recognition model on the model, since the complexity of the model is determined by both the time complexity and the space complexity, this study uses two indicators, training time and prediction speed. 100 experiments were carried out to find the average value of the model evaluation index. The experimental results are shown in Table 2:

| Model | Forecast speed (number/s) | Training time(min) |
|-------|---------------------------|--------------------|
| A     | 175                       | 16.02              |
| B     | 162                       | 16.35              |
| C     | 146                       | 15.54              |

From Table 2, from the perspective of prediction speed, model A has the fastest prediction speed, which can predict 175 sample data per second, and its prediction speed is significantly higher than the other two models, indicating that the use of migration learning can effectively improve disease prediction speed. From the perspective of training time, the training time of model A is 16.02 minutes, while the training time of model C is 15.54 minutes. The training time of model A is longer than that of model C. This may be because model A is advanced in obtaining disease recognition images. Features, improve the accuracy of disease recognition, adjust network parameters, and affect the speed of model training.

3.3. Model performance analysis
Model A is used to classify and identify 10 types of rice diseases, and the loss rate and accuracy of the training set and test set are simulated and analyzed to analyze the convergence performance of the model. The simulation analysis result is shown in Figure 4.
It can be seen from Figure 4 that as the number of training increases, the model training accuracy and test accuracy are gradually increasing. The training accuracy curve does not show large fluctuations. After 100 times, the curve stabilizes, and its training and testing accuracy rates are both above 96%. The training and testing loss rate curve shows a gradient downward trend, the change is relatively stable, and there is no over-fitting phenomenon, indicating that the model has strong generalization ability and high test accuracy. Transfer learning is beneficial to improve training and test accuracy and the speed of model convergence.
3.4. Model validity analysis

Use this model to perform predictive analysis on all samples in the test set to verify the effectiveness of the model. A total of 100 experiments were performed to find the confusion matrix of each disease in the test set; precision rate, recall rate and F1 average value. The results are shown in Table 3.

Table 3 Model a confusion matrix and classification comparison analysis table for predictive analysis of 10 diseases

| Type of disease | Disease category | Classification and comparison |
|-----------------|------------------|-----------------------------|
|                 | 0 1 2 3 4 5 6 7 8 9 | Precision rate (%) | Recovery rate (%) | F1 (%) |
| D0              | 48 0 0 0 1 0 0 0 0 1 | 96.2 | 95.5 | 95.85 |
| D1              | 0 50 0 0 0 0 0 0 0 0 | 98.1 | 97.2 | 98.04 |
| D2              | 0 0 50 0 0 0 0 0 0 0 | 97.3 | 96.1 | 97.19 |
| D3              | 0 1 47 0 0 2 0 0 0 0 | 97.6 | 95.4 | 96.49 |
| D4              | 2 0 0 0 43 1 0 0 1 2 | 95.2 | 96.2 | 95.70 |
| D5              | 1 0 0 0 0 49 1 0 0 0 | 97.9 | 95.3 | 96.58 |
| D6              | 0 0 0 0 0 0 49 0 0 1 | 97.2 | 95.7 | 96.44 |
| D7              | 0 0 0 0 0 0 0 50 0 0 | 98.3 | 98.4 | 98.45 |
| D8              | 1 1 0 0 0 0 0 0 48 0 | 97.7 | 96.9 | 97.30 |
| D9              | 1 0 0 0 1 3 0 0 0 45 | 95.3 | 95.5 | 95.40 |
| (AVG)           |                 | 97.08 | 96.22 | 96.75 |

Note: D0-Rice blast; D1-Sheath blight; D2-False smut; D3-Bacterial leaf blight; D4-Brown spot; D5-Bacterial brown spot; D6-Bacterial leaf streak rice blast; D7-Sheath rot; D8-Narrow leaf streak; D9-Red blight

It can be seen from Table 3 that the model A is used to predict the test set samples, and a good prediction effect is achieved. The average accuracy rate is 97.08%, the recovery rate is 96.22%, and the F1 value is 96.75%, indicating that the method is effective and feasible. The three diseases with the lowest F1 values are rice blast, flax spot and red blight. Mainly because these three diseases have many similarities in shape and color, they will affect the classification of diseases, resulting in lower F1 values.

4. Conclusions

In view of the fact that traditional classification and recognition methods rely heavily on image specific features and the recognition effect is not ideal, this study uses transfer learning to establish a disease recognition model based on the VGG16 architecture. This model is used to simulate 10 rice diseases and compare with other 2 the methods are compared and analyzed, and the following conclusions are obtained:

1) Using three recognition models to carry out simulation experiments, and analyze the classification and recognition accuracy and complexity of different models respectively. The results show that the classification and recognition accuracy of the three diseases are all above 95%, and the recognition effect of model A is the best, the average accuracy rate is 97.19%, and the balanced F score is 96.75%; Model A has the fastest prediction speed, reaching 175 samples per second.

2) Perform a simulation analysis on the performance of Model A. The training accuracy and prediction accuracy did not fluctuate greatly. After 100 trainings, the training and prediction accuracy reached 96% or more, indicating that the model is stable.

3) Using Model A to predict 10 rice diseases. From the experimental results, the average accuracy rate is 97.08%, the recovery rate is 96.22%, and the F1 value is 96.75%, indicating that the method is effective and feasible. The study found that the F1 value of the three diseases of rice blast, flax spot and red blight was low. This is because the three diseases have many similarities in shape and color,
which affects the classification effect of the diseases.

The study found that diseases with similar characteristics are easily misidentified, which reduces the recognition effect of the model. Therefore, how to collect a large number of high-resolution samples, obtain the typical characteristics of the disease, and use image processing technology to cut and separate, so that the disease model can extract the high-level recognition features of the image is an urgent problem to be solved. How the image recognition technology can effectively identify diseases in the natural environment and improve the practicability of the model is a topic worthy of study. At present, there are also researchers studying this. For example, the researcher Wang Zhen uses the UAV platform as image collection, processing and recognition, and his white ear recognition rate can reach 93.62%, and the false recognition rate is 5.44%, realizing accurate recognition of the diseased area in the natural environment [20]. This also provides an effective path for how to effectively identify diseases in the natural environment.

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