

Image recognition of four rice leaf diseases based on deep learning and support vector machine



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ABSTRACT

In the field of agricultural information, identification and prediction of rice leaf diseases has always been a research focus. Deep learning and support vector machine (SVM) technology are hot research topics in the field of pattern recognition at present. Their combination can not only solve the problem effectively, but also improve the recognition accuracy. In this study, firstly, we use convolution neural networks (CNNs) to extract the rice leaf disease images features. Then the SVM method is applied to classify and predict the specific disease. The optimal parameters of SVM model are obtained through the 10-fold cross validation method. The experimental results show that when the penalty parameter $C = 1$ and the kernel parameter $g = 50$, the average correct recognition rate of the rice disease recognition model based on deep learning and SVM is 96.8%. This accuracy is higher than that of the traditional back propagation neural networks models. This study provides a new method for the further research of crop diseases diagnosis by using deep learning.

1. Introduction

Rice, wheat and maize are the three major food crops in the world (Li, 2004). Among them, rice has the most sown area, the largest total yield and the highest yield per unit in China which has become one of the main grains of Chinese people. China's cultivated area accounts for about a quarter of the country's arable land, and the annual output accounts for half of the country's total grain output. For more details, we refer readers to the paper (Kavya et al., 2016; Pragati and Surekha, 2017; Yi and Deng, 2017; Shen et al., 2019; Ma and Wang, 2004; Lu et al., 2017). It has been estimated that there will be more than nine billion people in the world by 2050 (Godfray et al., 2010). Nevertheless, rice diseases have been seriously affecting rice production. Consequently, it is a big challenge for the agricultural community to ensure the food security of such a large population. During the growth of rice, many diseases are often accompanied, such as rice blast, sheath blight, jute leaf spot, rice curl disease, bakanae disease, bacterial leaf blight, and bacterial leaf streak disease. These diseases occur in every part of

rice, such as leaf, neck, and ear. Among them, rice blast, red blight, stripe blight and sheath blight are the four diseases with the largest occurrence probability and the widest influence.

Diseases will not only lead to production reduction, but also bring environmental pollution. When rice is attacked by diseases, they will seriously affect the yield of crops. Among them, a loss of 10–15% in rice production are caused by rice plant diseases (Peng et al., 2009). In serious cases, it can reach 40–50% or even no income, which will bring huge economic losses to the farmers who have worked hard for a year. However, farmers generally do not know enough about the diseases of rice or even crops, so they can not fully understand the occurrence of each disease and the specific characteristics of the disease spots, and thus can not judge the disease and apply medicine in time. As a result, too much, too little or even wrong medicine will be used, which will delay the treatment of disease and damage the soil and the environment. Therefore, it is very important to find the disease and identify the disease type as soon as possible.

In general, detection of rice plant diseases is based either on the

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visual assessment of the symptoms or the experimental result by culturing pathogens in the laboratory. The visual assessment is a subjective approach and prone to error. Whereas, culturing the pathogens in the laboratory is a time-consuming process and may not provide the result in time (Barbedo, 2013). Besides these limitations, both the conventional approaches require experts to identify the diseases and it is difficult for farmers to get access to experts due to the interior region of their agriculture field. These issues have prompted the research community to investigate various algorithms and develop automatic methods to detect and classify rice plant diseases, and simultaneously motivates the farmers to decide and choose the right pesticides.

With the development of computer and internet technology, recognition methods based on image processing and pattern recognition technology constantly emerge (Lai et al., 2009; Rahul et al., 2016; Kavya et al., 2016; Li et al., 2013; Pragati and Surekha, 2017). The main research fields include rice disease image acquisition methods, disease image preprocessing methods, feature extraction and optimization of disease spot image, and establishment of rice disease automatic recognition modeled by Bayesian classifier, back propagation neural network, support vector machine (SVM) and other methods (Tharwat et al., 2018; Dey et al., 2017; Guan, 2018; Qiu et al., 2019).

In recent years, digital image processing technology is becoming more and more mature and has been widely used in many fields which promotes the new development of these disciplines. The applications in the field of agriculture mainly includes the identification and diagnosis of crop diseases, pests and weeds (Burks et al., 2000; Gea et al., 2008; Sgaard, 2005), the identification and diagnosis of crop deficiency disease (Mao et al., 2005), the classification and inspection of crop seed quality (Zayas and Flinn, 1998; Steenhoek et al., 2001), the quality detection and classification of agricultural products (Fang et al., 2004), and some results have been achieved. Image processing technology is widely used in agriculture, especially in crop disease recognition which mainly includes the identification of leaf diseases of corn, rice, eggplant and other crops, fruit diseases of cucumber, tomato and other fruits, and common diseases of cashmere cotton, sunflower, tea, tobacco and other economic crops.

At present, many experts and scholars have used the technology of deep learning and SVM to identify and study the rice and general plant diseases. Ze-xin Guan (Guan et al., 2010) has used the image processing technology and the pattern recognition technology to respectively segment the rice disease images and extract the classify features, and a rice disease recognition system has been established. Through the analysis of the experimental results, it is concluded that this system has a better recognition performance. You-wen Tian et al. (Tian and Li, 2006) have studied the recognition of cucumber and corn diseases by using SVM, and have achieved good recognition results. Taking the wheat total erosion disease as the research object, Fu Wei (Fu, 2015) has used the unmanned aerial vehicle to take the wheat disease images and carried on the pretreatment and the characteristic parameter extraction of the collected disease images. Then, the disease degree of wheat total erosion disease has been obtained by comparing the color characteristic parameters. R. Pydipati et al. (Pydipati et al., 2006) have employed color co-occurrence method to determine texture-based hues. Saturation and intensity (HSI) color features combined with statistical classification algorithm have been used to identify diseases and normal citrus leaves under laboratory conditions. Yun-lan Tan et al. (Tan et al., 2019) have used the deep convolution network to establish the rice disease identification model to classify and identify eight kinds of rice diseases, of which the accuracy of sheath blight is 93%. Bo et al. have taken the image of vegetable and fruit diseases as the research object, then the image processing technology, the deep learning method and the convolution neural network (CNN) have been respectively used to preprocess the image, improve the recognition rate of the vegetable and fruit image and build the recognition model so as to accomplish the image recognition task (Bo et al., 2018). Shen Wei Zheng et al. (Shen et al., 2019) have studied the automatic identification method of rice

blast, sheath blight and bacterial leaf blight based on BP neural network. The parameters have been optimized by using the single factor analysis of variance and the effect of BP neural network model. The results have shown that the model has a good recognition performance.

Although the main methods used in the above studies include some traditional analysis methods, most of them still use a combination of multiple methods or propose a new research method. In pattern recognition, linear classifier based on statistics (Yusako et al., 2001a), Bayesian decision theory, artificial neural network (Pydipati et al., 2005; El-Faki et al., 2000; Ma and Wang, 2004), fuzzy recognition technology (Mohamed et al., 2006; Vioix et al., 2004; Qiu et al., 2002) and SVM (Tian et al., 2006) are widely used. At present, rice disease recognition based on digital image has become a research hotspot (Barbedo, 2013). Recently, CNN has also been applied to rice plant disease classification (Lu et al., 2017). Yong-gang Shi et al. (Shi et al., 2018) have proposed a segmentation method based on CNN and SVM to get the segmentation of hippo image. They use SVM to replace the output layer of CNN. The model can automatically extract image block features by training deep-seated network, then use the extracted image features to train SVM to improve image classification. The experimental results show that the segmentation accuracy of each region is greatly improved. In this study, in order to extract the effective feature parameters of rice disease images and establish the foundation of disease recognition system, we use mean shift method to separate the normal and abnormal parts of leaves so as to simplify the difficulty of image processing and further improve the processing speed. The motivation of using the mean-shift method as image segmentation method is that the area of the extracted spots is larger than that of the artificial threshold extraction. However, the existing image segmentation technology based on mean shift algorithm is not perfect, and the segmentation results are not stable. Therefore, a disease recognition model combining CNN and SVM is proposed to improve the recognition accuracy.

There are two main motivations to study the image recognition models of four rice diseases. (1) So far, this is still a challenge, and is becoming the main focus of rice disease recognition research. In order to obtain satisfactory disease recognition rate, this paper applies CNN and SVM to rice disease recognition. (2) According to the difference of rice disease spots, the mean shift algorithm and CNN are used to extract the optimal feature parameters.

There are two main contributions of this paper. (1) Aiming at the identification of four rice diseases, a new algorithm which combines CNN with SVM proposed in this paper. It is worth noting that the model can correctly and effectively identify rice diseases. (2) The experimental results show that the best combination of features and the best parameters of the model can not only improve the convergence speed, but also have higher recognition accuracy than the classical models such as feature extraction and disease recognition directly using CNN.

2. Materials and methods

2.1. Dataset

Rice leaf disease images used in this paper were taken in rural farmland by the Canon 660D digital camera in 2019, and some images were obtained by rice leaf disease atlas. In total, the rice leaf dataset contains 8911 images including 2274 images of healthy rice, 1634 images of rice blast, 1765 images of rice bacterial spot, 1678 images of rice streak leaf spot and 1560 images of rice sheath blight. Then, 6637 images of disease rice were clipped by manual clipping, which includes one or more sub-images whose size depends on the area of rice leaf lesions.

2.2. Image preprocessing

In this paper, we use the mean shift image segmentation algorithm (Liu and Chen, 2018; Zhao and Chen, 2018) to separate lesions from rice leaf disease images so that we can extract features of rice leaf lesion

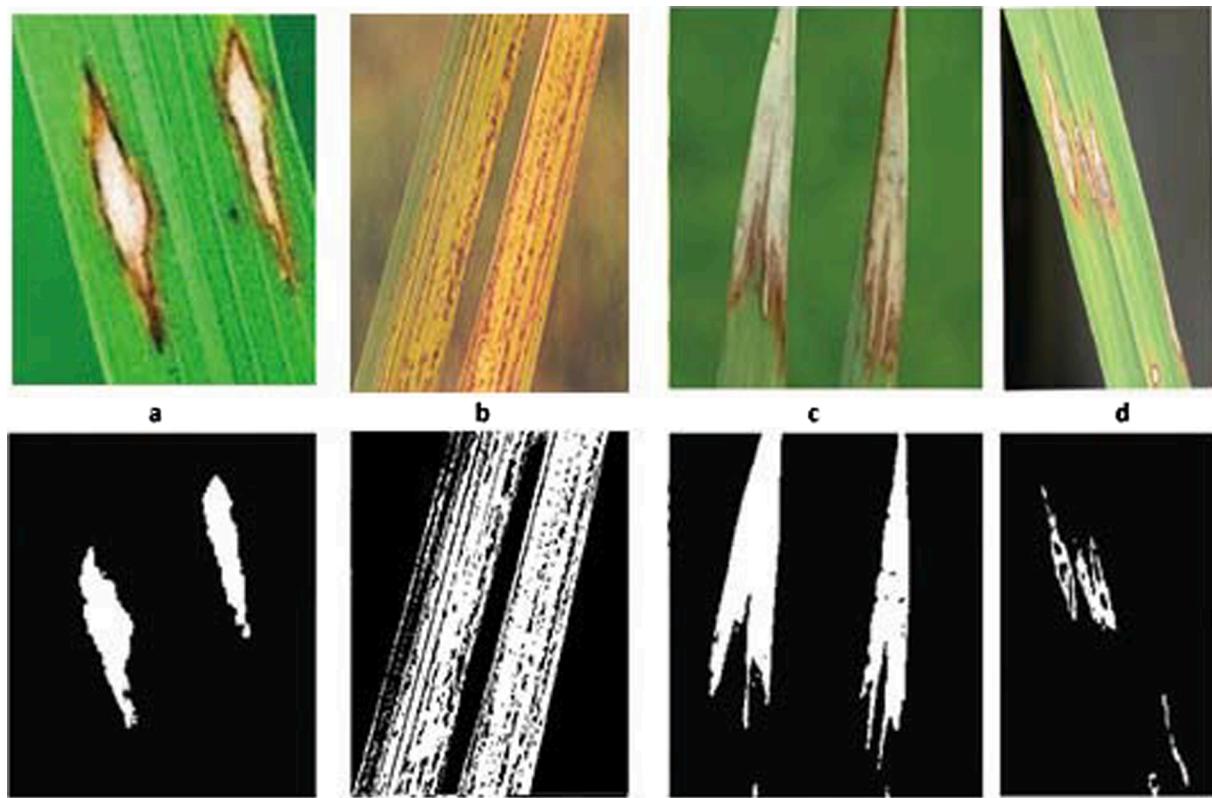


Fig. 1. Four rice leaf diseases images and corresponding segmentation images. a: rice blast b: red blight c: stripe blight d: sheath blight.

images. This method has better segmentation results than the traditional threshold segmentation method. The purpose of the image segmentation algorithm mainly includes two aspects: (1) It can not only remove more background noise of the lesion image, but also improve the quality of the image, so as to improve the accuracy of recognition. (2) It can reduce the amount of data, thus reducing the running time of the program. In order to reduce the running time of the program and improve the recognition efficiency of the program, the sizes of the rice disease images are compressed from 5213 * 3246 to 800 * 600. In this paper, the mean shift image segmentation algorithm is used to segment the sub-images obtained by artificial clipping. Firstly, cluster all pixels. Secondly, all the pixels converging to the same maximum value are classified. Finally, all the classes that meet the parameter conditions are merged. In order to ensure the accuracy of the experiment, the segmentation will be further completed through mean shift filtering, pre-segmentation and accurate segmentation (Song et al., 2006). The segmentation results of four kinds of rice leaf diseases are shown in Fig. 1.

From the images of leaf lesions of rice blast, red blight, stripe blight and sheath blight, we see that their colors and shape characteristics are different. The shape features of lesion images are extracted by artificial calculation method, and the color features are extracted by CNNs.

2.3. Shape feature extraction

In this paper, we select traditional shape features such as area, roundness and shape complexity. The purpose is to distinguish the shape characteristics of four kinds of rice leaf lesions effectively. Then, according to the images of lesion segmentation, we can get three new shape features: the number of lesions N , the area of lesions S and the ratio R of the number of lesions. The formula for calculating lesions area S is defined as Eq. (1).

$$S = \sum_{x=1}^n \sum_{y=1}^m f(x, y) \quad (1)$$

where n, m is the image coordinate value, $f(x, y)$ is a binary image function. The formula for calculating the roundness C of lesions is defined as Eq. (2).

$$C = d_{max} - d_{min} \quad (2)$$

where d_{max}/d_{min} are the maximum/minimum diameters of the cross section of lesions. The calculation formula of shape complexity E is defined as Eq. (3).

$$E = \frac{4\pi}{C} \quad (3)$$

The number of lesions N is obtained by the region pixel jump detection method. The ratio of lesion area to the number of lesions R is defined as Eq. (4).

$$R = \frac{S}{N} \quad (4)$$

The CNN algorithm (Palm, 2012) is implemented by using the deep learning matlab toolbox¹ developed by Palm, and the shape feature extraction algorithm of four rice disease spots is studied. The shape feature extraction effect of four kinds of rice leaf lesions are shown in Fig. 2.

According to the above formulas, five shape eigenvalues of four rice leaf lesions are calculated, including area, roundness, shape complexity, number of lesions and ratio of lesion area to number of lesions. The results are shown in Table 1.

As shown in Table 1, each group of same eigenvalue data is drawn into a curve. There is no cross or overlapping part in the data, which indicates that the shape features are quite different, which can be used as

¹ <https://github.com/rasmusbergpalm/DeepLearnToolbox#deeplearntoolbox>.

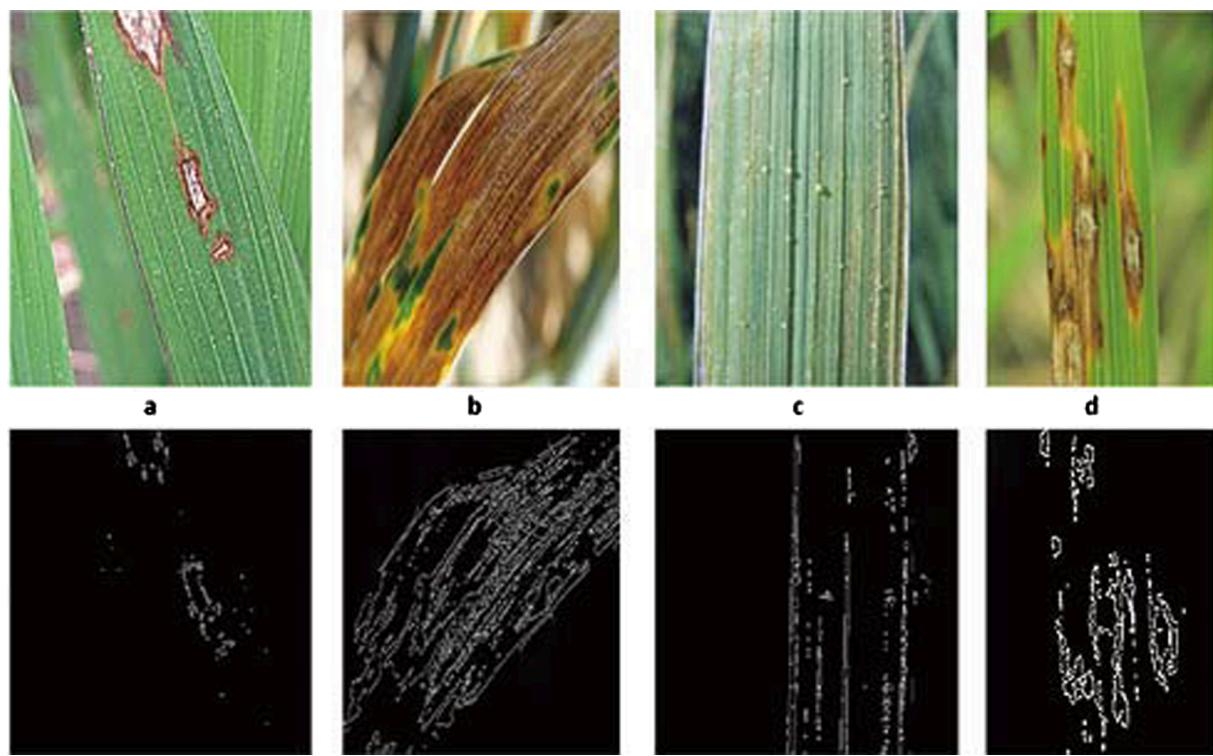


Fig. 2. Four rice leaf diseases images and corresponding feature extraction images. a: rice blast b: red blight c: stripe blight d: sheath blight.

Table 1
Shape characteristics of leaf lesions.

| Disease type | Area | Roundness | Shape complexity | Number of disease | Area to number ratio |
|---------------|-------|-----------|------------------|-------------------|----------------------|
| Rice blast | 82.2 | 3.0 | 8.6 | 3 | 27.4 |
| Red blight | 193.1 | 2.0 | 26.1 | 10 | 19.3 |
| Stripe blight | 102.3 | 3.1 | 25.3 | 41 | 2.5 |
| Sheath blight | 13.9 | 5.3 | 6.6 | 52 | 0.3 |
| Rice blast | 76.0 | 11.4 | 7.2 | 4 | 19.0 |
| Red blight | 236.1 | 1.7 | 34.5 | 13 | 19.7 |
| Stripe blight | 152.2 | 5.2 | 12.6 | 24 | 6.3 |
| Sheath blight | 23.6 | 5.1 | 4.5 | 58 | 0.4 |
| Rice blast | 68.1 | 12.3 | 7.3 | 2 | 34.1 |
| Red blight | 215.3 | 4.2 | 43.2 | 13 | 17.9 |
| Stripe blight | 120.4 | 4.1 | 16.2 | 36 | 3.3 |
| Sheath blight | 39.2 | 8.2 | 5.2 | 53 | 0.7 |
| Rice blast | 149.2 | 8.2 | 6.5 | 4 | 37.3 |
| Red blight | 84.1 | 3.1 | 36.6 | 9 | 9.3 |
| Stripe blight | 93.1 | 4.2 | 15.2 | 35 | 2.7 |
| Sheath blight | 49.2 | 3.5 | 4.7 | 43 | 1.0 |
| Rice blast | 74.1 | 5.6 | 8.3 | 4 | 18.5 |
| Red blight | 158.9 | 4.2 | 42.1 | 14 | 11.4 |
| Stripe blight | 93.1 | 3.7 | 16.4 | 37 | 2.5 |
| Sheath blight | 50.0 | 6.8 | 7.3 | 50 | 0.8 |

parameters to distinguish rice shape features. Therefore, we choose the area of lesions, the number of lesions and the ratio of the number of lesions as the shape characteristic parameters to distinguish four kinds of rice leaf lesions.

2.4. Color feature extraction

Spot color is one of the important criteria for agricultural experts to identify rice diseases (Su et al., 2018). Therefore, in the machine learning model of rice disease classification based on image, color can be used as the distinguishing feature. Ai-ping Yang et al. (Yang et al., 2019) have provided a more intuitive way to separate colors. In this paper, we extract the color feature of lesion images in *RGB*, *HSI* and *YCbCr* color space respectively so as to distinguish the color feature. Firstly, the size of the segmented rice lesion images is normalized to 64 * 64 pixels. Secondly, the *RGB* color space of all lesion images is converted into *HSI* and *YCbCr* color space. The conversion formula is as follows. The gray scale image of the disease spots with nine color components (*R*, *G*, *B*, *H*, *S*, *I*, *Y*, *Cb* and *Cr*) is obtained. Finally, the structure and weight of CNN are determined to train and extract the features of the lesion image.

$$N_r = \frac{R}{R + G + B} \quad (5)$$

$$N_g = \frac{G}{R + G + B} \quad (6)$$

$$N_b = \frac{B}{R + G + B} \quad (7)$$

The *RGB* color components *R*, *G*, *B* were converted to *N_r*, *N_g* and *N_b*. *N_r*, *N_g* and *N_b* are defined as Eq. (5), Eq. (6) and Eq. (7), where *N_r*, *N_g* and *N_b* represent the normalized values of *R*, *G* and *B*, respectively.

$$Y = 16 + (0.275 * R + 0.504 * G + 0.09 * B) \quad (8)$$

$$Cb = 128 + (-0.148 * R - 0.291 * G + 0.439 * B) \quad (9)$$

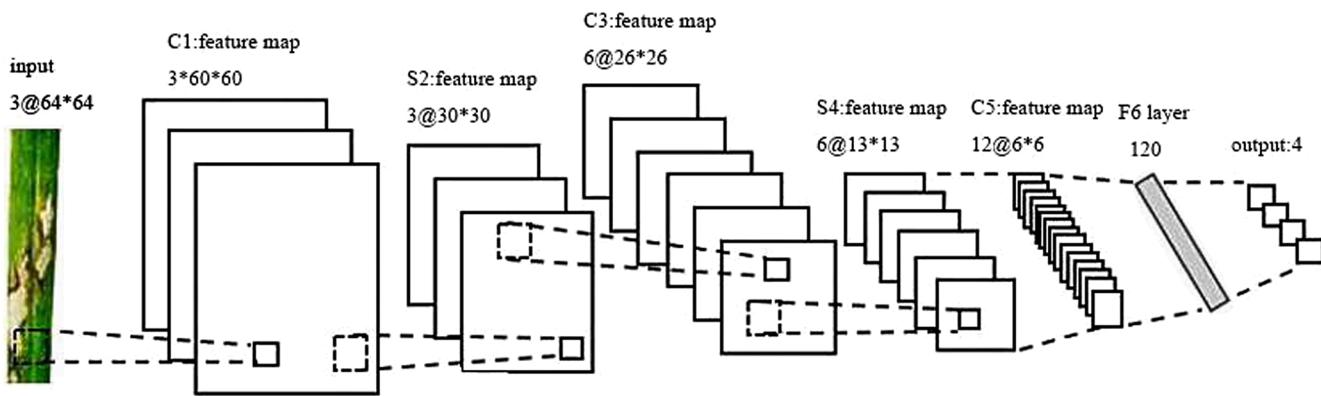


Fig. 3. The structure of convolutional neural networks.

$$Cr = 128 + (0.439*R - 0.368*G - 0.071*B) \quad (10)$$

The conversion equation of *RGB* to *YCbCr* is defined as Eq. (8), Eq. (9) and Eq. (10), where *Y*, *Cb*, *Cr* represent the luminance, blue-difference chrominance and red-difference chrominance components, respectively.

$$H = \begin{cases} \theta_{rgb} & \text{if } B \leq G \\ 360 - \theta_{rgb} & \text{if } B > G \end{cases} \quad (11)$$

$$S = 1 - \frac{3}{(R + G + B)} \quad (12)$$

$$I = \frac{1}{3}(R + G + B) \quad (13)$$

The conversion equation of *RGB* to *HSI* is defined as Eq. (11), Eq. (12) and Eq. (13). where $\theta_{rgb} = \cos^{-1} \left\{ \frac{\sqrt[3]{[(R-G)+(R-B)]}}{\sqrt[2]{[(R-G)^2+(R-G)(R-B)]}} \right\}$. The *HSI* color components *H*, *S* and *I* represent the hue, saturation and intensity, respectively.

2.5. Convolutional neural networks and model design

The CNNs structure is divided into seven layers, including input layer, convolution layer C1, sub-sampling layer S2, convolution layer C3, sub-sampling layer S4, convolution layer C5 and feature layer F6. In this study, we input 64 * 64 pixel lesion images in the input layer. In the layer C1, the convolution kernels are used to convolute the input images of the input layer and six feature maps are obtained. Each neuron in the feature graphs is connected to the neighborhood of the input images of 5 * 5. The size of the feature graphs is 60 * 60 pixels. Its advantage is that it can effectively prevent input connections from falling out of boundaries.

The S2 layer is a sub-sampling layer. Six feature maps of the layer C1 are pooled in the layer S2. Then, six feature maps with 30 * 30 pixels are obtained. Each unit in the feature graphs is connected to the 2 * 2

neighborhood of the corresponding feature graphs in the S1 layer. The four inputs of each unit in the S2 layer are added together, multiplied by a trainable parameter, then add a trainable bias. Because the 2 * 2 receptive fields of each cell do not overlap, the size of each feature map in the S2 layer is a quarter of that in the C1 layer.

The C3 layer is also a convolution layer that calculates the convolution from the S2 layer through the convolution core and obtains sixteen feature maps. The size of each feature map in the C3 layer is 26 * 26 pixels, in which the connection between the layer C3 and the layer S2 is full-link.

The S4 layer is a sub-sampling layer. Sixteen feature maps of the layer C3 are pooled and sixteen feature maps of the layer S4 are obtained. Each unit in the feature graph is connected to the 2 * 2 neighborhood of the corresponding feature graphs in the C3 layer, as the connection between the C1 layer and the S2 layer. Sixteen feature maps of the layer S4 are convoluted by using convolution kernels, and sixteen feature maps of the layer C5 are obtained.

The size of each feature maps in the C5 layer is 6 * 6 pixels. Sixteen feature map in the C5 layer are converted into column vectors of 1 * 2048. The F6 layer takes the eigenvector as the input of the CNNs, and outputs the result of disease identification through the Sigmoid excitation function. The initial weights of the networks are generated randomly and then adjusted by the back propagation algorithm.

In this paper, the learning rate of CNNs is fixed to 0.1, and the weights of the networks are adjusted once every sixty samples calculated, and the number of iterations is set to 100.

The structure of the CNNs model for rice disease identification designed in this paper is shown in Fig. 3.

3. Results and analysis

A total of 6637 disease images and 2274 healthy images were obtained by image feature extraction and segmentation. Effective disease spot images were divided into training set and testing set. Among them, 4757 lesion images are trained including 2017 images of healthy rice,

Table 2
Classification result of diseases based on color parameters.

| Color features | Number of disease | | Number of health | | Recognition accuracy of the Training set(%) | Recognition accuracy of the Testing set (%) |
|----------------|-------------------|-------------|------------------|-------------|---|---|
| | Train number | Test number | Train number | Test number | | |
| <i>R</i> | 279 | 164 | 257 | 28 | 93.40 | 90.00 |
| <i>G</i> | 313 | 165 | 201 | 40 | 75.29 | 72.10 |
| <i>B</i> | 353 | 223 | 283 | 30 | 96.30 | 92.35 |
| <i>H</i> | 272 | 182 | 122 | 18 | 82.48 | 80.24 |
| <i>S</i> | 264 | 166 | 126 | 6 | 76.83 | 74.32 |
| <i>I</i> | 271 | 204 | 104 | 12 | 95.39 | 92.00 |
| <i>Y</i> | 295 | 166 | 306 | 26 | 82.36 | 80.51 |
| <i>Cb</i> | 282 | 147 | 293 | 28 | 73.00 | 69.37 |
| <i>Cr</i> | 411 | 206 | 325 | 69 | 94.00 | 92.49 |

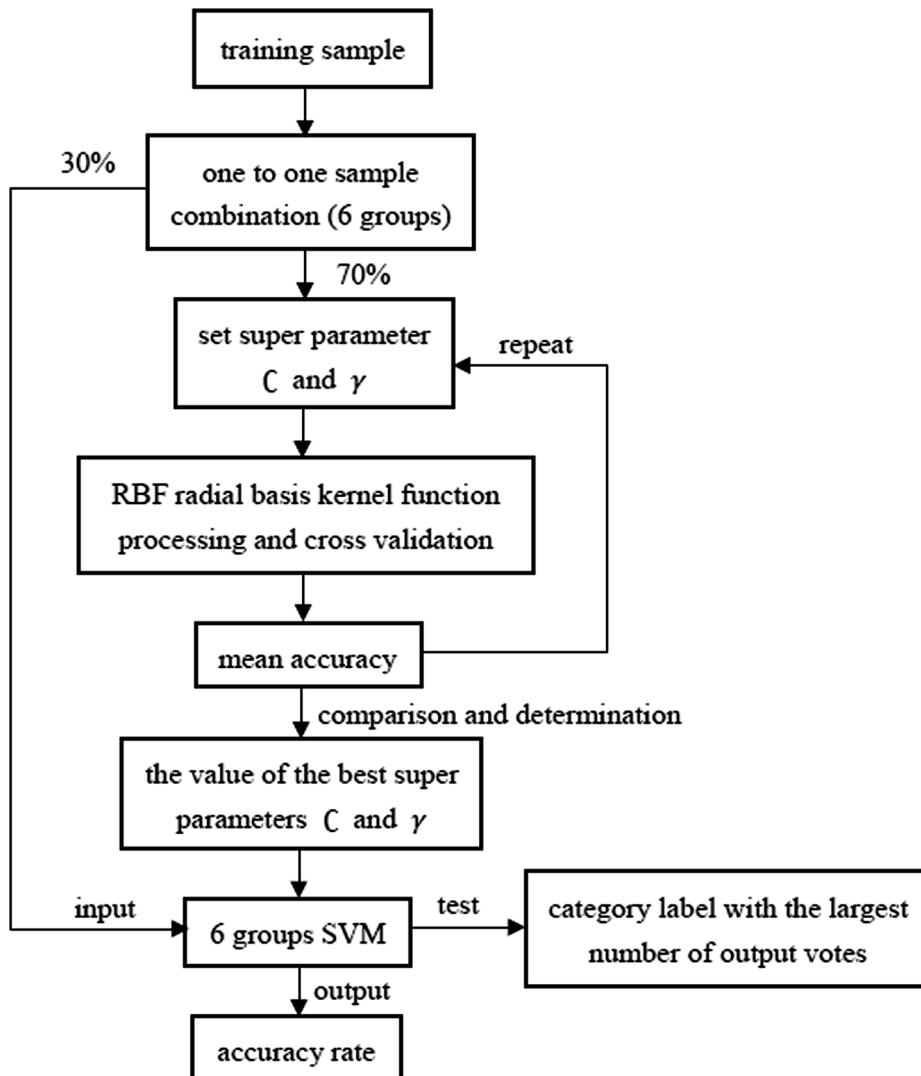


Fig. 4. The flow-chart of SVM applied to multi-classification Problems.

693 lesion images of rice blast leaf, 780 lesion images of red blight leaf, 705 lesion images of stripe blight leaf and 562 lesion images of sheath blight leaf. 1880 lesion images are tested including 257 images of rice healthy, 356 lesion images of rice blast leaf, 444 lesion images of red blight leaf, 428 lesion images of stripe blight leaf and 395 lesion images of sheath blight leaf. In this paper, the feature extraction of leaf lesion images is carried out by CNNs with gray level images of nine color components including R , G , B , H , S , I , Y , Cb and Cr . The recognition results of color feature extraction from lesion images based on CNNs are shown in Table 2.

Table 2 shows that R component and B component in RGB space, I component in HSI space and Cr component in $YCbCr$ space can be used as color characteristic parameters to identify four kinds of rice leaf lesions.

According to the results of extracting the shape and color feature parameters mentioned above, seven features are selected as the input direction of multi-class SVM, including three shape features (i.e., the area of lesions, the ratio of the number of lesions and the area of lesions) and four color features (i.e., the R and B components in RGB space, the I component in HSI space and the Cr component in $YCbCr$ space).

4. Establishment of disease image recognition model

4.1. Support vector machine

In this paper, SVM replaces softmax as the model output for the final classification task for four reasons: (1) In order to solve the problem of using softmax as CNN classifier in image classification task, the generalization ability of the model is insufficient, which can not adapt to rice image classification. In this paper, we make full use of the advantage of CNN to extract features automatically, and use SVM to replace softmax classification function to enhance the robustness and generalization of the model. (2) Due to the small number of sample images, and SVM has a better solution to small samples, nonlinear, high-dimensional and local minima learning problems(Burges, 1998). (3) Because of the penalty parameter in SVM, some redundant features can be removed and the classification effect can be improved. (4) Yi-chuan Tang (Tang, 2013) has used SVM to replace softmax layer to train the deep neural network. Experimental results show that SVM works better than softmax in facial expression recognition challenges of popular deep learning data sets MNIST, cifar-10 and the ICML 2013 Representation Learning Workshop face expression recognition challenge. So SVM is used as the final classifier. Radial basis function is used as the kernel function of the SVM, and the recognition results are compared and analyzed by choosing different penalty parameter C and kernel function parameter g . Thus, the

Table 3

Identification results of four rice diseases under the condition of parameter $C = 1$ and $g = 50$.

| Disease types | Identify the results | | Recognition accuracy of the training set(%) | Recognition accuracy of the testing set (%) |
|---------------|----------------------|-------|---|---|
| | C | g | | |
| Rice blast | 1.00 | 50.00 | 93.85 | 86.34 |
| Rice blast | 0.472 | 50.00 | 73.23 | 64.20 |
| Rice blast | 320.47 | 50.00 | 69.40 | 71.35 |
| Rice blast | 0.472 | 50.00 | 92.74 | 90.38 |
| Red blight | 4.00 | 50.00 | 76.83 | 74.32 |
| Red blight | 5.62 | 50.00 | 79.54 | 71.38 |
| Red blight | 4.00 | 50.00 | 82.56 | 80.41 |
| Red blight | 1.00 | 50.00 | 90.43 | 88.34 |
| Stripe blight | 50.00 | 50.00 | 84.00 | 78.22 |
| Stripe blight | 0.472 | 50.00 | 84.10 | 82.21 |
| Stripe blight | 1.00 | 50.00 | 95.30 | 92.39 |
| Stripe blight | 50.00 | 1.00 | 36.74 | 33.70 |
| Sheath blight | 5.62 | 50.00 | 75.43 | 72.57 |
| Sheath blight | 5.62 | 50.00 | 77.90 | 75.23 |
| Sheath blight | 1.00 | 50.00 | 88.49 | 85.00 |
| Sheath blight | 4.00 | 50.00 | 82.56 | 80.41 |

Table 4

Performance comparison of CNN with and without image segmentation algorithm.

| Model | Testing accuracy |
|--------------------------------|------------------|
| CNN with image segmentation | 92.75% |
| CNN without image segmentation | 82.26% |

optimal parameters of the SVM model for rice leaf disease identification are determined. SVM is applied to multi-classification problems. There are total four kinds of rice diseases, one SVM is designed between any two kinds of samples, and six SVMs are designed. The flow-chart is shown in Fig. 4.

4.2. Parameter determination

In this paper, grid search algorithm is used to compare the recognition accuracy under different combinations of penalty parameter C and kernel function parameter g , and then the optimal model parameters of SVM are determined. Penalty parameter C and kernel function parameter g all traverse all points in the grid with 0.1 as search step. For the training set to calculate three times of cross validation recognition accuracy, select the C value and g value when the recognition accuracy is the highest as parameters of SVM model, and record them as C_{best} and g_{best} respectively. The results are shown in Table 3. Table 3 shows that when $C = 1$, $g = 50$, the SVM has the best recognition results for four rice leaf diseases, which indicates that $C = 1$, $g = 50$ are the best model parameters of the SVM.

4.3. Experimental results

The proposed model is executed for 4757 training data followed by 1880 test data and the accuracy of training set is 98.79% and the test accuracy of 96.8%. In order to evaluate the performance of the proposed

Table 5

Performance comparison of CNN with and without SVM.

| Model | Testing accuracy |
|-----------------|------------------|
| CNN with SVM | 96.8% |
| CNN without SVM | 84.52% |

Table 6

Recognition accuracy of different models

| Model | Testing accuracy |
|-----------|------------------|
| CNN + SVM | 96.8% |
| AlexNet | 93.79% |
| VGG | 91.65% |

input → C1 → S2 → C3 → S4 → C5 → F6

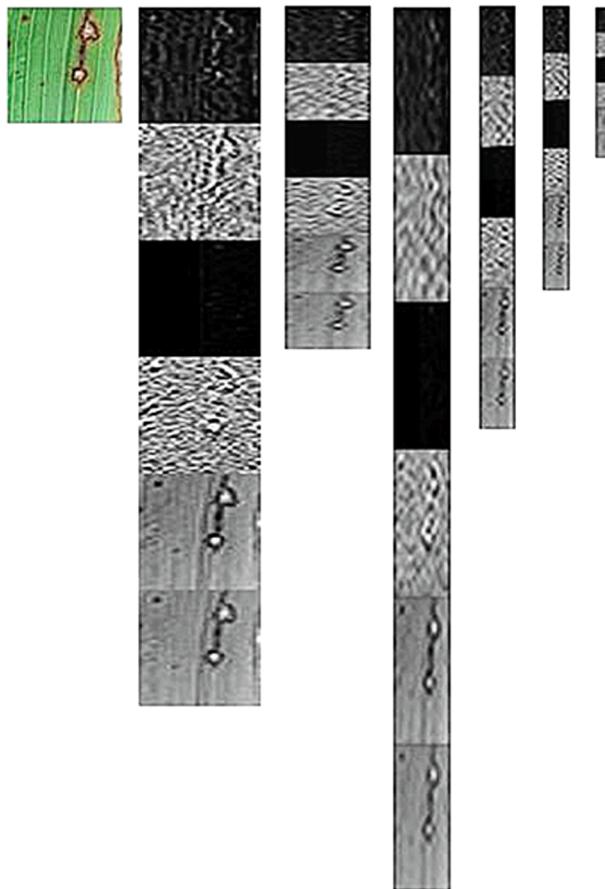


Fig. 5. Model output characteristic diagram.

model, we also implement a traditional CNN model without using image segmentation technology and SVM. The same data is executed on the CNN model, and it is trained, verified and tested without image segmentation technology and SVM. Table 4 shows the accuracy comparison of the proposed CNN model with Mean-Shift image segmentation algorithm and CNN without Mean-Shift image segmentation algorithm. It can be seen from the Table 4 that the accuracy of the CNN model using Mean-Shift image segmentation algorithm is 92.75%, while the accuracy of the CNN model without Mean-Shift image segmentation algorithm is 82.26%. It can be concluded that the proposed CNN combined with image segmentation technology can achieve higher accuracy. Compared without image segmentation technology, CNN combined with image segmentation technology has the best effect. Table 5 shows the accuracy

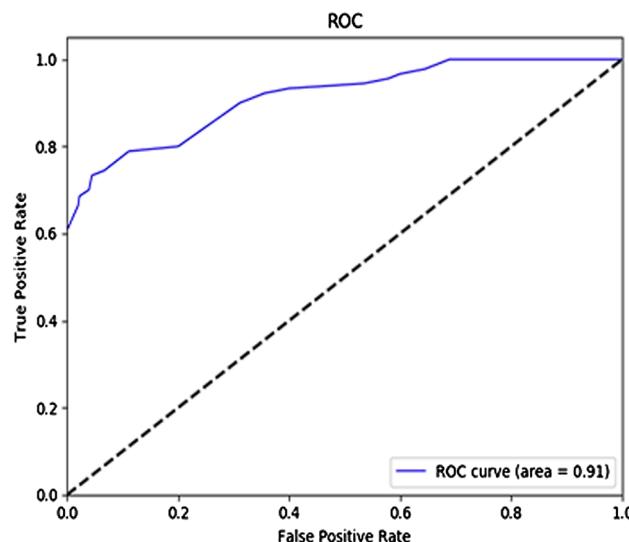


Fig. 6. ROC curve.

values of the two models during testing. The experimental results show that the accuracy of CNN combined with SVM model is 96.8%, and that of traditional CNN model is 84.52%. After that, we use the model proposed in this paper to compare with VGG and AlexNet models, and execute the same data for VGG and AlexNet models. The experimental results are shown in the Table 6. Table 6 shows the accuracy comparison of the proposed CNN model with VGG and AlexNet models. It can be seen from the Table 6 that the accuracy of the proposed CNN model is 96.8%, AlexNet model is 93.79%, and VGG model is 91.65%. It can be seen that the proposed model achieves the highest accuracy in the identification of rice leaf diseases, which demonstrates the effectiveness of the proposed model.

In this paper, the output characteristics of each layer of the model are shown in Fig. 5. It shows that the characteristics of rice leaf diseases extracted by this model are more obvious. Also, it shows that the model can effectively extract image features through local receptive fields and weight sharing, and has a certain translation invariance. Due to the fact that there are often class imbalances in the actual data set, there are more negative samples than positive samples (or vice versa), and the distribution of positive and negative samples in the test data may change with time. In this case, the receiver operating characteristic (ROC) curve can remain unchanged, so ROC is selected as the evaluation index of the model. As the value under the ROC curve, the area under curve (AUC) can directly evaluate the classifier. The higher the AUC value, the better the classification model. The calculation formula is defined as Eq. (14). The receiver operating characteristic curve of the model is shown in Fig. 6. From the trend of the curve, it can be seen that the model has good recognition performance. The results show that the disease recognition model proposed in this paper can effectively extract the implicit feature information in the dataset so as to achieve a better recognition result.

$$AUC = 1 - \frac{\sum_{i \in \text{positiveClass}} rank_i - \frac{M(1-M)}{2}}{M * N} \quad (14)$$

where M is the number of positive samples, N is the number of negative samples. The value of $rank$ represents the number of such combinations that can produce a positive sample.

The recognition results of the established disease identification model are shown in Table 7. The Table 7 shows that five of 257 rice health images were mistaken for sheath blight and three were mistaken for rice blast. The causes may be poor lighting and blurred images. Seven out of 356 rice blast images were mistaken for sheath blight, because the color and shape characteristics of early rice blast lesions were very similar to those of rice sheath blight, and the extracted characteristics of rice sheath blight lesions were similar, and three images were mistaken for health images. In order to ensure the normality of the images, there are some errors in the segmentation process, resulting in 15 images being mistaken for stripe leaf blight in 444 images of red blight lesions. Because the color and shape characteristics of 428 stripe leaf blight images were similar to those of rice blast, 7 images were mistaken for rice blast images, and 7 images were mistaken for health images. According to the identification of 395 images of rice sheath blight, 4 images were mistaken for stripe leaf blight disease and 8 images were mistaken for health images. The reason may be that there was stripe disease in the same rice leaf.

5. Conclusions

CNN is a valuable pattern recognition method both in theory and application. In this paper, the mean shift image segmentation method has been used to segment rice blast, red blight, stripe blight and sheath blight leaf lesion images. Based on the artificial calculation method and CNNs, the leaf lesions of four rice diseases have been extracted to determine the best combination of features. Then, SVM has been used to classify and recognize four kinds of rice leaf lesions under different parameters C and g . The experimental results have shown that when the parameter $C = 1$ and $g = 50$, the rice disease recognition rate based on deep learning and SVM is the highest, and the average correct recognition rate is 96.8%. In summary, the combination of deep learning and SVM can effectively identify rice leaf diseases and provide technical support for future crop fields.

CNN have achieved great performance breakthroughs in machine learning fields, but there still exists some research challenges. The first is that the CNNs may be composed of tens or hundreds of layers, each layer also includes thousands of neurons, how many layers and how many neurons are optimal at last. It has no choice but to rely on a great number of experiments. The second is that the efficient deep learning algorithm is still dependent on large-scale datasets. To improve rice diseases identification accuracy, we still need to provide thousands of high-quality rice diseases images samples. In future work, we plan to apply other deep architectures and other training algorithms which may achieve a better performance on recognition.

CRediT authorship contribution statement

Feng Jiang: Writing - original draft, Investigation, Software. Yang

Table 7
Identification results of four rice diseases $C = 1$ and $g = 50$.

| Classes | Number of Input Images | Identify the Results | | | | | Identify the Correct Number | Correct Recognition Rate (%) |
|---------------|------------------------|----------------------|------------|---------------|---------------|---------|-----------------------------|------------------------------|
| | | Rice blast | Red blight | Stripe blight | Sheath blight | Healthy | | |
| Healthy | 257 | 3 | 0 | 0 | 5 | 249 | 249 | 96.8 |
| Rice blast | 356 | 346 | 0 | 0 | 7 | 3 | 346 | 97.1 |
| Red blight | 444 | 0 | 429 | 15 | 0 | 0 | 429 | 96.6 |
| Stripe blight | 428 | 7 | 0 | 414 | 0 | 7 | 414 | 96.7 |
| Sheath blight | 395 | 0 | 0 | 4 | 383 | 8 | 383 | 96.9 |

Lu: Conceptualization, Supervision, Funding acquisition. **Yu Chen:** Methodology, Writing - review & editing, Project administration. **Di Cai:** Formal analysis, Visualization. **Gongfa Li:** Validation.

Declaration of Competing Interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

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Appendix A. Supplementary material

Supplementary data associated with this article can be found, in the online version, at <https://doi.org/10.1016/j.compag.2020.105824>.

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