

Rice Disease Image Recognition Based on Improved Multi-scale Stack Autoencoder

Jun Meng¹, Xingchen Lv¹, Lifang Fu¹ & Qiufeng Wu¹

¹ College of Arts and Sciences, Northeast Agriculture University, Hei Longjiang, China

Correspondence: Jun Meng, College of Arts and Sciences, Northeast Agriculture University, Hei Longjiang, China. Tel: 86-186-4511-6809. E-mail: 1135044376@qq.com; lvxingchen@neau.edu.cn

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Abstract

Recently, deep learning methods are widely used in the rice diseases identification. However, the actual image background of rice disease is complex, the classification performance is not ideal. Therefore, this paper proposed a multi-scale feature extraction method based on stacked autoencoder, named the multi-scale stacked autoencoder (MSSAE), to improve the recognition accuracy of rice diseases. This method extracts the complex rice disease image's features by two steps. In the first step, the images are preprocessed. Then, the MSSAE extract the multi-scale features through preprocessed rice diseases data in different scales. Through comparative analysis of experiments, the new method achieved greater than 95% precision in the detection of rice diseases. It indicated that the MSSAE model has an outstanding identification performance for actual crop disease image recognition.

Keywords: rice disease, image processing, stacked autoencoder, multi-scale features, image recognition

1. Introduction

Rice is one of the important food crops, and nearly half of the world's population takes rice as the main food (Meng, 2014). As a large agricultural country, China is also the country of origin of rice. Rice is one of the three major grain crops in China and occupies a large proportion in agricultural output (Chen, 2016). However, due to its own characteristics and the impact of its growing environment, rice is often harmed by diseases and insects, resulting in a decrease in rice production (Hu, 2017).

In the process of planting rice in the northern cold region, many diseases often occur. The rice blast and sheath blight had the most serious effect on rice yield, followed by bakanae disease, leaf sheath rot and damping off, etc (Lu et al., 2018). These diseases occur in every part of rice, such as leaf, neck and ear and the disease spot characteristics of the same disease are also different in different growing stages. These diseases caused the decline of rice quality and serious economic losses. At present, the main means of disease prevention are using pesticides and the development of disease-resistant varieties. However, these methods often fail to play a full role because they cannot accurately identify rice diseases, even lead to reduced rice production. Even for experienced experts, this is a very subjective and time-consuming task. Therefore, accurate identification of rice diseases is the primary task of rice disease control in China.

In recent years, lots of scholars have used machine learning to identify rice disease. Liang et al. (2019) proposed a new method for identification of rice blast based on convolutional neural network (CNN) (Lecun, 1995). Tan et al. (2019) according to the map of rice disease control (Sun, 2004) selected eight types of common rice diseases as the research objects, used fine-tuned and optimized to achieve a high recognition accuracy with a limited number of images. Qiu et al. (2019) proposed a new identification model aiming at the low recognition rate of traditional technology, and the identification accuracy reached over 90%. Liu et al. (2014) collected pictures of rice leaf diseases, compared their characteristic parameters of color, shape, texture and junction, these parameters were used for identification respectively, the recognition accuracy of a single characteristic parameter reached 96.71%. However, most scholars take pictures of experimental crops in laboratory or crops grown indoors by digital cameras. In this case, the background of the rice disease image is single, which cannot truly reflect the growing environment of the actual rice in the field. Under such conditions, there will be a large deviation in the actual field application.

In the field of image recognition model research, machine learning has been widely applied to every walk of life (Zhao et al., 2018; Gu et al., 2019; Wu et al., 2018; Liu et al., 2018). Many scholars are applying machine learning to disease recognition in agriculture. Guo et al. (2019) designed a multisensory recognition model based on AlexNet model, compared with the original network, the memory demand was reduced by 95.4%, and the recognition accuracy achieved 92.7%. Sun et al. (2017) proposed a convolutional neural network recognition model combining normalization and global pooling to identify plant diseases images in Plant Village data set, and the accuracy was 99.56%. Ren et al. (2019) used one-shot learning model (Sung et al., 2017; Lin et al., 2017) recognize diseases of 8 small sample data sets in Plant Village, and the recognition accuracy of this recognition method was improved 41.90%. Liu et al. (2018) identified four apple disease images and proposed a recognition method based on deep convolutional neural network, and the recognition accuracy achieved 97.62%. Amara et al. (2017) proposed a convolutional neural network model based on LeNet to identify the two banana diseases, and the accuracy rate reached 99.72%. The models in the above studies mainly adopted some traditional recognition methods, but did not analyze and discuss the complexity of the actual images. Therefore, more research is needed to improve the traditional recognition method, to adapt to the actual field images. In this paper, we established a model to recognize the rice disease of actual field in order to make the recognition model more applicable for the actual field. This paper assumes that each rice plant has only one disease.

The rest of the paper is structured as follows. Section 2.1 describes data acquisition. Section 2.2 describes the specific structure of the multi-scale stacked autoencoder used. Section 3.1 illustrates the image preprocessing. Section 3.2 illustrates multi scale selection. Section 3.3 illustrates the selection of the most parameters. Section 3.4 Comparison and analysis based on other models. Finally, part 4 will summarize the article.

2. Method

This section introduces how rice disease images are acquired and the basic theory of model establishment will be elaborated detail.

2.1 Image Acquisition

In this paper, the rice diseases were all from the experimental field of Northeast Agricultural University in Acheng. From August to September 2019, they were collected twice. Five common diseases of rice were collected and stored in JPG format, including 78 images of *ustilagrnoidea virens*, 70 images of grain blast, 54 images of panicle neck blast, 41 images of rice stripe virus, 31 images of leaf spot of flax, a total of 274 color disease images. The images are shown in Figure 1.

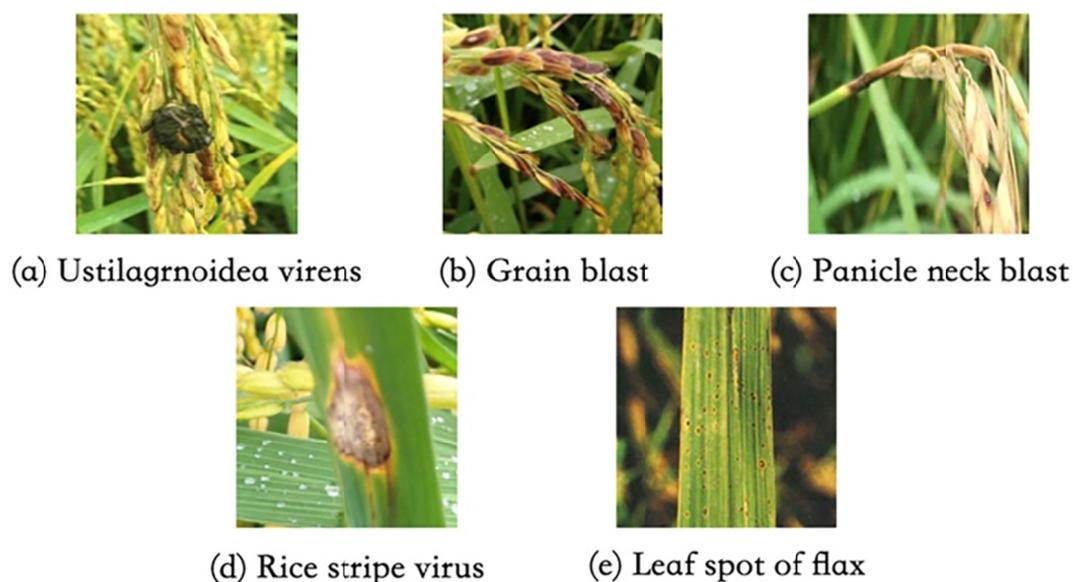


Figure 1. Images of rice disease

2.2 Model Approach

This section discusses in detail the construction process and algorithm flow of rice disease recognition model based on stack autoencoder.

2.2.1 Stacked Autoencoder (SAE)

Autoencoder, also known as Auto Associator or Diabolo Network, is an unsupervised learning algorithm. In practice, the number of hidden layer nodes is very close to or even greater than the number of input (Jia et al., 2018). Therefore, the number of active neurons in the hidden layer node can be reduced by adding certain keeping most neurons in a suppressed state. After adding sparsity limitation, the sparsity autoencoder is formed. For a data set containing m samples, the cost function is defined as Equation (1).

$$J(W, b) = \left[\frac{1}{2m} \sum_{i=1}^m \left\| \hat{x}^{(i)} - x^{(i)} \right\|^2 \right] + \frac{\lambda}{2} \sum_{l=1}^{n_l-1} \sum_{i=1}^{s_l} \sum_{j=1}^{s_{l+1}} (W_{ji}^{(l)})^2 \quad (1)$$

Where, L is the L hidden layer, λ is the regular term coefficient. The activation of neurons can be obtained by Equation (2).

$$a^{(l+1)} = f(z^{(l+1)}) = f(w^{(l)}a^{(l)} + b^{(l)}) \quad (2)$$

Then the average activation degree is expressed by Equation (3).

$$\hat{\rho} = \frac{1}{m} \sum_{i=1}^m [a_j^{(2)}(x^{(i)})] \quad (3)$$

Join the sparse parameters $\hat{\rho} = \rho$ (usually equal to 0 approximate value) and penalty factor $\sum_{j=1}^{s_2} KL(\rho \parallel \hat{\rho}_j)$. $KL(\rho \parallel \hat{\rho}_j)$ can be expressed by Equation (4).

$$KL(\rho \parallel \hat{\rho}_j) = \rho \ln \frac{\rho}{\hat{\rho}_j} + (1 - \rho) \ln \frac{1 - \rho}{1 - \hat{\rho}_j} \quad (4)$$

To further minimize the punishment factor. The overall cost function can be expressed as Equations (5).

$$J_{sparse}(W, b) = J(W, b) + \beta \sum_{j=1}^{s_2} KL(\rho \parallel \hat{\rho}_j) \quad (5)$$

Where, β is the weight of control sparsity penalty factor. Then the partial derivative of the cost function is solved by the Equations (6) and (7).

$$\nabla_{w^{(l)}} J(W, b; x, \hat{x}) = \delta^{(l+1)} (a^{(l)})^T \quad (6)$$

$$\nabla_{b^{(l)}} J(W, b; x, \hat{x}) = \delta^{(l+1)} \quad (7)$$

Finally, Softmax classifier was used for supervised training. The accuracy of the classifier was used as the output index to evaluate the feature expression ability. The Softmax classifier could be expressed by Equation (8).

$$J'(\theta) = -\frac{1}{m} \left[\sum_{i=1}^m \sum_{j=1}^k \{y^{(i)} = j\} \ln \frac{e^{\theta_j^T x^{(i)}}}{\sum_{l=1}^k e^{\theta_l^T x^{(i)}}} \right] + \frac{\lambda}{2} \sum_{i=1}^k \sum_{j=0}^n \theta_{ij}^2 \quad (8)$$

By gradient descent method, $J'(\theta)$ is gradually converged to the global optimal solution.

Through the above method, multi-layer autoencoder is trained, and the output of the first layer is taken as the input of the second features of the data are mapped layer by layer, finally abstracted into the activation value of the deepest layer network. Finally, input the extracted feature values into the Softmax classifier, and conduct supervision training according to the label of the sample. In this way, the stack autoencoder (SAE) is built, the training steps of SAE are shown in Figure 2. The concrete algorithm of stacked autoencoder is shown in Algorithm 1.

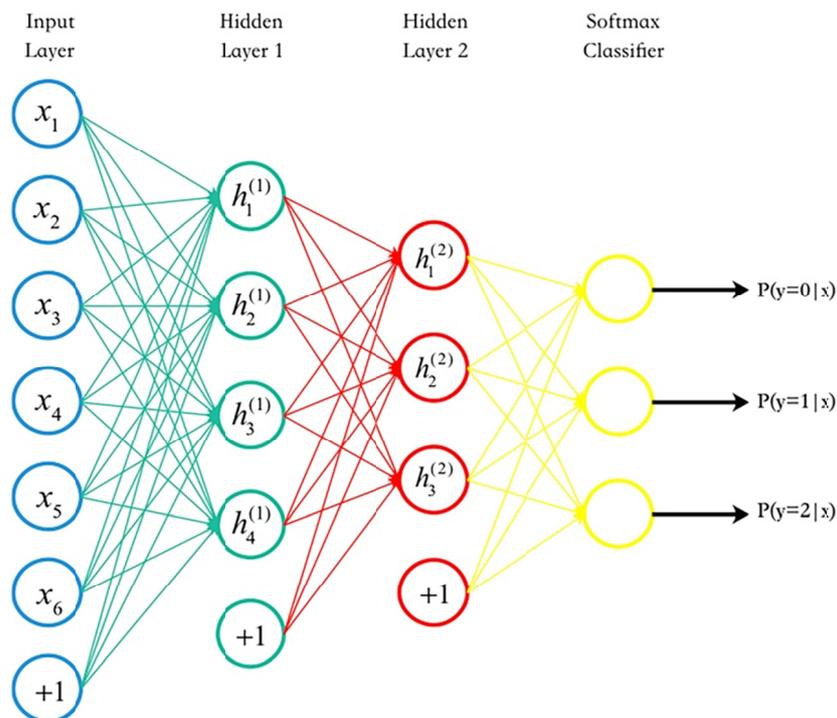


Figure 2. Architecture of stacked autoencoder

Algorithm 1 Stacked Autoencoder

1. **Begin**
2. Convert the covariance matrix into a real vector I of each pixel
3. The weight matrix W and the bias B were obtained from the pre-training network
4. Train the first hidden layer of autoencoder
5. For epoch = 1:k
6. Calculate the sample loss
7. Update the weight matrix W' and the bias b' using the gradient descent method of Equation (6)
8. End
9. Achieve the characteristic matrix H_1 of first hidden layer
10. Train the second hidden layer, using the eigenmatrix H_1 as input
11. Repeat steps 5 to 9 until all hidden layers are trained
12. Initialize the Softmax classifier and train it with training samples using the cost function in Equation (8)
13. Establish the whole network with the trained layers and Softmax classifier, then fine-tuning it with training samples using the cost function in Equation (8)
14. Classify each rice disease image using the whole network
15. **End**

2.2.2 Multi-scale Stacked Autoencoder (MSSAE)

The spots of different rice disease images have different sizes. It is difficult to fully reflect the different features of single scale extraction. In the real image of rice disease, there is multi scale information. Therefore, during the classification of rice disease, it is more reasonable to adopt a smaller scale window for small disease spot image, and a larger scale window for large disease spot image. Features that may not be detected at one scale, so it is necessary to extract features at several different scales and use them for the multi-scale feature is a promising approach to improve classification performance.

In this section, a multi-scale stacked autoencoder (MSSAE) is proposed for feature extraction of rice disease framework can be instructed as follow. Local spatial information is used to extract deep spatial features at

different scales. Then, the deep spatial features of different scales are sequentially combined to generate multi-scale features.

At the first step, we put all the input data into the pixel neighborhood window. In order to maintain the spatial relationship between the center pixel and adjacent pixels, the weight of each pixel is calculated according to Equation (9).

$$w_i = \frac{1}{1 + d_i} \tag{9}$$

Where, d_i is the spatial Euclidean distance from the i th pixel to the central pixel.

The corresponding weights of each neighbor can be calculated by Equation 9. Then, repeat the step above for all the image to obtain the matrix of pixels. Since the input of the MSSAE is a real vector, we flatten the neighborhood window into a vector.

At the second step, we use the training datasets to train the MSSAE. The training process of the SAE was described in detail in subsection 2.2.1.

Finally, enter the feature map into the Softmax classifier for classification. The specific feature splicing and fusion process is as follows: suppose the feature of the i scale is s_i , and the multi-scale eigenmatrix H can be expressed by Equation (10).

$$H = \sum_{i=1}^L s_i \oplus s_{i-1} \tag{10}$$

Where, \oplus represents the stitching and fusion of features, and L represents the number of features of different scales. After feature fusion, the multi-scale feature matrix H was sent to the Softmax classifier for classification, and the classification results were obtained. The MSSAE model is shown in Figure 3. The specific algorithm is shown in Algorithm 2.

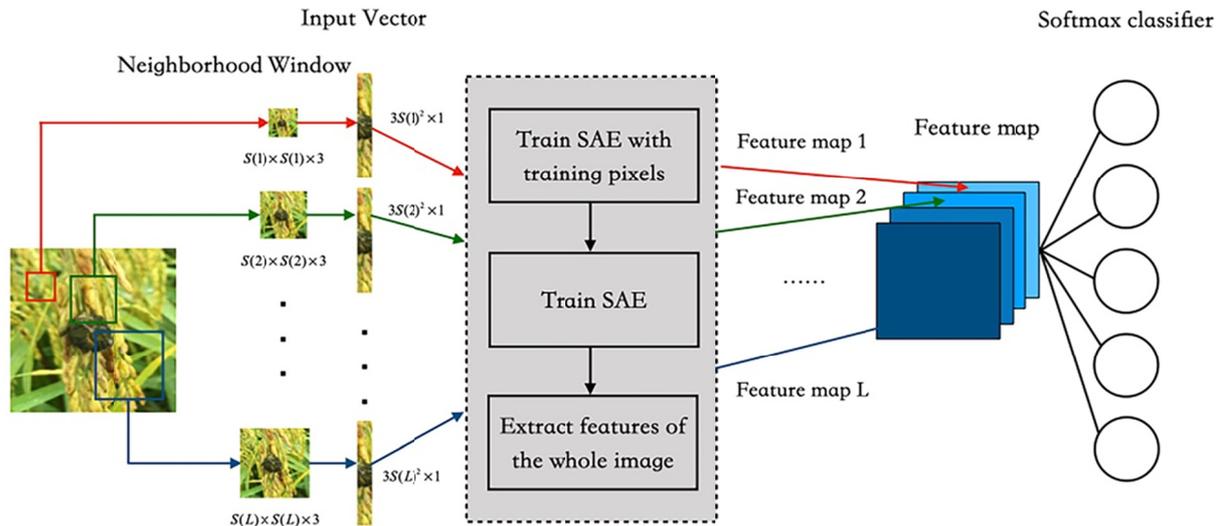


Figure 3. Multi-scale stacked autoencoder model

Algorithm 2 Multi-scale stacked autoencoder

1. **Begin**
 2. Initialize several neighborhood window scales: $s(1), s(2), \dots, s(L)$
 3. **For** each scale from $s(1)$ to $s(L)$
 4. Compute the weights according to Equation (9)
 5. **For** each pixel in the image
 6. Cur out the neighborhood to get an image of size $s(i) \times s(i) \times 3$
 7. Neighborhood pixel multiplied by corresponding weight
 8. Flatten the pixels into a vector with size $3, s(i)^2 \times 1$
 9. **End**
 10. Select the training set and input it to the SAE
 11. Train SAE by training set
 12. Extract the features of each pixel using a trained SAE
 13. Constitute the feature map using feature vector of each pixel
 14. **End**
 15. Extract features of different size and conduct feature fusion through Equation (10)
 16. The fused features are input into the classifier for classification
 17. **End**
-

3. Results

In this section, we discuss the experimental results. All experiments were implemented in MATLAB_R2018a under Windows 10, the processor was dual-core I5-8250, 128G SSD, the CPU was Intel core I7-6500U, and the main frequency was 2.5 ghz.

3.1 Images Processing

Due to the lack of rice diseases data, especially the panicle neck blast and leaf spot of flax, it is easily lead to over-fitting problem and reduce the accuracy of rice disease recognition. Therefore, we use two solutions to solve these problems:

The first approach is the data enhancement. We use reflection deformation, the image data for 90 degrees, 180 degrees, 270 degrees and vertical mirror of rotation (Mairal, 2010). In addition, histogram equalization was used to enhance the disease image and highlight the characteristics of disease spots.

The rotated instance diagram is shown in Figure 4. The enhanced sample information obtained is shown in Table 1.

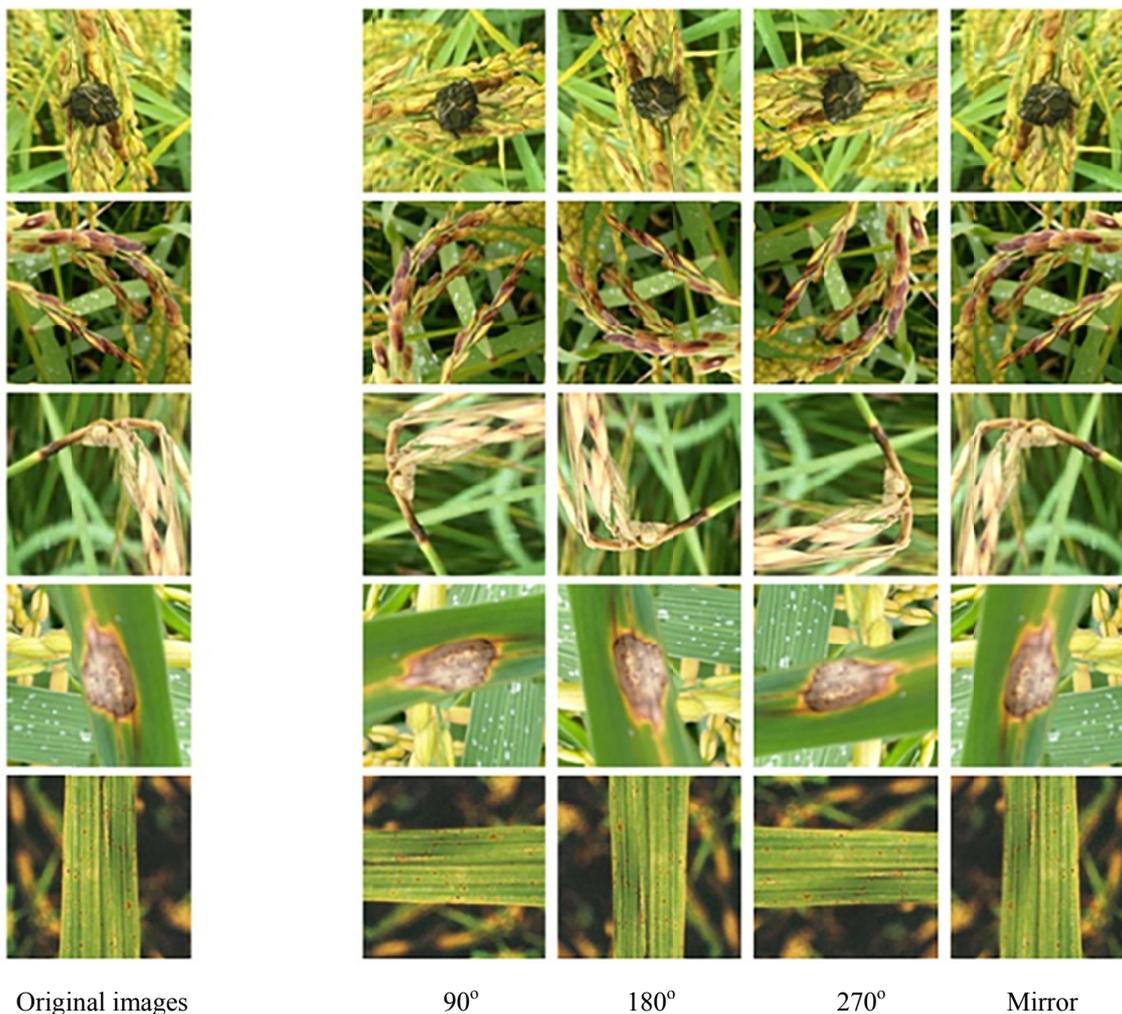


Figure 4. Example of data augmentation

Table 1. Rice disease image table

Category	Ustilagnoidea Virens	Grain Blast	Panicle Neck Blast	Rice Stripe Virus	Leaf Spot of Flax
Number of original images	78	70	54	41	31
Number of images after expansion	378	379	392	386	374

After image expansion, histogram equalization was used to enhance the image of rice disease, which made the image clearer and laid a foundation for subsequent image recognition. The result of histogram equalization is shown in Figure 5.

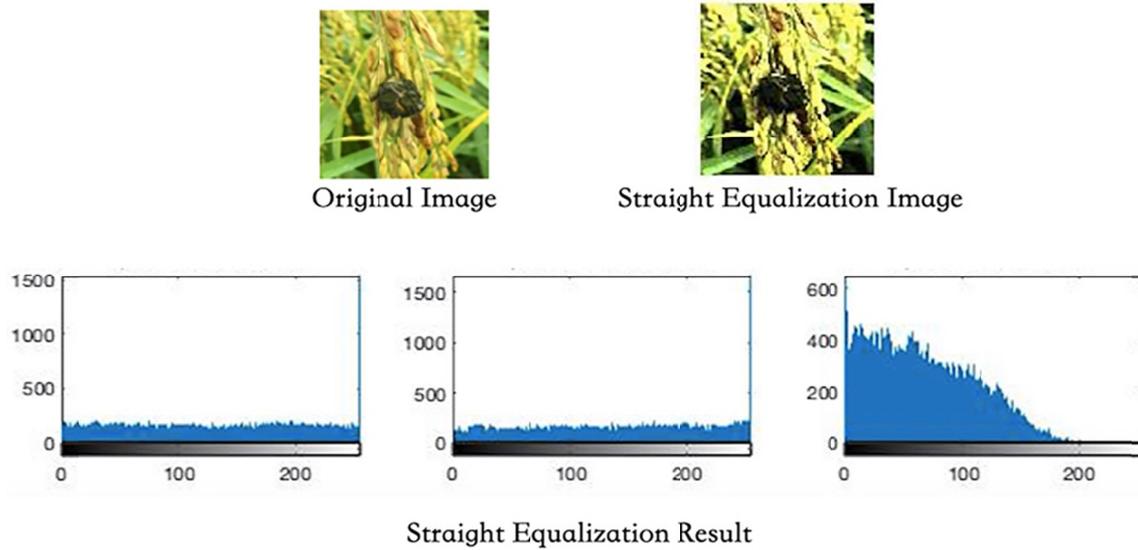


Figure 5. Contrast the original image with the straight equalization image

3.2 Scale Selection

An important part of MSSAE training is the selection of input image scale. In this section, we select the neighborhood window scales by experiment. Through the steps 2 to 14 in algorithm 2, use single scale image for feature extraction. Then input each single scale feature into Softmax classifier to obtain classification results. Therefore, we choose twelve different neighborhood window scales: 3×3 , 5×5 , 7×7 , 9×9 , 11×11 , 13×13 , 15×15 , 17×17 , 19×19 , 21×21 , 23×23 , 25×25 . We use two numerical indexes, the identification accuracy and computation time, to compare the performance of different single scales. The result of time is shown in Figure 6(a) and the classification accuracy is shown in Figure 6(b).

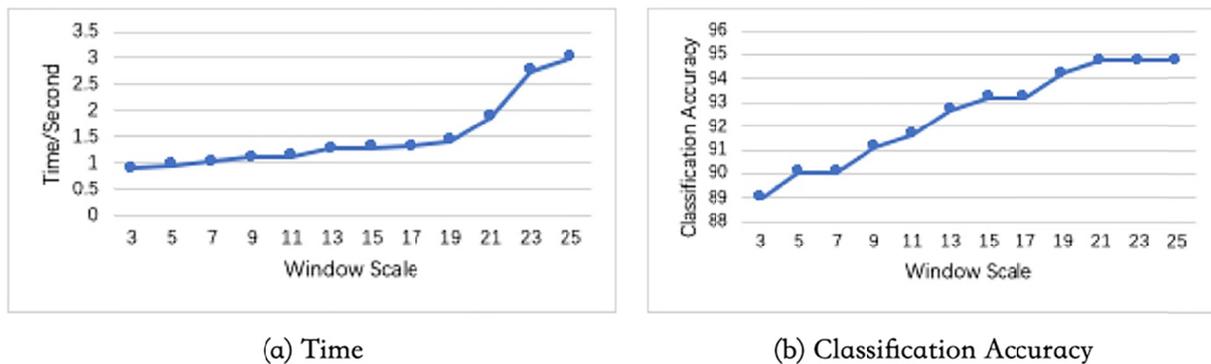


Figure 6. Scale selection

As can be seen from (a) and (b) in Figure 6, with the increase of neighborhood window scale, the accuracy and calculation time both increase. However, when the scale size is 3×3 , the recognition accuracy is less than 90%. When the scale size is more than 21×21 , the increase trend of accuracy becomes flat. When the scale size is more than 19×19 , the trend of time growth becomes steeper. Therefore, in order to balance the relationship between accuracy and time, neighborhood windows with scales of 5×5 , 7×7 , 9×9 , 11×11 , 13×13 , 15×15 , 17×17 and 19×19 are selected.

3.3 Model Parameters

The input size can be determined by 3.2. Then, the network parameters need to be determined. The parameters of the specific settings are shown as Table 2.

Table 2. Hyperparameters setting of SSAE

Hyperparameters				Indexes	
First hidden layer	Second hidden layer	Sparsity parameter	Iteration	Accuracy (%)	Time (s)
100	50	0.1	100	92.33	15.05
		0.1	200	92.13	18.59
		0.1	300	93.49	20.36
		0.1	400	93.89	24.35
		0.01	100	93.04	16.67
		0.01	200	93.19	20.73
		0.01	300	93.43	22.68
		0.01	400	93.68	26.73
200	100	0.1	100	93.19	20.78
		0.1	200	94.41	28.67
		0.1	300	94.76	32.77
		0.1	400	93.68	38.96
		0.01	100	92.65	23.98
		0.01	200	93.19	29.65
		0.01	300	95.78	34.12
		0.01	400	94.12	38.55
300	200	0.1	100	93.57	23.43
		0.1	200	93.66	27.65
		0.1	300	92.87	29.78
		0.1	400	93.45	32.90
		0.01	100	93.06	26.54
		0.01	200	94.67	29.57
		0.01	300	94.79	34.65
		0.01	400	93.28	39.01

As can be seen from Table 2, when the first hidden layer is 200, the second hidden layer is 100, the learning rate is 0.01, and the number of iterations is 300, the recognition accuracy is the best, 95.78%, and the required time is 34.12 seconds.

3.4 Results of Experimental

In order to quantitatively analyze and test the network performance, the precision (P), recall (R) and F1 scores (F1) were used for objective evaluation. The precision is the percentage of the correct portion of the test results. The recall is the percentage of the correct part of the test results to the actual correct part. In addition, the F1 score was given to evaluate the overall performance of the classifier (Fu et al., 2020). The calculation equations are as follow.

$$\text{Precision} = \frac{\text{True Positive}}{\text{True Positive} + \text{False Positive}} \quad (11)$$

$$\text{Recall} = \frac{\text{True Positive}}{\text{True Positive} + \text{False Negative}} \quad (12)$$

$$\text{F1} = \frac{2 \times \text{Precision} \times \text{Recall}}{\text{Precision} + \text{Recall}} \quad (13)$$

Where, true positive refers to the number of correctly identified rice disease, false positive refers to the number of incorrectly identified rice disease, false negative refers to the numbers of incorrectly identified rice disease as other.

The classification accuracy for every class is presented in Table 3 along with P, R and F1 scores coefficient values. The confusion matrix of the MSSAE method is shown in Table 4.

Table 3. Classification accuracy of rice disease

Class	SVM	Alex Net	Googlenet Net	SAE	MSSAE
Ustilagnoidea Virens	78.69	94.68	98.33	90.33	100
Grain Blast	82.67	90.62	94.13	90.13	98.62
Panicle Neck Blast	62.63	92.02	93.49	91.49	93.89
Rice Stripe Virus	71.55	89.71	94.89	91.89	92.04
Leaf Spot of Flax	85.65	93.64	93.04	89.04	98.80
P	78.18	92.48	96.71	90.19	97.88
R	71.67	90.60	94.28	92.79	96.79
F1	79.79	91.67	92.46	91.28	96.05

Table 4. Confusion matrix comparison of MSSAE

Class	P (%)	R (%)	F1 (%)
Ustilagnoidea Virens	100	100	99.59
Grain Blast	97.37	98.80	99.47
Panicle Neck Blast	94.87	96.37	93.11
Rice Stripe Virus	94.87	89.27	92.64
Leaf Spot of Flax	97.30	98.51	98.95

In Table 3, the P, R and F1 scores coefficient values of the MSSAE are the highest. The precision of the MSSAE is approximately 19.7%, 5.4%, 1.17% and 7.69% higher than that of the other methods. The recall of MSSAE is approximately 25.12%, 6.19%, 2.51% and 4% higher than that of the other methods. The F1 scores of the MSSAE is approximately 16.26%, 4.38%, 3.59% and 4.77% higher than that of the other methods.

4. Discussion

At present, most of the commonly used network models have low recognition accuracy for complex background images. For some images with complex backgrounds, it is difficult to accurately identify the location of disease spots by using machine learning.

In order to make the image recognition model better applied to the real field, this paper highlights the location of the disease spots by weighting the images. After image preprocessing, the features of the disease spots become clearer, which is conducive to the subsequent feature extraction. Through the multi-space of the image, the feature extraction is carried out with images of different sizes, finally the recognition and classification is carried out.

Results as shown in Table 3 in chapter 3, SVM has the lowest recognition accuracy, SAE is better, then convolutional neural network, and MSSAE has the highest recognition accuracy. MSSAE has high recognition accuracy for images with complex background.

In the process of identifying rice disease, the multi-scale stacked autoencoder presents some errors, some of which are shown in Figure 7 below.

Image to Recognize



Forecast: Leaf Spot of Flax
Fact: Grain Blast



Forecast: Rice Stripe Virus
Fact: Panicle Neck Blast

Image to Recognize



Forecast: Ustilagnoidea Virens
Fact: Rice Stripe Virus



Forecast: Grain Blast
Fact: Leaf Spot of Flax

Figure 7. Samples of misclassified

There are two reasons for this phenomenon:

(1) Grain blast and leaf spot of flax are similar in features, point by point, and similar in color, so it is easy to confuse leaf spot and grain blast.

(2) Most of the reasons for misidentification are due to the complex actual field background, which is easy to confuse the characteristics of some diseases.

5. Conclusions

In this paper, we proposed a multi scale staked autoencoder (MSSAE) method based on the staked autoencoder to extract the deep multi-scale features for rice diseases and obtained a high rice diseases recognition accuracy. The method preprocesses the image first. Then, extract the multi scale features by different scales images. Finally, the feature fusion method is proposed to obtain the feature matrix. It can be seen from the experiment that MSSAE has a high recognition accuracy rate for images with complex background, and can effectively overcome the noises. From the result, the classification accuracy of the MSSAE achieved as high as 95.78%, the computing time was only 34.12 seconds. This indicates that the new model can accurately identify rice diseases, prepared for accurate removing disease accurately in the future, and provided reliable support.

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