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Identification of Crop Diseases Based on Improved Genetic Algorithm and Extreme Learning Machine

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Abstract: As an indispensable task in crop protection, the detection of crop diseases directly impacts the income of farmers. To address the problems of low crop-disease identification precision and detection abilities, a new method of detection is proposed based on improved genetic algorithm and extreme learning machine. Taking five different typical diseases with common crops as the objects, this method first preprocesses the images of crops and selects the optimal features for fusion. Then, it builds a model of crop disease identification for extreme learning machine, introduces the hill-climbing algorithm to improve the traditional genetic algorithm, optimizes the initial weights and thresholds of the machine, and acquires the approximately optimal solution. And finally, a data set of crop diseases is used for verification, demonstrating that, compared with several other common machine learning methods, this method can effectively improve the crop-disease identification precision and detection abilities and provide a basis for the identification of other crop diseases.

Keywords: Crops, disease identification, extreme learning machine, improved genetic algorithm.

1 Introduction

The inspection of crop diseases is an important part of planting protection [Kurale and Vaidya (2018)], Due to the effect of temperature, humidity and other environmental factors, crops may be harmed in their growth processes by many kinds of diseases, such as common leaf spot and rust diseases [Khitthuk, Srikaew, Attakitmongcol et al. (2018)], imposing great threats to their growth. Therefore, the identification and detection of crop diseases have become an indispensible section in agricultural production. However, the traditional identification methods are generally based on manual operations, such as visual observation, artificial sorting, etc., which, due to the diversity and complexity of different diseases, cannot accurately identify the diseases of crops. Consequently, the inefficiency of subjective judgments by professionals and other traditional artificial methods have been gradually appearing, bringing great inconvenience to farmers, falling

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short of the purpose of the scientific production of agriculture, and even resulting in huge economic losses. Therefore, the identification of crop diseases has great economic and scientific significance for social production.

Over the recent years, with the rapid development of computer technology, the identification of crop diseases has become a hot issue, with more and more advanced methods applied in crop production and protection, such as image processing and machine learning with some satisfactory achievements made in this area. For example, Korkut et al. [Korkut, Gokturk and Yildiz (2018)] extracted various features from the leaf images of different crops by using the transfer learning method and tested the features using various machine learning agorithms, to finally achieve an identification rate of 94%; a satisfactory identification rate. Maniyath et al. [Maniyath, Vinod, Niveditha et al. (2018)] applied the image processing technology in such features as the color and texture of crop leaves, to identify and classify the disease images of different crops by using the method of random forest with a precision of 70.14%. Sardogan et al. [Sardogan, Tuncer and Ozen (2018)] considered that the color information extracted from a homogeneous color component would have limitations, so the characteristics of the color component of crop images were used to identify and classify the crops based on the convolution neural network model and learning vector quantization algorithm, with a final average identification precision of 86%. Rangarajan et al. [Rangarajan, Raja and Szczepanski (2018)] introduced multi-class SVM to identify crop diseases based on the analysis of SVM model, obtaining an average best precision of 81.3%, by using the combined ten texture features, the polynomial kernel function and LS method, thereby improving the training performance. Kaya et al. [Kaya, Kekl, Ensar et al. (2019)] proposed a local binary model and Histogram of Oriented Gradients of plant images to form new texture features and used extreme learning machine for classification, achieving good results. Although these researches provide important reference values for image preprocessing and feature extraction, they use the traditional extreme learning machine algorithm for identification and classification, without considering the impact of data scale in the training process, leaving much room for improvement. In conclusion, these disease-based identification methods can make up for the shortcomings of traditional methods and achieve better identification results, though there are still problems left in the experimental process. For example, in the process of crop disease feature extraction, the homogeneity and redundancy of sample features might be ignored, resulting in lower or higher identification rates and reducing the persuasiveness of their research results. As another example, when common machine learning methods are used to optimize the training process, parameters are needed to be adjusted many times or fall into a local optimum [Cai, Liu, Zhang et al. (2018)], leading to an instable training process and eventually a lowered precision and poor experimental.

In view of the low efficiency of traditional crop disease identification, as well as the shortcomings of the above methods, this study proposes a method of crop disease detection by using the improved genetic algorithm and extreme learning machine based on image processing and machine learning theory. Specifically, it will analyze the characteristics of crop images and fuse the optimal characteristics, and then introduce hill-climbing algorithm to improve the traditional genetic algorithms. In addition, it will promote their abilities in a global search, thus enhancing the global optimization of the initial weights and thresholds of the extreme learning machine, improving the network and promoting the precision of crop identification, while ensuring the robustness of the network. Finally, this study uses a data set of crop diseases for simulation to verify the feasibility of the method proposed and compares it with many other algorithms. The experimental results show that the new method can effectively improve the precision and effect of disease identification.

2 Data set and method

2.1 Data set

The target data set of this experiment comes from the data set of some crop diseases in the 2018 Global AI Challenge (www.challenger.AI), which is composed of 10 commonly-seen and different crop varieties, such as apple, corn, potato, and etc. Based on different disease characteristics of various crop leaves, they are classified into 27 health or disease types.

After careful observation and statistics of the disease characteristics of different crops, this study finds that the data set has the following problems: some crops have the same disease degree with different incidences if observed by naked eyes, which are not of good recognition significance; and some crop diseases have too many or too few samples to reach the research objectives of this topic. In order to better realize the scheme proposed in this study, the target data set is constructed on the basis of this data set. Specifically, different crop disease types with moderate or less sample sizes are selected as the target data set. Finally, five typical disease types of different crop leaves are selected according to the distribution of sample sheets in the data set. With 100 images of each disease, there are a total of 500 disease images. One set of disease samples is shown in Fig. 1.

Figure 1: Disease sample

2.2 Image preprocessing

By observation of the sample images in the data set, it can be found that the data set is not acquired in an ideal environment, and noises and other uncertain factors might appear in the collection process. In order to obtain better data relevant to the leaf disease areas, the sample images need to be preprocessed, mainly by image filtering and segmentation. The specific operations are as follows: first, the sample was cut and adjusted to the size of 256×256, for the purpose of improving the precision of the subsequent experiments; and then the filtering was carried out to remove the relevant noises. After comparative analysis of several commonly-used filtering methods, the median filtering method [Bae and Yoo (2018)] is found to have the best effect, retaining the details of the images very well, so the median filtering is used to filter the sample images. Then, in order to separate the disease areas from the background, K-means clustering algorithm [Tan, Li, Xia et al. (2019)] was used to segment the sample images in the principle of transforming the given sample image set from RGB space to lab color space, which is divided into k clusters according to the distance between the sample images. Finally, segmentation was performed by minimizing the sum of the squares of the distance between the image intensity and the cluster centroid. An example group of the sample pictures after filtering and segmentation are shown in Fig. 2, which shows that the diseases are very well presented and separated from the background.

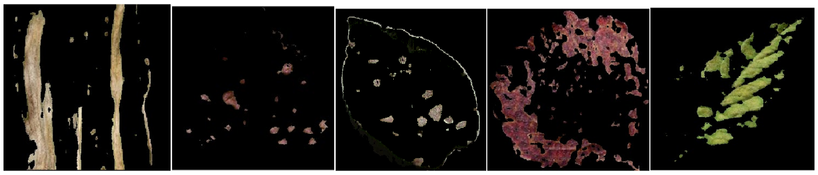


Figure 2: Sample after pretreatment

2.3 Feature extraction

Given the characteristics of the disease areas of crop leaves, this study will select the disease features from two aspects, color and texture.

2.3.1 Extraction of color feature

The color attributes of disease areas can directly reflect the characteristics of diseases. Compared with common RGB color space, the color space composed of HSV (hue, saturation and value) is more similar to human vision and has a higher utilization of color, so it is more suitable to act as the attribute for feature expression. After the disease segmentation images are obtained, the RGB color space of the sample image is transformed into HSV color space, and then the color moment of each channel of HSV is worked out for analysis [Karmakar (2019)]. A group of color moments of different diseases therein are shown in Fig. 3.

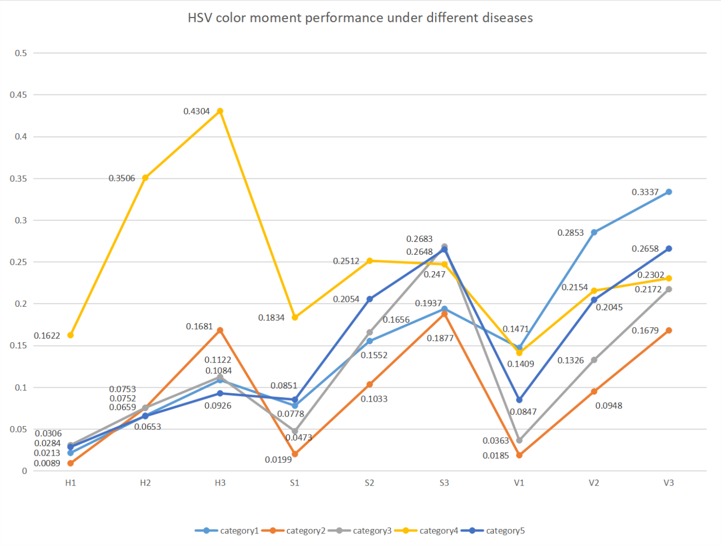


Figure 3: Color moment representation of different diseases

Since the color distribution information is mainly concentrated in the low-order moment, the color moment can more effectively represent the color characteristics of the images. Through quantitative analyses of the first-, second- and third-order moments of different color components, it can be seen that the first-order moments of H and S color components change significantly at different disease color degrees, while the difference of color moments in other color spaces is too little to be representative. Therefore, the first-order moments of H and S components can be selected as color features by using the formula below:

$$E_i = \frac{1}{N}\sum_{j-1}^{N} p_{ij} \tag{1}$$

$$\sigma_i = \sqrt{\frac{1}{N}\sum_{j-1} N(p_{ij} - E_i)^2} \tag{2}$$

where, E_i and σ_i represent the first- and second-order moments.

2.3.2 Extraction of texture feature

In addition to color features, texture features are also one of the main features of images. Texture features describe the repeated local patterns and their arrangement rules in images, which are generally generated by Gray Level Co-occurrence Matrix (GLCM) operators [Krithika and Selvarani (2017)] and LBP operators [Kou, Cheng, Zhuang et al. (2018)]. However, in order to avoid high dimensionality caused by too many or overlapping texture feature parameters, this study first uses LBP operators to obtain the local binary pattern images of disease images and then calculates the four texture feature parameters generated by GLCM. Local Binary Patterns (LBP) is a nonparametric linear dimensionality reduction operator to describe the local spatial structure of an image for local texture feature extraction. With a simple principle, low calculation workload and strong classification ability, LBP features are invariant to monotonic gray changes. In contrast, GLCM is a matrix correlation function determined by image angles and pixel distances, capable of reflecting certain texture feature information of images in terms of directions and changing amplitudes. It has four parameters: energy (E), entropy (H), moment of inertia (I) and correlation (C). This operation can make full use of the effectiveness of GLCM and LBP operators. The four texture features can be obtained by defining distance (d), direction (θ) and two gray values (*i*, *j*), among which:

$$E = \sum_{i=0}^{L-1}\sum_{j=0}^{L-1} P^2(i,j;d,\theta) \tag{3}$$

$$H = \sum_{i=0}^{L-1}\sum_{j=0}^{L-1} P(i,j;d,\theta)\lg P(i,j;d,\theta) \tag{4}$$

$$I = \sum_{I=0}^{L-1}\sum_{j=0}^{L-1} (i-j)^2 P(i,j;d,\theta) \tag{5}$$

$$C = \frac{\sum_{i=0}^{L-1}\sum_{i=0}^{L-1} ijP(i,j) - \mu_x\mu_y}{\sigma_x^2\sigma_y^2} \tag{6}$$

2.3.3 Multi-feature fusion

Since it is difficult to accurately express the attributes of the disease areas of crop leaves with single or complex features, after the extraction and analysis of the two main features of color and texture, the representative features obtained are fused by using a feature fusion strategy [Tan and Yu (2019); Xia, Chen, Chen et al. (2018)]. And finally, a six-dimensional feature vector is obtained, and then the min-max normalization of feature data is carried out, so that they can be mapped between 0 and 1 for follow-up test operation.

3 Improve the genetic algorithm to optimize the extreme learning machine

3.1 Extreme learning machine

Extreme Learning Machine (ELM) is a new model for single hidden layer feedforward neural network [Cheng, Zhao, Wang et al. (2019)], with such advantages as fast learning speeds and good generalization performance. Compared with the traditional feedforward network training models, the biggest feature of this model is that in the training process, both the connection weights between the input layer and the hidden one and the threshold values of hidden layer neurons are randomly generated without adjustment. With only the number of hidden layer neurons to be set, a unique optimal solution can be obtained. The network structure of the ELM is shown in Fig. 4.

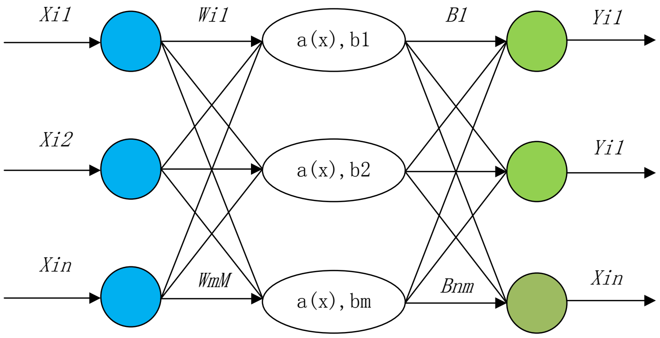


Figure 4: Elm network structure

where, m, M, and n are the number of neurons in the input layer, hidden layer and output layer, respectively; $a(x)$ is the excitation function of neurons; b is the threshold value of neurons in the hidden layer; and (x_i, y_i) is the training sample. The training model of ELM can be expressed as follows:

$$\sum_{\mathrm{i}=1}^{M} \beta_i a(\omega_i x_i + b_i) = o_j, j = 1,2...,N \tag{7}$$

where, $\omega 1i = [\omega_{1i}, \omega_{2i}, ..., \omega_{mi}]$ is the weight vector of input layer and hidden layer; $\beta i = [\beta_{i1}, \beta_{i2}, ..., \beta_{in}]^T$ is the weight vector of output layer and hidden layer; and $oi = [o_{i1}, o_{i2}, ..., o_{in}]^T$ represents the network output value. The cost function of ELM can be expressed as follows:

$$E(S, \beta) = \sum_{j=1}^{N} \| o_j - y_j \| \tag{8}$$

where, $s = (\omega_i, b_i, i = 1,2,3,...M)$. The model can calculate the weight β of output function and hidden layer by the value of cost function, so as to minimize errors. This operation can reduce the difference between the training results and the actual ones, so that the training results are closer and closer to the real one. In practical applications, if HH^T is not singular, then

$$\begin{aligned} \beta &= H^+ O = H^+ (HH^T)^{-1} O \\ &= H^T (\frac{1}{C} + HH^T) O \end{aligned} \tag{9}$$

H^+ is the generalized matrix of the H matrix, which in turn is the hidden layer matrix of the neural network. O is the vector of the predicted target value. It can be learned from the ridge regression theory that increasing the normal number $1/C$ can make the result more stable, thus improving the generalization ability of the model, i.e.,

$$f(x) = h(x) H^T (\frac{1}{C} + HH^T) O \tag{10}$$

As a supplement to the least square, the ridge regression can reduce the probability of "ill-conditioned matrix" and lose the unbiasedness in exchange for high stability of the numerical value.

3.2 Improved genetic algorithm

As a computational model, the Genetic Algorithm [Singh and Misra (2015)] simulates the natural selection of Darwin's Biological Evolution and the biological evolutionary process of genetic mechanism, i.e., the inheritance and selection law of "survival of the fittest" in the nature. Often used as one of the global search optimization algorithms, GA (Genetic Algorithm) begins with a population that represents a potential solution set of the problem to be solved, while each population consists of a certain number of individuals, each of which is genetically encoded. The workflow of the algorithm can be described as: firstly, a first-generation population is generated, and a better individual is gradually evolved out according to the principle of "survival of the fittest" and can be regarded as an approximate solution to the problem; in each generation, an individual is selected according to its fitness size in the problem domain, and then it is combined, crossed and mutated with the help of genetic operators of natural genetics to generate populations representing new solution sets [Viknesh and Manikandan (2017)]. This process will make the population of the later generation, like in the natural evolution, more adaptable to the environment than the previous generation, and finally, the optimal individuals in the last generation can be decoded as the approximate optimal solution of the problem. Therefore, the basic process of genetic algorithm can be described as follows:

1) Initialization of population: Set the evolutional generation counter $t = 0$ and the maximum evolutional generation T, and randomly generate M individuals as the initial population $P(0)$;

2) Individual evaluation: Calculate the fitness of each individual in the population $P(t)$;

3) Selection: operators will be selected and applied to the population. The purpose of selection is to directly pass down the optimized individual to the next generation or to generate a new individual through pairing and crossover, which is then passed down to the next generation. The selection operation is based on the fitness evaluation of the individuals in the population;

4) Crossover: The crossover operators are applied to the population, which play a core role in the genetic algorithm;

5) Mutation: The mutation operators are applied to the population, so as to change the genic values at certain loci of individual strings in the population. The next generation of population $P(t+1)$ is obtained after the selection, crossover and mutation operations on population $P(t)$;

6) Termination condition judgment: If $t = T$, the individual with the greatest fitness as obtained in the evolution process is taken as the optimal solution output, and then the calculation is terminated.

Although the GA algorithm has a good global search ability, it is prone to fall into the local minimum and then no longer make searches when dealing with multiple optimal solutions, thus failing to acquire the global optimum. For this problem, the hill-climbing algorithm [Sazaki, Primanita, Satria et al. (2018)] was introduced, which can guide and adjust the GA search direction in case that GA may fall into the local minimum, so as to keep searching in the optimal direction until obtaining the global optimal solution. In summary, the hill-climbing algorithm can be used to optimize the search procedure of genetic algorithm.

3.3 Improve the genetic algorithm to optimize the extreme learning machine

It is known from the ELM principle that the algorithm does not need to adjust the input weights and the hidden layer thresholds during the training process; instead, they are randomly generated. However, this may affect the generalization ability of ELM under the condition of uncertain training set sizes and imbalanced distributions. The learning ability of ELM can only be judged through multiple trainings, and the input weights and thresholds become important influencing factors of the learning performance of ELM. Therefore, to avoid performance loss during the training process, an improved genetic algorithm was introduced after the ELM training model was built for a better population-based global search strategy, so as to optimize the input weights and hidden layer thresholds of ELM, thereby improving the ELM network structure and optimizing the training effect. The optimization of ELM model by using the improved genetic algorithm can be divided into the following steps:

1) Construct an ELM crop identification model and initialize its network parameters; and then select an appropriate number of network nodes (e.g., the number of hidden layer nodes) as per the feature dimensions;

2) Initialize the population, take the input weight and the hidden layer threshold of the ELM model as the genetic solution objects, and conduct global searches for them to obtain the approximate optimal solution;

3) Perform DE optimization, calculate and compare the output errors of ELM, and perform such operations as mutation, crossover and selection, to generate the next-generation population;

4) Use the hill-climbing algorithm to perform optimization again in the next-generation population, that is, to select an initial individual to compare it with the individuals from the adjacent area for the fitness values, and keep the individuals with higher fitness values;

5) Determine whether the maximum number of iterations is reached or whether the initial individual has been replaced, or whether no better substitute can be found after the completion of iteration. If so, proceed to Step 6; otherwise, return to Step 3;

6) Terminate the algorithm, and take the optimal individual obtained at this time as the input weight and the hidden layer threshold of ELM.

The entire disease identification process of crop images is shown in Fig. 5.

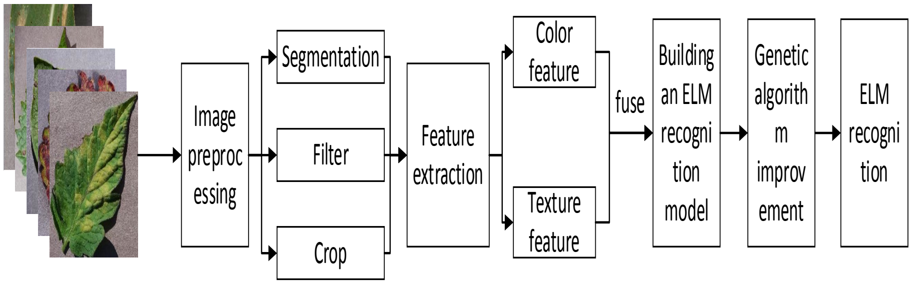


Figure 5: Identification process of crop diseases

4 Experimental process and result analysis

4.1 The process of experiment

During the experiment, training was made for five types of diseased crops for identification. And the specific moments in HSV color moments were used as color features, while the local binary mode and GLCM method were used to extract texture features. Because GLCM would produce four texture features in four different directions, i.e., 0°, 45 °, 90° and 135°, it could be learned by observing the data that the array differences in different directions were not big, so the mean values of the numerical values in the four directions could be selected as texture features. Color features and texture features were combined into a feature vector form as the input, including two color features and four texture features. The name numbers of different types of diseases were selected as the output label, which were defined as 1-5, respectively; and the DE_ELM model was used as the evaluator for the experiment. In order to improve the precision of the experiment, of the 500 disease images in this study, 350 were randomly selected as the training set, and the remaining 150 as the test set. A group of training data are shown in Tab. 1, with x1-x6 representing the features and y representing the categories.

Table 1: Example of training data

Disease/feature	x1	x2	x3	x4	x5	x6	y
Corn leaf spot	0.028	0.078	0.621	0.886	0.112	2.494	1
Grape black rot	0.009	0.020	0.933	0.211	0.039	12.045	2
Potato early blight	0.021	0.047	0.886	0.319	0.049	9.593	3
Strawberry leaf blight	0.162	0.183	0.708	0.628	0.078	5.345	4
Tomato leaf mold	0.031	0.085	0.733	0.618	0.058	4.831	5

4.2 Result analysis

According to the characteristics of genetic algorithm, other parameters are set as follows: the number of iterations is set to 100; the chromosome size 20; the crossover probability 0.7; and the mutation probability 0.05. the hill-climbing algorithm is added for improvement; and the feature parameters are extracted from the training set and the test set for training and testing, respectively. And a group of results are shown in Fig. 6 below.

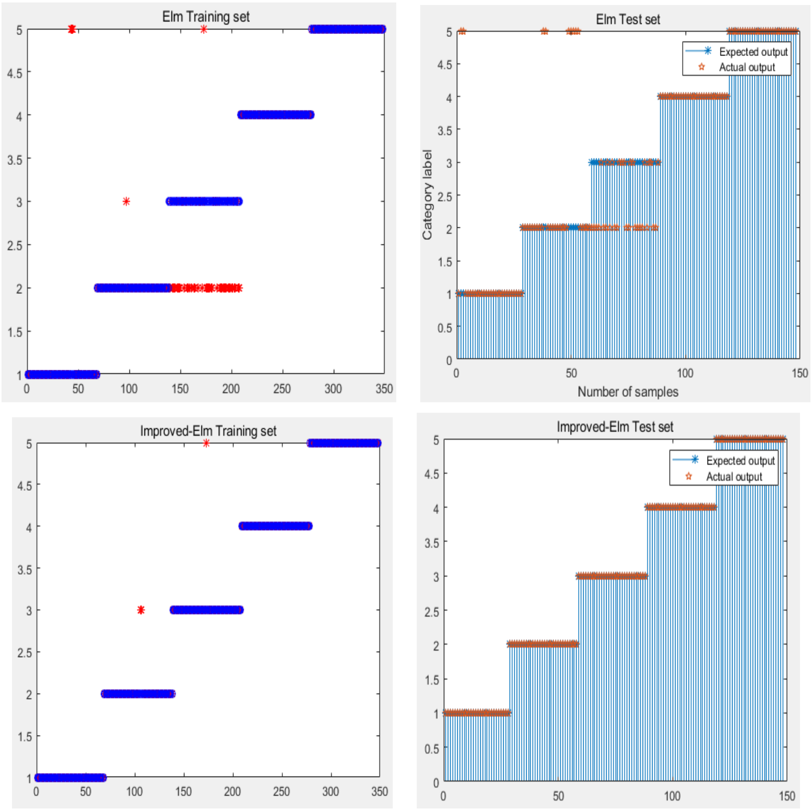


Figure 6: Experimental result

Figs. 6-1 and 6-2 show the identification results from traditional ELM training and testing, while Fig. 6-3 and Fig. 6-4 are the results from the improved training and testing. It can be seen from the figures that crop diseases were divided into five categories in the experiment, and the input results were set as categories 1-5. If the expected output is consistent with the actual output, the identification effect will be regarded as good; otherwise, the effect will be bad. When the unimproved extreme learning machine was used for training, due to a small-scale data set, good results were achieved after training the 350 images in the training set. Calculation shows an average identification precision of 83.9% and an error of 16.1%. However, it can be observed that there is a certain deviation in the second group of experimental data if the experimental data are instable or have a large difference, indicating that the training data may be instable under the traditional ELM, because the initial weights and thresholds of the algorithm cannot be very well determined. Figs. 6-3 and 6-4 demonstrate that after ELM is optimized with the improved genetic algorithm, the identification effect is improved. Although there are some data deviations in the training set, the overall stability is improved. After 80 iterations under the genetic algorithm, the average identification precision reaches 96.34%, with an error of 3.66%, meaning that satisfactory results have been achieved. Then, five different types of crop diseases are calculated, with the identification precision and error shown in Tab. 2.

Table 2: Disease identification accuracy of traditional elm and optimized ELM

Different categories	Corn leaf spot	Grape black rot	Potato early bligh	Strawberry leaf blight	Tomato leaf mold
Improved-ELM	97.60%	96.67%	94.37%	95.22%	97.84%
Improved-Error	2.40%	3.33%	5.63%	4.78%	2.16%
ELM	80.56%	75.26%	84.70%	90.34%	88.64%
Error	19.44%	24.74%	15.30%	9.66%	11.36%

The identification performance of optimized ELM and traditional ELM for each type of disease is shown in Tab. 2, which shows that the identification effect is improved for different types of diseases after the ELM model is optimized with the improved genetic algorithm: The identification precision is 12.44% higher than that of non-optimized ELM model, with the error reduced to 3.66%. Therefore, the method proposed in this study is verified.

In addition to comparison with the traditional ELM model, several commonly-used machine learning methods were selected in this study to carry out experiments on the five different types of diseases. Such machine learning methods include random forest and support vector machine, with their trainings carried out under the same experimental platform. Tab. 3 shows the identification accuracies and errors both from the above machine learning algorithms and from the algorithm proposed in this study.

Table 3: Recognition performance under different machine learning

Different categories	Corn leaf spot	Grape black rot	Potato early bligh	Strawberry leaf blight	Tomato leaf mold
Improved Elm	97.60%	96.67%	94.37%	95.22%	97.84%
	2.40%	3.33%	5.63%	4.78%	2.16%
ELM	80.56%	75.26%	84.70%	90.34%	88.64%
	19.44%	24.74%	15.30%	9.66%	11.36%
RF	93.80%	86.10%	89.65%	94.57%	92.39%
	6.20%	13.90%	10.35%	5.43%	7.61%
SVM	92.44%	87.90%	93.67%	95.19%	91.74%
	7.56%	12.10%	6.33%	4.81%	8.26%

As can be seen in the table above, in disease identification for different crops, the method proposed by this study has better performance than other methods in terms of accuracy and error. Based on table above, the average identification precisions of trainings under different machine learning methods are shown in Fig. 7, and the specific recognition accuracy and error for each crop disease are shown in Fig. 8.

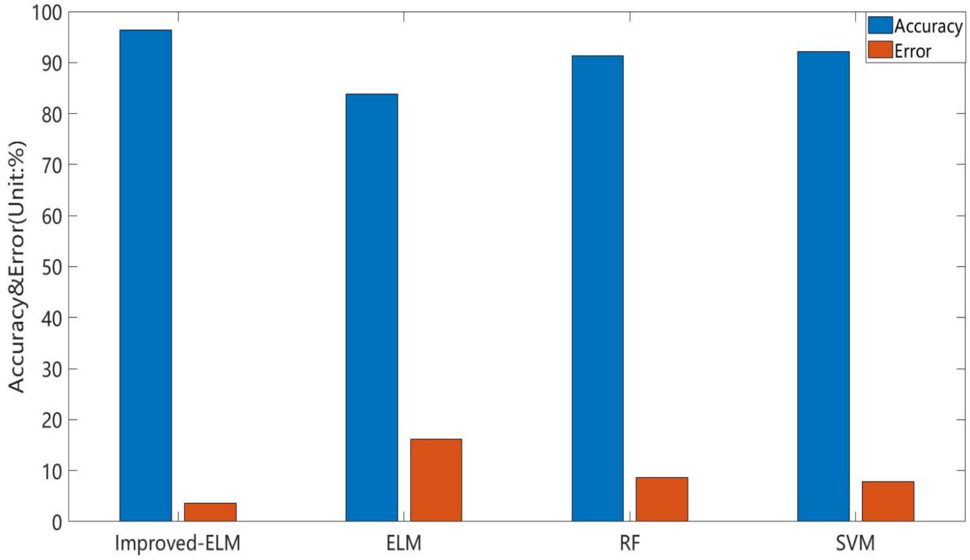
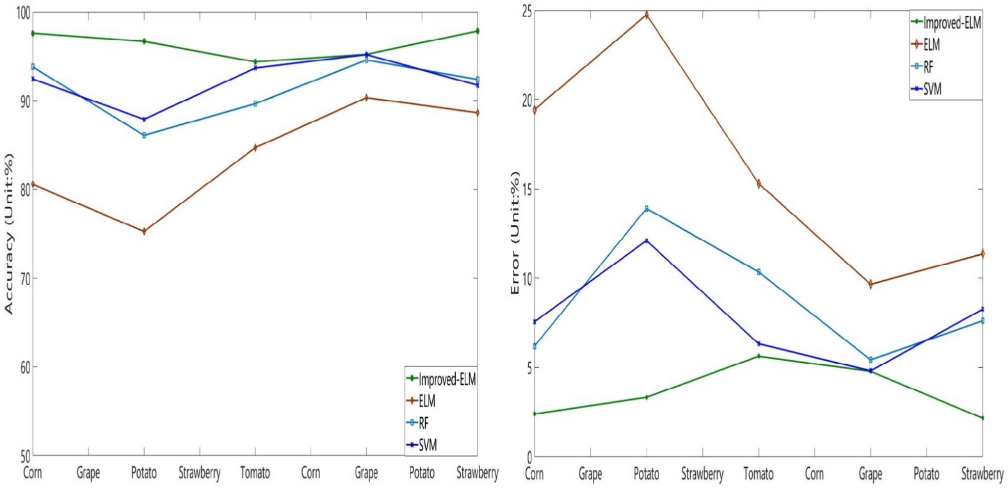


Figure 7: Average recognition accuracy and error



(a) Accuracy (b) Error

Figure 8: The specific recognition accuracy and error of each crop disease

As shown in Fig. 7, compared with other machine learning methods, the method proposed in this study has not only improved the average identification accuracy, but also reduced the error. From the discount trend in Fig. 8, it can be concluded that for the disease data characteristics of different crops, these commonly used machine learning algorithms generally perform well and, to a certain extent, can help effectively identify different types of diseases of crops. Compared with other machine learning methods, the ELM identification model optimized by the improved genetic algorithm performs better, so the effectiveness of this method is verified.

5 Conclusion

To address the shortcomings of traditional methods in crop disease identification, a new identification method is proposed based on the improved genetic algorithm and extreme learning machine. For different crop diseases, the hill-climbing algorithm was used to improve the genetic algorithm by optimizing the initial weight and threshold values of ELM, so as to obtain more powerful global search ability. This new approach is proved able to enhance the disease identification effect of ELM. Compared with other commonly-used machine learning identification methods, this new method can effectively improve the disease identification rate for different crops and improve the identification performance. Nevertheless, although this new method has delivered a high identification rate, the data set in this study has a small scale, leading to high identification deviation for some diseases in a complex context. So the validity of the method needs to be further verified against more characteristics of crop diseases and data sets.

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