



Identification of rice diseases using deep convolutional neural networks[☆]



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ABSTRACT

The automatic identification and diagnosis of rice diseases are highly desired in the field of agricultural information. Deep learning is a hot research topic in pattern recognition and machine learning at present, it can effectively solve these problems in vegetable pathology. In this study, we propose a novel rice diseases identification method based on deep convolutional neural networks (CNNs) techniques. Using a dataset of 500 natural images of diseased and healthy rice leaves and stems captured from rice experimental field, CNNs are trained to identify 10 common rice diseases. Under the 10-fold cross-validation strategy, the proposed CNNs-based model achieves an accuracy of 95.48%. This accuracy is much higher than conventional machine learning model. The simulation results for the identification of rice diseases show the feasibility and effectiveness of the proposed method.

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1. Introduction

Rice is one of the most important food crops in China and even in the world. Rice diseases have a devastating effect on rice production. Also, it is a major threat to food security. Thus, the diagnosis and identification of rice diseases play a very important role in ensuring the high yield, high quality and high efficiency of rice. The traditional method of detecting rice diseases requires lots of experts' experience and knowledge. With the development of computer and internet technology, farmers can search the rice diseases images database or consult the plant pathologists to judge rice

diseases remotely. The disadvantage is that not only the judgement is easy to be wrong, but also the efficiency is low.

In order to improve the accuracy and rapidity of the diagnosis results, many researchers have studied the automated rice diseases diagnosis based on pattern recognition and machine learning. Such as, using pattern recognition techniques [25], support vector machine [16], digital image processing techniques [2] and computer vision [1]. Meanwhile, these advanced techniques are not only applied to the diagnosis of rice diseases, but also to other crops, such as wheat [20], maize [34], cotton [29], tomato [5], etc.

The past 10 years have witnessed successful applications of deep convolutional neural networks (CNNs) in diverse fields including image classification [6,21], video classification [18], traffic sign recognition [17] and human action recognition [15], etc. The study of CNNs and related research have therefore gained persistent research interest since the early 1990s, see [10,12] and the references therein. During this period, Hinton and co-workers have done widely meaningful and fundamental research on deep neural network to improve algorithm performance and optimize architecture, see e.g. [3,23,24,27], and the references cited. A number of research have been made for CNNs to improve the original architecture of Krizhevsky et al. [21]. For example, Zeiler and Fergus [33] used stochastic pooling for regulation of CNNs and Simonyan and Zisserman [31] proposed very deep CNNs to 16–19 layers,

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which achieved the state-of-art accuracy on ImageNet Large-Scale Visual Recognition Challenge (ILSVRC) [26]. Especially, in March 2016, AlphaGo beat Lee Sedol in a five-game match, the first time a computer Go program has beaten a 9-dan professional, and it was a major milestone in artificial intelligence research [30,32]. LeCun et al. pointed out that deep convolutional neural networks have brought about breakthroughs in processing images, video, speech and audio in a survey paper published in Nature in 2015 [22].

Recently, several studies on automated plant disease diagnosis have been conducted using deep learning techniques [19,35]. Kawasaki et al. proposed a system based on CNNs to recognize cucumber leaf disease; it achieves an accuracy of 94.9% in distinguishing among melon yellow spot virus, zucchini yellow mosaic virus and a non-diseased class. Sanyal et al. have identified rice disease of brown spot and blast diseases by using color texture of rice leaf images [28].

As we all know that the machine learning technology is essential in the intelligent diagnosis of crop diseases. However, there exist some defects and difficulties in the above research, involving the recognition rate is higher for specific samples under certain circumstances. In the diagnosis model, some parameters are not optimal, the convergence speed of training algorithm is slow, and it is easy to fall into local minima, and so on.

So far, no research has been published which explores deep convolutional neural networks for rice diseases identification. The goal of this research is to construct deep convolutional networks model to achieve fast and accurate automated recognition by using rice diseases images. The 10 common rice diseases include rice blast (RB), rice false smut (RFS), rice brown spot (RBS), rice bakanae disease (RBD), rice sheath blight (RSHB), rice sheath rot (RSR), rice bacterial leaf blight (RBLB), rice bacterial sheath rot (RBSR), rice seeding blight (RSEB) and rice bacterial wilt (RBW).

The key motivation for developing the deep convolutional networks model for rice disease is to provide the farmers an easy-to-use system to detect early-stage infections by using common digital camera. Second, extracting effective features for identifying rice diseases is a critical but challenging task, and CNNs are highly expected to be automated feature learning from the raw inputs in a systematic way. Through the deep architecture, the learned features are deemed as the higher level abstract representation of low level raw rice disease images. In addition, to improve diagnostic results, the CNNs is regarded as one of the best classifications in pattern recognition tasks. So we develop the deep convolutional neural networks model for rice diseases identification in this paper.

In this paper, we present a novel rice diseases identification method based on deep convolutional neural networks. The proposed CNNs-based model can get higher classification ratio. On the basis of an analysis of structure and parameters in CNNs, the gradient-descent algorithm can be applied to train CNNs. A total of 500 rice leaves and stem images are pre-processed first, then the processed images are used to train CNNs. This CNNs model can improve the convergence speed while training the parameters in CNNs, and obtain a higher recognition accuracy than the conventional model. The main contribution of this paper is mainly twofold. (1) Convolutional neural network is first applied to the issue of the identification of rice diseases. Note that the proposed method can correctly and effectively recognize the 10 common rice diseases. (2) Experiment results show that the CNNs method can not only improve the convergence speed, but also obtain a higher recognition accuracy than other models: (1) standard BP algorithm; (2) support vector machine (SVM); (3) particle swarm optimization (PSO).

The advantages of the proposed CNNs are that images can be input directly to the model. First, sparse-auto encoding is used to learn the features from images. Second, we can classify images

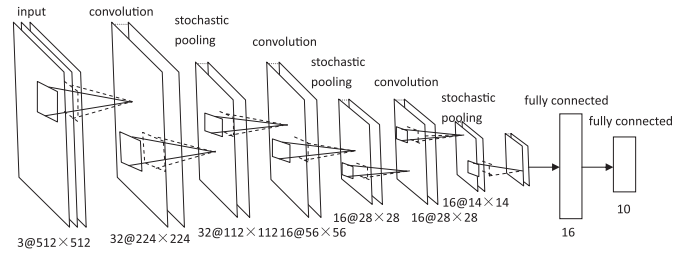


Fig. 1. The structure of deep convolutional neural networks.

Table 1
Related parameters of CNNs.

Layer name	Function	Weight filter sizes	Output tensor
Input			$3 \times 512 \times 512$
Conv1	Convolutional	16×16	$3 \times 224 \times 224$
Pool1	Stochastic pooling	5×5	$32 \times 112 \times 112$
Conv2	Convolutional	9×9	$64 \times 112 \times 112$
Pool2	Stochastic pooling	5×5	$64 \times 56 \times 56$
Conv3	Convolutional	5×5	$128 \times 28 \times 28$
Pool3	Stochastic pooling	5×5	$128 \times 14 \times 14$
Output	Softmax regression		$10 \times 1 \times 1$

from a reduced data set applying convolution and pooling. The stochastic pooling method is applied in the proposed CNNs model. For it is simple enough to randomly select elements in feature map according to their probability values, that is, the elements with large probability are easy to be chosen. Unlike max-pooling, the maximum element always chosen, and mean-pooling, the average value of the elements is chosen. Also, it strengthened generalization ability of the proposed CNNs model. Third, softmax regression learning algorithm can solve multi-classification problem. Finally, we can distinguish between 10 common different rice diseases.

The remainder of this paper is organized as follows. In Section 2, we describe the architecture and learning algorithm of CNNs. Section 3 introduces the rice disease identification method. The application of the developed CNNs to the problem of rice diseases recognition is presented in Section 4. Conclusions are given in Section 5.

2. Architecture of deep convolutional neural networks model

Inspired by classical and successful LeNet-5, AlexNet CNNs architecture and its performance improved by Ciresan et al. [6], Krizhevsky et al. [21] and LeCun et al. [23], we describe a kind of our multi-stage-CNNs configuration. The CNNs-based model includes convolution layer, stochastic pooling layer, and softmax layer. An illustration and related parameters are shown in Fig. 1 and Table 1.

The size of the input image is set to be $224 \times 224 \times 3$ according to the experience, which can be divided by 2, and computing capability of the computer. It is composed of many slices in the depth direction. One slice corresponds to many neurons, the weight in neurons can be thought as the convolution kernel, that is a square filter, such as 16×16 , 9×9 and 5×5 . These neurons respectively correspond to a local area in the image, and it is used to extract the feature of the region. Assume that the size of the input image is W , the size of the convolution kernel is F , the mobile stride of the convolution kernel is S , generally $S = 2$, padding P is used to fill in the input image boundary, usually $P = 0$, so the size of the image after convolution is $(W - F + 2P)/S + 1$. Then we get the output tensor.

2.1. Convolutional layer

The proposed CNNs are of hierarchical architecture, which contain three convolutional layers. The first convolutional layer is used to extract different low-level features from the input image, such as edges, lines and corners. The other two can get high-level features.

Each output map feature combines multiple input maps with convolutions. Generally, the output can be denoted by the following formula:

$$x_j^\ell = f\left(\sum_{i \in M_j} x_i^{\ell-1} * k_{ij}^\ell + b_j^\ell\right) \quad (1)$$

where ℓ represents the ℓ th layer, k_{ij} represents convolutional kernel, b_j represents bias and M_j represents a set of input maps. The detailed implementation of the CNNs can use a sigmoid function or a tanh function, also an additive bias can be applied in it. For example, the value of unit at position (x, y) in the j th feature map and the i th layer, denoted as v_{ij}^{xy} , is given by

$$v_{ij}^{xy} = \text{sigmoid}\left(b_{ij} + \sum_{p=0}^{P_i-1} \sum_{q=0}^{Q_j-1} w_{ij}^{pq} v_{(i-1)}^{(x+p)(y+q)}\right) \quad (2)$$

where $\text{sigmoid}(\cdot)$ is the sigmoid function, b_{ij} is the bias for the feature map, P_i and Q_j are the height and width of the kernel, and w_{ij}^{pq} is the kernel weight value at the position (p, q) connected to the (i, j) layer. The parameters of CNNs, such as the bias b_{ij} and the kernel weight w_{ij}^{pq} , are usually trained using unsupervised approaches [4,23].

2.2. Stochastic pooling layer

We use a stochastic-pooling layer to substitute a sub-sampling layer in CNNs [23]. Stochastic-pooling layer is used to reduce variance, it can compute the max value of a particular feature over a region of the image. Suppose the image features have small translations, it will ensure that we can obtain the same result. Stochastic pooling not only combines the advantages of meaning-pooling and max-pooling but also prevents over-fitting. It plays a very important role in rice diseases classification and detection.

In stochastic pooling, first, we need to compute the probabilities p for each region j according to the Eq. (3)

$$p_i = \frac{\alpha_i}{\sum_{k \in R_j} \alpha_k} \quad (3)$$

where R_j is pooling region j in feature map c , and i is the index of each element within it.

Then we sample from the multinomial distribution based on p to pick a location l within the region. The stochastic pooling operation can be denoted by $\text{Stochastic}(s)$, for each feature map c , the $\text{Stochastic}(s)$ is formulated by:

$$\alpha_{p,q}^{l,k} = \text{Stochastic}_{(m,n,i,j) \in p}(\alpha_{m,n}^{l-1,k} u(i, j)) \quad (4)$$

where $\alpha_{p,q}^{l,k}$ is the activation of the neuron at spatial coordinate (p, q) in feature map k in l th layer, $u(i, j)$ is the weighing window function.

The advantages of this implementation are that stochastic pooling layer not only makes the CNNs have faster convergence, but also improves generalization ability when processing superior invariant features.

2.3. Softmax regression

Softmax regression is applied in multi-class classification problem. The hypothesis function takes the form:

$$h_\theta(x) = \frac{1}{1 + \exp(-\theta^T x)} \quad (5)$$

Our goal is to train θ to minimize the cost function $J(\theta)$.

$$J(\theta) = -\frac{1}{m} \left[\sum_{i=1}^m \sum_{j=0}^l l\{y^{(i)} = j\} \log p(y^{(i)} = j | x^{(i)}; \theta) \right] \quad (6)$$

For training dataset $\{(x^{(1)}, y^{(1)}), \dots, (x^{(m)}, y^{(m)})\}$, $y^i \in \{1, 2, \dots, k\}$. In Softmax regression, the probability of classifying x as category j is:

$$p(y^{(i)} = j | x^{(i)}; \theta) = \frac{e^{\theta_j^T x^{(i)}}}{\sum_{l=1}^k e^{\theta_l^T x^{(i)}}} \quad (7)$$

Supervised learning algorithm is used to train the network to learn. The internal representation reflects the similarity among training samples. We design 10 classifications for rice disease identification. In order to know the feature representation learned by the deep convolutional neural network, the maximized activation neuron represents the recognized rice disease. At last, we visualize the image features by averaging image patches that are related with the neurons with stochastic response in an upper-layer.

2.4. Training algorithm

Also, we use back gradient-descent algorithm to train CNNs. It includes two stages of feedforward pass and back propagation pass. In feedforward pass stage, we consider a multiclass problem with c classes and N training samples. The squared-error function is given by

$$E^N = \frac{1}{2} \sum_{n=1}^N \sum_{k=1}^c (t_k^n - y_k^n)^2 \quad (8)$$

where t_k^n is the k th dimension of the n th pattern's corresponding label, and y_k^n is the value of the k th output layer unit in response to the n th input pattern.

Let ℓ represent the current layer, L denote the output layer and the input layer be denoted by l . The output of the current layer is defined to be

$$x^\ell = \text{sigmoid}(W^\ell x^{\ell-1} + b^\ell) \quad (9)$$

where W represents weight value matrix and b represents bias.

In back propagation pass stage, from higher layers to lower layers, the back propagated error can use the following recurrence function:

$$\delta^\ell = (W^{\ell+1})^T \delta^{\ell+1} \odot f'(W^\ell x^{\ell-1} + b^\ell) \quad (10)$$

where “ \odot ” represents elements multiplication. Finally, we will update the weight according to the following formulas:

$$\frac{\partial E}{\partial W^\ell} = x^{\ell-1} (\delta^\ell)^T \quad (11)$$

$$\Delta W^\ell = -\eta \frac{\partial E}{\partial W^\ell} \quad (12)$$

3. Rice disease identification method

3.1. Rice diseases images data acquisition and processing software

Rice diseases images database is created, which consists of a total of 500 rice diseases images. Some images of rice diseases

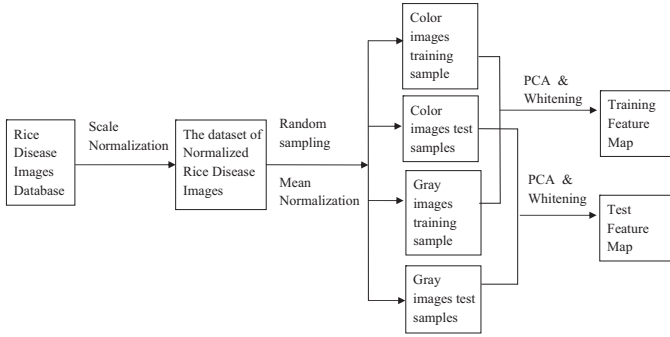


Fig. 2. Rice diseases images pre-processing procedure.

are captured from Heilongjiang Academy of Land Reclamation Sciences, China. The dataset consists of 500 common rice disease images. The 10 common rice diseases include rice blast (RB), rice false smut (RFS), rice brown spot (RBS), rice bakanae disease (RBD), rice sheath blight (RSHB), rice sheath rot (RSR), rice bacterial leaf blight (RBLB), rice bacterial sheath rot (RBSR), rice seeding blight (RSEB) and rice bacterial wilt (RBW). Canon EOS 5D Mark III (EF 24–70 mm F2.8L II USM) digital color camera has been used in capturing rice disease images with resolutions of 5760×3840 pixels. Some images of rice diseases are collected from agricultural pest and insect pests picture database (<http://bcch.ahnw.gov.cn/Right.aspx>). Some rice diseases images are scanned from book, titled with 'Rice Diseases and Insect Pests Atlas and Control Technology' [7,36].

The images are processed and analyzed by using digital image processing toolbox and stanford_dl_ex-masterCNNs toolbox in Matlab R2012a software.

3.2. Rice diseases pre-processing

In order to reduce the running time of matlab program, the size of the rice disease images are compressed from 5760×3840 to 512×512 . CNNs is a part-connected network, not a full-connected network. In full-connected network, if all nodes in input layer would connect all the nodes in hidden-layer, the parameters that be learned will become very much, and the training time will become very long. In part-connected network, the nodes in hidden layer just connect partial nodes in input layer. This method simulates the visual cortex in the human cerebral cortex, and different positions only respond to the local region. Since natural images are stable, that is, the statistical features of a part of an image are similar to those of other parts, so the characteristics of the parts which we learn are also applicable to other parts. Also, due to that all the rice diseases images are color images, the stationarity property does not hold across color channels, then we rescale the data in $[0, 1]$ and apply PCA and Whitening to get training feature and testing feature. The pre-processing procedure is shown in Fig. 2.

First, we turn the image into fixed-size 512×512 RGB image in order to reduce the dimension of training data and keep the details of the input image. Let n -dimensional vector x represent any one image, n is the product of the image width and height. The pre-processing on the N images in rice diseases database is computed from each pixel by the following formula:

$$x^i = \frac{\tilde{x}^i - \mu}{\sqrt{S + 8}} \quad (13)$$

where $\mu = \frac{1}{N} \sum_{j=1}^N x_j$, $S = \frac{1}{N} \sum_{k=1}^N (x_k - \mu)(x_k + \mu)^T$, \tilde{x}^i is the estimate of x^i .



Fig. 3. Rice sheath blight recognition image.

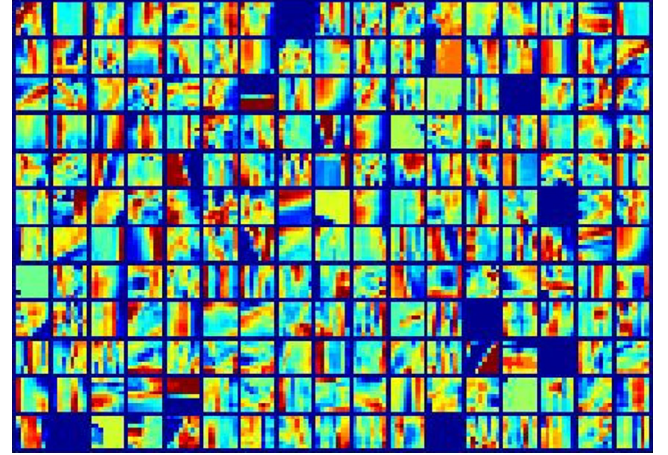


Fig. 4. Rice disease image patches.

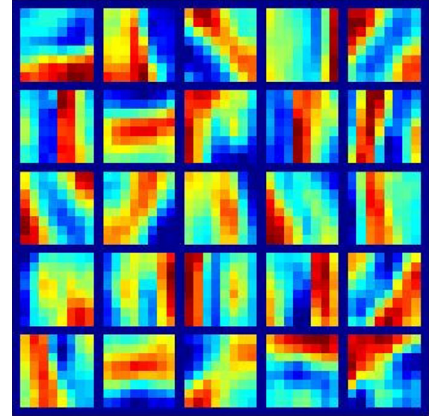


Fig. 5. The corresponding feature map of rice disease image patches.

Then apply ZCA-Whitening method to remove correlation between data X according to the following formula:

$$X_{ZCA, Whitening} = U \cdot \frac{x_{rot}}{S + \varepsilon} \cdot U^T \quad (14)$$

where $U = \text{svd}(S)$, $x_{rot} = U^T \cdot x$, the reasonable range of parameter ε is in 0.01–0.1.

4. Rice disease recognition simulation examples

The proposed CNNs model is applied to rice disease recognition problem. We use database of 500 images labeled of 10 kinds of rice diseases. One of the rice disease images is shown in Fig. 3.

Randomly select 10,000 12×12 patches from the 500 natural images, according to the pre-processing procedure introduced in Section 3.2, we get one of the rice disease image patches as shown in Fig. 4 and the corresponding feature map is shown in Fig. 5.

Table 2

Recognition performance using mean-pooling, max-pooling and stochastic pooling.

Different pooling	Mean-pooling	Max-pooling	Stochastic-pooling
Recognition accuracy (%)	92.11	93.24	95.48

Table 3

Recognition performance using different convolutional filter size.

Different convolutional filter size	5 × 5	9 × 9	16 × 16	32 × 32
Recognition accuracy (%)	93.15	92.56	93.29	92.48

Table 4

Simulation results using proposed method compared with BP, SVM and PSO.

Algorithm	CNN	BP	SVM	PSO
Accuracy rate (%)	95	92	91	88
Missing report rates (%)	5	8	9	12
False report rate (%)	0	0	5	10

Before training, we need to normalize the brightness and contrast of all the training samples patches. The experiment is that, for each sample, we subtract the mean and divide the standard deviation. In addition, when divided by the standard deviation with the denominator being 0, in order to avoid and suppress noise, we give the standard deviation of adding a small constant. For the range of gray scale [0, 255], the variance plus 10 can get better results.

Under the 10-fold cross-validation strategy to train and test, and compare the mean-pooling, max-pooling and stochastic pooling, the results are shown in Table 2, from which it can be seen that stochastic pooling gained better results. Also, compare the convolutional filter sizes of 5 × 5, 9 × 9, 16 × 16 and 32 × 32, the recognition performance is shown in Table 3.

As we can see, different convolutional filter sizes have little effect on the recognition results.

The compared results with BP method, support vector machine (SVM) method and particle swarm optimization (PSO) are shown in Table 4.

5. Conclusions

CNNs is a valuable pattern-recognition method both in theory and in application. In this paper, we proposed an innovative technique to enhance the deep learning ability of CNNs. The proposed CNNs-based model can effectively classify 10 common rice diseases through images recognition. The application to the rice disease identification shows that the proposed CNNs model can correctly and effectively recognize rice diseases through image recognition. Compared with the other model, the proposed method has a better training performance, faster convergence rate, as well as a better recognition ability than the other model.

Deep convolution neural networks have achieved great performance breakthroughs in machine learning fields, but there still exist 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 deal of experiments. The second is that the efficient deep learning algorithm is still depending on large-scale datasets, such as Imagenet ILSVRC containing millions of training examples. To improve rice diseases identification accuracy, we still need to provide thousands of high-quality rice diseases images samples. Furthermore, there are a large number of parameters in CNNs, and how to find the optimal parameters is also a research challenge.

In future work, we plan to apply other deep architectures and other training algorithms, such as the restricted Boltzmann ma-

chine [14] which achieves a better performance on object recognition. We can extend this model for fault diagnosis. Moreover, we plan to have a deeper analysis of the training method with and without labeled samples. The results in this paper could be further extended to the distributed state estimation problems for sensor networks [9] and nonlinear time-varying systems [8,11,13].

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