Research on Microbial Image Classification Algorithm based on Residual Network

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Abstract

With the progress in biology, food and other fields, the importance of microbial classification research has gradually increased. In this study, the residual network model based on deep learning was introduced to classify microbial species, and a residual network model was established for microbial classification by pre-processing and data enhancement of microbial images. The accuracy of the model is about 93% when experiments are carried out on the microbial image dataset. In the field of microbial classification, the classification efficiency is improved, and there is no need to manually classify microbial species.

Keywords

ResNet; Deep Learning; Microorganism.

1. Introduction

Most algal microorganisms are native lower organisms that can perform photosynthesis. Most are eukaryotic organisms, and a small number are prokaryotes (such as Cyanobacteria, etc.). They are mainly aquatic. Because of their small size, most individuals are only a few millimeters to tens of millimeters, and their morphological features usually require the use of tools to clearly see. There are many types of algal microorganisms belonging to most categories of the plant and animal kingdoms. They are large in number and widely distributed. They exist in all sea areas of the world. According to statistics, there are more than 1,300 types of plankton in my country alone , there are already more than 8,900 species of algae, which are a key component of marine life[1].

With the further improvement of technological level, the development of the environment is increasing, and the damage to the world's environment is becoming increasingly serious. On the one hand, algae microorganisms are an indispensable part of the ecosystem. On the other hand, they also cause various algae blooms, The real culprit behind red tide and other natural disasters is that the stability of the marine ecosystem has been severely damaged this year. Marine pollution and water body eutrophication are serious. Their distribution, quantity and type are closely related to human life and have profoundly affected human life[2]. So we need to classify and identify microbes to make people's lives better.

2. ResNet-18 Network Structure

ResNet-18 deep residual network[3] (ResidualNeuralNetwork) was proposed by He Kaiming and others. The main contribution of the residual neural network is the discovery of "Degradation" and the invention of the residual structure for this phenomenon. "Shortcutconnection" eliminates the neural network training problems caused by degradation phenomena. The residual structure is shown in Fig. 1. The residual structure solves the problem of being unable to achieve linear transformation

due to adding too many network layers for nonlinear transformation by adding additional connecting lines[4]. ResNet allows the output of a certain layer to directly skip one layer or multi-layer network and directly input to subsequent layers by introducing connecting lines in the residual block. In this way, even if some layers have meaningless transformations, subsequent layers can accept the information of previous layers without losing the gradient.
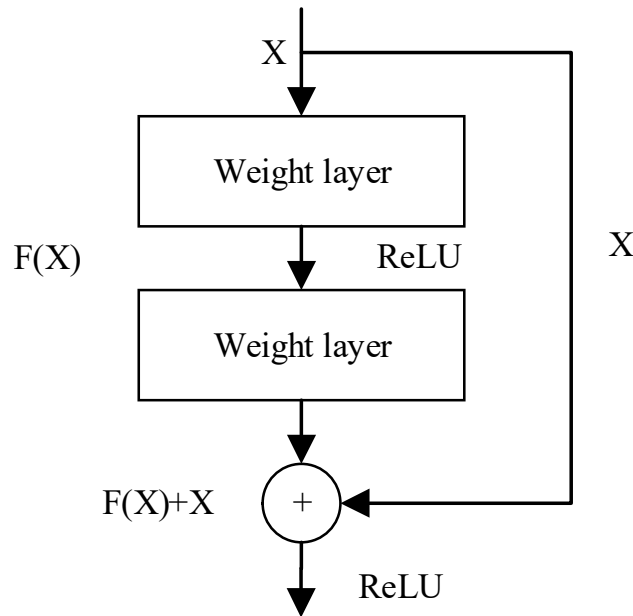

Fig. 1 residual structure

The Resnet18 network consists of 17 convolutional layers and 1 fully connected layer. The depth of the network is 18 layers, and the batch normalization layer and pooling layer are not calculated. The network structure of ResNet18 is shown in Table 1 below.

Table 1. ResNet18 Network structure table

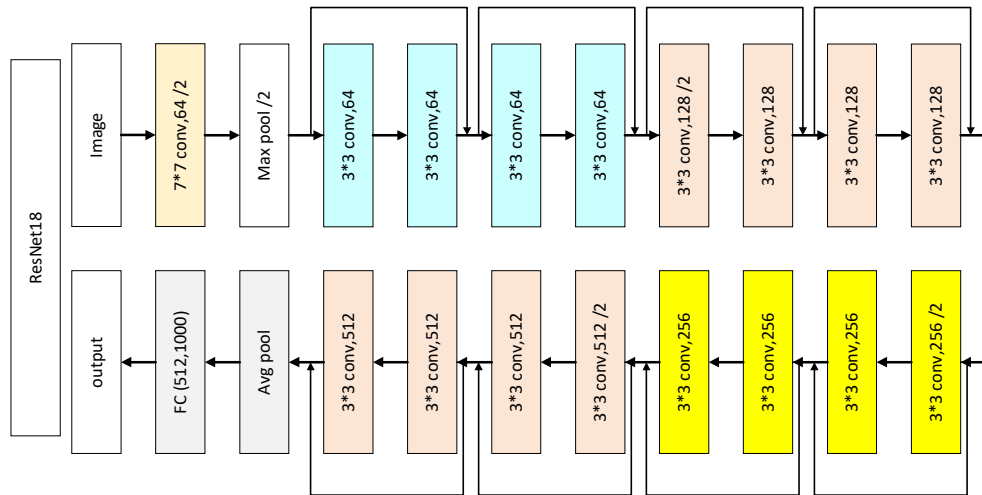| residual block	Conv1	Conv2_x	Conv3_x	Conv4_x	Conv5_x
ResNet18	7×7 $64, stride\ 2$ 3×3 Max pool stride 2	$\begin{bmatrix} 3 \times 3, & 64 \\ 3 \times 3, & 64 \end{bmatrix}$ $\times 2$	$\begin{bmatrix} 3 \times 3, & 128 \\ 3 \times 3, & 128 \end{bmatrix}$ $\times 2$	$\begin{bmatrix} 3 \times 3, & 256 \\ 3 \times 3, & 256 \end{bmatrix}$ $\times 2$	$\begin{bmatrix} 3 \times 3, & 512 \\ 3 \times 3, & 512 \end{bmatrix}$ $\times 2$
Output	112×112	56×56	28×28	14×14	7×7

Fig. 2 ResNet Network structure diagram

The ResNet network has four stages. In the first stage, the network model inputs a three-channel image with a data size of 224*224. It first passes through a 7*7 convolution layer and then is sent to the second stage through the maximum pooling layer. In this stage, 4 residual blocks are used to complete the feature extraction of the network. In each residual block, a 1*1 convolution kernel is used with step size adjustment to halve the size of the output feature map and double the number of channels to maintain information. The quantity remains unchanged to facilitate better feature extraction. The third stage is the average pooling layer that programs the input data into a one-dimensional vector and sends it to the fourth stage. The fourth stage uses a fully connected layer to integrate and map all one-dimensional features to the final output to obtain the predicted classification result.

The ResNet18 network uses the cross-entropy function method to calculate the loss value, combined with the Adam optimizer to improve the accuracy of the training model and reduce the loss value, and finally the classifier performs output recognition. The following is the formula for the cross entropy function:

$$H(p,q) = -\sum_{i=1}^{n} p(x_i) \, log(\, q(x_i)) \tag{1}$$

3. Experimental Design

The number of images for classification pre-training is 840[5]. The microbial images are randomly divided into a training set and a test set at a ratio of 8:2. The training uses the ResNet-18 network, which is sent to training after image preprocessing. The training rounds are 30 times, and the cross loss function is the CrossEnteropyLoss function. The specific training parameter settings are shown in the Table 2below.

Table 2. Training parameter table

criterion	CrossEnteropyLoss
epochs	30
optimizer	Adam
Step_size	5
gamma	0.5
bitch_size	32

In order to scientifically evaluate the microbial classification and identification model[6], it is necessary to select appropriate evaluation indicators as indicators to judge the quality of the model. For model evaluation, commonly used indicators include Accuracy, Precision, Recall, F1-score and other specific calculation formulas as shown in the table. Accuracy identifies the overall accuracy of the model and calculates both positive and negative samples. Accuracy is an evaluation of the accuracy of both positive and negative samples of the model. It is limited to reflecting the accuracy of the overall model and cannot evaluate the accuracy of the model as a whole. Make corresponding judgments about the performance of the model; Precision looks at how accurate the model as a whole is, so it only determines whether the positive samples of the model are correct; recall rate is the probability of the correct sample predicted by the model among the original samples. Ideally, the higher the precision rate and recall rate, the better. However, in actual processing, it is contradictory to have both of them high. When one of the two indicators increases, the other will decrease. Therefore, it is necessary in different situations. Determine which indicator is more important based on the actual situation, and achieve the goal by improving the corresponding indicator; in the process of model indicator evaluation, in order to take into account both the precision and recall rates, the F1 value is proposed. The F1 value combines precision and recall. The two indicators of recall can make a better comprehensive evaluation of the network model. as shown in Fig. 3.
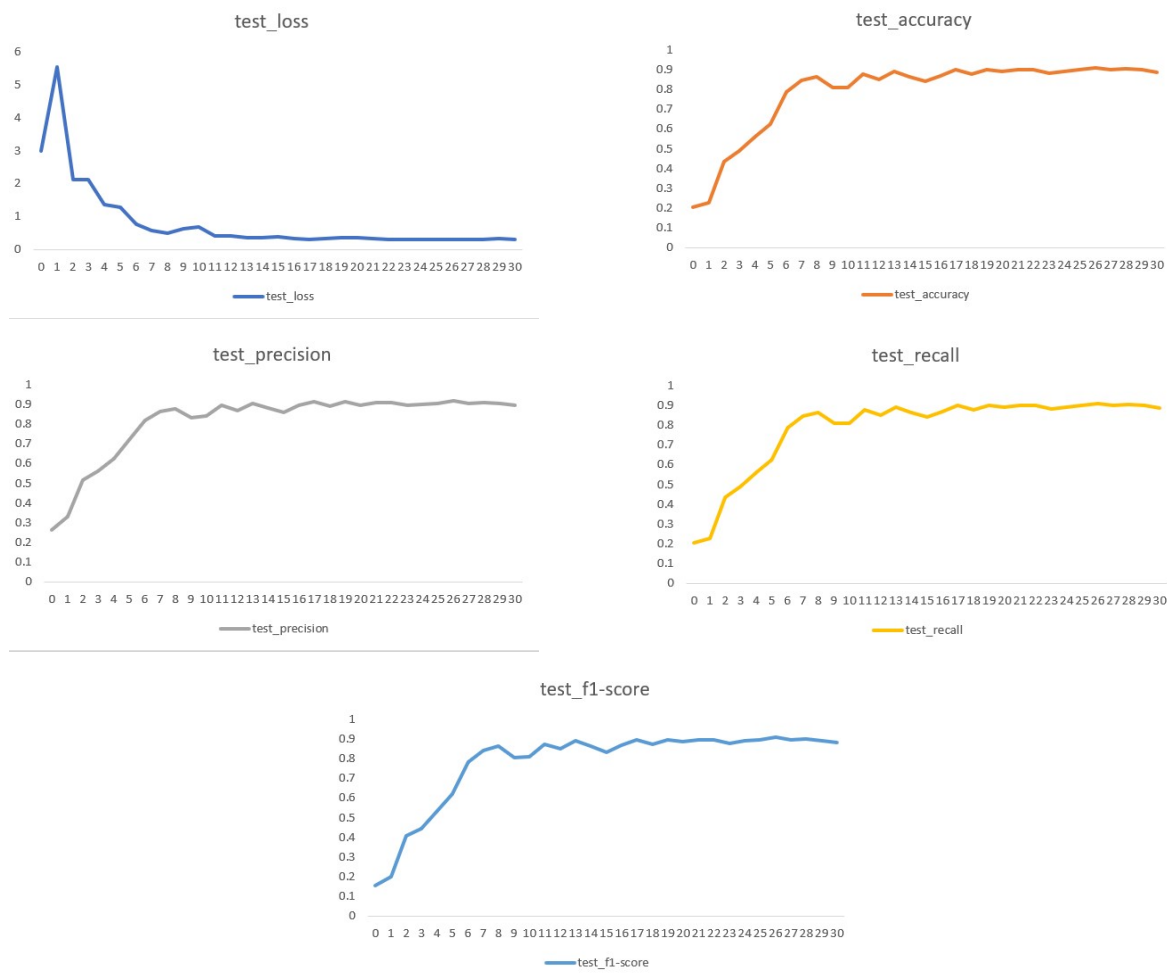

Fig. 3 Test set classification evaluation index

According to the experimental results, the accuracy of the entire set of microbial classification and identification algorithms reached 0.929 in the test set.

4. Conclusion

Through the research on microbial classification and recognition algorithms, a microbial data set for the classification algorithm was established. Through the training of the residual network ResNet18 network model, good recognition performance was achieved in predicting the microbial images of the test set. For the training set image recognition accuracy can reach 0.947, and for the test set image recognition accuracy can reach 0.929. This paper proposes the research of microbial classification and recognition algorithm and its systematic method, which solves some problems and deficiencies in the speed and accuracy of current microbial detection. The microbial classification and recognition and detection system can realize the automatic identification and detection function of microorganisms, and can store microorganisms and record their related information in the warehouse, but it is insufficient in the identification of microbial species and quantity. Only 21 microorganisms can be identified, and the network model is too simple. The system will be improved in the following aspects to make it more intelligent and rational.

Acknowledgments

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