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Data-Fusion Based on Transfer Learning for Plant Disease Recognition

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In this paper, the research focused on wild and introduced cultivated flowers with multiple diseases such as Stephanitis, Sooty Mould, Xanthosis, and Leaf Blight, utilizing transfer learning and data fusion technology to construct a plant disease detection model employing Faster R-CNN. The self-built data set collected during the flower growth cycle was trained and identified. To solve the problem of disease category imbalance in the actual collected data samples, the data of small category samples is enhanced from the perspective of category balance and label balance, and FocalLoss is used to improve the original classification loss function. Based on this self-built data set, the constructed IFRCNN disease detection model was compared with the SSD (Single Shot multibox Detector), ResNet18 and Yolov3 models. The results showed that for several common plant diseases in the dataset, the mAP of IFRCNN disease detection model was significantly higher than that of the other three models. It can effectively locate plant leaf disease areas, realize the detection of multiple diseases, and provide reference for accurate disease prevention and control.

KEYWORDS: Transfer Learning; FocalLoss; Faster R-CNN.

1. Introduction

Plant diseases and insect pests are one of the most serious natural disasters, which have a direct impact on the yield of agricultural crops, and are also one of the most complicated and difficult problems in plant growth and production, affecting global production and ecological security. FAO estimates that plant disease costs the global economy more than $220 billion a year. Data from China's forestry department shows that during the "11th Five-Year Plan" period, forest diseases and pests killed more than 40 million trees each year, causing an annual loss of more than 110 billion yuan. In recent years, factors such as global warming and frequent extreme weather have also made the occurrence of plant diseases and pests more frequent and widespread. Therefore, timely and accurate identification and control of plant diseases has become an urgent and important research topic. However, there is an increasing variety of plant pests and diseases, some of which are very similar to each other and difficult to distinguish. In addition, the limited scientific and cultural level of some cultivators, management negligence and other factors make the diseases and pests cannot be found timely and accurately, which leads to the delay of the best period of control. Thus, it can be seen that how to timely and accurately detect plant pests and diseases is a key problem faced by agriculture and forestry plants.

With the rapid development of deep learning, machine vision, Internet of Things and other technologies, researchers have put forward many solutions for this. Since 1980, from traditional shallow machine learning to deep learning has been well applied in plant pest identification. Through investigation, it is found that existing researches are mainly based on traditional image recognition methods and object detection methods based on deep learning, and most of them focus on cash crops such as fruits and vegetables and grains [2, 3, 5, 8, 10, 14, 15, 18, 23, 24] as research objects. For example, Mengistu et al. [11] cut and median filter the image of three important leaf diseases of coffee, and used K-means method to segment the image. After dimensionality reduction by principal component analysis, 5 gray co-occurrence matrix texture features and 6 color features are extracted, and feature optimization is carried out by genetic algorithm, the adaptive radial basis function (RBF) neural network classifier can recognize 2730 test samples with an accuracy of 90.07%. Chong et al. [13] experimented with histogram features of grayscale images of strawberry leaves by using support vector machine (SVM), K-nearest neighbor (KNN) and naive Bayesian Support vector machine. A recognition algorithm for strawberry snake eye disease based on gray histogram features was proposed.

The method of deep learning is to extract Galway's abstract features from a large number of samples by deepening the network structure. However, due to the limitation of the amount of data, the accuracy error of multi-scale and multi-target detection in complex natural scenes is large, especially in the special cases such as occlusion and texture similarity. Weiyin et al. [22] improved the feature extraction network of RetinaNet by combining DenseNet enhanced feature reuse, so as to improve the recognition rate of crop pests by the deep network model. Xuesong et al. [1] proposed a disease and insect detection algorithm for crops based on Res2NeXt50, which replaced 7×7 convolution with a new hybrid convolution, improved subsampling to enhance information fluidity, and reduced model computation. Yanxin et al. [9] used Darknet53 feature network, combined with K-means++ algorithm to classify the fused features and predict their positions, and constructed a YOLOv3-based tobacco disease detection model with a Miou of 0.81 and a mAP of 0.77. Singh et al. [21] reviewed the application of machine learning technology in plant disease detection from the perspective of data acquisition and availability of data sets. The effectiveness of most existing methods in field plant disease detection is very different, and the generalization ability has not been explored.

Currently, the emphasis of pest and disease detection in agriculture and forestry lies predominantly on crops. However, this paper delves into the study of diseases affecting both wild and introduced rhododendrons. It involves the systematic tracking and compilation of various diseases encountered during their growth cycle. Furthermore, leveraging data fusion technology, datasets of disease occurrences in natural settings have been meticulously constructed. By integrating the concept of transfer learning, we propose a pest detection model rooted in Faster R-CNN, aimed at enhancing the efficacy of prevention and control measures against flower diseases. In this paper, we will elucidate our work in detail across four dimensions: data collection and processing, the construction of our detection model, experimental outcomes, and potential future research avenues.

2. Disease Detection Model Based on Faster R-CNN

2.1. Plant Disease Data Set

Due to the intervention of pathogenic organisms or unfavorable environmental conditions, such as rainfall and temperature fluctuations, plants exhibit varying pathological features in their physiology, tissue structure, and morphology. Moreover, the characteristics of diseases and pests that may arise undergo significant changes with the shifting seasons and growth stages of plants. To gather more comprehensive and authentic experimental data, the experimental personnel conducted field tracking and data collection at the flower cultivation base of the local forestry science institute. This involved capturing actual images multiple times throughout the flower's growth cycle, ensuring comprehensive coverage. By utilizing diverse shooting equipment and varying factors like angles, distances, and brightness, the team aimed to incorporate as many disease and pest characteristics across different periods as possible into the collected data.

Table 1

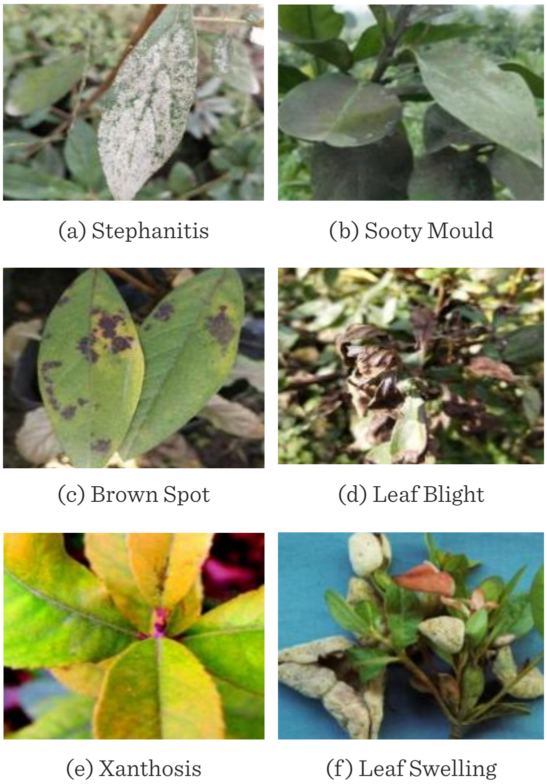
Details of the original data set

Serial Number	Disease Category	Number Of Original Samples
1	Stephanitis	880
2	Sooty Mould	330
3	Brown Spot	605
4	Xanthosis	1006
5	Leaf Swelling	818
6	Leaf Blight	115
Total		3754

In one year, a total of 3,754 disease pictures were tracked and taken (the detailed quantity of various samples is shown in Table 1), mainly including the pictures of multiple diseases in the growth process of six kinds of flowers, such as crown bug, brown spot and leaf blight (as shown in Figure 1).

Figure 1

Example of rhododendron leaf disease



(a) Stephanitis (b) Sooty Mould

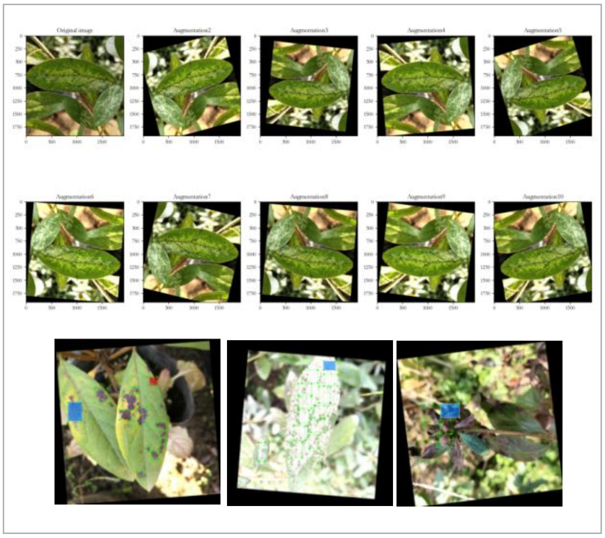
(c) Brown Spot (d) Leaf Blight

(e) Xanthosis (f) Leaf Swelling

Affected by many uncontrollable factors such as natural conditions and the unpredictability of plant growth, the original data set showed certain limitations in terms of the overall data amount and the distribution balance of various samples. This may cause some challenges to the subsequent data analysis and model training, so the original data set is extended by data enhancement in this paper. In the process of data enhancement, considering that color changes may have adverse effects on model training, operations such as overcoding and color transformation that may have a greater impact on model training are avoided in the process of enhancement. In particular, operations such as Gaussian blur, mirroring, rotation and brightness transformation are selected (as shown in Figure 2). In this paper, Gaussian noise, which is normally distributed, is used, and its value is distributed according to Gaussian probability distribution, and different images are generated by increasing the disturbance spectrum effect and the interference to the image data. This method can not only be used for data enhancement, but also improve the ability of the model to learn mapping rules from the input space during training, so that the model can show better adaptability and robustness in the face of unknown data. In addition, due to the great difference in the intensity of light at different times and in different weather during field detection in natural environment, the detection results are greatly affected. Therefore, the paper also enhanced the brightness of the samples and appropriately increased the noise, as shown in the last three sample examples in Figure 2.

Figure 2

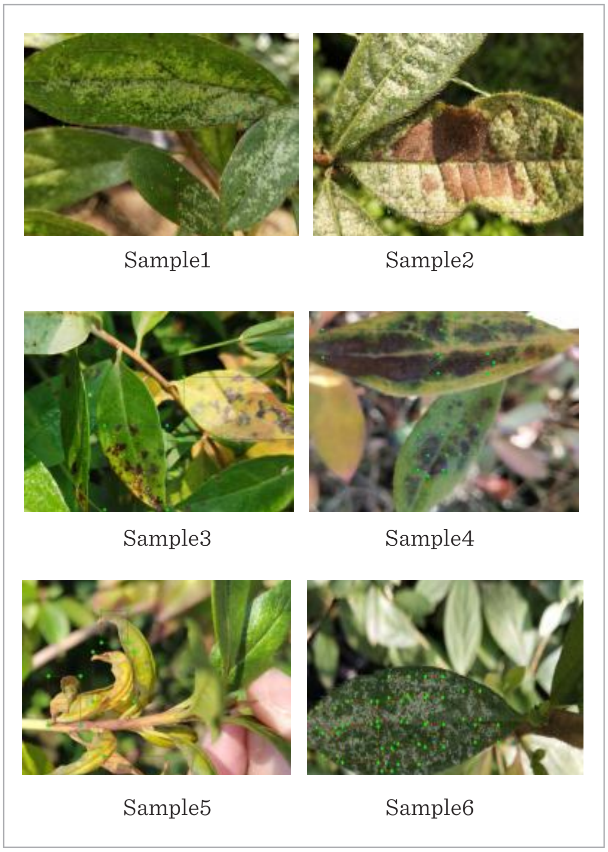
Sample data enhancement example



For the constructed data set, Exif elimination of the leaf image was done by the image preprocessing program written in python. The pre-processed images were manually classified according to disease category, and the annotation tool LabelImg was used to mark the disease area more efficiently. The pictures are taken in a natural environment, and most of the pictures contain multiple leaves, so the annotation is mainly done in two ways. One is to make large labels for disease areas per leaf (samples 1-3 in Figure 3), and the other is to make small labels for different disease areas in each leaf (samples 4-6 in Figure 3). In order to solve the problem of unbalance of data set caused by sample differences among different disease categories and improve the recognition performance of the model, sample balance was carried out on the original data set from the two perspectives of the number of labels and the number of pictures of each disease sample.

Figure 3

Example of sample labels



Sample1 Sample2

Sample3 Sample4

Sample5 Sample6

2.2. Construction of Detection Model

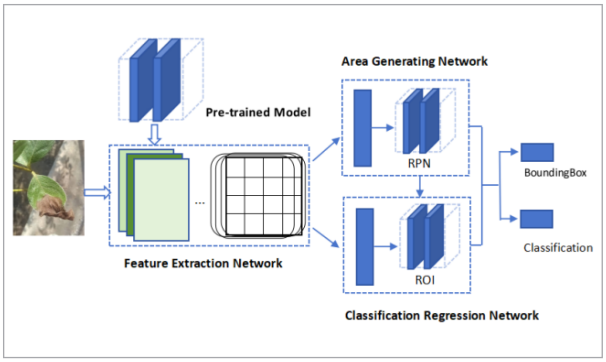
The Fast R model was proposed by Girshick et al. [4] in 2015, which was inspired by the SPP-Net model. The model adopts the multi-task learning mode of classification and regression simultaneously, and integrates three modules of feature extraction, region classification and boundary box regression, which not only saves the space used to store the middle layer features, but also greatly improves the efficiency of model detection. Even so, the model is still unable to meet the needs of real-time detection. Subsequently, Ren et al. [16] improved it and proposed the Faster R_CNN model in 2017.

On the basis of maintaining the good performance of Fast R-CNN, Faster R-CNN combines the recently popular deep learning term “attention” mechanism, and further introduces RPN (Region proposal networks) into Fast R-CNN network. Instead of the selective search method in Fast R_CNN model, a unified network with convolution features shared by two tasks is generated, and real time detection is realized. In this study, the Faster R-CNN as the main backbone network combined with Inception_v2 feature extraction network will be used to build a plant disease and insect detection model (as shown in Figure 3). At the same time, Focal Loss will be used to further optimize the detection algorithm to improve the detection ability of the model for small targets and rare categories. Through this combination, the model can not only identify and locate diseases and pests on plants in real time, but also accurately identify tiny disease spots or pests in a complex background, providing strong technical support for precision agriculture.

In this model, the input image is represented as a three-dimensional tensor with dimensions of Height (height), Width (width) and Depth (depth). The input image is first processed by a series of feature extraction networks that can effectively extract useful information to obtain a feature map for the following two key processing steps, forming the two branches in Figure 4. The above branch RPN (Region Proposal Network) is used as an independent module to calculate and generate candidate target regions. Through Softmax function and calculated offset, the classification of Foreground Anchors and the modification of the position and size of the anchors are completed respectively. The generated Proposals represent the possible locations of pests and diseases in the image. Therefore, these proposals are the key for the subsequent detection of pests and diseases. At the same time, the convolutional feature map is also input into the following branch ROI Pooling layer. It Maps the candidate Proposals obtained in the RPN network to the shared Feature Map, so that each candidate Proposal can correspond to an area in the Feature map, so that a Proposal feature map containing detailed information can be calculated. Finally, the model completes regression and classification operations through the fully connected layer to obtain the exact location and category of the pest target.

Figure 4

IFRCNN Disease Detection Model



2.3. Feature Extraction

The experiment in this paper employed a rigorous parameter-tuned transfer learning approach [12], fine-tuning the Inception_v2 network, which was pre-trained on the ImageNet dataset, to construct a feature extraction network suitable for plant disease detection. The Inception_v2 model, as the second generation of the Inception model developed by the Google research team based on Inception_v1, has a core design philosophy of replacing the original 5*5 convolution kernels in the Inception module with two smaller 3*3 convolution kernels. Through this optimization, not only the total parameters of the model are significantly reduced, but also the overfitting phenomenon is effectively alleviated [20]. In addition, the detection model incorporates Batch Normalization (BN) technology [6, 19] to independently standardize the input of each neuron, significantly reducing the coupling between gradient and parameter initialization, and effectively preventing the problem of gradient explosion and gradient disappearance. At the same time, in order to accelerate the training process and improve the convergence efficiency of the model, a higher learning rate is adopted in the training process.

At the commencement of the training process, the mean value (as Equation (1)) and variance (as Equation (2)) of each mini-batch throughout the iterations were initially extracted.

$$\mu_\beta = \frac{1}{m}\sum_{i=1}^{m} x_i \tag{1}$$

$$\sigma_\beta^2 = \frac{1}{m}\sum_{i=1}^{m} \left(x_i - \mu_\beta\right)^2 \tag{2}$$

In this context, m represents the number of samples in the mini-batch. Subsequently, each feature within the mini-batch undergoes standardization, as indicated by Equation (3).

$$\hat{x}_i = \frac{x_i - \mu_\beta}{\sqrt{\sigma_\beta^2 + \xi}}, \tag{3}$$

where ξ is a constant, which is used to prevent cases where the denominator is zero. Because, in practice, we usually do not want the mean of all the samples to be 0 and the variance to be 1. Therefore, in order to better adapt to the distribution of data, scaling parameters γ and migration parameters β are used to further process the normalized features to obtain the final output feature y_i.

$$y_i = \gamma * \hat{x}_i + \beta \tag{4}$$

The existing algorithms based on CNN have the problem of scale sensitivity of convolutional features in target detection task, while the leaf size is different in plant disease detection task due to distance. Common RoI pools simply fit preset feature lengths by copying feature values, a practice that distorts the original structure of small scale objects. Therefore, the deconvolution pooling layer of bilinear kernel is used in this paper to preserve the context information of small scale objects, thus helping to generate features that are faithful to the original structure.

2.4. Loss Function

Since plant pests and diseases are restricted by various uncertain factors such as natural environment, climate, season, etc., the characteristics of the collected pests and diseases differ greatly in different growth stages. In order to balance the losses of the majority and minority classes, the cross-entropy loss function with balance coefficient [7] was adopted in this paper. A typical binary cross entropy loss can be defined as Equation (5), where p_t represents the confidence that is predicted to be of the correct class.

$$L = \begin{cases} -\log(p_t) & y = 1 \\ -\log(1 - p_t) & y = 0 \end{cases} \tag{5}$$

In order to balance the imbalance between the background and the target class and the class proportion imbalance of the sample itself, the loss function is expressed as Equation (6) after the introduction of the balance factor.

$$\mathrm{FL}(p_t) = -\alpha(1 - p_t)^\gamma \log(p_t) \quad \gamma \geq 0, \tag{6}$$

where, γ is the regulatory factor, $(1 - p_t)^\gamma$ is used to reduce the loss contribution degree of easily classified samples and increase the loss proportion of difficult to classify samples, so that the model pays more attention to difficult to classify samples. The experimental results show that the best effect is obtained when the balance factor α=0.25 and the regulation factor γ=2.

3. Experiment

3.1. Training Process

The experiment is conducted on the Ubuntu 18.04 operating system, employing the deep learning algorithm framework, TensorFlow-GPU 1.13.1. The whole training process is carried out alternately by the region generation network and the detection network. The entire training procedure is conducted in an alternating fashion between the region generation network and the detection network. Initially, the pre-trained model of the feature extraction network is loaded, allowing the region generation network to undergo end-to-end training. Following this, the detection network is trained, leveraging both its own pre-trained model and the output proposals from the region generation network. During alternate training, the extraction parameters of the shared feature layer remain fixed, while the parameters of the detection network are employed to initialize the Region Proposal Network (RPN). Additionally, the parameters involved in the network's candidate region extraction process and the classification and regression components of the detection network are generated within the training region.

During the training process, it was found that if the network fine-tuned the parameters before adapting to the new data, a relatively large gradient may lead to the contamination of the originally trained better parameters. Consequently, during the migration of training processes, the new dataset undergoes a predefined number of epochs of initial training prior to the application of fine-tuning techniques. This approach aims to minimize the risk of altering parameters prematurely, before the network has fully acclimated to the new data, thereby preventing large gradients from corrupting the initially well-trained parameters. In this study, a smaller dataset was employed compared to those of ImageNet and COCO [17]. To prevent excessively rapid weight distortion in pretrained network models and maintain the smoothness of the weights, a reduced initial learning rate of 0.0002 was applied to the fine-tuned hidden layers. Additionally, the regularization coefficient was established at 0.0005 to curb overfitting. Compared to randomly initializing the weight parameters across all network layers, employing transfer learning through parameter fine-tuning proves more beneficial for the network's rapid convergence when starting with the training dataset.

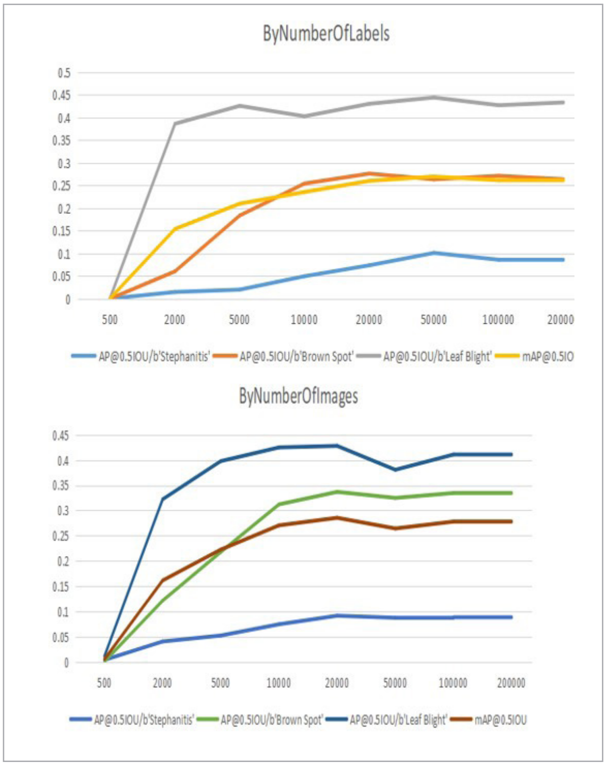
When RPN generates RoIs, Non-maximum suppression is used to suppress NMS=0.7, and 2000 RoIs with the highest probability are selected. In addition, in order to improve the processing speed, only 50 candidate boxes were selected in the experiment, and still maintained a good effect. The maximum number of iterations was set at 200,000, by which point the loss decreased to 0.001 and continued to exhibit a stable decline.

3.2. Analysis of Experimental Results

The experiment starts with the equilibrium analysis of the samples. The original data were processed from the two dimensions of the number of samples of different categories and the number of labels, and the enhanced pest and disease sample data set was randomly divided into a training set and a test set according to the ratio of 8:2, and random verification was done in the natural scene. To demonstrate the efficacy of the PD-IFR CNN model for disease and pest identification, this paper employs average precision (AP) and mean average precision (mAP) — metrics commonly utilized in the realm of target detection to objectively assess the performance of the disease recognition model. Figure 5 shows the experimental results of small label samples with the number of labels and the number of category samples balanced, taking the three typical diseases of Crown bug, brown spot and leaf blight as examples. At 5000step, the ap of the large-label model was 0.542893 for Stephanitis, 0.586503 for Brown Spot, and 0.309588 for Leaf Blight with small label. The detection effect of small labels is poor for diseases with features covering the whole leaf, such as Stephanitis.

Figure 5

AP@0.5 and mAP@0.5 under small labels

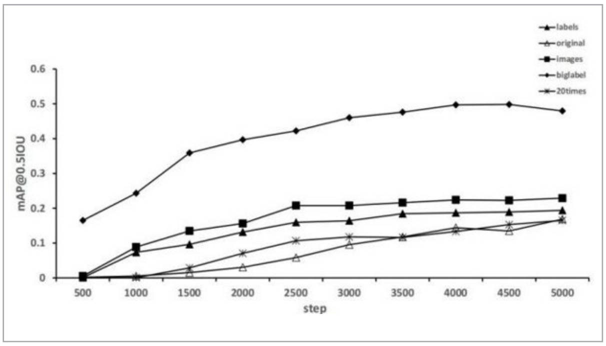


In summary, according to the application characteristics of plant disease and pest detection, the subsequent experiments in this paper adopted a combined data set with small labels and a variety of balancing strategies.

Figure 6 furthermore illustrates the mAP experimental findings pertaining to these three diseases, with an IOU threshold set at 0.5, subsequent to 5000 iterations of the process. It can be seen that the mAP of large labels is generally higher than that of small labels, which also verifies the defects of Faster-RCNN for small target detection mentioned above. However, the model trained according to the data set balanced by the number of pictures and the number of labels converges significantly faster than the original data set within 5000 steps. The model balanced by the number of images also performed slightly better than the model balanced by the number of labels. Because the unbalance rate of the model trained by the 20-

Figure 6

Experimental results of data sets based on different balancing strategies



fold expanded data set is roughly the same as that of the original data set, the convergence rate is similar to that of the original data set, although the size of the data set is larger after the data is enhanced by 20 times.

In order to further verify the detection performance of the model, the PD-IFRCNN detection model proposed in the paper was compared with three classical target detection models with ResNet18, Yolov3, Yolov5s and SSD as the core detection module on the self-built data set, and the results are shown in Table 3. The results further showed that the IFRCNN model had a good effect on the detection of various flower diseases. With the exception of yellows and coal contamination, which were slightly lower than Yolov3 and Yolov5s, respectively, most of the disease recognition maps showed significant improvements compared to several other models (Table 2). This indicates that the model detects all categories as well as possible, which means that the improved model can detect targets more accurately and be more comprehensive in recalling targets.

After comprehensively considering the aforementioned discussion, we conducted meticulous detection and testing procedures on flower leaf images sourced from the internet and disease-ridden leaf images randomly captured in the natural environment, encompassing varying distances and deflection angles. These images underwent rigorous screening and preprocessing to guarantee their diversity and representativeness. Figure 6 vividly showcases the visual outcomes of the model developed in this paper, wherein the rectangular boxes precisely designate the locations of diseases predicted by the model, further differentiating among various disease types through distinct colors and marking techniques. This outcome undeniably attests to the remarkable adaptability and detection accuracy of the methodology employed in this paper when confronted with multi-scale and multi-target detection tasks of leaf pests and diseases in a natural setting. The model introduced in this paper excels at accurately identifying and localizing disease areas, irrespective of whether the image is crisp and clear from a short distance or blurred and distant, or whether it captures the leaf in a straight or oblique angle. This not only underscores the model's robustness across diverse conditions but also underscores its immense potential for practical applications (as shown in Figure 7).

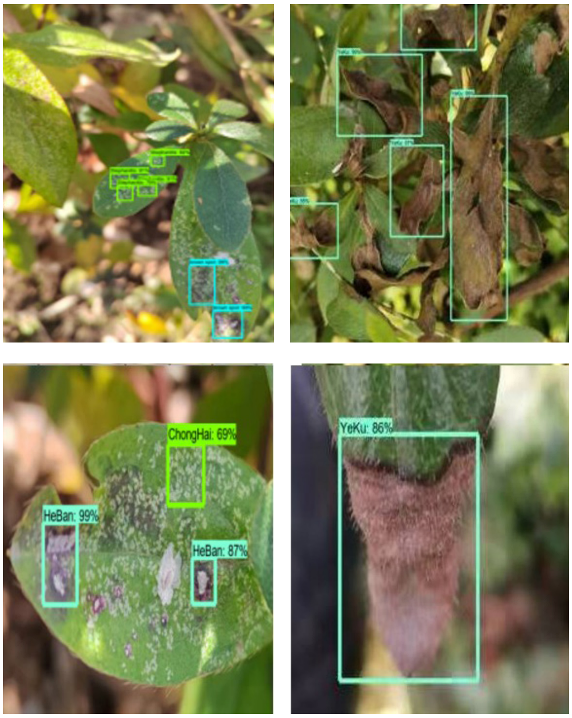
Table 2

Comparison of different models

Detection Model	mAP(%)					
	Leaf Swelling	Xanthosis	Stephanitis	Brown Spot	Sooty Mould	Leaf Blight
SSD	74.1	78.2	80.3	79.5	78.7	81.6
ResNet18	72.5	76.6	66.81	79.3	76.1	80.8
Yolov3	75.26	78.54	57.62	65.43	75.97	82.7
Yolov5s	78.7	75.3	65.3	79.1	81.1	81.7
PD-IFRCNN	78.5	77.6	81.5	80.3	79.1	83.8

Figure 7

Visual example of IFRCNN detection results



4. Conclusion

Leveraging the concepts of migration learning and data fusion technology, we propose a plant disease detection model named IFRCNN, which is based on the Faster R-CNN framework. This model employs the Inception network, known for its superior feature extraction capabilities, as its feature extraction backbone. Furthermore, it refines the Loss function by integrating Focal Loss, ultimately enhancing the model's accuracy in detecting plant diseases. In order to test the validity of the model, different data sets with different labels and different algorithm models were evaluated. The results show that the model has a good performance for the detection of many common diseases and pests, and it can be well adapted to the practical application in the natural scene. Nevertheless, the feature maps derived from Faster-RCNN through convolution are typically single-layered, resulting in a lower resolution. Consequently, the detection model is not particularly adept at identifying small objects at a distance, a point that is further substantiated by the comparative experimental data on size labels presented in this paper. In our subsequent efforts, we will refine the model's performance by focusing on two main avenues: broadening the spectrum of data samples for increased diversity, and integrating various-sized feature maps while elevating their resolution. These measures are aimed at bolstering the model's capability to generalize effectively.

Declaration of Conflicting Interests

The author(s) declared no potential conflicts of interest with respect to the research, author-ship, and/or publication of this article.

Data Sharing Agreement

The datasets used and/or analyzed during the current study are available from the corresponding author on reasonable request.

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