Identification of Abnormal Cucumber Leaves Image Based on Recurrent Residual U-Net and Support Vector Machine Techniques

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Abstract. Cucumber diseases arise and spread quickly, affecting the yield and quality of cucumbers. The correct diagnosis of diseases on cucumber leaves is an important factor determining the success of control measures. To support accurate identification of cucumber leaf diseases, we proposed a machine learning method to identify powdery mildew diseases, downy mildew diseases, blight diseases, and anthracnose diseases on cucumber leaves. Most of the features of these diseases are similar. Therefore, the automatic identification of these diseases presents many challenges. The proposed method uses the recurrent residual U-Net deep learning model and the traditional support vector machine technique to identify diseases on cucumber leaves with an average accuracy of 96.33%, higher than other methods.

Keywords: Cucumber leaf diseases · Recurrent residual U-Net · SVM · Identify diseases

1 Introduction

Plant disease identification based on computer vision often requires extraction of the shape, ridge, color, and other characteristics of disease spots. This method has low identification efficiency because it depends on farmers' expertise in the field of disease identification in crops [1]. With the rapid development of artificial intelligence technology in recent years, many researchers have conducted related studies based on deep learning technology to improve the accuracy of plant disease identification. The existing methods of plant disease analysis are mainly disease classification.

Amara [2] determined the disease of 60 × 60 banana leaves based on LeNet. Deep learning also plays an important role in detecting disease severity in plants. Wang [3] created a series of deep convolutional neural networks to diagnose disease severity using

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black rot images of apples in the Plantvillage dataset. The performance of the shallow learning networks learned from scratch and the deep learning models tuned by transfer learning were also evaluated. The best model is VGG16 learned by transfer learning and the overall accuracy in the test set is 90.4%.

Ferentinos [4] used an open database containing 87,848 images to identify 58 diseases of 25 different plants based on in-depth research. And the best efficiency was 99.53% in accuracy rate. Barbedo [5] investigated the identification of plant diseases from individual lesions and spots using the GoogLeNet architecture, and the obtained accuracy ranged from 75% to 100% for each crop. This variation in accuracy is due to differences in the number of images, the number of diseases, disease states, and degree of difficulty in identification. A CNN neural network usually requires many samples to learn. However, collecting the learning data required by the models is difficult and expensive in many applications [6]. Therefore, the study of data expansion is especially important.

In previous studies, many researchers combined deep learning with transfer learning under the condition of limited dataset [7] to classify plant diseases based on image processing and GPU. Srdjan [8] proposed a method for evaluating deep learning models to identify 14 different classes of plant diseases, including 13 diseases and healthy leaves. He used mixed data with a dataset size of 30,880 images and average accuracy of 96.3% for this method combined with transfer learning method. Liu [9] enhances the training dataset by rotating, mirroring and adding Gaussian noise, adjusting brightness, and adjusting contrast. This method helps to increase the size of the dataset by 12 times and reduce excessive repetition.

In addition to expanding data volumes, improvements in deep learning algorithms are critical to disease recognition outcomes. Through [10] studied the deep network architecture and used images from the PlantVillage dataset to form the data size of 34,727 training set samples, 8702 validation set samples and 10,876 set samples. Experiments show that DenseNets requires fewer parameters and reasonable computation time to achieve the most advanced performance compared to VGG and ResNet. Their accuracy reaches 99.75%.

Picon [11] proposed an improved algorithm based on deep learning neural networks to detect different plant diseases under real acquisition conditions, where different adaptive measures for detection Early disease presentation have been suggested. The obtained results showed that the AuC index of all analyzed diseases was higher than 0.80. Selvaraj [12] relearned three different CNN architectures using transfer learning. By using pre-trained disease recognition models, deep transfer learning was performed to generate networks that could make accurate predictions. Zhong [13] proposes three methods of regression, multi-label classification and focal loss function based on DenseNet-121 CNN to identify diseases on apple leaves. These methods achieved 93.51, 93.31 and 93.71% accuracy on the test dataset.

The disease identification methods in the study cannot automatically locate the disease area from the image and need to extract the disease area manually for identification. Deep learning can also be applied to identify plant diseases. However, at present research in this area is still at an early stage, especially in practical application, due to the continuous improvement of requirements for the identification of plant diseases and diseases.

This paper proposed a method for abnormal cucumber leaves image identification based on modified Recurrent residual U-Net and support vector machine techniques. Main contributions of this study are: (i) the types of abnormal cucumber leaves are explained; (ii) proposed a method for abnormal cucumber leaves image identification based on deep learning model combined on support vector machine techniques traditionally but with high accuracy results. The rest of the paper is organized as follows: Sect. 2 presents the features of abnormal cucumber leaves, and the proposed method for abnormal cucumber leaves identification in Sect. 3. Section 4 and 5 are the experimental results and conclusions, respectively.

2 The Features of Abnormal Cucumber Leaves

Cucumber is growing and increasing in area and production because it is easy to grow and grow in a short time. However, a fundamental cause affecting the area, yield and quality of cucumbers is the serious destruction of some major pests and diseases. There are many types of diseases on cucumber plants. In this section, we only summarize four common diseases such as powdery mildew, downy mildew, blight, and anthracnose. These abnormal presents as Fig. 1.

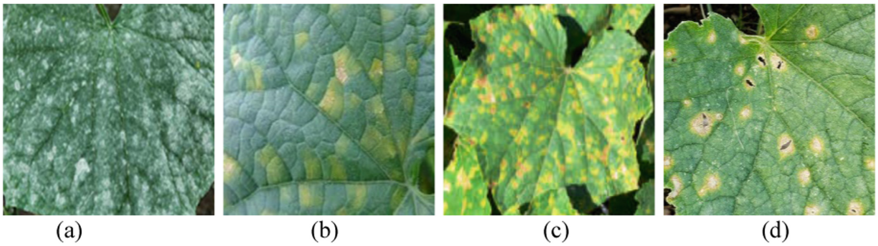

Fig. 1. Common abnormal on cucumber leaves (a) Powdery mildew disease (b) Downy mildew disease (c) Blight disease (d) Anthracnose disease

Powdery mildew disease appears initially as small, powdery white spots on the leaves. Then the leaves turn yellow, dry, and fall easily and gradually spread to other leaves and parts. The disease is most severe when the powdery mildew spreads down the trunk, branches, and flowers, causing the flowers to dry and fall off, causing the cucumber plant to weaken and then die. It greatly affects the yield and quality of cucumbers. Figure 1a presents a case study for this disease.

Downy mildew disease mainly affects leaves. Spots are small at first, pale green then turn yellow. The diseased spots have an edge-shaped base. When encountering high humidity, right on the underside of the leaf, there is a purple-red chalk layer, which is the spores of the fungus. The lesions coalesce into light brown areas. Severely diseased trees give poor yield and fruit quality, and the tree may die. Figure 1b presents a case study for this disease.

Blight disease appears with small spots of all shapes that may be colorless or green and then gradually turn yellow or light brown scattered throughout the location on cucumber leaves. In particular, the underside of leaves where the disease is located will appear a layer of gray-white mold. When they appear too much, the leaves are deformed, the leaves are torn. Plants cannot perform photosynthesis for a long time, causing the plant to die due to lack of nutrients. Figure 1c presents a case study for this disease.

Anthracnose disease appears initially on leaves with brown lesions forming concentric rings. When the fungal damage is more severe, the black fungal spots are in very prominent circles on the leaves. Figure 1d presents a case study for this disease.

Most of the features of these diseases are similar. Therefore, the automatic identification of these diseases presents many challenges.

3 Identification of Abnormal Cucumber Leaves Image

As present in the above section, most of the features of the abnormal cucumber leaf image are small differences. Therefore, we should choose the identification method that is suitable for this task. The identification method in this case study must ensure accurate feature extraction, avoiding loss information in image. This section clearly presents the proposed method for abnormal identification. To identify cucumber leaves images, the proposed method presented as Fig. 2, includes the stages as: features extraction by Recurrent residual U-Net (R2U-Net) combined on a support vector machine (SVM) for identification.

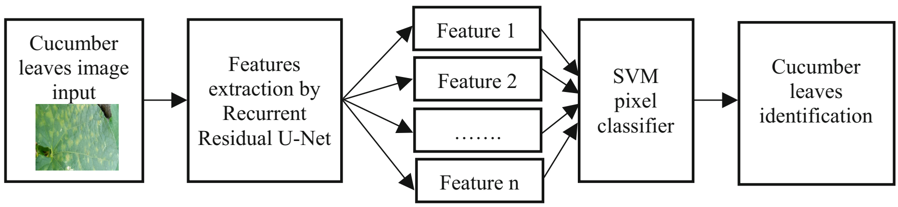

Fig. 2. The proposed method for identification of abnormal cucumber leaves image.

The R2U-Net model is improved from the U-net model. The R2U-Net model is improved by replacing Convolution layers with Recurrent Convolution layers and applying extra block residuals in each of its blocks. The R2U-Net model has two main parts: encoder and decoder. The task of the encoder in the R2U-Net model is to extract features of the image, and the decoder is to restore the image to its original size. Image recovery is done by concatenating feature maps from encoder to decoder. Both the encoder and decoder are built from the Recurrent Residual Convolution block [14].

The Recurrent Residual Convolution block is made up of two identical Recurrent Convolutional layers and a path to combine the results obtained when performing calculations over the two Recurrent Convolutional layers and the input of the block itself. Figure 3 illustrates the structure of the Recurrent Residual Convolution block.

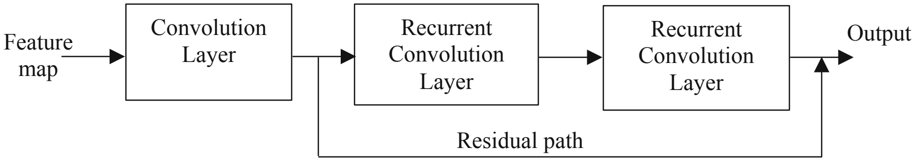

Fig. 3. The structure of the Recurrent Residual Convolution block

In the Recurrent Convolutional layer, it contains the Convolution layer. So, the size and number of filters of the Recurrent Convolutional layer is the size and number of filters of the Convolution layer within it. The architecture of the R2U-Net model is built as follows:

Assume that the cucumber leaf image of size 512 × 512 × 1 is the input image of the R2U-Net model. The image passes through the Recurrent Residual Convolution block of size 3 × 3, 32 filters and generates a feature map of size 512 × 512 × 32. This feature is passed through the Pooling layer of size 2 × 2 to obtain a new feature map of size 256 × 256 × 32. We continue to use 3 more sets with each set including 1 Recurrent Residual Convolution block size 3 × 3 and 1 Pooling layer size 2 × 2 with the number of filters of Recurrent Residual Convolution block is 64, 128, 256, respectively. The output of one feature map is 32 × 32 × 256. This feature map goes through a Recurrent Residual Convolution block of size 3 × 3 and the number of filters is 512 to obtain a new feature map of size 32 × 32 × 512. After that, this feature map will be included in the image resizing phase.

When executed on the first decoder, the above feature map is passed through a transpose convolution layer with size 2 × 2 and 256 filters. By concatenating this feature map with the feature map from the symmetric encoder, we get a new feature map of size 64 × 64 × 512. Continuing using a 3 × 3 Recurrent Residual Convolution block with 256 filters, a 64 × 64 × 256 feature map is created that is the same size as the feature map in the opposite encoder. We continue to do this with three decoders: through the Transpose Convolution layer, concatenating features in the symmetric encoder and a 3 × 3 Recurrent Residual Convolution block [14, 15].

The Transpose Convolution layer and the Recurrent Residual Convolution block have the same number of filters as 128, 64, and 32, respectively. At the end of this process, we get a feature map of size 512 × 512 × 32. The segmented image is the result of the feature map just obtained when passing through a 1 × 1 Convolution layer with a filter number of 1. And this image has a size of 512 × 512 × 1. All Convolution layers are followed by Batch normalization layer and ReLU activation function. Only the last Convolution layer uses Sigmoid function as function activated.

Support vector machines (SVM) can be used for disease identification on cucumber leaves. In the SVM algorithm, the data is as a point in n-dimensional space (where n is some number of objects there are) with the value of each object being the value of a particular coordinate. We do the identification by finding the hyperplane that distinguishes the two classes very well. In the SVM classifier, the SVM kernel is a function that takes a low-dimensional input space and transforms it into a higher-dimensional space. It converts an indivisible problem into a separable problem. It is mainly useful in non-linear decomposition problems. Specifically, it separates data based on labels or outputs that it validates. The features have been identified, extracted from the feature extraction in the above step, they are put into the SVM classifier to identify anomalies in the leaf image.

4 Experimental Results

The dataset, which is collected by us, used to perform the experiments. This dataset contains images taken under different lighting conditions. These images have different colors and orientations. The dataset has 154 images including: 32 powdery mildew images, 31 downy mildew images, 24 blight images and 67 anthracnose images. The size of all images is 512×512 pixels resolution with Portable Network Graphics (.png) file format. Some images are presented in Fig. 4.

Fig. 4. Some images in dataset

The experimentation used 70% dataset for data training and 30% for data testing to evaluate the results. These images augmented the dataset by scaling, clipping, rotation, etc. as in the Table 1. So, the size of the training dataset is expanded to 1000 images.

Table 1. Data augmentation parameters.

Transformation type	Description
Rotation	Randomly rotate image between ($-10°$, $10°$)
Clipping	Randomly clip images with angle between $-15°$ and $15°$
Flipping	Horizontal and vertical flip images
Translation	Randomly shift between -10% and 10% of pixels

The experimental programs were developed by the python language. The configuration hardware is on a computer of Intel core i7, 3.2 GHz CPU and 16 GB DDR3 memory. The diagram for cucumber diseases is presented as Fig. 5.

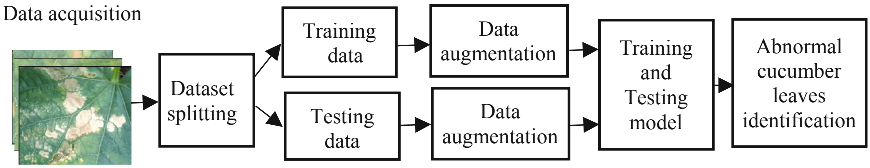

Fig. 5. The diagram for cucumber diseases identification.

To evaluate the identification result, the accuracy metrics are used. Sensitivity (Se) is defined as the ability to detect abnormal images, ranges from 0 to 1 and calculated as Eq. (1). TP (true positives) is the number of true positives. FN (false negatives) is the number of false negatives.

$$Se = \frac{TP}{TP + FN} \tag{1}$$

Specificity (Sp) is defined as the ability to distinguish images that have abnormal or not, ranges from 0 to 1 and is calculated as in the Eq. (2). TN (true negatives) is the number of true negatives. FP (false positives) is the number of false positives.

$$Sp = \frac{TN}{TN + FP} \tag{2}$$

Accuracy (Acc) is defined as the result accuracy of the proposed method in the test dataset, ranging from 0 to 1 (equivalent from 0% to 100%). The accuracy values are calculated as Eq. (3).

$$Acc = \frac{TP + TN}{TP + FN + TN + FP} \tag{3}$$

The experimentations are implemented in all images of above the datasets. Table 2 presented the evaluation of the abnormal leaf images identification between machine learning models, such as: SVM, VGG-16, VGG-19, U-Net and SVM method with the proposed method. The combination of the R2U-Net and SVM method is better than others.

Table 2. The evaluation of the abnormal leaf images identification (%) between machine learning models.

Disease leaf	Accuracy (%)				
	SVM method	VGG-16 method	VGG-19 method	U-Net + SVM method	Proposed method
Powdery mildew	78.124	87.342	91.119	91.981	94.163

(*continued*)

Table 2. (*continued*)

Disease leaf	Accuracy (%)				
	SVM method	VGG-16 method	VGG-19 method	U-Net + SVM method	Proposed method
Downy mildew	82.568	88.692	91.347	92.953	97.642
Blight	79.656	89.173	93.670	94.679	95.761
Anthracnose	78.359	86.228	89.181	91.267	96.751

Table 3. The results of identification average accuracy between the proposed method with the recent methods.

Method	Year	Dataset collection		
		Sensitivity	Specificity	Accuracy
Shanwen method [16]	2017	0.8252	0.9521	0.8783
Abdul method [17]	2021	0.8690	0.9696	0.9133
Nazar method [18]	2022	0.9221	0.9856	0.9516
Proposed method	2022	0.9398	0.894	0.9633

Table 3 presents the average accuracy of the proposed method is 96.33% while the average accuracy of Shanwen method [16], Abdul method [17] and Nazar method [18] are 87.83%, 91.33% and 95.16%, respectively.

As presented in the above, the R2U-Net architecture is improved by replacing Convolution layers with Recurrent Convolution layers and applying extra block residuals in each of its blocks. So, we get more features to improve the identification task. While Shanwen [16] proposed a method to recognize the rate of cucumber disease based on the Global-Local singular value decomposition. They used the watershed algorithm to segment from each cucumber disease leaf image and used a SVM classifier. Abdul [17] used LAB color space and region of interest to extract through K-mean clustering and SVM for identification. Nazar [18] used methods involving the fusion and selection of the features combined on VGG and Inception V3 deep learning models to be considered and fine-tuned. These methods have low accuracy.

5 Conclusions and Future Works

The correct diagnosis of diseases on cucumber leaves is an important factor determining the success of control measures. However, many diseases have similar symptoms, making local disease identification difficult, sometimes impossible. The application of machine learning in identification and classification of diseases on images of cucumber leaves is an inevitable trend. This paper proposed a method for abnormal cucumber leaves image identification based on modified Recurrent residual U-Net combined on support vector machine techniques. The results of the proposed method compare with other methods and are better than others. To crease the accuracy of the proposed method, improving deep learning architecture is necessary and experimenting on other datasets in future work.

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References

1. Mohanty, S.P., Hughes, D.P., Salathé, M.: Using deep learning for image-based plant disease detection. Front. Plant Sci. **7**, 1419 (2016)
2. Amara, J., Bouaziz, B., Algergawy, A.: A deep learning based approach for banana leaf diseases classification. Lecture Notes in Informatics (LNI). Gesellschaft Für Informatik, Bonn, pp. 79–88 (2017)
3. Wang, G., Sun, Y., Wang, J.: Automatic image-based plant disease severity estimation using deep learning. Comput. Intell. Neurosci. 1–8 (2017). https://doi.org/10.1155/2017/2917536
4. Ferentinos, K.P.: Deep learning models for plant disease detection and diagnosis. Comput. Electron. Agric. **145**, 311–318 (2018)
5. Arnal, B., Jayme, G.: Plant disease identification from individual lesions and spots using deep learning. Biosyst. Eng. **180**, 96–107 (2019)
6. Lee, S.H., Chan, C.S., Wilkin, P., et al.: Deep-plant: plant identification with convolutional neural networks. In: IEEE International Conference on Image Processing, pp. 452–456. IEEE (2015)
7. Pan, S.J., Yang, Q.: A survey on transfer learning. IEEE Trans. Knowl. Data Eng. **22**(10), 1345–1359 (2010)
8. Srdjan, S., Marko, A., Andras, A.: Deep neural networks based recognition of plant diseases by leaf image classification. Comput. Intell. Neurosci. **6**, 1–11 (2016)
9. Liu, B., Zhang, Y., He, D.J.: Identification of apple leaf diseases based on deep convolutional neural networks. Symmetry **10**(1), 11 (2016). https://doi.org/10.3390/sym10010011
10. Too, E.C., Li, Y., Njuki, S.: A comparative study of fine-tuning deep learning models for plant disease identification. Comput. Electron. Agric. **161**, 272–279 (2016)
11. Picon, A., Alvarez-Gila, A., Seitz, M., Ortiz-Barredo, A., Echazarra, J., Johannes, A.: Deep convolutional neural networks for mobile capture devicebased crop disease classification in the wild. Comput. Electron. Agric. **1**(161), 280–290 (2019)
12. Selvaraj, M.G., Vergara, A., Ruiz, H., et al.: AI-powered banana diseases and pest detection. Plant Methods **15**, 92 (2019). https://doi.org/10.1186/s13007-019-0475-z
13. Zhong, Y., Zhao, M.: Research on deep learning in apple leaf disease recognition. Comput. Electron. Agric. **168**, 1–6 (2020). https://doi.org/10.1016/j.compag.2019.105146
14. Mubashar, M., Ali, H., Grönlund, C., Azmat, S.: R2U++: a multiscale recurrent residual U-Net with dense skip connections for medical image segmentation. Neural Comput. Appl. 1–17 (2022). https://doi.org/10.1007/s00521-022-07419-7
15. Muhammad, A.K., et al.: Cucumber leaf diseases recognition using multi level deep Entropy-ELM feature selection. Appl. Sci. **12**(2), 593, 1–19 (2022). https://doi.org/10.3390/app12020593
16. Zhang, S., Xiaowei, W., You, Z., Zhang, L.: Leaf image based cucumber disease recognition using sparse representation classification. Comput. Electron. Agric. **134**, 135–141 (2017)

17. Abdul, R., Zain, T., Shoaib, U.D.M, Ahmed, Z., Muhammad, U.K., Sumair, A.: Cucumber leaf disease classification using local tri-directional patterns and haralick features. In: 2021 International Conference on Artificial Intelligence, pp 258–263 (2021). https://doi.org/10.1109/ICAI52203.2021.9445237
18. Nazar, H., et al.: Multiclass cucumber leaf diseases recognition using best feature selection. CMC-Comput. Mater. Contin. **70**(2), 3281–3294 (2022). https://doi.org/10.32604/cmc.2022.019036