



Technical Note Fourier Domain Adaptation for the Identification of Grape Leaf Diseases

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Abstract: With the application of computer vision in the field of agricultural disease recognition, the convolutional neural network is widely used in grape leaf disease recognition and has achieved remarkable results. However, most of the grape leaf disease recognition models have the problem of weak generalization ability. In order to overcome this challenge, this paper proposes an image identification method for grape leaf diseases in different domains based on Fourier domain adaptation. Firstly, Fourier domain adaptation is performed on the labeled source domain data and the unlabeled target domain data. To decrease the gap in distribution between the source domain data and the target domain data, the low-frequency spectrum of the source domain data and the target domain data is swapped. Then, three convolutional neural networks (AlexNet, VGG13, and ResNet101) were used to train the images after style changes and the unlabeled target domain images were classified. The highest accuracy of the three networks can reach 94.6%, 96.7%, and 91.8%, respectively, higher than that of the model without Fourier transform image training. In order to reduce the impact of randomness, when selecting the transformed image, we propose using farthest point sampling to select the image with low feature correlation for the Fourier transform. The final identification result is also higher than the accuracy of the network model trained without transformation. Experimental results showed that Fourier domain adaptation can improve the generalization ability of the model and obtain a more accurate grape leaf disease recognition model.

Keywords: grape leaf diseases; Fourier domain adaptation; image identification; farthest point sampling

1. Introduction

As one of the four principal fruits in the world, the grape is a nutrient-rich source of minerals, amino acids, glucose, vitamin C, and fiber [1]. Notably, items made from grapes including wine, raisins, and juice are highly valuable commercially [2]. The demand for grapes is driven by rising economic levels and an expanding worldwide population. However, a number of leaf diseases impede the high-yield high-quality grape industry's sustained expansion. As a result, effective prevention of grape leaf diseases is urgently needed.

In the field of grape leaf disease identification, image processing technologies play a crucial role. Currently, the predominant method relies on convolutional neural networks (CNNs) for effective feature extraction and classification from images. Apart from CNNs, other image processing techniques are also applied in grape leaf disease recognition. Traditional machine learning algorithms such as support vector machines (SVM), random forests, and k-nearest neighbors (KNN) can be effective, especially with smaller datasets and simpler feature sets. Image segmentation techniques are important for accurate localization and identification of disease areas by segmenting images into distinct regions or



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Copyright: © 2024 by the authors. Licensee MDPI, Basel, Switzerland. This article is an open access article distributed under the terms and conditions of the Creative Commons Attribution (CC BY) license (https:// creativecommons.org/licenses/by/ 4.0/). objects using methods like thresholding, region growing, and edge detection. In recent years, computer vision technology, especially convolutional neural networks (CNN), has achieved some satisfactory results in plant disease identification, when plant disease identification networks trained in the training dataset are applied in the test dataset in the case of a training dataset and test dataset all from the same domain [3]. However, the image distribution of the grape leaf diseases dataset collected in the fields is domain migration due to some factors such as different varieties, growth periods, locations, weather, etc. [4]. It leads to the grape leaf diseases identification network being trained on the one grape leaf diseases domain dataset, namely generalization problem in plant disease identification. Therefore, it is necessary to propose a grape leaf disease identification network with strong generalization ability to solve weak generalization due to domain migration.

Aiming at the weak generalization ability of grape leaf disease recognition, the research methods based on deep learning include data enhancement [5], model fine-tuning [6], and domain adaptation. The first method is to expand the dataset of rice leaf disease by data enhancement (such as flipping, translating, building an antagonistic network, etc.) to enhance the diversity of the original dataset of grape leaf disease. The recognition network trained on this kind of dataset of grape leaf disease learns richer data features and prevents over-fitting, thereby enhancing the generalization ability of the recognition network. However, the data on grape leaf diseases collected by the recognition network are not consistent with the data of the source domain, in other words, the accuracy of the recognition network will decrease when the data of the source domain are inconsistent with the data of the target domain, that is, the generalization ability will not improve significantly. The second model is based on the original grape leaf disease dataset, which is trained in the new grape leaf disease dataset to adjust the weights and parameters of the network. However, model fine-tuning can only improve the generalization ability on a single grape leaf disease dataset and needs to be trained again when applied to other fields. In order to improve the generalization ability of the grape leaf disease recognition model in many different fields, this chapter adopts the field adaptive method to improve the generalization ability. The third model maps the distributed datasets of grape leaf diseases into a special feature space, which makes the same disease data close to each other and then trains the target function in the feature space. There is no limit to the number of source domains and target domains, so the domain adaptive method can improve the generalization ability of the recognition model.

The shift between two distributions should be minimized through domain adaptation. Some classical methods minimize the distance between the transformed source domain and the target domain by finding a mapping function, such as transfer component analysis (TCA) [7], joint distribution adaptation (JDA) [8], and dynamic distribution adaptation (DDA) [9]. All of them are based on the common difference metric maximum mean difference (MMD). However, due to the limited expression ability of these metrics, even minimizing MMD cannot guarantee the alignment of the two domain datasets. Another popular method is generative adversarial network (GAN), which can enhance the generalization ability of the model by training the robustness of the model on adversarial samples. It minimizes domain differences by using trained discriminators to maximize confusion between source domain and target domain representations [10]. However, most of the target domains do not have manual labeling in reality. When the label distribution is inconsistent, adversarial training makes it very easy to close the features of different categories in different data domains, resulting in the negative effect of adversarial domain adaptation.

Thus, a grape leaf disease identification method based on Fourier domain adaptation is proposed in this paper that does not require any training to perform the domain alignment with a small number of target domain labels. The method includes a simple Fourier transform and its inverse and three convolutional neural networks, namely Alexnet [11], Vgg13 [12], and Resnet101 [13]. Firstly, the low-order frequency of the target image is replaced by the low-order frequency of the source image by calculating the fast Fourier

transform (FFT) [14]; afterward, the transformed image is reconstructed by inverse FFT (iFFT) using the primitive annotation of the source domain. Then, the source domain images and generated images are constructed into a new dataset, which is then trained in three different networks. In order to reduce the trouble caused by the randomness of style transformation, this paper still uses the farthest point sampling method to select images with significant differences for transformation.

In this paper, a grape leaf disease identification method based on Fourier domain adaptation is proposed to identify the types of grape diseases. The main contributions of this paper are as follows:

- 1. A grape leaf disease identification method based on Fourier domain adaptation to identify three common types of grape diseases;
- 2. The (fast) Fourier transform (FFT) is used for the adaptive method of grape leaf disease identification from different domains;
- Reducing the impact of randomness on experiments using the farthest point sampling method.

The organizational structure of this paper is as follows. In the next section, we introduce the materials and methods. Section 3 includes experiments and gives the results of experiments. Section 4 is the discussion on Fourier domain adaptation for identification of grape leaf diseases. Section 5 provides the conclusion.

Related Work

Due to factors like lighting, posture, and image quality, even identical models can exhibit significant performance disparities in similar tasks. Domain adaptation, a facet of transfer learning, seeks to mitigate the discrepancies between two distributions. Deep visual domain adaptation methods have historically been categorized into two groups, which are one-step DA and multi-step DA [15].

One-step DA can be further classified into three subcategories [16]. Discrepancy-based methods involve fine-tuning to reduce domain migration [17–20]. Adversarial-based approaches employ discriminators to foster confusion through adversarial objectives [21–24]. Instruction-based techniques utilize data reconstruction, which is used as an auxiliary task to guarantee feature consistency [25–28]. Many projects are based on the idea that the disparity between two domains can be reduced by improving deep network models with labeled or unlabeled target data. These works focus on employing several strategies to align the statistical distribution shift between the source and target domains. maximum mean discrepancy (MMD), correlation alignment (CORAL), Kullback–Leibler divergence (KLD), H divergence, and other methods are frequently used to measure and lessen distribution shifts. Another class of domain adaptation techniques that has lately gained interest is adversarial learning. This method uses a domain discriminator to determine if a data point comes from the source domain or the destination domain through an adversarial objective, which is intended to promote domain confusion while decreasing the discrepancy between the source domain and target domain mapping distributions. An example shows how to create simulated samples similar to the target sample while retaining source domain annotation data by using source images, noise vectors, or a combination of both. Alternatively, the feature extractor uses labels from the source domain to learn a discriminating representation. Using a domain-confusion loss, this representation is then utilized to translate target domain data into the unified space, producing domain-invariant representations. The aforementioned techniques fall under the one-step DA subcategory.

Similar to the single-step DA, multi-step DA has three subcategories [29]. With hand-crafted approaches, specialists identify intermediate domains based on their knowledge [30]. Instance-based techniques comprise intermediate domains by picking specific data segments from additional datasets, hence training the deep network [31]. By freezing previous trained networks and using their intermediate expressed as inputs for next networks, representation-based approaches promote transfer [32]. The multi-step DA technique starts from the intermediate domain where the correlation between the localization and the source domain and the target domain is stronger than their direct relationship. One-step DA is then used to transfer knowledge between the source, intermediate, and destination domains, minimizing information loss. It is important for multi-step DA to select the intermediate domain and use it efficiently. The common approach is to extract central data portions from auxiliary datasets to form meta-structure domains, subsequently training the deep learning network. The selective learning algorithm (SLA) serves as a notable technique, gradually choosing relevant unlabeled data from intermediate domains. This approach functions as a bridge to bridge the substantial distribution gap, enabling knowledge transfer between distant domains. SLA is adeptly employed to address the distant domain transfer learning (DDTL) challenge. It leverages supervised autoencoders or supervised convolutional autoencoders as base models, accommodating various input types.

With image-to-image translation carried out via low-frequency spectra components exchange (amplitudes only), Fourier domain adaptation (FDA) supplies a workable substitute for the aforementioned techniques while still achieving the same outcomes on natural images. The outcomes of adapting this technique for cityscapes, medical imaging, digit recognition, item recognition, and adaption between the actual world and the virtual world are all excellent [33]. However, its use in agricultural modernization has not been very widespread.

2. Materials and Methods

This paper mainly studies the identification of grape leaf diseases by Fourier domain adaptation. In this section, the paper first introduces the data used in the experiment and then introduces the methods proposed in this study.

2.1. Materials

The images of grape leaf diseases acquired in this paper are from the AI Challenger 2018. To download this data, please visit the link in the Data Availability Statement at the end of the article. We obtained 2808 RGB images of total data and classified two domains according to the severity of the disease and the general condition of the disease, as shown in Table 1. The subjects were black measles fungus, black rot fungus, and leaf blight fungus, as seen in Figure 1.

Table 1. The number of each class of diseases.

Disease	Source Dataset	Target Dataset	Total
Black Measles Fungus	478	577	1055
Black Rot Fungus	528	435	963
Blight Fungus	720	70	790
Total	1726	1082	2808

Among them, the source domain dataset entails the data with more serious diseases and the image disease of the target domain dataset is general. In subsequent experiments, the images will be processed according to the needs of each experiment. The source domain dataset is allocated in a ratio of 8:2 as the training set and the validation set. The target domain dataset is used as the test set and the accuracy obtained in this paper is the recognition accuracy of the test set. Black measles fungus can be easily identified as brown streaking lesions on any part of the leaf. Black rot fungus appears as a small spot on the leaves and then becomes round and white tan, often surrounded by brown rings. Blight fungus is characterized by the presence of a white powdery (ash-like) coating in patches on both sides of the leaves and the affected leaves turn pale and curl up. Source data





Target data

Figure 1. Examples of grape leaf disease image.

2.2. Methods

2.2.1. Motivation and Intuition

In recent years, much of the ongoing work in grape leaf disease identification has relied heavily on training within the same dataset. Nonetheless, real-world agricultural scenarios present certain challenges: (1) securing a significant volume of grape leaf disease data is arduous, particularly in the confines of a single grape planting base. (2) Model generalization, even when trained on identical datasets, necessitates enhancement. This entails that despite optimal training, the model may not deliver satisfactory outcomes when applied to datasets with diverse environmental contexts.

During our quest to enhance model generalization, we uncovered the potential of domain adaptation. This technique has demonstrated success across various domains in improving model generalization. However, certain methodologies rely on sensor-derived features to address the statistical distribution shift. Unfortunately, merely matching means and covariances falls short in consistently aligning distinct domains. Moreover, some methods, although effective, entail intricate computational processes that are not particularly user-friendly for practical agricultural applications.

Our intuition in doing so stems from the observation when image classification maintains a high level of performance; a low level of spectrum (amplitude) can change significantly. No matter whether something in the picture is a plant leaf or a disease, it should not be affected by sensors, light sources, or other factors. Fourier transform is simpler than other methods and they can be registered.

To handle the case where the model's generalization capability needs to be enhanced and the dataset for grape leaf disease is difficult to obtain, Figure 2 depicts the suggested Fourier transfer's processing flow. Images of three different grape leaf diseases that were captured in a field location serve as the input. They separated the leaves from the captured photos and categorized each sick leaf into severe and general categories. The classification of three CNN identification models for grape leaf diseases was conducted and the outcomes were compared. The target domain data from the grape leaf disease dataset are visualized using the most accurate VGG13 identification finding and then the farthest point sampling method is used to reduce the chance of model success.



Figure 2. Spectral transfer of grape disease leaf image.

2.2.2. Fourier Domain Adaptation

To facilitate discussion, we first introduce some notation. The source dataset is defined as $D^s = \{ (x_i^s, y_i^s) \sim P(x^s, y^s) \}_{i=1}^{N_s}$, where $x^s \in \mathbb{R}^{H \times W \times 3}$ is a color image of grape leaves and $y^s \in \mathbb{R}$ is the category label related to x^s described as having two domains, S for the source and T for the target. The target dataset, which lacks category labels, is denote as $D^t = \{ (x_i^t) \}_{i=1}^{N_t}$. Typically, when the recognition network trained on D^s tries on D^t , its performance will decrease. In order to diminish the domain gap between the two domains, we propose Fourier domain adaptation for the identification of grape leaf diseases.

 \mathcal{F}^{A} : $\mathbb{R}^{H \times W \times 3}$ and \mathcal{F}^{P} : $\mathbb{R}^{H \times W \times 3}$ represent the amplitude and phase of an RGB image Fourier transform \mathcal{F} , respectively. For the image *x*, the transformation is shown in Formula (1) as follows:

$$\mathcal{F}(x)(m,n) = \sum_{h,w} x(h,w), -j2\pi (\frac{h}{H}m + \frac{w}{W}n), j^2 = -1$$
(1)

which the FFT method may implement effectively. \mathcal{F}^{-1} is the inverse Fourier transform that returns the phase and amplitude of spectral signals to picture space. All images are in RGB format, so the red channel, green channel, and blue channel are used as independent two-dimensional signals, respectively, and then 2D FFT is applied to each channel. In this way, the characteristics and spectral information of each color channel can be analyzed in the frequency domain to support subsequent image processing and analysis. Additionally, we represent a mask with M_{β} , whose value is zero except for the central region where $\beta \in (0, 1)$.

$$M_{\beta}(h,w) = \mathbb{1}_{(h,w)\in[-\beta H:\beta H,-\beta H:\beta H]}$$
⁽²⁾

here, we will suppose that (0,0) is the image's center. Because β is not measured in pixels, selecting β is independent of the size or resolution of the image. There are two randomly selected photo definitions of $x^s \sim D^s$, $x^t \sim D^t$; Fourier domain adaptation is represented by the following Formula (3):

$$x^{s \to t} = \mathcal{F}^{-1}\Big(\Big[M_{\beta} \circ \mathcal{F}^{A}(x^{t}) + (1 - M_{\beta}) \circ \mathcal{F}^{A}(x^{s}), \mathcal{F}^{P}(x^{s})\Big]\Big)$$
(3)

in the formula, x^t is the target image, which takes the place of the source image's low-frequency portion of its amplitude. $\mathcal{F}^A(x^s)$ is the source image. The picture $x^{s \to t}$, whose

content is identical to x^s but will resemble the appearance of a sample from D^t , is then projected back to the changed spectral representation of x^t , with its phase component unaltered. The mask M_β , which is depicted in green in Figure 2, shows the procedure.

According to Equation (3), $\beta = 0$, $x^{s \to t}$ will be rendered exactly as the original source image x^s . On the other hand, the amplitude of x^s will be replaced by that of x^t when $\beta = 1.0$. Figure 3 shows how β is an impact. The image $x^{s \to t}$ approaches the goal image x^t as β approaches 1.0 but also shows noticeable artifacts, as can be seen from the enlarged blue and yellow boxes area in Figure 3. We choose $\beta \leq 0.15$. But in Table 1, similar to a straightforward multi-scale pooling strategy, we display the impact of various β selections along with the average of the generated models.



Figure 3. Effect of the size of the domain β .

2.2.3. FDA for Image Identification

We proposed our identification approach of grape leaf diseases based on the Fourier domain adaptation technique. Firstly, it consists of swapping the low-frequency amplitudes of the source image spectrum with those of those of the target image, the style of which should be borrowed. Then, the generated new image and the source domain image are combined into a new dataset, which is put into AlexNet, VGG13, and ResNet101 for image identification training and tested with the target domain dataset to obtain the identification results. It shows an image identification model for grape leaf diseases based on Fourier domain adaptation with VGG13 as an example in Figure 4.



Figure 4. FDA for image identification, taking VGG13 as an example.

Farthest point sampling (FPS) is a widely utilized sampling algorithm recognized for its capability to ensure uniform sampling of samples. This methodology operates by iteratively selecting the furthest point from the existing set of sampled points. The algorithm follows the following detailed steps:

- i. Select a point, which is denoted by p_0 , from the data point as the initial point to form the initial sampling point set: $s = \{p_0\}$;
- ii. By calculating the distance from all points to p_0 , an N-dimensional array called *l* is generated. Select the point corresponding to the maximum value in *l* as p_1 . Update the sampling point set: $s = \{p_0, p_1\}$;
- iii. Calculate the distances from all points to p_1 . For each point p_i , the distance from it to p_1 is compared with the value in l[i]. If the distance from p_1 to p_i is less than the value in l[i], the distance is used to update l[i]. Therefore, the array l always stores the nearest distance from each point to the sampling point set s;
- iv. Proceed by selecting the point consistent with the maximum value in the array l as p_2 . Renew the sampling point set: $s = \{p_0, p_1, p_2\}$. Repeat Step 2 to Step 4 iteratively until the quantity required of n target sampling points is achieved.

This process ensures a gradual selection of points that maximizes the spatial spread, effectively achieving uniform and diverse sampling.

3. Results

In this section, we introduce the training details, parameter adjustment experiments, and comparative experiments of the grape leaf disease recognition model based on Fourier domain adaption and discuss the experimental results.

3.1. Training Details

The experiment uses Pytorch as the deep learning framework for Python and uses NVIDIA GeForce RTX 3080 Ti to build and implement the network model. The acceleration process of this experiment is realized by calling a graphics processing unit (GPU). Table 2 shows the workstation specifications.

Table 2. Workstation specifications.

Hardware	Software
CPU: Intel Core i9-10900K	Windows10
RAM: 128 GB	CUDA12.1.112 + CUDNN8.0
GPU: NVIDIA GeForce RTX 3080 Ti	Pytorch Stable (2.3.0)

With the purpose of the availability of the proposed grape leaf disease identification method based on Fourier domain adaptation, we conducted three types of experiments. The first experiment is the parameter adjustment experiment about the Fourier transform. The training set consists of the source domain image and the style transformation image containing the features from the target domain and label from the source domain after one Fourier transform; the test set is the target domain dataset. There are two sub-experiments in this experiment: (1) β selected 0.01, CNN network selected Alexnet. The learning rate has four parameters of 0.0001, 0.0005, 0.001, and 0.01 and the batch_size has four parameters of 4, 8, 16, and 32, which are one-to-one correspondence. After 16 experiments, two groups of batch_size and learning rate combinations with better training effects were obtained; (2) β has three parameters of 0.01, 0.05, and 0.09, epochs have three parameters of 50, 100, and 200, and the CNN network has three networks of Alexnet, Vgg13, and Resnet101. Combined with the two combined parameters obtained in the experiment, (3) the best grape leaf disease identification model with single-scale Fourier domain adaptation was obtained after 54 groups of experiments.

The second experiment is a comparative experiment. The source domain image without Fourier transform is trained in the same Vgg13 network under the same parameters and conditions. The results obtained are compared with the results of Fourier transform training, which proves that the proposed method has practical significance and effects.

In the third experiment, in order to eliminate the randomness of the model, we propose a fusion farthest point sampling algorithm. Three images with far feature distance are selected in the target domain dataset and their features are adaptively transferred to the source domain dataset through the Fourier domain. In total, 1434 images are obtained and 478 images in the source domain are added to obtain 1912 training set images, which are put into Vgg13 for training and tested with target domain images.

In the grape leaf disease identification experiment, the performance of the method was evaluated by accuracy, which is the percentage of the predicted correct sample in the total sample.

3.2. Parameter Adjustment Experiment

The first test is the proposed grape leaf diseases identification network based on the Fourier domain adaptation with a single scale on the source domain: 956 images of each category \rightarrow target domain; 239 images of each category. In order to experiment with better performance of the model, we choose different hyper-parameter configurations (learning rate, batch size, and epochs) to adjust the identification performance of the model. The learning rate is selected as 0.0001, 0.0005, 0.001, and 0.01, the batch size is selected as 4, 8, 16, and 32, and the epoch is selected as 50, 100, and 200. The experiment is divided into two parts. Firstly, two groups with higher accuracy are selected through the combination of learning rate of 0.01 and batch size 4. All networks use Alexnet, shown as in Table 3. Then, we used these two sets of parameters to train on the three classical networks of CNN, combined with epochs selected as 50, 100, and 200. In addition, three kinds of β were selected for experiments.

Learning Rate	Batch_Size	Accuracy	
	4	65%	
0.0001	8	45.5%	
0.0001	16	27.0%	
	32	33.3%	
	4	79.8%	
0.0005	8	88.1%	
0.0005	16	65.4%	
	32	60.4%	
	4	81.9%	
0.001	8	78.7%	
0.001	16	76.4%	
	32	65.7%	
	4	93.2%	
0.01	8	91.4%	
0.01	16	92.6%	
	32	91.4%	

Table 3. Parameter adjustment experiment.

When β is selected as 0.01, 0.05, and 0.09, the experimental process is shown in Tables 4–6. After 54 experiments, the final results are as follows: when $\beta = 0.01$, Vgg13 network is selected for training, epochs = 100, learning rate = 0.0005, epoch = 8, and the accuracy is the highest, which can reach 96.2%. When $\beta = 0.05$, select the Vgg13 network for training, set epochs = 200, learning rate = 0.0005, epoch selection 8, and the highest accuracy can also reach 96.2%. When $\beta = 0.09$, the Vgg13 network is selected for training. When epochs = 100, learning rate = 0.01, epoch 4 is selected, the accuracy is the highest, and the highest accuracy can be achieved, which is 96.7%.

Learning Rate	Epochs	Models	Accuracy	
		Alexnet	90.9%	
	50	Vgg13	95.8%	
		Resnet101	90.8%	
		Alexnet	88.1%	
0.0005	100	Vgg13	96.2%	
		Resnet101	83.8%	
		Alexnet	92.1%	
	200	Vgg13	95.5%	
		Resnet101	84.5%	
		Alexnet	94.7%	
	50	Vgg13	95.5%	
0.01		Resnet101	90.7%	
		Alexnet	93.2%	
	100	Vgg13	95.5%	
		Resnet101	89.0%	
		Alexnet	92.5%	
	200	Vgg13	93.6%	
		Resnet101	89.7%	

Table 4. The experimental process when $\beta = 0.01$.

Table 5. The experimental process when $\beta = 0.05$.

Learning Rate	Epochs	Models	Accuracy	
		Alexnet	89.8%	
	50	Vgg13	94.6%	
		Resnet101	88.6%	
		Alexnet	91.6%	
0.0005	100	Vgg13	93.3%	
		Resnet101	91.8%	
		Alexnet	90.7%	
	200	Vgg13	96.2%	
		Resnet101	90.7%	
		Alexnet	93.7%	
	50	Vgg13	95.7%	
0.01		Resnet101	87.4%	
		Alexnet	91.6%	
	100	Vgg13	93.4%	
		Resnet101	90.1%	
		Alexnet	91.8%	
	200	Vgg13	93.4%	
		Resnet101	88.7%	

Table 6. The experimental process when $\beta = 0.09$.

Learning Rate	Epochs	Models	Accuracy
		Alexnet	91.1%
	50	Vgg13	95.1%
		Resnet101	88.8%
		Alexnet	89.1%
0.0005	100	Vgg13	94.3%
		Resnet101	91.2%
		Alexnet	94.6%
	200	Vgg13	94.4%
		Resnet101	87.0%
0.01		Alexnet	90.4%
	50	Vgg13	96.5%
		Resnet101	90.0%
		Alexnet	94.0%
	100	Vgg13	96.7%
		Resnet101	90.1%
		Alexnet	91.5%
	200	Vgg13	93.2%
		Resnet101	90.8%

3.3. Contrast Test

The grape leaf disease identification model based on the Fourier domain adaptation was compared with the method without Fourier domain adaptation, using the same identification network. This experiment uses the same number of source domain datasets and target domain datasets. The network selects Vgg13 and other parameters are shown in Table 7. From Table 7, we can see that the prediction results of our model are better.

Table 7. Contrast Test.

Model	β	Learning Rate	Batch_Size	Epochs	Accuracy
Model without FDA Model with FDA	0.01	0.005	8	100	86.9% 96.2%
Model without FDA Model with FDA	0.05	0.005	8	200	90.7% 96.2%
Model without FDA Model with FDA	0.09	0.01	4	100	92.6% 96.7%

In order to further analyze the recognition effect of the Fourier domain adaptation method proposed in this chapter on grape leaf diseases, this experiment uses the confusion matrix to compare and analyze the recognition effect of the grape leaf disease recognition model with Fourier domain adaptation and the grape leaf disease recognition model without Fourier domain adaptation on grape leaf diseases, mainly analyzing the recognition accuracy of the three diseases, when $\beta = 0.09$, learning rate = 0.01, batch_size = 4, and epoch = 100.

According to Figures 5 and 6, the number of correct recognitions of black measles fungus, black rot fungus, and leaf blight fungus by the recognition model without Fourier domain adaptation is 184, 185, and 187, respectively. After adding Fourier domain adaptation, the number of correct recognitions is 195, 193, and 194. It can be seen from the confusion matrix that the recognition accuracy of various grape leaf diseases based on the adaptive recognition method in the Fourier domain adaptation has been significantly improved and the recognition accuracy of black measles fungus has been improved the most, indicating that the domain adaptive effect of black measles fungus is the best.



Figure 5. Confusion matrix without Fourier domain adaptation.



Figure 6. Confusion matrix with Fourier domain adaptation.

3.4. FPS for FDA

In previous experiments, we used a single image to perform Fourier transform. In order to reduce the contingency of the method, we use the farthest point sampling method to take the features of the image as input and obtain three images with unrelated features. Then, they are adapted to the Fourier domain with the source domain images, respectively, and 1912 style-transformed images are obtained and then put into the network for training. The parameters used are Learning rate = 0.005, batch size = 8, epochs = 100, respectively. The results are compared with the proposed method, as shown in Table 8. At the same time, the random sampling method is also used to select any three images to perform the same experiment and the results are shown in Table 8.

β Model Accuracy 89.7% FPS for FDA 93.7% 0.01 random sampling for FDA 96.2% FDA FPS for FDA 92.5% 0.05 random sampling for FDA 83.8% 96.2% FDA FPS for FDA 91.2% 0.09 random sampling for FDA 90.2% FDA 96.7%

Table 8. Comparison of FDA's results with other methods using a random sampling method.

4. Discussion

Fourier domain adaptation is a promising approach for identifying grape leaf diseases and has the potential to improve the precision and robustness of disease detection in a wide range of environments and grape varieties. This discussion explores the impact, advantages, possible problems, and future associated with the use of the FDA.

FDA may be able to extract more discriminating characteristics from grape leaf images by exploiting the Fourier domain, thereby allowing a more precise diagnosis of the disease than conventional approaches. The ability to detect minute changes in the spectrum related to disease increases the sensitivity and specificity of detection. FDA's intrinsic adaptability makes it possible for this model to be extended to all types of wine and environments. This robustness is critical in agricultural environments where variations in lighting, soil composition, and grape varieties are common. Traditionally, a large number of supervised learning methods are based on tagged data. FDA's Domain Adaptive Ability allows for less reliance on large-scale annotation datasets in the destination field, which can be used in real-world situations that might be difficult or costly to acquire.

However, FDA's effectiveness depends on obtaining high-quality and sufficient diversity of data in the origin and destination areas. The provision of representative datasets covering different disease phases, environment, and varieties of wine is crucial for robust model performance. While FDA solves the problem of domain displacement, it is difficult to adapt to the underlying domain, especially when there are significant domain differences. It is necessary to optimize the adaptive intensity in order to avoid over-fitting to the features of the source domain but also to keep the key data of the object domain. While FDA's models are effective, they tend to be a black box, which presents a challenge to the interpretation of acquired representations and decision making. It is crucial to make the model transparent and readable, especially in the field of agriculture when interested parties are looking for workable ideas and interpretations.

Furthermore, future work could concentrate on enhancing the granularity of disease detection within grape leaves. Specifically, researchers could aim to identify and segment individual disease spots or lesions on the leaf surface. This would involve advancing techniques beyond simple disease detection to achieve instance segmentation, where each distinct disease spot is identified and delineated separately. By moving toward instance segmentation, the FDA approach can provide more detailed and precise information about the distribution and severity of diseases on grape leaves.

In the future, research of Fourier domain adaptation, exploring the influence of different color spaces, can help to select a color space with the best performance. By comprehensively utilizing the advantages of different color spaces, researchers can optimize the performance of disease recognition systems and improve the accuracy and reliability of different diseases.

In addition to disease-specific advancements, integrating the FDA with state-of-theart image processing methods such as semantic segmentation holds promise. Semantic segmentation enables the labeling of each pixel in an image with its corresponding class, facilitating a more comprehensive understanding of the spatial distribution of diseases on grape leaves. By leveraging these advanced image processing techniques alongside the FDA, researchers can further refine disease detection capabilities, enhance model interpretability, and ultimately contribute to more effective and robust disease management strategies in viticulture.

In summary, the FDA demonstrates tremendous potential in the field of plant disease detection due to its capability to detect the presence of different regions. Future directions include expanding datasets to encompass a wider range of disease types and classes, advancing toward instance-level disease spot identification and integrating with state-of-the-art image processing techniques like semantic segmentation. These directions not only expand the applicability of the FDA but also have the potential to lead innovation in crop disease diagnosis and management practices.

5. Conclusions

A grape leaf disease recognition model with strong generalization ability is proposed based on Fourier domain adaptation. By exchanging the low-frequency amplitude of the source image spectrum with the low-frequency amplitude of the target image spectrum, the Fourier transform designed in this study is applied to the adaptive method of grape leaf disease recognition in different domains, which does not require any large amount of calculation and complex model and improves the generalization ability of the recognition model. The results showed that the accuracy of the model trained by the selected three β values to identify grape leaf diseases in the target domain can reach 96.2%, 96.2%, and 96.7%. In the research of agricultural disease image classification, how to improve the generalization ability of image classification conveniently is still a difficult problem. Fourier domain adaptation can solve this problem in some cases. The low-level statistical data of the image can change greatly without affecting the underlying scene. This preprocessing can replace complex architecture or laborious data enhancement, so as to solve some problems in image recognition of grape leaf diseases and improve the recognition generalization ability. In the future, it is hoped that this method can be applied to actual production.

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