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A Two-stage Approach for Plant Disease Classification Based on Deep Neural Networks and Transfer Learning

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***Abstract*—In recent times, drastic changes in the climate have brought about a dramatic increase in the prevalence of crop diseases. Such diseases are a huge threat to sustainable agriculture, especially for third-world countries whose economies still rely much on agriculture. Proper disease detection is an essential prerequisite to get timely treatment of crops and prevent reduction in crop yield. In most plant diseases, the leaves may contain some texture variations, which may help in identifying the diseases. However, an identical disease may not appear in a similar fashion for different plant species and visible texture differences may be very negligible. In most cases, plant diseases are classified for all species together, which may miss the species-specific symptoms. In this paper, we propose a two-stage classification scheme to classify plant diseases that divides the whole classification pipeline into two parts: a plant species detection part and a subsequent species-specific disease detection part. In both stages, we employ some efficient deep convolutional neural network (CNN) architectures, namely EfficeintNetB3, NASNetLarge, DenseNet201, MobileNetV2, VGG16 and InceptionV3 with effective transfer learning. Two publicly available datasets, namely Plant Village and IPM, are considered in this paper. Comparative analysis reveals that the proposed two-stage method can perform better than the conventional single-stage methods reported in the literature for plant disease detection.**

***Index Terms*—Crop Diseases, Convolutional Neural Network, Classification, Transfer Learning, Unseen crops**

I. Introduction

With the rising food demand and decreasing arable land, the need for healthy crops is more than ever before. Early detection of crop diseases is very important, which mostly relies on manual inspection. In this case, the accuracy of the diagnosis strongly depends on the human specialists' knowledge. Hence, automated crop disease detection technique that can precisely perform the task has great demand. Different machine learning algorithms were widely used for this purpose where a major difficulty was to finalize the desired hand-crafted features. As an alternative, most of the research works are now concentrating on deep learning methods using the convolutional neural network (CNN). Several research works on disease detection of isolated crops have been conducted over the past few years, including maize [1], cassava [2], tomato [3] [4] [5], apple [6], wheat [7] among others. However, when a generic model is created to detect disease for numerous crops, comparatively poor performance is obtained. A common problem, in this case, is that the images of different diseases may have similar patterns and on the other hand, different plant species may have similar diseases but with variations in images. Due to a shortage of disease-specific data, in most cases, transfer learning is used by utilizing large datasets of various images. In [8], an improved generalization is proposed to classify diseases of the crops that have never been observed before (different than the training data distribution). The characteristics gained from models trained with crop-disease classes are investigated qualitatively and the parameters are applied to other architectures to improve accuracy [9]. In [10], a new conditional multi-task learning (CMTL) approach is shown, which allows the distribution of host species and disease characteristics learned simultaneously with a conditional link between them. Deep ensemble neural networks are also used in several other studies [11] [12]. Even though these methods are quite innovative, in most cases they classify diseases without classifying the plants and thus plant-specific characteristics cannot be fully utilized in disease classification. Moreover, they cannot perform well when completely unseen plant leaf images need to be detected which are taken in an uncontrolled environment.

The most difficult challenge is to recognize plant disease in real-world photographs taken in the crop field, where the data distribution is expected to be quite different from that of images in the training dataset. In this paper, a two-stage deep neural network-based scheme is developed to better address this challenge, where both the plant type and disease are classified. To provide more robust performance, in the two-stage classification method: first, multi-stage transfer learning is used to recognize the plant species, and then, a species-specific trained network is proposed to identify the appropriate disease group. Instead of building a new architecture, we experimented with existing, highly effective, and thoroughly

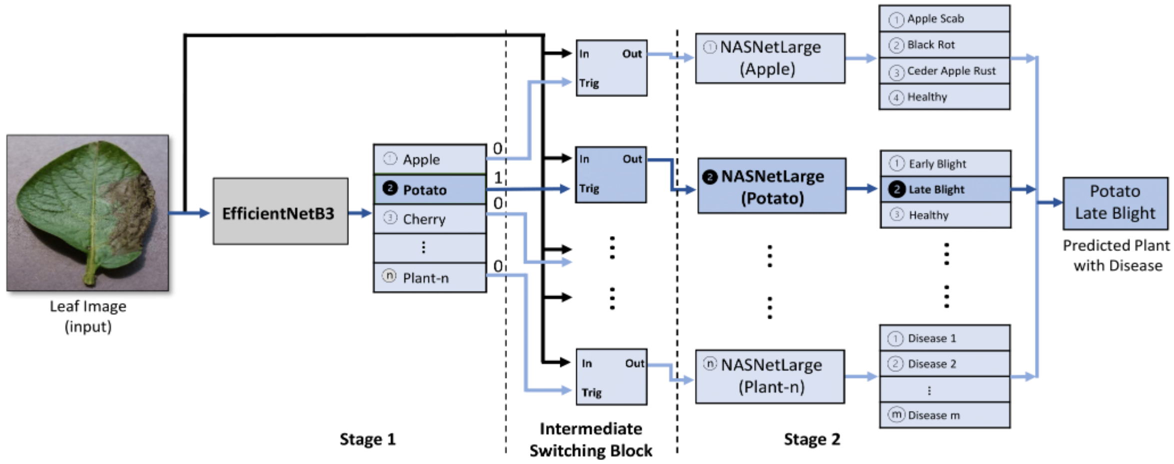


Fig. 1: Proposed Two-stage Classification Scheme. Here n (=14) denotes the total number of plant species considered.

researched architectures, and better performance was obtained than the existing studies. The proposed strategy is compared with a few of the recently proposed methods for plant disease detection on publicly available datasets.

II. Datasets

One of the most well-studied datasets in the area of plant disease detection is the 'Plant Village' (PV) dataset. In this investigation, the first publicly available version of the PV dataset is used. There are 38 crop disease pairings, such as Potato Late Blight, Apple scab, Tomato bacterial spot, etc., and 14 types of plant species in this dataset, such as Apple, Tomato, Orange etc. A variety of setups is tested in this research, including the one used in the original study [9], in which 80% of the data is utilized for training and 20% for validation. To further assess the strength of the trained models, another widely used dataset, called IPM, is used, first published in [9]. Images in this dataset are not captured in a controlled setting like those in the PV dataset. A total of 118 images were obtained from reputable sources to form the dataset. There are 10 plant species and 19 crop disease pairs in the IPM dataset, and all of those are common to the PV dataset.

III. Proposed Methodology

The proposed method provides the classification of plants as well as their diseases. This is essential to utilize plant-specific characteristics in the learning process. Unlike conventional methods, it offers two results that help better analysis of the diseases. Moreover, when a plant type is known, only the second stage model of the proposed method needs to operate, which is obviously more effective than a conventional generic model of plant-independent disease classification. Different types of deep learning networks are investigated for performing the classification task in two stages. Some of these techniques have been able to detect plant diseases very accurately when images are acquired in a controlled environment and/or less number of plant disease classes are considered or only common types are considered [8]. But in noisy images, most of the techniques do not perform well. The proposed method first recognizes the plant type and then in the second stage, disease prediction is performed for that plant. The detailed structure of the two-stage classification system is depicted in Figure 1. As illustrated, the entire structure contains an intermediate switching block with n number of switches. The introduction of this block serves as a convenient means to link up both stages.

A. First Stage: Plant Type Classification

In the first stage, an image of a plant leaf is taken as input. There are two major concerns, a large number of classes with the class imbalance and the scarcity of training samples. In order to handle the challenges, various types of image augmentation are incorporated, such as scaling, shearing, zooming, horizontal and vertical flip, rotation, and brightness control. Instead of building a new architecture, existing effective deep neural architectures are tested. Considering the limited number of training data, transfer learning is applied. Input images are fed to a pre-trained CNN model that predicts the plant species. In this research, a transfer learning and fine-tuning strategy are employed because of its superior advantages over other strategies.

The models are created and loaded with pre-trained weights from the ImageNet [13]. The ImageNet database contains about 1.2 million pictures linked to 1000 very diverse classes. In this study, many types of CNN architectures with different depths are used: NASNetLarge, EfficientNetB3, DenseNet201, MobileNetV2, VGG16, and InceptionV3. Concerning the inputs, during the training, the image at the input of the model is resized according to the architectures. Among these models, the EfficientNetB3 architecture uniformly scales all dimensions of depth/width/resolution using a compound coefficient.

The output can be considered as a one-hot encoded 14-length vector where the one denotes the predicted plant species. As a result, the corresponding switch is activated, transmitting the input image to the model attached to the

TABLE I: Comparison of different CNNs for plant type detection

Model	Plant Village (Train set)		IPM (Test set)	
	Accuracy (with augmentation)	Accuracy (without augmentation)	Accuracy (with augmentation)	Accuracy (without augmentation)
EfficientNetB3	99.94	99.96	**87.29**	**78.81**
NASNetLarge	99.95	99.97	80.51	73.73
DenseNet201	99.98	100.00	82.20	70.34
MobileNetV2	99.90	99.99	73.73	66.95
VGG16	99.85	99.89	62.71	61.86
InceptionV3	99.93	99.98	76.27	69.49

switch's output. There are 14 switches in the intermediate switching block corresponding to each of the elements in the output vector of the first stage model. For one inference, only one switch is activated, while the remaining 13 stay inactive. Before the next inference, all switches are made inactive again and the process continues.

B. Second Stage: Disease Classification

In our study, there are 14 different pre-trained disease classification models in the second stage, all based on the same CNN architecture; and each of them is trained with data from a single plant species only. Then, this single-species pre-trained model of the second stage predicts the disease type of the given leaf image. As there are only a few disease classes for a single plant, the second model can easily identify the disease more accurately and this disease detection technique is quite fast. But if the first stage can't detect the plant type correctly then, the second stage result is insignificant. Because the second stage result is dependent on the first stage. To avoid this limitation there are a few more alternatives available, such as single-stage classification, but the performance of those methods is not satisfactory. The CNN architectures that were tested in the first stage were also applied in the second stage. However, NASNetLarge was chosen as it uses a reinforcement learning search method to find the best architecture configurations.

IV. Experiment and Result

The performance of the proposed two-stage plant disease detection scheme is evaluated in terms of accuracy that is defined as

$$Accuracy = \frac{Correctly\ classified\ samples}{Total\ number\ of\ samples}$$

To train the model which is used in the first stage, the PV dataset is divided into 14 classes by considering only the type of plant species, and 80% of the whole dataset is used for training and 20% for validation. And for both stages, the training is carried out over a total of 25 epochs and the 'Categorical Cross Entropy' loss function is used.

After the completion of training and validation, the models are tested on IPM dataset. Table I presents the performance of the models employed in the first stage. It can be seen that EfficientNetB3 and NASNetLarge models with augmentation perform very well compared to others. For the EfficientNetB3 model with augmentation, 87.29% accuracy was found.

TABLE II: Comparison of two-stage classification system with other approaches to detect both plant and disease type

1st stage	2nd stage	IPM (Test set)
EfficientNetB3	**NASNetLarge**	**54.24**
GoogLeNetBN [8]		39.50
VGG16 [14]		44.54
InceptionV3 [15]		26.89
GoogLeNet [9]		31.69

In the second stage, the model is trained considering only a specific type of plant but different diseases (e.g all potato leaves containing various diseases). Table II presents the performance of the models employed in the second stage. It is found that the NASNetLarge model performed comparatively better in the 2nd stage. Finally, the EfficientNetB3 model with augmentation is used for the first stage, and the NASNetLarge model for the second stage. As a result, a promising accuracy of 54.24% is achieved using the completely unseen IPM dataset (9.7% improvement compared to the 2nd best method). As expected, the results are found not very satisfactory when only a single stage is used.

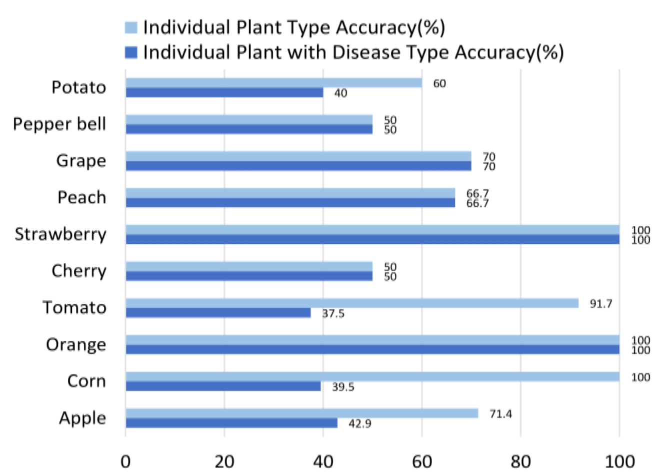
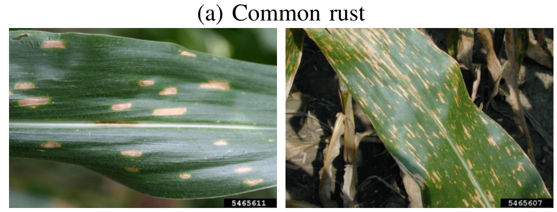


Fig. 2: Crop-wise accuracy on IPM dataset in detecting only plant type and detecting both plant and disease type

Figure 2 depicts the results of each plant class in the IPM dataset. Here for each type of plant, plant type classification performance along with the disease type classification performance is shown pairwise. It is found that the performance in the second stage varies among different plants. Although the first stage of our model produced excellent results for the Tomato and Corn classes, the performance degrades in the second stage for both classes. For example, the proposed method can accurately recognize all of the test images of the Corn plant in the first stage, but only 39.5% of the total test images of the Corn plant in the second stage provides correct results. One possible reason for this particular case is that the images of different Corn plant diseases are nearly identical. The images of 'Common rust' and 'Cercospora leaf disease Gray leaf spot,' as shown in Figure 3, are very similar, and similar to other methods, performance deteriorates in 10 test cases. However, it is very inspiring that for the most common species, such as orange (100%), strawberry (100%), and grape(70%), very satisfactory performance is achieved in both stages, which was not true for other comparing methods. This indicates that by enhancing the training data with more diversified samples, a better model can be obtained for both plant and disease classification.

(a) Common rust



(b) Cercospora leaf spot Gray leaf spot

Fig. 3: Examples of Corn leaves from the IPM dataset that are confused with classes of (a) Common rust and (b) Cercospora leaf spot Gray leaf spot.

V. Conclusion

In this paper, an efficient two-stage classification scheme based on different deep CNN architectures is demonstrated for detecting both plant and disease types. During training, augmentation techniques have been employed and shown to enhance classification performance. Based on extensive experimentation on different networks, in the first stage of the proposed method for plant species classification, the EfficientNetB3 model, while in the second stage for the species-specific disease classification, the NASNetLarge model is employed, which offers comparatively better classification performance. It is found that for some plants, such as Corn plants and tomatoes, even a very high accuracy is obtained at the first stage, comparatively the performance deteriorates in the second stage. One obvious reason is the similarity in the images of the disease types. On top of that, there is a scarcity of images with class diversity, which is tackled reasonably by applying augmentation (a significant enhancement is shown irrespective of the deep CNN architecture). On the contrary, a very satisfactory performance is achieved by using the two-stage proposed method for the most common species, such as oranges, strawberries and grape, a very satisfactory performance is achieved in both stages. This indicates that the proposed method can serve as a potential tool in the agricultural sector with more diversified training data to classify both plants and diseases.

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