Decision-making support system for fruit diseases classification using Deep Learning

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Abstract—**Fruit diseases are a continuous hazard to farmers. By applying computer vision-based techniques, precision agriculture can support the farmers in the decision making for fruit disease control. Features extraction is an essential task for the computer vision pipeline. Nowadays, in general, feature extraction for fruit diseases are handcrafted. However, empirical results in different domains confirm that features learned by Convolutional neural networks (CNNs) provide significant improvements in accuracy over handcrafted features. CNNs have been applied in many computer vision tasks, replacing the hand-engineered models. In general, a large-scale image dataset is necessary for training a CNN. However, there are not many fruit disease images available to compose the dataset. We propose to train a tiny and efficient deep convolutional network developed to run in the mobile devices to classify healthy peach fruits and three peach diseases. Based on transfer learning techniques and data augmentation strategies, the proposed model achieves a Macroaverage F1-score of 0.96. The model does not misclassify any disease class. This achievement shows the potential of using small CNN models for fruit disease classification when having a small quantity of training data.**

Index Terms—**fruit diseases, deep convolutional network, small dataset, precision agriculture**

I. INTRODUCTION

Fruit diseases are a continuous hazard to farmers and responsible for substantial economic losses. The anthracnose is an example of fruit disease, whether left unchecked can cause severe fruit rot infection [1]. In this sense, precision agriculture provides many technologies for supporting farmer's decision making.

In the literature, there are various published works that use computer vision models for fruit disease identification or classification [2], [3], [4], [5], [6], [7], [8]. However,

these models tend to use handcrafted feature vectors (i.e., designed by hand). These types of features have a low-level representation [9]. In the other hand, the convolutional neural networks (CNNs) can learn to extract low-level, mid-level, and high-level features [10]. Empirical results in different domains confirm that representations learned by CNNs provide significantly improvements in accuracy over handcrafted features [11].

Because the state-of-art CNNs have millions of parameters, for a good prediction accuracy and generalization, it is necessary to have large-scale training data. Unfortunately, for fruit diseases, there are not many images available for composing the dataset. A common approach to overcome the lack of large-scale dataset for deep learning training is to apply the transfer learning and data augmentation techniques [12]. In this article, we propose to apply the transfer learning using the CNN MobileNetV2 [13], pre-trained in the ImageNet dataset [14], and data augmentation, in order to investigate the diseases classification results in our relatively small peach fruit disease dataset, as illustrated in Fig. 1. Although the CNN approach has already been used in different context (e.g., leaf tree disease in large scale dataset [15]). The novelty of the current work is related to the prediction capabilities considering a small fruit disease dataset. Also, the model is designed to run on mobile devices. This paper is structured as follows. In Section II, summarizes the related work. Section III describes the methodology. Section IV includes the analysis and discussion of results. The conclusions are given in Section V.
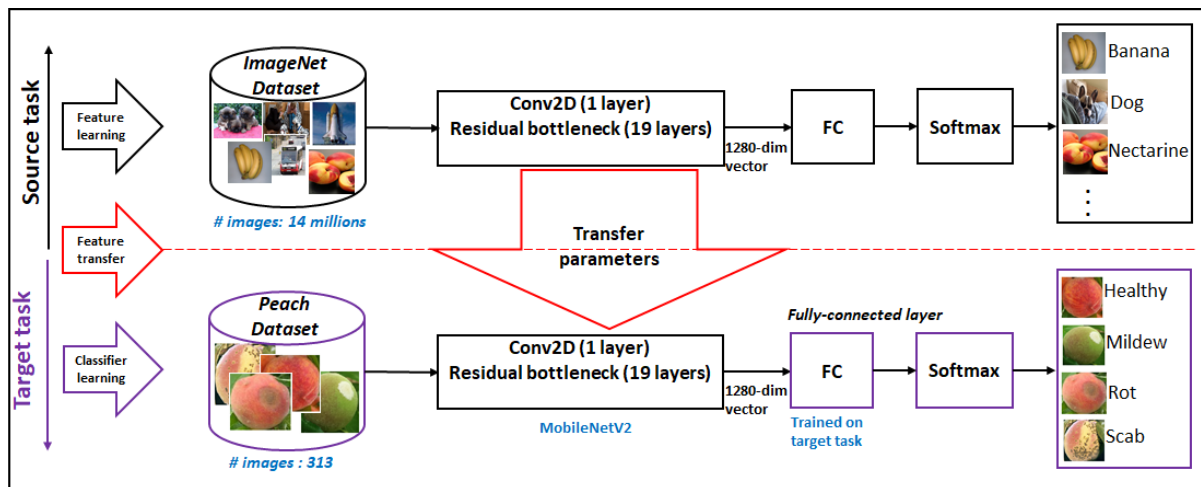
Fig. 1. MobileNetV2 transferring parameters: The model was firstly trained on the ImageNet dataset (source task). This model and its pre-trained parameters are available on the Tensorflow-Hub. Pre-trained parameters are transferred to the target task (fruit disease classification). Furthermore, a fully connected layer is trained on our peach disease dataset to compensate for the difference between the source and target data images.

II. RELATED WORK

Dubey and Jalal [2] propose a method for apple disease (blotch, rot, and scab) classification. The pipeline of the method consists of image fruit segmentation applying K-means, feature extraction from segmented images (global color histogram, color coherence vector, and local binary), and then apply the support vector machine as a classifier. The method achieved an average precision of 0.93, using 50 images per class. This method required finding manually the useful features from the images to discriminate each fruit disease class.

Samajpati and Degadwala [3] fuse color and texture features from apple images and use the random forest to classify scab, rot, and blotch diseases. They used 70 images for training and 10 for testing of each class. This non-automatic method required selecting manually the features (from color and texture) representing each fruit disease class.

Bhange and Hingoliwala [16] suggest a solution for pomegranate fruit disease detection. The method starts with pre-processing by enhancing the images. After that apply K-means clustering algorithm for segmentation. For feature extraction, they construct a feature vector with color, texture, and morphology from the segmented image. As a classifier, they proposed to use K-nearest neighbors.

Similarly to [16], Behera et al. [17] propose an orange disease classification approach with pre-processing, segmentation, and feature extraction. In the pre-processing phase, it is performed image enhancement and L*a*b color transformation. It is used the Gary level co-occurrence matrix for extracting the following features: contrast, correlation, energy, homogeneity, mean, standard deviation, entropy, RMS, variance, smoothness, kurtosis, skewness, and IDM. The authors used the SVM classifier, perform testing in 40 images, and achieved an accuracy of 0.9.

Abirami and Thilagavathi [18] proposed a method for classification of fruit diseases using neural networks (NN) as classifier. First, they perform image pre-processing, then segmentation to produce binary images by thresholding and finally creating feature vectors applying the local binary pattern. They reported test accuracy for 100 images of 0.92 for bacterial disease and 0.86 for fungal diseases with ten hidden layers NN.

Ayyub and Manjramkar [7] performed a method for identifying and classifying rot, scab, and blotch apple fruit diseases. The feature extraction approach combines color, texture, and shape image information. Training a multiclass support vector machine, they report an average accuracy of 0.96.

III. MATERIALS AND METHODS

A. Dataset

Our peach dataset is composed of RGB images collected from the open websites platform Forestry Images [19], PlantVillage [20], Pacific Northwest Pest Management Handbooks [21], Utah State University [22], University of Georgia [23], as well as from the APPIZÊZERE (Associação de Protecção Integrada e Agricultura Sustentável do Zêzere). The dataset has 313 RGB images split into four classes: Healthy, Rot, Mildew, and Scab, as shown in the Table I. Fig. 2 shows the dataset class instances and their visual examples.

TABLE I. Dataset Statistics

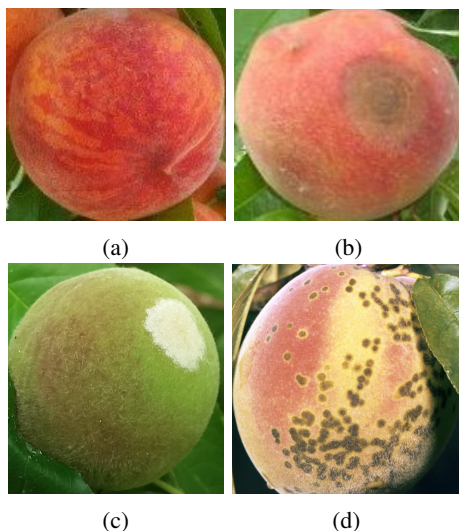| Classes	Images	Training	Testing
Healthy	124	99	25
Rot	106	84	22
Mildew	58	46	12
Scab	25	20	5
Total	**313**	**249**	**64**

Fig. 2. Peach fruit images and their classes: (a) Healthy. (b) Rot. (c) Mildew. (d) Scab.

As mentioned before, CNNs can suffer from poor generalization, whether trained with a small quantity of data. A common approach to overcome this problem is to apply data augmentation. We performed the data augmentation technique in our dataset, according to Table II. We have performed other augmentations, but theses ones shown in the table led to the best results.

TABLE II. Data Augmentation

Transformation	Values
Rotation	40
Width-shift	0.15
Height-shift	0.15
Zoom	0.2
Horizontal-flip	True

B. Model Assessment

To evaluate the model performance, we used the Precision (1), Recall (2), and F1-score (3), which is a function of Precision and Recall metrics. In the field of disease identification and classification, True Negative (TN) samples are dominant. It means that the dataset composition is uneven (i.e., unbalanced), and the TN can largely contribute to the model test results. In this context, F1-score is a suitable metric to assess the proposed method.

$$Precision = \frac{TP}{TP + FP} \qquad (1)$$

$$Recall = \frac{TP}{TP + FN} \qquad (2)$$

Where TP is True Positive (means the number of correctly classified); FP is False Positive (means the number of misclassified as belonging to the class); FN is False Negative (is the number of cases that should be classified as belonging to the class).

$$F1\text{-}score = \frac{2 \times Precision \times Recall}{Precision + Recall} \qquad (3)$$

C. Convolutional Neural Network Architectures

We have mentioned the deep neural networks overfitting problem due to a small quantity of data for training. Unfortunately, the available fruit diseases datasets have a relatively small quantity of images. Taking this restriction into account, we select the MobileNetV2 CNN model to investigate the peach fruit diseases. MobileNetV2 is a general-purpose computer vision neural network designed to support classification, object detection, semantic segmentation, and run in mobile devices and real-time applications.

1) MobileNetV1: The main key to reduce the computational cost and model size is splitting the typical convolution into two layers: a depthwise convolution and a pointwise convolution. The depthwise convolution is performed by applying one filter kernel per input channel and the pointwise convolution by applying a linear combination in the depthwise output layer. In total, the MobileNetV1 has 28 layers [24].

2) MobileNetV2: It has an initial fully convolution layer followed by 19 bottleneck layers, according to Table III. Its building block (bottleneck layer) is based on MobileNetV1 structure with two additional layers that perform expansion in the low-dimensional input to a high dimension and filtered with a lightweight depthwise convolution. In the end, the features are again projected back to a low-dimensional representation with a linear convolution.

TABLE III. MobileNetV2 structure: Each line describes a sequence of 1 or more equal layers, respected to n. All layers in the same line have the same number c of output channels. The first layer of each sequence has a stride s and all others use stride 1. The expansion factor applied to the input is t.

Input	Operator	t	c	n	s
224^2 x 3	conv2d	-	32	1	2
112^2 x 32	bottleneck	1	16	1	1
112^2 x 16	bottleneck	6	24	2	2
56^2 x 24	bottleneck	6	32	3	2
28^2 x 32	bottleneck	6	64	4	2
14^2 x 64	bottleneck	6	96	3	1
14^2 x 96	bottleneck	6	160	3	2
7^2 x 160	bottleneck	6	320	1	1
7^2 x 320	conv2d 1x1	-	1280	1	1
7^2 x 1280	avgpool 7x7	-	-	1	-
1 x 1 x 1280	conv2d 1x1	-	k	-	-

D. *Implementation Details*

The experiment was developed in the deep learning frameworks Keras, TensorFlow, and TensorFlow-Hub.

1) Keras & TensorFlow: Keras is a high-level deep learning API that runs on top of the machine learning platform TensorFlow, which efficiently executes low-level tensor operations on CPU, GPU, or TPU. We used the Keras application version 1.0.8 and TensorFlow-GPU 2.0.0. The image data preparation resize, and augmentation also was performed with Keras processing library.

2) TensorFlow Hub: TensorFlow Hub is a repository for publication and consumption of reusable parts of machine learning models across different tasks supporting transfer learning. In the TensorFlow Hub, a module is a piece of TensorFlow graph. In our work, we used a pre-trained MobilenetV2 classifier module. The image input dimension for the model is 224x224x3.

3) Experiment: Using the Keras API, a fully connected layer and a Softmax activation function were added to the model. We compile the model with optimizer adam, loss function sparse categorical crossentropy, and metrics accuracy. We split the dataset according to Table I and performed the training with 20 epochs and batch size of 16.

IV. RESULTS AND DISCUSSION

This article proposes the use of a deep learning-based solution for classifying Rot, Mildew, and Scab diseases in peach fruits, which represents a contribution, considering that previous methods were all handcrafted. We used a MobileNetV2 CNN architecture, fine-tuned based in a set of images collected from well known datasets and data augmentation techniques. Fig. 3 and Fig. 4 show the training report for the best result achieved. The error for training and validation is about 0.2, and the difference between each other is very small, indicating that the model does not suffer overfitting for 20 training epochs.

The Table IV presents the classification report for the model assessment. In this table, we can evaluate the model for each class and the total performance of the model. We can see that the best classification performance for an individual class is the Scab disease with F1-score of 1.00. Fig. 2(d) shows that the visual black spots can provide useful features for discriminating the Scab disease. Rot and Mildew diseases both have classification results of 0.96 F1-score. And lastly, the Healthy fruit class with an F1-Score of 0.94. The total performance of the model achieved the Macro-average F1-score of 0.96. One important finding is that the only misclassification was for the Healthy fruit class (Fig. 5 summarizes the classification errors). The model does not misclassify any disease class. This result is an important achievement, because misclassification in the disease investigation for infection and control has a high cost.
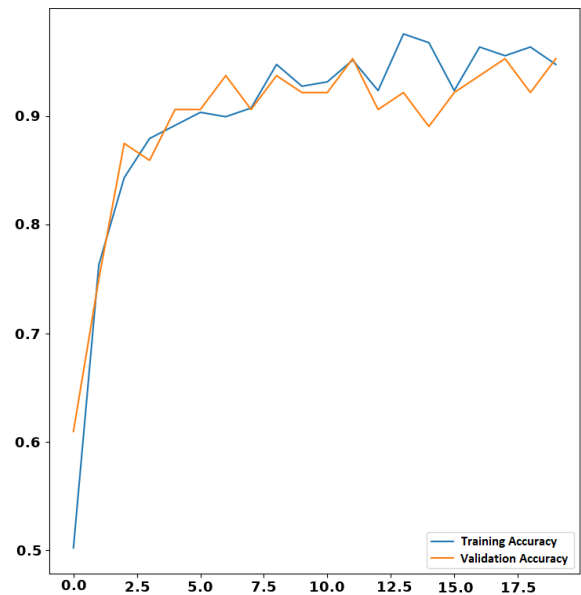

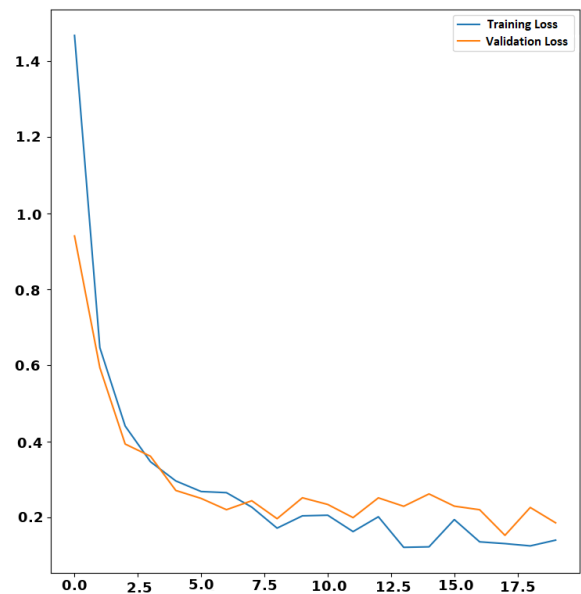Fig. 3. Training and Validation Accuracy.

Fig. 4. Training and Validation Loss.

TABLE IV. Classification Report

Class	Precision	Recall	F1-score	Support
Healthy	1.00	0.88	0.94	25
Mildew	0.92	1.00	0.96	12
Rot	0.92	1.00	0.96	22
Scab	1.00	1.00	1.00	5
Macro-avg F1-score	0.96	0.97	**0.96**	64

Fig. 5. Confusion Matrix.

V. CONCLUSIONS

Scab disease had the best individual classification with F1-score of 1.00, followed by Rot and Mildew classes with both of 0.96 F1-score. The Healthy class had a classification of 0.94 F1-Score. The total performance of the model achieved a Macro-average F1-score of 0.96. The model does not misclassify any disease class, which is very important in disease investigation for infection and control. These achievements show the potential of using CNN for fruit disease classification with a small quantity of training data.

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