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A Deep Learning-based Approach for Banana Leaf Diseases Classification

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Abstract:

Plant diseases are important factors as they result in serious reduction in quality and quantity of agriculture products. Therefore, early detection and diagnosis of these diseases are important. To this end, we propose a deep learning-based approach that automates the process of classifying banana leaves diseases. In particular, we make use of the *LeNet* architecture as a convolutional neural network to classify image data sets. The preliminary results demonstrate the effectiveness of the proposed approach even under challenging conditions such as illumination, complex background, different resolution, size, pose, and orientation of real scene images.

Keywords: Banana plant diseases, Deep learning, Classification

1 Introduction

Crop diseases are major sources of famine and food insecurity on our planet. In fact, it is estimated that plant pathogens may account for annual crop yield losses of up to 16% globally [Oe06]. Furthermore, the current solutions to fight different diseases demand the massive use of crop protection products, which are dangerous for the environment and the user. Microscope and DNA sequencing-based methods are effective to identify and discover different kinds of diseases. Even though many of the farmers around the world do not have access to these diagnostics tools, the vast majority of them possesses a cell phone. In fact, the Ericsson company forecasts that mobile subscriptions will reach 9.3 billion in 2019 and 5.6 billion of these will be smartphone subscriptions [Mo15]. Hence, a phone based tool that helps in diagnosing crop diseases based on capturing and analyzing automatically a picture of a plant leaf is a promising solution.

In this paper, we take a first step towards such a tool. However, we limit our study to classify banana leaves diseases. Banana is threatened by different types of diseases, such as *banana sigatoka* and *banana speckle*. The black sigatoka is caused by the fungus *Mycosphaerella fijiensis*. Its symptoms start by minuscule, chlorotic spots and it then develops into thin brown streaks that are bounded by leaf veins (see Fig.1). Leaf speckle is a fungal disease. Its symptoms start as light brown little spots and with time they increase in size

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and become black. Left untreated, these diseases will kill the plant. If, however, they are diagnosed early, they can be treated and the plant can be saved.

(a) Black Sigatoka (b) Banana Speckle

Figure 1: Example of two banana diseases

Given the limited availability of resources and expertise on banana pathology worldwide, the need for a system to classify and identify banana diseases automatically is urgent. Also, the proliferation of using phones and the internet all over the world make it easily accessible to all kind of people. Computer vision and machine learning techniques have been applied to different disease detection such as tomatoes, grapes, potatoes and cotton. Motivated by advances in computer vision, especially convolutional neural networks (CNNs), which managed to produce remarkable results in the field of image classification, we propose a new system based on CNNs for banana plant disease recognition. Our method, based on LeNet architecture [Le89] requires minimal image preprocessing. The model can learn visual features directly from images. The developed model is able to recognize two different types of diseased leaves out of healthy ones.

The rest of the paper is organized as follows: in Section 2, we present the related work. Section 3 explains technical details of the proposed approach and the architecture of the used convolutional neural network. Furthermore, experimental evaluation and results are reported in Section 4. Finally, Section 5 concludes the paper and provides an outlook to future work.

2 Related work

Plant diseases cause major production and economic losses in agriculture and forestry. Recent developments in agricultural technology have led to a demand for a new era of automated non-destructive methods of plant disease detection. Hence, a number of approaches have turned to computer vision and machine learning techniques to create a fast method for plant diseases detection at the early onset of the symptoms. Most of the studies presented in the literature of plant disease identification follow the steps shown in Fig. 2 [Al11, Cu10, PC13].

As shown in Fig. 2, the identification process starts by an image acquisition step where different digital devices are used to capture healthy and infected plant images. Then, further analysis is needed to edit the image and prepare it for later treatment, such as image enhancement, segmentation, color space conversion and filtering. In particular, image segmentation methods, like thresholding, are frequently used to detect boundaries in images.

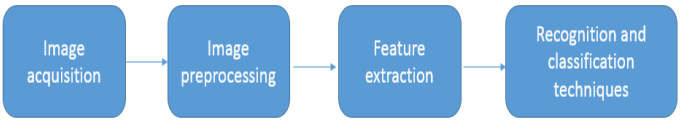

Figure 2: General steps applied to plant disease identification

Within the feature extraction step, features such as color, shape and texture are calculated from the image. Finally, the classification step is performed. Different classification algorithms are used in the literature such as neural network [Sa13], support vector machine [BKS16] and rule based classification [Cu10, Sc16]. In the following, we present a set of the state-of-the-art approaches following the general architecture in Fig. 2.

An automated tool is presented in [Cl15] to measure the foliar bleaching of leaf caused by the insect known as Corythucha ciliata (SAY). In this study, a CCD camera was used for collecting infected plant images. The authors used the digital color image analysis discrimination method in which the original RGB leafs images were converted into HIS and L*a*b color spaces. The leaves containing the disease are determined based on the color difference between them and the healthy leaves. The method is based on the use of the *Otsu method* to isolate the leaf from its background and the chlorophyll histogram to detect discolorations caused by the lace bug. In [Al11], a color based approach is introduced to identify five types of leaf diseases which are *early scorch*, *cottony mold*, *ashen mold*, *late scorch* and *tiny whiteness*. The approach starts by identifying green pixels based on the calculation of a global threshold according to the *Otsu method*. After removing of non green pixels, the infected areas are clustered using the K-means technique. Furthermore, texture features are extracted using the co-occurrence matrix as an input to a neural network to identify the disease. In [Cu10], the authors develop an automatic threshold method to separate the infected areas from the healthy ones. They use a multispectral CCD camera to capture the images of the leaves then each leaf image is converted from the RGB format to the HIS format. After the infected and healthy pixels are segmented, the RIA (Ratio of Infected Area) and RCI (Lesion Colour Index) values were calculated. Based on these values, the approach is able to determine if a leaf is healthy or not.

Another approach, represented in [BKS16], starts by a segmentation step of the leaf in order to remove the background using the guided active contour. The approach then computes the deviation of each pixel from the green color in order to segment the symptom. The greener the pixel the healthier the part of the leaf is. The segmented symptoms and lesions are then transformed from the RGB space to the HSV, L*a*b* and CMYK color spaces. The classification step is then performed using color histograms. A new system is introduced in [MBP16] to classify different diseases that infect the paddy plants such as brown spot disease, leaf blast disease and bacterial blight disease. In this system, the authors extract the scale invariant feature transform (SIFT) feature and then use KNN and SVM for classification. [Ob14] introduce a prototype for the detection of mycotic infections on tomato crops. The authors have created a manually annotated dataset of 147 im-

ages including 31 and 28 images of healthy and infected plant leaves, respectively. Then they use different color descriptors (Color Structure Descriptor (CSD), Scalable Color Descriptor (SCD) and Color Layout Descriptor (CLD)) to characterize the leaflets. The authors reported that the CSD showed better results as compared to SCD and CLD. The author in [Sa13] presented a disease identification approach of a medical herb called Phyllanthus Elegans Wall (Asin-Asin Gajah) which is used to cure breast cancer. The proposed method starts by enhancing contrast as a preprocessing step before segmentation and features extraction from leaves images. Then, two feed forward neural networks which are multi-layer perceptrons and radial basis function RBF were applied to classify the images into healthy or unhealthy.

Even though different methods have achieved good classification results in identifying and recognizing some of the diseases, they suffer from some limitations. For example, segmentation is used in most methods as the first step in the leaf disease analysis. If the leaf image is captured with a black background, the segmentation is straightforward and no obstacles should be faced. However, when the background contains other leaves or plants, the segmentation may be questionable. Most of the methods will fail to effectively extract the leaf from its background which will lead to unreliable results. Also, some disease symptoms do not have well represented edges and they could gradually fade into healthy tissue [Ba16]. This may disturb solutions like color based methods and thresholding. Furthermore, a number of the methods rely on hand-crafted features such as color histograms, texture features, shape features and SIFT that requires expensive work and depends on expert knowledge. However, these methods do not generalize well and they are not effective when dealing with a large amount of data that could contain significant varieties. For example, the black leaf streak disease in banana produces heterogeneous symptoms and hence requires more powerful methods to detect them effectively. Hence, in our work we will investigate the application of convolution neural network (CNN) which is a method that avoids segmentation and hand-crafted features. Also, the presence of a large amount of banana leaves data and powerful computing infrastructure made CNN a suitable candidate for the current application.

In the next section, we detail the proposed method for banana disease identification.

3 Proposed method

To deal with the mentioned challenges, we introduce a deep learning-based approach to classify and identify banana leaves diseases. The general architecture of the proposed framework is illustrated in Fig. 3. The figure shows that the framework consists of two main components: *image preprocessing* and *deep learning-based classification*. In the following, we present details about each component.

3.1 Image preprocessing

The dataset stored in either local or global repositories contains a large number of images of healthy and infected leaves. The images are taken with a standard digital camera. Each

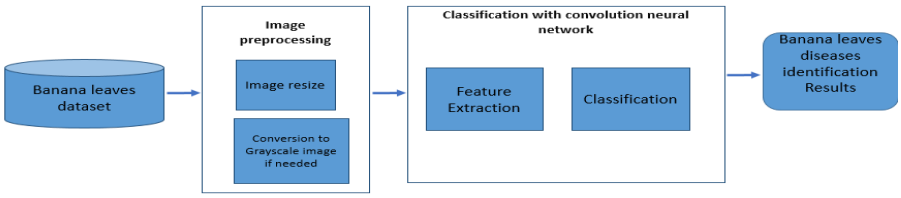

Figure 3: Proposed framework architecture.

image has three channels which are red (R), green (G), and blue (B). In our experiments we will test the applicability of our approach to both the RGB images and the grayscale images. To this end, we perform a preprocessing step where each image in our dataset is resized to $60 \star 60$ pixels and converted to grayscale.

3.2 Deep learning based classification

Neural networks contains multiple neurons arranged in layers. The neurons in the adjacent layers are connected to each other. These neurons learn how to convert inputs (pre-extracted and pre-processed features) into corresponding output (labels). In particular, convolutional neural networks (CNNs) are a family of multilayered neural networks and are considered as the first successful trial for deep learning approachs where many layers of a hierarchy are successfully trained in a robust manner. CNNs are known for their robustness toward low variation in inputs, they require low preprocessing for their execution. They are also able to extract appropriate features while simultaneously performing discrimination [De14, ARK10]. More specifically, in the current implementation we make use of the LeNet [Le89] architecture for the convolution neural network.

As shown in in Fig. 4, a CNN is composed of three main parts which are convolution, pooling and fully connected layers. The convolution and pooling layers act as feature extractors from the input images while the fully connected layer acts as a classifier. The essential purpose of convolution is to extract features automatically from each input image. The dimensionality of these features is then reduced by the pooling layer. At the end of the model, the fully connected layer with a softmax activation function makes use of the learned high-level features to classify the input images into predefined classes. In summary, the LeNet model is composed of two main parts: the first part is the self-taught feature extraction model and the second part is the classification model. In the rest of this section, we will detail these two components.

3.2.1 Feature extraction model

The feature extraction model is the part where the network learns to detect different high-level features from the input images. It consists of a sequence of convolution and pooling layers.

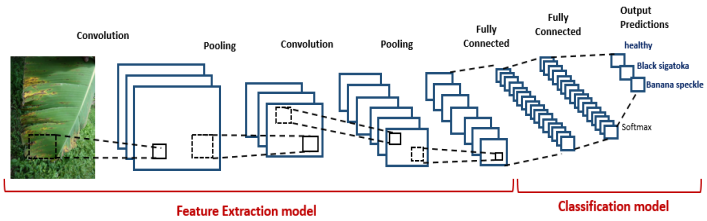

Figure 4: A graphical depiction of a LeNet model

- **Convolution map.** The convolution layer is an elementary unit in the CNN architecture. The goal of convolution is to extract features from the input image. It consists of a set of learnable filters. Each filter is applied to the raw pixel values of the image taking into account the red, green and blue color channels in a sliding window fashion, computing the dot product between the filter pixel and the input pixel. This will result in a 2-dimensional activation map of the filter called the *feature map*. Hence, the network learns filters (ie. edges, curves) that will activate when they find known features in the input.The CNN learns the values of these filters on its own during the training process. The Convolution operation is presented in Equation 1. A convolution layer is configured by the number of convolution maps it contains M_i, the size of the filters which are often squared $k_x \star k_y$. The feature map M_i is computed as follows:

$$M_i = b_i + \sum_k W_{ik} \star X_k \tag{1}$$

where $\star$ is the convolution operator, X_k is the k^{th} input channel, W_{ik} is the sub kernel of that channel and b_i is a bias term. In other words, the convolution operation being performed for each feature map is the sum of the application of k different 2D squared convolution features plus a bias term. Hence, In comparison with traditional image feature extraction that relies on crafted general feature extractors (SIFT, Gabor filter, etc), the power of CNN is noted in its ability to learn the weights and biases of different feature maps which lead to task specific powerful feature extractors. Moreover, the rectified nonlinear activation function *(ReLU)* is performed after every convolution to introduce nonlinearity to the CNN. The ReLU is a very popular activation function which is defined as $f(x) = max(0,x)$ where x is the input to a neuron.

- **Max-pooling map:** In the architecture of convolutional neural network, convolution layers are followed by sub-sampling layers. Each sub-sampling layer reduces the size of the convolution maps, and introduces invariance to (low) rotations and translations that can appear in the input. A layer of max-pooling is a variant of such layer that has shown different benefits in its use. The output of max-pooling layer is given by the maximum activation value in the input layer over sub windows within each feature map. The max-pooling operation reduce the size of the feature map.

3.3 Classification model

Within the classification step we use fully connected layers where each neuron provides a full connection to all learned feature maps issued from the previous layer in the convolution neural network. These connected layers are based on the softmax activation function in order to compute the classes scores. The input of the softmax classifier is a vector of features resulting from the learning process and the output is a probability that an image belongs to a given class. The softmax function ς takes as input a C-dimensional vector z and outputs a C-dimensional vector y of real values between 0 and 1. This function is calculated as below:

$$y_c = \varsigma(\mathbf{z})_c = \frac{e^{z_c}}{\sum_{d=1}^{C} e^{z_d}} \quad for\, c = 1 \cdots C \tag{2}$$

In the next section, we will present the conducted experiments and results.

4 Experimental Evaluation

To validate the performance of the proposed approach, we conducted a set of experiments using a real dataset of banana diseases obtained from the PlantVillage project [HS15, MHS16]. The plant village project [3] contains thousands of images of healthy and diseased crop plants that are open and available on the web. The images in our dataset are annotated as belonging to three different categories which are healthy (1643 images), black sigatoka (240 images) and black speckle (1817 images). Fig. 1 illustrates some samples of the dataset which contains in general 3700 images. These images are captured with different sizes, orientation, poses, backgrounds and illumination. In our implementation we used the deeplearning4j [4] as an open source deep learning library which supports the use of GPUs to make the execution of the deep learning algorithms faster. Our goal is to evaluate the predictive performance of our model on unseen data of banana diseases. Hence, in our experiments, we decided to test all the different range of train and test set splits to evaluate the robustness of our proposed algorithm and its ability to avoid overfitting. This means that a percentage of the whole dataset is used for training and the rest is used for testing. The training dataset varies from 80%, 60%, 50%, 40 % to 20 % with the use of the same hyper parameters described in Table 1. These parameters are determined empirically according to a series of experiments carried on the whole dataset that give the best results of classification.

Table 1: hyper parameters choices

Parameter	optimization algorithm	learning rate	momentum	weight decay	batch size	activation function	iterations
Value	SGD	0.001	0.9	0.005	10	Sigmoid	30

As shown in Table 1, the stochastic gradient descent (SGD) algorithm is used in our model to learn the best set of weights and biases of the neural network that minimize the loss

[3] https://www.plantvillage.org/en/
[4] https://deeplearning4j.org/

function. While learning, the SGD algorithm works by randomly choosing a small number of training inputs. We refer to this as the batch size which is set to 10. The learning rate is set to 0.001. It is the rate at which a function move through the search space. A small learning rate leads to more precise results but it requires more training time. The momentum is an additional factor to determine how fast the SGD algorithm converges on the optimum point. It is set to 0.9.

To evaluate the effectiveness of the proposed system, we make use of a combination of *accuracy*, *precision*, *recall*, and *F1-score*. Results are reported in Table 2 across all our experimental configurations.

Table 2: Precision, recall, accuracy and F1 score for the corresponding experimental configuration.

		Color				Gray Scale			
Train	Test	Accuracy	Precision	Recall	F1-score	Accuracy	Precision	Recall	F1-score
20%	80%	0.9861	0.9867	0.986	0.9864	0.9444	0.9479	0.9444	0.9462
40%	60%	0.9861	0.9865	0.9859	0.9863	0.9757	0.9764	0.975	0.976
50%	50%	0.9972	0.9970	0.9972	0.9971	0.8528	0.889	0.8527	0.8705
60%	40%	0.9676	0.969	0.9677	0.9683	0.9282	0.9314	0.9283	0.9298
80%	20%	0.9288	0.9299	0.9288	0.9294	0.8594	0.8678	0.8594	0.8636

these results were obtained using our deep learning model for identifying three banana images classes (healthy, black sigatoka and black speckle). As shown in Table 2, our model was able to find good results when applied to classify the diseases of banana from its leaves. The obtained results confirm the the importance of the color information in plant disease identification. Hence, a green color always refer to a healthy leaf while a leaf with black or brown spots may be considered unhealthy.

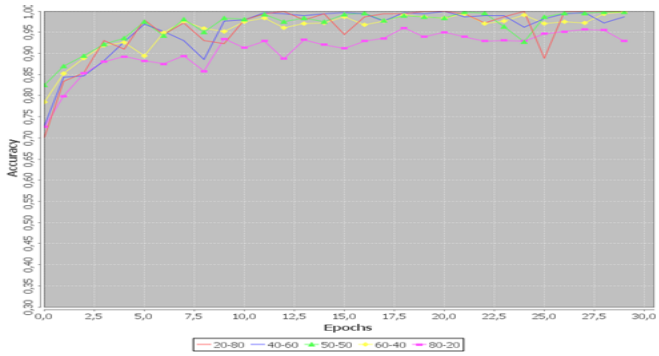

Figure 5: Comparison of progression of overall accuracy grouped by train-test set splits

Fig. 5 shows the accuracy of the different train and tests splits choices while the number of iterations is varied. As we can see, in some splits the model take more time to converge. However in most of the test splits, the model starts to stabilize from iteration 25 and achieve good accuracy at the final iteration.

5 Conclusion

Agriculture suffers from a severe problem, plant diseases, which reduces the production and quality of yield. Besides, the shortage of diagnostics tools in underdeveloped countries has a devastating impact on their development and quality of life. Hence, there is an urgent need to detect the plant diseases at the early stage with affordable and easy to use solutions. To this end, in this paper, we presented an approach based on convolution neural networks to identify and classify banana diseases. The proposed model can serve as a decision support tool to help farmers to identify the disease in the banana plant. Hence, the farmer can take a picture of the leaf with the symptoms and then the system will identify the type of the disease. Our main contribution is to apply deep neural networks to detect two famous banana diseases which are banana sigatoka and banana speckle in real scene and under challenging conditions such as illumination, complex background, different images resolution, size, pose and orientation. After several experimentations our system was able to find good classification results. This has proven that the proposed method can significantly support an accurate detection of leaf diseases with little computational effort. Encouraged by the optained results, we intend in our future work to test more banana and plants diseases with our model. Besides, we will target the automatic severity estimation of the detected disease since it is an important problem that can help the farmers in deciding how to intervene to stop the disease.

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