# Tomato Disease Classification using AlexNet

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Abstract—This work employs the AlexNet architecture for tomato diseases detection. The experimental setup is divided into two categories: In the first case a 10-class classifier is trained with healthy (1 class) and diseased (9 classes) leaf images and in the second case 9 different 2-class classifiers are trained with healthy (1 class) and diseased (1 class) leaf image. All cases are tested for three training scenarios. Finally, we point a particular feature of the PlantVillage dataset.

*Index Terms*—Classification, plant, disease, leaves, AlexNet, PlantVillage.

## I. INTRODUCTION

The latest advances in Neural Networks (NN) have produced complex classifiers without the need to analytically define the discriminating function. The particular case of plant diseases detection has been discussed in depth in various works that either concentrate on the feature extraction methods or the classification procedure. In some cases like [8] they utilize solely Support Vector Machine (SVM) kernels and base the success of the classifier to the feature extraction method. In other works, like [3], [6], [7], [9] the features are learned through various architectures and then the classifier uses a series of fully connected layers.

In the following section we do a literature overview, in section III we describe the experimental setup and in section IV we present the experimental results. Section V concludes the paper.

### **II. LITERATURE OVERVIEW**

The target problem is the detection of plant diseases through images. As a classification problem, it requires a classifier as the function that discriminates one or more diseases from the healthy plants and a quality dataset. The characteristics of a good dataset are a large number of samples and those examples to be as typical as possible. The sections that every works states specifically are the dataset, the feature extraction method and the classification method.

## A. Datasets

Datasets are publicly available only in 4 papers. Specifically, in [1], [3], [5] they use the PlantVillage dataset and in [4] they use the NLB dataset. Nevertheless, in any of the works listed in this summary, data consists of high-resolution labeled plant

leave images. In cases like [2] the dataset is also augmented with common practices, like mirroring, rotating and translating the images, to introduce invariance to the classifier.

## B. Feature Extraction

In [3], [5]-[7], [9] the images, apart from being preprocessed (equalization, cropping) are forwarded directly to the classifier. The image is used either as is or in patches. For the latter case, in [2] and [4], an annotation tool is used to label each patch in order to train the classifier. In all other works the images are used as is. In [1], the proposed feature extraction method provides some insight on how features are obtained through a Convolutional NN (CNN). They visualize the features after each layer in a 5-layer CNN with a the InceptionV3 module. In that manner, they highlight that the neurons are activated on ROIs, without prior annotation. In [8], [10], [11] they use texture based information. Specifically, they compute the Color/Gray level Co-Occurrence Matrix (CCM/GLCM) that count the occurrences of shorty sequences in the image. Also in [10], the authors use transforms like Discrete Cosine Transform (DCT) and Discrete Wavelet Transform (DWT) to feed as input to the classifier, in various combinations.

## C. Classification

The classification is done by NNs, SVMs, K-Nearest Neighbors (**KNN**) and Decision Trees. Specifically, in [2] they compare KNN with a Multilayer Perceptron (**MLP**) NN. Likewise, in [3] They compare 2 NN architectures with SVM and Random Forest. In, [8] they compare 4 different SVM kernels. In [10] they compare KNN, SVM, Randrom Forest (RF), Bayesian and RNN classifiers. Lastly, when NNs are utilized the architectures used are AlexNet (or CaffeNet), GoogleNet, while in [4], [9]–[11] the architecture is custom.

For reference purposes, in Table 1 we mention only the best performance in terms of accuracy all of the above works yielded.

## III. EXPERIMENTAL SETUP

As the problem is to classify tomato diseases from plant leaves, it makes sense to test not only how a 10-class classifier learns, but how sensitive and specific is a binary classifier in discriminating healthy images from a single disease. Also, as stated in III-A, the classes are not balanced. For these reasons we created 9 binary classifiers, one for each disease, besides the 10-class one. Each, network, was trained using the Cross

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Study	Feature Extraction	Classification	Best Accuracy
[2]	- <sup>a</sup>	GoogleNet	t.l. <sup>b</sup> : 99.18%
[3]	_ <sup>a</sup>	GoogleNet	99.35%
[4]	Hand picked	CNN	97.8%
[5]	Hand picked	MLP	81.12%
[6]	- <sup>a</sup>	CaffeNet	t.1.:96.3%
[7]	- <sup>a</sup>	AlexNet	88.3%
[8]	4 rot. GLCMs*9 metrics	Linear SVM	99.83%
[9]	3-layer CNN	1-layer FC	92.5%
[10]	Otsu+GLCM/DCT/DWT	SVM	94.45%
[11]	K-means/Otsu+HSI CCM	NN	94.67%

TABLE I Results in bibliography

<sup>a</sup> Features extracted by the NN, <sup>b</sup> transfer learning.

Entropy loss function, and the Stochastic Gradient Descent method. As proposed by Sladojevic et al. [13] each network was tested for 3 training scenarios, to visualize the impact of transfer learning in the plant disease detection problem:

· Shallow retraining

The model is pre-trained on the ImageNet dataset with 1000 output classes and only the 3 final fully connected layers are fine tuned using our dataset

• Training from scratch

The model is randomly initialized according to He, Zhang, Ren, Sun [15] and trained solely on our dataset.

• Deep retraining

The model is pre-trained as in shallow retraining, but this time all the parameters of the network are fine tuned.

For all cases the networks are trained for 30 epochs. In terms of iterations, for the 10-class classifier, this translates to 21,590 iterations. For the binary classifiers the number of iterations changes in accordance to the size of the dataset for that class. Finally, since training from scratch requires randomly initializing the network, it is appropriate to test the network over a number of tries. Therefore we trained the network 20 times and averaged the results to compare them to the other two scenarios.

# A. Dataset

The PlantVillage dataset is publicly available <sup>1</sup> and it was published by Hughes and Salathé [16] in 2015. It contains 55,100 pictures of 38 classes of diseased plant leaves and 1 class of healthy leaves per plant. For our experiments we selected only tomato related classes. Namely, our selection comprises of 18,179 images from 9 tomato plant diseases and a single healthy class. In Table 2 there are the number of images per class. Fig. 1 shows one sample image from each class. For training and validating the network we used an 80%-20% split. In addition, as it is obvious the classes are not balanced. This is also a reason why we needed to test the discrimination of healthy against single-disease classes. As it can be seen the background is similar across the dataset and thus the network should be able to neglect it and pick up features only from the leaves. [13] et al. provide also a segmented version

<sup>1</sup>PlantVillage: https://github.com/spMohanty/PlantVillage-Dataset



Fig. 1. (a) Bacterial spot, (b) Early blight, (c) Healthy, (d) Late blght, (e) Leaf mold, (f) Mosaic virus, (g) Septoria leaf mold, (h) Spider mites, (i) Target spot, (j) Yellow leaf curl virus.



Fig. 2. The AlexNet architecture as presented in [14].

of the dataset, were manually the background was set to 0. However, we observed that the segmentation is not perfect and in many cases also sets to 0 foreground regions of interest. This probably happens because lesion related regions on the leaf have similar color values to the background.

TABLE II DATASET DESCRIPTION

#	Class Name	Train Size	Validation Size
0	Bacterial spot	1702	425
1	Early blight	800	200
2	Healthy	1273	318
3	Late blight	1526	382
4	Leaf Mold	761	191
5	Septoria leaf spot	1417	354
6	Spider mites	1341	335
7	Target Spot	1123	281
8	Yellow Leaf Curl Virus	4286	1071
9	Mosaic virus	299	74

# B. Network Architecture

We used the AlexNet deep neural network, from Krizhevsky et al. [14], with 5 convolutional layers and 3 fully connected layers, interchanging features between layers of the same level. Fig. 2 shows in detail the AlexNet architecture. We selected this network for its simplicity of implementation and short training time.

# **IV. RESULTS**

As shown by Fig. 3, shallow and deep retraining show similar behaviour. Since both start from the same pre-training, the initial error is the same. However, deep retraining is achieving convergence to a lower minimum. That is expected since the network is optimizing many more parameters and thus searches for the minimum in a higher dimensional space. Regarding training from scratch, for the first 4 or so epochs,



Fig. 3. Loss of 10-class AlexNet for Shallow, From scratch and Deep training, over 30 training epochs.



Fig. 4. Confusion matrices for (a) Shallow retraining, (b) From scratch training and (c) Deep retraining. Rows show the predicted class and columns the true class. Color intensities are logarithmic. All cells sum to 100%.

the loss drops steadily with a small rate, and after that, it converges to the neighborhood above deep loss. This, shows that even without the pre-training session, the network approaches nearly the same minimum as the deep retraining model. Fig. 4 shows the confusion matrices for each training scenario. Deep retraining provides a matrix closer to the identity than the other training cases as expected.

In order to test the 1 vs. 1 response of the network, we set up 9 additional experiments to check how well the classifier distinguishes a single disease. Results are accumulated in

TABLE III Accuracy & Cross Entropy Loss for 10 classes

Scenario	Accuracy	Cross Entropy Loss
Shallow	89.98%	0.55
Scratch	96.01%	0.17
Deep	96.20%	0.11

TABLE IVSENSITIVITY & SPECIFICITY

	Sensitivity/Specificity			
#	Shallow	Scratch	Deep	
0	0.96/0.99	0.97/0.99	0.98/1.00	
1	0.68/1.00	0.87/0.99	0.97/1.00	
2	1.00/0.98	1.00/0.99	1.00/0.99	
3	0.88/0.99	0.94/1.00	0.97/1.00	
4	0.84/1.00	0.98/1.00	0.94/1.00	
5	0.95/0.97	0.97/1.00	1.00/1.00	
6	0.66/1.00	0.95/0.99	0.82/0.99	
7	0.83/0.97	0.88/0.99	0.96/0.99	
8	0.98/0.99	0.99/1.00	0.97/1.00	
9	0.96/1.00	0.99/1.00	0.97/1.00	

Table 4.

### A. Notice on the PlantVillage dataset

Finally, we would like to point out a characteristic of the dataset. As it might be clear from Fig. 1, that some classes appear to have been recorded under different conditions. For example, class Healthy appears to be noisy. For that reason, we made the following analysis to each class. We computed the 2D Fast Fourier Transform (FFT) and masked out the base band as shown in Fig. 6. Next, we summed up the values of the remaining frequencies for every image and created the histogram of that summations. The results are shown in Fig. 7 and indicate that the healthy class contains higher frequencies, than the other two classes. This doesn't necessarily mean that all the classes are separable by that metric alone, or that the network exploits only on the spectral content of the images. However, it makes clear that many of the classes (only three of them shown for the sake of space) are easily separable due to the different noise introduced in each class.

## V. CONCLUSION

We have employed the AlexNet architecture for tomato diseases detection. The results were very accurate indicating that the dataset is a rather easy one as highlighted by our remarks in section IV.

In the near future we will present results on our custom dataset using RGB and multispectral images.

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Fig. 5. Loss of binary AlexNets for Shallow, from Scratch and Deep training, over 30 epochs. (a to i) correspond to classes 0 to 9, except for 2 (healthy class).



Fig. 6. (a) 2D FFT of an image from the healthy class (in dB), (b) the mask used to filter the contents of the FFT.



Fig. 7. Histogram of high frequencies for Health, Bacterial spot and Late blight classes.

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