Use of Convolutional Neural Networks in the Diagnosis of Corn Diseases

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Abstract- The detection of corn (maize) crop diseases is traditionally carried out by farmers, based on their experience accumulated over a period of field practice. However, the visual observation may represent a risk of error due to subjective perception. This article presents an approach based on Deep Learning to identify diseases that affect corn crops. A public database with 3,852 images of maize plant leaves was used, divided into four classes: healthy corn, exserohilun leaf spot (northern leaf blight), common corn rust (common rust) and cercosporiosis (cercospora leaf/gray leaf). The proposed model used Convolutional Neural Networks (CNN) techniques for image classification. The four experiments indicated results with an average accuracy above 94.5%. These results in the identification and diagnosis of plant diseases can contribute significantly as a tool to the improvement of the production chain that affect corn crops.

Keywords - Corn Diseases, Classification, Data Augmentation, Convolutional Neural Networks

I. INTRODUCTION

Plant diseases are considered one of the main influencing factors in food production, being responsible for the significant reduction in physical or economic productivity of crops and, in certain cases, can even be an impediment to this activity [1]. Corn is attacked by pests and diseases that occur throughout the development of the crop; from sowing to harvesting the grains. Productivity can be significantly compromised if these pests and diseases are not properly managed. The importance that each species assumes varies according to the region and growing season, with correct identification being a crucial point in management programs [2].

The detection of diseases in agriculture is traditionally carried out by farmers, based on their experience accumulated over a long period of field practice, analyzing the components of the plant, such as leaves and fruits. On the other hand, visual observation by farmers represents a risk of error due to subjective perception. Therefore, it is necessary to develop automated, practical, reliable and economical solutions capable of monitoring plant health, providing significant information for the decision-making process, for example, the correct dosage of pesticides [3], [4], [5], [6].

Machine learning is a field of computational intelligence that is concerned with building computer programs that automatically improve with experience. Over the past years, many successful machine learning applications have been developed, from data mining programs that learn how to detect fraudulent credit card transactions, to information filtering systems that learn users' reading preferences, to autonomous vehicles, which learn to drive on highways without the driver participation [7], [8], [9].

A particular type of machine learning, called deep learning, allows computational models composed of multiple processing layers to learn data representations with multiple levels of abstraction. These methods drastically improved the state of the art in speech recognition, image recognition and text recognition, as well as establishing a new frontier in other domains, such as drug discovery and genomics [10].

Deep learning has been widely studied and applied in different segments of agricultural sciences. An example of these applications that can help growers on crops are those capable of visually identifying and classifying diseases and pests that plague agriculture. Among many deep learning techniques, convolutional neural networks (CNN) are probably the most used model. CNN are a special class of artificial neural networks, a bioinspired method, which simulates the functioning of a massive set of neurons to process a task in parallel and quickly [11]. A CNN is composed of several layers that use the convolution operation to extract features from the images [12]. This operation is carried out from a sliding data window, called a convolutive filter, which runs through the entire network input and operates in an analogous way to the superposition of receptive fields. The model can contain several filters, whose values are adjusted during the training process to obtain different features from the input. In the end, these extracted features become inputs to a learning algorithm applied to classification or regression, according to the type of problem. It is common among the convolutive layers to perform other operations to reduce the feature space. The most common is the subsampling, or pooling layer. Other operations can be included as well, such as normalization and zeropadding [13]. At the end of the convolutive layers, the flattening operation takes place, where the matrix with the extracted features is placed in the form of a vector and thus it passes to the last stage, the fully connected neural network, also called multilayer perceptron [8].

The recognition and classification of plant leaf diseases is a problem with many challenges to overcome. The analysis in the process of identification of diseases by the leaves can create a large number of false positives, for example, the symptoms of phyto-toxicity are associated with some disease due to similar leaf lesions. Before the usage of convolutional neural network, traditional machine learning classification methods such as SVM (support vector machine) [14] and K-means [15] were used to classify plant diseases.

Patil and Bodhe [16] applied the classic image processing technique to detect diseases in sugarcane leaves using threshold segmentation to determine leaf area and triangle threshold for the injured area. An approach proposed by Singh and Misra [17] uses genetic algorithms for image segmentation, which is an important aspect for the detection of diseases in a plant leaf. Pydipati [18] used the color co-occurrence method (CCM) to determine whether texture-based color, saturation and intensity (HSI) characteristics, in conjunction with statistical classification algorithms, can be used to identify diseased citrus leaves and normal under laboratory conditions. According to Jabal [6], feature extraction is a promising approach capable of resolving dichotomies between data sets constructed with images in controlled environments and images captured in the real world. This present study applied computer vision techniques, based on deep machine learning, to classify, from images of corn plant leaves into four categories: healthy corn, cercosporiosis, common rust and helminthosporiosis. Through the use of deep neural networks model, known as convolutional neural networks (CNN) [8], this study aims to play an important role in the detection and diagnosis of diseases that affect the corn crop.

II. METHODOLOGY

The proposed methodology uses the PlantVillage data set, provided by Hughes [19], containing 54,306 images of plant leaves and 38 different classes, each class corresponding to a different crop disease. Each class has three different versions: original color image, grayscale image and segmented image.

Only images related to corn were selected for the present study, totalizing 3,852. All images consist of maize plant leaves and are divided into four classes, healthy maize and three types of maize diseases: helminthsporiosis or exserohilun leaf spot (northern leaf blight), common corn rust (common rust) and brown eye spot (cercospora leaf/gray leaf), as shown in Fig. 1 and Table I.



Fig. 1. Samples from the corn plant disease dataset used in three versions of images (color, grayscale and segmented). (a) Corn leaf with cercosporiosis. (b) Corn leaf with common rust. (c) Corn leaf with helminthsporiosis. (d) Healthy corn leaf [19].

Table I. Subset of maize images from the PlantVillage dataset.

Class	Name	Image Quantity	Sample	Description
Healthy Corn	Zea mays	1.162		Predominance of green color throughout the leaf without stains
Northern Leaf Blight	Exserohilum turcicum	985		Small oval spots, than elongated spots are elliptical in gray or brown
Common Rust	Puccinia sorghi	1.192		Small pieces are round until the oval is found on the surface of the leaf at the top and bottom
Cercospora Leaf Gray Leaf	Cercospora zea- maydis	513		Grayish-brown spots on the entire leaf surface

The identification of corn diseases from images of their leaves involved four phases: image acquisition, image preprocessing, feature extraction and classification [20].

The image data provided by Hughes [19] have a particular characteristic: the number of images per class is not uniform. The number of images of leaves with cercosporiosis is much smaller than that of the other classes. This detail can negatively affect the training of machine learning models, as they depend on a considerable number of samples (examples) to make mathematical correlations and extract the necessary features for the image classification process. Thus, it was decided to use CNN, which are recognized in the literature as excellent image classifiers. To do so, it was necessary to experiment with different scenarios, in order to find the best model configuration for the chosen data set. Some CNN scenarios were trained with the original number of images. The technique known as data augmentation was used to automatically generate more images of cercospora class in the scenario 4. With the new generated images, CNN was again trained and submitted to the test and validation data.

The four scenarios experienced in the convolutional neural networks implemented in this study differ among themselves, in this way: CNN of scenario 1 is a typical deep neural network used in image classification; the network of scenario 2 differs for a longer training period (150 epochs); in the scenario 3 network, the cross-validation training model was used and; in the last (4th) scenario, data augmentation was implemented to supply the low number of samples in one of the classes.

Another pre-processing step carried out was the images dimension transformation. The original format of the corn leaves images used is 1080x1080 and, in order to be submitted to CNN for the feature extraction, they need to be in the 150x150 format.

For the chosen data set, four different architecture scenarios and CNN parameters were tested. These scenarios are described in Table II.

Table II. Configurations Used in CNN Networks in the 4 Scenarios.

CNN Parameters				
	Scenario 1	Scenario 2	Scenario 3	Scenario 4
Training Model	70% training	85% training	Cross	70% training
0	15%	25%	Validation	15%
	validation	validation and	K = 10	validation
	15% test	test		15% test
Data Augmentation	No	No	No	Yes
Input Layer	1 neuron	1 neuron	1 neuron	1 neuron
	RGB 3	RGB 3	RGB 3	RGB 3
	channels	channels	channels	channels
	150x150 color	150x150 color	150x150 color	150x150 color
Convolutional Layer	32 neurons	32 neurons	32 neurons	32 neurons
	conv filters	conv filters	conv filters	conv filters
	3x3 ReLU	3x3 ReLU	3x3 ReLU	3x3 ReLU
	activation	activation	activation	activation
Pooling Layer	2 x 2	2 x 2	2 x 2	2 x 2
Convolutional Layer	32 neurons	32 neurons	32 neurons	32 neurons
	conv filters	conv filters	conv filters	conv filters
	3x3 ReLU	3x3 ReLU	3x3 ReLU	3x3 ReLU
	activation	activation	activation	activation
Pooling Layer	2 x 2	2 x 2	2 x 2	2 x 2
Convolutional Layer	64 neurons	64 neurons	64 neurons	64 neurons
	conv filters	conv filters	conv filters	conv filters
	3x3 ReLU	3x3 ReLU	3x3 ReLU	3x3 ReLU
	activation	activation	activation	activation
Pooling Layer	2 x 2	2 x 2	2 x 2	2 x 2
Convolutional Layer	128 neurons	128 neurons	128 neurons	128 neurons
	conv filters	conv filters	conv filters	conv filters
	3x3 ReLU	3x3 ReLU	3x3 ReLU	3x3 ReLU
	activation	activation	activation	activation
Pooling Layer	2 x 2	2 x 2	2 x 2	2 x 2
Convolutional Layer	256 neurons	-	256 neurons	256 neurons
	conv filters		conv filters	conv filters
	3x3 ReLU		3x3 ReLU	3x3 ReLU
	activation		activation	activation
Dealing Large	2 x 2	-	2 x 2	2 x 2
Pooling Layer	212			5.7.5
Convolutional Layer	512 neurons	-	512 neurons	512 neurons
Convolutional Layer	512 neurons conv filters	-	512 neurons conv filters	512 neurons conv filters
Convolutional Layer	512 neurons conv filters 3x3 ReLU	-	512 neurons conv filters 3x3 ReLU	512 neurons conv filters 3x3 ReLU
Convolutional Layer	512 neurons conv filters 3x3 ReLU activation	-	512 neurons conv filters 3x3 ReLU activation	512 neurons conv filters 3x3 ReLU activation
Convolutional Layer Pooling Layer Pooling Layer	512 neurons conv filters 3x3 ReLU activation 2 x 2	-	512 neurons conv filters 3x3 ReLU activation 2 x 2	512 neurons conv filters 3x3 ReLU activation 2 x 2
Convolutional Layer Pooling Layer Convolutional Layer Convolutional Layer	512 neurons conv filters 3x3 ReLU activation 2 x 2 1024 neurons	-	512 neurons conv filters 3x3 ReLU activation 2 x 2 1024 neurons	512 neurons conv filters 3x3 ReLU activation 2 x 2 1024 neurons
Pooling Layer Pooling Layer Convolutional Layer Convolutional Layer	512 neurons conv filters 3x3 ReLU activation 2 x 2 1024 neurons conv filters	-	512 neurons conv filters 3x3 ReLU activation 2 x 2 1024 neurons conv filters	512 neurons conv filters 3x3 ReLU activation 2 x 2 1024 neurons conv filters
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Pooling Layer Convolutional Layer Convolutional Layer Convolutional Layer Pooling Layer Flattening Layer Fluty-Connected	512 neurons conv filters 3x3 ReLU activation 2 x 2 1024 neurons conv filters 3x3 ReLU activation 2 x 2 128 64 neurons	- - - 64 64 neurons	512 neurons conv filters 3x3 ReLU activation 2 x 2 1024 neurons conv filters 3x3 ReLU activation 2 x 2 128 64 neurons	512 neurons conv filters 3x3 ReLU activation 2 x 2 1024 neurons conv filters 3x3 ReLU activation 2 x 2 128 64 neurons
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Pooling Layer Convolutional Layer Convolutional Layer Convolutional Layer Pooling Layer Flattening Layer Fully-Connected Layer (MLP) Dropout Layer Output Layer	512 neurons conv filters 3x3 ReLU activation 2 x 2 1024 neurons conv filters 3x3 ReLU activation 2 x 2 128 64 neurons ReLU activation 50% chances 4 neurons	- - - - - - - - - - - - - - - - - - -	512 neurons conv filters 3x3 ReLU activation 2 x 2 1024 neurons conv filters 3x3 ReLU activation 2 x 2 128 64 neurons ReLU activation 50% chances 4 neurons	512 neurons conv filters 3x3 ReLU activation 2 x 2 1024 neurons conv filters 3x3 ReLU activation 2 x 2 128 64 neurons ReLU activation 50% chances 4 neurons
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The general diagram visually describing the CNN architecture proposed for scenario 2 in this study is shown in Fig. 2.



Fig.2. CNN architecture used in scenario 2.

Fig. 3 shows the dimensionality reduction in the corn leaf image during the feature extraction process through the layers of CNN.



Fig. 3. Corn leaf images during the feature extraction process through the CNN layers.

The computational application was developed with Python programming language, using Spyder integrated development environment. For deep learning implementations, Keras library was used, which uses TensorFlow in the underlying layer.

The hardware and software resources used in this study to the neural model implementation are shown in Table III.

Table III. Hardware and Software specifications

Hardware	Description	Software	Description
CPU	Intel Core	Sistema Operacional	MS Windows 10 Home Single
	I7-7700HQ		64-bits
	CPU @		
	2.8GHz		
GPU	NVIDIA	Anaconda Navegador	v 1.10.0
	GeForce		
	GTX 1050		
	4GB		
	GDDR5		
RAM	DDR4	Spyder IDE	v 4.1.5
	16GB		
SSD	512GB	Python	v 3.8.5

All data and codes are available at https://github.com/npca-ufra/classificacao-doencas-milho.

III. RESULTS

In the first tested scenario, CNN obtained an accuracy of 95.1% and the loss function reached 0.15. The confusion matrix indicates that 25 images were incorrectly classified between the leaf spot and cercosporiosis classes.

CNN in scenario 2 obtained an accuracy of 96.3% and the loss function reached 0.23. The confusing matrix indicates that 23 images were wrongly classified between the leaf spot and cercosporiosis classes and 2 between common rust and cercosporiosis classes.

In scenario 3, the neural network achieved 94.5% average accuracy, as it used cross validation training model. The loss function averaged 0.30. The confusion matrix indicates that 11 images were incorrectly classified between the leaf spot and cercosporiosis classes.

Data augmentation technique was used in the CNN of scenario 4 for the cercosporiosis class, which originally had 513

samples. After applying the method, the class reached 1,027 images, a similar amount to that of the other classes. In this scenario, an accuracy of 95.7% was obtained and the loss function reached 0.17. The confusing matrix indicates that 15 images were wrongly classified between the leaf spot and cercosporiosis classes and 1 between common rust and cercosporiosis classes. The learning curves for the test data of the 4 scenarios are shown in fig. 4. The confusion matrices are shown in fig. 5.







Fig. 5. Confusion matrices to all CNN scenarios. Scenario 3 used crossvalidation training model and * represents the fold with greater accuracy.

IV - CONCLUSION

In this work, a computational model was proposed to classify images and diagnose diseases from corn leaf images. The model was based on deep learning technique and was applied to a public image bank. For the chosen and tested data set, the convolutional neural network obtained a high rate of accuracy within the expected for the four scenarios experienced. It was observed that CNN did not need more than 30 epochs to converge, learn the problem and classify efficiently. It was also observed that, for this corn images data set, extracted from the PlantVillage database, the use of techniques such as cross-validation, as well as data augmentation, did not significantly increase the result.

A next step to be taken is the application of the same Artificial Intelligence approach for image data of Brazilian corn plants, specially those produced in the state of Pará, as well as for a greater number of other diseases that affect this important production chain.

In this context, it is understood that the implementation of this type of agro-technology tool in the early diagnosis of diseases in plants can add value and optimize the application of financial resources, allowing the increase in the profitability of the producer and the viability of the crops. It also allows the reduction of the impact of pests on crops through the automated identification of diseases.

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