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TOMATO LEAF DISEASE DETECTION USING CNN WITH LOCAL INTERPRETABLE MODEL AGNOSTIC EXPLANATIONS

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ABSTRACT

Black-box classification models must be easy for the receiver to understand in order to be used in agriculture. By providing a plant-specific explanation for a given classification, Local Interpretable Model-Agnostic Explanation (LIME) increases the potential for any complicated classifier to function as a safety aid in any environmental scenario. This study is conducted on tomato leaf to test the usability of LIME in prediction of tomato leaf disease. The tomato crop is a significant staple with a high commercial value on the Indian market and also main ingredient of Indian food. A simple convolutional neural network model is modified in this paper to demonstrate the application of LIME and characterize illnesses in tomato leaves. Convolutional neural net- works do have some drawbacks including poor explainability. unfortunately, consumers must comprehend the reasoning behind deep convolutional neural network forecasts in many real-world applications before deciding whether or not to believe the predictions. A novel genetic algorithm-based solution (LIME) is suggested to address this problem by automatically evolving local explanations that might help users evaluate the predictability of the result.

Keywords: Explainable Machine Learning, Local Explanations, Model- agnostic Explanations (LIME), Evolutionary Deep Learning, Image Classification, CNN.

1. INTRODUCTION

A large portion of the population of India is dependent on the agriculture industry. In India, tomatoes are the most widely consumed vegetable. Tomatoes include beta- carotene, vitamin C, and the three most significant antioxidants: vitamin E and vitamin C (Agarwal et al.,2000). They are also abundant in potassium, a mineral that is vital for optimum health. India is the third-largest tomato producer in the world, with an approximate 3,50,000 hectares under tomato crop cultivation and a production volume of 53,00,000 tonnes (Tm et al., 2018). Diseases are prevalent in the tomato crop at all phases of its growth due to the sensitivity of crops and the climatic circumstances. Plants with diseases account for 10% to 30% of all crop losses. To avoid any severe losses in yield and the quantity of the agricultural output, it is crucial to identify such illnesses in the plant. Due to its complexity and length, manually monitoring plant diseases is a challenging and time-consuming process. Therefore, it is necessary to decrease the amount of human labour required for this operation, while also producing accurate forecasts and guaranteeing the farmers lives are hassle-free. Visually discernible patterns might be challenging to understand at first glance, which causes many farmers to infer the wrong information about the disease (Khirade et al.,2015). Therefore, the farmers preventative measures may be inefficient and occasionally detrimental. Because they lack professional guidance on how to handle crop infestations, farmers typically band together and employ common disease preventive strategies. In certain cases, over or under- application of the pesticide has led to crop damage because of insufficient awareness of the disease's severity or a misunderstanding of it. This is the driving force behind the suggested methodology, which strives to precisely identify and categorize pathogens in the tomato crop. The methods outlined in the study is relevant to the most prevalent ailments that affect tomato plants, including Yellow Leaf Curl, Septorial Leaf Spot, and Bacterial Leaf Spot. Any leaf image submitted for analysis might be labelled as healthy or belonging to one of the disease classifications. A portion of PlantVillage's repository, which holds 54,306 images of 14 crops infected with 26 illnesses, was used as the database for the evaluation. Around 18160 images of tomato leaf diseases are included in the subset. The three main steps of the proposed methodology are data gathering, pre-processing, and classification. As previously indicated, the photos utilized to apply the suggested methodology were obtained from the publicly accessible dataset known as Plant Village. Before putting them into the classification model, the photos were resized to a standard size in the following phase. In the final stage, the input photos are classified using a modest modification of the deep learning convolutional neural network

(CNN) standard model, which comprises of the convolutional, activation, pooling, and fully connected layers. The following is the setup of paper: Section 2 focuses on the noteworthy research in the relevant field. The actions used to acquire the required findings are explained in Section 3 along with the model and proposed technique. Section 4 demonstrate the experimental set- ting. The results and an examination of the suggested methodology are covered in Section 5. The paper's conclusion is found in Section 6, which also outlines the direction of future research.

2. LITERATURE REVIEW

To correctly move to the right direction, it is crucial to acknowledge the prior research that has been done in this field. In order to accurately classify plant leaf diseases, image processing and deep learning techniques have been extensively used in this important research area. In this paper, we go over the methods that have been used the most frequently in related literature. Figures 1 and 2 depict two typical tomato plant illnesses, while Figure 3 depicts healthy tomato leaves. If done manually, keeping track of a sizable field of crops is a laborious operation. It is essential to reduce the amount of human labor required for plant management. As a result, this is a prominent research area that draws several researchers.

In literature, plant diseases are mentioned in a number of research. An effective approach to determine if a tomato leaf is healthy or has been put forth by Mokhtar et al., (2015). The image that was provided as input was first pre-processed by removing the background and noise using the erosion technique. The enhanced image's texture features were extracted using the Gray Level Co-occurrence Matrix (GLCM). Using the linear kernel function and the SVM classifier, the suggested system has a 99.83% accuracy rate. The accuracy obtained is insufficient to predict or distinguish between healthy and diseased leaves. Additionally, the disease's type was not specified.

Khirade et al., (2015), have presented several segmentations, feature extraction, and classification algorithms that identify and detect the type of the disease employing the diseased image to do classification in order to address the issue with the aforementioned research. The leaf image that was provided as the system's input was pre- processed, either by smoothing it out or by improving it with histogram equalization. Different segmentation methods, such as K-Means clustering, have been applied to identify the impacted area. The segmented region's features were extracted and with the help of GLCM algorithm calculations were made. Artificial neural networks (ANN) or back propagation neural networks were used to diagnose diseases after feature extraction. The disadvantage of using K-Means clustering to segment the im- age is that the proposed process was semi-automated because the user had to specifically choose the cluster that included the diseased part.

In order to extract features that aid in the disease diagnosis of tomato leaves, Mokhtar et al. (2015) describes an approach that applies the Gabor wavelet transformation technique. The SVM classifier was trained using the retrieved characteristics, which subsequently identified the disease type found on the affected tomato leaf. The pre-processing procedure involved resizing the images, removing noise, and removing the back- ground. In order to recognize the textual patterns of the impacted leaf and extract the necessary information, the paper used the Gabor transformation. SVM was used to classify diseases using various kernel functions, and the performance was assessed using the cross-validation technique. According to experimental results of the suggested methodology, an accuracy of 99.5% has been demonstrated. The primary drawback of the Gabor transformation for feature extraction that, it is very computationally demanding.

Figure 1: Tomato Septoria leaf

Figure 2: Tomato Spider mites Two spotted spider mite

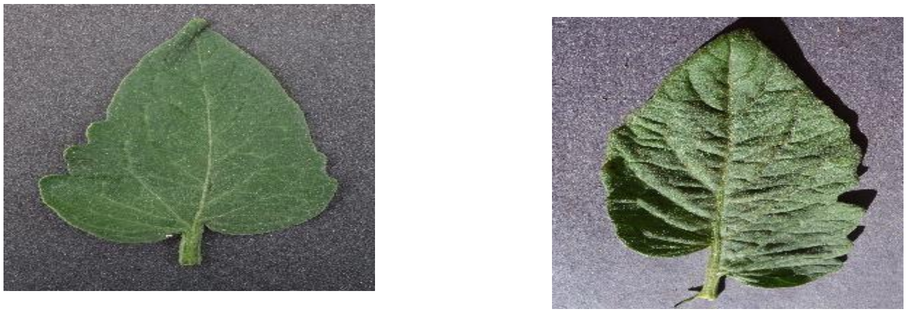

Figure 3: Tomato healthy

The classification of the diseased tomato leaves into numerous classes, including Tomato Late Blight, Septoria Spot, Bacterial Spot, Bacterial Canker, Tomato Leaf Curl, and Healthy, has been done by Sabrol et al., (2016) using a straightforward methodology. For the implementation, a dataset of 383 images taken which were captured using a digital camera. Otsu's image segmentation algorithm has been used for image segmentation. In order to create colour features, RGB colour components were used, while the regionprops function was used to create shape features, and GLCM was used to create texture features. To create a feature extraction module, all the extracted features were concatenated. The decision tree classifier has been trained to classify data using supervised learning techniques. Despite their high accuracy, decision trees have a number of drawbacks, including overfitting in noisy data scenarios and a limited amount of user control.

In order to identify 26 illnesses in 14 different crop species, deep convolutional neural networks have been trained in [6]. For this, the authors adopt the widely used GoogleNet by Szegedy et al., (2015) and AlexNet by Krizhevsky et al., (2012) architectures. This has been accomplished by using a public repository that has 54,306 pictures of both diseased and healthy plant leaves. The dataset has been created by collecting the images of the plant leaves in a controlled environment. The authors used two different methods for model training be- fore doing a performance analysis on both of these architectures. In the first instance, it is done from scratch, and in the second, transfer learning is used. The technique of modifying pre-trained weights gained by training models on the ImageNet dataset is referred to as transfer learning. The Caffe framework has been used to create the model, giving it 99% accuracy. This illustrates how feasible this strategy is. The model accuracy drops to 31.4% when tested against a set of sample test photos acquired from online public data sources that are significantly different from the train set due to the train and test sets having different distributions and this is a common issue with neural networks.

Jihen et al., (2017) suggest a method for identifying and categorizing the banana sigatoka and banana speckle illnesses that affect banana leaves. They worked under some difficult circumstances to develop deep learning models. These circumstances include lighting, a complicated background, various image resolutions, sizes, and orientations. They successfully illustrate the precision of this method and the significantly low computational effort needed.

3. EXPERIENTIAL WORK

The proposed approach includes the four important stages, first is Data Acquisition followed by Data pre-processing, Classification and result explanation using LIME. Flow diagram is shown in Fig. 4 and current section includes the brief discussions of the same.

Figure 4: Proposed Methodology

3.1 Data Acquisition

The tomato leaf disease images have been taken from the Plant Village repository which has the tomato leaf disease images. There are almost 18160 photos in the obtained dataset, divided into 10 different classes. Images of all the main leaf diseases that potentially harm the tomato crop are included in the dataset. Each image that was downloaded was saved in the uncompressed JPG format and by default uses the RGB color space.

3.2 Data Preprocessing

The collected dataset was made up of mostly noise-free images, hence noise removal was not required as a preprocessing step. To hasten model training and make it computationally practical, the images in the dataset were downsized to a resolution of 60x60. Standardizing the input or target variables has the tendency to accelerate the training process. This is accomplished by strengthening the numerical parameters of the optimization problem. Additionally, it is ensured that the various default values used for startup and termination are suitable. For our purposes, we use the mean and standard deviation to normalize the photos such that all of the pixel values fall within the same range. It is referred to as the Z-score in the context of machine learning.

3.3 Classification

Convolutional neural networks can be used to create a computer model that takes unstructured image inputs and transforms them into pertinent categorization output labels (CNN). They belong to the class of multi-layer neural networks, which can be trained to learn the features needed for classification. They perform autonomous feature extraction and require less pre-processing than traditional approaches, which improves performance. We investigated a number of common deep learning architectures for tomato leaf disease detection, including AlexNet (Krizhevsky et al., 2012) and GoogleNet (Szegedy et al., 2015), and found that a proposed architecture produced the best results.

A straightforward CNN model which has three layers: convolutional, activation, pooling, and fully connected layer. An adaptation of the model is used for the classification of tomato leaf diseases. Compared to the original CNN architecture, it has various additional blocks of convolutional, activation, and pooling layers. Fig. 5 depicts the model utilized in this study. A convolutional, an activation, and a max pooling layer make up each block. In this architecture, three Convolutional, 3 Max Pooling, one flattened layer and two fully connected layer are used. First fully connected layer uses ReLU activation function and second fully connected layer uses softmax activation function. such blocks are used, followed by completely connected layers and softmax activation. While fully connected layers are used for classification, convolutional and pooling layers are applied to extract features. The network's non- linearity is introduced using activation layers.

Convolutional layer extracts features using convolutional operation. The complexity of the retrieved features grows as the depth increases. As we move from one block to another, the number of filters gradually increases but the size of the filter remains fixed at 3x3. In the first convolutional block, there are 16 filters; this number rises to 32 in the second and 64 in the third. Due to the usage of pooling layers in each of the blocks, the size of the feature maps was reduced, demanding the increase in the number of filters. In order to maintain the size of the image after applying the convolution process, the feature maps are additionally zero-padded. The max pooling layer is used to shorten the length of the feature maps, accelerate training, and make the model less sensitive to input variations. For maximum pooling, the kernel size is 3x3. ReLU activation layer is used in each of the blocks for the introduction of nonlinearity. Also, Dropout regularization technique has been used with a keep probability of 0.2 to avoid overfitting the train set. Dropout regularization randomly drops neurons in the network during each iteration of training in order to reduce the variance of the model and simplify the network which aids in prevention of overfitting. Finally, the classification block consists of two sets fully connected neural network layers each with 512 and 10 neurons respectively. First fully connected layer uses reLU activation function and second fully connected layer uses softmax activation function to compute the probability scores for the ten classes.

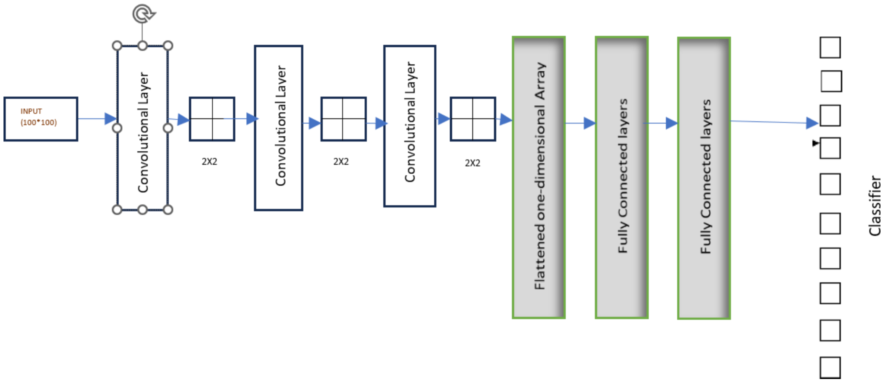

Figure 5: Proposed Model Architecture

3.4 LOCAL INTERPRETABLE MODEL AGNOSTIC EXPLANATION (LIME) KIT

Although a deep learning model can obtain quite good classification results, it is difficult to understand how the classification results are derived because of its black-box characteristics. How to interpret the reasoning mechanism of the deep-learning model has become an important topic of research. In recent years, among the deep-learning methods, LIME is a new evaluation method for the interpretability of the model (Ribeiro et al., 2016), i.e., whether it is possible to understand the importance of the deep-learning model for the interpretability of the image in the subsequent classification and prediction. The problem with model interpretability is that it is difficult to define the decision boundary of the model in a way that humans can understand. As shown in Figure 6, LIME is a Python library that attempts to generate some local feature-circle super-pixels. This can be used to explain the principle on which the model is based, which is usually difficult to describe, and to help with understanding whether the basis on which the model applies its decisions is appropriate or not.

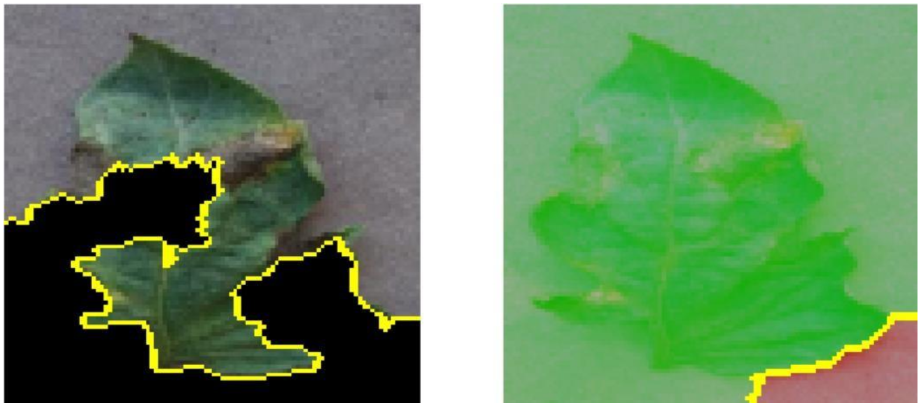

Figure 5: Tomato leaf's early blight prediction using LIME

Now we know why our model classifies our image as tomato early blight. On the left image, we can see that only the super-pixels where the leaf is visible are shown. This means that our model classifies our image as a tomato early blight because of these parts of super-pixels.

On the right image, the area of super-pixels colored in green are the ones that increase the probability of our image belongs to a tomato early blight class, while the super- pixels colored in red are the ones that decrease the probability.

4. EXPERIMENTAL SETTING

The implementation of the proposed methodology has been carried out on the PlantVillage dataset. It consists of around 18160 images belonging to 10 different classes of tomato leaf diseases. Keras, a neural network API written in Python, has been used for the model implementation. Out of the 18160 images, 4800 images were set aside for testing and 13360 images were used for training. In order to increase the dataset, automatic data augmentation techniques have been used by randomly rotating the images by a small amount of 40 degrees, horizontal flipping, vertical and horizon- tal shifting of images. The optimization was carried out using Adam optimizer with categorical cross entropy as the loss function. Batch size of 1920 has been used and the model has been trained for 100, 200 and 300 epochs. The initial learning rate has been set to 0.0001 and it is reduced by a factor of 0.3 on plateau where the loss stops decreasing. Early stopping has also been used in order to monitor the validation loss and stop the training process once it increases. All the experiments were performed on Intel Core i7- nvidia GPU.

5. RESULT AND ANALYSIS

To evaluate the performance of the proposed model, a set of quantitative metrics comprising of accuracy, precision, recall and F1-score have been used. The results are reported in Table 1. They show the highest values of the quantitative metrics obtained until the corresponding epoch number.

Table 1. Measure of Performance

No. of Epochs	Accuracy	Precision	Recall	F1-Score
100	0.9141	0.9012	0.9012	0.9012
200	0.9552	0.9447	0.9447	0.9447
300	0.9785	0.9682	0.9682	0.9682

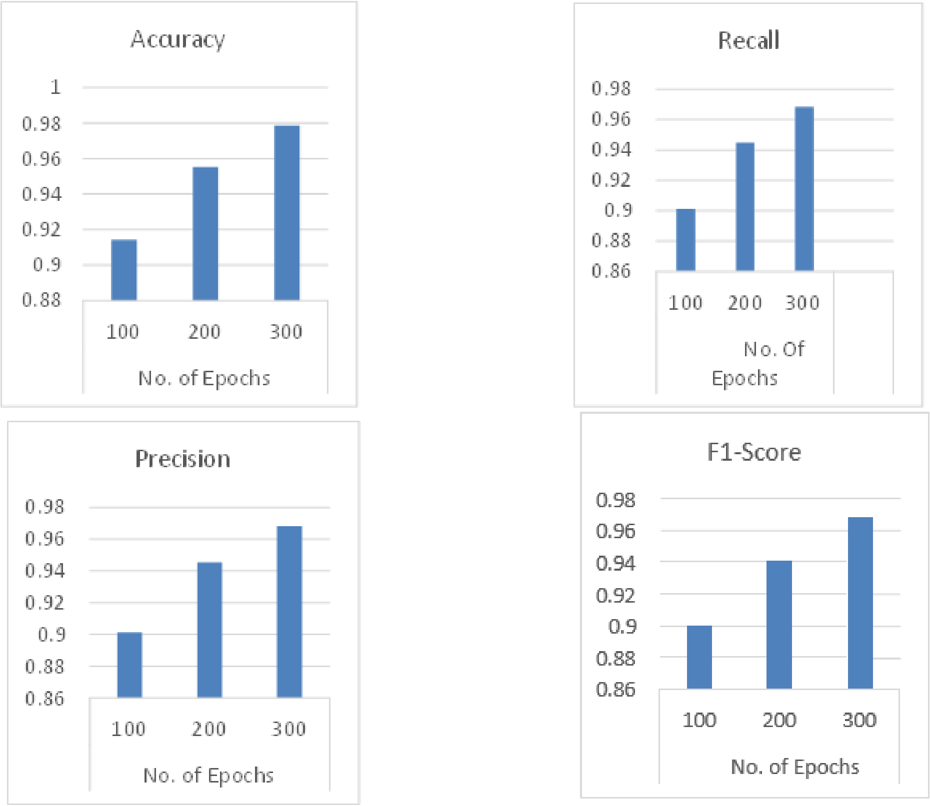

Figure 7: Graphical representation of measure of performance

A highest validation accuracy of 95.8% was obtained over 300 epochs of training, while a high 97.85% of training accuracy was reported. An average validation accuracy of 94% has been obtained. This is an effective measure of the classification made by the deep learning model. The plots of train accuracy, recall, F1-Score and precision against the epochs is provided a means of visualization and indication of the speed of model convergence. Metrics do show a significant improvement in the last 100 epochs. The results show that the model performs well on the dataset and can be used as a means for classification of the 10 tomato leaf diseases with minimum resource requirements. The implementation process requires minimum hardware requirements unlike large neural networks which generally have high computational resource requirements or the use of a Graphics Processing Unit. This is due to a smaller number of training parameters owed to the presence of fewer layers with less filter sizes and smaller train size images. Unlike other state of the art models, the model implementation can be carried out on CPU with minimum time owing to the simplicity. Also, the variation of the LeNet model adopted is simple to understand and easy to implement. The model thus, provides a simple and effective way of solving the problem of plant disease detection with results comparative to Tm et al., (2018), where the authors deal with plant diseases of multiple crops. With less resource constraints and minimal data, the model gives comparative results to traditional state of the art techniques.

6. CONCLUSION AND FUTURE WORK

Agricultural sector is still one of the most important sectors over which the majority of the Indian population relies on. Detection of diseases in these crops is hence critical to the growth of the economy. Tomato is one of the staple crops and its price in India is very high currently even though it is produced in large quantities. Hence, this paper aims at detection and identification of 10 different diseases in the tomato crop. The proposed methodology uses a convolutional neural network model to classify tomato leaf diseases obtained from the Plant Village dataset. The architecture used is a simple convolutional neural network with minimum number of layers to classify the tomato leaf diseases into 10 different classes. Different learning rates and optimizers could also be used for experimenting with the proposed model as a part of the future work. It could also include experimentation with newer architectures for improving the performance of the model on the train set. Thus, the above-mentioned model can be made use of as a decision tool to help and support farmers in identifying the diseases that can be found in the tomato plant. With an accuracy of 96-97% the methodology proposed can make an accurate detection of the leaf diseases with little computational effort. The primary focus of this research work is to show how using Local Interpretable Model Agnostic improves the understanding of classification better.

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