DEEP TRANSFER LEARNING FOR AUTOMATED DIAGNOSIS OF TOMATO PLANT LEAF DISEASES

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Abstract

Worldwide food production is being stressed by extreme weather conditions, fluctuating temperatures, and global affairs. With a global output of millions of tons annually, tomatoes stand as a pivotal staple in agricultural practices worldwide. Early-stage identification and classification of diseases in tomato plants can be a cost-effective measure for farmers, potentially reducing the need for expensive crop sprays and enhancing overall food yield. In the realm of disease detection and control, there is considerable potential for transformative impact through technological innovations. In a multitude of domains, deep learning algorithms, a subset of artificial intelligence, have autonomously demonstrated their recognition and applicability in real-life situations. This paper seeks to employ deep transfer learning for the classification of various distinct tomato diseases namely, bacterial spot, early blight, late blight, leaf mold, mosaic virus, septoria leaf spot, target spot, and yellow leaf curl virus with the healthy state. The approach in this work uses tomato leaf images as input, which is given to convolutional neural network architectures. In addition, these models utilize transfer learning principles from well-established deep learning networks. The assessment of performance involved rigorous examination through multiple data split strategies and diverse metrics. Moreover, to mitigate the influence of randomness, the experiments were repeated 6 times. The six categories were classified with mean values of 98.3% precision, 98.2% F1 score, 98.1% recall, and 98.4% accuracy.

Introduction

Agriculture is the lifeline of food security, catering to the production needs of both commercial and local sectors. Its paramount importance is highlighted for small-scale farmers, providing them with a key source of income in the absence of alternative employment opportunities. Tomatoes stand out as a sustainable choice due to their lower water and fertilizer requirements compared to other crops. Tomatoes, due to their nutritional richness and ubiquitous presence in various recipes, hold a pivotal role as a vital crop and staple food product globally [1]. According to the Food and Agriculture Organization (FAO), tomatoes are ranked as the sixth most abundant vegetable worldwide [2]. In 2021, the global production of tomatoes reached a staggering 189 tons in 5 million hectares area of harvestation. Despite their prominence, the tomato plant remains vulnerable to numerous diseases caused by bacteria, viruses, or fungi, directly impacting productivity.

Tomatoes rank among the most commonly consumed fruits globally on a daily basis. Given their widespread use in toppings like ketchup, sauce, and puree, tomatoes boast a high global utilization rate [3]. In Europe, an individual's yearly tomato consumption stands at around thirty-one kilograms, while in North America, this figure rises to approximately forty-two kilograms per person. The substantial demand for tomatoes underscores the necessity for the development of early detection technologies capable of identifying viruses, bacteria, and other contaminations [4]. Numerous studies have explored the application of artificial intelligence-based technologies to enhance the resistance of tomato plants against diseases. The conventional approach to disease detection in farming involves seeking guidance from plant pathologists or relying on personal experience and public resources. The hurdles lie in the significant time investment, effort, and technical knowledge required, affecting both professionals and farmers. Consequently, technological solutions geared toward facilitating disease detection and identification have the potential to significantly reduce costs while improving the accuracy and speed of disease control.

In this context, recent strides in artificial intelligence (AI) have unleashed a myriad of applications across diverse disciplines. AI systems encapsulate domain knowledge within their models through the intricate processes of training and validation, endowing them with decision-making capabilities of considerable sophistication and complexity [5]. Notably, deep learning algorithms, and specifically convolutional neural networks (CNNs), have emerged as powerful tools for discerning intricate relationships and features in real-life processes, especially in direct image-based decision-making and object detection. Unlike traditional neural networks comprising input, output, and hidden layers, deep learning involves a more extensive layering architecture, allowing the capture of input features and details across multiple scales. Among the plethora of deep learning AI algorithms, convolutional neural networks stand out as particularly adept at processing images as input. Within a CNN, layers conduct a series of convolution operations using filters of varying sizes, often followed by a rectified linear unit (ReLU) activation function [6]. The output from the ReLU is a feature map, subsequently down-sampled by a pooling layer. Generally, the final layer preceding the output in a CNN is a fully connected layer, amalgamating diverse features learned from preceding layers and feeding them into the output layer.

This paper presents the following key contributions:
1. Advancing deep learning models made for diagnosing tomato plant leaf diseases focusing on a variety of unique diseases like early blight, mosaic virus, septoria leaf spot, late blight, target spot, and yellow leaf curl.
2. Implementation of transfer learning using six deep convolutional neural network models to classify leaf images into ten classes.
3. Evaluation of the performance of the various deep learning models through the use of multiple metrics covering various aspects of detection and classification capabilities.

The subsequent sections of this paper are organized as follows: detailed presentations on the data, convolutional network models, and the setup of performance evaluation metrics. The

following section delves into the performance evaluation results, comparing them with related literature and providing a discussion on the models. The paper concludes in the final section.

Literature Review

Le et al. [7] introduced a methodology for classifying various plant leaf diseases. The initial step involved a pre-processing phase utilizing morphological opening and closing methods to eliminate unwanted information from the suspected samples. Subsequently, key points were extracted using the filtered local binary pattern method with contour mask and coefficient k (k-FLBPCM). The calculated feature vector underwent training of an SVM classifier for classification [8]. While this approach demonstrates robustness in diagnosing plant leaf-related diseases with an accuracy of 98.63%, its performance diminishes when applied to distorted images.

Similarly, a framework known as Directional Local Quinary Patterns (DLQP) was introduced for calculating a descriptive set of sample features, which were then utilized for SVM training. This technique exhibits enhanced performance in categorizing plant leaf abnormalities, achieving an accuracy of 97.80%. However, it shows degraded results when handling blurry input images. In another study, Sun et al. [9] proposed a solution for crop disease categorization. Initially, the input image was segmented using Simple Linear Iterative Cluster (SLIC) to form several blocks. Feature computation from these image blocks was conducted using fuzzy salient region contours and the Gray Level Co-occurrence Matrix (GLCM). The extracted key points vector was employed to train the SVM method for classifying various plant diseases [10]. Although this methodology demonstrates superior results in plant leaf disease recognition with an accuracy of 98.50%, it comes at the cost of high computational requirements.

Tan et al. [11] in their research, captured images of chili plant leaves and employed a processing technique to determine the health status of the chili plant, ensuring targeted application of chemicals to diseased plants. Their approach utilized MATLAB for feature extraction and image recognition. Pre-processing steps involved Fourier filtering, edge detection, and morphological operations. The integration of computer vision expanded the image processing paradigm for object classification, employing a digital camera for image capture [12].

In a related study, Badnakhe [13] compared the efficacy of the Otsu threshold and the k-means clustering algorithm for analyzing infected leaves. Their findings indicated that k-means clustering yielded lower feature values but offered enhanced clarity compared to other methods. The RGB image was employed for disease identification, utilizing k-means clustering to identify green pixels. Subsequently, Otsu's method was applied to obtain varying threshold values. For feature extraction, the color co-occurrence method was used, with the RGB image converted to the HSI translation. Texture statistics were computed using the SGDM matrix, and features were calculated through the GLCM function [14].

Materials and Methods

Figure 2 illustrates a flow encompassing all phases of the proposed approach. Utilizing Convolutional Neural Networks (CNNs) eliminates the need for explicit feature extraction, and relevant image parts do not require separation through segmentation. These tasks, among others, are implicitly handled by the intricate operations of the deep learning models. Repurposing a broadly pre-trained deep learning model for a specific application involves several key modifications. Firstly, the classification layer is replaced to arrange with the number of classes in the application. Secondly, the learnable layer that combines features from previous layers is replaced with a new layer [15], which may be a fully connected layer or a convolution 2d layer depending on the CNN model. Thirdly, to expedite training, some initial layers can be frozen, meaning their weights will not be updated during training. The number of frozen layers is determined empirically based on application requirements, testing performance, and training speed. In this work, no layers were frozen due to available hardware for extensive training. Fourthly, the dataset is prepared by resizing images to meet CNN requirements, and it is split into training and validation subsets. Image augmentation operations may also be applied to introduce more variety into the dataset and enhance the learning process. Finally, the CNN network is retrained with the tomato dataset, and its performance is evaluated in this concluding step [16].

Plants play a crucial role in global food supply, and the impact of plant diseases on production can be mitigated through proactive monitoring. However, the manual surveillance of plant diseases by agricultural experts and botanists is labor-intensive, challenging, and prone to errors. To enhance disease monitoring and reduce the risk of severe outbreaks, machine vision technology, specifically artificial intelligence, emerges as a valuable solution [17]. An alternative approach to mitigating disease severity involves the collaborative efforts of computer technologies and human expertise. In this study, we propose a solution for detecting tomato plant diseases using a deep learning-based system that leverages image data of plant leaves. Our approach utilizes a deep learning architecture based on a recently developed convolutional neural network, trained in segmented and non-segmented tomato leaf images. Employing a supervised learning approach, we utilize the Inception Net model to detect and recognize various tomato diseases in this research work.

Proposed Methodology

The dataset encompasses 15,452 publicly available tomato leaf images, each illustrating features associated with nine distinct tomato diseases, alongside representations of the healthy state. The distribution of images per class is as follows: 2127 for bacterial spot, 1000 for early blight, 1909 for late blight, 952 for leaf mold, 373 for mosaic virus, 1771 for septoria leaf spot, 1676 for spider mites, 1404 for target spot, 5357 for yellow leaf curl virus, and 1591 for healthy leaves. Each image corresponds to a photograph of a single leaf, representing one of the ten health classes [18]. All photos were taken against a neutral background, providing a relatively uniform appearance across all images. Additionally, each leaf is positioned at the center of its respective image. The dataset was obtained in JPEG format with a resolution of 256 _ 256.

Exemplar leaf images showcasing the nine diseases and healthy leaves are presented in Figure 1.
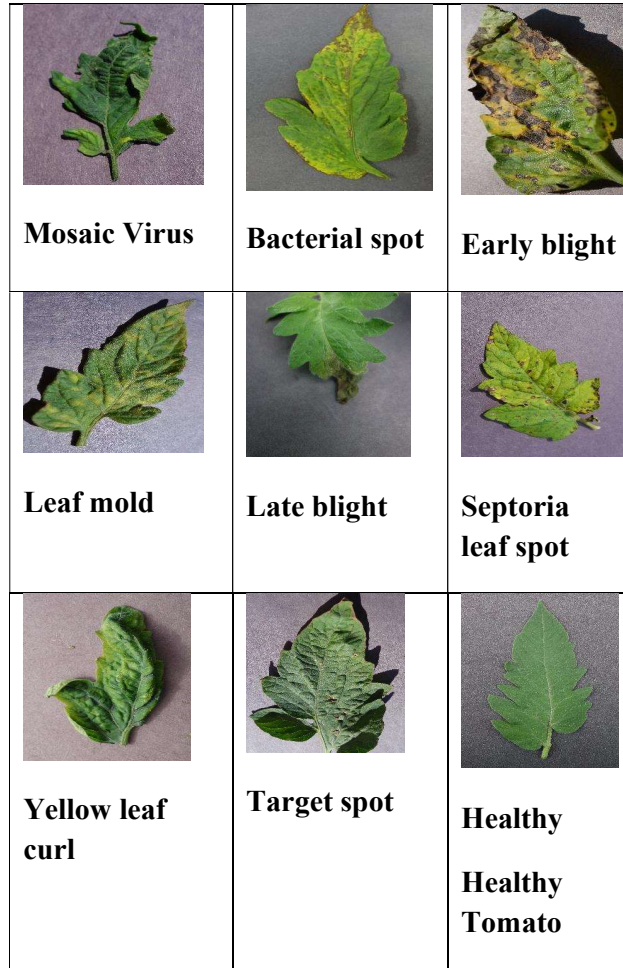

Mosaic Virus	Bacterial spot	Early blight
Leaf mold	Late blight	Septoria leaf spot
Yellow leaf curl	Target spot	Healthy
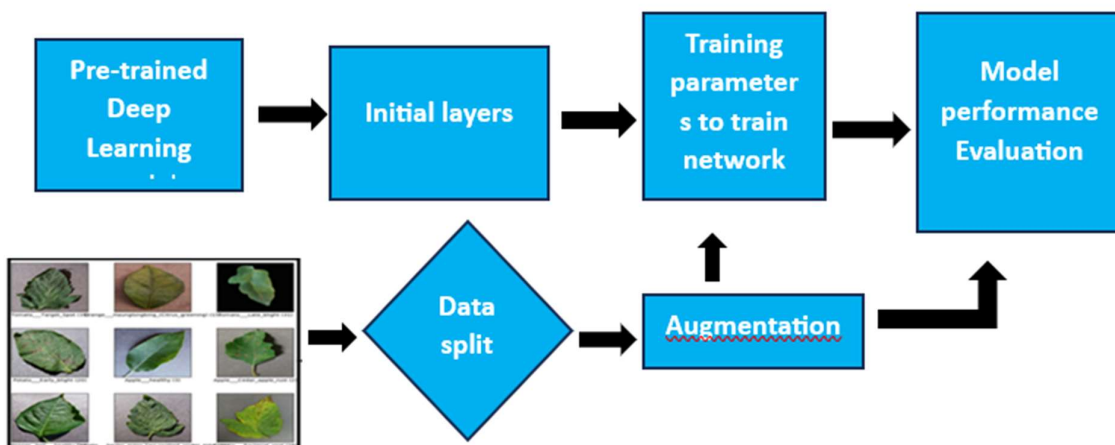
Healthy Tomato

Figure 1. Sample images

Figure 2. Flow of the proposed model

In this study, the customization, retraining, and application of eleven deep-learning CNN models were explored for the classification of tomato diseases based on leaf images. These models varied in the input size, structure, and computational efficiency of their internal operations. Notably, the hyperparameters governing the training of these models, such as the number of iterations, were kept consistent throughout the research. The CNN models encompassed DenseNet, GoogLeNet, Inceptionv3, ResNet 101, ResNet 18, SqueezeNet, and Inceptionv3. Training was conducted using uniform hyperparameters across all models, with the number of training epochs [19]. This decision was informed by the observed training and validation behavior of the models. The system's available memory permitted a batch size of 16, and the solver optimization algorithm employed for network training was fast-converging stochastic gradient descent with momentum (SGDM) [20].

$$\text{Accuracy} = \frac{\text{True positive} + \text{True negative}}{Positive + Nega} \tag{1}$$

$$\text{Precision} = \frac{\text{True positive}}{\text{True positive} + Fal \quad positive} \tag{2}$$

$$\text{Recall} = \frac{\text{True positive}}{\text{True positive} + \text{False negative}} \tag{3}$$

Results and Discussion

Performance evaluation was undertaken to assess and compare the classification capabilities of the various deep transfer learning models, employing well-established and indicative performance metrics. The evaluation was conducted over 10 repetitions to account for random variations in the selection of data subsets, and the time requirements for training/validation were documented for all models across different configurations. Three data split strategies 50,70 and 90 were employed to examine the models' abilities to learn from varied amounts of data and to identify potential underfitting or overfitting issues. Table 1 presents the mean values over 10 runs for the overall F1 score, precision, and recall using 50% of the data for training. DenseNet exhibited the highest mean F1 score at 97.5%, demonstrating exceptional performance, while SqueezeNet performed the least favorably with a 91.7% F1 score. These findings are further supported by the confusion matrices for the best and worst-performing models, as illustrated in Table 2. The matrix for SqueezeNet reveals a concerning pattern of misclassifying leaves with diseases as healthy, particularly for spider mites and target spots.

Table 1. Model accuracy

Name of the model	Accuracy	Precision	Recall
DenseNet	98.3%	98.6%	91.2%
GoogleNet	92.4%	93.6%	93.9%
ResNet 101	98.3%	98.1%	97.8%
ResNet18	96.9%	97.3%	96.3%
SqueezeNet	89.7%	91.9%	95.6%
InceptionV3	97.5%	98.0%	96.8%

Table 2. Confusion Matrix

	Bacterial spot	Early blight	Healthy	Late blight	Mosaic virus	Septoria leaf spot	Yellow leaf curl
Bacterial spot	1023		1			2	5
Early blight	2	436		6			
Healthy		1	765			1	
Late blight		1		185	2		
Mosaic virus					676		
Septoria leaf spot		2		3		881	
Yellow leaf curl					1		2682

While the current number of images has yielded satisfactory results, it is prudent to explore the impact of enlarging the training dataset. Deep learning models, unlike traditional machine learning algorithms, are known to exhibit improved performance with larger datasets. Table 2 depicts the mean values over 10 runs for the overall F1 score, precision, recall using 70% of the data for training. All models demonstrated enhanced performance, with diminishing returns. SqueezeNet improved to a 91.8% F1 score, while DenseNet exhibited the best performance with an F1 score of 97.5%. The corresponding confusion matrices in Table 2 support these performance values and highlight a substantially improved diagnosis, particularly regarding the misclassification of late blight and yellow leaf curl as healthy. While most other models experienced reduced fluctuation, smaller models such as SqueezeNet and GoogLeNet did not seem to benefit significantly from additional training data, particularly concerning their sensitivity to random choices of images for inclusion in the training set.

Conclusion

Tomatoes, as a crucial mass-produced agricultural commodity, face susceptibility to diseases leading to potential yield losses. Leveraging deep transfer learning and established models has demonstrated significant potential in various applications within the existing literature. This study focuses on the specific task of identifying tomato diseases through infected leaf images. Customizing and retraining eleven deep-learning models using leaf images as input, we aimed to identify nine tomato diseases along with healthy plants. The performance of these models

was compared across six common metrics and training/validation times. While all models performed admirably, DenseNet emerged as the top performer, achieving values exceeding 99% for all metrics. Conversely, the SqueezeNet model exhibited the fastest training and the shortest inference time. The transfer learning approach employed here is characterized by inherent credibility and reduced complexity. It obviates the need for explicit image processing or feature extraction, making it conducive to implementation in standalone smartphone applications. Such applications could prove invaluable for plant pathologists and farmers, offering swift and effective disease recognition and control. Future endeavors may involve the evolution of models through incremental learning during deployment. Additionally, the approach could be adapted for disease identification in tomato fruit images, potentially requiring 3D deep learning models to cover all sides of the fruit. Other models or ensembles of models could also be explored to address the same problem.

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