Tomato Disease Classification using Convolutional Neural Networks

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Abstract— Research on methods that use images to identify and categorize plant diseases is expanding as a field of study. These programs help find plant illnesses as they happen. Fungal, bacterial, and viral infections are the most harmful to plants. Five major tomato diseases have been classified in this study: Bacterial Spot, Black Mold, Gray Spot, Late Blight, Powdery Mildew, and healthy tomato plant leaf. The classification is done by extracting color, shape, and texture features from healthy and unhealthy tomato plant images. Following the segmentation phase, the feature extraction method is carried out. Features extracted from segmented pictures are used as inputs to a classification algorithm. These five categories were used to finalize the illness categorization system. The variety of five kinds of tomato images vielded an overall 98% classification accuracy. Furthermore, various research gaps have been identified to achieve a more open approach to detecting tomato diseases.

Keywords— Tomato, NumPy, RandomRotation, Convolutional Neural Networks (CNN), DenseNet

I. INTRODUCTION

Plant diseases are aberrant conditions that interrupt normal plant growth, resulting in crop yield losses. Favorable environmental conditions and crop kinds determine the occurrence and spread of these diseases. Various plant disease control programs have been developed to mitigate these losses. Significant progress has been made in recognizing and classifying plant diseases in recent decades. Early and precise disease identification may help in the execution of preventive measures to reduce loss of output and maintain high-quality crops. Image recognition technology to identify plant diseases has become more popular, fueling the development of visual applications and digital technologies.

Numerous studies (references) have proposed and studied image processing techniques for automatically recognizing and quantifying plant diseases. These strategies aim to create a system that can detect plant diseases without relying on domain specialists. The condition can be identified by extracting typical features from the affected regions of infected plant photos using image processing techniques. For spotting disease-infected plants, pattern recognition approaches such as neural networks (references number) and support vector machines (references number) are often used. Color, shape texture, and other attributes are among the features extracted from digital photos of plant diseases.

This work focused on recognizing many diseases that usually impact horticulture plants to automate identifying and evaluating plant diseases using image processing. The study assessed photos of plant leaves infected with Bacterial Spots, Black Mold, Gray Spots, Late Blight, and Powdery Mildew in tomato plants. In this study, there were seven processes for diagnosing tomato plant illnesses—step 1. Load a total of six types of images. Step 2. It has created training and testing datasets. Step 3. To perform segmentation on training and testing datasets. Step 4 and Step 5. Color, shape, and texture attributes extracted from segmented images of healthy and infected tomato plants. Step 6. Load training data into the classification model. Step 7. Visualize the result using a confusion matrix. The primary objective of this classification model is to provide a lightweight framework for disease prediction in tomatoes.

The paper addresses the need for automated systems to detect and classify plant diseases, which can help identify early conditions and prevent crop yield losses. The authors specifically target five major tomato diseases: Bacterial Spot, Black Mold, Gray Spot, Late Blight, and Powdery Mildew, along with healthy tomato plant leaves.

- 1. The methodology involves the extraction of color, shape, and texture features from segmented images of healthy and diseased tomato plants. The extracted features are then inputted into a classification model based on Convolutional Neural Networks (CNN). The model architecture includes layers such as Conv2D, MaxPooling2D, Flatten, and Dense layers, followed by a SoftMax activation function for multi-class classification.
- The authors report an overall classification accuracy of 98% on the dataset used in their study. They also identify research gaps and suggest future directions, including collecting more extensive and diverse datasets, improving model interpretability, and integrating other imaging modalities for accurate disease detection.
- 3. The paper includes a literature review that discusses the use of CNNs and transfer learning techniques in tomato disease classification and the challenges and limitations in the field. It also compares the proposed architecture with other related works regarding accuracy.

The remaining paper is structured as follows: The Literature Review in section $\underline{2}$. Section $\underline{3}$. exhibits the Methodology and the architecture. Section $\underline{4}$. exhibits the Result and Discussion section. Section $\underline{5}$. exhibits Conclusion. Finally, section $\underline{6}$. exhibits References.

II. LITERATURE REVIEW

Tomato diseases threaten tomato crops worldwide, resulting in economic losses and decreased food supply. The traditional disease detection methods rely on visual inspection by human experts, which can be time-consuming and subjective. With the advancement of computer vision and deep learning techniques, CNNs have shown promising results in automating the classification of tomato diseases based on leaf images. This literature review aims to provide insights into the state-of-the-art approaches employed in this field.

Methodologies: The reviewed studies employed various CNN architectures, including popular models like YoloV5 and DenseNet. Transfer learning, where pre-trained models are fine-tuned for tomato disease classification, was widely used to leverage the learned representations from large-scale image datasets. Data augmentation techniques, such as rotation, flipping, and scaling, were employed to augment the training dataset and improve model generalization.

Challenges and Limitations: Despite progress in tomato disease classification using CNNs, several challenges and limitations exist. Variations in image quality, illumination, and background clutter can affect model performance. The need for large-scale and diverse tomato disease datasets is another limitation. Additionally, the lack of interpretability of CNN models hinders understanding the learned features and decision-making processes.

Future Directions: Future research can focus on collecting more extensive and diverse datasets encompassing a more comprehensive range of tomato diseases, growth stages, and environmental conditions to address the existing challenges. Developing techniques for model interpretability and explaining the classification decisions of CNN models can enhance trust and adoption. Integration of other modalities, such as spectral imaging and hyperspectral imaging, can provide complementary information for accurate disease detection.

III. METHODOLOGY

Tomato crops play a crucial role in global food security and agricultural economies. However, diseases significantly threatened potato production, leading to yield losses and decreased quality. Therefore, accurate and timely disease detection is essential for effective disease management strategies. In recent years, computer vision techniques and intense learning models, like CNN and DenseNet, have shown promising results in automating the detection and classification of potato diseases. We implemented VGGNet19 and integrated it with a custom CNN architecture.

A. Image Acquisition

We have used the downloaded dataset. We have taken 3978 images from Kaggle across six labels: Bacterial spot, Black mold, grey spot, Healthy, Late blight, and Powdery mildew. The images used for each category are displayed below in Fig. 2. Table 1 gives the image count for each lab.



Fig. 1: Leaves Sample

Label Name	Number of Images
Bacterial Spot	704
Black Mold	428
Gray Spot	537
Healthy	678
Late Blight	627
Powdery Mildew	1004

Table 1: Label List

A. Image Preprocessing

We loaded the images with the cv2.imread function and resized the photos into 256*256. After resizing, we converted the images into a NumPy array. We have taken a batch size of 32. So, we had a length of 125 in our dataset. We have taken 80% for training the model, 10% for validation, and 10% for testing. The images are randomly shuffled 1000 times, and TensorFlow AUTOTUNE enables prefetching elements from the dataset. Prefetching overlaps the preprocessing and model execution, allowing the model to train on a batch of data while the next set is being prepared. In data augmentation, we have used the Random Flip function from Keras with the parameter of "horizontal and vertical" and Random Rotation with the parameter of 0.2. Features from RGB images were extracted using color histograms. These procedures improve training performance by avoiding redundant data loading, increasing the diversity of training examples, and enhancing its ability to handle variations and distortions in real-world data.

B. Proposed Methodology

Any image application can benefit from preprocessing methods that enhance image quality and characteristics. Detecting plant diseases is no different. The collection contains images with irrelevant context for identifying tomato diseases in leaves. To get around this, we convert the picture from RGB color space to a NumPy array. Then, we balanced the pixel value. Next, an input layer is defined to accept image data with specific dimensions, represented by SIZE and N ch. This allows the model to process images of varying sizes and channel depths. The architecture consists of 16 layers and a total of sixteen layers. It includes one resize and rescale layer, six Conv2D layers, six MaxPooling2D layers, one Flatten layer, and two Dense layers. DenseNet utilized 64 channels, elementwise addition, and channel-wise addition for

parameterization.

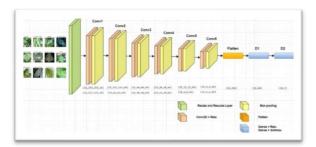


Fig. 2: Proposed Model

The model begins by preparing the input image through resizing and rescaling. The subsequent Conv2D layers learn image features using filters and ReLU activation. The MaxPooling2D layers then reduce the spatial dimensions while retaining crucial information. These steps are repeated, allowing the model to extract increasingly complex features. The Flatten layer converts the output to a 1D tensor. The Radial Basis Function (RBF) kernel was used in multi-SVM. The Dense layers learn high-level representations and capture relationships in the data. Finally, the last Dense layer uses SoftMax activation to produce output probabilities for each class. These layers enable the model to extract important image features and accurately classify them into the appropriate category.

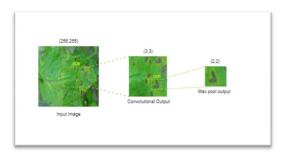


Fig. 3: Input-Output Layers

Softmax and Relu are used in neural networks to introduce non-linearity to the network's output. The purpose of an activation function is to determine the outcome of a neuron or a layer of neurons in the network based on its input. Without activation functions, the web would be a linear transformation, and multiple linear transformations can be collapsed into a single linear transformation.

$$f(\varkappa) = \begin{cases} 0 & \text{for } \varkappa < 0 \\ \varkappa & \text{for } \varkappa \ge 0 \end{cases}$$

$$f(x) = \log_e(1 + e^x)$$

A. Experimental Setup

Python is utilized in the model, which typically aims towards a less complicated, more straightforward language while providing programmers with a workaround and utilizing Keras. The deep learning architecture has been decided upon. To compute mathematical operations, we have used NumPy, and to Visualize our datasets, we have used pandas and matplotlib.

IV. RESULT AND DISCUSSION

Infectious diseases of crops pose a global danger to agricultural production. However, with the help of AI advancements in detection and categorization, these dangers may be monitored and eradicated in their infancy with remarkable speed and precision. In this study, we introduced a convolutional neural network (CNN) architecture for identifying diseases in tomatoes. By applying augmentation methods to a more significant number of photos in the dataset, we were able to boost the accuracy of our tests significantly. A mean testing accuracy of 98% was attained by the suggested design.

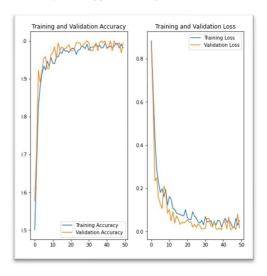


Fig. 4: Average Accuracy and Loss Curve

This accuracy score can be improved by adding more images to the dataset. In this study, we give a confusion matrix detailing the many sorts of accuracy and the computed and reported performance measurements. Finally, a comparison of the suggested architecture's testing accuracy to that of similar works was offered. The proposed architecture outperformed the relevant efforts in terms of overall testing accuracy.

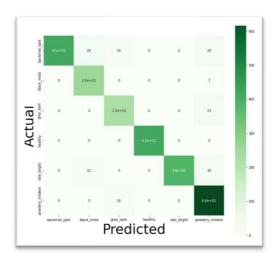


Fig. 5: Actual vs. Predicted Graph

Table 2 Comparison results of related works and the proposed architecture

	Year	Description	Accuracy
			(%)
[1]	2020	Random Forest	97.00
		classifier	
[3]	2021	Convolutional	98.00
		Neural Network	
[4]	2017	Support Vector	95.00
		Machine	
[6]	2017	CNN+VGG	96.00
Proposed	2023	Densenet121	98.00
Model			

V. CONCLUSION

This paper uses CNN architecture to develop an automated and easily accessible system. The most significant diseases in tomatoes, Bacterial spot, Black mold, Gray spot, Late blight, and Powdery mildew, are identified with little computational effort. Our approach will offer farmers a feasible, efficient, and timesaving way of disease identification. We plan to integrate more diseases of various plant species into the system. We will dedicate our future works to automatically estimating the severity of the detected disease. Our future works to estimate the severity of the detected disease automatically.

VI. REFERENCES

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