

TOMATO LEAF DISEASE DIAGNOSIS USING CNN

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ABSTRACT

Tomato is a horticultural crop that is cultivated globally, but it faces increasing threats from various diseases, including bacterial spot, tomato mosaic, and yellow leaf curl, which are the most prevalent and devastating, leading to significant crop losses. Early and accurate detection is crucial for effective management of these diseases. A convolutional neural network (CNN) approach has been introduced in the present study to precisely classify these specific tomato leaf diseases. A dataset comprising a total of 9,448 leaf images, representing three diseases and healthy samples, were used to train the CNN model. The evaluation metrics, including precision, recall, and F1-score values, ranged from 0.96 to 0.99, 0.97 to 1.00, and 0.98 to 1.00, respectively. The model achieved a promising accuracy of 98.99% in detecting these diseases.

INTRODUCTION

Tomato (*Solanum lycopersicum* L.) holds a significant position in horticulture globally and ranks as the second most consumed vegetable after potato. Notably, India stands as the world's second-largest tomato producer, contributing to a substantial portion of the global tomato production. According to the Food and Agriculture Organization of the United Nations (FAOSTAT, 2021), worldwide tomato production reaches 189.134 million tonnes, whereas in India, it amounts to 21.181 million tonnes (FAOSTAT, 2021). However, tomato cultivation faces a considerable challenge due to susceptibility to various diseases, which adversely affect both yield and quality. An annual crop loss of 20–30% has been reported by various plant diseases (Kashyap *et al.*, 2017). To address these challenges, it is imperative to deploy accurate and prompt disease diagnosis methods that empower farmers to mitigate crop losses effectively. Deep learning, specifically Convolutional Neural Networks (CNNs), has become a leading approach in agricultural disease identification. Kamilaris and Prenafeta-Boldú (2018) detail how CNNs specialize in image classification, surpassing traditional methods by directly identifying patterns from images, thereby eliminating manual interventions. This innovation leads to reduced crop losses, improved crop health, and increased yields. Abdel-Hamid *et al.* (2014) highlighted the potential of CNNs, paving the way for their incorporation in agriculture. Subsequent research, including works by Bangari *et al.* (2022) and Dhaka *et al.* (2021), underscores the paramount role of deep learning, particularly CNNs, in contemporary agricultural practices. In a study, Ahmed and Yadav (2023) provide an in-depth exploration of machine and deep learning for plant disease

diagnosis. Their methodology revolves around image preprocessing, augmentation, and CNNs' in-depth utilization. Their approach includes various machine learning techniques to optimize accuracy. Emphasizing data augmentation and vast datasets, their work exemplifies a blueprint for researchers, spotlighting pivotal areas and the intricacies that affect real-time agricultural disease detection. In summary, deep learning, with CNNs at its helm, has revolutionized disease identification in agriculture, promoting sustainable yields and enhanced crop health. This research paper aims to present a novel and advanced approach for the diagnosis of tomato leaf diseases using convolutional neural networks (CNNs). The study leverages a comprehensive database plant village comprising images of both healthy and diseased tomato leaf samples. The tomato diseases of the present study are Bacterial spot, Tomato mosaic, and Yellow leaf curl caused by *Xanthomonas species*, *Tomato Mosaic Virus* (ToMV), and *Tomato Yellow Leaf Curl Virus* (TYLCV), respectively. The primary objective is to develop an accurate and efficient model capable of categorizing tomato leaf diseases swiftly. Critical disease classes, including bacterial spot, tomato mosaic, yellow leaf curl (Czosnek and Laterrot (1997), Xu *et al.* (2021), Navas-Castillo *et al.* (1999), Abrahamian *et al.* (2021)) and healthy leaves, are meticulously selected to enhance model performance. Employing data preprocessing techniques, such as resizing and normalization, ensures dataset consistency. Data augmentation techniques, such as re-scaling, shearing, magnification, and horizontal flipping, contribute to a more robust training dataset. In this study, a CNN model is developed using the Keras module within the Tensor Flow framework. The architecture comprises Convolutional Layers followed by Max Pooling Layers, designed to extract relevant features

while reducing input image dimensions. Dense layers with Rectified Linear Unit (ReLU) activation add nonlinearity and facilitate complex pattern learning. Training the model employs the Adam optimizer and categorical cross-entropy loss, with accuracy as the primary evaluation metric. The successful outcome of this work has a significant impact on the detection of these diseases and their management.

MATERIALS AND METHODS

Dataset Selection and Preprocessing

For this study, a dataset comprising 9448 images sourced from the PlantVillage dataset was chosen. The dataset contained both healthy and diseased tomato leaf samples, categorised into four classes, including images of healthy tomato leaves as well as leaves affected by bacterial spot, tomato mosaic, and yellow leaf curl. To facilitate model assessment, the dataset was split into training (80%) and testing (20%) sets.

Image Resizing and Normalisation

The original images, initially at 256x256 pixels, were resized to 224x224 pixels. This resizing step serves two key purposes: it reduces computational complexity and ensures compatibility with the chosen CNN architecture. Furthermore, pixel values underwent normalisation to the range enhancing convergence and stability during training (Pushpa, 2022; Pawara *et al.*, 2017).

Data Augmentation

Data augmentation techniques were applied to the training set to diversify the dataset and improve model generalization. Techniques such as horizontal rotation, zooming, shearing, and rescaling were implemented using TensorFlow's Image

Data Generator module (Anandhakrishnan and Jaisakthi, 2022; Attallah, 2023; Kukacka *et al.*, 2017). These augmentations bolster the model's capacity to learn from various variations within the dataset.

CNN Model Architecture

The CNN architecture used in this study was designed for image classification tasks, particularly categorising images into four distinct classes. The architecture consists of three convolutional layers, each followed by a max-pooling layer. This combination enables hierarchical feature extraction from input images, progressing from low-level features to higher-level representations (Lee *et al.*, 2015; Zhang *et al.*, 2020). The convolutional layers employ filters to capture features of varying complexity. Subsequent max-pooling layers down-sample the feature maps, preserving essential information while reducing spatial dimensions. The resulting feature maps are then flattened into a 1D vector for input into two fully connected, dense layers. These dense layers, with 128 neurons and 4 neurons, respectively, are connected sequentially. They learn high-level features and produce the final classification output, representing predicted probabilities for each class (Tugrul *et al.*, 2022; Anandhakrishnan and Jaisakthi, 2022; Agarwal *et al.*, 2020; Pushpa, 2022).

RESULTS AND DISCUSSION

Tomato crops face numerous challenges, among which bacterial spot, tomato mosaic, and yellow leaf curl are particularly detrimental. Each of the disease has its own characteristic symptoms on the leaves (Figure.1). Bacterial spot, caused by various *Xanthomonas* species, manifests as small, dark, water-soaked spots on leaves, which can become necrotic and are often surrounded by a yellow halo. When

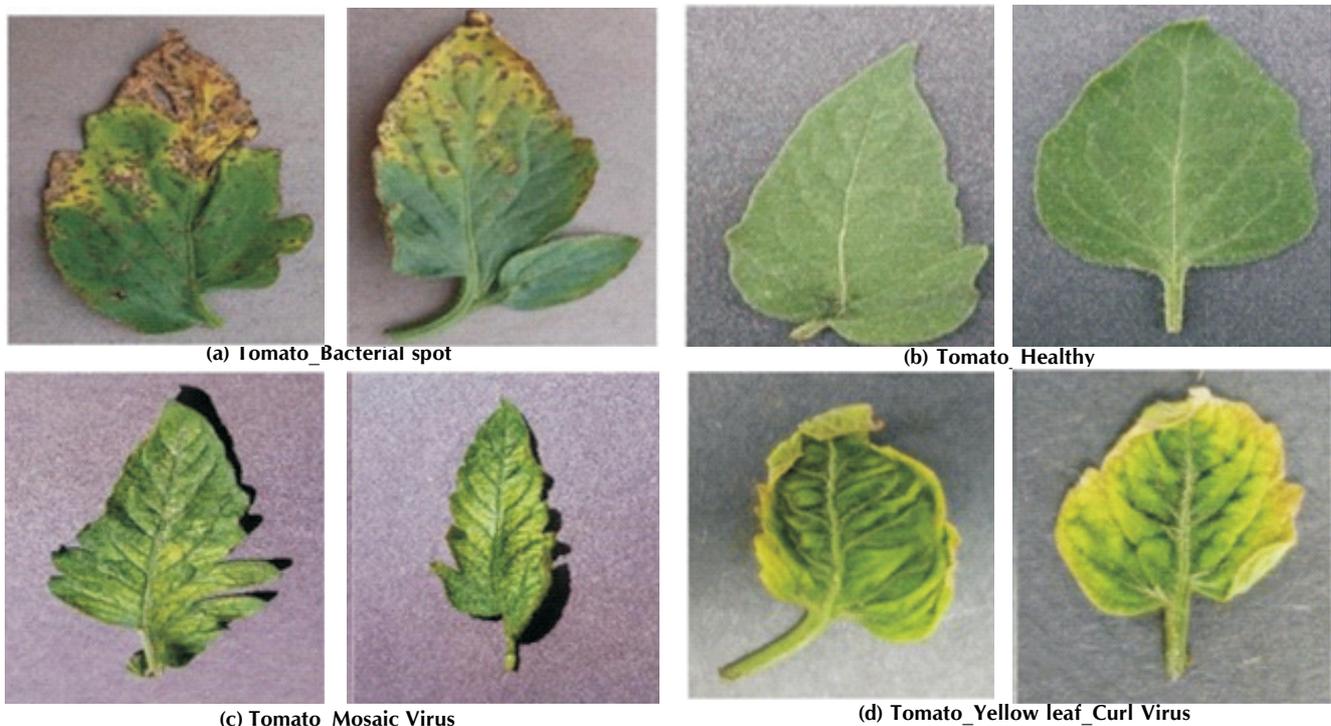


Figure.1: Images from the dataset showing healthy and diseased Tomato leaves

Table 1: Model Summary

Layer (type)	Output Shape	Param #
conv2d (Conv2D)	(None, 222, 222, 32)	896
max_pooling2d (MaxPooling2D)	(None, 111, 111, 32)	0
conv2d_1 (Conv2D)	(None, 109, 109, 64)	18496
max_pooling2d_1 (MaxPooling2D)	(None, 54, 54, 64)	0
conv2d_2 (Conv2D)	(None, 52, 52, 128)	73856
max_pooling2d_2 (MaxPooling2D)	(None, 26, 26, 128)	0
flatten (Flatten)	(None, 86528)	0
dense (Dense)	(None, 128)	11075712
dense_1 (Dense)	(None, 4)	516

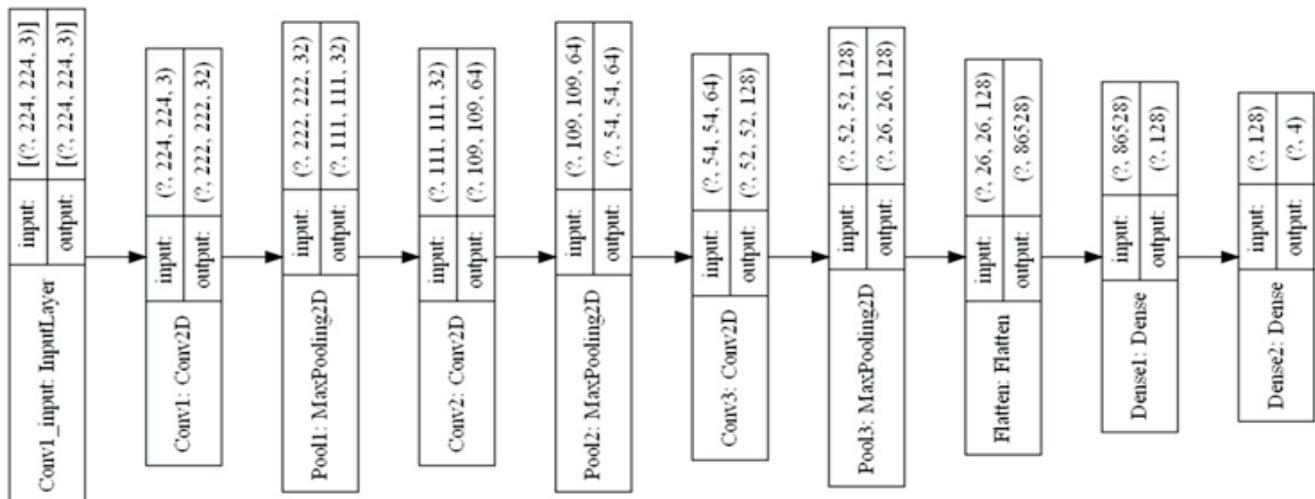
Total params: 11,169,476

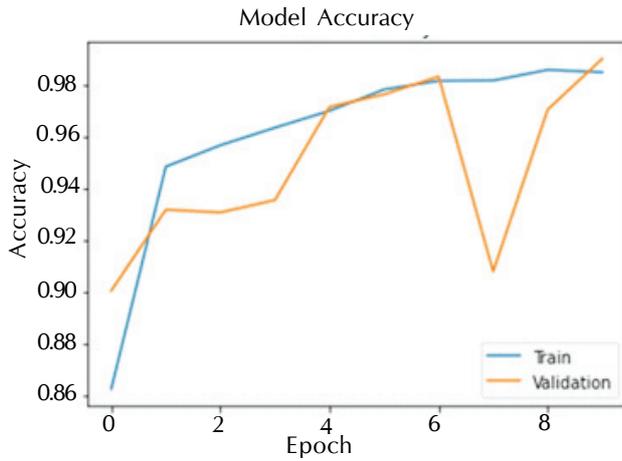
Trainable params: 11,169,476

Non-trainable params: 0

this disease is severe, it leads to extensive blighting and can also create raised, rough spots on the fruit (Abrahamian *et al.*, 2021). Tomato mosaic, induced by the ToMV, sees infected plants present a mottled green-yellow pattern on their leaves, which may become necrotic or distorted in extreme cases. The fruit might also display a similar mottled coloration (Xu *et al.*, 2021). Lastly, the tomato yellow leaf curl, attributed to the TYLCV and spread by whiteflies, causes upward leaf curling, yellowing, and stunting in affected plants, leading to smaller fruits and reduced yield (Czosnek and Laterrot., 1997; Navas-Castillo *et al.*, 1999). The present study focused on the detection of three severe diseases of tomato using a Convolutional Neural Network (CNN) model trained on leaf images. The proposed method used characteristic symptoms of each disease on the leaves as markers for detection. The

CNN model consisted of three pivotal convolutional layers, each increasing in complexity, and three max-pooling layers. The model additionally included a Flatten layer and two dense layers. Adam combined with a categorical cross-entropy loss function was used to optimise the training. The model underwent ten training epochs, and the results showed an overall accuracy of 99% for the detection of three tomato diseases. The study demonstrated the ability of deep learning models, specifically CNNs, to diagnose tomato leaf diseases rapidly and accurately. The use of characteristic symptoms of each disease on the leaves as markers for detection is a promising method, as it allows for the identification of specific diseases based on their unique symptoms. Table.1 and Figure.2 detail the proposed CNN model's structure and performance. The model's architecture is based on prior research that demonstrated CNN's prowess at capturing hierarchical data representations. For instance, Shrestha *et al.* (2020) proposed a CNN-based method for plant disease detection that obtained an accuracy of 88.80% during testing. Another study utilised a CNN model to detect plant diseases in a polyhouse with an optimal prediction accuracy of 85 percent (Radha and Swathika, 2021). Several other studies have also proposed using CNN models for plant disease detection (Al-Tuwaijari *et al.*, 2020; Sable *et al.*, 2021; Shrestha *et al.*, 2020; Radha and Swathika, 2021). Other studies have utilised various techniques for plant disease detection, including the support vector machine (SVM) algorithm (Al-Tuwaijari *et al.*, 2020), optimised CNN models (Mubarokah *et al.*, 2022), and feature extraction algorithms (Hussein and Abbas, 2018). Comparing the SVM algorithm to the CNN algorithm, Al-Tuwaijari *et al.* (2020) found that the CNN algorithm was more accurate and effective in the detection and classification of plant leaf diseases. Mubarokah *et al.* (2002) proposed a CNN model optimised for the classification and detection of Begomovirus disease in tomato leaves. A study comparing various feature extraction algorithms discovered that the combination of four methods produced outstanding results (Hussein and Abbas, 2018). Toda and Okura (2019) used CNNs to classify 38 categories of diseased or healthy leaf images with a 99.35% degree of accuracy.

**figure 1: Model Summary**



Graph.1: CNN Model Accuracy and Loss

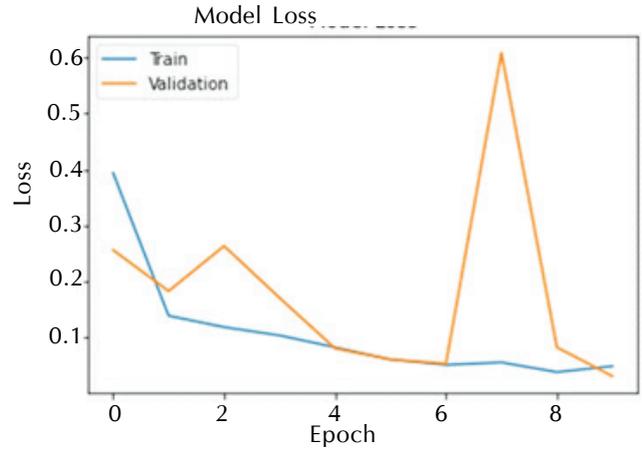


Table 2: Epoch Result

```

Epoch 1/10
236/236 [=====] - 545s 2s/step - loss: 0.3934 - accuracy: 0.8626 - val_loss: 0.2558 - val_accuracy: 0.9004
Epoch 2/10
236/236 [=====] - 598s 3s/step - loss: 0.1383 - accuracy: 0.9483 - val_loss: 0.1824 - val_accuracy: 0.9317
Epoch 3/10
236/236 [=====] - 609s 3s/step - loss: 0.1181 - accuracy: 0.9565 - val_loss: 0.2631 - val_accuracy: 0.9306
Epoch 4/10
236/236 [=====] - 507s 2s/step - loss: 0.1033 - accuracy: 0.9633 - val_loss: 0.1704 - val_accuracy: 0.9354
Epoch 5/10
236/236 [=====] - 2317s 10s/step - loss: 0.0820 - accuracy: 0.9698 - val_loss: 0.0800 - val_accuracy: 0.9714
Epoch 6/10
236/236 [=====] - 450s 2s/step - loss: 0.0603 - accuracy: 0.9781 - val_loss: 0.0602 - val_accuracy: 0.9762
Epoch 7/10
236/236 [=====] - 448s 2s/step - loss: 0.0506 - accuracy: 0.9814 - val_loss: 0.0528 - val_accuracy: 0.9831
Epoch 8/10
236/236 [=====] - 452s 2s/step - loss: 0.0550 - accuracy: 0.9815 - val_loss: 0.6085 - val_accuracy: 0.9078
Epoch 9/10
236/236 [=====] - 462s 2s/step - loss: 0.0377 - accuracy: 0.9856 - val_loss: 0.0819 - val_accuracy: 0.9703
Epoch 10/10
236/236 [=====] - 427s 2s/step - loss: 0.0483 - accuracy: 0.9847 - val_loss: 0.0305 - val_accuracy: 0.9899
    
```

Table 3 : Classification Report

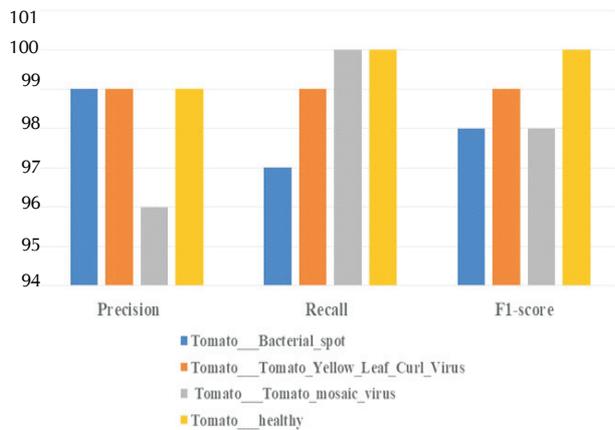
	Precision	Recall	F1-score	Support
Tomato__Bacterial_spot	0.99	0.97	0.98	426
Tomato__Tomato_Yellow_Leaf_Curl_Virus	0.99	0.99	0.99	1072
Tomato__Tomato_mosaic_virus	0.96	1.00	0.98	75
Tomato__healthy	0.99	1.00	1.00	319
Accuracy			0.99	1892
macro avg	0.98	0.99	0.99	1892
weighted avg	0.99	0.99	0.99	1892

The proposed CNN model, described in Table.1 and Figure.2. The model has a total of three convolutional layers. Convolutional Layer 1: Applies 32 filters to the input images, resulting in feature maps of size (None, 222, 222, 32). Convolutional Layer 2: Applies 64 filters to the previous layer’s output, resulting in feature maps of size (None, 109, 109, 64). Convolutional Layer 3: Applies 128 filters to the previous layer’s output, resulting in feature maps of size (None, 52, 52, 128). The model includes three max-pooling layers, each

following a convolutional layer. Max Pooling Layer 1: Performs down-sampling on the output of Convolutional Layer 1, resulting in feature maps of size (None, 111, 111, 32). Max Pooling Layer 2: Performs down-sampling on the output of Convolutional Layer 2, resulting in feature maps of size (None, 54, 54, 64). Max Pooling Layer 3: Performs down-sampling on the output of Convolutional Layer 3, resulting in feature maps of size (None, 26, 26, 128). The Flatten layer converts the 3D feature maps into a 1D vector, preparing the data for the fully connected layers. Flatten Layer: Reshapes the feature maps to a 1D vector of size (None, 86528). The model includes two fully connected dense layers following the flatten layer. Dense Layer 1: This dense layer has 128 neurons and is fully connected to the flattened input. It learns high-level representations of the features extracted by the convolutional layers. Dense Layer 2: The final dense layer has 4 neurons, corresponding to the number of classes (or categories) in the classification task. It produces the final output of the model, representing the predicted probabilities for each class. The model was compiled using the Adam optimizer, a stochastic gradient descent variant featuring adaptive learning rates. Categorical cross-entropy was chosen as the loss function for multi-class classification. Accuracy served as the evaluation metric to gauge the model’s performance. Training employed the train data generator, with updates to model weights based on 32-batch gradients. Similarly, in several other studies have used CNN model for plant disease detection (LeCun *et al.*, 1998; Krizhevsky *et al.*, 2012; Simonyan and Zisserman, 2015; Scherer *et al.*, 2010; Goodfellow *et al.*, 2016; Zeiler and Fergus, 2014; Kingma *et al.*, 2015).

Further, this study training process spanned ten epochs, and the training and validation results were tracked and recorded for subsequent analysis. Various techniques were employed to evaluate the trained CNN model. Training and validation accuracy and loss were visualised using line plots generated from the history object (Table.2 and Graph.1). Model predictions were generated for the test dataset, enabling the creation of a confusion matrix to compare actual and predicted class labels (Figure.3). Additionally, classification reports were generated, providing precision, recall, F1-score, and support metrics for each class (Table.3 and Graph.2).

However, the rise in validation loss in specific epochs, such as Epoch 8, points to potential overfitting, which is a challenge



Graph 2: Classification Report

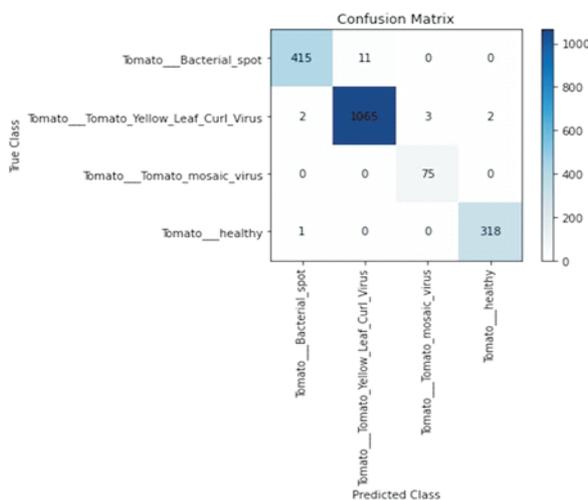


Figure 3: Confusion matrix of the proposal model

that researchers seek to mitigate. Finally, we have obtained impressive overall accuracy of 99% for detection of diseases of tomato. The study's findings provide a promising avenue for the development of effective and efficient methods for plant disease detection.

CONCLUSION

This study showed that Convolutional Neural Networks have the ability to effectively classify tomato leaf diseases of the study such as bacterial spot, tomato mosaic, and yellow leaf curl with an overall accuracy of 99%. The proposed CNN model's high accuracy holds promise for transforming disease diagnosis and control in tomato cultivation, thereby contributing to global food security by increasing crop yields and reducing disease losses. Future study should focus on optimising the model and exploring its practical application in agricultural environments.

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