

YOLOv11-Based Deep Learning System for Accurate and Real-Time Tomato Disease Classification

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Abstract

Tomato is one of the most important vegetable crops that are traditionally and economically valued in Nigeria, but its productivity is challenged by various diseases that reduce its yield and quality. The conventional method of identifying plant diseases is through manual inspection alone, but this is inefficient, time-consuming, and prone to errors. This study proposes a system for detecting and classifying tomato diseases using the YOLOv11 model in real-time. The proposed system utilized the PlantVillage dataset of 18,160 images of diseased and healthy tomatoes, categorized into ten classes of diseased and one class of healthy tomatoes. Data processing, transfer learning and hyperparameter optimisation were applied to improve performance. The trained YOLOV11 model classified with an accuracy of 99.2% and mean average precision (mAP@0.5) of 0.93. It was deployed on a lightweight web application, developed with React.js and FastAPI integrated together. This set up allow users to upload images and receive instant predictions. A comparative analysis with existing works demonstrated the precedence of this method in accuracy and speed. The system has potential for deployment in real-life farming contexts. This will curb the issues of dependency on expert physical inspection, minimise yield losses and ultimately contribute to food security in Nigeria.

Keywords: Tomato diseases, deep learning, YOLOv11, PlantVillage dataset, Precision Agriculture.

1. Introduction

At the time of Nigeria’s independence, agriculture was the backbone of the economy, provided stability and the potential for long-term growth. Research indicates that the sector controlled about 60% to the country’s GDP in the early 1960s. However, by 1999 to 2000 , this contribution had dropped to between 40% and 42%. This decline can be linked to the aftermath of the Civil War in 1967 and the discovery of crude oil in the early 1970s, which shifted the nation’s focus away from agriculture and hindered its development due to a lack of visionary planning (Ugwukah, 2022).

Till date, the sector is yet to regain its position in the economy. Food insecurity remains a pressing issue in Nigeria today, as millions of households are struggling to access sufficient, safe and nutritious food. To address this issue, the Nigerian government and various global stakeholders have promoted the need to boost local food production, with a particular focus on staple crops and high-value cash crops like tomatoes.

Tomato fruit is a good source of phosphorus, iron and vitamins (Irina et al., 2024). The fruit contains B complex vitamins, thiamin, niacin and riboflavin which are important in a healthy diet. Tomatoes are one of the most consumed vegetable fruits in Nigeria, playing a significant role in the diets of many households and serving as an essential ingredient in traditional dishes. Nigeria is the second largest producer of tomatoes in Africa according to Nyarko et al. (2023), contributing significantly to the agricultural economy. Tomato farming provides thousands of jobs and promotes agro-industrial processes like tomato paste production. Despite its importance, tomato’s value chain faces challenges in Nigeria and diseases are one of these problems.

The tomato plant can be infected with over 200 various diseases as it is more prone to disease than any other vegetable plant. some of the diseases include early blight, late blight, leaf mold, Septoria leaf spot, spider mites, yellow leaf curl virus, mosaic virus, target spot and bacterial spot) can create favorable conditions for their spread (Nyarko et al., 2023). Without early and accurate detections, farmers often resort to excessive use of chemical pesticides, which are harmful to the environment thereby increasing losses and by extent, cost of farming.

Disease control in tomato farming today is majorly carried out using manual identification method. This method has over time been proven to be inefficient, time consuming, requires expert knowledge, tiring and prone to human errors. These gaps underline the need for innovative solutions leveraging on modern technology to boost agricultural productivity. Luckily, advancements in Artificial Intelligence (AI) is paving the way to change the dynamics of disease management and control in agriculture. By analyzing images of affected plants, these technologies can detect diseases based on visual symptoms.

In recent years, computer vision and ML have emerged as transformative tools in agriculture (Ghate et al., 2025). Machine learning (ML), a subset of AI, offers solutions to complex problems such as disease detection and crop management. ML refers to the use of algorithms that allow systems to produce output or make predictions without being explicitly programmed just by simply learning patterns from input data. In the context of this project, ML algorithms can analyze images of plant parts, identify patterns associated with plant specific diseases and classify them with high accuracy. This capability is significant

for farmers because it allows early detection of diseases and enables timely interventions and minimize losses. Among the many ML techniques, convolutional neural networks (CNNs) have been developed to be the most effective for image-based tasks due to their automatic feature extraction ability from images. CNNs are inspired by the structure and functioning of the human visual cortex, consist of layers that process image data to recognize unique patterns and distinguish between healthy and diseased plants. Architectures like YOLO (You Only Look Once), SSD (Single Shot MultiBox Detector), EfficientDet and RetinaNet are renowned for classification, real-time object detection, as well as ResNet (Residual Network) and GoogLeNet address issues like vanishing gradients, allowing deeper networks to train effectively. These advancements create a strong platform for the development of automated systems that detect diseases. This is a practical approach that could be taken to enhance the management of crop health in Nigeria. The purpose of the research is to reduce the reliance on expert inspections to detect diseases in plants. The research will empower farmers with the necessary information to make timely interventions to address the detected diseases. This will enhance the health of the crops. The research will be useful to the people of Nigeria in the following ways: The research will help to curb the spread of diseases in tomato plants. The detection of the diseases will help to enhance the health of the plants. The research will help to empower farmers with the necessary information to make timely interventions to address the detected diseases. The research will be useful to the people of Nigeria in the following ways: The research will help to curb the spread of diseases in tomato plants. The detection of the diseases will help to enhance the health of the plants. The research will help to empower farmers with the necessary information to make timely interventions to address the detected diseases.

There has been a lot of research on the detection of tomato plant diseases using various deep learning architectures. However, these approaches are not precise in their results. Additionally, the approaches are becoming obsolete. The research aims to use a recent approach to detect tomato plant diseases. The project will include the design, implementation, and deployment of a Disease Detection System for Tomato Plants. The model will include the following: Pre-processing and augmentation of the images to enhance the quality of the data. The images will be segmented to detect the region of interest (ROI) using the standard YOLO bounding box detection approach. The model will also include the implementation of an efficient feature extractor. The model will also include the implementation of an efficient classifier.

2. Related Works

Disease detection in plants has always relied on machine learning. Initially, the focus was on image processing techniques such as thresholding and segmentation (Suneetha et al., 2026). Later, machine learning techniques such as k-NN and SVM were applied. Though these techniques were effective to a certain extent, some issues were encountered (Zhang et al., 2025). Later, deep learning techniques were applied. The focus was on CNN. The performance was good. For instance, Olowu et al. (2025) applied a deep learning model for detecting diseases in tomatoes. The model was trained and tested using 6,124 images belonging to five different diseases. The model was compared against a lightweight CNN. The results were good. The accuracy obtained by the lightweight CNN was 97.6%, while

that obtained by the VGG16 model was 92.8%. Another study by [Geetha et al. \(2020\)](#) applied a combination of K-means clustering and GLCM for segmenting images and KNN for detecting diseases in tomatoes. The results were good but lacked scalability. Another study by [Sivagami and Mohanapriya \(2021\)](#) obtained high accuracy using a modified K-means clustering and ANFIS. The results were good but lacked scalability. Later, Siamese networks were applied for detecting diseases in plants ([Thuseethan et al., 2024](#)). Hybrid feature selection and transfer learning were applied for achieving near perfect results. The accuracy obtained by the model was near perfect. Later, the YOLO family was applied to detecting diseases in plants ([Attallah, 2023](#)). The accuracy obtained by the model was better than that obtained by the CNN model ([Rajamohanan and Latha, 2023](#); [Jing et al., 2023](#)). The latest version of the model is known as YOLOv11. The model has several modifications. The modifications include a C3k2 block that replaces C2f. Another modification is the use of C2PSA for achieving parallel spatial attention. The third modification is the use of an optimal version of Spatial Pyramid Pooling-Fast ([He et al., 2025](#)). This study applied YOLOv11 for tomato disease classification, integrating real-time deployment through a web platform to bridge the gap between research and practical usage.

3. Methods

The work used a publicly accessed secondary datasets, known as the PlantVillage dataset found on Kaggle for the training and testing. This PlantVillage dataset consists of 54,303 healthy and unhealthy leaf images divided in 38 categories by species and disease, including that of apple, blueberry, corn (maize), soybeans, tomato, potato and 8 other plants. The images have high-resolution ranging from 500×500 to 2560×1920 pixels of coloured and segmented tomato leaves, capturing different diseases conditions as well as healthy samples. it contains of 18,160 tomato leaf images across ten classes, including healthy and nine classes of diseased samples. These disease classes are bacterial spot, early blight, late blight, Septoria leaf spot, spider mites, leaf mold, target spot, tomato mosaic virus, and yellow leaf curl virus. The colored tomato leave image files were extracted and used for the YOLOv11 classification model to accurately classify tomato plant diseases.

Various image processing techniques were applied to the dataset, to improve the model’s generalization ability. The preprocessing stage included rotations, flipping, scaling, contrast changes, and addition of noise. This process allows the model to identify patterns of disease regardless of the image’s resolution. In training the model, resizing of the images was done to a fixed input shape of 256×256 . The PlantVillage dataset has good lighting conditions, minimal background noise, making it suitable for training the model. Shadows are absent, backgrounds are clean, and the structures of the leaves are in clear focus. The dataset was split into training, validation, and test sets in a ratio of 70:15:15, but class balance is not yet even.

3.1. System Design

It follows a well-defined, step-by-step approach in order to ensure a reliable classifier that identifies diseases in tomato plants. In addition, a diagrammatic representation of the system’s architecture is provided in [Figure 1](#). All stages of the system are important, as they emphasize how accurate a prediction will be.

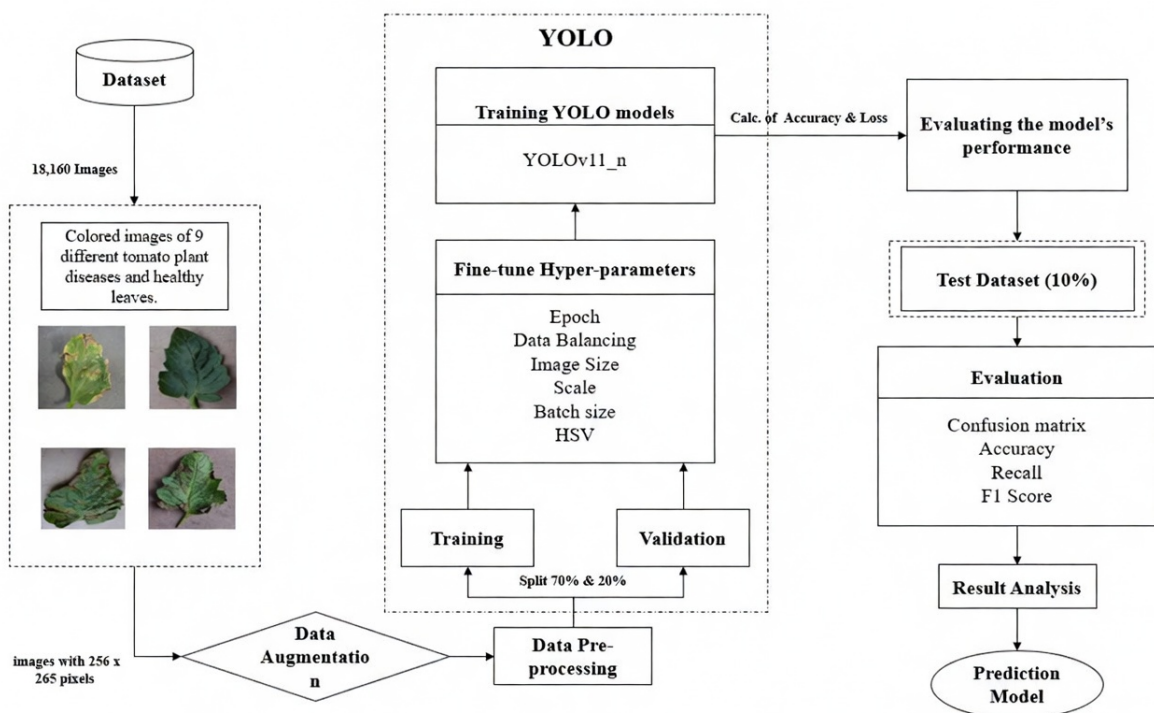


Figure 1: Tomato Disease Classification System Architecture

It uses a state-of-the-art deep learning technique, YOLOv11, for its ability to detect objects in real-time with high precision and speed. It begins with loading weights, which are pre-trained on a dataset called MS COCO, in order for the system to have a general idea about features in images. Then, training occurs by inputting images into a dataset, which are then fed into a deep learning network for fine-tuning its parameters via a technique called backpropagation and gradient descent optimization. In addition, several hyperparameters are optimized, such as learning rate, batch size, and activation functions, in order to optimize results further. Transfer Learning is incorporated in order to reduce computational time and optimize results on a different, smaller dataset for tomato diseases. Adaptive Learning Rate Optimization is used with Learning Rate Schedulers in order to optimize results further, while Loss Function Optimization uses advanced mathematical formulas in order to minimize errors and optimize results further.

The stages in YOLOv11 optimize feature extraction, classification accuracy, and real-time deployment. It integrates deep learning techniques, preprocessing methods, and a user-friendly deployment framework to assist farmers and researchers in early disease detection. It is modular and organised into three main components: The Backbone, the Neck, and the Head.

The model is based on the YOLOv11 architecture. This architecture is divided into three major components:

- i. Backbone: This section extracts low-level and high-level features using convolutional layers and C3k2 blocks. This is where the input image of size $256 \times 256 \times 3$ undergoes

a series of convolutional operations. These layers perform down-sampling, reducing spatial dimensions while capturing low-level features like edges, textures, and shapes to improve accuracy and speed:

- (a) **Deep convolutional layers:** In the backbone of YOLOv11 each convolutional block uses filters to extract specific patterns from the image. A convolution is defined as:

$$Conv(C_{in}, C_{out}, K, S)$$

C_{in} : Number of input channels

C_{out} : Number of output channels (filters)

K : Kernel size (usually 3×3)

S : Stride (typically 2 for downsampling)

- ii. **Neck:** In this section, it aggregates multi-scale features through path aggregation and spatial attention (C2PSA).
- iii. **Head:** This last block contains bounding boxes and probabilities for the categories of tomato disease. This block is used to interpret the refined features to arrive at the output classes. After the features are extracted, the data passes through fully connected layers to perform the disease classification.
- (a) **Fully connected layers:** The features are mapped to a high-dimensional space to enable the differentiation of various diseases.
- (b) **Softmax activation:** The final classification layer uses the SoftMax function to ensure that the most probable tomato disease is classified.

$$p_k = \frac{e^{z_k}}{\sum_{j=1}^{10} e^{z_j}}$$

p_k : Probability of class k

z_k : Logit (score before activation) for class k

10: Total number of classes.

This formula converts logits z_k into probabilities p_k over 10 classes.

- (c) **Optimization of cross-entropy loss function:** The loss function seeks to minimize misclassification errors by adjusting the model's weights based on incorrect predictions.

$$L = - \sum_{k=1}^{10} y_k \log(p_k)$$

3.2. Hyperparameters

The main hyperparameters used for training are presented in Table 1.

3.3. Evaluation metrics

This study used precision, Recall, mAP@0.5 and F1 score as evaluation metrics for the performance of the model.

Table 1: YOLOv11 Training Hyperparameters

Parameter	Value
Learning rate	0.001
Batch size	16
Epochs	30
Optimizer	SGD
Dropout	0.3

4. Results and Discussion

4.1. Model Training Performance

The accuracy of the YOLOv11 model on the test set was 99.2%, which is a clear indication of its classification capabilities. The convergence of training was also effective, as depicted in Figure 2, where the loss reduces from 1.57 to 0.14 over 30 epochs. The model showed particular strength in detecting common diseases like bacterial spot and late blight (Figures 3(a) and 3(b) show prediction samples), while maintaining strong performance across all nine disease classes. The mean average precision (mAP@0.5) of 0.93 indicates excellent localization of disease symptoms on leaf images. Table 2 shows the precision, Recall, F1-Score and Support for each of the classes and overall accuracy of the system.

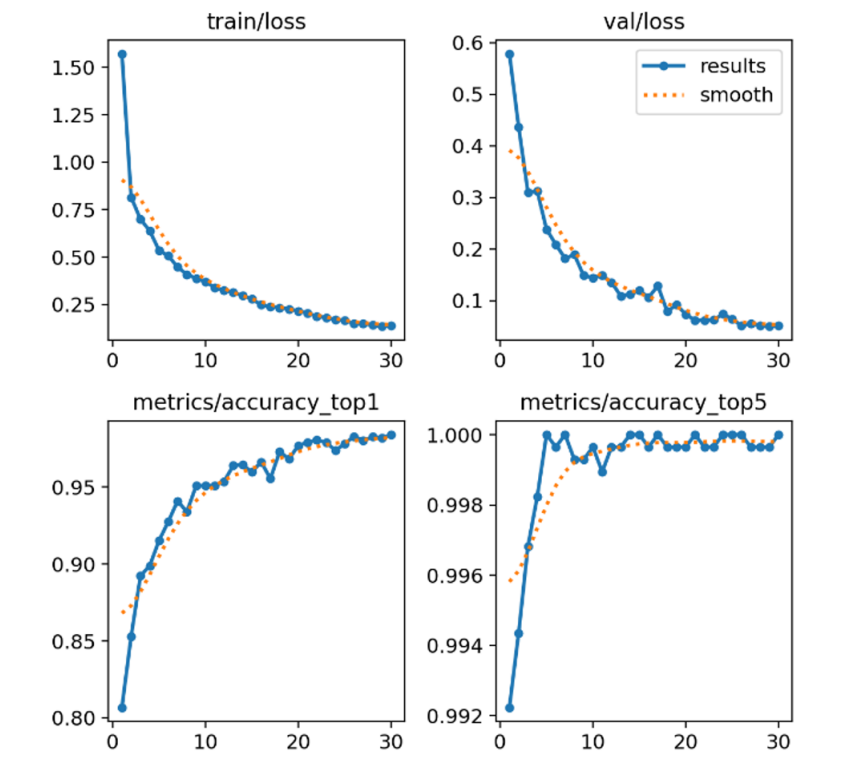


Figure 2: Accuracy Graph

Table 2: Validation Evaluation Results

Class	Precision	Recall	F1-Score	Support
Bacterial_spot	1.000	1.000	1.000	287
Early_blight	1.000	0.970	0.985	197
Healthy	0.984	1.000	0.992	317
Late_blight	1.000	0.997	0.999	375
Leaf_Mold	1.000	0.995	0.997	191
Septoria_leaf_spot	1.000	0.994	0.997	353
Spider_mite	0.997	0.971	0.984	343
Target_Spot	1.000	0.993	0.996	271
Yellow_Leaf_Curl_Virus	0.964	1.000	0.982	400
Tomato_mosaic_virus	1.000	1.000	1.000	75
accuracy	0.992	0.992	0.992	0.992



Figure 3: Validation Information

4.2. Confusion Matrix Analysis

The confusion matrix (Figure 4(a)) and its normalized form (Figure 4(b)) reveal excellent performance across all nine tomato disease classes. In Figure 4(a), most classes achieved high correct prediction counts. For instance, Bacterial spot recorded 287 correct predictions, Early blight 191, and Healthy 317, while Late blight and Septoria leaf spot had 374 and 351 correct predictions respectively. Similarly, Tomato Yellow Leaf Curl Virus and Tomato Mosaic Virus achieved perfect recognition with 400 and 75 correct predictions each. These are high numbers that demonstrate just how well this model is able to identify a variety of different states of tomato leaf condition. Figure 4b helps to clear up this data by normalizing it and showing class-by-class accuracy. Most of these classes are well above 95% correct, but Healthy, Tomato Yellow Leaf Curl Virus, and Tomato Mosaic Virus are all represented

by a perfect score of 1.00. Leaf Mold and Septoria leaf spot are just a hair under that, represented by a score of 0.99, but Late blight comes in at a very strong 0.98. The what-else category is a little weaker, represented by a score of 0.96 for Target Spot and 0.95 for early blight, indicating a little cross-contamination between visually similar diseases. The overall accuracy of this system is very strong, demonstrating its overall robustness and its strong potential for practical application in agriculture.

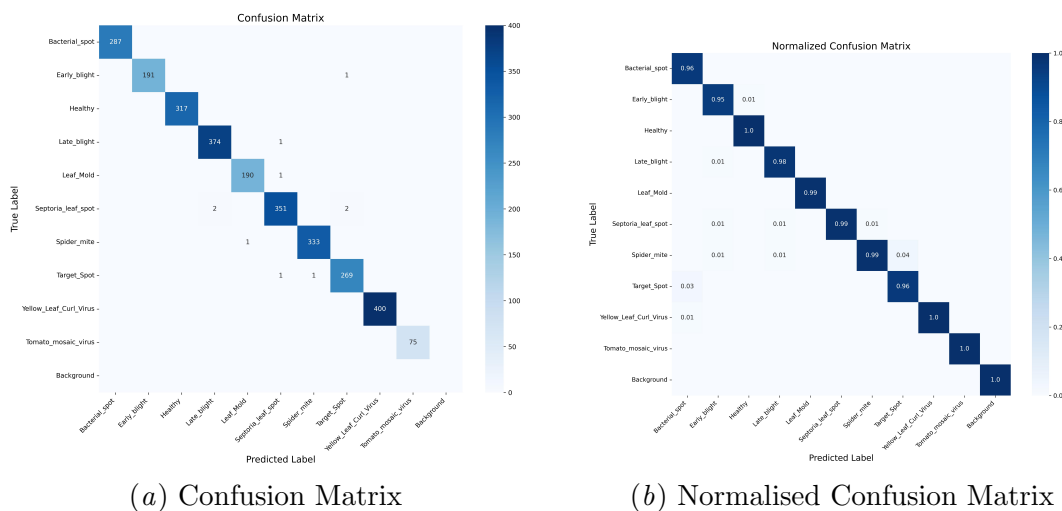


Figure 4: Confusion Matrices

4.3. Comparative Analysis

The evaluation results are highlighted in Table 3, which compares the proposed YOLOv11 model with other approaches.

Table 3: Comparative Analysis of Tomato Disease Classification Approaches

Method	Accuracy (%)	mAP@0.5
K-means + ANFIS (Sivagami and Mohanapriya, 2021)	98.6	-
Siamese Networks (Thuseethan et al., 2024)	96.9	-
VGG16 Olowu et al. (2025)	92.8%	-
CNN Olowu et al. (2025)	97.6%	-
YoLov5 (Pandeya et al., 2023; Rajamohanam and Latha, 2023)	97.0, 0.93	0.76, 0.95
YoLov8 (Liu et al., 2024; Shen et al., 2025)	94.6,- %,	0.95, 0.798
Proposed Model	99.2	0.93

4.4. Real-world Deployment

The model was then deployed to a web app for real-time testing. The user interface is designed to be user-friendly using React.js, while the server-side is implemented using FastAPI

to deploy the trained YOLOv11 model for disease classification. Users can upload images, as depicted in Figure 5, showing the classification results and confidence percentage.

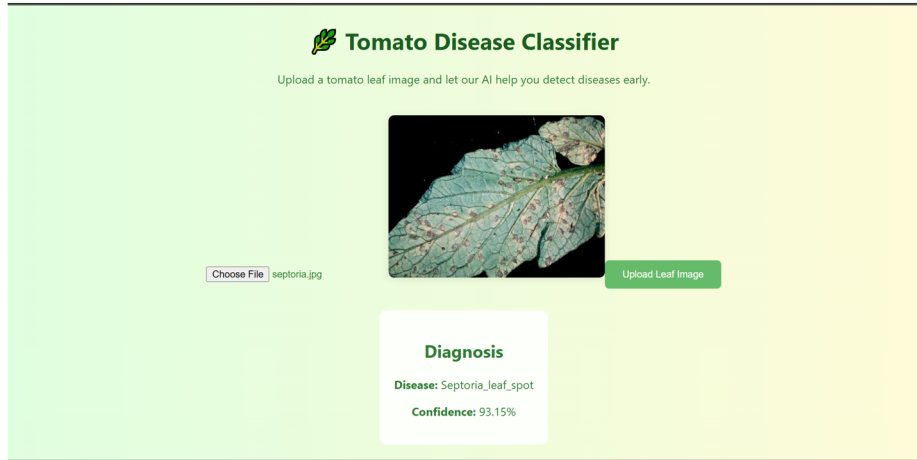


Figure 5: Displays the User Interface

4.5. Discussion

From the results, it is clear that the YOLOv11 model is highly effective for the classification of tomato diseases. This is because the model achieved a 99.2% accuracy with a mean average precision at 0.5 of 0.93, making the model robust for the differentiation of the various diseases affecting the leaves of the tomato plants, which are very similar. This is supported by the confusion matrix, which indicates a few errors, with the model successfully differentiating the diseases, including the early blight disease, which is related to the bacterial spot disease. The precision, recall, and F1 scores for the different classes are all above 0.95, which makes the model highly effective for the detection of true positives while keeping the false positives low. When comparing the results with the previous methods, including the ANFIS method (Sivagami and Mohanapriya, 2021) and the Siamese network (Thuseethan et al., 2024), the results indicate that the YOLOv11 model not only improves the classification accuracy but also improves the speed of the model, which makes the model more efficient for the differentiation of the diseases affecting the tomato plants. This is supported by the results shown in Table 3, which indicate that the YOLOv11 model performs better than the YoLov5 model (Pandeya et al., 2023), especially with regards to the average precision, which is 0.93 compared to 0.76. This is because the model incorporates architectural tweaks, which improve the effectiveness of the model, including the use of the C3k2 block, which improves the effectiveness of the model with regards to the extraction of features, as well as the use of the C2PSA attention mechanism, which improves the effectiveness of the model with regards to the extraction of features from the diseased areas, thereby improving the effectiveness of the model with regards to the bounding boxes as well as the differentiation of the diseases affecting the tomato plants.

The results are highly beneficial for the practical applications, which makes the model highly efficient for the differentiation of the diseases affecting the tomato plants, making

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5. Conclusion

The project was a success in that a robust system for the classification of diseases in tomato plants was created using the YOLOv11 deep learning model. The system was able to accurately classify and detect different diseases in tomato plants. The PlantVillage dataset for tomato leaf images was downloaded and used in the creation of the model. The model was able to attain an impressive accuracy rate of 99.2% in the classification of the different diseases affecting tomato plants. The model was also able to make real-time predictions using a user-friendly interface created using React.js and FastAPI. The average inference time for the model was 420 milliseconds. The model was able to outperform existing models such as K-Mean+ANFIS, Siamese Networks, VGG15, CNN, YOLOv5, and YOLOv8 in terms of speed and precision. The model has the potential to help in the early detection of diseases in plants and can be adapted for use in other fields. The use of the model can help in the development of a more efficient and effective method for detecting diseases in plants.

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