

Performance Analysis YOLO11n Model for Chili Leaf Diseases Detection

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ABSTRACT

Chili plants are a strategic agricultural commodity with high economic value, yet their production is often disrupted by disease attacks causing significant yield reduction. Early and accurate detection of chili leaf diseases is crucial for implementing precision agriculture practices. This research implements the YOLO11n (You Only Look Once version 11 nano) model for automated chili leaf disease detection using the "Chili Plant Leaf Disease and Growth Stage Dataset from Bangladesh" containing 1,856 high-resolution images across six categories: Bacterial Spot, Cercospora Leaf Spot, Curl Virus, Healthy Leaf, Nutrition Deficiency, and White Spot. The model was trained for 100 epochs on Google Colab with Tesla T4 GPU using 640×640 pixel input resolution. Evaluation results demonstrate excellent detection performance with precision of 83.7%, recall of 84.3%, mAP@0.5 of 92.3%, and mAP@0.5:0.95 of 74.5%. Per-class analysis reveals that Nutrition Deficiency achieved the highest performance (mAP@0.5 = 99.2%), while Curl Virus presented the greatest detection challenge (recall = 55.6%). The lightweight YOLO11n architecture with only 2.58 million parameters and 6.3 GFLOPs, making it highly suitable for deployment on edge devices such as agricultural drones, mobile applications, and IoT monitoring systems. This research contributes to smart agriculture applications by providing an efficient and accurate solution for automated chili leaf disease detection under real field conditions.



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INTRODUCTION

Chili plants are a strategic agricultural commodity in Indonesia with high economic value, yet their productivity is frequently hindered by disease attacks that cause significant yield reduction ((Ninis Putri Arafa et al., 2024). Consequently, early and accurate detection of chili leaf diseases is a crucial element in implementing precision agriculture to minimize losses and enable timely intervention (Siti Choiriyah & Aji Supriyanto, 2025). Major diseases frequently attacking these plants include *Bacterial Spot*, *Curl Virus*, and *Cercospora Leaf Spot*, which act as destructive pathogens across various growth stages of chili plants (Anthony A. Moreira-Morrillo et al., 2022).

Conventional methods for plant disease diagnosis generally rely on visual inspection by agronomists. This approach has significant limitations regarding scalability, consistency, and accessibility, particularly in rural areas with limited expert availability, making it inefficient for

large-scale farming (Jenny Rahma Hidayat & Jemakmun, 2025). Over the last decade, *Computer Vision* and *Deep Learning* technologies have emerged as transformative solutions for automated plant disease detection, offering methods that are faster, cost-effective, and capable of real-time operation (Abhishek Upadhyay et al., 2025).

In the context of plant disease recognition, the *object detection* paradigm offers distinct advantages over simple image classification. While classification only identifies the presence of a disease in an image, object detection provides richer spatial information by localizing lesions or symptoms via *bounding boxes* (Leo Thomas Ramos & Angel D. Sappa, 2025). This localization information is vital for practical field applications, such as precision pesticide spraying, severity assessment, and monitoring disease progression (Leo Thomas Ramos & Angel D. Sappa, 2025).

Among various *Deep Learning* architectures, the *You Only Look Once* (YOLO) algorithm has become the industry standard in agricultural applications due to its superiority in inference speed and computational efficiency (Peiyuan Jiang et al., 2022). The evolution of YOLO continues with the latest generation, YOLO11, which introduces key architectural enhancements to balance efficiency and accuracy (Rahima Khanam & Muhammad Hussain, 2024). The YOLO11n (*nano*) variant is specifically designed as a lightweight model for implementation on resource-constrained devices to maximize resource utilization efficiency (Areeg Fahad Rasheed & M. Zarkoosh, 2024).

Although recent YOLO architectures have been widely applied for disease detection in various commodities such as maize, rice, and tomatoes, research regarding the specific application of YOLO11 for chili disease detection remains very limited (Akansh Vishwakarma & Murugan A, 2025; Daya Rameshbhai Thummar, 2025; Jie He et al., 2025). Furthermore, a major challenge in current research is the reliance on datasets captured under controlled laboratory conditions, which often fail to represent the true variability of field conditions and limit model generalization in the real world (Abhishek Upadhyay et al., 2025; Muhammad Shafay et al., 2025). This gap needs to be addressed by utilizing datasets that reflect visual challenges in actual agricultural lands.

This research aims to bridge this gap by implementing the YOLO11n model using a recently published dataset, the "*Chili Plant Leaf Disease and Growth Stage Dataset from Bangladesh*" released in February 2025 (Md Asraful Sharker Nirob et al., 2025). This dataset offers high-resolution images collected directly from farmlands under agronomist supervision, covering six classes of leaf conditions relevant to Asian agroecological conditions. This study evaluates the performance of YOLO11n in detecting chili diseases and analyzes its feasibility for deployment on *edge computing*-based smart farming monitoring systems.

MATERIALS AND METHODS

1. DATASET

The dataset used in this research is the "*Chili Plant Leaf Disease and Growth Stage Dataset from Bangladesh*" available on Mendeley Data Repository with DOI 10.17632/w9mr3vf56s.1. This dataset was published on February 19, 2025, by a research team from Daffodil International University, Bangladesh, and is licensed under Creative Commons Attribution 4.0 (CC BY 4.0). For example image of dataset on Figure 1. Data collection was conducted manually from chili gardens in Charpolisha, Jamalpur, Bangladesh, during the period October 2024 to February 2025 under agricultural expert supervision. This data collection approach ensures realistic field

condition representation with natural variability in lighting, camera angles, backgrounds, and disease severity levels (Md Asraful Sharker Nirob et al., 2025).

The dataset consists of two main categories: (1) Chili Leaf Disease Dataset and (2) Chili Growth Stage Dataset. This research focuses on the first category containing chili leaf images with various health conditions.

Chili Leaf Disease Dataset includes:

- Total original images: 1,856 high-resolution images in .jpg format
- Augmented dataset: 12,000 images resulting from data augmentation
- Disease classes: 6 categories covering 5 diseases and 1 healthy condition

The six classes used in this research are:

1. Bacterial Spot: Caused by *Xanthomonas* spp. bacteria, characterized by dark brown necrotic lesions with yellow halos on leaf surfaces
2. Curl Virus: Viral infection transmitted by whitefly (*Bemisia tabaci*), causing leaf curling and deformation with color changes
3. Cercospora Leaf Spot: *Cercospora capsici* fungal infection producing circular lesions with gray centers and dark brown edges
4. Nutrition Deficiency: Nutrient deficiency symptoms that may include chlorosis, marginal necrosis, or systemic color changes due to nitrogen, phosphorus, potassium, or micronutrient deficiency
5. White Spot: White or pale lesions on leaf surfaces that can be caused by various pathogens or abiotic conditions
6. Healthy Leaves: Healthy leaves without disease symptoms, serving as control class to distinguish normal conditions from pathological conditions

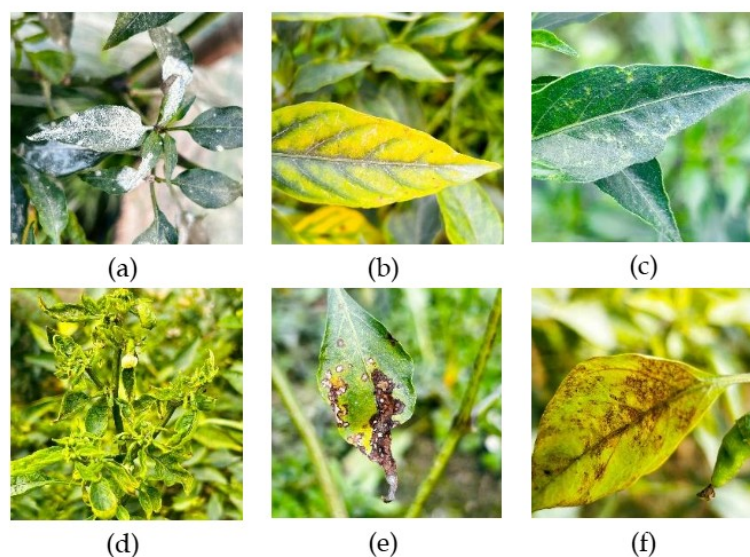


Figure 1. Sample of dataset (a) White Spot, (b) Nutrition Deficiency, (c) Healthy leaf, (d) Curl Virus, (e) Cercospora leaf spot, (f) Bacterial Spot

2. YOLO11n Model Architecture

YOLO11 is the latest evolution of the YOLO family integrating architectural innovations to improve detection accuracy, particularly for small object detection, while maintaining computational efficiency (Glenn Jocher & Jing Qiu, 2024). The YOLO11 architecture consists of three main components: backbone for feature extraction, neck for multi-scale feature fusion, and detection head for prediction. This structure allows the model to extract visual information, combine features from various resolution scales, and generate accurate predictions of disease location and type. The data processing flow is illustrated in Figure 2.

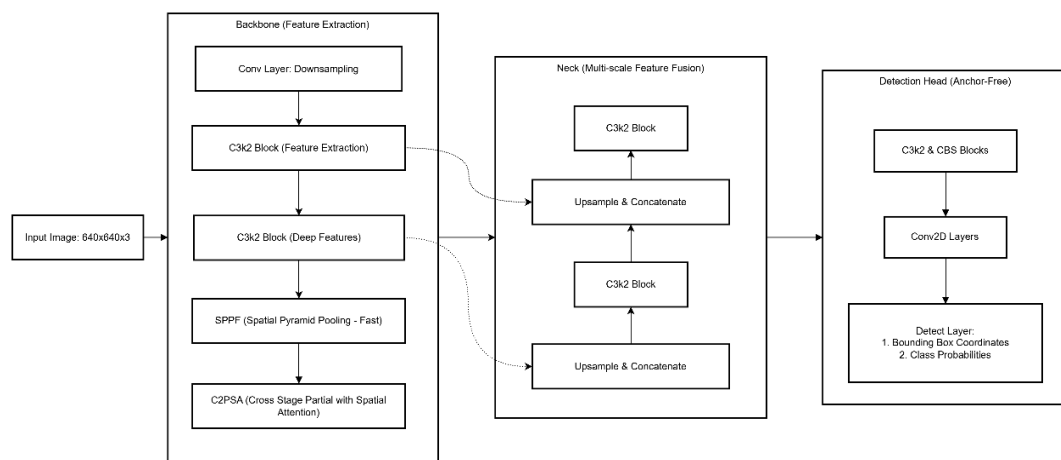


Figure 2. Schematic diagram of the YOLO11n architecture utilizing C3k2 and C2PSA modules for efficient detection

2.1 Backbone (Feature Extraction)

This component functions to extract visual features from the input image. YOLO11n introduces the C3k2 (*Cross Stage Partial with kernel size 2*) block to replace the C2f block used in previous versions. The C3k2 block utilizes a smaller kernel size to accelerate computation and reduce parameter count without compromising the quality of extracted features (Tariq & Javed, 2025). Additionally, there is the C2PSA (*Convolutional block with Parallel Spatial Attention*) module which applies a spatial attention mechanism. This module processes features to prioritize pixel areas containing important information, such as disease lesions, and reduce the influence of the background (Rahima Khanam & Muhammad Hussain, 2024).

2.2 Neck (Feature Fusion)

The Neck component is responsible for combining features from various network depth levels to handle object size variations. YOLO11n utilizes a PANet (*Path Aggregation Network*) structure that connects high-resolution features from the initial backbone layers with semantic features from the final layers (Hidayatullah et al., 2025). The dashed lines in the diagram indicate these feature concatenation paths. This process ensures the model simultaneously acquires detailed texture information to detect small-sized diseases and contextual information for larger diseases ((Rahima Khanam & Muhammad Hussain, 2024).

2.3 Detection Head (Final Prediction)

The Head component processes the combined features to generate the final output in the form of bounding boxes and disease class probabilities. YOLO11n employs an anchor-free approach, where the model directly predicts the object center and its dimensions without relying on pre-determined reference boxes (*anchor boxes*) (Hidayatullah et al., 2025). Furthermore, the detection process is performed separately (*decoupled head*), splitting the tasks of object location determination and disease type classification into different processing paths to improve the accuracy of each task (Rahima Khanam & Muhammad Hussain, 2024).

3. Performance Evaluation Metrics

Quantitative evaluation of the YOLO11 model is conducted using standard object detection indicators to assess the network's capability in generalizing features from the training set to the test set. The primary metrics employed include Precision, Recall, and Mean Average Precision (mAP), which are derived from the confusion matrix elements: True Positives (TP), False Positives (FP), and False Negatives (FN).

3.1 Precision

Precision quantifies the accuracy of positive predictions generated by the model. It is defined as the ratio of correctly identified positive instances to the total number of positive predictions. This metric indicates the model's ability to minimize false positive detection errors (Rahminda & Oktaviany, 2025).

3.2 Recall (Sensitivity)

Recall measures the proportion of actual positive instances that are correctly identified by the model. A high recall value signifies the model's effectiveness in minimizing false negatives, ensuring that significant objects are not overlooked during inference (Zhang, 2025).

3.3 Mean Average Precision (mAP)

mAP is a comprehensive metric that calculates the average of the Average Precision (AP) values across all classes. In the context of YOLO11 evaluation, two specific variations are standard:

- **mAP@0.5:** This metric represents the mean average precision calculated at an Intersection over Union (IoU) threshold of 0.50. It assesses the model's performance under moderate localization strictness (Akansh Vishwakarma & Murugan A, 2025; Rahima Khanam & Muhammad Hussain, 2024).
- **mAP@0.5:0.95:** This metric computes the average mAP over a range of IoU thresholds from 0.50 to 0.95, with a step size of 0.05. It serves as a rigorous benchmark for evaluating the robustness of the model's bounding box localization accuracy (Rahima Khanam & Muhammad Hussain, 2024).

4. Training Loss Functions

The YOLO11 architecture employs a compound loss function to optimize network parameters during backpropagation. This function aggregates components responsible for bounding box regression, class probability prediction, and distribution precision to ensure model convergence.

- **Box Regression Loss (CIoU)** To optimize spatial localization, YOLO11 utilizes the Complete Intersection over Union (CIoU) loss. Unlike standard IoU, CIoU accounts for three

critical geometric factors: overlap area, central point distance, and aspect ratio consistency between the predicted box and the ground truth. This approach enhances the precision of bounding box regression and accelerates convergence during the training phase (Mao & Hong, 2025).

- Distribution Focal Loss (DFL) YOLO11 integrates Distribution Focal Loss (DFL) within its detection head to manage ambiguity in bounding box boundaries. DFL models the box coordinates as general distributions rather than deterministic values, allowing the network to focus on learning the probability density around the target labels. This mechanism is particularly effective for refining localization in scenarios where object boundaries are indistinct or occluded (Mao & Hong, 2025).
- Classification Loss (BCE/Focal Loss) For object classification, the model employs Binary Cross Entropy (BCE) or its variant, Focal Loss. These functions are designed to calculate the error between predicted class probabilities and ground truth labels. Focal Loss specifically addresses the issue of class imbalance by down-weighting the loss assigned to well-classified examples ("easy" samples) and focusing the training process on hard-to-classify examples, thereby preventing background dominance during training (Mao & Hong, 2025).

RESULTS

1. Training Data Distribution

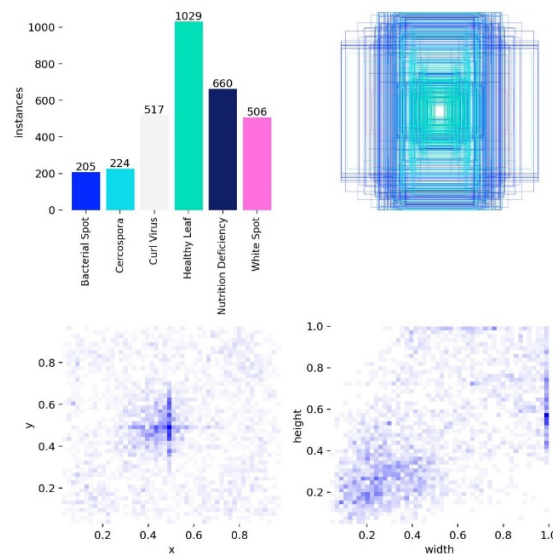


Figure 3. displays label distribution in the training dataset

Based on the Figure 3, the dataset is significantly dominated by the Healthy Leaf class with 1,029 instances, followed by Nutrition Deficiency (660) and Curl Virus (517), while classes such as Bacterial Spot and Cercospora represent the minority with around 200 instances each. The center coordinate (x , y) analysis confirms that the objects are primarily centered within the frames, while the width and height visualizations show a diverse range of bounding box sizes—from small scales to nearly full-frame—indicating that the model will be trained on varied camera distances and perspectives.

2. Training Process Summary

YOLO11n model training was conducted for 100 epochs using Tesla T4 GPU with CUDA 12.6 support on the Google Colab platform. Total training time required was 0.393 hours (approximately 24 minutes) to process 1,464 training images and 367 validation images. Training configuration used batch size 32, input resolution 640×640 pixels, and AdamW optimizer with initial learning rate 0.001. The training process showed stable convergence with consistent loss reduction. At the beginning of training (epoch 1), box loss, cls loss, and dfl loss values were 3.215, 4.308, and 4.214 respectively. At the end of training (epoch 100), these values decreased to 0.7899, 0.8856, and 1.344, indicating effective learning by the model.

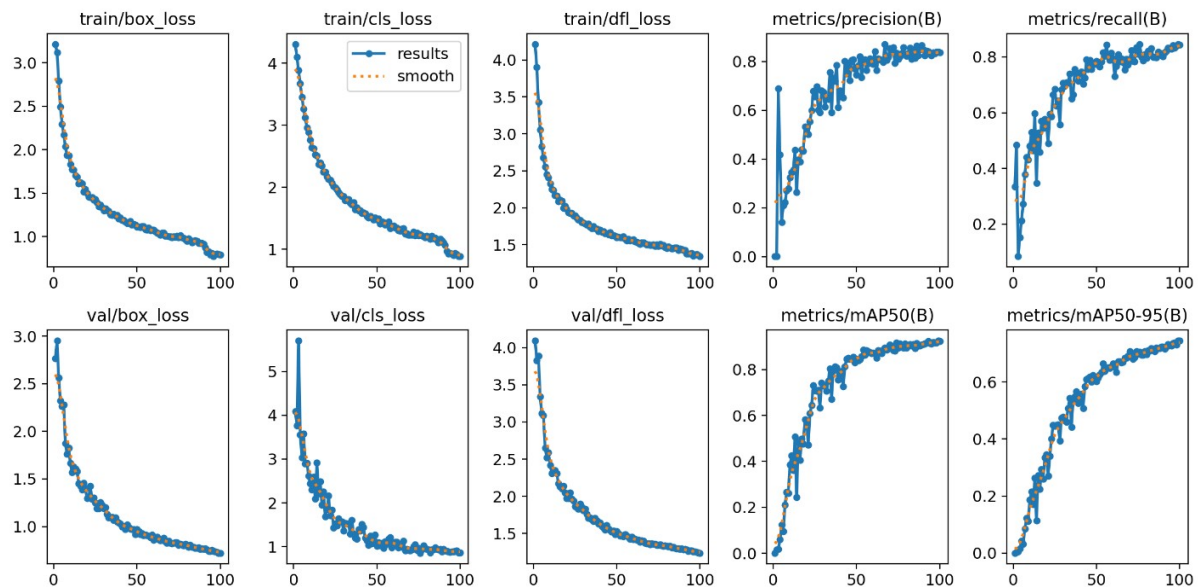


Figure 4. Training and validation metrics progression graph over 100 epoch

3. Overall Model Performance Analysis

The YOLO11n model achieved excellent detection performance on the chili leaf disease dataset. Table 1 presents a summary of overall model evaluation metrics on the validation set consisting of 367 images with 525 object instances. The mAP@0.5 value of 92.3% indicates that the model is capable of detecting and localizing chili leaf diseases with high accuracy at the standard IoU threshold of 0.5. The mAP@0.5:0.95 value of 74.5% reflects model performance at various localization precision levels, which is a stricter and more comprehensive metric.

Table 1. Model Evaluation Metrics

Metric	Value
Precision	0.837
Recall	0.843
mAP@0.5	0.923
mAP@0.5:0.95	0.745
F1-Score	0.840
Inference Speed	
Preprocessing	0.2 ms/image

Inference	1.9 ms/image
Post Processing	1.6 ms/image
Total	3.7 ms/image
Model Complexity	
Parameters	2.582.322
GFLOPs	6.3
Layers	100

4. Per-Class Performance Analysis

Table 2 presents detection performance for each disease class and leaf condition. This analysis provides insight into model detection characteristics for each category.

Table 2. Per-Class Detection Performance on Validation Set

Class	Images	Instances	P	R	mAP50	mAP50-95
Bacterial Spot	32	34	0.797	0.971	0.959	0.856
Cercospora	48	53	0.841	0.799	0.896	0.702
Curl Virus	63	90	0.971	0.556	0.900	0.520
Healthy Leaf	104	170	0.752	0.824	0.890	0.747
Nutrition Deficiency	94	109	0.854	0.991	0.992	0.904
White Spot	30	69	0.809	0.920	0.902	0.739

Classes with Highest Performance:

- Nutrition Deficiency achieved the best performance with mAP@0.5 of 99.2% and mAP@0.5:0.95 of 90.4%. The very high recall (99.1%) indicates that almost all nutrition deficiency instances were successfully detected. Distinctive visual characteristics in the form of systemic color changes (chlorosis) facilitate model identification of this condition.
- Bacterial Spot showed excellent performance with mAP@0.5 of 95.9% and recall of 97.1%. The characteristic dark brown necrotic lesions with yellow halos provide visual features that are easy for the model to learn.

Classes with Detection Challenges:

- Curl Virus showed the highest precision (97.1%) but lowest recall (55.6%), indicating that although detections made were very accurate, the model missed almost half of existing instances. Morphological variability in virus induced leaf deformation is the main challenge.
- Healthy Leaf had the lowest precision (75.2%) but good recall (82.4%). Visual characteristic overlap with early-stage diseases can cause false positives.

5. Precision-Recall Curve Interpretation

The Precision-Recall curve in Figure 3 shows the trade-off between precision and recall for each class at various confidence thresholds. The Nutrition Deficiency and Bacterial Spot classes show the most ideal curves with AUC approaching 1.0, while Curl Virus shows significant recall decline with increasing confidence threshold.

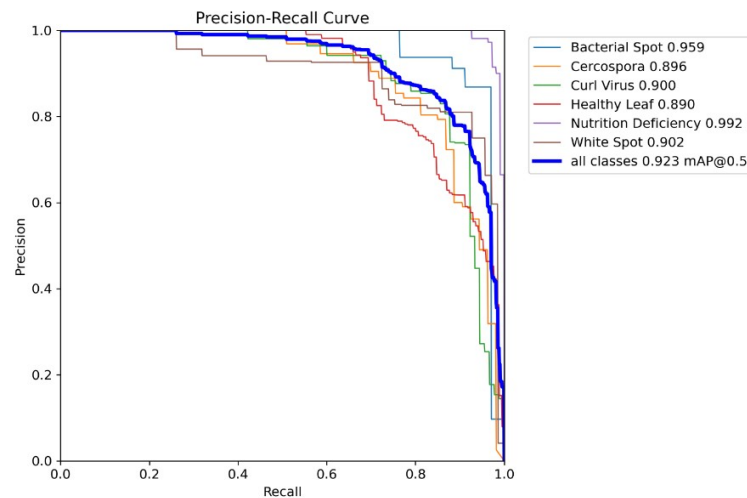


Figure 5. Precision-Recall curve for each class

6. F1-Confidence Curve Analysis

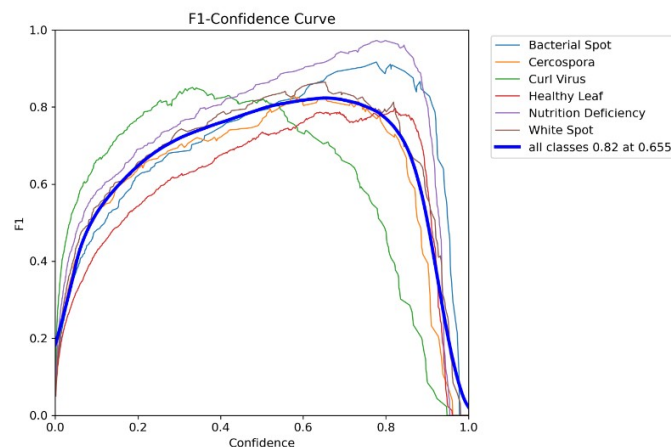


Figure 6. F1-Score versus confidence threshold curve for each disease class

Figure 5 displays the F1-Score versus confidence threshold curve. The optimal F1-Score point for the overall model is at a confidence threshold around 0.4-0.5, where the best balance between precision and recall is achieved.

7. Confusion Matrix Analysis

The confusion matrix in Figure 6 reveals model classification error patterns:

1. Dominant diagonal: High values on the diagonal indicate good classification accuracy for all classes.
2. Inter-class errors, There are several misclassification patterns:
 - Curl Virus sometimes goes undetected (background), contributing to low recall
 - There is slight confusion between Healthy Leaf and early-stage diseases
 - White Spot and Cercospora Leaf Spot have some visual overlap
3. False Negatives: The background column shows the proportion of undetected objects by the model for each class.

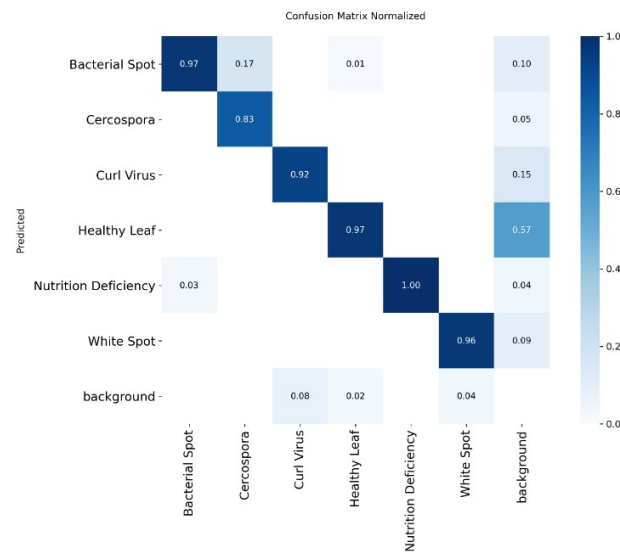


Figure 7. Normalized Confusion Matrix showing prediction proportion per class

8. Detection Results Visualization

Figure 5 displays example model detection results on validation images. The model successfully detected and localized various disease types with accurate bounding boxes and high confidence cores.

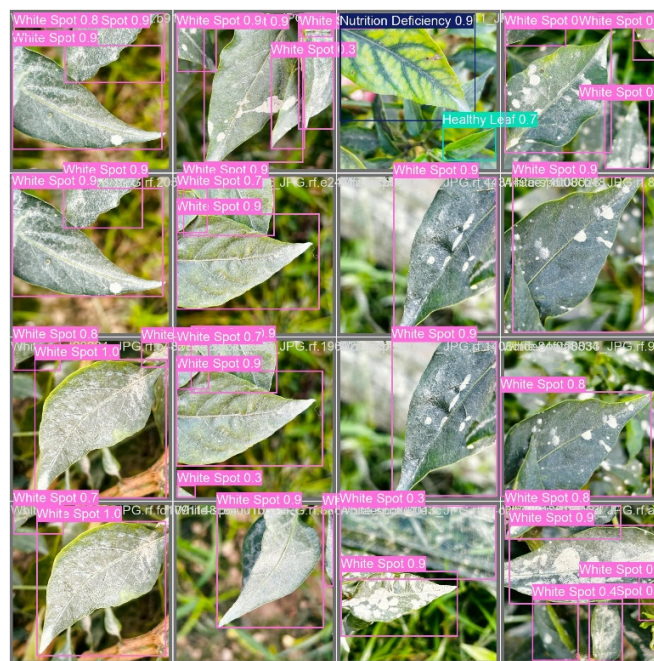


Figure 8. Example model predictions on validation batch, showing bounding boxes and confidence scores for each detection

CONCLUSION

This study successfully implemented and evaluated the YOLO11n model for automated detection of chili leaf diseases using the Chili Plant Leaf Disease and Growth Stage Dataset from Bangladesh (2025). The experimental results demonstrate that YOLO11n achieves strong detection performance with mAP@0.5 of 92.3% and mAP@0.5:0.95 of 74.5% across six leaf condition classes. These results confirm that lightweight object detection architectures can provide both high accuracy and computational efficiency for smart agriculture applications.

The model shows an effective balance between performance and efficiency, with only 2.58 million parameters and 6.3 GFLOPs. This lightweight configuration makes YOLO11n highly suitable for deployment on edge devices such as agricultural drones, mobile-based diagnostic applications, and IoT monitoring systems.

Per-class evaluation reveals that Nutrition Deficiency and Bacterial Spot achieve the highest detection performance due to their distinctive visual characteristics. In contrast, Curl Virus presents the greatest challenge, particularly in recall, indicating that morphological variability and subtle visual symptoms require further optimization strategies.

Overall, this research contributes to the development of efficient and practical deep learning-based plant disease detection systems under real-field conditions. Future work should focus on expanding dataset diversity to improve generalization across different agroecological regions, enhancing augmentation strategies to address difficult classes, and validating the model performance on real edge hardware platforms for practical deployment scenarios.

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