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The Accuracy and Efficiency of YOLO Algorithms in Identifying Plant Leaf Diseases

Milan Narendra Gohel[1], Dr. Hiren Kavathiya[2]
[1]Department of Computer Engineering, Atmiya University, India, milan.gohel@atmiyauni.ac.in
[2]Department of Computer Science, Atmiya University, India, Hiren.kavathiya@atmiyauni.ac.in

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Abstract

Plant diseases are one of the biggest challenges of world agriculture, leading to enormous output losses and economic damages. Early and accurate detection of these diseases may help to increase crop yield, improve resource efficiency, decrease costs and environmental impact and assist the production of high-quality food. In recent years, deep learning (especially computer vision approaches) has become a strong tool for a number of tasks such as picture classification, segmentation and object detection. Such techniques include the You Only Look Once (YOLO) family of neural networks, a state-of-the-art technology for accurate object detection. In this work, we use YOLOv5, YOLOv7 and YOLOv8 models for citrus disease detection with the CCL’20 dataset. During training, a number of data augmentation techniques are used to improve the model performance, such as picture translation, scaling, flipping and mosaic augmentation. The model performance was evaluated using the Mean Average Precision (mAP) for Intersection over Union thresholds from 50% to 95% (mAP@50–95). The results showed that the YOLOv8 model performed better than the other variations, with significant improvements compared to the benchmarks reported in previous studies. After hyper-parameter adjustment, the improved model reached a mAP@50-95 of 96.1% on the test set for detection of the citrus diseases. The model attained the mAP@50-95 of 95.3%, 96.0% and 97.0% for Anthracnose, Melanose and Bacterial Brown Spot respectively for each disease. Furthermore, the model could reliably identify both single and many cases of the same and different diseases inside a single image, illustrating the robustness of recent YOLO architectures. Finally, the trained YOLOv8 model has been successfully installed into the Roboflow platform which is ready for practical applications in citrus disease monitoring.

Keywords; Plant Disease Detection, Deep Learning, YOLOv5, YOLOv7, YOLOv8

INTRODUCTION

Agriculture is a backbone of national economic development through the rise of crop production. Plant disease early detection is crucial not only for global food security but also for preventing economic damages to farmers. Detection in time can prevent loss of yield, overuse of pesticides and other economic consequences and allows for early action. Agriculture is the source of food for human consumption and supplies critical feed for livestock and raw materials for the food processing industry. Plants as primary energy sources provide nutritional and therapeutic values. In the agricultural practice, the problem of plant disease detection is especially essential since the illnesses can arise at any stage of the crop growth and can cause significant reduction in both the yield and the economic value. Worldwide, plant diseases contribute for 10-16% of agricultural production losses, amounting to around $220 billion in economic effect. By 2050, food production would need to almost double, rising by over 70%, to feed a burgeoning population. The most serious crop losses occur in African countries, ranging from estimates of 20% to 40%. The challenges of food security are pressing issues worldwide and are increasing as a result of plant diseases, climate change and the scarcity of arable land.

Precision Agriculture uses sophisticated technologies, data analytics, and automation to increase crop yields while lowering resource use, cutting costs and and limiting environmental impacts. This means farmers may better target their use of water, fertilizers and pesticides to the correct places in need, at the right time.

“Early detection of plant diseases enables the detection of infected areas and helps a more strategic input management. Disease detection in conjunction with Precision Agriculture Technologies (PATs) can be connected with Variable Rate Technology (VRT) for precise allocation of resources and improved crop output. Traditional approaches like as manual field inspections for disease diagnosis are labor-intensive, time-consuming and impracticable for large-scale farming. The automatic detection task is more complicated due to the natural variation of leaf morphological features such as form, size, hue, direction and illumination. Reliable accuracy in disease recognition has been a challenge for traditional machine learning techniques. Thus, there is an urgent demand for enhanced deep learning approaches capable of identifying many incidences of similar or different diseases inside a single image. To overcome these difficulties, modern deep learning models have been proposed for plant disease detection with better performance and robustness. This work aims at assessing the effectiveness of YOLO-based models (YOLOv5, YOLOv7, and YOLOv8) for plant disease detection. These models are trained on a high-quality annotated dataset and are compared with benchmark studies. The research shows that YOLO structures can detect and pinpoint several occurrences of disease in a single image, and can handle changes in leaf form, size, color, orientation and lighting.The paper is organized as follows. The Related Work part presents the Evolution of YOLO models and Previous Literature on Plant Disease Detection. The dataset, pre-processing techniques, and model parameters are outlined in the Materials and Methods section. The Results and discussion section discusses results of model training, hyper-parameter optimization, comparison of performance, benchmark comparison and deployment considerations. And last, the Conclusion section gives insights from the study, and ideas for future research.

II. LITERATURE REVIEW

Many studies have been conducted on early detection of plant diseases and pests to avoid the spread and to reduce the crop losses. A CNN based model was created for citrus fruit and leaf diseases detection with 94.55% testing accuracy [1]. Also, CNN architectures like VGG16 and InceptionV3 have been employed for identification of rice diseases and pests with a mean validation accuracy of 97.12% [2]. Automatic categorization and detection of plant diseases using machine learning (ML) and deep learning (DL) algorithms have been widely employed in the literature [3]. Studies on two-stage and single-stage DL models for plant disease identification showed that DL methods have generally worked better than conventional ML approaches [4][5][6].

YOLO (You Only Look Once) is a fast and efficient one-stage object detection technique [7]. YOLO predicts the bounding box coordinates and class probabilities in one step, improving accuracy and processing efficiency. It blends numerous object detection modules into a single neural network, which allows it to grasp the context of the classes of objects and their appearance [8]. With the development of YOLO, there have been several improvements. YOLOv1 used the GoogleLeNet architecture and divided the input photos into grid cells, then improved the bounding boxes via Non-Maximum Suppression (NMS). Later variants used Darknet-19 and Darknet-53 backbones, anchor boxes with clustering algorithms, and multi-scale training to improve small object detection. It was further improved by adding CSPDarknet53 architecture, Cross Stage Partial (CSP) connections, Spatial Pyramid Pooling (SPP), Path Aggregation Network (PANet) and Self-Adversarial training (SAT) for better speed and accuracy.

YOLOv5 used CBS and C3 modules, focus modules, and SPP for backbone, top-down FPN and bottom-up PAN for multiscale feature detection, and enhanced data augmentation for better generalization [9]. Later, YOLO variations incorporated EfficientRep backbones, Rep-PAN, decoupled heads, and Task Alignment Learning (TAL) for optimal label assignment . YOLOv7 incorporated CSPVoVNet architecture, enhanced ELAN modules, compound model scaling and planned re-parameterization convolutions and batch-normalized convolutions and EMA models for more reliable inference. YOLOv8 improved the architecture with C2f modules, SPPF, a combined FPN-PAN multi-scale fusion module, and anchor-free detection, and used mosaic augmentation during training to improve performance [10]. These improvements in the YOLO have greatly increased the efficiency and accuracy of object identification and are very useful for plant disease detection. For example, the F1 score of 83.4% was attained for detecting turmeric diseases using modified YOLOv3-tiny with residual CNN layers [11]. The optimized YOLOv4 with EfficientNet obtained 95.3% of F1 and 96.4% of accuracy for citrus illnesses [12]. An enhanced YOLOv5 model with squeeze-and-excitation modules achieved an accuracy of 91.07% and mAP of 94.10% for detecting tomato virus infections [13]. YOLOv5l was utilized to detect citrus greening with a Micro F1 score of 85.19% [14]. Hybrid models comprising single-stage YOLO and two-stage models like Faster-RCNN achieved mAP of 85.2% [6].

However, single-stage models are better on larger datasets [15]. The improved YOLOv5s models achieved 93.1% mAP, better than YOLOv4-tiny and YOLOX-s. Multi-crop disease detection utilizing repeated augmentation, focused loss and early halting was achieved using a YOLOv5-CAct model with 94.24% mAP [15]. For jute disease diagnosis, YOLO-JD obtained 96.63% mAP, whereas lightweight YOLOv4 models with MobileNet v3 backbones reached 97.21% mAP for cucumber leaves [16]. Apple-YOLO (version of YOLOv5s) diagnosed apple leaf illnesses with 96.04% mAP at 34 FPS [17]. Comparative experiments with two-stage and single-stage models comprising CenterNet2 and Scaled YOLOv4 P7 showed high performance for citrus disease detection with mAP of 94.8% for Melanose and 93.9% for Bacterial Brown Spot [9]. YOLOv7 obtained 65% mAP for general plant disease detection [18]. An EfficientDet based model with SSD modules achieved 85.52% mAP [26]. Alternaria alternata and Thrips citrus illnesses were detected by YOLOv5 and Mask RCNN models with 99% average precision [19]. In tea leaf disease identification, YOLOv7 obtained 98.2% mAP, which outperformed CNN, Deep CNN, DNN, AX-RetinaNet, and improved DCNN [20]. In grape disease detection, Fusion Transformer (FTR) YOLO achieved 90.67% mAP [21].

Despite these developments, research gaps persist. Many research use limited or low quality datasets which can affect the model training and validation. To address the above shortcomings, this study uses a high-quality expert-annotated dataset of citrus diseases [5] to conduct a comprehensive evaluation of YOLO models for plant disease detection accuracy.

III. RESEARCH METHODOLOGY

A. Data Collection

The picture dataset employed in this investigation was taken from the Conghua Orchard located at Conghua District, Guangzhou, China and is specifically intended for citrus plant disease identification [5]. This unstructured dataset contains a total of 2,684 photos of which 427 images are of healthy leaves. It detects three major forms of diseases of citrus. Disease A - Anthracnose (37%) Disease B - Melanose (35%) Disease C - Bacterial Brown Spot.

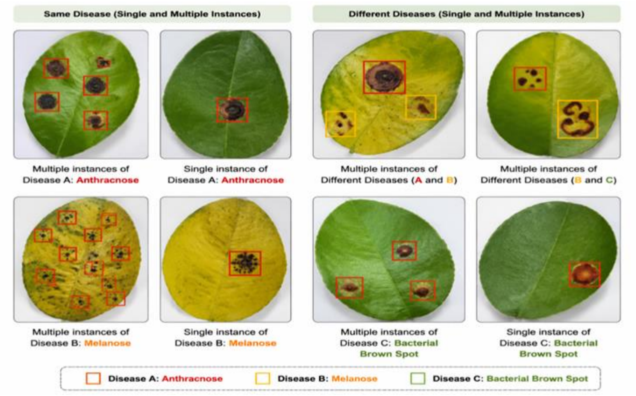
The dataset has a wide range of leaf properties such as variances in form, size, color, orientation and illumination conditions. Several photos have multiple cases of the same or distinct diseases on a single leaf, which represent actual world settings for disease identification. All photos are identified with professional annotations for precise disease identification. The dataset comprises a total of 10,332 annotations and is provided in both XML and JSON formats. This high quality dataset is available in the public domain for study and practical applications [22, 23].

B. Data Pre-processing

Data preparation is a very important step to improve the quality of data for better exploration and modelling. Preprocessing of unstructured data like photographs includes conversion of annotation files into a common format, structuring the information in a hierarchical fashion for learning algorithms and use of data augmentation techniques to prepare the images for training of the model.

In this paper the dataset is RGB photos of resolution 1000 × 1000 pixels. Annotations were transformed from JSON to YOLO Darknet text format . Healthy photos received null annotations. The YOLO text files have one line per item, with the numerical class label (beginning from zero) and the normalized center coordinates, height and breadth of the object. The normalization ensures that annotations are still consistent after the image has been scaled. The data is separated into training , validation and testing directories , each having subfolders for photos and labels according to the selected data split technique . We prepared a configuration file (data.yaml) specifying the paths to the training, validation and test photos, number of classes and an array of object names. The data set was separated into training, validation and test sets in the ratio of 70:20:10. The training set contains 1,878 RGB photos with 7,095 annotations in four classes, including 313 healthy leaf images.

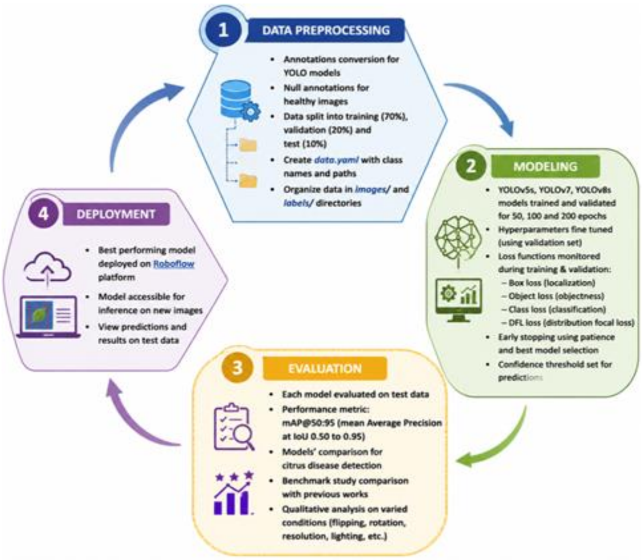
To further enrich the dataset and increase the generalization of the model, data augmentation was employed. These were horizontal and vertical flipping, rotation with random angles, clockwise and counterclockwise rotation with 90°, random blurring, padding, cropping, and color changes such as brightness, contrast, saturation and hue variations. Some examples of single and numerous occurrences of the same disease on a leaf, and single and multiple occurrences of various diseases on a leaf are shown in Figure 1.



C. Modeling

In the modeling stage, we train and test deep learning algorithms. We measure their performance with the Mean Average Precision (mAP) over Intersection over Union (IoU) levels from 50% to 95% (mAP@50–95). In this study, the preprocessed dataset of healthy and sick citrus leaves was used to train the YOLO variants YOLOv5s, YOLOv7 and YOLOv8s. The models were evaluated on different samples with the addition of flip, random rotation and resolution modification to validate the capacity of the models to detect diseases and mark the damaged regions on the images properly. Hyper-parameters were tuned and overfitting was avoided using validation datasets. The models were trained for 50, 100 and 200 epochs to see the performance at varied training lengths. Some of the loss measures seen during training and validation are:• Box loss: how well the algorithm predicts the center of an item and how well the anticipated bounding box covers the object.

- Object loss (objectness loss) – Probability of the object being in the suggested area of interest.
- Class loss (classification loss): Checks the capacity of the model to correctly categorize the detected object.
- Distributed Focal Loss (DFL): Treats the dense distribution of box centers as a discretized probability distribution for more accurate localization.The confidence threshold was specified as the minimum score at which a prediction was considered valid by the model. Additionally a patience parameter was set, which is the amount of epochs to wait without significant improvement before early ending the training, which guarantees the best performing model.The overall workflow is illustrated in Fig. 2 encompassing data preprocessing, model training, evaluation and deployment phases.



To evaluate the trained models, the mean Average Precision (mAP) measure over Intersection over Union (IoU) threshold from 50% to 95% (mAP@50–95) was used. This measure takes into account both precision and recall, as well as IoU. The measure of how many of the diseases found by the model were actually right is called precision. The measure of how many of the actual disease occurrences were detected by the model is called recall. These measurements together make mAP an unambiguous and fair metric of the models' ability to detect and localize plant illnesses in the images.

$$Precision = \frac{TP}{TP + FP} \qquad (Eq. 1)$$

$$Recall = \qquad TP$$

4

IoU (Intersection over Union) is a statistic used to find the overlap between two bounding boxes (usually the predicted and ground truth boxes) . It is computed as the ratio of the intersection area to the union area of the two boxes. The value of IoU is 1 when the projected bounding box perfectly matches the ground-truth, whereas the value of 0 implies no overlap at all. If they partially overlap, the IoU is between 0 and 1, which tells us how much the forecast and the real object agree.

$$IoU = \frac{\text{Intersection Area of Predicted Bounding Box and Ground Truth}}{\text{Union Area of Predicted Bounding Box and Ground Truth}} \quad (Eq.3)$$

The model will do well when both precision and recall are high. Average Precision (AP) is the area under the precision-recall curve. A threshold (e.g. 50 % IoU) is utilized to assess if a predicted bounding box counts as a genuine positive . To reduce bias, the IoU threshold is increased from 50% to 95% in 5% increments. The threshold can be changed and both accuracy and recall values can be plotted against each other, resulting in the precision-recall curve. AP@50–95, which is the average of AP values over this range, provides a full evaluation of how stable and consistent the model is at different thresholds, demonstrating how resilient it is in correctly identifying objects

Mean Average Precision (mAP) is the mean of the Average Precision (AP) values over all object classes and is an important evaluation metric for object detection tasks. We test the effectiveness of the models using mAP over IoU levels from 50% to 95% (mAP@50-95). A benchmark research was performed on the same dataset of citrus plant disease to assess the performance of multiple models in identifying plant illnesses [9]. This benchmark is used as a reference to evaluate the models developed in the present study. Benchmark findings showed that the CenterNet2 model had the best overall mAP of 91.4% across all disease classes. Specifically, the AP value of Melanose attained by CenterNet2 is 94.8%. The AP values of Anthracnose and Bacterial Brown Spot achieved by the Scaled YOLOv4 P7 model are 92.8% and 93.9%, respectively.Table 1 displays the mAP values of all models tested for each citrus disease. It also displays the best performing model for each disease specific category. These results are a good reference point and serve as a benchmark for the evaluation of performance improvements and the assessment of the YOLO-based models in this work.

Model	mAP (%)	Disease (AP (%))
Scaled YOLO v4 P7	89.3	Anthracnose (**92.8**), Bacterial Brown Spot (**93.9**)
CenterNet2	91.4	Melanose (**94.8**)

Here, each YOLO model YOLOv5s, YOLOv7, and YOLOv8s was trained for 50, 100, and 200 epochs, respectively, to evaluate the steady increases in performance. The benchmark study for citrus disease diagnosis also used a maximum of 200 epochs for the YOLO models [5].All experiments were conducted in an environment of Google Colab Python with a Tesla T4 GPU (15,102 MiB), 2 CPU cores and 12.7 GB of RAM. We rapidly implemented, trained, and evaluated the YOLO models using the essential Python modules such as PyTorch and Ultralytics.

RESULTS AND DISCUSSIONS

Models' Training and Hyperparameter Fine Tuning

The hyperparameters and training settings of the models were set as follow: IoU threshold of 0.6; Adam optimizer with the initial learning rate of 0.001; and the value of patience as 20 for early halting. batch size was 16, size of input images was 512 pixels, number of worker threads was 8, all optimized by available CPU resources. Other regularization options include weight decay (0.001), box loss gain (7.5), class loss gain (0.5) and object loss gain (0.7).

To improve model generalization and performance we used data augmentation. The augmentation settings comprised modifications in HSV color space with hue set at 0.015, saturation to 0.7 and value to 0.4. Spatial transformations were image translation 0.1, scaling 0.5, horizontal flipping with probability 0.5 and mosaic augmentation with probability 1.0. These setups ensured that models were trained on a diverse and robust dataset, increasing their capability to identify and classify citrus plant diseases effectively

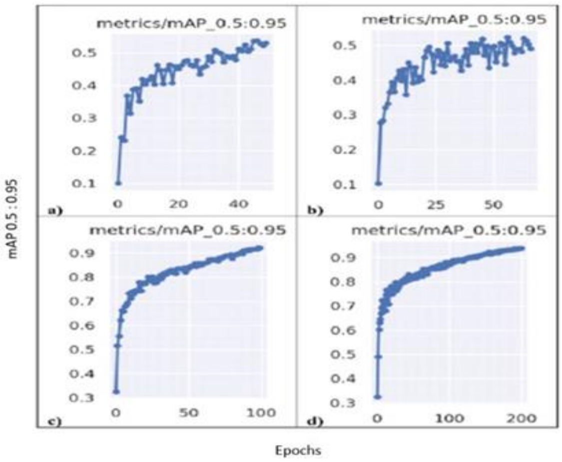


Figure 3. YOLOv5s training performance, mAP w.r.t epochs. a) for 50 Epochs, b) performance with early stopping at 67 Epochs, c) for 100 Epochs, and d) performance for 200 Epochs

Figure 3a depicts the performance metric of YOLOv5s trained for 50 epochs. The mAP@50-95 is 52.97% and the performance metrics graph displays spikes in the first epochs but these are lowering with the number of epochs and the performance is continuously growing. 2.18, 0.02 and 0.02 for training box loss, object loss and class loss, respectively. The validation box loss, object loss and class loss were 1.63, 0.01 and 0.02 correspondingly. The validation box and object losses are smaller than the training losses. The losses of boxes and objects for both training and validation are decreasing as the number of epochs increases. It is also observed that the class loss values are still dropping with number of epochs.

Figure 3b displays the performance characteristics of YOLOv5s early stopping at 67 epochs. The mAP@50-95 is 49.01% and the performance metric graph shows more spikes and model performance has declined with the number of epochs which suggests an issue in model training. The results show that the performance is diminishing with more epochs, so some hyperparameters are fine-tuned to optimize the model performance i.e., IoU threshold of 0.7, weight decay of 0.0005, box loss gain of 0.05, class loss gain of 0.5 and object loss gain of 1.0. The image augmentation parameters are fixed.

Figure 3c provides YOLOv5s performance metrics for 100 epochs. The mAP@50-95 is 92.17% and performance metric graph shows that mAP@50-95 is still increasing with number of epochs therefore model performance is improving progressively. While. Figure 3d: Evaluation metrics of YOLOv5s on 200 epochs. The mAP@50-95 is 93.82%, and the performance metric graph has been improved steadily compared to the previous findings.

Figure 4 shows the training and validation loss of YOLOv5s for 200 epochs. The training box loss, object loss and class loss are 0.0115, 0.0089 and 0.0001 correspondingly. The validation box loss, object loss and class loss are 0.0088, 0.0047 and 0.0001 correspondingly. The validation losses are less than the training losses. Box loss and object loss for training and validation are continuously reducing, class loss for training and validation converges to the minimum.

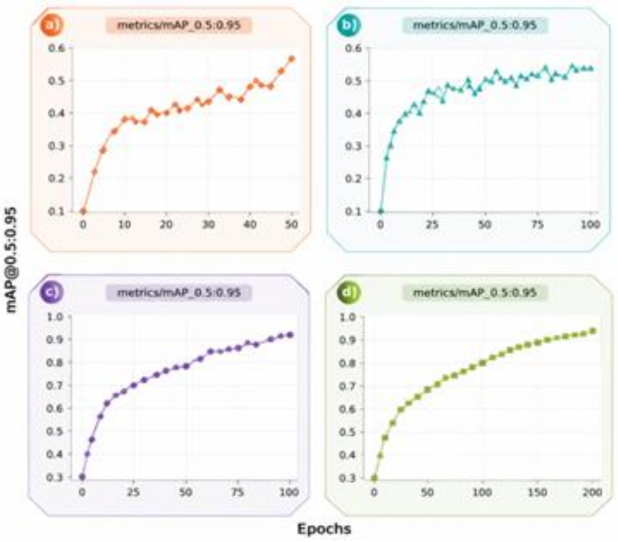


Figure 4. YOLOv5s Training and Validation Losses (200 Epochs)

The YOLOv7 model was trained for 50, 100 and 200 epochs with the following hyperparameters: confidence threshold 0.001, IoU threshold 0.7, Adam optimizer with an initial learning rate 0.001, batch size 16, input image size 512, weight decay 0.0005, box loss gain 0.05, class loss gain 0.3 and object loss gain 0.7.The YOLOv8s model was trained with the same amount of epochs and settings, except the loss-related parameters that were tuned to a box loss gain of 7.5, class loss gain of 0.5, and a distributed focal loss of 1.5. The image augmentation parameters for both the models were: HSV (hue=0.015, saturation=0.7, value=0.4), translation=0.1, scale=0.5, horizontal flip=0.5, mosaic=1.0.As expected, model performance improved with more epochs, although increases were slow (Figure 5). mAP@50-95 exhibited an increased trend across all models with extended training. Specifically, the mAP of YOLOv5s was 93.9%, which was 5.1% higher than the performance at 50 epochs, YOLOv7 was 92.7%, which was 4.6% higher than the performance at 50 epochs, and YOLOv8s was 96.8%, which was 3.0% higher than the performance at 50 epochs. The results indicate that further training and correct hyperparameter tuning can enhance the accuracy of citrus disease diagnosis.

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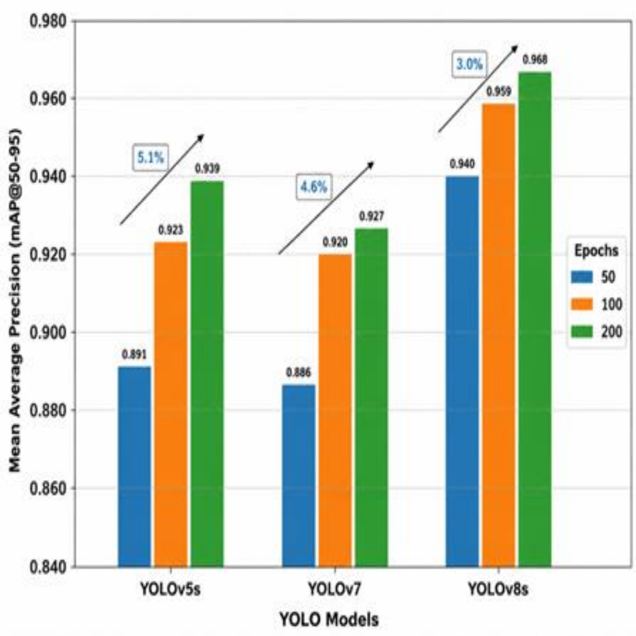


Figure 6. Overall mAP values for all diseases detection for train, test, and validation datasets of the 200 epochs trained models

Figure 7 shows the performance comparison of YOLOv5s, YOLOv7 and YOLOv8s models in recognizing each type of citrus illness in the test dataset. Among these, YOLOv8s consistently exhibited the greatest detection accuracy across all disease classes. Therefore, YOLOv8s is chosen as the top performing model on this dataset with mAP@50-95 values of 95.5%, 96.9% and 97.1% for Disease-A (Anthracnose), Disease-B (Melanose) and Disease-C (Bacterial Brown Spot), respectively. This also indicates the better ability of it to accurately detect different types of citrus leaf diseases.

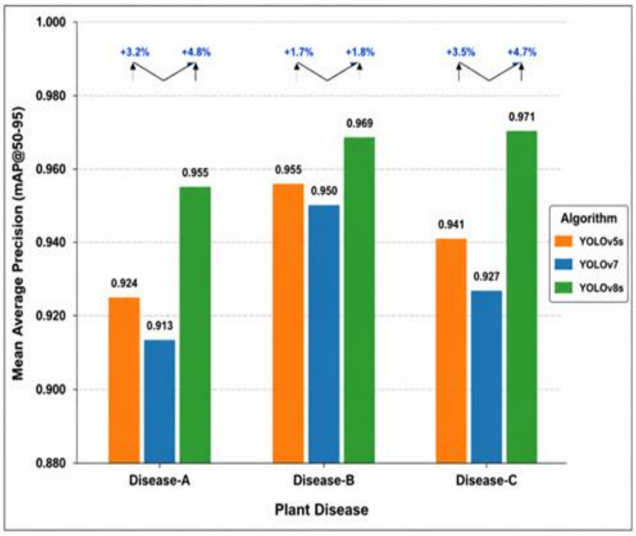


Figure 7. mAP Performance comparison of YOLOv5s, YOLOv7, YOLOv8s models for detection of each citrus disease on the test dataset

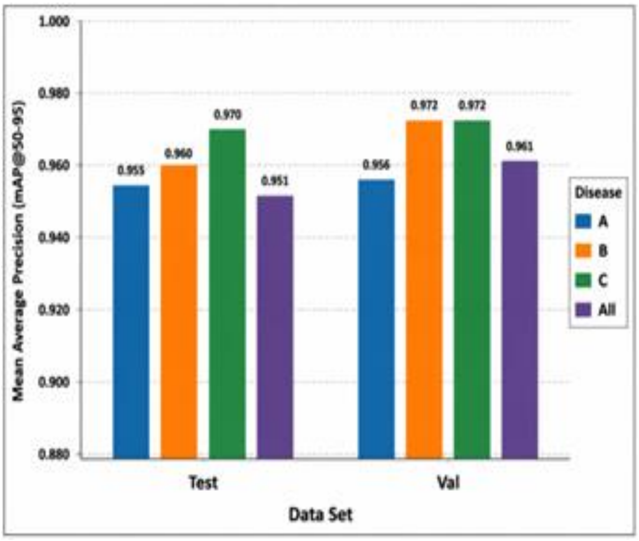


Figure 8. YOLOv8s final trained model mAP values for each disease on validation and test dataset

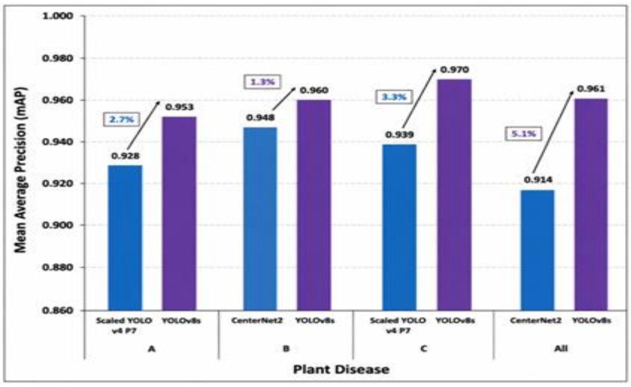
Figure 9. YOLOv8s model predictions after training for 200 epochs. As you can see, the model correctly detects and labels both healthy leaves and sick parts in the test photos. It can predict single or several instances of same or distinct diseases in a single image. It outputs bounding boxes with high confidence values. The experimental results show that the model is reliable and successful in identifying diseases of citrus plants under real-world situations

Figure 9. Predicted bounding boxes and labels with confidence value (YOLOv8s - Test Data)

The experimental results show that the YOLOv5s, YOLOv7, and YOLOv8s models trained for 200 epochs perform much better than the models trained for 50 or 100 epochs. Among these, the YOLOv8s model trained for 200 epochs had the best accuracy, topping YOLOv5s and YOLOv7 in both individual citrus illness detection and overall mean Average Precision (mAP) across all disease classes. The results suggest that longer training with well-tuned hyperparameters improves the models' capacity to identify and pinpoint illnesses in citrus plants reliably.

C. Comparison to Benchmark Study

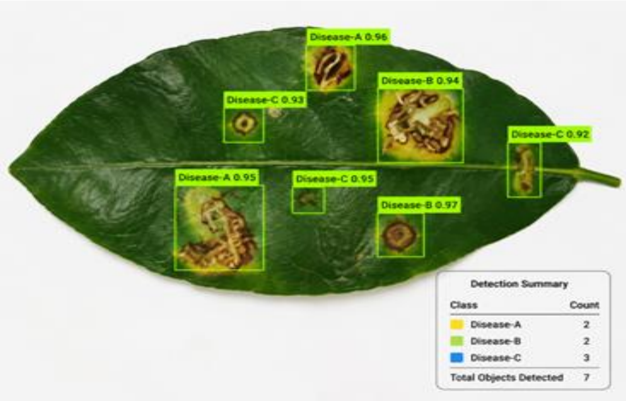
Figure 10 shows a comparison between the models from the benchmark study and the YOLOv8s model produced in this work for the detection of certain citrus illnesses. The results show that YOLOv8s performs better than the benchmark models and attains higher accuracy for each disease category. The YOLOv8s model achieves mAP values of 95.3%, 96.0%, and 97.0% for Disease-A, Disease-B, and Disease-C, respectively, indicating its powerful capacity to accurately detect individual diseases in the present dataset.



Performance comparison of the benchmark model, CenterNet2 and the YOLOv8s model established in this study for the detection of all citrus illnesses is shown in Fig. 10. The results show that YOLOv8s exceeds the benchmark, with a mean Average Precision (mAP) of 96.1%, which is 5.1% better than the CenterNet2 baseline. From these findings, it can be inferred that the YOLOv8s model gives better accuracy for individual disease identification and also better mean precision for all citrus plant illnesses in the CCL'20 dataset.

D. Model Deployment

The best model for citrus plant disease identification was selected as the YOLOv8s model [23] which was trained and verified for 200 epochs and is deployed on the Roboflow platform [24]. Figure 11. Web interface for uploading photos for automated detection of citrus plant diseases in the test dataset. This application reflects the model's practicality, offering an interactive and user-friendly tool for real-time illness identification



Detection Summary

Class	Count
🟨 Disease-A	2
🟩 Disease-B	2
🟦 Disease-C	3
Total Objects Detected	7

Figure 11. Web Interface of the deployed model

The system allows users for registration or sign in and uploading photographs for testing system by selecting Model option from side menu. You can use sliders to vary the confidence and overlap levels. You can use a dropdown menu to change the label display mode. Also the sample photographs of the test set are given to see the model performance in the detection of citrus plant illnesses instantly. The main goals of this investigation have been successfully met. The models YOLOv5s, YOLOv7 and YOLOv8s were successfully designed to detect and localize numerous copies of the same or distinct diseases in one image. The models are resilient to changes in leaf form, size, colour, orientation and illumination conditions. The model performance was extensively assessed using mean Average Precision (mAP@50-95%). Among the models, YOLOv8s was put on a web interface that allowed real-time display of the detected citrus plant illnesses on the test dataset.

IV. CONCLUSION

In the current work, the models YOLOv5, YOLOv7 and YOLOv8 were used for detecting illnesses in citrus plants. Among them, YOLOv8s achieved the highest detection accuracy, with a mAP@50–95% of 96.1% for overall citrus disease detection and mAP@50–95% values of 95.3%, 96.0%, and 97.0% for Anthracnose, Melanose, and Bacterial Brown Spot, respectively. This model can be a useful tool for farmers to detect diseases, identify the areas afflicted improve the yield of crops, optimize the use of resources, cut costs and minimize environmental impact. It is also capable of being integrated with Precision Agriculture Technologies (PATs).

The lightweight YOLOv8s variant is especially well suited for implementation on IoT devices such as precision agriculture instruments. The rest of the bigger YOLO variants, YOLOv8m, YOLOv8l and YOLOv8x, can be trained on bigger datasets for more complex detection scenarios. Experimental findings show the high speed and accuracy of the model, but more validation is necessary to guarantee dependable real-time performance under field circumstances.

In future model should be trained and tested on different dataset with different type of disease and plant species. Integration with PATs may include airborne crop monitoring through high definition drone photography and field mapping utilizing Global Navigation Satellite System (GNSS) technology. The applications would allow for exact identification of affected regions, targeted pesticide treatment, effective disease management and eventually, increased agricultural yields.

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