



## Deep learning-based detection of co-occurring diseases in mustard (*Brassica juncea*) crop using YOLOv11

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### ABSTRACT

Mustard [*Brassica juncea* (L.) Czern.] is an essential crop in agriculture, but its yield is often restricted by different kind of diseases, affecting both farmers and the edible oil industry. Recent advancements in artificial intelligence have transformed plant disease detection by enabling precise identification of various diseases. However, their detection and management become more challenging when crops are affected by multiple co-occurring diseases. To address this challenge, present study was carried out to implement deep learning algorithm for precise detection of co-occurring disease in mustard crop. A dataset consisting of 329 diseased leaf images of mustard crop with co-occurring symptoms of *Alternaria* blight and white rust diseases were collected during the 2023–2024 from the experimental fields of ICAR-Indian Agricultural Research Institute, New Delhi. Dataset processed through annotation and augmentation to boost detection accuracy of the network. A YOLO-based detection model (YOLOv11 and its variants) was trained and validated. Their performance was evaluated using the test dataset. Among the YOLOv11 variants, YOLOv11-x showed the highest performance by achieving mAP@50 score of 96.2% with average F1-score of 93.8% on validation data, performing 4.8% relatively better than the least complex model (YOLOv11-n), highlighting its superior detection capability. Furthermore, YOLOv11-x also surpassed previous YOLO models (YOLOv8, YOLOv9, and YOLOv10) in detection accuracy. The experimental results demonstrated the effectiveness of YOLOv11 for co-occurring disease detection in mustard crops.

**Keywords:** Artificial intelligence, Deep learning, Disease detection, YOLOv11 architecture

Mustard [*Brassica juncea* (L.) Czern.] is a vital oilseed crop, valued for its edible oil, protein-rich animal feed, and use as a condiment. Oilseed crops constitute a significant portion of India's agricultural sector, accounting for approximately 19% of the global cultivated area. However, their contribution to total global production remains comparatively low, at only 2.7% (Mishra *et al.* 2024). The mustard crop is highly vulnerable to various diseases that limit its growth and productivity. Crop diseases interfere with normal growth patterns, disrupt essential physiological processes, and damage plant structures, thereby adversely affecting farmers who depend on these crops for their livelihood and trade. In many instances, different pathogens target multiple plant structures, including stems, leaves and roots, leading to complex interactions and often worsening the overall damage. Such infections

are common in environments where multiple pathogens coexist, and crops are vulnerable to their combined effects. Mustard is also affected by fungal infections such as *Albugo candida*, which causes white rust, and *Alternaria brassicicola*, responsible for *Alternaria* blight, occurring at same time. These pathogens are prevalent in mustard fields, causing significant crop losses (Meena *et al.* 2011, Gupta *et al.* 2023) with reported losses reaching up to 70% in the case of *Alternaria* blight (Monika and Kidwai 2017) and 17–34% for white rust (Vignesh *et al.* 2011). Moreover, the co-occurrence of multiple diseases in crops remains underexplored for accurate diagnosis and effective disease management.

Advancements in artificial intelligence (AI), with specific emphasis on deep learning and computer vision have significantly improved the precision and efficiency of plant disease detection, enabling accurate identification of multiple diseases from complex image patterns (Haque *et al.* 2022). In computer vision, the introduction of the YOLO (You Only Look Once) object detection model (Redmon *et al.* 2016) marked a significant advancement in real-time detection frameworks. The unified detection strategy of YOLO significantly improves computational

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efficiency and detection speed, making it highly suitable for automated crop disease diagnosis applications (Hussain and Khanam 2024). Several deep learning-based models have been developed for mustard disease identification. Hridoy *et al.* (2022) proposed the MPNet architecture for mustard disease detection. Sharma *et al.* (2021) introduced a deep learning framework combining convolutional and recurrent networks for assessing downy mildew severity, and Jain *et al.* (2024) developed a CNN-based model to estimate white rust severity.

Despite the increasing use of deep learning in plant disease detection, important gaps remain in both model capability and problem complexity. Many studies have applied YOLO-based object detection models such as YOLOv3, YOLOv5, and YOLOv8 for crop insect and disease identification. However, these studies mainly focus on single-disease detection that do not address the more challenging scenario where multiple diseases occur simultaneously on the same plant tissue. Moreover, the latest YOLO architecture, YOLOv11, which incorporates advanced attention-based module and enhanced multi-scale detection heads, remains unexplored for mustard disease detection, particularly in co-occurring multi-disease scenarios. Further, non-YOLO detection models such as Faster R-CNN and SSD, although capable of localisation, have higher computational cost and slower inference, which limits real-time use. In contrast, classification models like ResNet, DenseNet, MobileNet, and Xception assign a single label per image and cannot detect or localise multiple co-occurring diseases on the same leaf. To address these gaps, the present study developed a novel field-collected dataset exclusively capturing co-occurring *Alternaria* blight and white rust on the same mustard leaf under real field conditions. The study validated multiple trained YOLO variants (YOLOv8, YOLOv9, and YOLOv10) on co-occurring disease dataset and compare against YOLOv11 evaluating detection accuracy, localisation precision and inference efficiency.

## MATERIALS AND METHODS

To develop an effective disease detection model, images of mustard leaves infected with *Alternaria* blight and white rust were collected and preprocessed through annotation and augmentation (Fig. 1), followed by training and validation of YOLO-based detection models on the prepared dataset.

For this study, image data were collected during the winter (*rabi*) season of 2023–24 from mustard crop fields at the ICAR-Indian

Agricultural Research Institute (28°38'23" N, 77°09'27" E; at an elevation of 228.6 m amsl), New Delhi. The mustard crop was grown under typical field conditions representative of the Indo-Gangetic plains. Images were captured at multiple growth stages of the crop, specifically from the vegetative stage through the flowering and pod-filling stages, as these represent the critical periods of maximum disease incidence and progression for both *Alternaria* blight and white rust. Images of mustard diseases were captured using a OnePlus Nord CE2 smartphone equipped with a 64 MP main rear camera and an 8 MP ultra-wide-angle lens. All images were captured under natural field illumination during morning and mid-morning hours (8:00–11:00 AM) to ensure consistent, well-balanced natural lighting and to minimise shadow interference. A dataset of mustard leaves simultaneously infected with white rust and *Alternaria* blight were collected, including samples where both diseases co-occur on the same leaf. Disease identification and annotation were performed under the direct supervision of plant pathology experts, ensuring accurate ground-truth labeling of both diseases. The final dataset comprised 329 annotated images, each containing instances of both diseases present simultaneously on the same leaf.

Image preprocessing was performed to standardise image quality and improve detection performance. All collected leaf images were resized to 2,048 × 2,048 pixels and annotated using Labellingm annotation tool, generating bounding box coordinates in YOLO (.txt) format. The initial dataset comprised 329 images containing 2,200 *Alternaria* blight and 3,070 white rust instances. To enhance dataset diversity and improve model generalisation, six augmentation techniques were applied to each image, including rotation (90° and 180°), horizontal and vertical flipping, and brightness and contrast adjustments. Since the original dataset consisted of only 329 images, augmentation was necessary to mitigate overfitting and improve model robustness. The augmented images were combined with

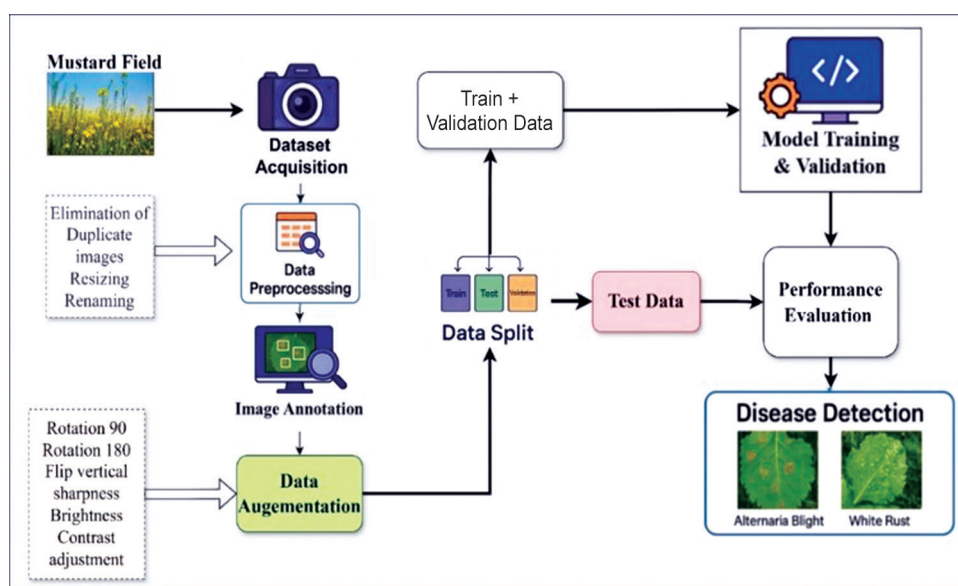


Fig. 1 Workflow of detection model for co-occurring diseases in mustard crop.

the original dataset, resulting in a total of 2,303 images (approximately a  $7\times$  increase), with corresponding annotations comprising 15,400 *Alternaria* blight and 21,490 white rust instances. During augmentation, spatial transformations such as rotation and flipping altered object positions within the image; therefore, a dedicated pipeline was implemented to ensure that the bounding box coordinates were consistently transformed in alignment with the augmented images. The dataset was then split into training, validation, and test sets in an 85:10:5 ratio.

In 2016, Redmon *et al.* (2016) introduced YOLO detection framework. Unlike two-stage region-based detectors that decouple region proposal and classification, YOLO formulates detection as a unified regression problem, directly predicting bounding box coordinates and class probabilities from the full image using a single convolutional neural network. Specifically, the input image is divided into grid, where each grid cell is responsible for predicting a fixed number of bounding boxes along with corresponding confidence scores and class probabilities. This unified formulation reduces computational redundancy and eliminates intermediate processing steps, resulting in an efficient detection pipeline with significantly improved inference speed compared to earlier complex detection frameworks (Du 2018).

YOLOv11, introduced by Jocher and Qiu (2024), represents an advanced evolution of the Ultralytics YOLO family, designed to achieve an optimal balance between detection accuracy, computational efficiency, and real-time performance. The architecture (Fig. 2) follows a systematic three-stage design consisting of a backbone, neck, and detection head, where each component plays a distinct role in feature extraction, aggregation, and prediction.

This unified and optimised architecture enables

YOLOv11 to deliver superior localisation precision, improved small-object detection, and faster inference performance, making it highly suitable for complex real-world detection tasks such as multi-disease identification in agricultural crops.

The detection performance was evaluated using standard object detection metrics, including Precision (P), Recall (R), F1-score, Average Precision (AP), and Mean Average Precision (mAP). The F1-score, representing the harmonic mean of precision and recall while average precision measures the area under the precision-recall curve for each class.

$$P = \frac{TP}{TP + FP}$$

$$R = \frac{TP}{TP + FN}$$

Where TP, True positives; FP, False positives; FN, False negatives.

$$F1 = 2 \times \frac{P \times R}{P + R}$$

$$P = \int_0^1 P(r) dr$$

Mean Average Precision (mAP) is calculated as  $mAP = \frac{1}{n} \sum_{i=1}^n AP_i$ , averaging AP across all classes. Higher values of these metrics indicate improved detection accuracy and localisation performance.

The experimental analysis was conducted on an NVIDIA DGX system powered by an AMD EPYC 7742 64-Core processor with NVIDIA A100-SXM4-40GB GPUs running Ubuntu 20.04 LTS. The deep learning environment utilised

Python 3.8.10, PyTorch 2.4.1, and Jupyter Notebook. The YOLO models were trained on annotated datasets using optimised hyperparameters, including an image size of 640, 500 epochs, batch size of 9, SGD optimiser with a learning rate of 0.01, momentum of 0.937, weight decay settings, and a patience value of 200, ensuring stable convergence, improved generalisation, and enhanced detection performance.

## RESULTS AND DISCUSSION

This study utilised a dataset comprising 329 annotated images of mustard leaves, featuring 2,200 instances of *Alternaria* blight

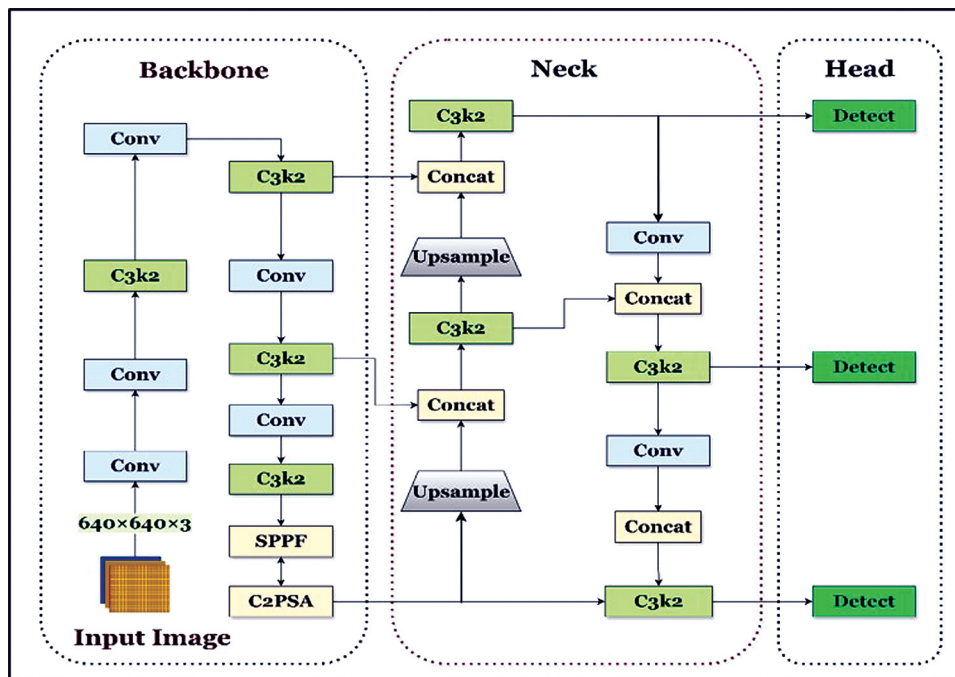


Fig. 2 Architectural design of YOLOv11 detection network.

and 3,070 instances of white rust. To enhance model generalisation and detection performance, advanced data augmentation approaches were implemented. We trained YOLOv11 models of different scales: Nano (n) - minimalistic, Small (s) - efficient, Medium (m) - standard, Large (l) - enhanced, and Extra Large (x) - powerful. The architecture of each model is characterised by differing layer counts and parameter sizes, which define its computational complexity and impact its capacity for feature extraction and detection accuracy. We also conducted a comparative analysis with preceding YOLO model (YOLOv10, YOLOv9, and YOLOv8) to assess advancements in detection accuracy and computational efficiency.

Each YOLOv11 variant was trained for 500 epochs and evaluated using precision, recall, F1-score, mAP @50, and mAP @50–95 to ensure a consistent and comprehensive comparison under identical validation settings. The results (Table 1) indicated a clear performance progression with increasing model capacity. Among all variants, YOLOv11-x demonstrated the best overall performance, achieving the highest F1-score (0.938), which reflects an optimal balance between precision (0.967) and recall (0.911). This balance is important in disease detection tasks where both accurate identification and minimal missed detections are critical. In contrast, YOLOv11-n recorded the lowest F1-score (0.874), due to comparatively lower precision (0.903) and recall (0.847) which can be attributed to its lightweight architecture. YOLOv11-l also showed competitive performance, matching YOLOv11-x in recall (0.911) and achieving one of the highest mAP @50 values (0.963), indicating strong localisation capability. A notable improvement was observed in mAP @50–95, which increased from 0.641 in YOLOv11-n to 0.859 in YOLOv11-x, highlighting enhanced robustness and generalisation across varying IoU thresholds. Although YOLOv11-m and YOLOv11-l reported similar mAP @50 values (0.963), YOLOv11-x surpassed them in mAP @50–95, reinforcing its superior performance under stricter evaluation criteria.

From a computational perspective, the YOLOv11 family demonstrated a well-defined trade-off between model complexity and detection performance, characterised by variations in the number of parameters, GFLOPs, and training time/epoch. The lightweight YOLOv11-n variant, with 2.59M parameters and 6.4 GFLOPs, offers high computational efficiency, achieving the fastest inference speed (1.6 ms) along with a moderate training time of

49.30 sec/epoch. This makes it particularly suitable for real-time applications and deployment on edge devices with limited computational resources. As the architecture scales to larger variants, there is a substantial increase in parameters and computational operations, leading to improved feature representation and detection accuracy. For instance, YOLOv11-s and YOLOv11-m, with 9.43M and 20.05M parameters, respectively exhibited increased GFLOPs (21.6 and 68.2), enabling better learning of complex patterns while maintaining reasonable training times (35.87 sec and 38.69 sec/epoch). This trend agreed with Ramos and Sappa (2025) who also reported improved precision, recall and mAP with increasing model size for YOLOv11 in tomato leaf disease detection. However, Khan *et al.* (2025) reported opposite trend where the smallest YOLOv8n model performed best for large weed plants in cotton, but showed lower accuracy for small weeds.

Further scaling to YOLOv11-l (25.31M parameters, 87.3 GFLOPs) and YOLOv11-x (56.88M parameters, 195.5 GFLOPs) introduced higher computational demand due to increased network depth and representational capacity. This scaling improved the model's ability to capture fine-grained spatial features and enhances localisation precision. Despite this increase, YOLOv11-x maintained a practical inference time of 6.0 ms and a training time of 47.95 sec/epoch, indicating efficient utilisation of computational resources relative to its performance gains. Fig. 3 presents both the input images and the corresponding detection outputs generated by the YOLOv11-x model, clearly demonstrating its capability to identify co-occurring diseases within the same mustard leaf. The output images illustrate precise localisation through well-defined bounding boxes over infected regions, along with associated class labels and confidence scores. It can be observed that the model successfully detected multiple instances of *Alternaria* blight and white rust simultaneously, even when the symptoms overlap or appear in close proximity.

The comparative results (Fig. 4) provided a clear evaluation of detection performance across YOLOv8, YOLOv9, YOLOv10, and YOLOv11 using key metrics, including precision, recall, F1-score, mAP @50, and mAP @50–95. YOLOv11 attained a precision of 0.981, which reflects relative improvement of approximately 10.6% over YOLOv8 (0.887), 13.5% over YOLOv9 (0.864), and 1.9% over YOLOv10 (0.963). This indicates a substantial reduction in false positive detections and improved classification

Table 1 Performance and computational complexity comparison of YOLOv11 variants

| Model     | Parameters (M) | GFLOPs | Precision | Recall | F1-score | mAP @50 | Time/Epoch (sec) |
|-----------|----------------|--------|-----------|--------|----------|---------|------------------|
| YOLOv11-n | 2.59           | 6.4    | 0.903     | 0.847  | 0.874    | 0.918   | 49.30            |
| YOLOv11-s | 9.43           | 21.6   | 0.953     | 0.905  | 0.928    | 0.968   | 35.87            |
| YOLOv11-m | 20.05          | 68.2   | 0.963     | 0.906  | 0.934    | 0.963   | 38.69            |
| YOLOv11-l | 25.31          | 87.3   | 0.955     | 0.911  | 0.933    | 0.963   | 65.12            |
| YOLOv11-x | 56.88          | 195.5  | 0.967     | 0.911  | 0.938    | 0.962   | 47.95            |

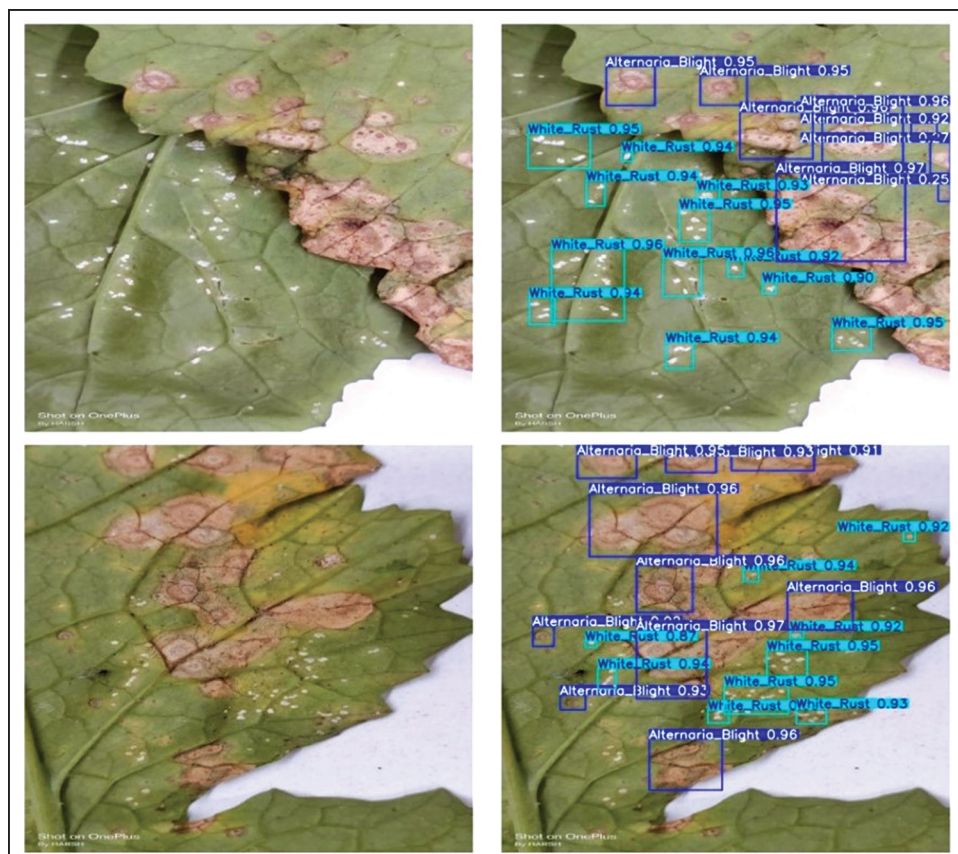


Fig. 3 Visualisation of plant disease detection using YOLOv11-x model.

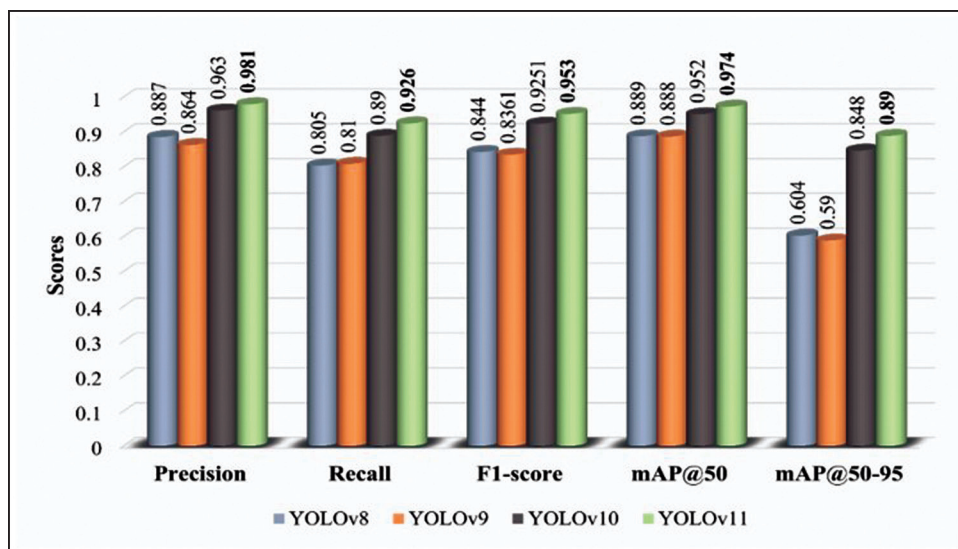


Fig. 4 Comparison of the best-performing YOLOv11 variants with other YOLO variants across key metrics on test data.

reliability. In terms of recall, YOLOv11 achieved 0.926, representing relative increase of about 15.0% compared to YOLOv8 (0.805), 14.3% over YOLOv9 (0.810), and 4.0% over YOLOv10 (0.890). This improvement highlights the model's enhanced ability to correctly identify disease instances, minimising missed detections. The F1-score further confirmed this balance, where YOLOv11 attained 0.953, relatively outperforming YOLOv8 (0.844) by 12.9%, YOLOv9 (0.836) by 14.0%, and YOLOv10 (0.925)

by 3.0%, demonstrating a well-optimised trade-off between precision and recall. A similar pattern is evident in localisation performance. YOLOv11 achieved a mAP @50 of 0.974, which represents approximately 9.6% proportional improvement over YOLOv8 (0.889), 9.7% over YOLOv9 (0.888), and 2.0% over YOLOv10 (0.952). For mAP @50–95, YOLOv11 achieved 0.890, showing a substantial 47.4% increase over YOLOv8 (0.604), 50.8% over YOLOv9 (0.590), and 4.9% over YOLOv10 (0.848). This performance indicates better generalisation and more precise bounding box regression across varying IoU thresholds.

In conclusion, the results showed improved detection performance with increasing model capacity, where YOLOv11-x achieved the highest precision (0.967) and recall (0.911), while YOLOv11-s achieved the highest mAP @50 (0.968), and YOLOv11-n showed comparatively lower performance. These findings highlight the trade-off between computational efficiency and detection accuracy across variants. Furthermore, evaluation on the test dataset showed that YOLOv11 outperformed earlier YOLO versions, achieving a mAP @50 of 0.974 and mAP @50–95 of 0.890. These results

highlight the superior performance of the YOLOv11-x variant in accurately detecting and localising co-occurring disease instances.

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