Precision Phenotyping for Weight Prediction in Soybean

Yu-Hang He, Lan-Qi Sun, Qi-Yuan Zhang, Wen-Hao Su,*

College of Engineering, China Agricultural University, 17 Qinghua East Road, Haidian, Beijing 100083, China

*Corresponding author: wenhao.su@cau.edu.cn

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Abstract.

Rapid, non-destructive quantitative analysis of plant architecture is crucial for accelerating soybean crop breeding and optimizing field management. This study developed a high-throughput phenotyping framework that integrates advanced computer vision with machine learning techniques, enabling the automatic extraction of complex morphological traits and accurate yield prediction at the individual-plant level. By incorporating the "Reparameterized Convolution" (RepConv) and "Cross-Stage Parallel Convolution" (CSPPC) modules, the framework enhances feature extraction and edge detection while preserving inference efficiency. It achieved a mean average precision (mAP) of 91.1% for pod detection and 94.0% accuracy for stem/branch recognition. A regression ensemble model, built on pod count, estimated seed number, and stem-branch biomass area, delivers high-precision predictions of individual plant weight, effectively capturing non-linear relationships between architecture and yield. The system further supports vertical distribution quantification at 10-cm intervals, aiding in the selection of lodging-resistant varieties and the optimisation of combine harvester cutting height to reduce field losses.

Keywords.

Soybean crop; Phenotyping,;Machine learning, Yield prediction.

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Introduction

In soybean breeding research, the rapid, high-throughput acquisition of soybean phenotypes is a critical step; however, traditional methods have often been overly labor-intensive, inefficient, and costly (Okada et al., 2024). Consequently, the use of neural network models for high-throughput soybean phenotyping has gradually become a trend (Wang et al., 2025). By capturing plant images or spectral data using automated imaging equipment and combining them with deep convolutional neural network algorithms, it is possible to extract features from field plants (Falk et al. , 2020). Learning deeper and more abstract features has significantly improved the efficiency and accuracy of phenotyping. Furthermore, the multi-organ phenotypic traits of soybean plants (such as pods and stems) are closely correlated with individual plant weight (Patrício et al., 2018). Therefore, this study developed an improved model for the precise detection of multi-organ phenotypes and the prediction of individual plant weight in soybeans. This will provide breeders with objective, quantifiable screening criteria, accelerating the development of high-yielding, high-quality varieties.

Materials and Methods

The original dataset consists of 890 pod images and 900 stem images, all of which have been annotated at the instance level (37,545 pods and 4,015 stems). The pods are classified into three categories 1, 2, and 3， based on the number of seeds. Data augmentation was performed using horizontal and vertical flipping, brightness adjustment, and rotation. After a 5-fold expansion, the dataset comprised 4,450 pod images, 4,500 stem images, and 4,400 primary root images. The augmented dataset was randomly split into training, validation, and test sets in a 7:2:1 ratio.

To improve the accuracy and efficiency of multi-organ segmentation of soybeans in complex field scenarios, this study implemented a lightweight modification to the YOLOv11-seg network: A RepConv module was embedded into the backbone network. This module consists of five stacked convolutional layers (including batch normalization and ReLU) and achieves a training convergence rate one-tenth that of traditional models, making it particularly suitable for the efficient segmentation of small, densely clustered objects such as soybean pods. Additionally, the original C3k2 structure was replaced with a CSPPC module, leveraging the low computational cost and T-shaped receptive field advantages of PConv to it accurately captures fine-grained features such as stem edges and internodes, as well as coarse-grained information like main stem morphology and branch distribution(Fig. 1). This effectively mitigates blurred segmentation boundaries caused by occlusion and interleaving, reduces the false negative rate for thin and weak branches, and maintains high FLOPS on CPU, GPU, and ARM devices, meeting the real-time inference requirements of portable field devices while demonstrating good generalization under few-shot conditions. The synergistic effect of these two improvements significantly enhances the segmentation accuracy and mask fit for pods and stems without increasing the inference burden, providing lightweight and highly effective technical support for high-throughput phenotyping

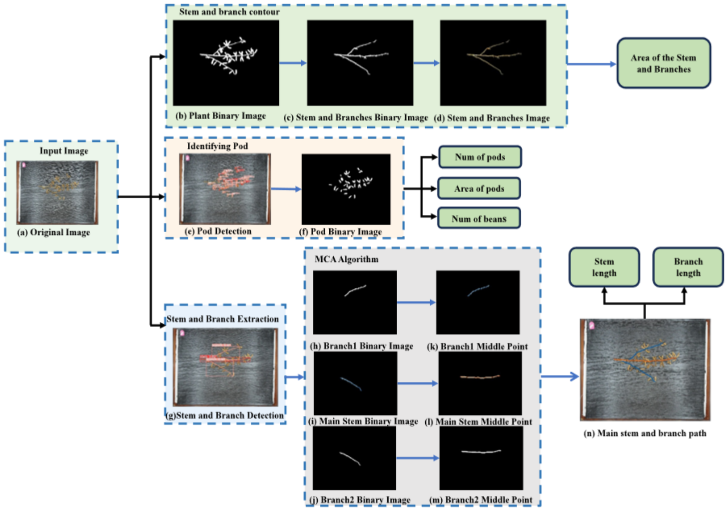

Fig 1. A Model for Soybean Instance Segmentation and Phenotypic Information Extraction Based on an Improved YOLOv11-seg.

Results and Discussion

Compared to the baseline model, YOLOv11-seg-RepConv demonstrated outstanding performance in soybean pod recognition. In the pod detection and segmentation tasks, it achieved a Box mAP50 of 94.6% and a Mask mAP50 of 90.6%. Furthermore, it demonstrated high accuracy in distinguishing between similar pod varieties. YOLOv11-seg-CSPPC achieved a Box mAP50 of 94.3% and a Mask mAP50 of 95.3% in the soybean stem and branch detection and segmentation tasks.

The processing efficiency evaluation was conducted on a fixed hardware platform, using a test set consisting of 3,862 soybean plant phenotype images with a resolution of 6,000 $\times$ 4,000 pixels. The total processing time was 31,193 s, with an average processing time of approximately 8.08 s per image. By process stage, YOLO model inference accounted for 65% of the processing time per image, detailed canopy analysis accounted for 20%, and image I/O and interface rendering accounted for 15%. In batch processing mode, the asynchronous thread mechanism effectively prevented interface blocking, while the deduplication logic ensured that no image was processed more than once, resulting in a 100% completion rate.

Conclusion

This study successfully developed an improved YOLOv11-seg model. By introducing RepConv and CSPPC modules, the model achieved accurate identification of the number of soybean pods and main stem branches at maturity, as well as the extraction of phenotypic information. The optimized model not only demonstrates excellent recognition accuracy and fast recognition speed but also offers the advantage of lightweight deployment. This study also developed a model for predicting the weight of individual mature soybean plants, representing an innovative and significant advancement in soybean breeding.

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