Georgia Peanut Commission
2025 progress report

Evaluation and development of high-throughput phenotyping technologies for peanut.

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During the 2025 season, several improvements were made to enhance the robot's reliability and efficiency. A dual-camera system mounted on a rigid steel frame was fully integrated with the on-board computer for precise synchronization, capturing two-row peanut plots simultaneously. We optimized traction to double operational speed to 1.0 m/s, halving the time required to scan each field, while navigation paths were streamlined to minimize travel between plots. A sunshade prototype was used to reduce lateral light and shadows, improving lighting consistency and contributing to more robust pod detections.

Images were captured every 35 cm, yielding roughly 30 images per plot, and automatically assigned to plots using GPS coordinates and timestamps. Plot-level images were generated through a three-step stitching pipeline. Left and right images were first combined using LightGlue and Superpoint to match feature points, followed by Procrustes alignment and blending with the Minimum Error Boundary Cut algorithm. Consecutive frames were then stitched vertically using the same approach, producing fully stitched stereo images for each plot.

Area of visible peanut pods was computed for each plot-level stitched image (Figure 1) using a YOLOv11 pod detection model trained on 2023–2024 data. Model performance was validated on 2024 field images (mAP50 = 90.3%, mAP95 = 54.8%). The model provided bounding boxes and area for each detected pod, which were then compared to manual yield measurements collected by harvesting and weighing each plot. A strong linear relationship was observed between visible pod area and actual yield ($R^2 = 0.7$). Using linear regression analysis, our predictions achieved an RMSE of 494 lbs/A and a mean absolute percentage error of 7.59% (Figure 2).

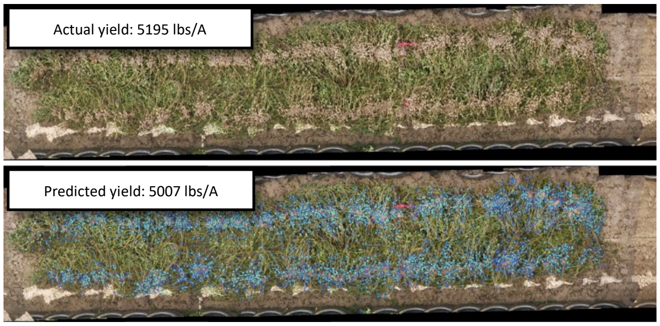

Figure 1. Area of visible peanut pods detected by our method. Blue pixels indicate detected peanut pods.

Field trials in 2025 were conducted at two UGA research farms, Ponder and ASF, across five fields and three trial types: PYT, IYT, and AYT. The robot scanned a total of around 1,000 two-row plots, with each 20' x 6' row planted at six seeds per foot. Predicted yield values were used to rank genotypes within each trial. Overall ranking accuracy compared to manual yield measurements was 83.6%, with per-trial accuracies of 79.5% in IYT, 75.8% in PYT, 72.7% in AYT, and 65.2% in PYT_HO, demonstrating that the pipeline can effectively distinguish high- and low-yielding genotypes. This can reduce the need to harvest non-promising lines early in the program.

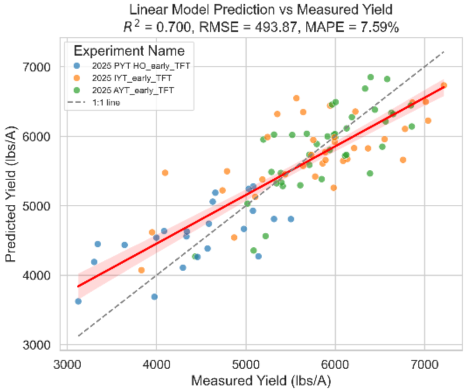

Figure 2. Predicted yield versus actual yield

Ongoing work will continue testing the system across multiple locations and soil conditions to evaluate performance under diverse growing environments. Further improvements to the robot and imaging system will increase speed, reliability, and data quality, supporting more efficient and accurate field-based phenotyping in peanut breeding programs.