# EVALUATION AND DEVELOPMENT OF HIGH-THROUGHPUT PHENOTYPING TECHNOLOGIES FOR PEANUT

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Progress on phenotypic measurements using robotic HTP system

A FLIR Blackfly industrial camera (Teledyne FLIR, Oregon, United States) with a wide field of view was used to capture the imaging data. Images were captured over the raised beds by defining a straight
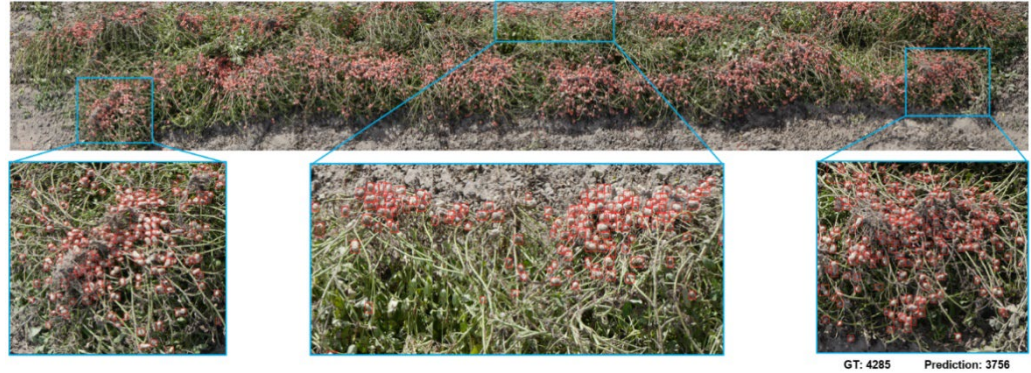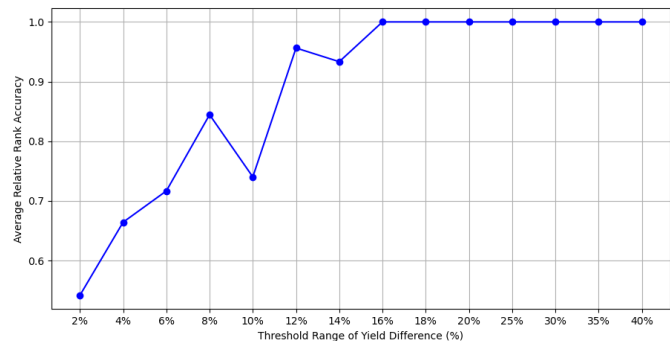

Figure 1. *Illustration of plot-scale pod detection. Red rectangles frame detected pods.*

path for the robot to follow. The images belonging to each plot were manually segmented and then stitched sequentially to generate plot-scale images using the Local Feature Transformer (LoFTR) (Sun et al., 2021) feature matching method. A new customized detector for plot-scale pod counting was developed and tested. The peanut pod detector was updated to solve previous performance issues found when detecting pods in bright and dark areas of the canopy. A model based on the Real-Time Detection Transformer (RT-DETR) (Lv et al., 2023) was used to substitute the previous YOLOv8 detector. This new model allowed for more robust and consistent pod detections (Figure 1).

Plot-level pod counts were validated against manual estimation of pod number using linear regression analysis, achieving an $R^2 = 0.6$. We found that while pod number estimation performed well, predicting yield solely based on pod number is not ideal. The size and weight of peanut pods vary significantly among genotypes, and there is considerable variability even within a single plant due to their

indeterminate flowering habit, varying maturity stages, and other environmental factors. For more precise estimates, it is essential to consider other factors, such as genotype-specific pod weight.

The concept of relative ranking accuracy was proposed to quantify how well algorithm-estimated yields align with manual-measured yields for ranking genotypes. This is especially useful for identifying higher- or lower-yielding genotypes. For each genotype, its yield was compared to the yield of every other genotype. The relative ranking accuracy for each genotype was calculated as the percentage of consistent

Figure 2. *Relative ranking accuracy as influenced by magnitude of yield difference between genotypes.*

comparisons (algorithm and manual measurements gave the same result) out of all possible comparisons. On average, plot-level yield estimations were highly consistent with manual measurements (over 85% accuracy), confirming its reliability in ranking genotypes by yield, even with slight differences in absolute yield values. Accuracy improved as yield differences increased (Figure 2), with relative ranking accuracy surpassing 90% when yield differences exceeded 12%. This high accuracy is valuable for distinguishing lower-yielding genotypes from the most promising ones during early breeding generations.