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Deep learning for maize mutants: Phenotyping individual plants using UAS images

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Using Unoccupied Aerial Systems (UASs) to collect image data for field phenotyping enables the coverage of large spatial scales, but the extraction of phenotypes at the level of an individual plant remains a challenge. Phenotypes are generally extracted at the plot level after manual delineation of the plots in an orthomosaic image. However, this approach is impractical when individual plant phenotypes are of interest, such as in mutant screenings, heterozygous population trials, and other cases where individual plants in a plot or a landscape may be very diverse. For mutant studies in particular, UASs have had limited utility since one typically wants to identify individual plants with outlier phenotypes. Current mutant population screenings require scientists to walk through the field on a regular basis to manually identify and record plants of interest. If UAS software could be designed to identify these plants, much larger studies could be conducted with lower labor costs. Here, we use deep Convolutional Neural Network (CNN) models to detect individual maize plants in raw UAS images followed by the extraction of individual phenotypes. The predictions from the CNN models are used to identify plants in the orthomosaic image to derive information on plot location. For the extraction of phenotypes, plant pixels are segmented from the background and traits including color-based indices and canopy coverage are calculated. Individual plant height is derived from the corresponding Digital Surface Model (DSM). This project will contribute to a more efficient approach for the phenotyping of individual plants using UAS images.