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January 14, 2023

NAPPN Annual Conference Abstract: Automated root phenotyping via deep learning-based landmark detection using SLEAP

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A high-throughput image analysis pipeline was developed to facilitate root phenotyping by reducing time-consuming labeling while maintaining phenotyping accuracy. This pipeline leverages a deep learning-based tool named SLEAP (SLEAP Estimates Animal Poses) which is designed to automate the detection of distinct morphological landmarks. By training SLEAP to detect the root branch points, tips, and midline of each root imaged in a gel cylinder, we were able to robustly and efficiently recover the root system geometry. We trained models to identify these landmarks on primary, lateral, and seminal roots across a range of crop plants, including soybean, rice, canola, and pennycress. We find that our SLEAP models are robust across genotypes and experiments, enabling automated root system quantification at the rate of hundreds of plants per hour. Using predictions of root landmark locations, we developed Python-based pipelines to extract phenotypic traits, including tip depths, root lengths, convex hulls, root angles, measures of curviness, and lateral root distribution (available at https://github.com/talmolab/sleap-roots). In order to extract meaningful patterns from this high-dimensional description of plant phenotypes, we use machine learning-based methods for dimensionality reduction and manifold embedding, allowing us to capture the statistical structure of root phenotypes present in our screens. In future work, we will use these quantitative phenotypic traits as a predictor for root system traits that enhance carbon sequestration capabilities in genome-wide association studies.