Root Phenotyping Using Pose Estimation

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Abstract

Image segmentation is commonly used to estimate the location and shape of plants and their external structures. Segmentation masks are then used to localize landmarks of interest and compute other geometric features that correspond to the plant's phenotype. Despite its prevalence, segmentation-based approaches are laborious (requiring extensive annotation to train), and error-prone (derived geometric features are sensitive to instance mask integrity). Here we present a segmentation-free approach which leverages deep learning-based landmark detection and grouping, also known as pose estimation. We use a tool originally developed for animal motion capture called SLEAP (Social LEAP Estimates Animal Poses) to automate the detection of distinct morphological landmarks on plant roots. Using high-throughput phenotyping method Root Architecture 3-D Imaging Cylinder (RADICYL) across multiple species, we show that our approach can reliably and efficiently recover root system topology at greater accuracy, faster speed, and with fewer annotated samples than segmentation-based approaches. In order to make use of this landmark-based representation for root phenotyping, we developed a Python library (*sleap-roots*) for trait extraction directly comparable to existing segmentation-based analysis software. We show that landmark-derived root traits are highly accurate and can be used for common downstream tasks including genotype classification and unsupervised trait mapping. Altogether, this work establishes the validity and advantages of pose estimation-based plant phenotyping. To facilitate adoption of this easy-to-use tool and to encourage further development, we make *sleap-roots* , all training data, models, and trait extraction code available at: https://github.com/talmolab/sleap-roots.

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