

Few-Shot Learning Enables Population-scale Analysis of Leaf Traits in *Populus trichocarpa*

Background

- Plant phenotyping is time-consuming and expensive, often requiring large groups of researchers to meticulously measure biologically relevant plant traits and is a bottleneck in mapping phenotypes.
- Image-based plant phenotyping is a method to characterize and categorize plants within and across species. There exists a need to develop methods for fast and accurate image-based plant phenotyping that alleviate the data gathering and annotation bottleneck across species and populations.

Approach

- We apply few-shot learning with convolutional neural networks to extract the leaf and vein architecture from high-resolution scans of *P. trichocarpa* leaves of natural variant genotypes from a common garden. These machine-learning methods maximize accuracy while minimizing the number of training images; this resulted in fast and accurate extraction of complex morphological and topological traits that were validated with real-world measurements.

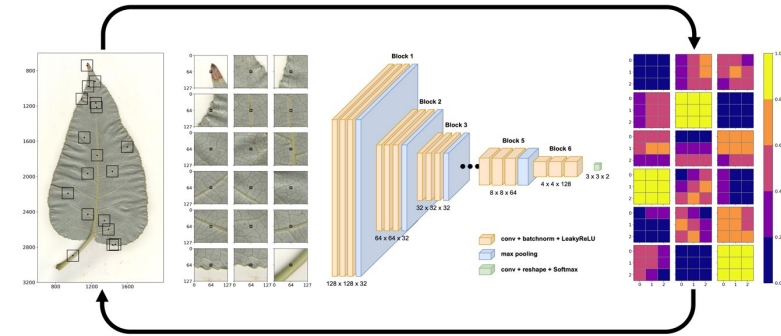
Results

- The leaf segmentation model was trained with 50 images and was applied to 2,906 top and bottom leaf scans, achieving equivalent speed and accuracy compared to a state-of-the-art computer vision model.
- The vein segmentation model used eight training images and was applied to 1,453 bottom leaf scans, exceeding the state-of-the-art across both computational and biological accuracy metrics.
- Open-source tools (e.g., RhizoVision Explorer) extracted 68 novel traits over the population; a genome-wide association study identified 30 unique genes potentially controlling vein density in *P. trichocarpa*.

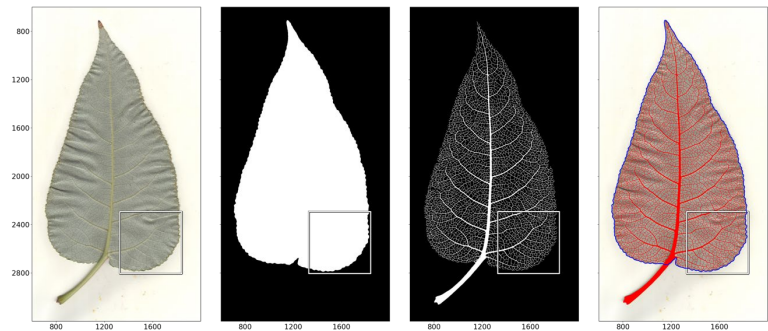
Significance

- These methods make accurate predictions at population scale with no image or sample preprocessing and with very few training samples. These capabilities enable in-depth studies of mechanisms underlying plant physiology, biomechanics, and structure within and across genotypes at unprecedented scale and accuracy.
- We have open-sourced all data, code, and results in the hope that this work becomes a valuable community resource and helps reduce barriers with high-throughput image-based plant phenotyping.

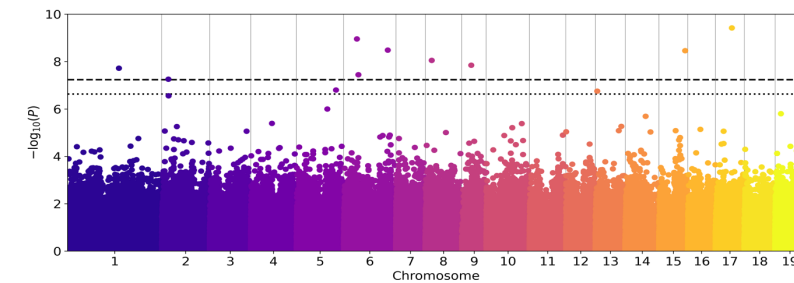
Lagergren, J., et al., (2023) *Plant Phenomics SPJ*, DOI: 10.34133/plantphenomics.0072.



The complex task of whole-image segmentation is broken into iterative pixel-level decisions, by which we maximize predictive accuracy across the population using very few images for training.



Resulting leaf and vein segmentations of a *P. trichocarpa* leaf.



GWAS reveals 30 genes potentially controlling vein density.