

Bioimage informatics

Plant 3D (P3D): a plant phenotyping toolkit for 3D point clouds

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Associate Editor: Jinbo Xu

Received on January 28, 2020; revised on March 16, 2020; editorial decision on March 24, 2020; accepted on March 25, 2020

Abstract

Motivation: Developing methods to efficiently analyze 3D point cloud data of plant architectures remain challenging for many phenotyping applications. Here, we describe a tool that tackles four core phenotyping tasks: classification of cloud points into stem and lamina points, graph skeletonization of the stem points, segmentation of individual lamina and whole leaf labeling. These four tasks are critical for numerous downstream phenotyping goals, such as quantifying plant biomass, performing morphological analyses of plant shapes and uncovering genotype to phenotype relationships. The Plant 3D tool provides an intuitive graphical user interface, a fast 3D rendering engine for visualizing plants with millions of cloud points, and several graph-theoretic and machine-learning algorithms for 3D architecture analyses.

Availability and implementation: P3D is open-source and implemented in C++. Source code and Windows installer are freely available at <https://github.com/iziamtso/P3D/>.

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Supplementary information: [Supplementary data](#) are available at *Bioinformatics* online.

1 Introduction

New technological advances in plant phenotyping are now being used to generate large volumes of data detailing the 3D shoot architectures of various plant species, grown in different environments, in both the lab and in the field. This has raised the challenge of automatically extracting phenotyping features, such as leaf size, shape and quantity (Huang *et al.*, 2018), branch lengths and angles (Bucksch *et al.*, 2017) and growth rates, amongst others. These features are important for numerous tasks, including quantifying plant biomass and yield (Mathan *et al.*, 2016), understanding plant responses to stressful conditions (Minervini *et al.*, 2016), mapping genotypes to phenotypes and building predictive structural-functional models of plant growth (Sievanen *et al.*, 2014).

2 The Plant 3D software package

We developed a tool called Plant 3D (P3D) to perform common phenotyping tasks using high-resolution 3D point clouds of plant architectures. 3D scanning avoids common issues with camera-based imaging, including camera calibration, image registration, object occlusion and inconsistencies in illumination—especially as these factors vary across labs and experimental setups (Perez-Sanz *et al.*, 2017). P3D is open-source and is bundled with a stand-alone Windows application (Fig. 1). P3D is written in C++ using

OpenGL, QT, TensorFlow and the point cloud library. P3D can visualize and process data imported as a 3D point cloud (pcd or txt formats) or a mesh (obj format).

The tool focuses on four phenotyping tasks described below (Supplementary Information). Technical details of all algorithms are provided in Ziamtsov and Navlakha (2019).

Lamina versus stem classification. The first task is to classify each point in the point cloud as belonging to either a lamina structure (e.g. leaf, cotyledon) or a stem structure (e.g. petiole, branch) (Fig. 1A). A point cloud consists of a list of (x, y, z) coordinates of the object of interest (a plant architecture). P3D computes fast point feature histogram features (Rusu *et al.*, 2009) for every point in the cloud, and then feeds these features into a deep neural network for binary classification. This classification is the first step toward computing leaf-related features (using lamina points) and morphology/shape-related features (using stem points).

P3D's rendering engine allows classification results to be visualized, with zooming and panning capabilities for evaluation of performance.

Lamina counting and segmentation. The second task is to segment or cluster all of the lamina points into subsets, where each subset represents an individual lamina (Fig. 1B). P3D uses a conditional region growing method that clusters lamina points based on similarity of their curvature (anisotropy), normal vectors and fast point feature histogram features. This step produces a set of lamina—which are individually colored—and can then be used for analyses of

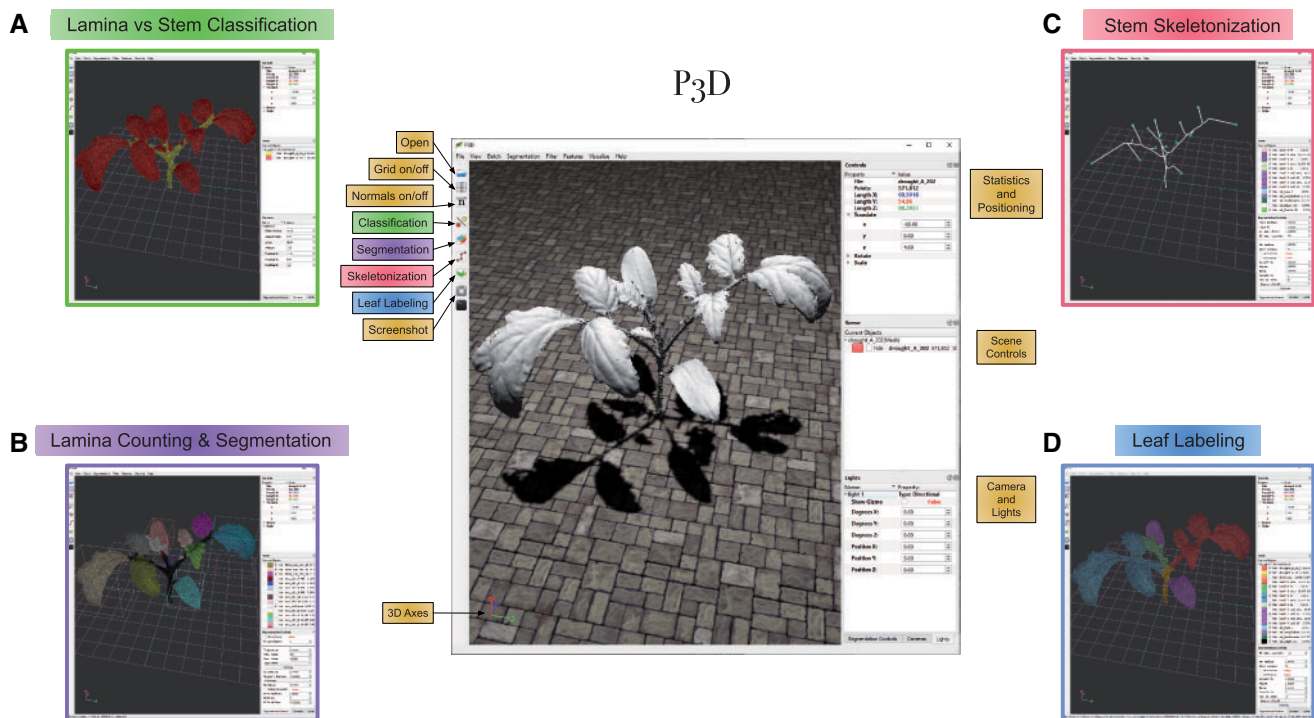


Fig. 1. Overview of the P3D tool. Center panel shows the overall GUI and an example scan of a tomato plant on growth Day 20. Examples of the four phenotyping tasks are shown in panels (A–D). (A) Classification of the point cloud into lamina points (red) and stem points (yellow) using a deep learning classifier. (B) Segmentation of the lamina points into individual lamina (shown in different colors). (C) Skeletonization of the stem points into a 3D graph-theoretic tree. White lines show the tree, and green dots signify the 3D locations of lamina found in the previous step. (D) Clustering of individual lamina into whole leaves. Three leaves are shown (red, green and blue), as well as two cotyledons (purple). Orange points signify stem points. (Color version of this figure is available at *Bioinformatics* online.)

lamina size, shape, arrangement (Kuhlemeier, 2017) and quantity (Giuffrida *et al.*, 2018).

Stem skeletonization. The third task is to generate a skeleton of the stem points (Delagrange *et al.*, 2014) (Fig. 1C). The P3D skeletonization algorithm outputs a graph-theoretic tree, with nodes following along the shape of the plant from the root through potential branching points to lamina end-points, and with edges corresponding to the stem structure connecting the nodes. Morphological traits of plant architectures are useful for studying plant geometry (Bucksch *et al.*, 2017), nutrient transport efficiency (Conn *et al.*, 2017), spatial distribution of branches and morphogenesis (Prusinkiewicz and Lindenmayer, 1996).

Whole leaf labeling. The fourth task builds upon the first three tasks and identifies whole leaves (Fig. 1D). Biologically, a single ‘leaf’ of (e.g.) a tomato plant consists of all the stem tissue (petioles and petioles) and all the individual lamina that are downstream of a single branching-point from the primary stem. Similar analyses of leaf traits can be then performed.

Additional features. P3D includes methods to downsample very large point clouds, methods to remove outliers and smoothen the data, and a shading editor to model light capture by plants. There is, of course, significant diversity in plant structures across the entire plant kingdom, and our methods currently have only been tested on Solanaceae species. However, P3D has a modular structure, which can be extended to handle other leaf and branching structures in the future.

3 Conclusions

P3D helps tackle several basic phenotyping challenges to better understand the structure of plant architectures. As 3D point clouds become a standard data type for digitizing plant architectures in the lab and in the field, we hope the P3D tool can help accelerate next-generation plant phenotyping.

Funding

S.N. was supported by the Pew Charitable Trusts, the National Science Foundation under award CAREER DBI-1846554, and funding from the Simons Center for Quantitative Biology at Cold Spring Harbor Laboratory.

Conflict of Interest: none declared.

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