Comparison of open-source image-based reconstruction pipelines for 3D maize root phenotyping

suxing liu[1,1], Alexander Bucksch[1,1], Wesley Paul Bonelli[1], and Peter Pietrzyk[1]

[1]University of Georgia

November 30, 2022

Abstract

Understanding root traits is essential to improve water uptake, increase nitrogen capture and raise carbon sequestration from the atmosphere. However, high-throughput phenotyping to quantify root traits for deeper field-grown roots remain a challenge. Recently developed open-source methods use image-based 3D reconstruction algorithms to build 3D models of plant roots from multiple 2D images and can extract root traits and phenotypes. Most of these methods rely on automated image orientation (Structure from Motion)[1] and dense image matching (Multiple View Stereo) algorithms to produce a 3D point cloud or mesh model from 2D images. Until now it is not known how the performance of these methods compares to each other when applied to field-grown roots. We investigate commonly used open-source pipelines on a test panel of twelve contrasting maize genotypes grown in real field conditions in this comparison study [2-6]. We compare 3D point clouds in terms of number of points, computation time, and model surface density. This comparison study will provide insight into the performance of different open-source pipelines for maize root phenotyping, and illuminates trade-offs between 3D model quality and performance cost for future high-throughput 3D root phenotyping.

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Suxing Liu[a,b,c], Alexander Bucksch[a,b,c]

[a]Department of Plant Biology, University of Georgia, Athens, GA, USA, 30605;

[b]Warnell School of Forestry and Natural Resources, University of Georgia, Athens, GA, USA, 30605;

[b]Institute of Bioinformatics, University of Georgia, Athens, GA, GA, USA, 30605.

ABSTRACT

Understanding root traits is essential to improve water uptake, increase nitrogen capture and raise carbon sequestration from the atmosphere. However, high-throughput phenotyping to quantify root traits for deeper field-grown roots remain a challenge. Recently developed open-source methods use image-based 3D reconstruction algorithms to build 3D models of plant roots from multiple 2D images and can extract root traits and phenotypes. Most of these methods rely on automated image orientation (Structure from Motion) and dense image matching (Multiple View Stereo) algorithms to produce a 3D point cloud or mesh model from 2D images. Until now it is not known how the performance of these methods compares to each other when applied to field-grown roots. We therefore, investigate commonly used open-source methods on a test panel of twelve contrasting maize genotypes grown in real field conditions in this comparison study. These methods include COLMAP [1], VisualSFM [2], OpenMVG [3], Meshroom [4], Multi-View Environment [5] and Regard3D [6]. We compare the 3D point cloud model density, number of points, and computation time. In addition, we compare computed traits to a manually measured ground-truth for each generated 3D model to gain insight into the dependency of trait measurements on method accuracy. The computed traits include distance between whorls and the number, angles, and diameters of nodal roots. This comparison study will provide first insight into the trade-off between model accuracy and trait accuracy for future high-throughput phenotyping pipelines.

Keywords: 3D reconstruction, maize roots, 3D point cloud

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