

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

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## 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.

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

## 1. INTRODUCTION

Root phenotyping is essential to improve water uptake, nitrogen capture and carbon sequestration[7] [8-12]. However, root phenotyping requires advanced methods to measure and quantify complex root architectures. With the development of computer vision techniques, image-based root phenotyping with commodity cameras has emerged as a cost efficient and accessible alternative to high-end imaging devices.

2D image-based root phenotyping methods provide abundant trait measurements [13]. Examples for such 2D approaches are DIRT [14], archiDART [15], EZ-Root-VIS [16], GiA Roots [17] and RhizoVision [18]. Unfortunately, 2D images can only record partial information of a dense and highly occluded 3D maize root structure. Therefore, quantifying important traits such as whorl number and the distance, and number of crown roots is challenging [19].

Methods for 3D phenotyping are promising to resolve even highly occluded branching structures [20] [21-23]. One of the key challenges in 3D root phenotyping method is to reconstruct a 3D representation of the

root [19]. The available open-source image-based 3D reconstruction pipelines can process large sets of unordered and diverse images and generate a dense colored point cloud model or a triangulated textured mesh [24]. However, the performance of each pipeline varies dependent on the computing environment and object complexity. Therefore, we asked the question which pipeline produces the need model detail in the shortest time for field-grown maize root.

In this study, we compared commonly used open-source pipelines on a test panel of twelve contrasting genotypes of field-grown maize roots. These methods include COLMAP [1] [2], VisualSFM [3], OpenMVG [4], Meshroom [5] and Multi-View Environment (MVE) [6]. We compare the 3D point cloud model in their visual quality, density, number of points, and computation time.

## 2. MATERIAL AND METHODS

### 2.1 Image dataset

Plants were grown at The Pennsylvania State University's Russell E. Larson Agricultural Research Center (40° 42' 40.915" N, 77° 57' 11.120" W) which has a Hagerstown silt loam soil (fine, mixed, semi-active, mesic Typic Hapludalf). Twelve genotypes were selected, including six inbred lines (B101, B112, DKIB014, LH123HT, Pa762, PHZ51) and six hybrid lines (DKPB80 x 3IIH6, H96 x 3IIH6, LH59 x PHG29, Pa762 x 3IIH6, PHG50 x PHG47, PHZ51 x LH59). These genotypes represent the extremes of dense vs. sparse, large vs. small, and maximum and minimum number of whorls selected from a full diversity panel published in [7]. We selected one plant for each genotype, in total 12 root samples for this initial comparison.

We captured images for each genotype by a prototype of the imaging chamber that was conceptually introduced in [25] (Fig. 1). Images were captured by ten imaging cameras (Image Source DFK 33ux183 USB 3.0, 12mm focal length V1228-MPY2 12 Megapixel Machine Vision Lens). A computing cluster of ten Raspberry Pi 4 synchronizes the image capture of the ten cameras using a server-client design. For each genotype, between 301 and 360 images with image resolution at 5,472×3,648 per maize root were captured using a manual rotation stand. Sample images for each genotype was shown in Figure. 1.



Figure 1. 3D root imaging chamber.

### 2.2 Methods

We tested the performance of the pipelines and its combination, including COLMAP, COLMAP+PMVS (Patch-based Multi-view Stereo), VisualSFM, Meshroom and OpenMVG+MVE [1, 2, 6, 24, 26-35]. 3D root models were computed by the five different pipelines on a Dell Workstation. (OptiPlex 7080, 10th Generation Intel® Core™ i9-10900K, 20 MB Cache, 10 Cores, 20 Threads, 3.7 GHz to 5.3 GHz, 125 W, 64 GB RAM, 4 x 16 GB, DDR4, M.2 2280, 1 TB hard drive, Gen 3 PCIe x4 NVMe, Class 40 SSD). In addition, we use GPU to facilitate the computation if the pipeline supported. The GPU model with the DELL workstation was (GeForce RTX 2070 SUPER, NVIDIA Corporation TU104, nvcc: NVIDIA (R) Cuda compiler driver).

## 3. RESULTS AND DISCUSSION

We compared the performance of five 3D reconstruction pipelines and combinations thereof. The tested pipelines include COLMAP, COLMAP+PMVS (Patch-based Multi-view Stereo), VisualSFM, Meshroom and OpenMVG+MVE. We computed overall 60 point clouds models of field-grown maize roots.

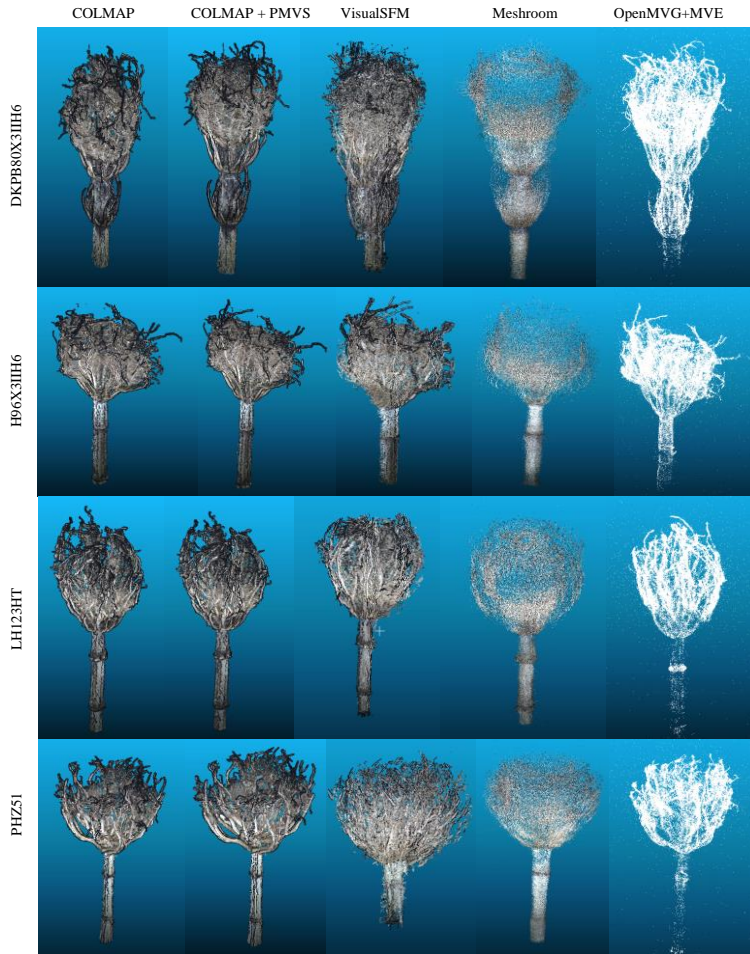


Figure 2. Visual comparison of four genotypes of models

“Properties” items. We also use a tool for computing geometric features provided by CloudCompare to estimate the density of point cloud models. Surface density is defined here as the number of neighbors within spherical neighborhood radius  $R$ , divided (normalized?) by the neighborhood surface  $= N / (\pi \cdot R^2)$ . We use the constant  $R = 0.005118$  to compute the surface density for each model. The comparison of number of points and surface density are shown in Figure 3 and 4 respectively. COLMAP and OpenMVG+MVE produced the largest point sets, achieving on average 94 and 49 times of Meshroom respectively. Meshroom produced the smallest point clouds. COLMAP+PMVS and VisualSFM also averaged 14 and 9 times more points than Meshroom, respectively. COLMAP and VisualSFM produced models with the greatest surface density, however, COLMAP, OpenMVG+MVE, COLMAP+PMVS and Meshroom achieves 94, 31, 14, 8 times of VisualSFM in average.

#### 4. CONCLUSION

By comparing the performance of all the 3D reconstruction pipelines and its combination in this study, we found out that COLMAP, COLMAP+PMVS and VisualSFM are the three pipelines which can generate colored 3d root models directly. Although the computation time of COLMAP is 12-times slower than the VisualSFM, COLMAP achieved 10 times greater number of points, and a 94 times higher surface density

We selected four genotypes and visually compare the model quality in Figure 2. COLMAP and COLMAP+PMVS both achieve good visual quality and models are complete. VisualSFM did not achieve good quality and lost details due to the limited number of input images. Meshroom failed to generate complete models. OpenMVG+MVE captures some details compared with VisualSFM, but the color information was not stored.

In addition to visual quality, we compare 3D model quality by computing total number of points and surface density of all sixty root models, as well as recordings the computation time, as shown in Figure 3. COLMAP consumed almost 29 times the average time OpenMVG+MVE, 5 times of Meshroom in average, while COLMAP+PMVS consumed only 3 times of OpenMVG+MVE in average.

COLORMAP+PMVS required runtimes similar to VisualSFM. We use CloudCompare [36] to load each point cloud model and record its number of points in its

in our test dataset. A combination of COLMAP+PMVS resulted in similar computation time with VisualSFM, but the model quality achieved 2 and 14 times of VisualSFM in term of number of points and surface density.

Our initial study is a good indicator, however further experiments are needed evaluate the quality of root traits and whole root descriptors to a manually measured ground-truth for a larger amount of 3D models. In that way, we will gain insight into the dependency of trait measurements on method accuracy.



Figure 3. Comparison of time cost, number of points and surface density of 3D models

## DATA AVAILABILITY STATEMENT

GitHub link for all the scripts for running the test:

[https://github.com/Computational-Plant-Science/3D\\_review\\_scripts/tree/master](https://github.com/Computational-Plant-Science/3D_review_scripts/tree/master)

Cyverse link to all the 3D model results:

[https://data.cyverse.org/dav-anon/iplant/home/lxs1980/3D\\_model\\_compare.zip](https://data.cyverse.org/dav-anon/iplant/home/lxs1980/3D_model_compare.zip)

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