Comparison of Open-Source Three-Dimensional Reconstruction Pipelines for Maize-Root Phenotyping

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Abstract

Understanding three-dimensional (3D) root traits is essential to improve water uptake, increase nitrogen capture, and raise carbon sequestration from the atmosphere. However, quantifying 3D root traits by reconstructing 3D root models for deeper field-grown roots remains a challenge due to the unknown tradeoff between 3D root-model quality and 3D root-trait accuracy. Therefore, we performed two computational experiments. We first compared the 3D model quality generated by five state-of-the-art open-source 3D model reconstruction pipelines on 12 contrasting genotypes of field-grown maize roots. These pipelines included COLMAP, COLMAP+PMVS (Patch-based Multi-view Stereo), VisualSFM, Meshroom, and OpenMVG+MVE (Multi-View Environment). The COLMAP pipeline achieved the best performance regarding 3D model quality versus computational time and image number needed. Thus, in the second test, we compared the accuracy of 3D root-trait measurement generated by the Digital Imaging of Root Traits 3D pipeline (DIRT/3D) using COLMAP-based 3D reconstruction with our current DIRT/3D pipeline that uses a VisualSFM-based 3D reconstruction (Liu et al., 2021) on the same dataset of 12 genotypes, with 5~10 replicates per genotype. The results revealed that, 1) the average number of images needed to build a denser 3D model was reduced from 3000~3600 (DIRT/3D [VisualSFM-based 3D reconstruction]) to 300~600 (DIRT/3D [COLMAP-based 3D reconstruction]); 2) denser 3D models helped improve the accuracy of the 3D root-trait measurement; 3) reducing the number of images can help resolve data storage capacity problems. The updated DIRT/3D (COLMAP-based 3D reconstruction) pipeline enables quicker image collection without compromising the accuracy of 3D root-trait measurements.

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Comparison of Open-Source Three-Dimensional Reconstruction Pipelines for Maize-Root Phenotyping

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Abstract

Understanding three-dimensional (3D) root traits is essential to improve water uptake, increase nitrogen capture, and raise carbon sequestration from the atmosphere. However, quantifying 3D root traits by reconstructing 3D root models for deeper field-grown roots remains a challenge due to the unknown tradeoff between 3D root-model quality and 3D root-trait accuracy. Therefore, we performed two computational experiments. We first compared the 3D model quality generated by five state-of-the-art open-source 3D model reconstruction pipelines on 12 contrasting genotypes of field-grown maize roots. These pipelines included COLMAP, COLMAP+PMVS (Patch-based Multi-view Stereo), VisualSFM, Meshroom, and OpenMVG+MVE (Multi-View Environment). The COLMAP pipeline achieved the best performance regarding 3D model quality versus computational time and image number needed. Thus, in the second test, we compared the accuracy of 3D root-trait measurement generated by the Digital Imaging of Root Traits 3D pipeline (DIRT/3D) using COLMAP-based 3D reconstruction with our current DIRT/3D pipeline that uses a VisualSFM-based 3D reconstruction (Liu et al., 2021) on the same dataset of 12 genotypes, with 5~10 replicates per genotype. The results revealed that, 1) the average number of images needed to build a denser 3D model was reduced from 3000~3600 (DIRT/3D [VisualSFM-based 3D reconstruction]) to 300~600 (DIRT/3D [COLMAP-based 3D reconstruction]); 2) denser 3D models helped improve the accuracy of the 3D root-trait measurement; 3) reducing the number of images can help resolve data storage capacity problems. The updated DIRT/3D (COLMAP-based 3D reconstruction) pipeline enables quicker image collection without compromising the accuracy of 3D root-trait measurements.

Introduction

Root phenotyping is essential in research projects aiming to improve water uptake, nitrogen capture, and carbon sequestration (Ault, 2020; Lynch, 2019; Lynch & Wojciechowski, 2015; Paustian et al., 1997; Smith et al., 2007). However, this approach requires advanced methods to measure and quantify complex root architectures in the field environment.

With the development of computer vision techniques, image-based root phenotyping with industrial cameras has emerged as a cost-efficient, highly scalable,

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and accessible alternative to expensive high-end imaging devices. Established 2D image-based root-phenotyping methods, such as DIRT (Bucksch et al., 2014), archiDART (Delory et al., 2016), EZ-Root-VIS (Shahzad et al., 2018), GiA Roots (Galkovskyi et al., 2012), and RhizoVision (Seethepalli et al., 2020) provide highly accurate trait measurements. However, 2D imaging approaches can only capture partial information from dense and highly occluded 3D maize-root architectures. Therefore, quantifying important traits, such as crown root number and whorl number, and their distances remains challenging.

The use of 3D imaging techniques in root phenotyping is promising because of their ability to leverage multiple views of a given scene to resolve occlusion in dense root architectures (Bucksch, 2014; Clark et al., 2011; Dowd et al., 2022; Topp et al., 2013). However, 3D imaging methods, such as X-ray CT (Shao et al., 2021) or magnetic resonance imaging (MRI; van Dusschoten et al., 2016), are 100–1000 times more expensive than multicamera systems (Liu et al., 2021), and they do not meet the needs of large-scale field studies due to the restriction on their operation cost and difficulties in deploying in the field environment. Moreover, 3D-imaging methods incur labor costs for highly trained staff and custom shielded rooms for operations. Therefore, X-ray CT and MRI techniques are unsuitable for capturing root architecture with high throughput. In contrast, multicamera systems can scale at a fraction of the cost of 3D-imaging methods and require neither highly trained staff nor custom facilities for their operation.

Fortunately, open-source image-based 3D reconstruction pipelines COLMAP (Schonberger & Frahm, 2016), COLMAP+PMVS (Furukawa & Ponce, 2007), VisualSFM (Wu, 2011), Meshroom (Griwodz et al., 2021), and OpenMVG+MVE (Moulon et al., 2016) Fuhrmann et al., 2014) enable 3D reconstructions of root-system architectures from large sets of unordered images obtained using multicamera systems (Liu et al., 2021) Hoppe et al., 2012).

However, which pipelines have the best performance when generating 3D root models? Until now, it has not been quantified if the model quality sufficient to measure root traits can be seen as a trade-off between the number of images and computation time.

To answer the question above, we performed two computational experiments. We compared the 3D model quality generated by the above five open-source 3D model reconstruction pipelines on 12 samples from 12 contrasting genotypes of field-grown maize roots in the first computational experiment. The 3D model quality comparison includes visual quality, number of points and surface density of a 3D point cloud model, and computation time. The COLMAP pipeline achieved the best performance regarding 3D model quality, which represented the optimal tradeoff between the point cloud metrics number of points and surface density, image number, and runtime. Therefore, in the second computational experiment, we implemented COLMAP in the 3D reconstruction pipeline in DIRT/3D (Liu et al., 2021) and compared the accuracy of 3D root traits generated by DIRT/3D (COLMAP-based 3D reconstruction) pipeline with our

current DIRT/3D (VisualSFM-based 3D reconstruction) pipeline from the same dataset, including 12 genotypes with 5~10 replicates per genotype (Liu et al., 2021). For abbreviation purposes, we shall now refer to DIRT/3D (COLMAP-based 3D reconstruction) pipeline as DIRT/3D (COLMAP), and DIRT/3D (VisualSFM-based 3D reconstruction) pipeline as DIRT/3D (VisualSFM).

In the following section, we discuss the methodology including root sample collection, two computational experiments and statistical analysis method. Then, reconstructed models of various maize genotypes are visually and quantitatively assessed for the quality of retrieved traits measurement.

Materials and Methods

Root Sample Collection

We used the same root samples as described in (Liu et al., 2021), including 12 genotypes with 5~10 replicates per genotype. The plants were grown at Pennsylvania State University's Russell E. Larson Agricultural Research Center, which has Hagerstown silt loam soil (fine, mixed, semi-active, mesic Typic Hapludalf; Liu et al., 2021). The selected genotypes represent extremes of dense vs. sparse, large vs. small, and maximum and minimum number of whorls selected from a full diversity panel. The 12 genotypes included 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). Sampling followed the shovelomics protocol, which minimizes variation by selecting similar representative architectures. Shoots were removed above all root-producing nodes and air-dried on a greenhouse bench. Then, the roots were transported to the lab for imaging.

Three-Dimensional Root-Model Reconstruction and Three-Dimensional Trait Computation

Computational Experiment 1:

Image Capture and Computational Methods

The image collection was conducted in an imaging chamber prototype built for Pennsylvania State University (Shi et al., 2019). Since this imaging chamber was equipped with a higher resolution camera than the cameras described in (Liu et al., 2021), we selected 12 roots from all the roots samples, with each root representing one genotype. We captured images of each root using this prototype imaging chamber, as conceptually introduced in (Shi et al., 2019). The images were captured using 10 cameras (Image Source DFK 33ux183 USB 3.0, 12mm focal length V1228-MPY2 12 Megapixel Machine Vision Lens) arrayed around a central focal point. Image capture was synchronized using a cluster of 10 Raspberry Pi 4s with a server-client design. For each sample, between 300 and 360 images with an image resolution 5,472×3,648 were taken.

We captured 12 sets of images. Then, we computed 60 3D root models for each image collected with all five 3D reconstruction pipelines (COLMAP,

COLMAP+PMVS VisualSFM, Meshroom, and OpenMVG+MVE). The 3D root-trait measurement was conducted using the same pipeline as that described in (Liu et al., 2021).

Computational Environment

We conducted the first computational experiment 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 used Graphics Processing Units (GPU)to facilitate the computation if the software-supported GPUs. The GPU model with the DELL workstation was a GeForce RTX 2070 SUPER, NVIDIA Corporation TU104, nvcc: NVIDIA (R) Cuda compiler driver. All the pipelines were tested under command-line interface (CLI) to generate related 3D root models in point cloud format. The scripts for the workstation are on GitHub (https://github.com/Computational-Plant-Science/3D_review_scripts/tree/master, folder Computational_test_1).

Computational Experiment 2:

Image Capture and Computational Methods

We used the same image dataset as in Computational Experiment 1. However, for each root sample, we used only a subset of 600 images to simulate reduced time for image capturing.

We computed all 100 3D root models for the 12 genotypes from a subset of 600 images with DIRT/3D (COLMAP). The 3D trait measurement of the roots was conducted using the same pipeline as that described in (Liu et al., 2021).

Computational Environment

The computation was conducted on the high-performance-computing (HPC) resource SAPELO2 at the Georgia Advanced Computing Resource Center (GACRC). We ran DIRT/3D (COLMAP) in a Docker container and recorded the running time for each execution of the container. The Docker container was retrieved from Docker hub (named as computationalplantscience/dirt3d-reconstruction and computationalplantscience/dirt3d-traits). All the scripts for this computational experiment are on GitHub (https://github.com/Computational-Plant-Science/3D_review_scripts/tree/master, folder Computational_test_2).

Three-Dimensional Model Quality Computation

We used CloudCompare v2.12.alpha **(Girardeau-Montaut, 2016)** to compute the number of points in the 3D point cloud model and to estimate the surface density of a point cloud in Computational Experiments 1 and 2. We loaded each point cloud model into CloudCompare v2.12.alpha using the software's graphical user interface. We then retrieved the number of points via the "Properties" tab.

The surface density S was estimated by counting the number of neighbors N

inside a sphere of radius R for each point. The surface density S is defined as follows:

$S = N / (Pi*R^2)$

Statistical Analysis

The CORREL function in Microsoft Excel (Microsoft 365 A3) and the Analysis ToolPak add-in for Excel were used to compute correlation coefficients between the two sets of trait measurements derived from DIRT/3D (COLMAP) and DIRT/3D (VisualSFM). In addition, the built-in R-squared formula RSQ in Microsoft Excel (Microsoft 365 A3) was used to compute the *R-squared value* in the regression analysis.

Results

Computational Experiment 1: Qualitative and Quantitative Comparison of Three-Dimensional Model Quality from Five Open-Source Three-Dimensional Reconstruction Pipelines

Visual Assessment

We selected 12 field-grown maize roots from 12 different genotypes to compute 3D point clouds using all five pipelines. For each root sample, 300~600 images were captured, and 60 3D point cloud models were generated.

Figure 1 provides a visual comparison of the computed 3D models with the pipelines COLMAP, VisualSFM, OpenMVG, Meshroom, and MVE. Among all the tested 3D reconstruction pipelines, COLMAP and COLMAP+PMVS achieved good visual results, in terms of model completeness, with no obvious disconnection of roots or missing parts of the root system. With the reduced image dataset, VisualSFM tended to omit fine details, such as brace roots at the margins of the point cloud. Meshroom produced models with large interior gaps. OpenMVG+MVE displayed finer details than VisualSFM but does not provide color information per point.
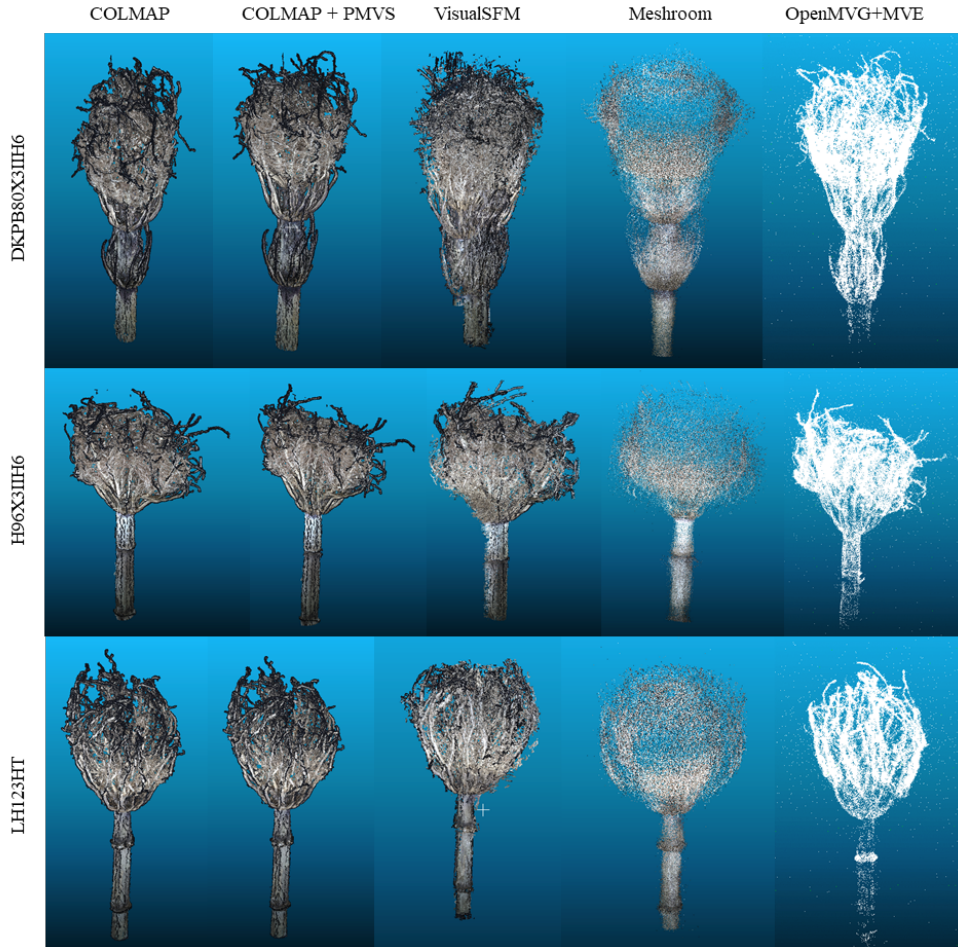
Figure 1. Visual comparison of three reconstructed maize genotypes. The 3D root models in each row compare the same genotype across different 3D reconstruction pipelines. The 3D root models in each column compare a 3D reconstruction pipeline across different genotypes.

Quantitative Assessment

We assessed the two sets of point cloud metrics (number of points and surface density) for each 3D point cloud model. "Number of points" represents the total of 3D points generated by a 3D reconstruction pipeline. "Surface density" is the average density across the surface of the root architecture. The comparison results for the number of points are illustrated in Figure 2. The COLMAP pipeline produced the largest number of points, achieving, on average, 94 times the number of points of Meshroom, which generated the fewest points. In general, COLMAP outperformed all the other tested pipelines regarding the number of points per root system (see Figure 2).
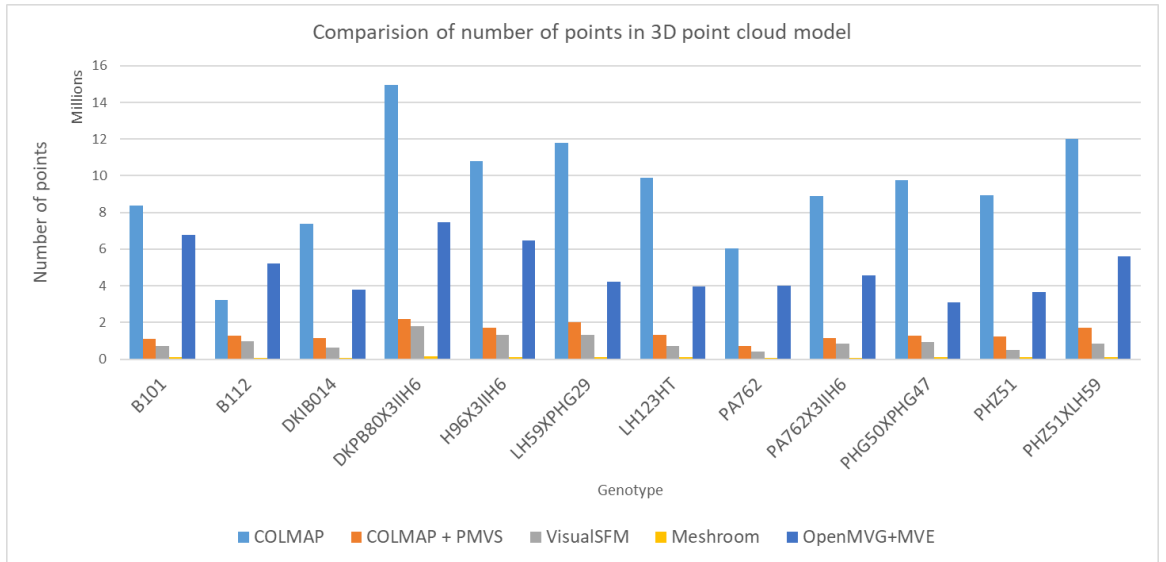
Figure 2. Comparison of the number of points in 3D models. The five pipelines are color labeled, and the lengths of bars represent the value of the number of points in each 3D point cloud model.

In addition to the number of points, we compared the surface density of the point clouds generated by each pipeline. Higher surface density values are desirable for point cloud characteristics. The comparison of surface density in Figure 3 reveals that COLMAP and OpenMVG+MVE produced the models with the largest surface density. The surface density generated by COLMAP was, on average, 94 times the surface density generated by VisualSFM, whereas OpenMVG+MVE was 31 times the surface density of VisualSFM. VisualSFM generated models with the lowest surface density among all the pipelines.
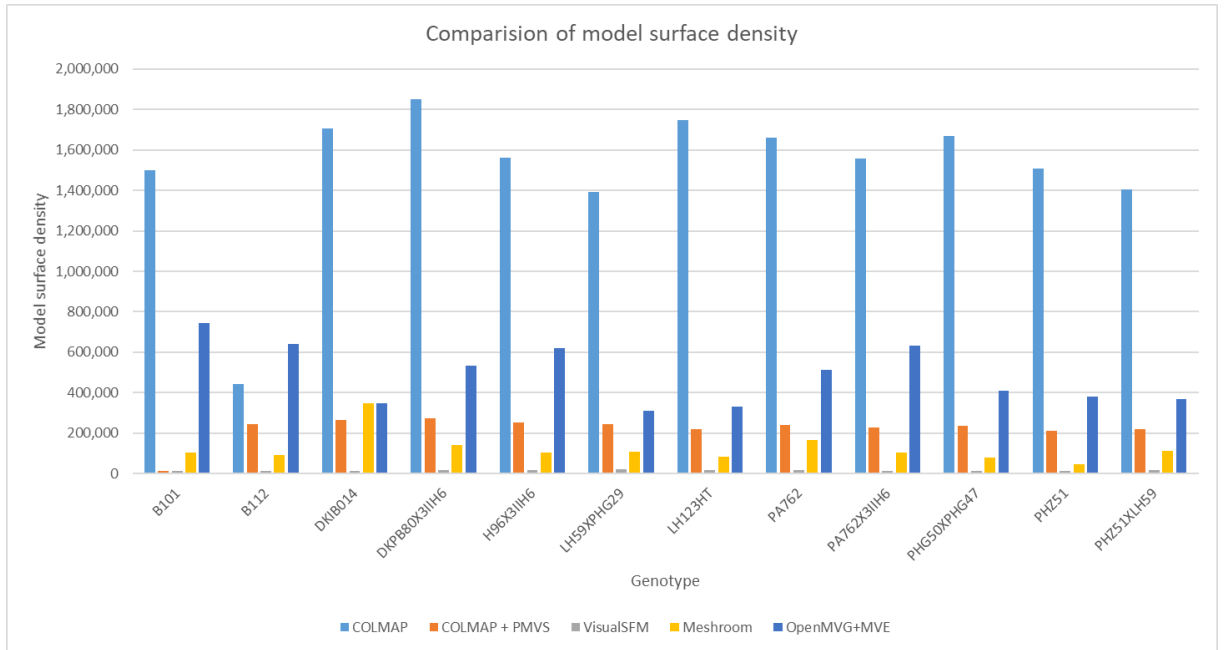
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Figure 3. Comparison of surface density of 3D models. COLMAP produced models with the highest surface density among all the pipelines, whereas VisualSFM produced the lowest surface density. The five tested pipelines are color labeled, and the lengths of the bars represent the value surface density of each 3D point cloud model.

Although COLMAP produced the best 3D model results regarding the number of points and surface density, its computation time was almost 29 times longer than the quickest algorithm (OpenMVG+MVE), and five times longer than Meshroom, on average. COLMAP+PMVS was significantly faster than COLMAP, and needed, on average, three times longer than OpenMVG+MVE to produce the 3D model. COLMAP+PMVS required a similar time to compute the 3D point cloud as VisualSFM, as illustrated in Figure 4.
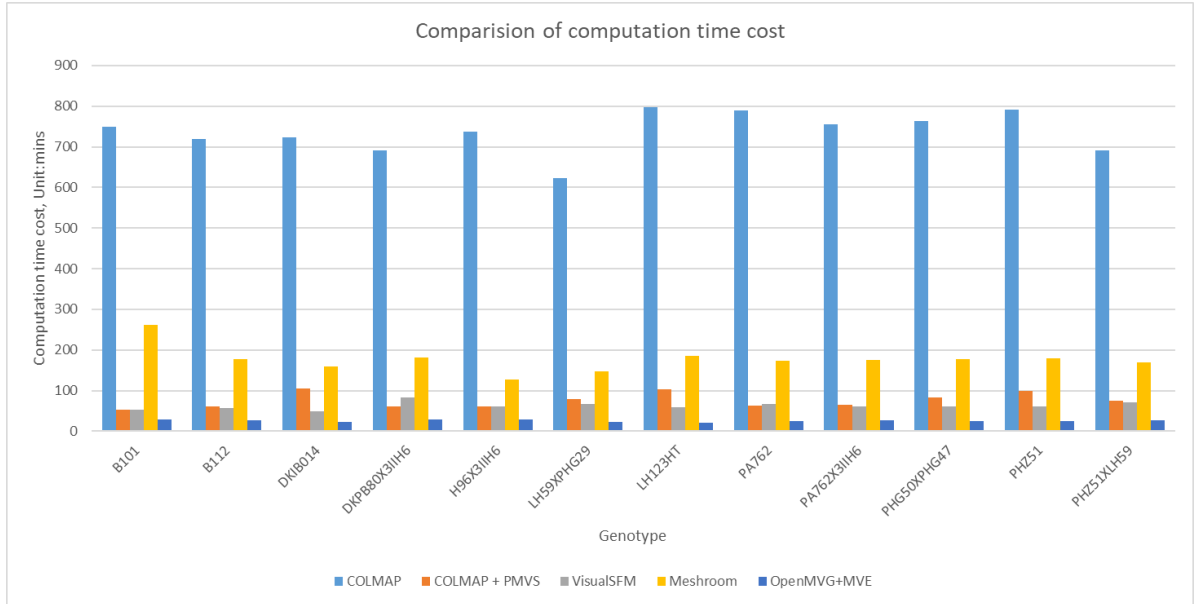
Figure 4. Comparison of computation times per 3D reconstruction pipeline. The five tested pipelines are color labeled, and the lengths of the bars represent the time needed to compute the point cloud model. Although COLMAP generated the best 3D models among all the pipelines regarding number of points and surface density, it also took the most computational time, on average. Meshroom was the second most time-consuming pipeline. COLMAP+PMVS took the least computational time, on average.

Computational Experiment 2: Comparison of Three-Dimensional Trait Accuracy with Maximal Surface Density Three-Dimensional Models

COLMAP produced higher surface density compared with the other tested algorithms, using around 600 images per sample based on the comparison results in Computational Experiment 1. In the second computational experiment, we tested whether the increased surface density enabled similar trait measurement accuracy using COLMAP, with around 600 images, to the original version of DIRT/3D (Liu et al., 2021) using 3600 images with VisualSFM. Therefore, we implemented COLMAP in the 3D reconstruction pipeline in DIRT/3D (Liu et al., 2021) and named it DIRT/3D (COLMAP) to distinguish it from the old DIRT/3D (VisualSFM).
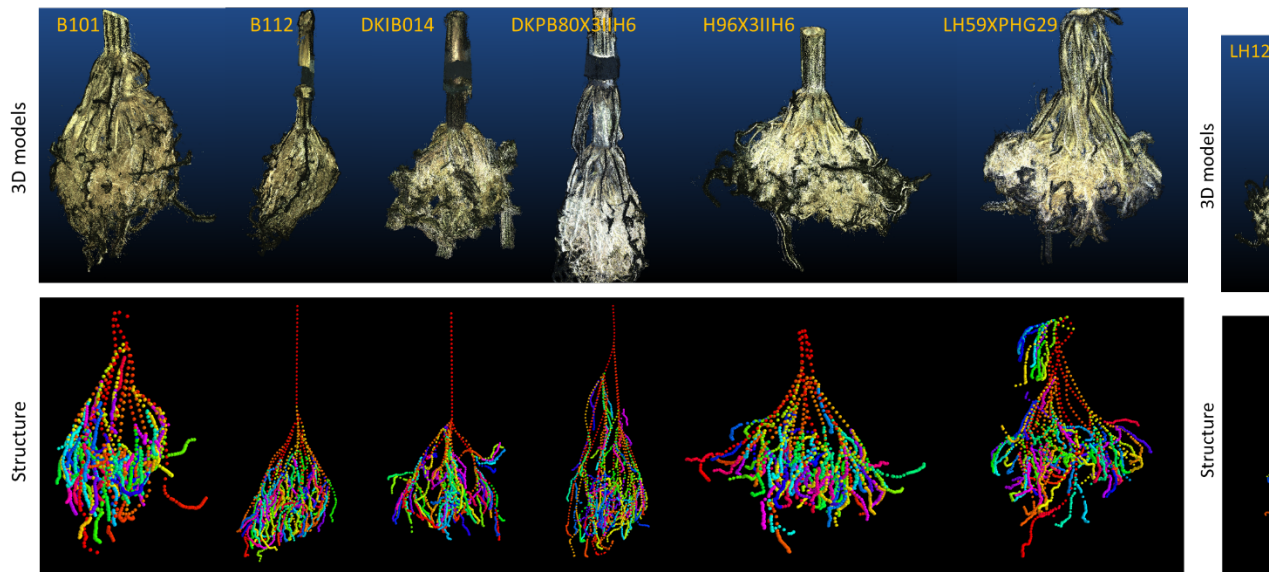
Figure 5. 12 sample 3D root models and their related computed root structure DIRT/3D (COLMAP). The rows named "3D models" provide examples of the computed 3D root point clouds per genotype. The rows named "Structure" illustrate the computed root architecture representation as skeletal curves.

In this computational experiment, we used the same maize-root image dataset as described in DIRT/3D (Liu et al., 2021). The full dataset includes 12 genotypes with 5~10 replicates per genotype. For each root sample, we down sampled the images from around 3600 images to 600 for this test. A visualization of the 12 example 3D root models and their skeletal curves is provided in Figure 5.
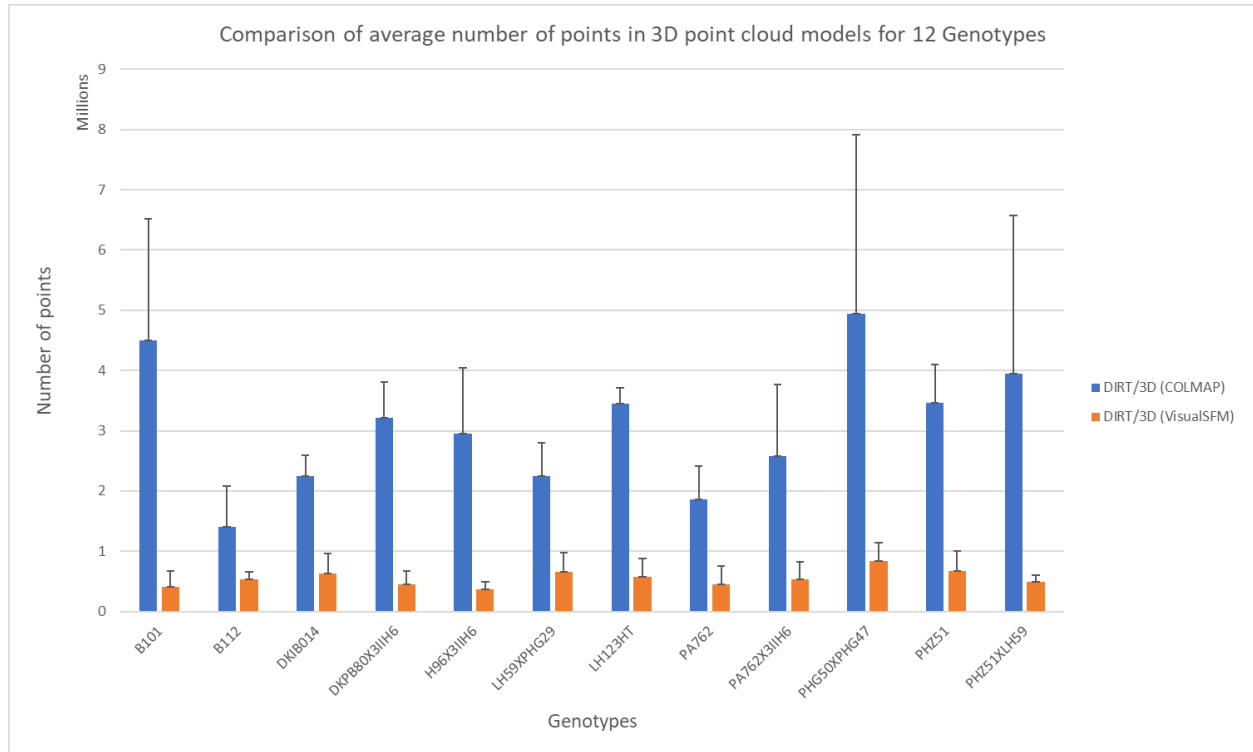
Figure 6. Comparison of the number of points in 3D models generated by DIRT/3D (COLMAP) and DIRT/3D (VisualSFM). The average numbers of points for the genotypes are rendered in different color bars. The lengths of the bars represent the value of the number of points. Black lines represent standard deviation.

We also compared the average number of points for each genotype for all samples within the genotype (see Figure 6). The comparison revealed that the number of points generated from DIRT/3D (COLMAP) increased, on average, six times compared with that of DIRT/3D (VisualSFM). The largest increase of the number of points was observed for Genotype B101. The average number of points generated by DIRT/3D (COLMAP) was approximately 11 times higher for B101 than in the 3D models generated by DIRT/3D (VisualSFM). The smallest increase of the number of points was observed for Genotype LH59XPHG29; the average number of points increased by about three times when changing from DIRT/3D (VisualSFM) to DIRT/3D (COLMAP).
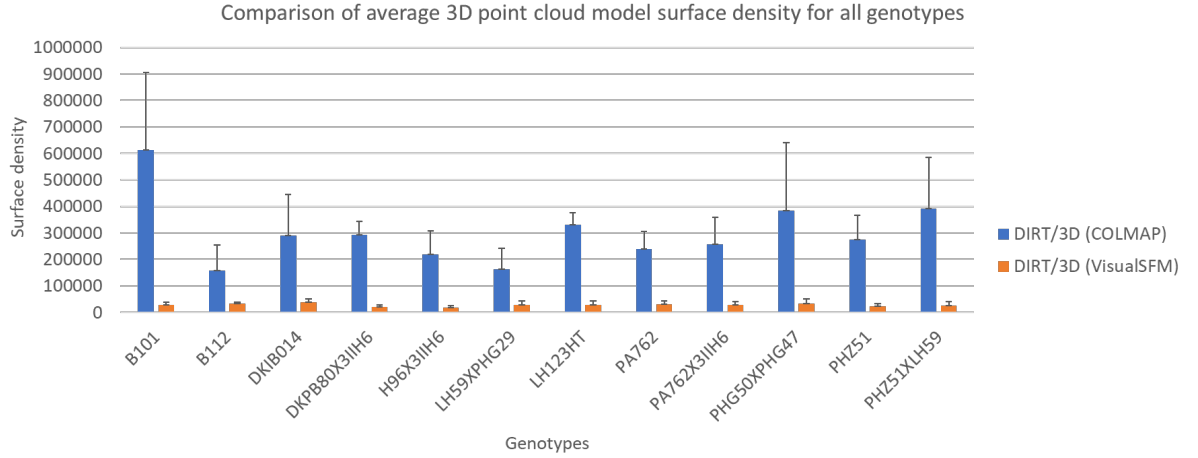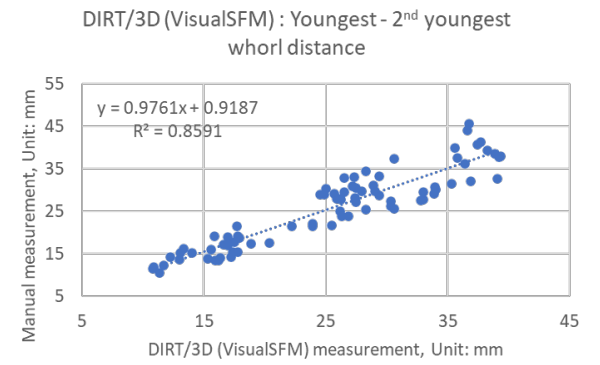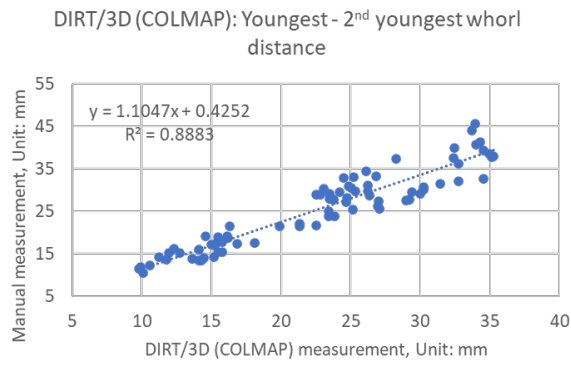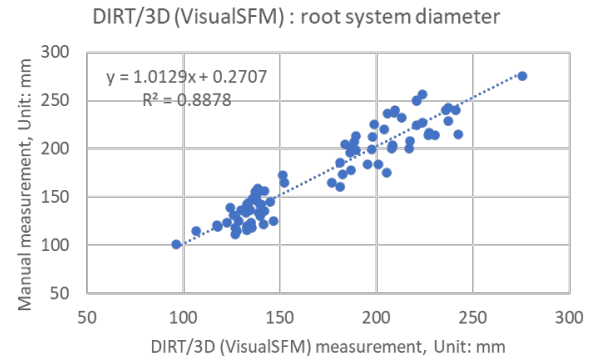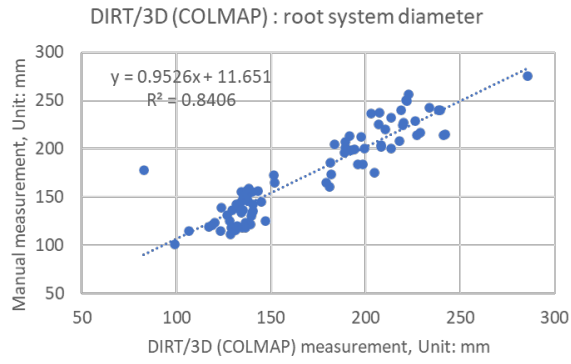
Figure 7. Comparison of surface density in 3D models generated from DIRT/3D (COLMAP) and DIRT/3D (VisualSFM). Average surface density for each genotype is rendered in different color bars, with the lengths of the bars representing the value of surface density. Standard deviation is represented as black lines. Surface density is defined as the number of neighbors divided by the neighborhood surface area.

In addition to the average number of points, we further compared the surface density of 3D models generated by DIRT/3D (VisualSFM) and DIRT/3D (COLMAP). The results in Figure 7 reveal that the model surface density improvement is significant between DIRT/3D (VisualSFM) and DIRT/3D (COLMAP). The results indicate that the surface density of the 3D model generated by DIRT/3D (COLMAP) increased 11 times, on average, compared with that of DIRT/3D (VisualSFM).
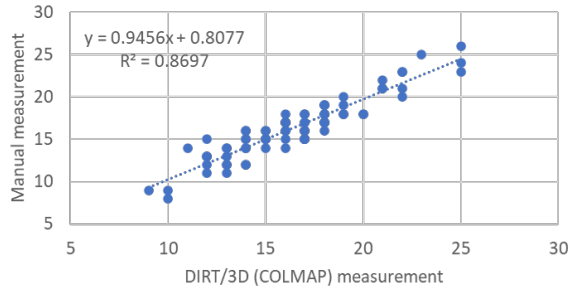
The largest increase in surface density was observed for Genotype B101, which increased 22 times from the DIRT/3D (VisualSFM) implementation to the DIRT/3D (COLMAP) implementation. The smallest increase in surface density was for Genotype B112, which still increased five times.

In our traits measurement accuracy comparison, we used the manual measurements of ten 3D root traits and compared their correlations with the DIRT/3D (VisualSFM) and DIRT/3D (COLMAP). The correlation analysis of these traits revealed r^2>0.80 and $P < 0.001$ (Figure 8). These traits include complete root crown traits and individual root traits, as described in (Liu et al., 2021).
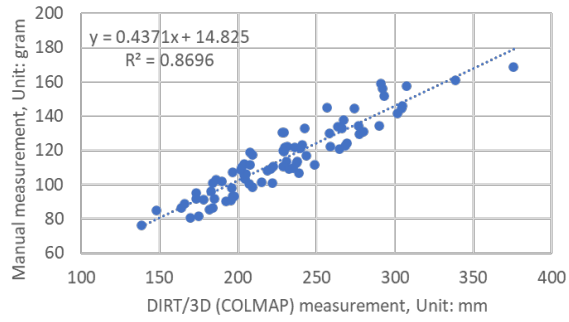
(A) Traits of complete root crown (RCs)

DIRT/3D (COLMAP) : root system diameter

$y = 0.9526x + 11.651$
$R^2 = 0.8406$

X-axis: DIRT/3D (COLMAP) measurement, Unit: mm
Y-axis: Manual measurement, Unit: mm

DIRT/3D (VisualSFM) : root system diameter

$y = 1.0129x + 0.2707$
$R^2 = 0.8878$

X-axis: DIRT/3D (VisualSFM) measurement, Unit: mm
Y-axis: Manual measurement, Unit: mm

DIRT/3D (COLMAP): Youngest - 2nd youngest whorl distance

$y = 1.1047x + 0.4252$
$R^2 = 0.8883$

X-axis: DIRT/3D (COLMAP) measurement, Unit: mm
Y-axis: Manual measurement, Unit: mm

DIRT/3D (VisualSFM) : Youngest - 2nd youngest whorl distance

$y = 0.9761x + 0.9187$
$R^2 = 0.8591$

X-axis: DIRT/3D (VisualSFM) measurement, Unit: mm
Y-axis: Manual measurement, Unit: mm

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DIRT/3D (COLMAP): number of youngest nodal root

$y = 0.9456x + 0.8077$
$R^2 = 0.8697$

Manual measurement

DIRT/3D (COLMAP) measurement

DIRT/3D (VisualSFM) : number of youngest nodal root

$y = 0.9271x + 1.0075$
$R^2 = 0.8656$

Manual measurement

DIRT/3D (VisualSFM) measurement, Unit: mm
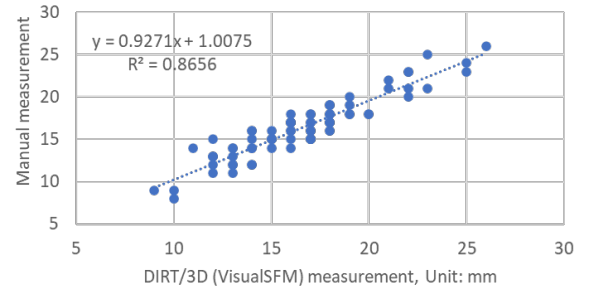
DIRT/3D (COLMAP): root biomass /volume

$y = 0.4371x + 14.825$
$R^2 = 0.8696$

Manual measurement, Unit: gram

DIRT/3D (COLMAP) measurement, Unit: mm

DIRT/3D (VisualSFM) : root biomass /volume
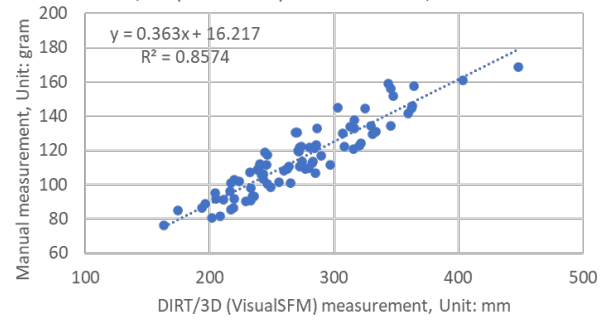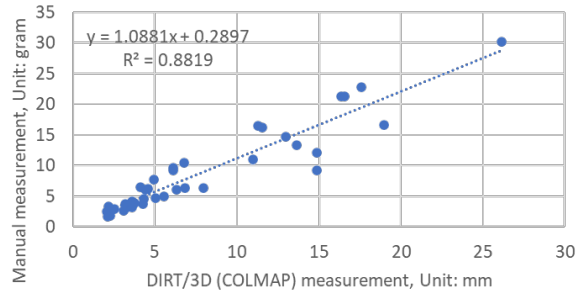
$y = 0.363x + 16.217$
$R^2 = 0.8574$

Manual measurement, Unit: gram

DIRT/3D (VisualSFM) measurement, Unit: mm

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DIRT/3D (COLMAP): 2nd youngest nodal-3rd youngest nodal whorl distance

$y = 1.0881x + 0.2897$
$R^2 = 0.8819$

DIRT/3D (VisualSFM): 2nd youngest nodal-3rd youngest nodal whorl distance

$y = 1.0018x + 0.2727$
$R^2 = 0.8887$
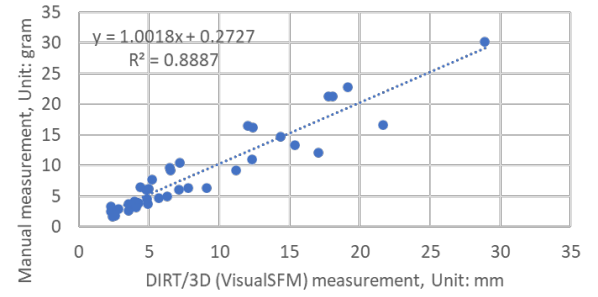
DIRT/3D (COLMAP): number of 2nd youngest nodal root

$y = 1.1207x - 0.003$
$R^2 = 0.9062$
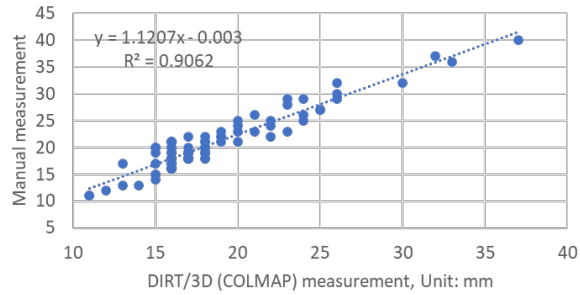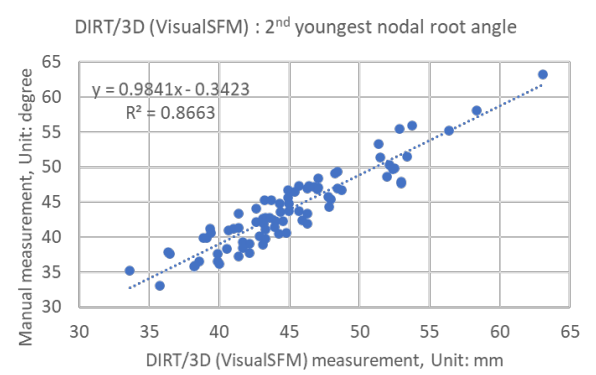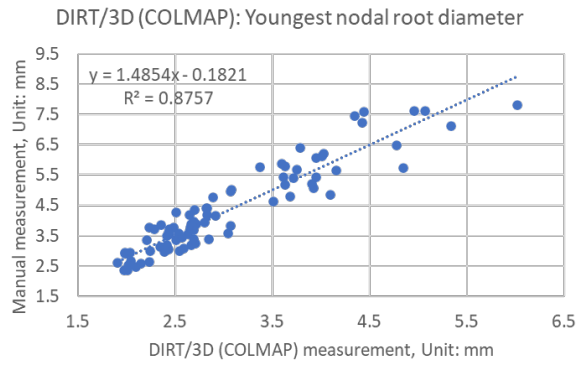
DIRT/3D (VisualSFM) : number of 2nd youngest nodal root

$y = 0.9908x - 0.2029$
$R^2 = 0.8821$
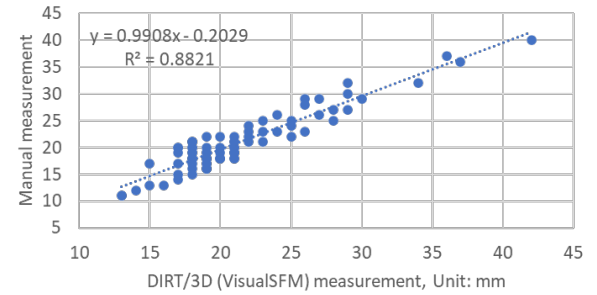
(B) Traits of individual roots (IRs)

DIRT/3D (COLMAP): Youngest nodal root diameter

$y = 1.4854x - 0.1821$
$R^2 = 0.8757$

Manual measurement, Unit: mm
DIRT/3D (COLMAP) measurement, Unit: mm

DIRT/3D (VisualSFM) : Youngest nodal root diameter

$y = 1.1094x - 0.1406$
$R^2 = 0.8551$

Manual measurement, Unit: mm
DIRT/3D (VisualSFM) measurement, Unit: mm

DIRT/3D (COLMAP): 2nd youngest nodal root angle

$y = 0.9354x + 1.8733$
$R^2 = 0.8025$

Manual measurement, Unit: degree
DIRT/3D (COLMAP) measurement, Unit: mm

DIRT/3D (VisualSFM) : 2nd youngest nodal root angle

$y = 0.9841x - 0.3423$
$R^2 = 0.8663$

Manual measurement, Unit: degree
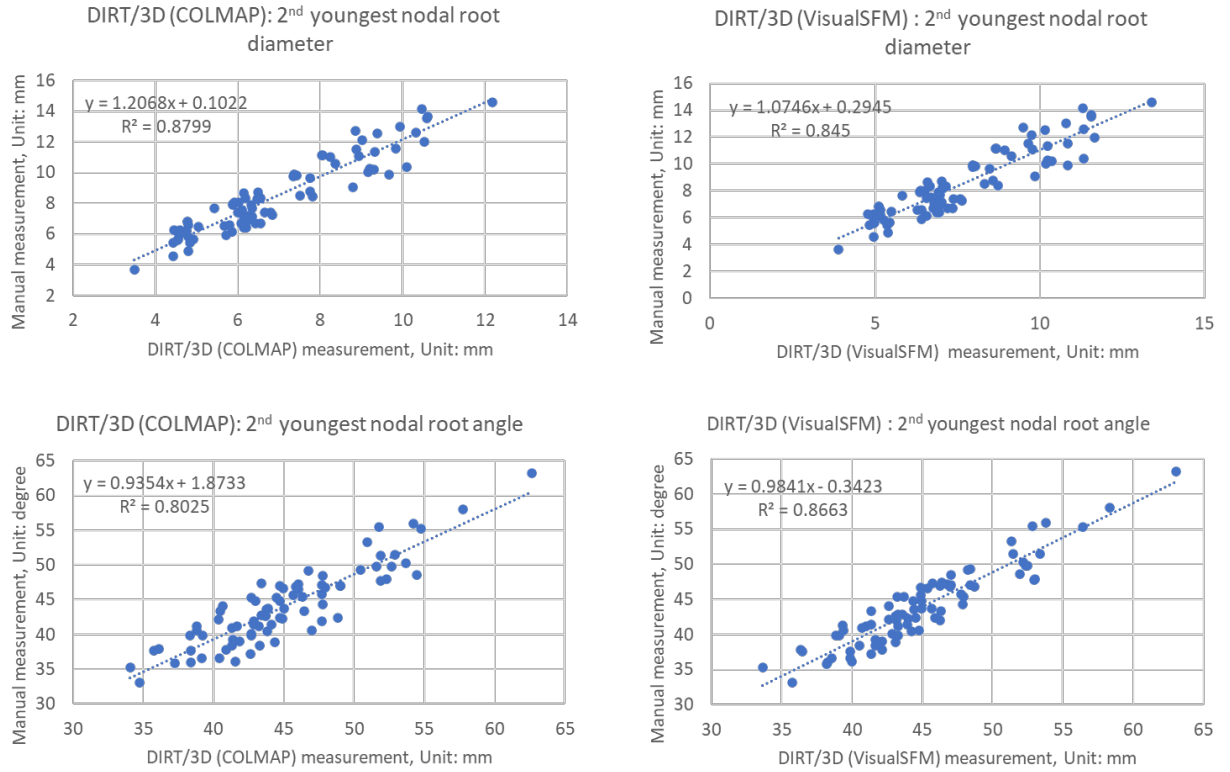DIRT/3D (VisualSFM) measurement, Unit: mm

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Figure 8. Comparison of correlation analysis of 10 traits. Results computed by DIRT/3D (COLMAP) and DIRT/3D (VisualSFM). The Y-axis represents the manual measurement values, whereas the X-axis represents the DIRT/3D (COLMAP) or DIRT/3D (VisualSFM) computed values. R^2 represents *R-squared value* in regression analysis. The dotted blue lines represent the linear trending lines of the correlation.

Regarding the complete crown root traits, we observed the improvement of trait measurement accuracy for most of the traits, except root-system diameter and second-youngest nodal–third-youngest nodal whorl distance, see Figure 8(A).

Regarding the individual root traits, we observed the improvement of trait measurement accuracy for the youngest nodal root diameter and second-youngest nodal root diameter, see Figure 8(B). This improvement might benefit from the surface density increase of DIRT/3D (COLMAP) over DIRT/3D (VisualSFM). Of note is that DIRT/3D (VisualSFM) resulted in $r^2 > 0.8$ in the original datasets, with around 3600 images per sample root; however, DIRT/3D (COLMAP) only required around 600 images per sample root, with the correlations improving despite reducing the number of input images.

DISCUSSION and conclusions

The first computational experiment evaluated five open-source pipelines regarding their 3D reconstruction quality in field-maize root systems. All five pipelines produce point clouds as output. We quantified reconstruction quality based on the point count and surface density, and we quantified efficiency as total computing time. In our evaluation, COLMAP and COLMAP+PMVS generated the largest number of points and highest surface density compared with the VisualSFM pipeline. Although the computation time of COLMAP was around 12-times slower than the VisualSFM implementation used in the original DIRT/3D paper (Liu et al., 2021), COLMAP achieved 10 times the number of points, and 94-times higher surface point density.

However, does an improvement in 3D model quality benefit the accuracy of root traits measurement? Therefore, the obvious increase in surface point density when using COLMAP in Computational Experiment 1 formed the hypothesis that a drastically reduced input image set can produce equally good trait measurements as the 3600 input images of the original VisualSFM implementation of DIRT/3D (VisualSFM). We tested this hypothesis in our second computational experiment by using around 600 images as input to DIRT/3D (COLMAP). We then computed the correlation of the DIRT/3D traits against the same manual ground truth used in DIRT/3D (VisualSFM). We observed slightly better correlations for the traits extracted with the COLMAP implementation of DIRT/3D (COLMAP) than with DIRT/3D (VisualSFM).

Overall, our experiments indicate it is possible to reduce the image-capturing time and trade it against increased computation time without significantly compromising the accuracy of the trait measurement. This finding suggests potential reductions in imaging time and effort, which typically require a trained staff member to place each root in the 3D scanning device manually and wait for the scanning to finish before placing the next root (Liu et al., 2021). Reducing the number of images from 3600 to around 600 reduces scanning time from seven minutes to four minutes per root and can reduce data transfer times from the scanner to online storage at CyVerse (Devisetty et al., 2016) from 15 minutes to six minutes (based on our second experiment). This outcome promises to streamline the most labor-intensive step of the root-phenotyping process.

We found that reductions in scanning and computation time are possible without excessively diminishing model quality. Our results highlight the need for further exploration of tradeoffs in root-image processing and demonstrate that neither customized operating rooms nor highly trained staff are necessary to operate a high-throughput root-imaging system. Our 3D imaging system promises to excel in high-throughput applications as an inexpensive and scalable 3D scanning solution for 3D root phenotyping.

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those of the author(s) and do not necessarily reflect those of the founders.

Conflict of Interest

The authors declare no conflict of interest.

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Optional Sections

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_model_reconstruction_demo

https://github.com/Computational-Plant-Science/3D_model_traits_demo

Cyverse link to all the 3D model results:

https://data.cyverse.org/dav-anon/iplant/home/lsx1980/3D_model_compare.zip

References

All in-text reference citations must be formatted using the author-year system and must be listed in alphabetical order. Please do not use numbering for your references.

References and citations should follow APA style. For more information about reference formatting, please see our style guide, starting in chapter 1, page 10.

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