4D STRUCTURAL ROOT ARCHITECTURE MODELING FROM DIGITAL TWINS

BY X-RAY COMPUTED TOMOGRAPHY

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ABSTRACT:

Background

Breakthrough imaging technologies are a potential solution to address the plant phenotyping bottleneck regarding marker-assisted breeding and genetic mapping. X-Ray CT (computed tomography) technology is able to acquire the digital twin of root system architecture (RSA) but computational methods to quantify RSA traits and analyze their changes over time are limited. RSA traits extremely affect agricultural productivity. We develop a spatial-temporal root architectural modeling method based on 4D data from X-ray CT. This novel approach is optimized for high-throughput phenotyping considering the cost-effective time to process the data and the accuracy and robustness of the results. Significant root architectural traits, including root elongation rate, number, length, growth angle, height, diameter, branching map, and volume of axial and lateral roots are extracted from the model based on the digital twin. Our pipeline is divided into two major steps: (i) first, we compute the curve-skeleton based on a constrained Laplacian smoothing algorithm. This skeletal structure determines the registration of the roots over time; (ii) subsequently, the RSA is robustly modeled by a cylindrical fitting. The experiment was carried out at the Ag Alumni Seed Phenotyping Facility (AAPF) from Purdue University in West Lafayette (IN, USA).

Results

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Roots from three samples of tomato plants at two different times and three samples of corn plants at three different times were scanned. Regarding the first step, the PCA analysis of the skeleton is able to accurately and robustly register temporal roots. From the second step, the volume from the cylindrical model was compared against the root digital twin, reaching a coefficient of determination ($R^2$) of 0.84 and a $P < 0.001$.

Conclusions

The results confirm the feasibility of the proposed methodology, providing scalability to a comprehensive analysis to high throughput root phenotyping.

**KEYWORDS**: phenotyping; imaging; proximal sensing; 3D modeling; skeleton; root system architecture (RSA); X-ray CT (computed tomography); digital twin.

1. BACKGROUND

Plant roots are critical for water and nutrient uptake from soils [1, 2]. Roots can form complex networks composed by different type and age of roots [3]. The spatial arrangement of the root system is called Root System Architecture (RSA). Considering that RSA can affect crop performance, selecting crops based on specific RSA could lead to improve agricultural productivity [4]. However, our understanding of RSA development in soil is limited by the complexity of the root phenotyping in situ. Because of the opaque nature of soil, progress made in non-destructive root phenotyping has been limited to systems such as the rhizotron, which acquires two-dimensional images of root growing in transparent enclosures.

Plant science community requires advance approaches in the characterization of RSA using novel image-based technologies [5], to quantify the 3D dynamics in RSA [6, 7]. Three tomographic techniques are currently available for non-destructive 3D phenotyping: X-ray Computed Tomography (CT), Magnetic Resonance Imaging (MRI) and Position Emission Tomography (PET). Recent technological innovations in scan resolution and the throughput in image processing made X-ray CT the current state of the art technology for non-destructive root phenotyping in soil [8]. Generally speaking, a regular X-ray CT has a source and a detector. The source is responsible for passing the X-ray beams through a sample, which absorbs a portion of these beams, while the detector will record this attenuated signal as two-dimensional projections. The attenuation is based on the material properties and electron-density; thus, the internal structure of the scanned sample becomes visible by contrasting the different elements inside depending on how much X-ray they absorb based on their chemical composition and characteristics [9]. Further, a 3D reconstruction of the sample material can be generated based on the 2D projections by scanning it at different positions [10].

A shape descriptor highly recommended in plant science is the curve-skeleton. It is able to describe the hierarchies and extent of branching plant networks [11]. Methods for skeleton extraction are primarily grouped in volumetric and geometrics, depending on the computed interior or only surface representation. As a common drawback, volumetric approaches potentially lose details and
have numerical instability caused by inappropriate discretization resolution [12]. In contrast, geometric methods approximate the medial surface by extracting the internal edges and faces. Medial axis skeleton and Reeb-graph-based methods are a couple of examples that are established using the geometric principles. In the 3D space, the medial axis usually fails when the planes occurrence.

For methods in 3D modeling, there are as well two categories. The first one includes voxel approaches, where volumetric models are constructed by partitioning the point cloud into voxels. The capability of these methods in model irregular surfaces is limited. The other category comprises parametric surface methods. The circular cylinder is the most dominant shape-fitting approach, because of its balancing between simplicity and realistic modeling [13].

Analysis of root models derived from X-ray CT images allows quantification of root growth over time and in response to external stresses, but there are several major challenges associated with this data. These include root segmentation and 3D modeling, which involve extracting the root digital twin from X-ray radiographs, and computing root architecture measurements from resulting models. The RootTine protocol was design to segment the root in a faster and automated way to be implemented in high-throughput (HTP) systems [14]. However, this method only computes the root length as a phenotyping trait by medial axis-based skeletonization processes. RootForce [15] is one of the latest developments in semi-automatic segmentation based as well in RootTine. It is able to extract more traits, for instance root volume and root growth angles by Reeb Graph-based skeletonization.

RooTrack is another tool for not only root segmentation but also for visually object tracking by identifying boundaries in image cross-sections. The main advantage is detecting and differentiating multiple roots from different plants in the same image. Still, this methodology is not yet applicable to HTP or automated procedures [16]. These tools mainly tackle the root segmentation issue from X-ray data as a primary challenge. The focus of this paper is to model temporal digital twins of roots to quantify traits as well as to record the topological and hierarchical branching structure, after the segmentation from the soil is already done. To the best of our knowledge, no research has been done to parametrize 3D root surfaces or even label their different branches. In our methodology, the temporal analysis of roots is solved throw skeleton extraction, while the spatial quantification is performed by a shape-fitting approach.

In this paper, we propose a spatial-temporal root architectural model from digital twins obtained by X-ray CT (computed tomography). Values of essential root traits were extracted as phenotypic data to quantitatively assist growth analyses and RSA description. The proposed methodology consists of two phases. In the first, we compute a curve-skeleton as a powerful descriptor for analyzing root system networks. We use a constrained Laplacian smoothing algorithm which directly performs on the mesh domain, followed by a connectivity surgery and embedding refinement process. As a result, this skeletal structure controls the registration process in temporal series. Secondly, the root system is robustly reconstructed by generating a flexible cylinder model. This non-linear optimization problem is solved by nonlinear squares iterative solution. The full pipeline is optimized for quantifying accurate and robust results, allowing high-throughput root phenotyping using X-ray CT systems.
2. MATERIALS AND METHODS

2.1. Materials

The digital twin of the root system can be obtained in 3D by X-ray CT. This technology allows us to non-destructively, comprehensively and accurately monitor the exact same plant root even at different points in time under controlled conditions. Our system scans pots with photon energies in the 225 keV range, and is able to scan pots 20 cm in height in less than 7 minutes. The resulting voxel size is set at 200 μm. The Focus-Detector distance is 800 mm. Both X-ray detector and X-ray tube are fixed within the system. A pot rotation stage allows 360° for the measurement. A vertical translation axis optionally extends the vertical field of view. Table 1 summarizes the rest of the technical specifications of the system.

Table 1. Technical specifications of the X-ray CT system.

| Parameter               | Value                                      |
|-------------------------|--------------------------------------------|
| X-ray cabin             |                                            |
| Pot diameter            | 100-200 mm                                 |
| Maximum pot height      | 400 mm                                     |
| Footprint dimension     | 2500 * 1500 * 3500 mm³                     |
| Maximum sample height   | 2500 mm                                    |
| Maximum weight          | 6 ton                                      |
| X-ray source            |                                            |
| High Power tube         | 225 kV                                     |
| Voltage                 | ≤ 200 kV                                   |
| Power                   | ≤ 200 W                                    |
| Cooling device          | Included                                   |
| Detector system         |                                            |
| Type                    | Flat Panel Detector                        |
| Radiation Hard detector|                                           |
| Size                    | 300 * 250 mm²                              |
| Pixel matrix            | 3500 * 2900                                |
| Pixel pitch             | 84 μm                                      |

The experiment was performed at the Ag Alumni Seeds Phenotyping Facility (AAPF) at Purdue University in West Lafayette (IN, USA). In this facility, plants are transported in standard carriers to the X-ray CT system from the loading position by a mechanical conveyor belt. During the summer of 2019, root systems from three tomato plants at two different times and three corn plants at three different times were scanned. The pots were circular with 180 mm-diameter and 200 mm-height for tomato and 400 mm-height for corn. The type of pot media in the pots is sifted sphagnum peat moss with a moisture inferior at 20% of relative humidity.

Table 2 summarize the main characteristics of the digital twins of the roots used in this study (additional file as Data S1: dataset), whereas Figure 1 their visualizations by X-ray CT.

Table 2. Root digital twin dataset.

| Sample | Scanned date  | Scan ID | Num. vertices | Num. faces |
|--------|---------------|---------|---------------|------------|
| Tomato | July 2nd, 2019| 111     | 120468        | 240928     |
|        | July 18th, 2019| 112     | 252550        | 505148     |
| Date       | ID 12 | ID 13 | ID 21 | ID 22 | ID 23 |
|------------|-------|-------|-------|-------|-------|
| July 3rd, 2019 | 121   | 131   | 211   | 221   | 231   |
| July 18th, 2019 | 122   | 132   | 212   | 222   | 232   |
| July 23rd, 2019 | 132   | 132   | 213   | 223   | 233   |
| Corn       |       |       |       |       |       |
| July 9th, 2019 | 211   | 231   | 211   | 231   | 231   |
| July 15th, 2019 | 212   | 232   | 212   | 232   | 232   |
| July 23rd, 2019 | 213   | 233   | 213   | 233   | 233   |

**Figure 1.** Visualization of the root samples from tomato (a) and corn (b) used in this study.

### 2.2 Methodology

In this study, we developed an approach that can be used to enable high throughput root phenotyping tasks. It includes a 4D structural root architectural modeling from digital twins by X-ray CT. These digital twins were obtained using RootForce tool [15]. RootForce approach is based on Frangi’s vesselness method [17], extended for the semi-automatic segmentation of roots.
Beforehand, a thresholding is applied to select a range of attenuation coefficient according to the type of soil and plants used in the experiment. Then, the Hessian-based Frangi vesselness filter is used for small roots detection while larger roots are detected based on their 3D homogeneity using a 3D-Gaussian filter. The small and large vessel structures are then merged using upper and lower merging thresholds. Here, the value range of the attenuation coefficient was 0.07 to 0.19 with root diameters of 0.4, 0.5, 0.6, 1.0 and 1.2 mm. The upper and lower threshold of the merging parameters were respectively 25 and 1000 for the corn roots and respectively 100 and 1000 for the tomato roots. A size filter was used to eliminate unconnected fragment with a minimum volume of 25 mm³ for the corn roots and 50 mm³ for the tomato roots. The minimum root diameter that can be segmented with RootForce is about 2.5 voxels in diameter. Here, using a resolution of 200 μm cubic voxel size for the reconstruction, the minimum detectable root diameter is approximately 0.5 mm. Once the segmentation process is done, we apply our model approach. It consists of two clearly differentiated phases: the computation of the curve-skeleton which serves for the registration of temporal series, and the RSA cylindrical model of the digital twin for spatial analysis. Figure 2 summarizes the workflow to follow.

**INPUT DATA**
- **ROOT DIGITAL TWIN**
  - By X-ray CT
  - Image acquisition
  - 3D reconstruction
  - Root segmentation
  - 3D mesh: noise & gap removal

**SKELETONIZATION**
- Laplacian-based contraction:
  - connectivity surgery
  - refinement
  - Root registration over time
  - Elongation rate

**ROOT DYNAMICS**
- **TEMPORAL ANALYSIS**
- **SPATIAL ANALYSIS**
  - Flexible cylinder fitting
  - Branching map
  - Volume, diameter, length, height, angle of axial and lateral roots

**Figure 2.** Workflow of the methodology proposed: from the digital twin of the root, first we extract the curve-skeleton to register temporal series of the same root and secondly, we model the RSA by a flexible cylinder fitting.

### 2.2.1. Skeletonization

The curve-skeleton is essentially a structure that abstracts the model volume and topological characteristics. For this study, we choose a robust skeleton extraction method via Laplacian-based contraction [12, 13]. The algorithm works directly on the mesh, without a resampled volumetric representation. Thereby, it is pose-insensitive, and invariant to global rotation. The method first contracts the mesh geometry into a zero-volume skeletal shape, removing details and noise by applying an iterative Laplacian smoothing that tightly moves all the vertices along their curvature normal directions. After each iteration, a connectivity process is carried out, removing all the collapsed faces from the degenerated mesh until no triangles exist. The challenge of this step is to carefully control the contraction procedure so that it leads to a collapsed mesh with sufficient skeletal nodes to maintain a fine correspondence between the skeleton and the original geometry. As a consequence, the contraction does not alter the mesh connectivity and retains the key features, guaranteeing to be homotopic to the original mesh. Finally, to refine the skeleton’s
geometric embedding, we describe a process that moves each skeletal node to the center of mass of its local mesh region. The potential limitation of this skeleton extraction is that it only works for closed mesh models with manifold connectivity since the Laplacian contraction algorithm operates for every individual vertex.

This skeletal structure drives the registration process in temporal series. Thus, we can automatically perform a growth analysis of the RSA, quantified by the elongation rate as a trait. To register temporal series, Principal Component Analysis (PCA) is performed [19]. In general, the principal components are eigenvectors of the data's covariance matrix. More specifically, this statistical analysis uses the first and second moments of the curve-skeleton, resulting in three orthogonal vectors centered on its center of gravity. The PCA summarizes the distribution of the lines along the three dimensions and models the principal directions and magnitudes of the curve-skeleton distribution around the center of gravity. Thereby, the registration of temporal series is carried out by overlapping the principal component axes. The elongation rate is measured in the first principal direction.

2.2.2. RSA model

We use a group of geometric primitives to model the surface and topology of the root. The circular cylinder is the simpler primitive. In the case of trees acquired by TLS, the circular fitting is the most robust primitive in the sense of a well-bounded volumetric modelling error, even with noise and gaps in the data, compared with more complex primitives which are more sensitive to data quality [14]. Thereby, our modeling is based on circular cylinder fitting as an optimal parametrization to provide significant traits of the RSA such as diameters, specific surfaces and volumes from the main root and ramifications. We use the approach of [20], where they model point clouds of individual trees acquired from TLS (Terrestrial LiDAR Scanner) by a cylindrical parametrization. This process is scale independent because only neighbor-relations and relative sizes are needed. To apply this approach, the 3D mesh of the root digital twin is transformed into a regularized point cloud [21]. For that, randomly sampled points over the mesh are extracted by fixing a desired density, (5 points/mm$^2$) and a restored point cloud is obtained. Subsequently, we apply Dart Throwing Poisson Disk sampling to the point cloud to make the points appear more uniform by culling those points that are close to a randomly selected point [22]. In this step, a threshold based on Euclidean distance between points of 1 mm is set. After this process, a significant reduction of points is achieved because the Poisson subsampling approach considers the local point distribution, retaining key elements of the structure.

Once the regularized point cloud is achieved, the cylinder fitting is applied. The process has 2 consecutive phases: first, the point cloud is segmented into the main root and its ramifications, and secondly, the surface and volume of the segments are robustly fitted with geometric primitives, specifically cylinders. This non-linear optimization problem is solved by nonlinear squares iterative solution. The topological distribution of the RSA is also recorded. Mathematically, the model is raised by a local approach in which the point cloud is covered with small sets corresponding to connected surface patches in the root surface. In that way, the RSA and size properties, such as volume and branch size distributions, can be approximated.
3. EXPERIMENTAL RESULTS

All the experimental results obtained below were run on a 3.6-GHz desktop computer with an Intel CORE I7 CPU and 32-GB RAM. First, the digital twin of the root obtained by X-ray has to be previously closed and repaired to be able to apply our approach. For this purpose, we follow the procedure already explained by [23], which incorporates several automatic and sequential tasks: (i) filling of holes through algorithms based on interpolators of radial basis function [24]; (ii) repairing of meshing gaps by threshold distance algorithms [25]; (iii) removing of topological noise, allowing the mesh to be re-triangulated locally [26]; (iv) removing of topological and geometric noise by anti-aliased Laplacians filters [27].

Once the mesh is repaired, the skeleton extraction and the RSA model pipelines are run. The code from the RSA model saves (i) general values of the entire root as total volume, height, length, number and order of branches, and the mean and maximum diameter of the crown, (ii) branching map of the root that includes the topological relation of each ramification, (iii) volume, length, angle, height, azimuth and zenith of each branch, and (iv) length, diameter, angle and coordinates of all the cylinders that belong to each branch. Figure 3 and 4 show both results for a tomato and a corn root sample. In the zoom window, we can appreciate the complexity and accuracy of the model. In our RSA model, each branch is labeled in a unique color and quantified. This is a brand-new solution that is able to quantify branching patterns, which are critical for biologists to understand water and nutrient uptake. In the supplementary material, we made a video that shows the segmented root, the skeleton and the RSA model, for tomato and for corn (Video S2: 4D Structural Root Architecture Modeling).
**Figure 3.** Tomato root sample with a zoom window: digital twin by X-ray CT system (a), curve-skeleton extraction based on a constrained Laplacian smoothing algorithm, where the mesh is in orange and the skeleton is in red (b), and the RSA model based on a flexible cylinder fitting, where each ramification is in different color (c).

**Figure 4.** Corn root sample with a zoom window: digital twin by X-ray CT system (a), curve-skeleton extraction based on a constrained Laplacian smoothing algorithm, where the mesh is in orange and the skeleton is in red (b), and the RSA model based on a flexible cylinder fitting, where each branch is in different color (c).

From the RSA model, different traits are extracted. Table 3 summarize the general values of the entire roots.

**Table 3.** General values of the RSA model for each sample (volume, volume of the main root, total length, length of the main root, number of branches, maximum order of ramifications and maximum and mean crown diameter).

| Scan ID | Vol. [mm³] | Vol. Main Root [mm³] | Total Length [mm] | Main Root Height [mm] | Num. Branches | Max. order Branches | Crown Diam. Max [mm] | Crown Diam. Mean [mm] |
|---------|------------|----------------------|-------------------|----------------------|---------------|---------------------|----------------------|----------------------|
|         |            |                      |                   |                      |               |                     |                      |                      |
4. VALIDATION RESULTS AND DISCUSSION

The volume of each digital twin of the root is measured by Cloud Compare software [28], that computes the volume within the solid mesh. Moreover, number of branches from digital twins are estimated by a visual analysis. Table 4 shows several metrics between the digital twin and the cylindrical model of each root of these two parameters. In particular, the root mean square error (RMSE), the relative RMSE (RRMSE), the average systematic error (ASE), and mean percent standard error (MPSE) were calculated as follow:

\[ \text{RMSE} = \sqrt{\frac{\sum_{i=1}^{n} (y_{\text{model}}^{i} - y_{\text{dig twin}}^{i})^2}{n}} \]  

\[ \text{RRMSE} = 100 \times \frac{\text{RMSE}}{y_{\text{dig twin}}} \]  

\[ \text{ASE} = \frac{100}{n} \sum_{i=1}^{n} \left( \frac{y_{\text{model}}^{i} - y_{\text{dig twin}}^{i}}{y_{\text{dig twin}}^{i}} \right) \]  

\[ \text{MPSE} = \frac{100}{n} \sum_{i=1}^{n} \left( \frac{y_{\text{model}}^{i} - y_{\text{dig twin}}^{i}}{y_{\text{dig twin}}^{i}} \right) \] 

where \( y_{\text{model}}^{i} \) is the parameter estimated from the model of the \( i^{th} \) scan, \( y_{\text{dig twin}}^{i} \) is the measured parameter from the digital twin of the \( i^{th} \) scan, \( \bar{y}_{\text{dig twin}} \) is the mean of the measured parameter from the digital twin per scan, and \( n \) is the number of scans.
Table 4. Statistic metrics of number of branches and volume where RMSE is the root mean square error, RRMSE is the relative RMSE, ASE is the average systematic error, and MPSE is the mean percent standard error.

| Parameter       | Root  | RMSE | RRMSE (%) | ASE (%) | MPSE (%) |
|-----------------|-------|------|-----------|---------|----------|
| # branches [number] |       |      |           |         |          |
| Tomato          | 2.48  | 8.76 | 1.37      | 1.67    |          |
| Corn            | 1.76  | 8.31 | 5.94      | 0.44    |          |
| Total volume [mm³] |       |      |           |         |          |
| Tomato          | 1087.66 | 36.92 | -29.01   | 0.48    |          |
| Corn            | 4470.03 | 25.11 | -23.63   | 2.86    |          |

From the results of this table, we can affirm that our model detects branches mainly by excess in tomato and corn. Moreover, for tomato branches were estimated by default more than for corn. Regarding the volume discrepancies, they are larger for corn in absolute values. In relative quantities, the error in tomato is larger. For both, always the volume is estimated by default. The errors in the number of branches detected could have been caused by segmentation problems. Figure 5 (a) represents a part of the RSA model from the ID 121 tomato scan. Each detected branch is in a distinct color. We can see that the loss of the tracking of the branches could have generated new false branches. This issue is high-lighted with a red circle in the figure. Another type of common errors is the volume discrepancies between the digital twin and the RSA model, mainly generated when the shape of the branch is not cylindrical and when the diameter of each segmented branch does not decrease along the length. This topological property is used in the branch segmentation of the model. Figure 5.b represents a part of the ID 223 corn scan, where the digital twin is represented by points and the model by polyhedrons in the same color. The shape of the branches could generate errors to fit cylindrical solids.
Figure 5. Errors in the number of detected branches due to loss of tracking in the segmentation process. Branches are on different colors with a red circle remarking this issue (a); and volume discrepancies in between the digital twin, represented with dense points, and the RSA model represented with polyhedrons with similar colors (b).

The relative volume of the RSA model is compared against the relative volume from the digital twin measured by Cloud Compare software [28]. We split the digital twins in 10%, 20%, 30%, 40%, 50%, 60%, 70%, 80% and 90% of the total volume (starting from the top) and we run the model with these parts to evaluate its performance, which reached an $R^2$ of 0.82 for tomato and 0.74 for corn with a $P < 0.001$, as Figure 6 displays. When tomato and corn measurements are together, the $R^2$ improves to 0.83.
Figure 6. Volume correlation between the RSA model and the digital twin for each scan sample: tomato (a) and corn (b).

Moreover, this methodology is able to temporally analyse the root dynamics through a registration process based on a PCA of the skeleton from the root mesh. Figure 7.a shows the same tomato root sample registered at two different times (July 2nd and 18th, 2019), with a slot of 16 days. The elongation rate is mapped in Figure 7.b, where the maximum value is 2.58 cm on the upper-right ramification. Figure 8 illustrates the same temporal sample where the convex hull is individually computed (Figure 8.a and 8.b) and as well the variation in time (Figure 8.c). The convex hull value for Figure 8.a is 229.87 cm³ and for Figure 8.b is 519.76 cm³.

Figure 7. Tomato root sample in July 2nd and 18th, 2019, registered by a PCA of the skeleton (a) and the elongation rate mapped in 3D (b).
Figure 8. Mesh of the tomato root sample from July 2nd (a) and 18th (b), together with its convex hull. Both convex hulls registered and superimposed in solid and transparent faces (c).

Table 4 recaps the maximum and mean value of the elongation rate for the temporal series of each sample and the convex hull volume reached by each root.

| Scan ID | CH Volume [cm$^3$] | Max. elongation [cm] | Mean elongation [cm] |
|---------|---------------------|----------------------|----------------------|
| 111     | 2298.71             |                      |                      |
| 112     | 5197.62             | 2.58                 | 0.63                 |
| 121     | 6183.22             |                      |                      |
| 122     | 15525.64            | 3.02                 | 0.97                 |
| 131     | 5762.72             |                      |                      |
| 132     | 9502.78             | 1.98                 | 0.62                 |
| 211     | 50631.14            |                      |                      |
| 212     | 64718.84            | 5.23                 | 1.07                 |
| 213     | 64131.16            | 4.02                 | 0.76                 |
| 221     | 58427.65            |                      |                      |
| 222     | 58146.56            | 3.75                 | 0.98                 |
| 223     | 63539.13            | 4.14                 | 0.77                 |
| 231     | 61435.67            |                      |                      |
| 232     | 62898.37            | 4.01                 | 0.87                 |
| 233     | 63957.62            | 3.89                 | 0.79                 |
5. CONCLUSIONS

In conclusion, the proposed pipeline aims to automatically extract phenotypic data of RSA from digital twins obtained by non-invasive X-ray CT. This pipeline is able to analyze both spatial and temporal root dynamics. As potential advantages, we find this methodology fully automatic, fast, precise and sufficiently robust to provide scalability for high throughput root phenotyping. Determining the contribution of structural root traits to crop performance is vital to overcome climate change, environmental degradation and food insecurity. Moreover, structural root traits that are accurately extracted from X-ray data will enhance our understanding of the relationship between the plant phenome and plant function in ecosystems, which is the end goal of functional phenomics [29]. Moreover, this computationally low-cost workflow will potentially increase the usability of imaging technologies for high-throughput phenotyping regarding genetic mapping and phenotypic selection in breeding programs.

DECLARATIONS

Availability of data and materials
The dataset supporting the conclusions of this article is included within the article (additional files Data S1: dataset and Video S2: 4D Structural Root Architecture Modeling).

Competing interest
The authors declare that they have no competing interests.

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Author’s contributions
M.H. conceived the idea, developed the data analysis pipelines and software, performed the data analysis and visualization, and wrote the manuscript; V.M., A.I. and A.S. contributed to writing the manuscript. V.M., A.I. and Y.Y. contributed to the method development and data analysis; M.T. and Y.Y. supervised the research and edited the manuscript. All authors have read and agreed to the published version of the manuscript.

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