

ROOT PHENOTYPING FROM X-RAY COMPUTED TOMOGRAPHY: SKELETON EXTRACTION

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ABSTRACT

Breakthrough imaging technologies are a potential solution to the plant phenotyping bottleneck in marker-assisted breeding and genetic mapping. X-Ray CT (computed tomography) technology is able to acquire the digital twin of root system architecture (RSA), however, advances in computational methods to digitally model spatial disposition of root system networks are urgently required.

We extracted the root skeleton of the digital twin based on 3D data from X-ray CT, which is optimized for high-throughput and robust results. Significant root architectural traits such as number, length, growth angle, elongation rate and branching map can be easily extracted from the skeleton. The curve-skeleton extraction is computed based on a constrained Laplacian smoothing algorithm. This skeletal structure drives the registration procedure in temporal series. The experiment was carried out at the Ag Alumni Seed Phenotyping Facility (AAPF) at Purdue University in West Lafayette (IN, USA). Three samples of tomato root at 2 different times and three samples of corn root at 3 different times were scanned. The skeleton is able to accurately match the shape of the RSA based on a visual inspection.

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

1. INTRODUCTION

Root System Architecture (RSA) is the connection between plants and soils, being the critical piece to water and nutrient extraction from (Seethepalli et al., 2020, Postma et al., 2017). The plant science community requires advanced approaches in the characterization of root system architecture (RSA) that support emerging root phenotyping technologies (Bucksch et al., 2014b).

The curve-skeleton is identified as a powerful descriptor for analyzing root system networks (Bucksch, 2014a). From the literature, there are several methods to extract the curve-skeleton from a solid, usually classified into two key types: volumetric and geometric (Cornea et al, 2007). This classification relies on the solid representation, depending on using an interior representation or a surface representation. Regarding volumetric approaches, they normally used a volumetric discrete representation, either a regularly partitioned voxelized representation or a discretized function demarcated in the 3D space. The potential loss of details within the solid and numerical instability due to inappropriate discretization resolution are the general disadvantages (Au et al., 2008). In the other hand, geometric approaches directly work on the meshes or point sets. The most common used geometric methods are the Voronoi diagram (Brandt and Algazi, 1992) and medial axis (Marie et al., 2016). Furthermore, currently, reeb-graph-based methods have increased the popularity (Mohamed et Hamza, 2012). There are another group of approaches, which are not classified within the two main types.

In this paper, we propose a skeleton extraction from root digital twins obtained by X-ray CT. Thereby, values of essential root traits can be extracted as phenotypic data to quantitatively assist growth analysis and RSA description. We use a constrained Laplacian smoothing algorithm which is performed directly on the mesh domain, followed by a connectivity surgery and embedding refinement process. This skeletal structure controls the correspondences between root ramifications over time, driving the registration procedure in temporal series. This challenging process is optimized for accurate, repeatable, and robust data, allowing high-throughput root phenotyping from X-ray CT systems.

2. MATERIALS AND METHODS

2.1. Materials

X-Ray CT is an emerging 3D imaging technology able to non-invasively scan the underground root with high speed and efficiency. The digital twin of the root structure in 3D can be precisely obtained. 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 in less than 7 min for 20 cm in height with photon energies in the 225 keV range. The resulting voxel size will be 200 μ m. The Focus-Detector distance is 800 mm. Both X-ray detector and X-ray tube are fixed within the system. A rotation stage allows 360° for measurement. There is as well a vertical translation axis to optionally extend the vertical field of

view. Table 1 summarizes the rest of the technical specifications of the system.

The experiment was set up at the Ag Alumni Seed 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, three samples of tomato root at 2 different times and three samples of corn root at 3 different times were scanned (Table 2). The pots were circular with 200 mm-height for tomato and 400 mm-height for corn.

<i>Parameter</i>		<i>Value</i>
<i>X-ray cabin</i>	<i>Pot diameter</i>	100-200 mm
	<i>Maximum pot height</i>	400 mm
	<i>Footprint dimension</i>	2500 * 1500 * 3500 mm ³
	<i>Maximum sample height</i>	2500 mm
	<i>Maximum weight</i>	6 ton
<i>X-ray source</i>	<i>High Power tube</i>	225 kV
	<i>Voltage</i>	≤ 200 kV
	<i>Power</i>	≤ 200 W
	<i>Cooling device</i>	Included
<i>Detector system</i>	<i>Type</i>	Flat Panel Detector Radiation Hard detector
	<i>Size</i>	300 * 250 mm ²
	<i>Pixel matrix</i>	3500 * 2900
	<i>Pixel pitch</i>	84 µm

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

<i>Sample</i>	<i>Scanned date</i>	<i>Scan ID</i>	<i>Num. vertices</i>	<i>Num. faces</i>
<i>Tomato</i>	July 2 nd , 2019	111	120468	240928
	July 18 th , 2019	112	252550	505148
	July 3 rd , 2019	121	183968	367920
	July 18 th , 2019	122	361248	722628
	July 9 th , 2019	131	110899	224002
	July 23 rd , 2019	132	427124	854604
	July 9 th , 2019	211	688928	1378152
	July 15 th , 2019	212	834648	1669464
	July 23 rd , 2019	213	1106486	2213120
<i>Corn</i>	July 9 th , 2019	221	729842	1459864
	July 15 th , 2019	222	935870	1871920
	July 23 rd , 2019	223	1211190	2422576
	July 9 th , 2019	231	765291	149761
	July 15 th , 2019	232	938634	1877412
	July 23 rd , 2019	233	1207404	2414924

Table 2. Root digital twin dataset.

2.2. Methodology

The curve-skeleton is essentially a 1D structure that abstracts the model's volume and topological characteristics (Bucksch, 2014a). For this study, we choose a robust skeleton extraction method via Laplacian-based contraction (Au et al., 2008). The algorithm works directly on the original mesh, without a resampled volumetric representation. Thereby, it is pose-

insensitive, including global rotation invariant. 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, guarantying 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 only works for closed mesh models with manifold connectivity since

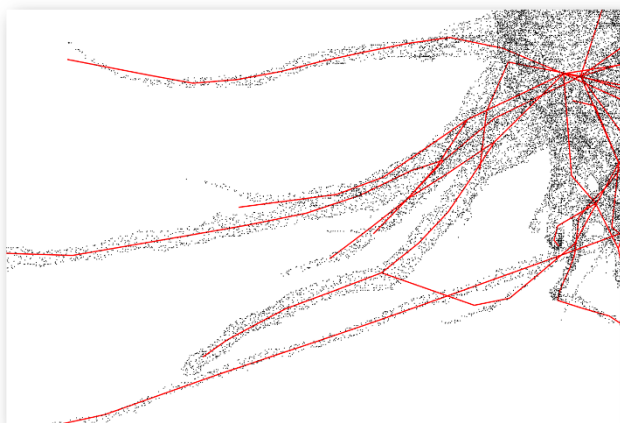
the Laplacian contraction algorithm operates for every individual vertex.

Once we have the skeleton, significant root architectural traits as number, length, growth angle, and branching map can be easily extracted. Furthermore, this skeletal structure controls the correspondences between root ramifications over time, driving the registration procedure in temporal series. Thus, we can automatically perform a growth analysis of the diverse ramifications, quantified by the elongation rate trait.

3. EXPERIMENTAL RESULTS AND DISCUSSION

Figure 1 and 2 illustrate the skeleton extracted from tomato and corn root samples from the digital twins, respectively. Before the skeleton in relative units, a small figure is provided that represents the digital twin of the root in black with the skeleton embedded in red. Based on a visual inspection, we can affirm that the skeleton algorithm may fail when there are several

narrow areas very closed. Two different errors can exist: they cannot be defined by the skeleton or the skeleton is out of the mesh. Figure 3 shows these issues in tomato (Figure 3.a) and corn (Figure 3.b).



(a)



(b)

Figure 3. Problematic zoom samples of the skeleton extraction in tomato (a) and corn (b), in red with the digital twin in black.

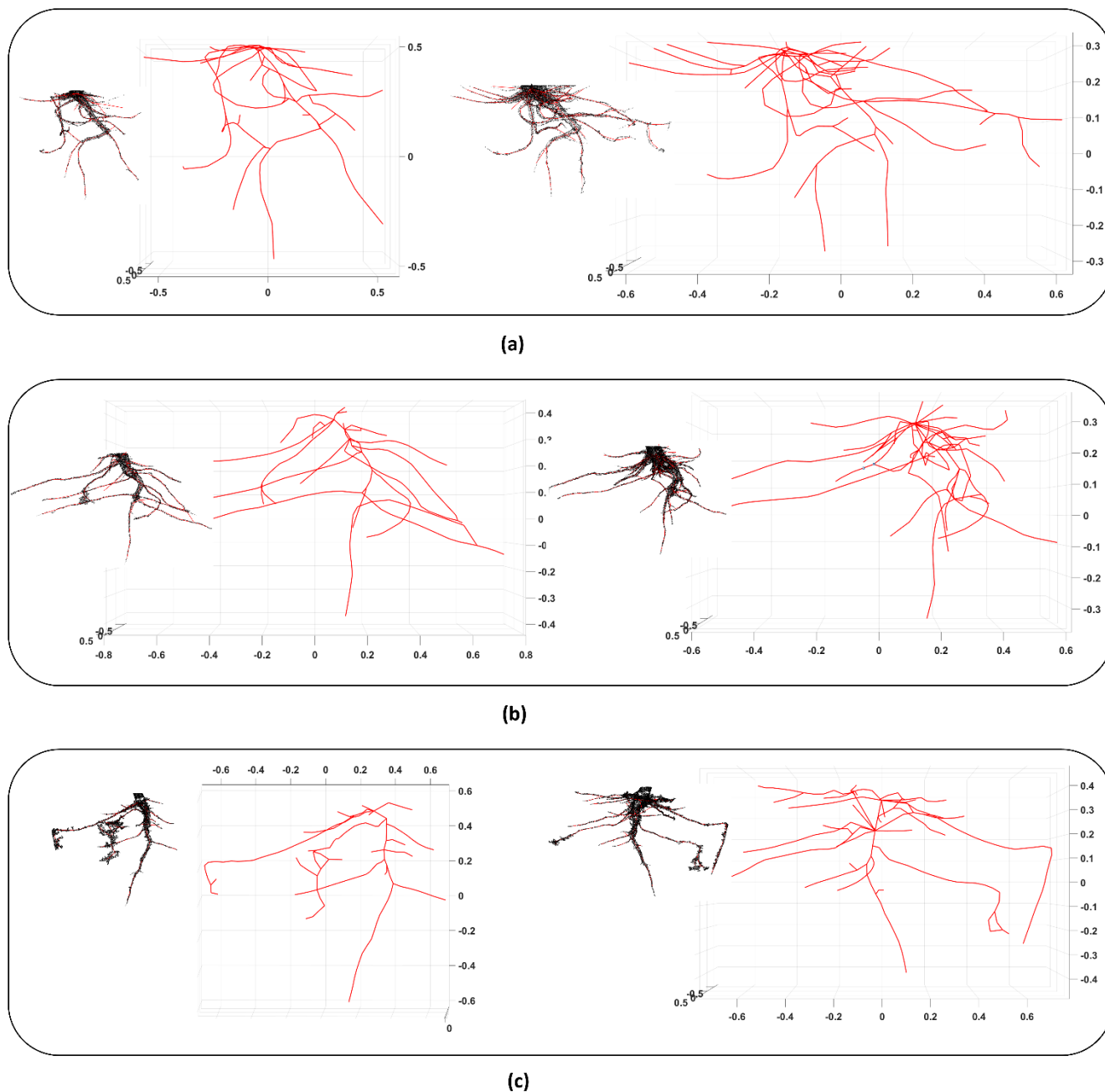


Figure 1. Skeleton of tomato root samples in relative units and a small figure representing the digital twin in black with the embedded skeleton in red: scan ID 111 and 112 (a), scan ID 121 and 122 (b) and scan ID 131 and 132 (c).

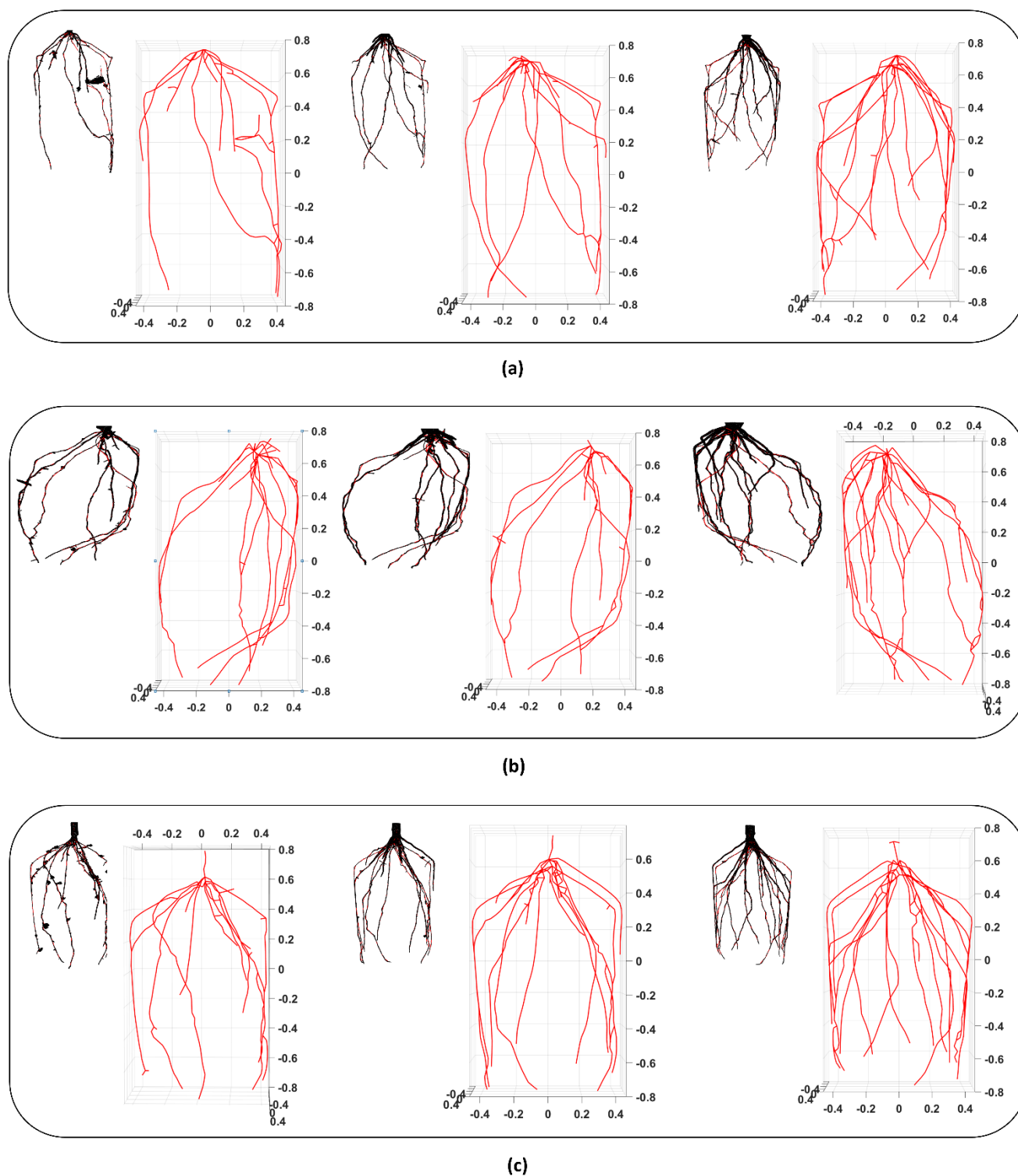


Figure 2. Skeleton of corn root samples in relative units and a small figure representing the digital twin in black with the embedded skeleton in red: scan ID 211, 212 and 213 (a), scan ID 221, 222 and 223 (b) and scan ID 231, 232 and 233 (c).

Results are analytically being evaluated, with particular attention for the abstraction and analysis of RSA traits in particular datasets as well as in temporal series.

4. CONCLUSIONS

In conclusion, the proposed pipeline aims to automatically extract phenotypic data of RSA from digital twins obtained by non-invasive X-ray CT. Moreover, the ease of this workflow will potentially increase the usability to imaging technologies regarding genetic mapping and phenotypic selection for in breeding programs (Herrero-Huerta et al., 2019, Herrero-Huerta et al., 2020).

This skeletal structure controls the correspondences between root ramifications over time, driving the registration procedure in temporal series. As further studies, analyzing temporal series throw the skeleton from different plant species will be needed. The root phenotypic data may serve as significant information for emerging disciplines as functional phenomics, which is poised to combat major global challenges such as climate change, environmental degradation, and food insecurity (York, 2017).

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REFERENCES

Au, O. K. C., Tai, C. L., Chu, H. K., Cohen-Or, D., & Lee, T. Y. (2008). Skeleton extraction by mesh contraction. *ACM transactions on graphics (TOG)*, 27(3), 1-10.

Brandt, J. W., & Algazi, V. R. (1992). Continuous skeleton computation by Voronoi diagram. *CVGIP: Image understanding*, 55(3), 329-338.

Bucksch, A. (2014). A practical introduction to skeletons for the plant sciences. *Applications in plant sciences*, 2(8), 1400005.

Bucksch, A., Burridge, J., York, L. M., Das, A., Nord, E., Weitz, J. S., & Lynch, J. P. (2014). Image-based high-throughput field phenotyping of crop roots. *Plant Physiology*, 166(2), 470-486.

Cornea, N. D., Silver, D., & Min, P. (2007). Curve-skeleton properties, applications, and algorithms. *IEEE Transactions on visualization and computer graphics*, 13(3), 530.

Herrero-Huerta, M., Govindarajan, S., Cherkauet, K. and Rainey, K. (2019) 'Triple S: A new tool for Soybean High Throughput Phenotyping from UAS-based Multispectral Imagery'. *Proc. SPIE 11007, Advanced Environmental, Chemical, and Biological Sensing Technologies XV, 110070K*. DOI: 10.1117/12.2519376.

Herrero-Huerta, M., Rodriguez-Gonzalez, P. and Rainey, K.M. (2020) 'Yield prediction by machine learning from UAS-based multi-sensor data fusion in soybean'. *Plant Methods* 16, 78. DOI: 10.1186/s13007-020-00620-6.

Marie, R., Labbani-Igbida, O., & Mouaddib, E. M. (2016). The delta medial axis: a fast and robust algorithm for filtered skeleton extraction. *Pattern Recognition*, 56, 26-39.

Mohamed, W., & Hamza, A. B. (2012). Reeb graph path dissimilarity for 3D object matching and retrieval. *the visual computer*, 28(3), 305-318.

Postma, J. A., Kuppe, C., Owen, M. R., Mellor, N., Griffiths, M., Bennett, M. J., ... & Watt, M. (2017). OpenSimRoot: widening the scope and application of root architectural models. *New Phytologist*, 215(3), 1274-1286.

Seethepalli, A., Guo, H., Liu, X., Griffiths, M., Almtarfi, H., Li, Z., ... & York, L. M. (2020). Rhizovision crown: An integrated hardware and software platform for root crown phenotyping. *Plant Phenomics*, 2020.

York, L. M. (2019). Functional phenomics: an emerging field integrating high-throughput phenotyping, physiology, and bioinformatics. *Journal of Experimental Botany*, 70(2), 379-386.