

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

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.

Full Text

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