High-throughput 2D+t root system architecture reconstruction and modelling from time-lapse phenotyping data

Romain Fernandez[1,2], Amandine Crabos[3], Morgan Maillard[3], Philippe Nacry[3], Christophe Pradal*[1,2,4]

[1] *CIRAD, UMR AGAP Institut, F-34398 Montpellier, France.*
[2] UMR AGAP Institut, Univ Montpellier, CIRAD, INRAE, Institut Agro, F-34398 Montpellier, France
[3] Institute for Plant Sciences of Montpellier (IPSiM), Univ Montpellier, CNRS, INRAE, Institut Agro, Montpellier, France.
[4] Inria & LIRMM, Univ Montpellier, CNRS, Montpellier, France

For correspondence: christophe.pradal@cirad.fr

Keywords: spatio-temporal plant model, root system architecture, high-throughput phenotyping, time-lapse tracking, computer vision

Background: High-throughput phenotyping is crucial for modelling root system development. In recent years, imaging automata have been developed to acquire Root System Architecture (RSA) of many genotypes grown in Petri dishes to explore the Genetic x Environment (GxE) interactions. Time-lapse phenotyping offers novel possibilities to characterise RSA and a golden path to build and fine-tune "digital twins" of root systems, by coupling mechanistic functional models and root system architectures characterized in both space and time. Such goals require methods for acquiring dynamic parameters such as the organ apparition rate or the growth rate of individual organs or inferring latent parameters from observations, and feeding geometrical and topological models with such parameters to simulate root system development. However, getting an accurate description of the topology, geometry, and dynamics of a growing root system remains a challenge.

Materials and Methods: We designed a high-throughput phenotyping method, combining an imaging device and an automatic analysis pipeline based on registration and topological tracking (see Figure 1). First a registration pipeline is built to address the alignment issue. Then root systems are segmented and labeled with root segments apparition time. A novel root topological tracking algorithm is applied that combines temporal and spatial information and solves ambiguities introduced by root crossing. This pipeline reconstructs the full RSA parameterized with development time, saved in the standard format RSML (Lobet et al, 2015). The method was tested on a challenging *Arabidopsis* seedling dataset, including numerous root occlusions and crossovers.

Results and Discussion: The pipeline allows to accurately characterize the topology and geometry of observed root systems in 2D+t. Static phenes are estimated with high accuracy (R^2=0.996 and 0.923 for primary and second-order roots length, respectively). These performances are similar to state-of-the-art results obtained on root systems of equal or lower complexity. The main result of our pipeline is to estimate the development of root architecture accurately and automatically (R^2=0.938 for lateral root growth estimation). The estimated architecture and development is captured into a model that allows us to simulate the whole RSA growth. We illustrate this capability by building a realistic time-lapse movie, and generate synthetic observations intended to feed deep learning models.

Conclusions: We designed a novel and fully automated 2D+t architecture reconstruction method. It has been used to characterize developing patterns of root systems grown under various environmental conditions and dissect structure and development to simulate a continuous spatio-temporal architectural model from a sparse time-series of images. It provides a unique geometrical and topological substrate for mechanistics models of root

systems and can be used for testing new hypotheses on actual time-lapse data. The architecture parameterized in space and time could be used further to simulate additional observation time-points in order to train segmentation models for improving phenotyping pipelines.
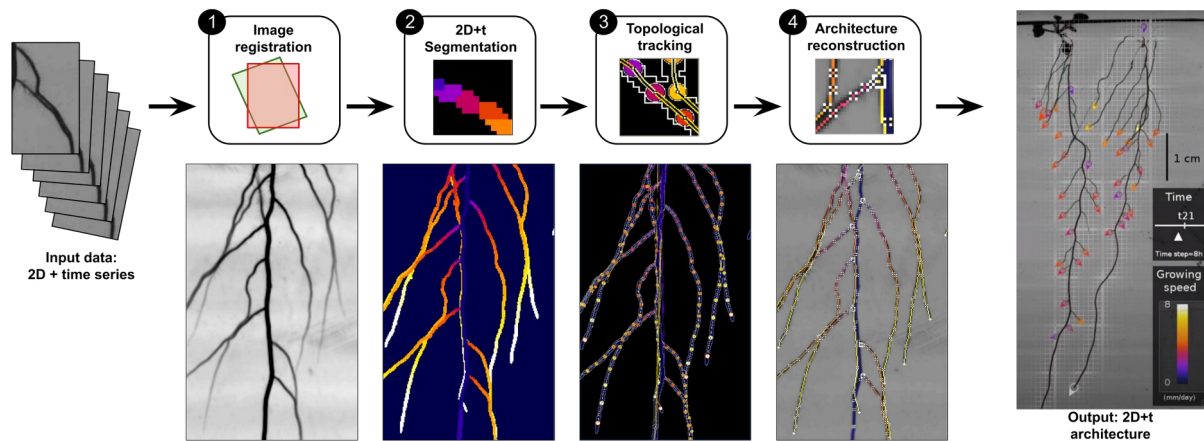

Figure 1: *The automatic processing pipeline. Upper line: pipeline steps, bottom line: outputs of the successive steps.*

References

Fernandez et al., 2022, *bioRxiv,* doi: 10.1101/2022.07.13.499903
Lobet et al., 2015, *Plant physiology* 167(3):617-27, doi: 10.1104/pp.114.253625
Maurel and Nacry, 2020, *Nature plants* Jul;6(7):744-9, doi: 10.1038/s41477-020-0684-5
Takahashi and Pradal, 2021, *Breeding Science* 71(1):109-16, doi: 10.1270/jsbbs.20126
Yasrab *et al.*, 2021, *Remote Sensing*, Jan 20;13(3):331, doi: 10.3390/rs13030331