

SPROUTS: An Integrated Desktop Application for High-Throughput Root Phenotyping

Kinjalk Parth Sebastian Varela Andrew D.B. Leahey

Carl R. Woese Institute for Genomic Biology, University of Illinois at Urbana-Champaign, Urbana, IL, USA

kinjalk2@illinois.edu, sv79@illinois.edu, leahey@illinois.edu

Abstract

Traditional manual extraction of quantitative traits from minirhizotron imagery remains a major bottleneck in plant science. In this work, we introduce SPROUTS (Smart Phenotyping of Roots: Optimized User-friendly Tools), a standalone, cross-platform desktop application that streamlines the root phenotyping pipeline. SPROUTS integrates a human-in-the-loop workflow that supports interactive validation and correction with two novel end-to-end deep learning models for root traits: Pix2PixRoot for generative root skeletonization and RootSeg-ResNet for area segmentation. It also provides practical visualization interfaces for root trait insights tailored for biologists. SPROUTS illustrates how combining specialized models into an easy-to-use tool can democratize plant phenotyping and support FAIR principles.

1 Introduction

The quantitative analysis of root systems is fundamental to advancing crop genetics and understanding plant-environment interactions [2]. Minirhizotron imagery provides a non-destructive method for observing root system depth and distribution in the field. However, extracting traits from the resulting imagery is notoriously slow and labor-intensive, limiting high-throughput analysis of root systems [1]. Currently, there is a trade-off between analytical capability and accessibility among the available landscape of computational tools. Accessible open-source desktop applications are widely adopted but are typically based on traditional image processing [5] or involve a two-step process [7], which tend to be prone to noise from complex soil background [6]. This forces a choice between cutting-edge models that may require complex setups and user-friendly tools that may lack analytical accuracy. We introduce SPROUTS to bridge this gap: a standalone desktop application that integrates novel deep learning models with a full suite of interactive tools for biologists.

2 Materials and Methods

2.1 General Description

SPROUTS features a built-in data visualization dashboard powered by Plotly/Dash. The application successfully integrates a complex computer vision pipeline into a simple and responsive desktop application. The interactive interface allows for the rapid correction of segmentation outputs, root trait generation, and visualization, turning a multi-software, multi-day task into a streamlined process that can be completed in a single session. The visualizations provide immediate biological context to the quantitative data, enabling researchers to identify trends and outliers without exporting data to external statistical software. The system’s efficiency is a key result; on a standard consumer laptop equipped with an NVIDIA GTX 1660Ti GPU, SPROUTS can process 60,000 minirhizotron images for root area in under two hours. This throughput refers to fully automatic batch inference (no HIL); SPROUTS also provides a Review mode for optional human-in-the-loop correction and dataset curation, but models remain frozen during inference and user edits are exported for offline fine-tuning.

2.2 Human-in-the-Loop Correction, Annotation and Visualization

A central feature of SPROUTS is its human-in-the-loop workflow. The application includes a specialized annotation module (Fig. 1, top) where users can instantly visualize model-generated masks and make precise edits using intuitive paint-style tools (brush, eraser, fill). This serves two critical functions: (1) to ensure that the final data for any given study are of the highest human-verified quality, and (2) to facilitate the rapid creation of high-quality curated ground-truth datasets for training or fine-tuning future models.

2.3 Root Traits Prediction

The analytical core of SPROUTS features two custom-trained deep learning models, each optimized for a specific phenotyping task and engineered to run efficiently on

consumer-grade GPUs:

- **RootSeg-ResNet:** For determining root area, we designed a segmentation model using a ResNet-18 backbone [3]. The architecture is augmented with a spatial attention mechanism to focus on relevant root features (Fig. 1, top), with 72.46 mIoU; area prediction $R^2=0.912$, MAE = 2.44 mm².
- **Pix2PixRoot:** For determining root length, we developed a conditional Generative Adversarial Network (cGAN) based on the Pix2Pix framework [4]. This model excels at the image-to-image translation task of converting a raw root image directly into a clean, one-pixel-wide skeleton, from which length is calculated (Fig. 1, bottom), achieving $R^2=0.89$, F1@2px (± 2 -pixel tolerance) = 79.

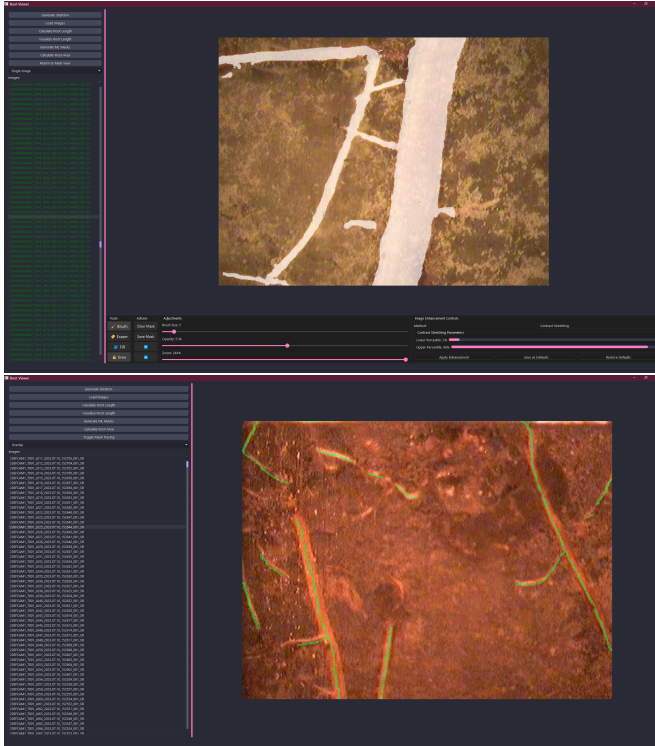


Figure 1. The SPROUTS interface showing (top) RootSeg-ResNet mask overlaid with refinement tools, and (bottom) Pix2PixRoot-predicted root skeleton overlaid on the root images for inference and sanity-checks

2.4 Integrated Visualization of Insights

This module allows researchers to perform immediate, interactive exploratory analysis on the data they have just processed and verified. Users can dynamically generate plots of root growth over time, compare development across different genotypes, and visualize trait distributions by soil depth (Fig. 2), significantly accelerating biological hypothesis testing.

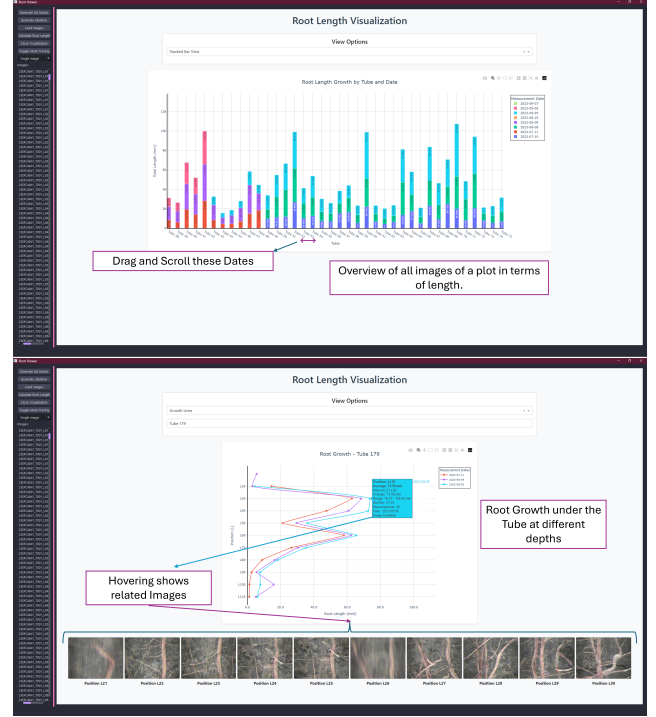


Figure 2. **Top:** Stacked bar visualization showing cumulative root length by tube and measurement date, with colored segments indicating growth contributions from each measurement period. This enables quick identification of high-performing tubes and assessment of overall field productivity. **Bottom:** Spatial root growth distribution within a single tube across multiple measurement dates, showing root density profiles along the tube length over time to reveal spatial colonization patterns. Together, these visualizations form a multi-granularity suite for temporal growth comparison, field-wide productivity assessment, and spatial-temporal root development analysis.

3 Conclusion

We introduce SPROUTS, a standalone desktop application that provides an end-to-end solution that integrates robust deep learning models into an accessible end-user interface, streamlining access to root phenotyping tools. By combining specialized models for segmentation and skeletonization with human-in-the-loop correction and integrated visualization, SPROUTS delivers a seamless, robust workflow. It reduces the technical and financial barriers to high-throughput phenotyping. Future work will expand the model library to cover additional root traits and enable users to share and deploy custom fine-tuned models within the SPROUTS ecosystem. Additionally, incorporating pre-planting field plot mapping data that documents genotype distribution across experimental plots will enable spatially-aware, genotype-specific root phenotyping analysis with enhanced visualization capabilities at both plot and field scales. A public GitHub release is planned by February 2026, pending institutional approvals.

References

- [1] Felix Maximilian Bauer, Lena Lärm, Shehan Morandage, Guillaume Lobet, Jan Vanderborght, Harry Vereecken, and Andrea Schnepf. Development and validation of a deep learning based automated minirhizotron image analysis pipeline. *Plant Phenomics*, 2022, 2022. [1](#)
- [2] Joseph G Dubrovsky and Brian G Forde. Quantitative analysis of lateral root development: pitfalls and how to avoid them. *The Plant Cell*, 24(1):4–14, 2012. [1](#)
- [3] Kaiming He, Xiangyu Zhang, Shaoqing Ren, and Jian Sun. Deep residual learning for image recognition. In *Proceedings of the IEEE conference on computer vision and pattern recognition*, pages 770–778, 2016. [2](#)
- [4] Phillip Isola, Jun-Yan Zhu, Tinghui Zhou, and Alexei A Efros. Image-to-image translation with conditional adversarial networks. In *Proceedings of the IEEE conference on computer vision and pattern recognition*, pages 1125–1134, 2017. [2](#)
- [5] Anand Seethepalli, Kundan Dhakal, Marcus Griffiths, Haichao Guo, Gregoire T Freschet, and Larry M York. Rhizovision explorer: open-source software for root image analysis and measurement standardization. *AoB PLANTS*, 13(6): plab056, 2021. [1](#)
- [6] Radka Slovak, Christian Göschl, Xiaoxue Su, Koji Shimotani, Takashi Shiina, and Wolfgang Busch. A scalable open-source pipeline for large-scale root phenotyping of arabidopsis. *The Plant Cell*, 26(6):2390–2403, 2014. [1](#)
- [7] Abraham George Smith, Eusun Han, Jens Petersen, Niels Alvin Faircloth Olsen, Christian Giese, Miriam Athmann, Dorte Bodin Dresbøll, and Kristian Thorup-Kristensen. Root-painter: deep learning segmentation of biological images with corrective annotation. *New Phytologist*, 236(2):774–791, 2022. [1](#)