

Plant Root Phenotyping Pipeline.

To begin the plant analysis process, launch the interface by entering "chronoroot" in the command line. This will open the main analysis window.

ChronoRootAnalysis

Plant Analysis | Analysis Overview | Plant Overlay | Generate Report | Report

Individual plant root analysis

Select Project Folder

Select Video Folder

Raspberry Module (should be the raspberry number)

Camera (should be the camera number)

Plant Number (should be a number, to identify plant)

Identifier (variety identifier, e.g. WT, Col0)

Analysis and postprocessing parameters

☐ Save Cropped Images (useful to make growth videos, takes extra time and disk space)

Set processing limit (in days, 0 means no limit)

Capture interval (in minutes, usually 15 minutes)

Emergence distance (in millimeters, default: 2 mm)

Save

Preview video

Analyze Plant

Process all plants

Load config json from file

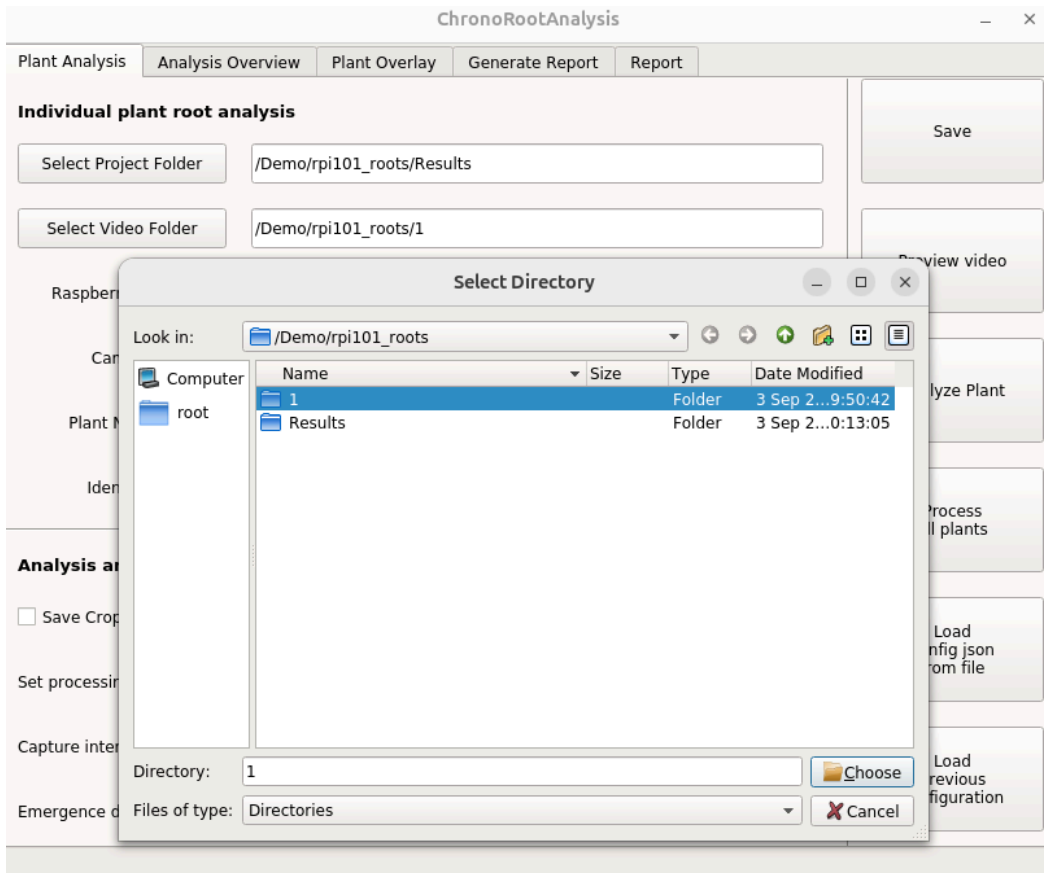
Load previous configuration

Interface Components:

- **Select Project Folder:** Specifies the storage location for your analysis results. A project encompasses a complete experimental setup involving one or more Raspberry Pi modules.
- **Select Video Folder:** Identifies the video file for current processing. Videos must be processed sequentially, one at a time.
- **Plant Identification Fields:** The Raspberry Pi Module, Camera, Plant Number, and Identifier fields allow you to tag each plant according to its origin (camera and module), position on the plate, and biological variety.

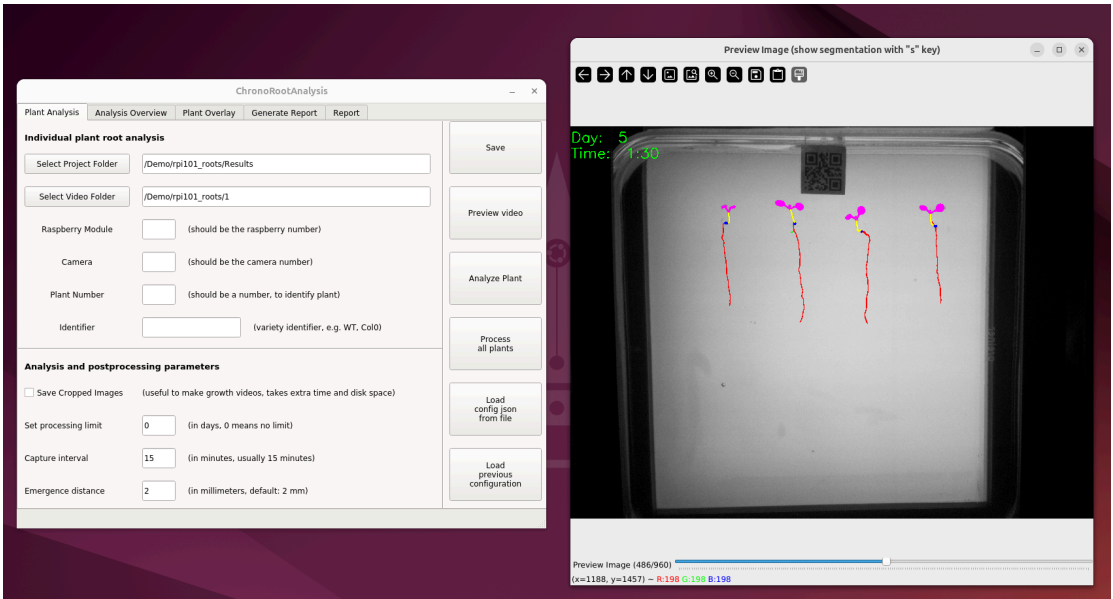
Getting Started:

Begin by creating a dedicated folder for storing results, then select the first video from the Demo dataset. A popup window will prompt you to choose the appropriate folders.



Video Preview and Setup:

Click the "Preview Video" button to view your selected video. Use the scrollbar to navigate between frames and press the "S" button to toggle the segmentation overlay for visual inspection.



Complete the plant identification details for the first plant you wish to analyze.

The screenshot shows the ChronoRootAnalysis application window. The 'Plant Analysis' tab is active, displaying fields for project and video folder selection, and input for Raspberry Module, Camera, Plant Number, and Identifier. Below these are analysis and postprocessing parameters, including a checkbox for saving cropped images and numeric inputs for processing limit, capture interval, and emergence distance. A sidebar on the right contains buttons for Save, Preview video, Analyze Plant, Process all plants, Load config json from file, and Load previous configuration.

Individual plant root analysis	
Select Project Folder	/Demo/rpi101_roots/Results
Select Video Folder	/Demo/rpi101_roots/1
Raspberry Module	1 (should be the raspberry number)
Camera	1 (should be the camera number)
Plant Number	1 (should be a number, to identify plant)
Identifier	A (variety identifier, e.g. WT, Col0)

Analysis and postprocessing parameters	
<input type="checkbox"/> Save Cropped Images	(useful to make growth videos, takes extra time and disk space)
Set processing limit	0 (in days, 0 means no limit)
Capture interval	15 (in minutes, usually 15 minutes)
Emergence distance	2 (in millimeters, default: 2 mm)

Save

Preview video

Analyze Plant

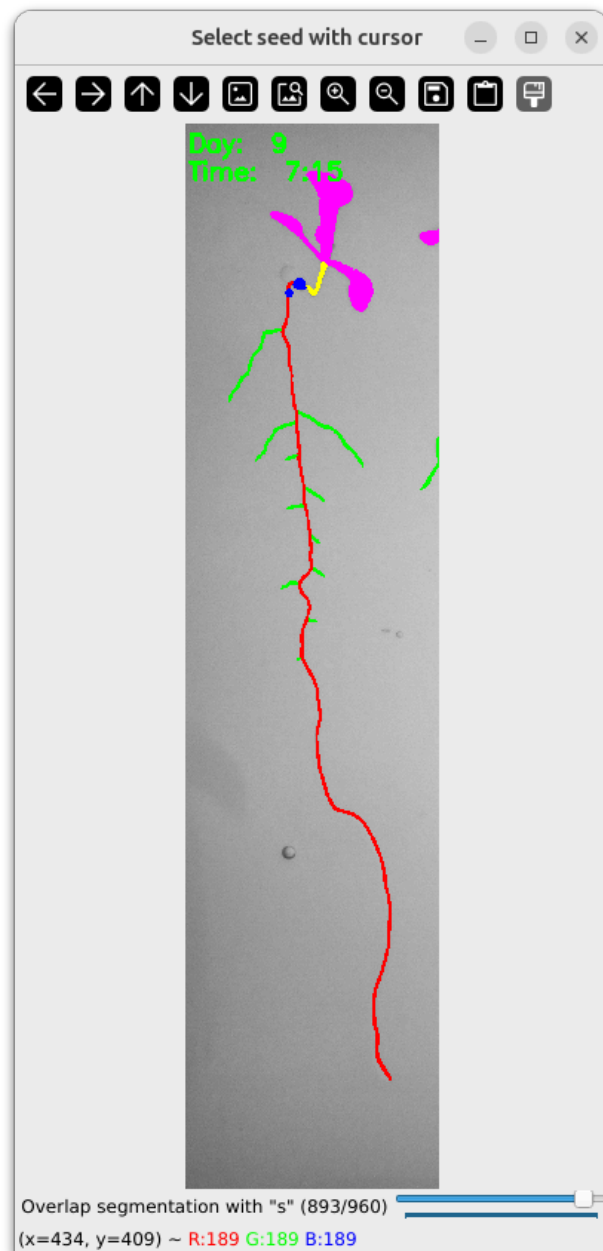
Process all plants

Load config json from file

Load previous configuration

Plant Analysis Workflow:

1. **ROI Selection:** Click "Analyze Plant" to open the ROI (Region of Interest) selector. Manually define the analysis area and press double-enter to confirm your selection.
2. **Seed Point Selection:** Choose the seed point carefully, as this will remove any segmentation above it and establish the starting point for graph construction. This serves as a manual validation and cleaning step.
3. **Validation:** Review the complete sequence using the scrollbar and visualize the segmentation by pressing "S". Press Enter when satisfied with the results.
4. **Repeat Process:** Complete this workflow for all 4 plants in the demo. Feel free to compare varieties using patterns like A-B-A-B or A-B-C-D to observe behavioral differences.



Quality Control and Batch Processing:

Navigate to the "Analysis Overview" tab to monitor experiment progress and error rates. Poor ROI selection or incorrect seed point positioning may cause errors in graph creation. Once individual plant processing is complete, return to the "Plant Analysis" tab and select "Process All Plants."

ChronoRootAnalysis								
Plant Analysis		Analysis Overview		Plant Overlay		Generate Report		Report
	Variety	Raspberry	Camera	Plant Number	Result ID	Error Rate	Status	Finish Date
1	A	1	cam_1	plant_1	Results_0	0.0	Finished	2025-09-03 20:24:44
2	B	1	cam_1	plant_2	Results_0	0.008	Finished	2025-09-03 20:26:21
3	A	1	cam_1	plant_3	Results_0		Not finished	
4	B	1	cam_1	plant_4	Results_0	0.0	Finished	2025-09-03 20:29:22

Refresh

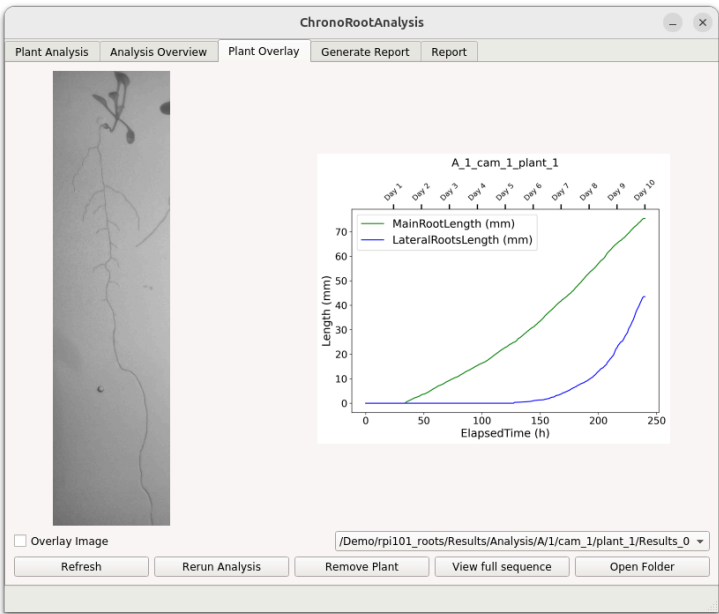
Open Path

Remove Plant

Rerun Analysis

Visual Inspection:

The "Plant Overlay" tab provides visual inspection capabilities for both segmentation results and plant root performance analysis. This interface allows you to discard problematic plants or restart the entire process if needed.



Report Generation:

After completing individual plant analyses, you can generate comprehensive reports. The demo dataset includes 10 complete days of plant growth data—feel free to experiment with different report types. The system can perform interval testing (for example, every 6 hours) to compare different varieties using statistical methods such as the Mann-Whitney U test to determine if varieties show statistically significant differences.

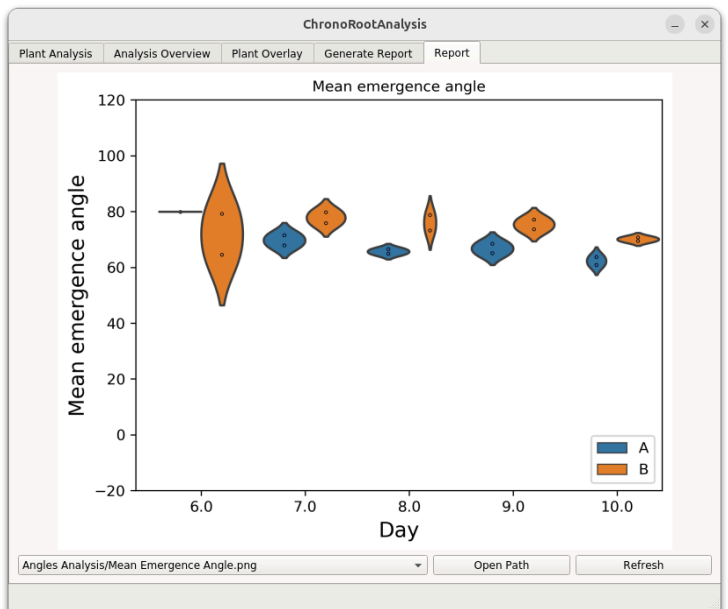
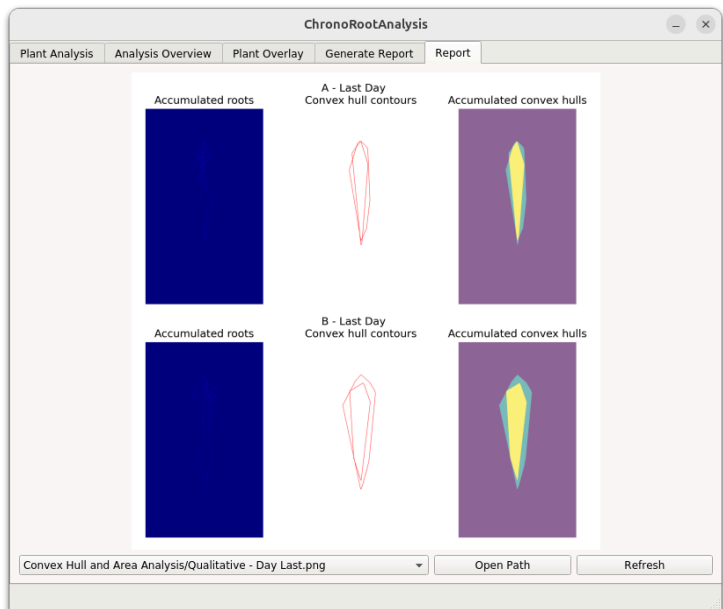
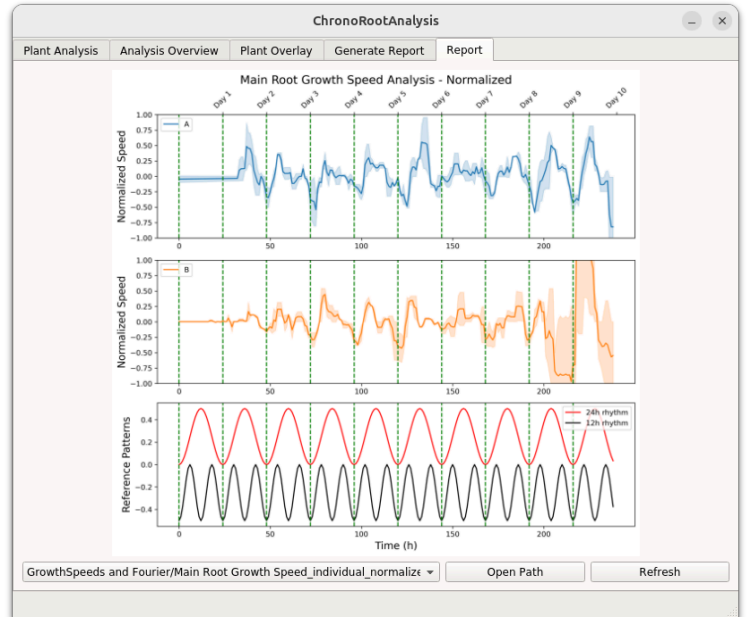
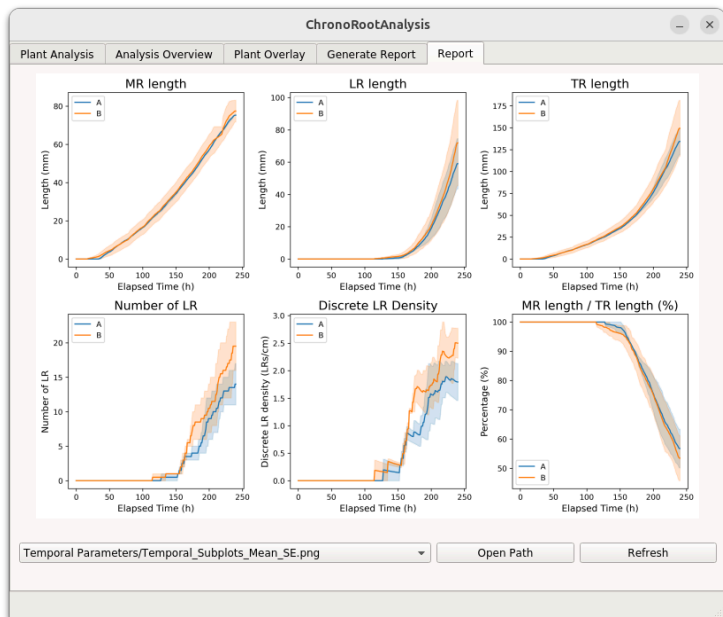
PS: If working with longer datasets and wanting to limit processing time, set the processing limit to your desired number of analysis days.

The screenshot shows the 'ChronoRootAnalysis' application window with the 'Generate Report' tab selected. The interface includes a 'Select Project Folder' button and a text field containing '/Demo/rpi101_roots/Results'. Below this, there are several sections of settings, each with a checked checkbox and associated controls:

- Average intervals before testing:** A checkbox is checked. To its right is a label 'Time series stats interval (dt, in hours)' and a text field with the value '6'. Below this is a descriptive sentence: 'Hypothesis testing uses Mann-Whitney test every dt interval. If selected, an average value will be used, or a step (i*dt) otherwise'.
- Perform Functional PCA on time series:** A checkbox is checked. To its right is an unchecked checkbox labeled 'Normalize FPCA Boxplots' and a text field labeled 'Number of components' with the value '2'.
- Do Convex hull analysis:** A checkbox is checked. To its right is an unchecked checkbox labeled 'Save images for each day'. Below this is a label 'Days to report' and a text field with the value '6,7,8,9,10', followed by the text '(Numbers separated by commas)'.
- Evaluate Growth Speeds and perform Fourier Analysis:** A checkbox is checked. To its right is a label 'Speeds stats interval (dt, in hours)' and a text field with the value '6'.
- Do Lateral Root Angles Analysis:** A checkbox is checked. To its right is a label 'Emergence distance' and a text field with the value '2', followed by the text '(in millimeters, default: 2 mm)'. Below this is a label 'Days to report' and a text field with the value '6,7,8,9,10', and another label 'First LR Tip Stats interval (dt, in hours)' with a text field containing '6'.

At the bottom of the window, there are two input fields: 'Processing limit' with the value '0' and 'Capture interval' with the value '15'. To the right of these fields are five buttons: 'Save', 'Process all plants', 'Generate report', and 'Load previous configuration'.

The system automatically generates comprehensive reports containing various figure types. All raw figures and images are saved within the report directory for detailed analysis and further investigation.



< > Home / Documents / ChronoRootDATA / Demo / rpi101_roots / Results / Report



Angles Analysis



Convex Hull and Area Analysis



FPCA



GrowthSpeeds and Fourier



Individual plant plots



Temporal Parameters



Convex_Hull_Data.csv



LateralRootsData.csv



Synchronized FirstLR.csv



Temporal_Data.csv