Root System Analyser – Documentation



Quick-start

- 1. Download latest .m files from http://www.csc.univie.ac.at/rootbox/rsa.html
- 2. Extract files in one directory
- 3. Run RSA_GUI.m in Matlab

Requirements

The software was tested with Matlab 2010b and Matlab 2012 and requires the Image Processing Toolbox and Bioinformatics Toolbox.

Root System Analyser can work with all 2D images created with different imaging techniques. The only limitations are that (1) the images must offer a sufficient resolution such that a segmented binary image can be created, where roots are white pixels and the background are black pixels and (2) all pixels that belong to the roots must be connected. Currently, there is no automatic segmentation provided in the software. Generally this is non-trivial task and we advise to use the free tools <u>GIMP</u> or <u>ImageJ</u> to create such segmentation. Depending on the imaging technique there might be more specialised software available.



Full automatic detection of a single measurement

- 1. Open (1) image file
- 2. Press 'detect' (2): automatic detection starts
- 3. Check detection results: First select the 'select root' radio-button (3), click at the root to select it (the root turns yellow). The bottom right corner of the screens shows information about the selected root.
- 4. Save results (4): saves the detected roots in a .mat file and copies the structure in the Matlab workspace. The workspace then contains the adjacency matrix (*A*) of the graph, nodes coordinates (*nodes*), edge coordinates (*edges*), and information on the detected roots (*tips*).
- 5. With the Open (1) menu, you can also open an existing Matlab workspace and modify results.

Manual initial roots

If the tap root is not detected correctly, or there are multiple primary roots, an initial root system can be predefined manually.

- 1. Open (1) image or Matlab workspace (or press the reset button if a root system is already detected in the Matlab workspace).
- 2. Choose the ,add root' radio-button (5)

- 3. First, click the base node of the root, after that, click at the tip node of the root. Repeat this to create an initial root system. Colours of the roots represent the order of the roots. Always start at the roots with lowest order, and add lateral roots only once the base root is created.
- 4. Press detect (2): to detect the remaining roots automatically
- 5. Save results (4)

Manual correction of results

If roots are detected wrong individual roots can be deleted:

- 1. Choose the 'remove' radio-button (6)
- 2. Click at the root you want to remove

New roots can be added:

- 1. Choose the 'add root' radio-button (5)
- 2. First, click the base node of the root, after that, click at the tip node of the root.

Root tracking in an image sequence

- 1. Store single image files that belong to one sequence in one folder
- 2. Run the Matlab script CreateDynamicMAT.m
- 3. This script creates a Matlab Workspace that contains the graph information of the final root system as well as arrays with information about the individual images and the corresponding measurement times.
- 4. Start with the first measurement (7)
- 5. Press detect (2): roots are detected automatically in the first image
- 6. Manual correct results in this image (as described above)
- 7. Press detect next (8): roots are detected in the next image with the detected roots as an initial root system
- 8. Repeat steps 6 and 7 until images of the sequences are analysed.

Output

If the user saves the results, a .MAT file is created with all relevant information. Additionally, the values are copied to the current Matlab workspace. Note that this file .MAT can be reopened.

The output workspace includes:

Information on the graph representation:

A: a sparse matrix containing the adjacency matrix of the graph (entries are the edge indices) *nodes*: nodes coordinates <Nx2 double> where N is the number of nodes

edges: list of edge coordinates <Ex1 cell> where E is the number of edges. Each cell contains <Cx2 double>, where C is the number of edge coordinates

For each measurement:

D: distance maps of the image <Nx1 cell>, where N is the number of images in the sequence. Each cell contains a distance map of the corresponding binary image *times*: measurement times in days <Nx1 double>.

The tracked roots:

tips: <Nx1 cell> where N is the number of images in the sequence. Each cell contains a <Rx1 struct> where R is the number of tracked roots. Each root structure contains the following fields: *number* (root identification number), *order* (branching order), *ct* (approximated time of emergence), *predecessor* (parent root identification number), *prelength* (distance between branching point to the parent root base), *length* (root length at the observation time), *area* (area of the root in the image), *path* (nodes that belong to each individual root).