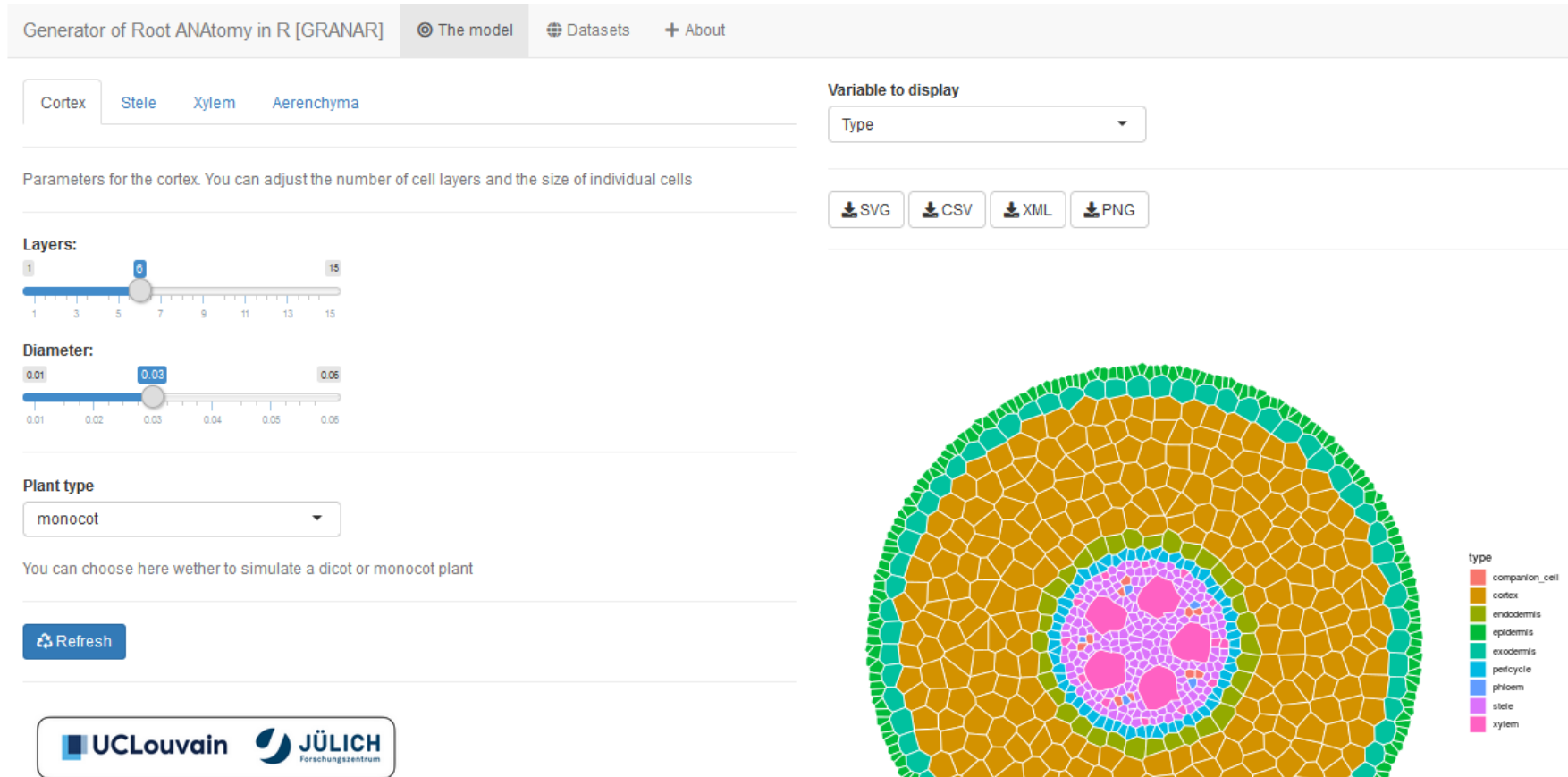


SIMULATING ROOT ANATOMIES

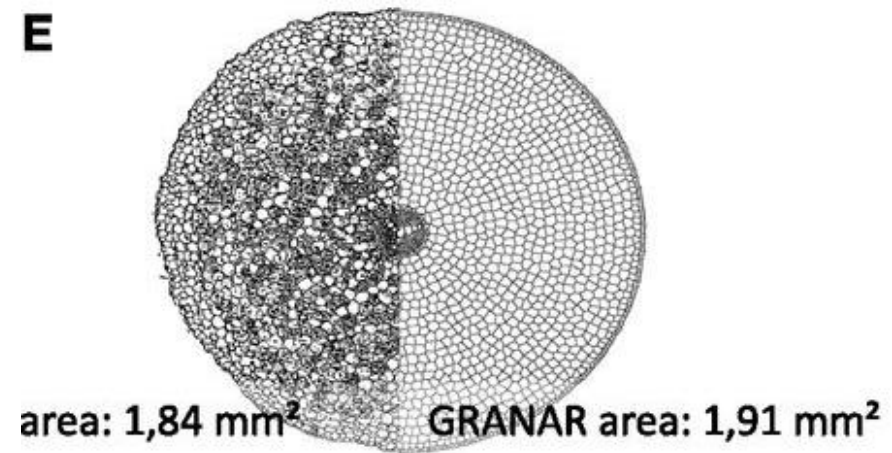
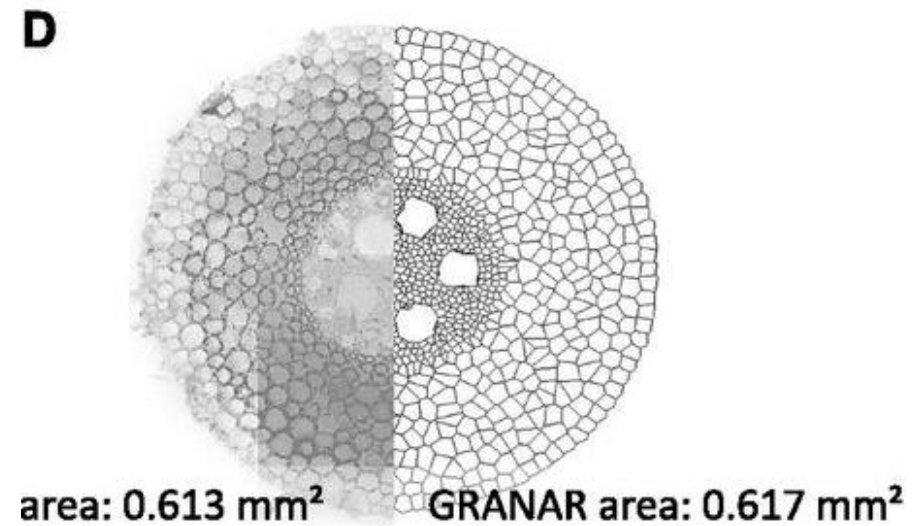
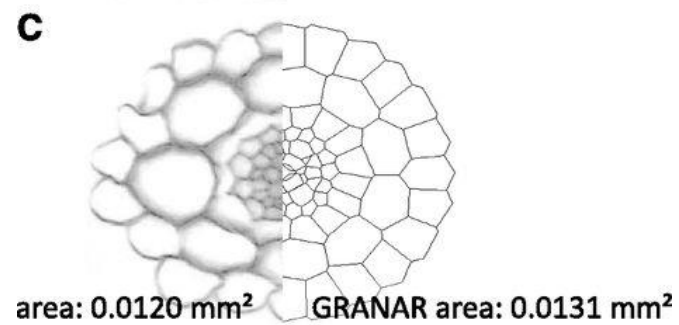
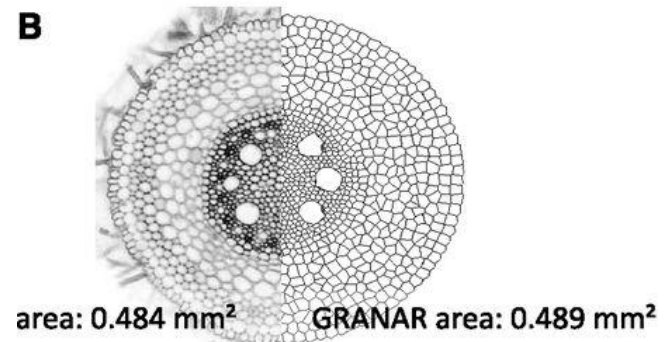
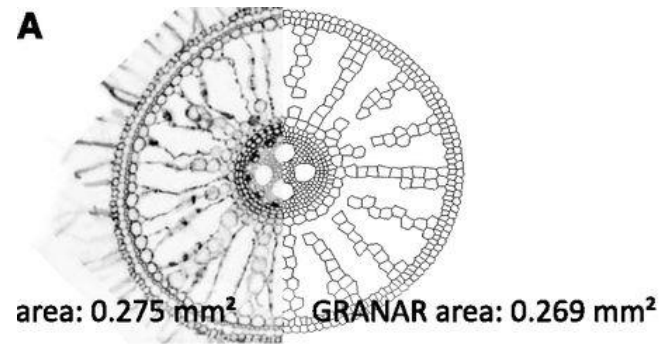
- GRANAR -

<https://plantmodelling.shinyapps.io/granar/>

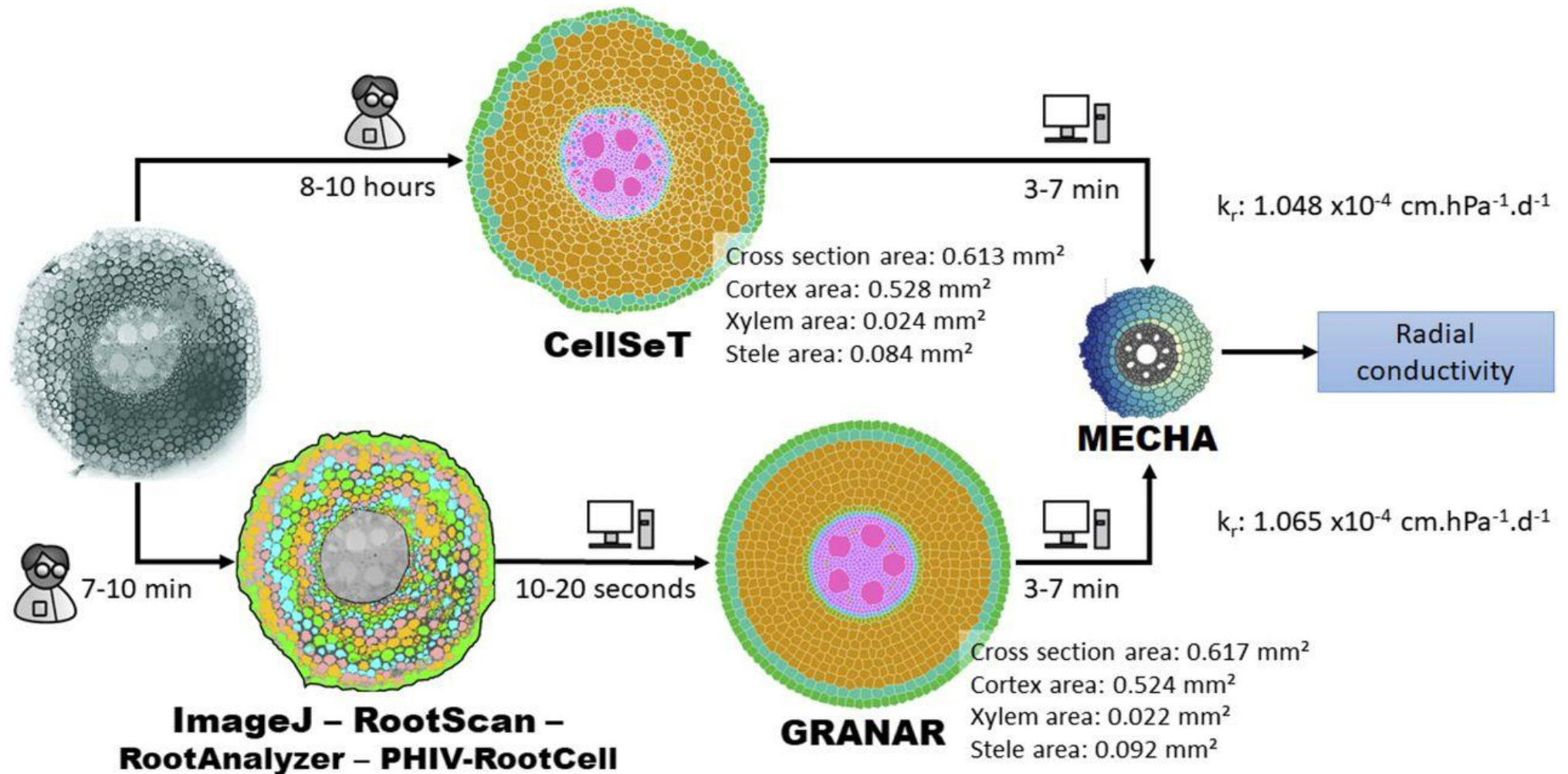


<https://doi.org/10.1104/pp.19.00617>

DIVERSITY OF ROOT ANATOMIES WITH GRANAR



COUPLING GRANAR AND MECHA TO ESTIMATE K_r



<https://doi.org/10.1104/pp.19.00617>

SIMULATING ROOT ANATOMIES

- GRANAR -

<https://plantmodelling.shinyapps.io/granar/>

1. Change
anatomical
parameters

2. Run
GRANAR

Generator of Root ANAtomy in R [GRANAR] The model Datasets + About

Cortex Stele Xylem Aerenchyma

Variable to display
Type

Parameters for the cortex. You can adjust the number of cell layers and the size of individual cells

Layers: 1 3 5 7 9 11 13 15

Diameter: 0.01 0.03 0.06

Plant type
monocot

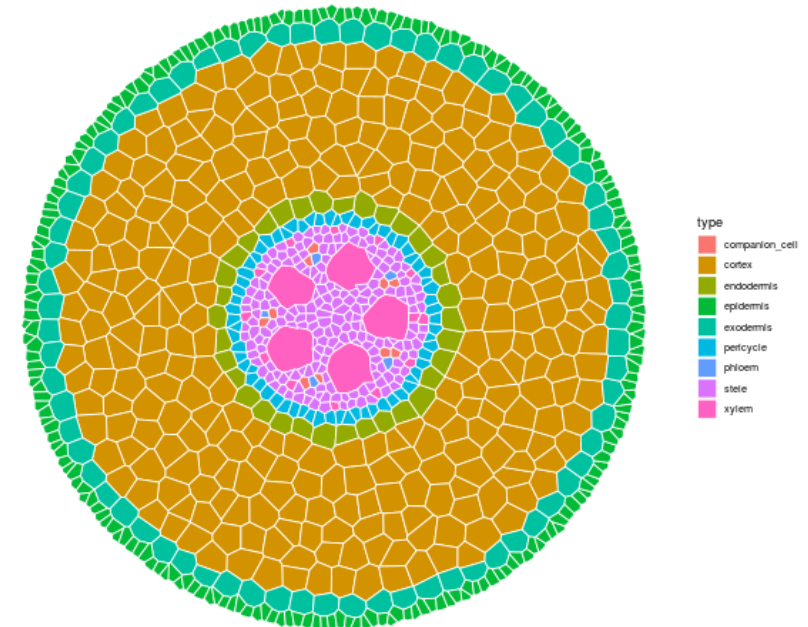
You can choose here whether to simulate a dicot or monocot plant

Refresh

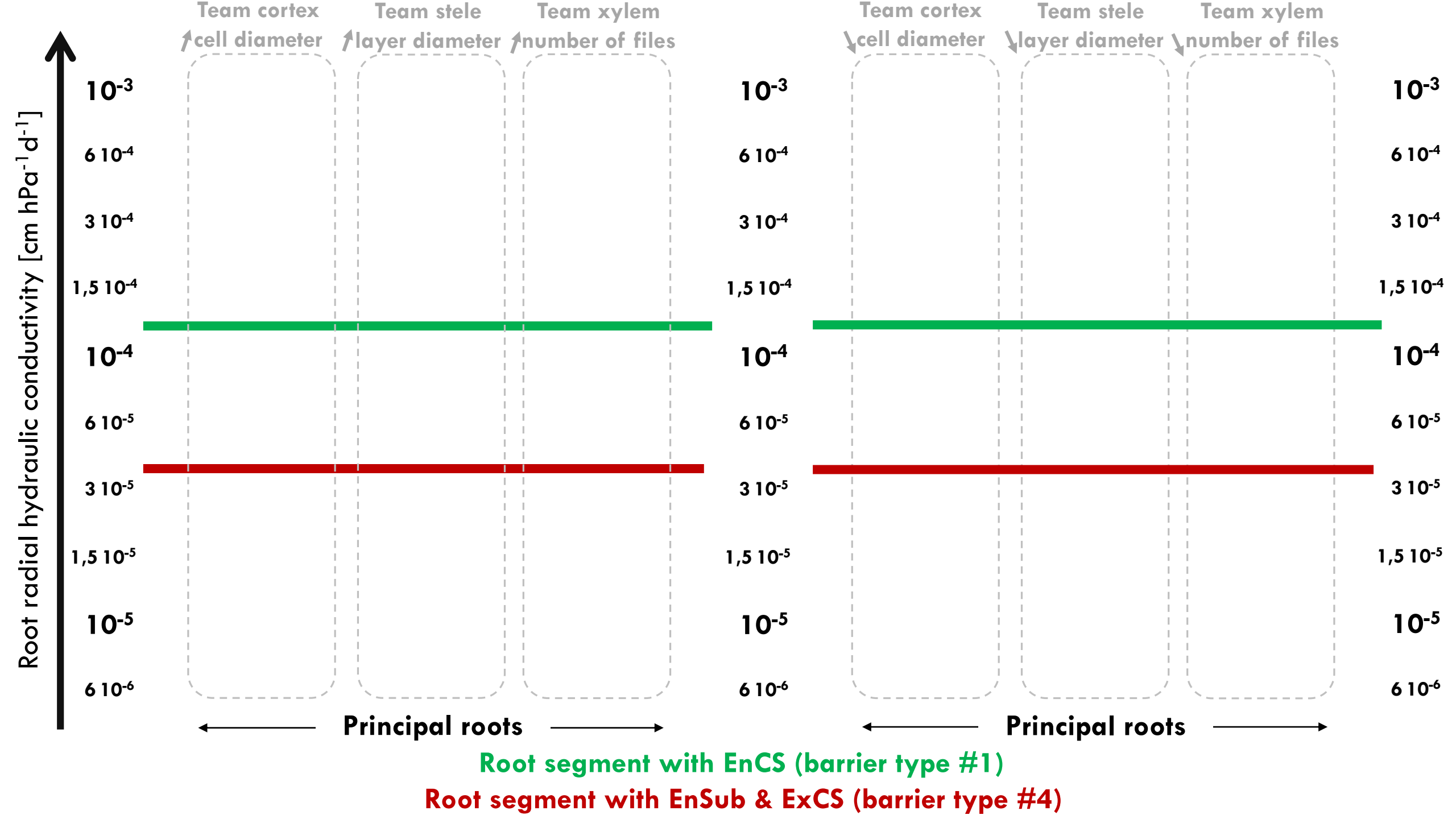
UCLouvain JÜLICH Forschungszentrum

SVG CSV XML PNG

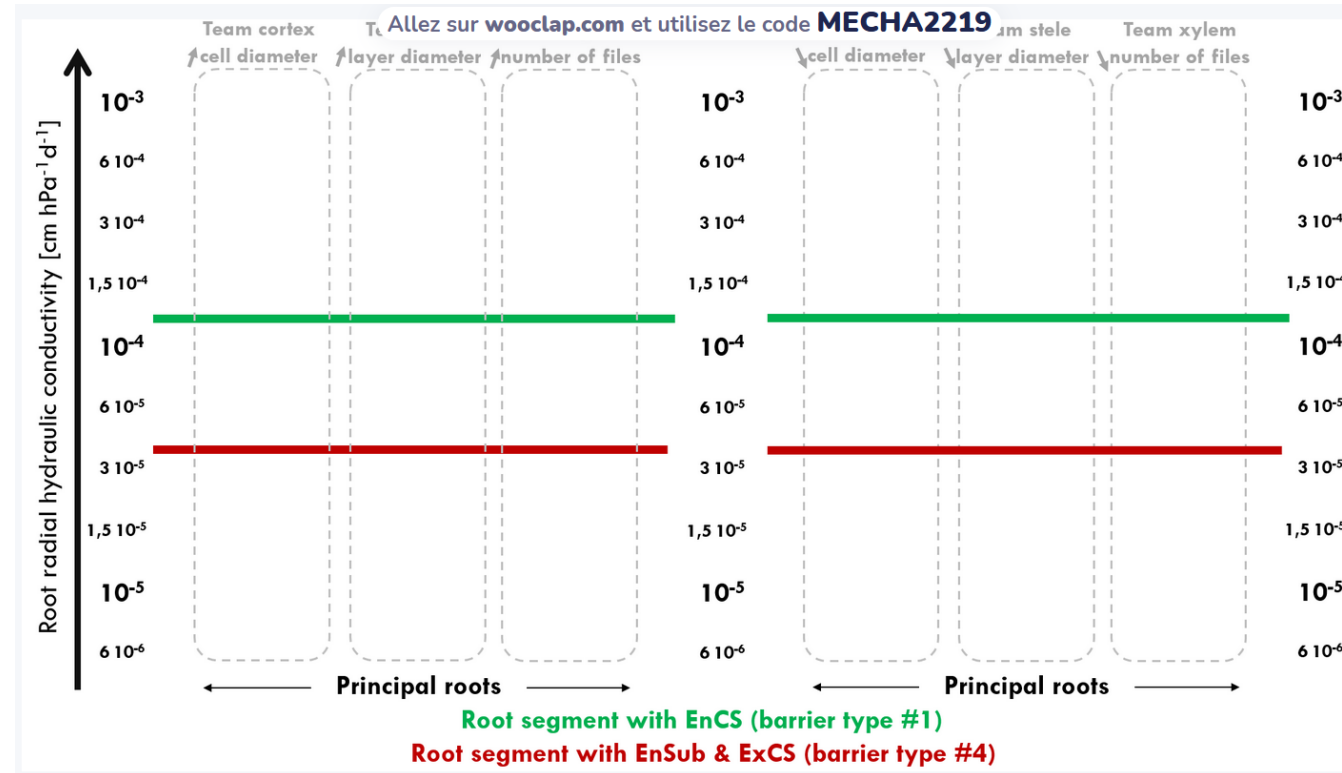
3. Download the .xml file



<https://doi.org/10.1104/pp.19.00617>



Add updates radial conductivities in your team's column !



1

Allez sur wooclap.com

2

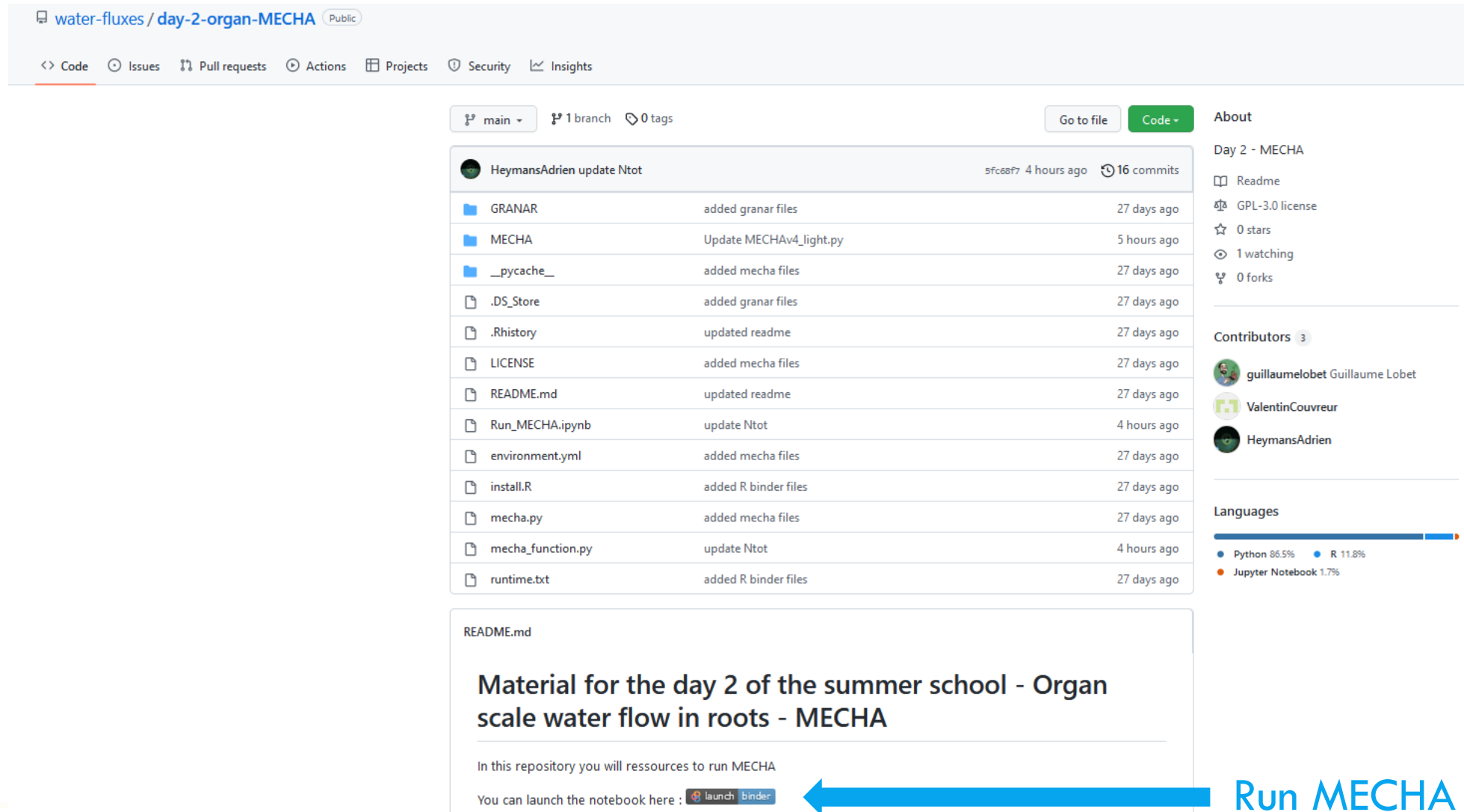
Entrez le code d'événement dans le bandeau supérieur

Code d'événement
MECHA2219

MODELLING WATER FLOW AT THE ORGAN SCALE

- MECHA -

<https://github.com/water-fluxes/day-2-organ-MECHA>



The screenshot shows the GitHub repository page for 'water-fluxes/day-2-organ-MECHA'. The repository is public and has 16 commits. The commit history table lists the following files and their update times:

File	Commit Message	Time Ago
GRANAR	added granar files	27 days ago
MECHA	Update MECHAv4_light.py	5 hours ago
__pycache__	added mecha files	27 days ago
.DS_Store	added granar files	27 days ago
.Rhistory	updated readme	27 days ago
LICENSE	added mecha files	27 days ago
README.md	updated readme	27 days ago
Run_MECHA.ipynb	update Ntot	4 hours ago
environment.yml	added mecha files	27 days ago
install.R	added R binder files	27 days ago
mecha.py	added mecha files	27 days ago
mecha_function.py	update Ntot	4 hours ago
runtime.txt	added R binder files	27 days ago

The README.md file contains the following text:

Material for the day 2 of the summer school - Organ scale water flow in roots - MECHA

In this repository you will find resources to run MECHA

You can launch the notebook here : [launch binder](#)

The right sidebar shows the repository's metadata: 0 stars, 1 watching, 0 forks. The contributors list includes guillaumelobet, ValentinCouvreur, and HeymansAdrien. The languages section shows Python (86.5%), R (11.8%), and Jupyter Notebook (1.7%).

Run MECHA via Binder

MODELLING WATER FLOW AT THE ORGAN SCALE

- MECHA -

Once on Binder... let's open the Jupyter Notebook!

The screenshot shows the Binder Launcher interface. On the left is a file explorer with a search bar 'Filter files by name'. The file list includes:

Name	Last Modified
GRANAR	4 hours ago
MECHA	4 hours ago
Y: environme...	4 hours ago
R install.R	4 hours ago
LICENSE	4 hours ago
mecha_fun...	4 hours ago
mecha.py	4 hours ago
README.md	4 hours ago
Run_MECH...	4 hours ago
runtime.txt	4 hours ago

The main area is titled 'Launcher' and contains three sections:

- Notebook**: Contains icons for Python 3 (ipykernel), R, RStudio [↗], and Shiny [↗].
- Console**: Contains icons for Python 3 (ipykernel) and R.
- Other**: Contains icons for Terminal, Text File, Markdown File, Python File, R File, and Show Contextual Help.

A blue arrow points from the text 'Double click on Run_MECHA.ipynb' to the 'Run_MECH...' file in the file explorer.

MODELLING WATER FLOW AT THE ORGAN SCALE

- MECHA -

Once on Binder/Jupyter Notebook... let's run MECHA!

File Edit View Run Kernel Tabs Settings Help

Filter files by name

/ MECHA / cellsetdata /

Name	Last Modified
current_root.xml	a day ago
current_root_tap.xml	a day ago

Launcher Run_MECHA.ipynb

2. Click on play

MECHA: Upon this generated cross-section and the cell hydraulic properties defined in Hydraulic.xml MECHA estimates the radial hydraulic conductivities (for three scenarios: 1 = an endodermal casparian strip, 2 = a fully suberized endodermis, 3 = fully suberized endodermis and a casparian strip on the exodermis.

Change kernel to Python to launch the following script. Once the kernel is changed, all variables stored in R are gone.

1. Click on a cell

```
[2]: from mecha_function import *  
  
mecha()  
  
Importing geometrical data  
Import Geometrical data  
Creating network nodes  
Creating network connections  
Importing hydraulic data  
Maturity #0 with apoplastic barrier type #1  
Radial conductivity: 0.00016366878594094897 cm/hPa/d  
Maturity #1 with apoplastic barrier type #4  
Radial conductivity: 4.794135423239936e-05 cm/hPa/d  
End of mecha
```

3. k_r for root with Casp

4. k_r for suberised root

MODELLING WATER FLOW AT THE ORGAN SCALE

- MECHA -

Once on Binder... let's update the root anatomy!

The image shows a Binder interface with a file explorer on the left and a launcher panel on the right. The file explorer shows a directory structure with a folder named 'MECHA' highlighted. The launcher panel has sections for 'Notebook', 'Console', and 'Other'. A blue arrow points from the 'MECHA' folder in the file explorer to the 'Notebook' section in the launcher panel.

File Explorer:

Name	Last Modified
GRANAR	5 hours ago
MECHA	5 hours ago
environment.yml	5 hours ago
install.R	5 hours ago
LICENSE	5 hours ago
mecha_function.py	5 hours ago
mecha.py	5 hours ago
README.md	5 hours ago
Run_MECHA.ipynb	3 minutes ago
runtime.txt	5 hours ago

Launcher Panel:

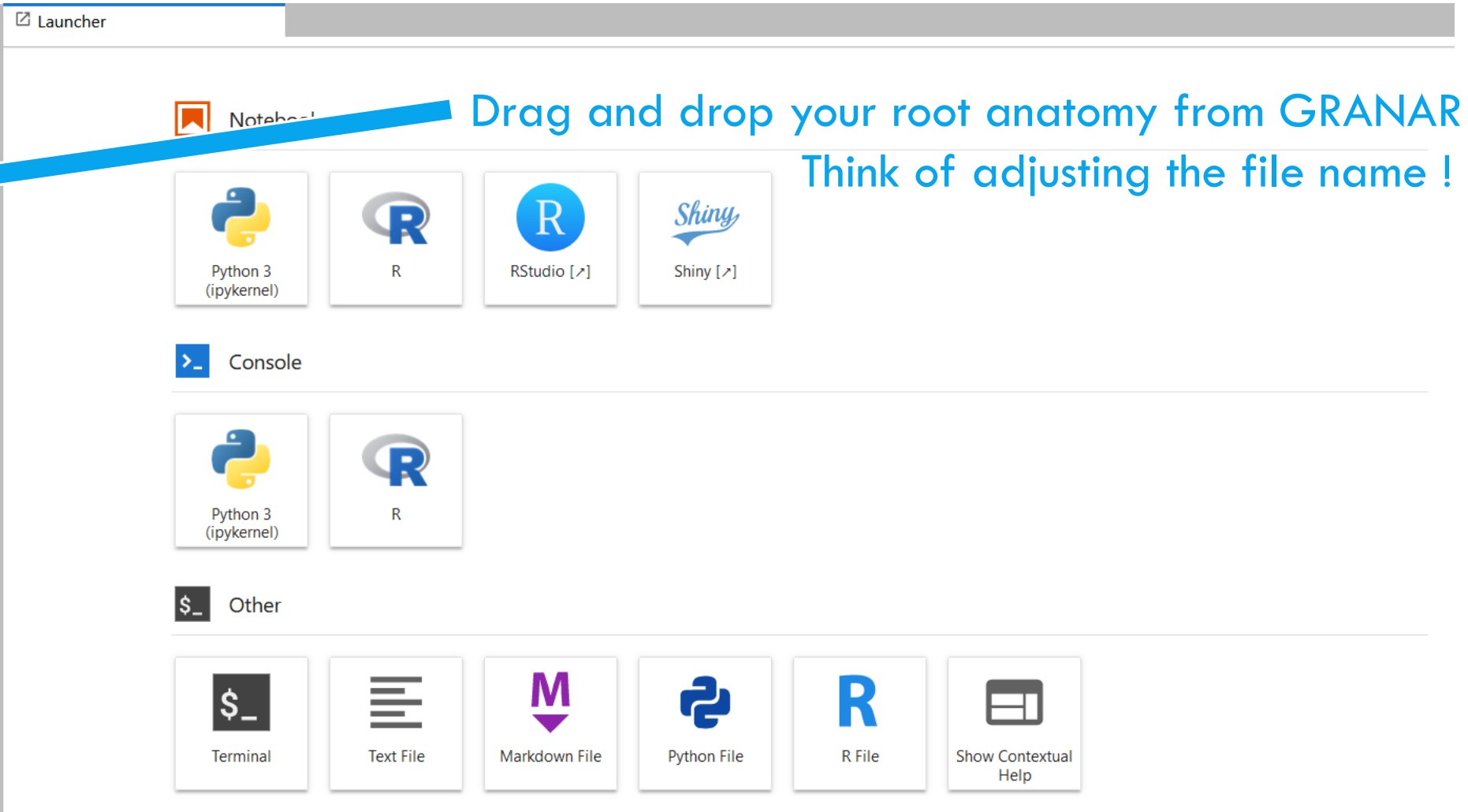
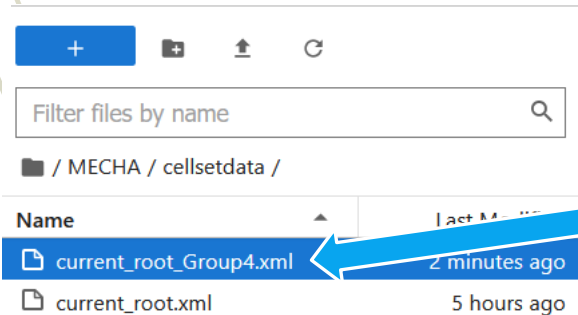
- Notebook:** Python 3 (ipykernel), R, RStudio [↗], Shiny [↗]
- Console:** Python 3 (ipykernel), R
- Other:** Terminal, Text File, Markdown File, Python File, R File, Show Contextual Help

Double click on folders MECHA/ then cellsetdata/

MODELLING WATER FLOW AT THE ORGAN SCALE

- MECHA -

Once on Binder... let's update the root anatomy!



Drag and drop your root anatomy from GRANAR
Think of adjusting the file name !

MODELLING WATER FLOW AT THE ORGAN SCALE

- MECHA -

Once on Binder... let's update the root anatomy!

Filter files by name

/ MECHA /

Name	Last Modified
cellsetdata	5 hours ago
Projects	5 hours ago
MECHAv4_l...	5 hours ago

Go to the folder `MECHA/Projects/granar/in/`

Launcher

Python 3 (ipykernel)

R

RStudio [↗]

Shiny [↗]

Console

Python 3 (ipykernel)

R

Other

Terminal

Text File

Markdown File

Python File

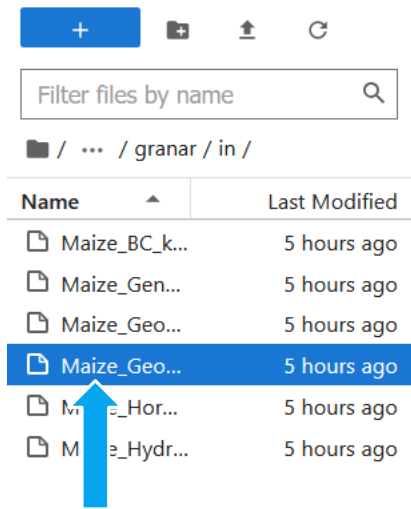
R File

Show Contextual Help

MODELLING WATER FLOW AT THE ORGAN SCALE

- MECHA -

Once on Binder... let's update the root anatomy!



1. Open the file
'Maize_geometry_aer.xml'

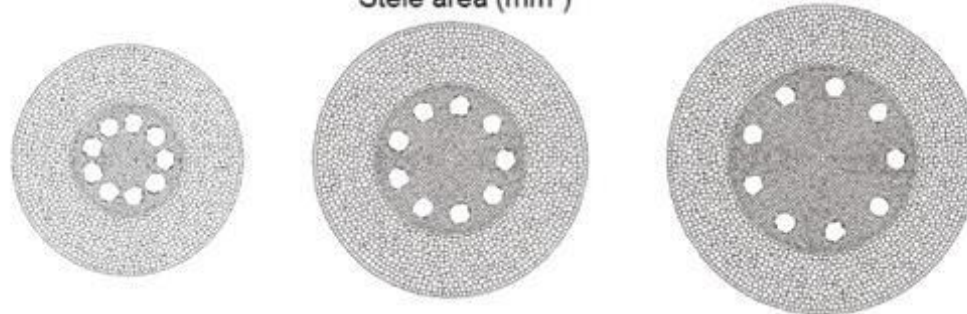
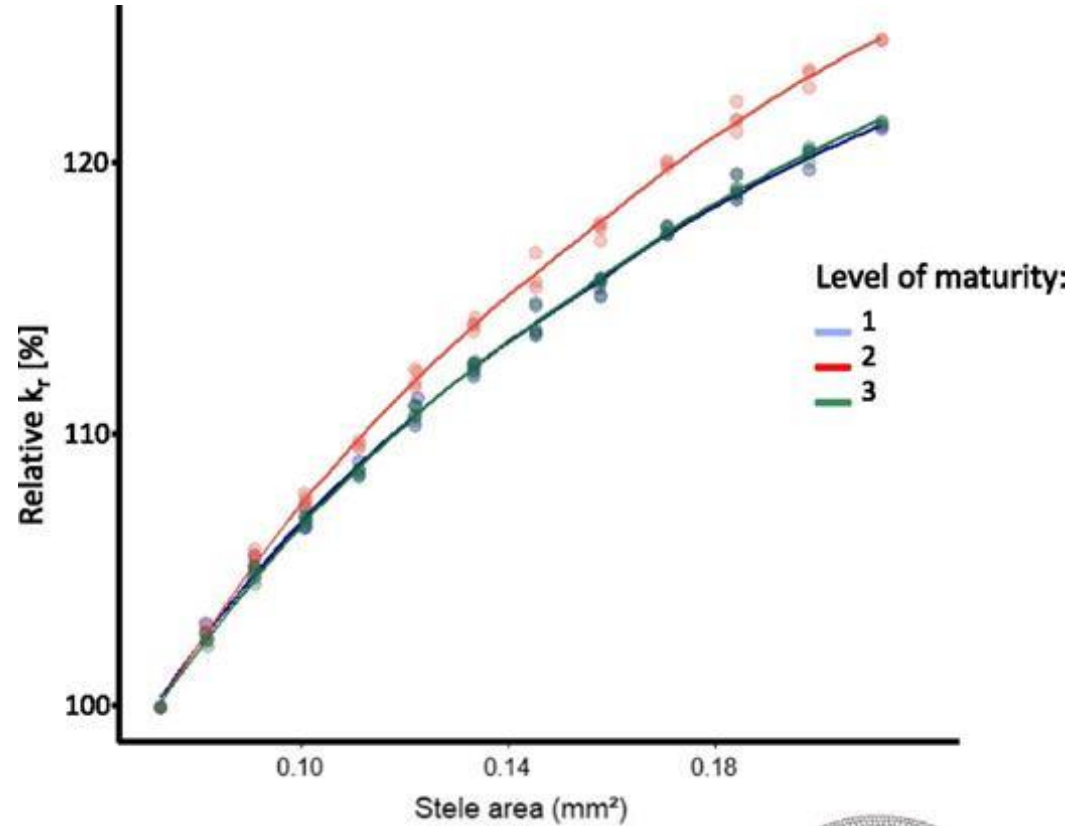
```
1 <?xml version="1.0" encoding="utf-8"?>
2
3 <param>
4   <!-- Plant type -->
5   <Plant value='Root' />
6
7   <!-- Image path and properties -->
8   <path value='current_root.xml' />
9   <im_scale value="1000" /> <!-- #image scale (micron per pixel) -->
10
11   <!-- Maturity Level
12   0: No apoplastic barriers
13   1: Endodermal Casparian strip (radial walls)
14   2: Endodermal suberization except at passage cells
15   3: Endodermis full suberization
16   4: Endodermis full suberization and exodermal Casparian strip (radial walls) -->
17   <Maturityrange> <!-- All the listed barrier types will be simulated and reported in separate files "b1",
18   "b2", "b3",... -->
19   <Maturity Barrier="1" height="200" Nlayers="1"/>
20   <Maturity Barrier="4" height="200" Nlayers="1"/>
21   </Maturityrange>
22   <Printrange>
23   <Print_layer value="0"/>
24   </Printrange>
25   <Xwalls value="1" /> <!-- 0: No transverse walls in the 2D simulations; 1: Transverse walls included in 2D
26   simulations -->
27   <PileUp value="0" /> <!-- 0: Simulating different levels of maturity separately (2D); 1: Simulating all levels
28   of maturity interconnected (3D) -->
29
30   <!-- Topological info (passage cells and intercellular spaces) -->
31   <passage_cell_range>
32     <passage_cell id="-1" /> <!-- ID number of passage cells in the endodermis, ideally in front of early
33     metaxylem vessels -->
34   </passage_cell_range>
35   <aerenchyma_range>
```

3. Update the name of folder in
which the new outputs will be stored

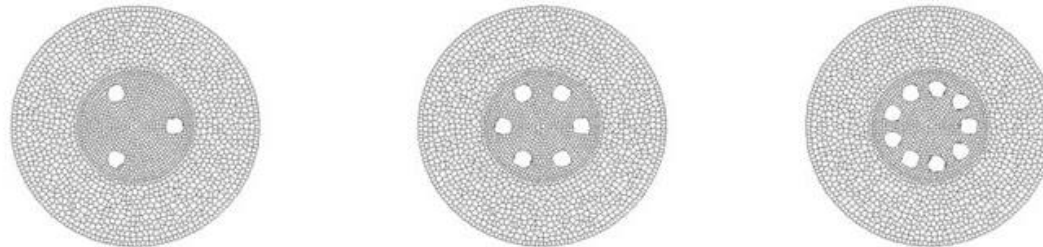
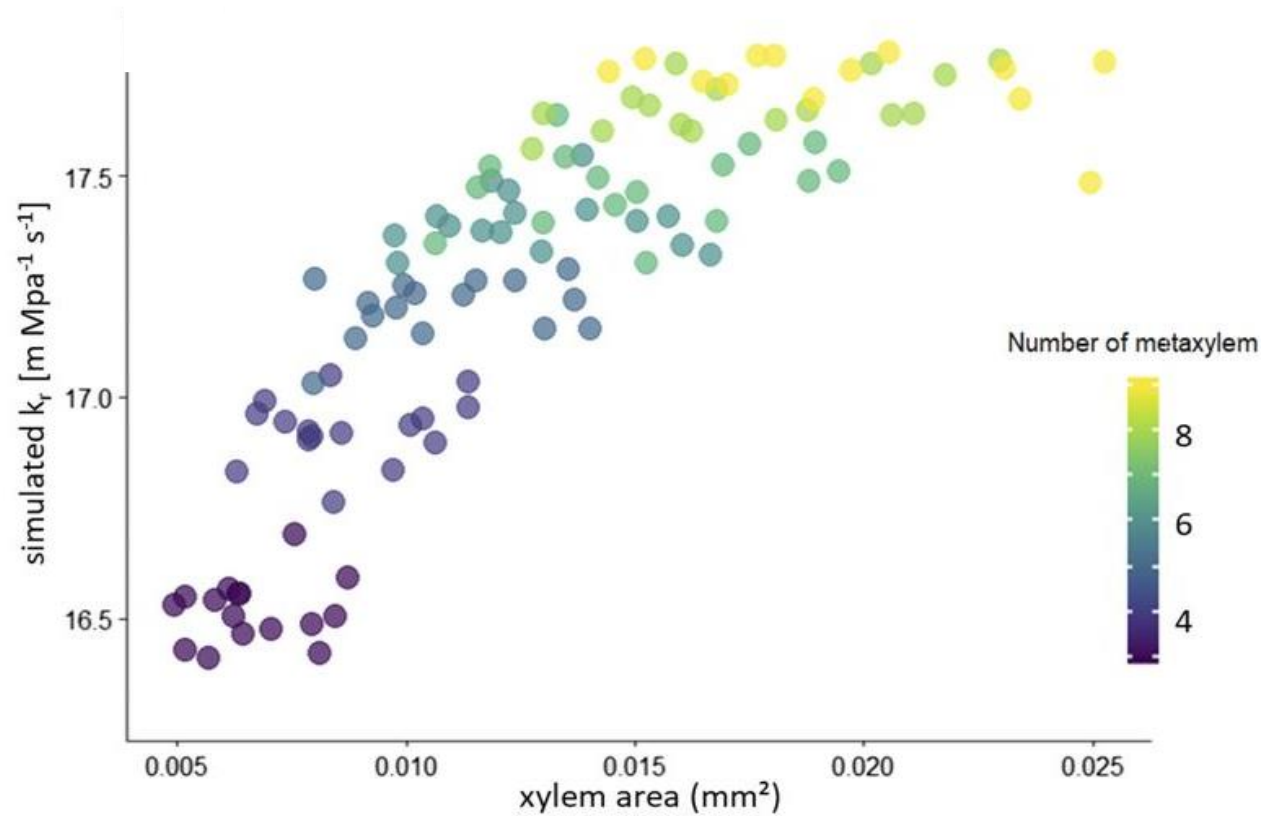
2. Update the name of the dragged
GRANAR output, so it corresponds to
your new root anatomy file name
(e.g. 'Principal_root_largeStele.xml')

4. In Run_MECHA.ipynb, run the cell « from
mecha_function ... » and check new kr values

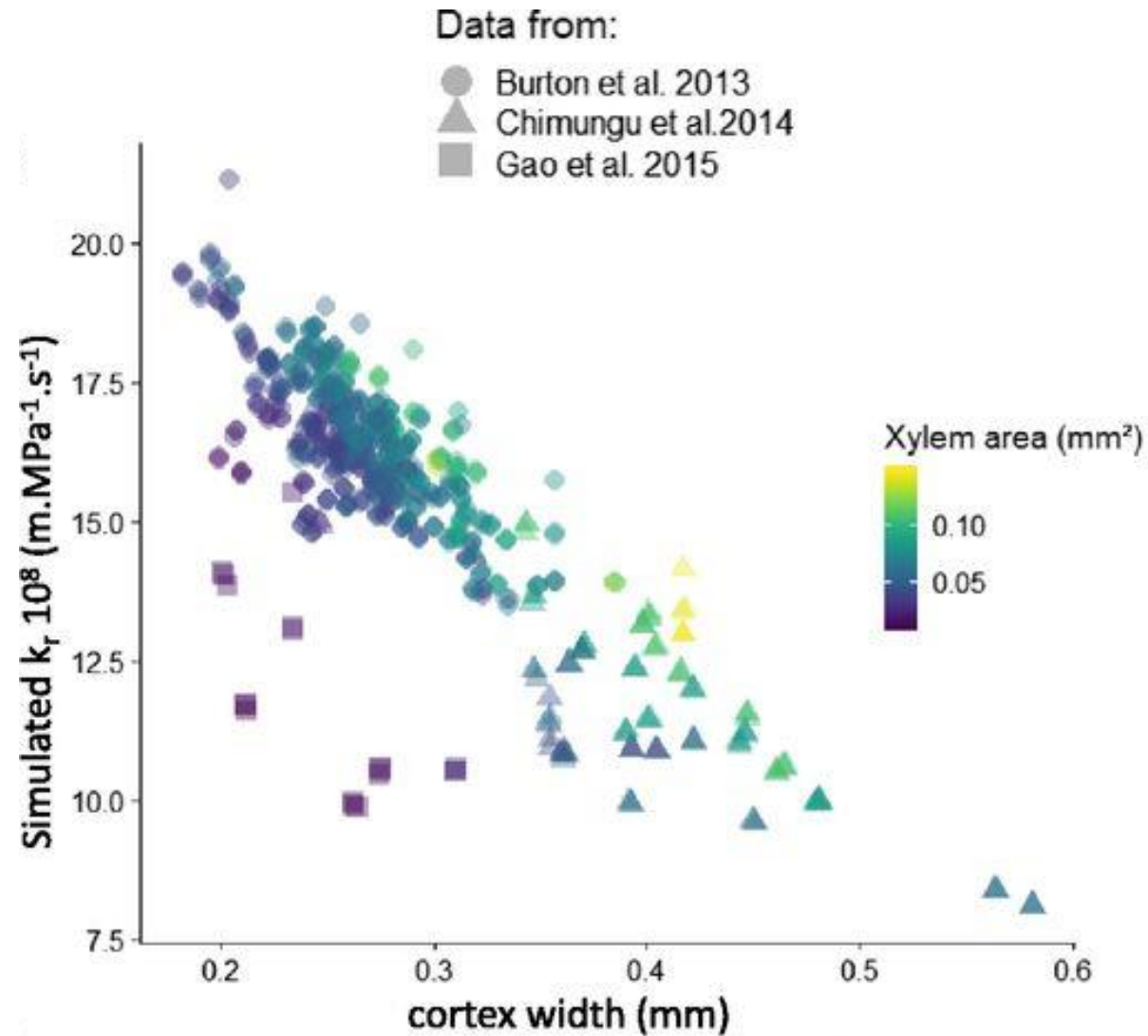
SENSITIVITY ANALYSIS



SENSITIVITY ANALYSIS



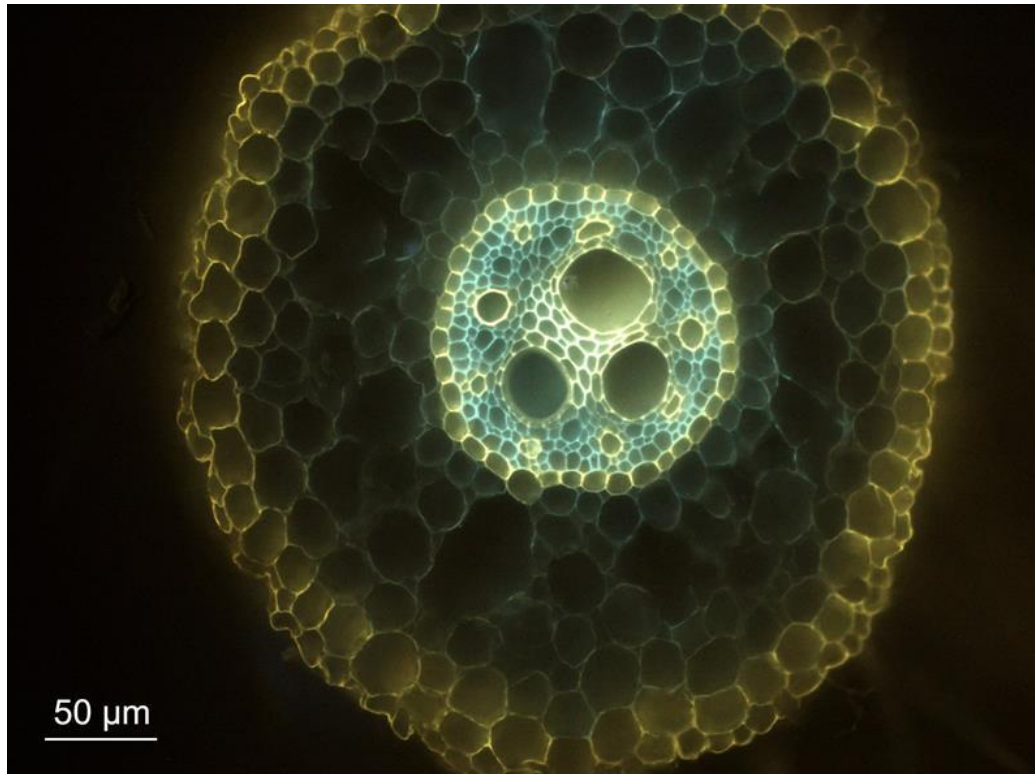
SENSITIVITY ANALYSIS



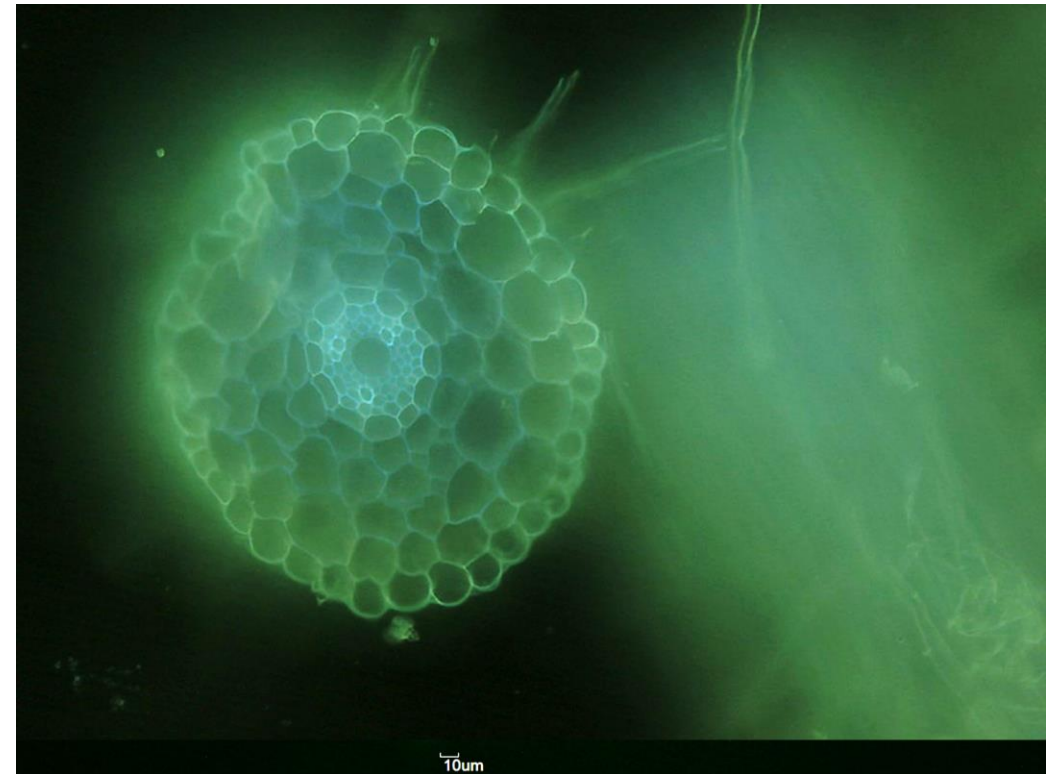
HANDS ON GRANAR

➡ Try to reproduce one of these anatomies on the ShinyApp

<https://plantmodelling.shinyapps.io/granar/>



Principal root maize B73



Lateral root maize B73

Devoir anatomie - architecture

<https://github.com/LBRAI2219-2023/ressources>

➡ Exercice individuel

Le but du devoir est de combiner les analyses des modèles anatomiques (GRANAR, MECHA) et architecturaux (MARSHAL).

En particulier, vous devez :

- générer une anatomie avec GRANAR (Shiny app)
- utiliser cette anatomie pour estimer des paramètres hydrauliques locaux avec MECHA (via Binder)
- utiliser ces valeurs de conductivité dans un système racinaire complet à l'aide de MARSHAL

Encore plus précisément, vous devez répondre aux questions suivantes (analyse de sensibilité)

- quel est l'effet de l'anatomie sur K_r
- quel est l'effet de l'anatomie des racines primaires sur K_{rs}
- quel est l'effet de l'anatomie des racines latérales sur K_{rs}

Vous devez choisir un des deux types architecturaux fournis par défaut dans la Shiny app de MARSHAL (**simplified or not**)

Les anatomies **de base** des racines principales et latérales doivent ressembler aux images ci-dessus.

Pour l'analyse de sensibilité, modifiez UN SEUL paramètre anatomique au choix (de +50% à -50%).

Le répertoire contient un RMD permettant de faire tourner Marshal et un permettant de faire tourner GRANAR.

Vous devez nous fournir un graphique qui permette de répondre à chacune des questions

SIMULATING ROOT ANATOMIES

- GRANAR -

<https://github.com/water-fluxes/day-2-organ-GRANAR>

The screenshot shows the GitHub repository page for 'water-fluxes / day-2-organ-GRANAR'. The repository is public and has 1 watch, 0 forks, and 0 stars. The main branch is 'main'. The repository contains a file tree with the following files and their last commit times:

File	Commit Message	Time Ago
GRANAR	Thin lateral root for LBRAI2219 - GRANAR inputs	1 hour ago
outputs	updated paths	8 months ago
.DS_Store	updated paths	8 months ago
DAY2_2.pdf	Add files via upload	7 months ago
GRANAR_MECHA.Rmd	change repo structure	8 months ago
LICENSE	change repo structure	8 months ago
Modeling Water fluxes in the s...	Add files via upload	7 months ago
README.md	Update README.md	7 months ago
Run_GRANAR.ipynb	Update Run_GRANAR.ipynb	8 months ago
install.R	change repo structure	8 months ago
runtime.txt	updateruntime	8 months ago

The README.md file is displayed below the file tree. It contains the following text:

Material for the day 2 of the summer school - Organ scale water flow in roots - GRANAR

In this repository you will find resources to run GRANAR

You can launch the notebook here : [launch](#) [binder](#)

A blue arrow points from the 'binder' link in the README to the text 'Run GRANAR via Binder' on the right side of the slide.

Run GRANAR via Binder

RUNNING GRANAR

3. Click play

2. Click on
Run_GRANAR*

1. Change
kernel into R

Estimation of hydraulic properties using modeling tools

GRANAR:

Upon a small set of anatomical features the GRANAR model is able to reconstruct a generic root cell network for mono and dicotyledon.

Change kernel to R to launch the following script.

```
[1]: # Loading R Library
library(tidyverse)
library(plyr)
library(deldir)
library(sp)
library(xml2)
library(viridis)

source("../GRANAR/R/granar.R")
```

NameError Traceback (most recent call last)
/tmp/ipykernel_61/2087669825.py in <module>
1 # Loading R library
----> 2 library(tidyverse)
3 library(plyr)
4 library(deldir)
5 library(sp)

NameError: name 'library' is not defined

COUPLING GRANAR AND MECHA TO ESTIMATE K_r

Filter files by name

/ outputs /

Name	Last Modified
current_root.xml	3 minutes ago
Maize_Geometry.x...	3 minutes ago
Maize_Hydraulics.x...	3 minutes ago

1. New root anatomy in output folder

