THE 1ST INTERNATIONAL SUMMER SCHOOL ON ADVANCED SOIL PHYSICS

MODELING WATER FLUXES IN THE SOIL-PLANT SYSTEM

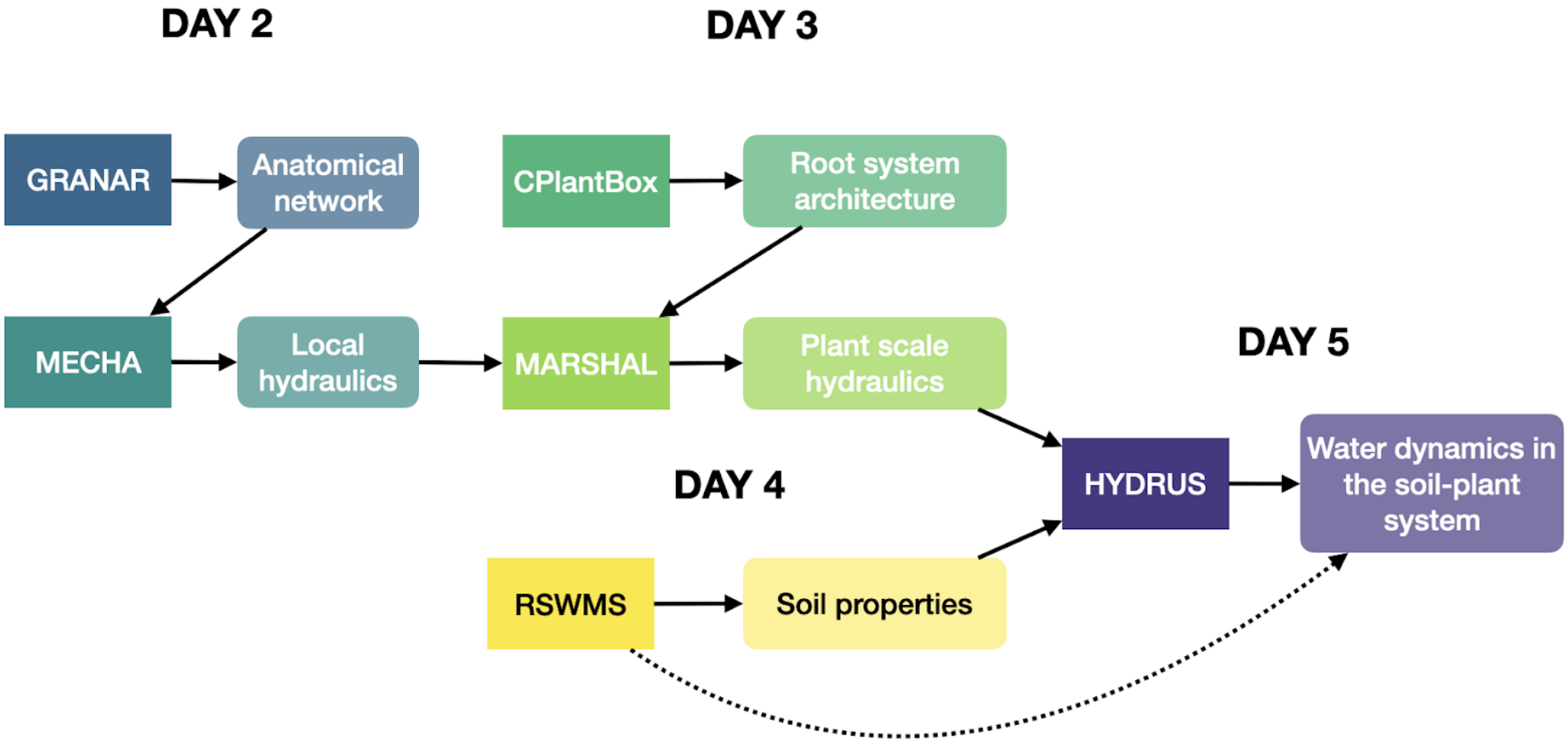
MODELLING ROOT ANATOMY - GRANAR

GUILLAUME LOBET

UCLouvain

ISMC
International Soil Modeling Consortium

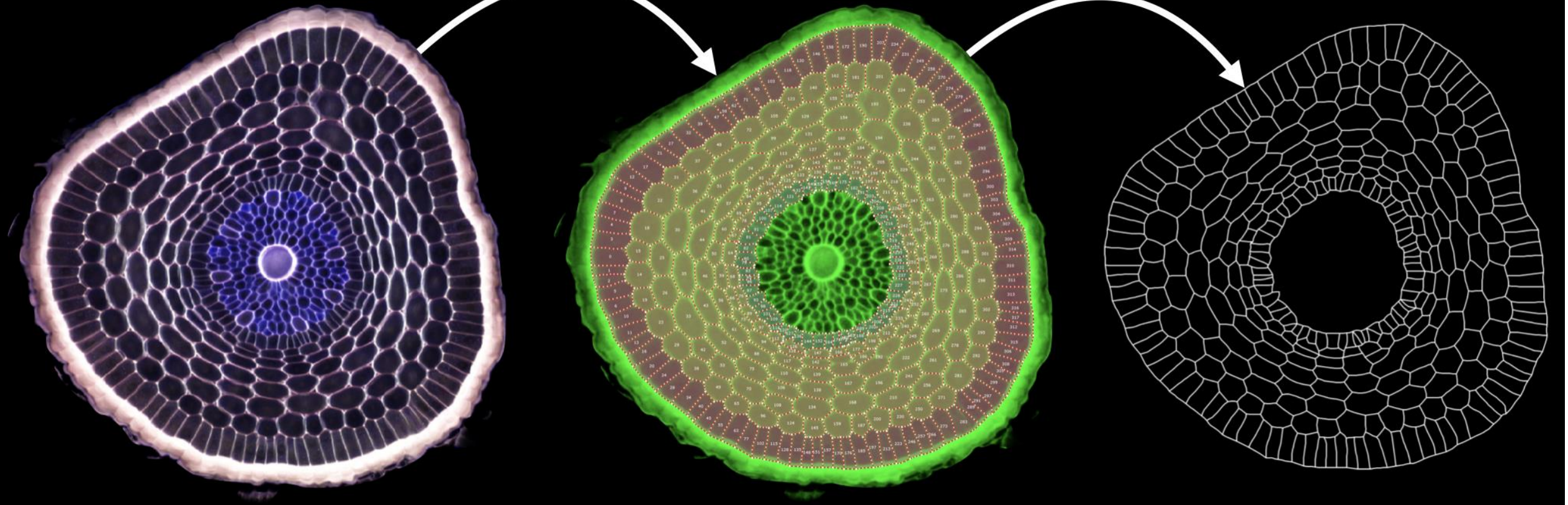
ENVITAM


DAY 2
DAY 3
GRANAR
Anatomical network
CPlantBox
Root system architecture
MECHA
Local hydraulics
MARSHAL
Plant scale hydraulics
DAY 5
DAY 4
HYDRUS
Water dynamics in the soil-plant system
RSWMS
Soil properties

ROOT CONDUCTIVITY = ANATOMY + CONDUCTIVITIES

CELLSET

XML



Pound et al, 2012

Plant Cell

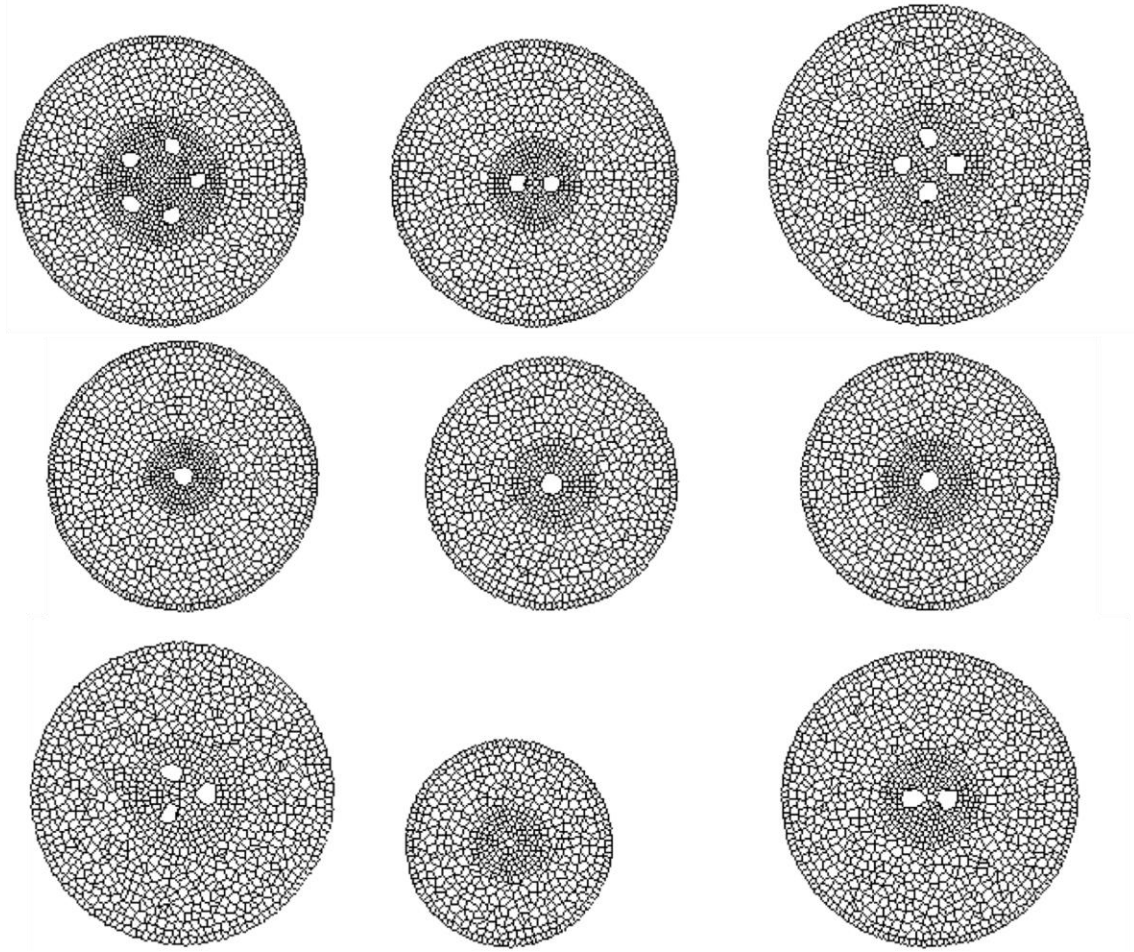
GENERATOR OF ANY TYPE OF ROOT ANATOMY IN R
GRANAR

XYLEM VESSELS
∅ XYLEM VESSELS

CORTEX LAYERS
∅ CORTEX CELLS

∅ STELE

% AERENCHYMA



Heymans A, Couvreur V, LaRue T, Paez-Garcia A, Lobet G. GRANAR, a Computational Tool to Better Understand the Functional Importance of Monocotyledon Root Anatomy. Plant Physiol. 2020;182: 707–720. doi:10.1104/pp.19.00617

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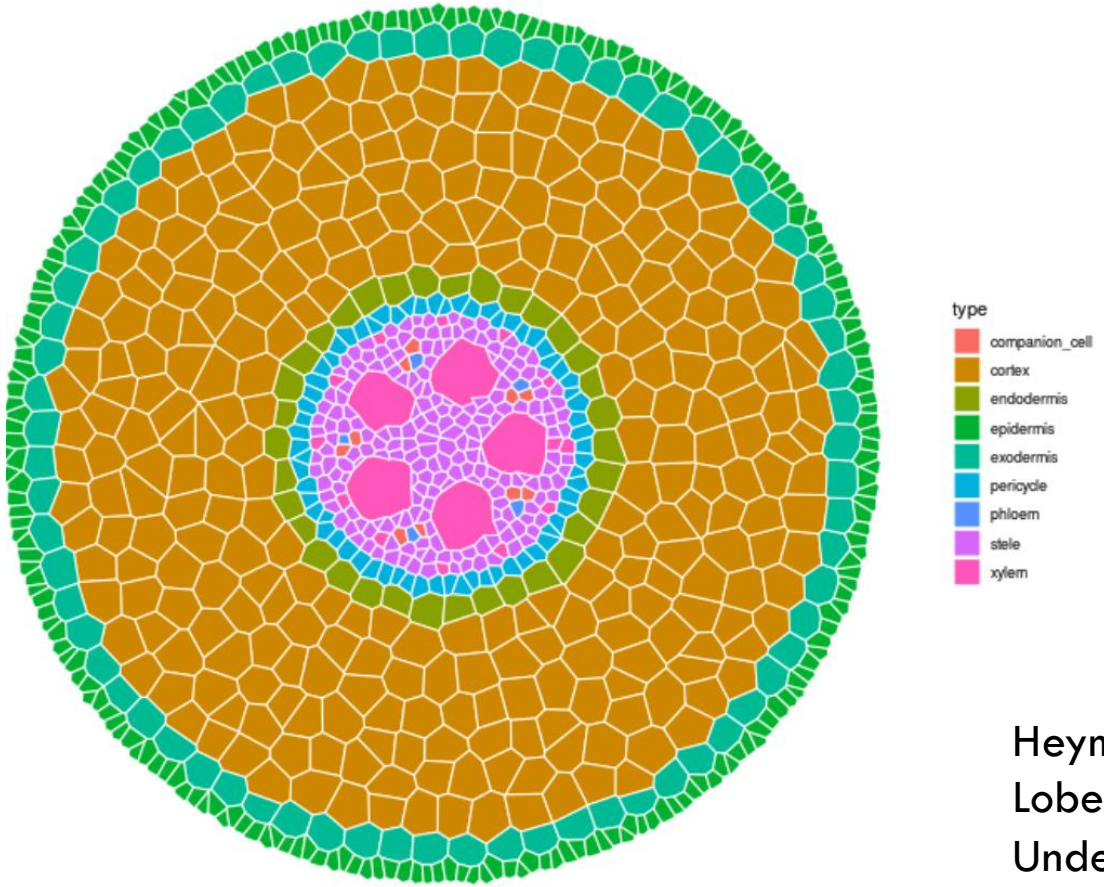

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GENERATOR OF ANY TYPE OF ROOT ANATOMY IN R
GRANAR

INPUT FILE OF GRANAR

```
<?xml version="1.0" encoding="utf-8"?>

<granar>
    
    <!-- General parameters -->
    <planttype param="2" /> <!-- 1 = monocot / 2 = dicot -->
    <randomness param="3" />
    
    <!-- Cell layers -->
    <stele cell_diameter="0.0044" n_layers="1" layer_diameter = "0.027" order="1"/>
    <pericycle cell_diameter="0.0056" n_layers="1"  order="2"/>
    <endodermis cell_diameter="0.0083" n_layers="1"  order="3"/>
    <cortex cell_diameter="0.0227" n_layers="1"  order="4"/>
    <epidermis cell_diameter="0.0147" n_layers="1" order="6"/>


    <!-- Vessels-->
    <xylem max_size="0.0045" n_files="3" order="1.5" ratio ="1" />
    <phloem max_size="0.01" n_files="3" />
    
    <!-- Other cell types -->
    <aerenchyma proportion="0" n_files="10"/>

</granar>
```

RUNNING GRANAR

```
# Load one parameter file for GRANAR
params <- read_param_xml("GRANAR/model_params/Zea_mays_2_Heymans_2019.xml")

 # # # # # # # # # # # # # # # #
#  To change paramter value   #
 # # # # # # # # # # # # # # # #

# Xylem size (diameter)
params$value[params$type == "max_size" & params$name == "xylem"] <- 0.026

# aerenchyma proportion
params$value[params$type == "proportion" & params$name == "aerenchyma"] <- 0.2
# number of lacuna
params$value[params$type == "n_files" & params$name == "aerenchyma"] <- 15

# Generate the anatomy
sim <- create_anatomy(parameters = params, verbatim=F, paraview = F)
```

PLOTTING RESULTS

```
# To visualize the anatomy and the scenario that are going to be tested.
# you can use the plot_anatomy function.
plot_anatomy(sim, col = "segment", apo_bar = 1)
plot_anatomy(sim, col = "segment", apo_bar = 2)
plot_anatomy(sim, col = "segment", apo_bar = 3)

# To visualize cell type:
plot_anatomy(sim) # default type
```

EXPORTING RESULTS

```
# write geometry
write_anatomy_xml(sim, "./outputs/current_root.xml")
# give explicit location of root lacuna in geometry
aer_in_geom_xml(sim, path = "./outputs/Maize_Geometry.xml")
```

EXERCICE

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

- Run the jupyter notebook on binder
- Try modifying the parameters in the R code
- Try modifying the parameters directly in the input files
- Generate one specific anatomy for every group (see printed documents)