

Xylogenes Dynamics Simulator 2

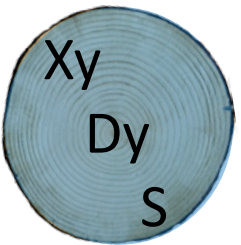
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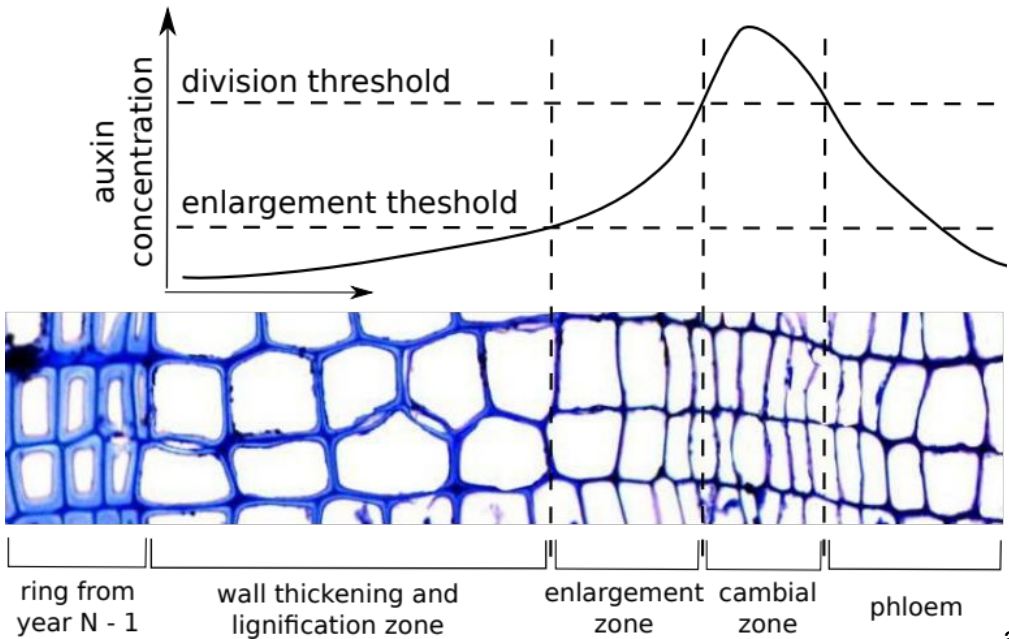
XyDyS (Xylogenesis Dynamics Simulator)

- XyDyS is an open-source software for modeling and simulating the dynamics of wood formation in conifers.
- Freely available at <https://forgemia.inra.fr/felix.hartmann/xydys>.
- Focused on understanding the internal regulation of wood formation (basic research in developmental biology).
- Hypothesis-driven approach: a tool for quantitatively testing various hypotheses.
- XyDyS has been presented and illustrated in two research articles:
 - 1) Hartmann *et al.* (2017) Modelling wood formation and structure: power and limits of a morphogenetic gradient in controlling xylem cell proliferation and growth. *Annals of Forest Science*.
 - 2) Hartmann *et al.* (2021) Modelling the spatial crosstalk between two biochemical signals explains wood formation dynamics and tree-ring structure. *Journal of Experimental Botany*.



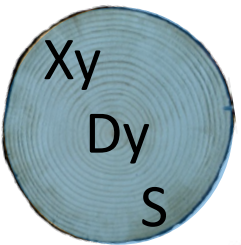
Initial motivation:

The auxin gradient as a morphogenetic gradient?



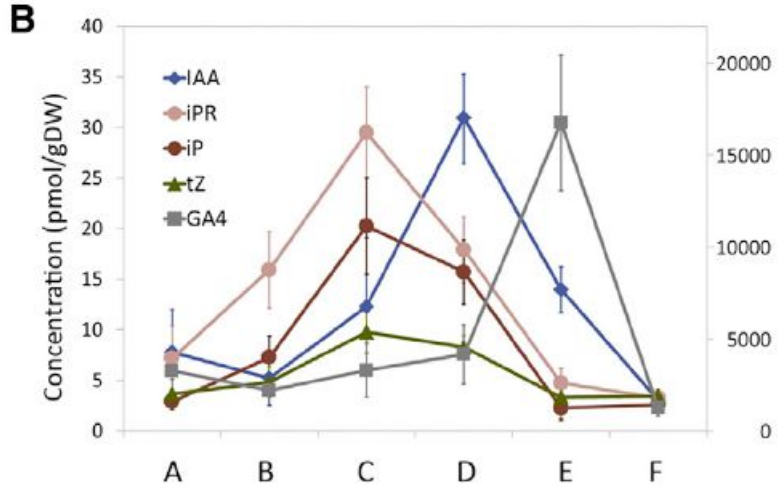
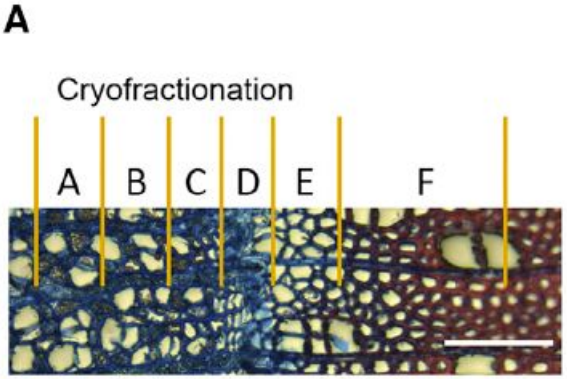
adapted from Bhalerao and Fischer (2014)

Does the auxin gradient provide enough information to cells to guide the development of the tissue into mature wood?



Further motivation:

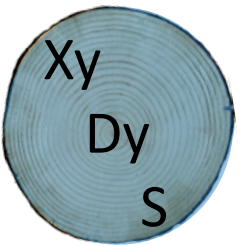
Actually, there are many gradients across the tissue



from Immanen *et al.* (2016)

- auxin
- cytokinins
- gibberellins
- peptides (CLE42)
- ...

It would be nice to have a tool to easily model and simulate how these gradients regulate wood formation!



A user-friendly interface

A graphical interface allows to build, tune, and explore models.

A variety of outputs are possible to visualize the results of simulations.

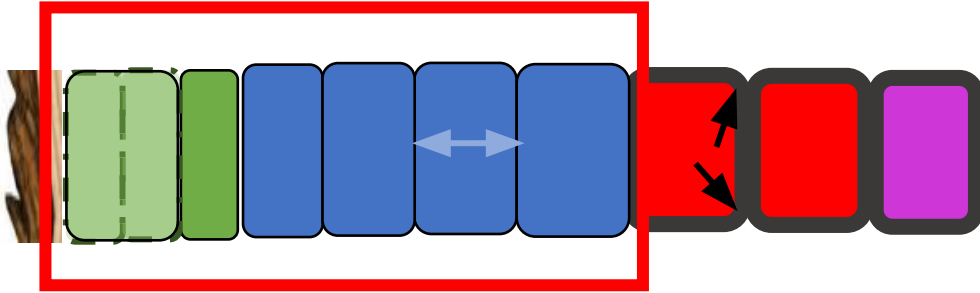
The screenshot displays the XyDyS software interface with several components:

- Simulation Control Panel:** Includes tabs for Model, Signals, and Advanced. Parameters include Start (day of year: 90), Cambium activation (day of year: 91), Stop (day of year: 300), Initial number of cells (6), and Initial cell diameter (6.0). A Run button is present.
- Simulation Status:** Shows "Simulation finished after 2170.6 s." and a Draw cell file button.
- Options:** Checkboxes for division threshold, end of enlargement threshold, strain rates, and colored zones. Buttons for Plot cell diameters, Plot growth, Plot growth speed, Plot cell accumulation, Plot number of cells in each phase, Plot cell entry rate in each phase, Plot cell residence times, Plot mean rates, Load settings, and Save settings.
- Plots:**
 - Signal concentration vs. μm :** A scatter plot with a blue trend line showing signal concentration increasing from 0 to 14 as distance from the cambium decreases.
 - Length (μm) vs. Day of year:** A line graph showing cell length increasing from 0 to approximately 2500 μm over 200 days.
 - Number of cells vs. Day of year:** A line graph showing the number of cambial cells (green line) and enlarging cells (blue line) over 300 days.
 - Cell diameter (μm) vs. Cell index:** A line graph showing cell diameter decreasing from approximately 45 μm to 10 μm across 80 cells.
- Visualizations:** Three images of tree trunks at different stages of growth, corresponding to different points in the simulation.

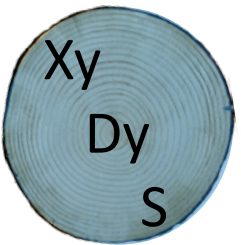


Resolved cell phases and processes

Only cell division and expansion are modeled.

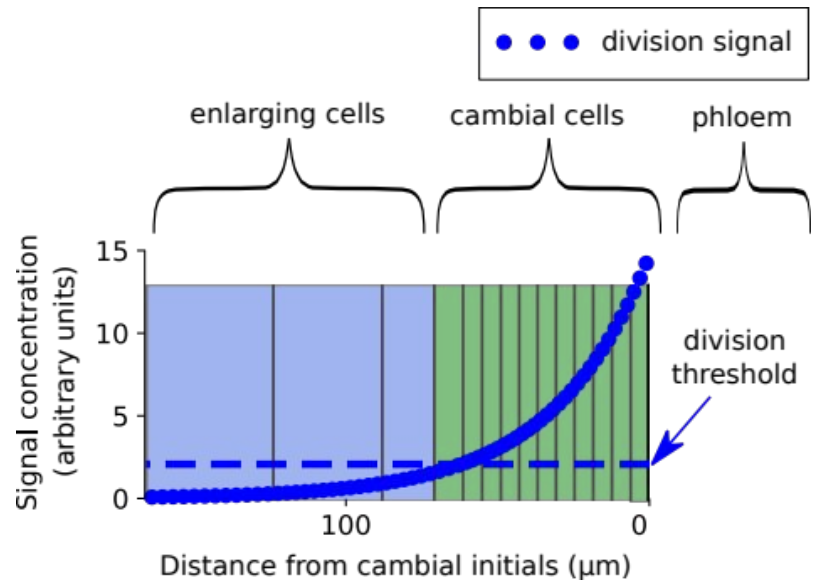
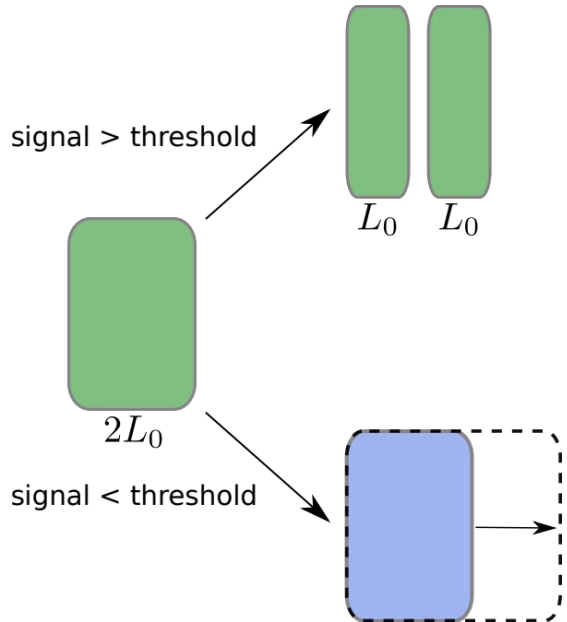
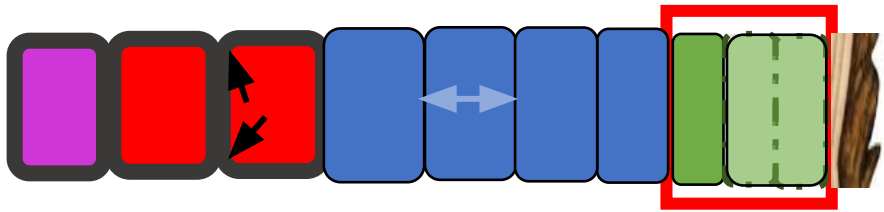


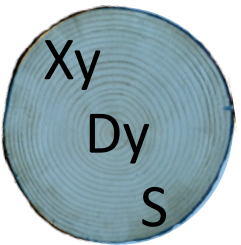
Secondary cell wall thickening and lignification are not considered.



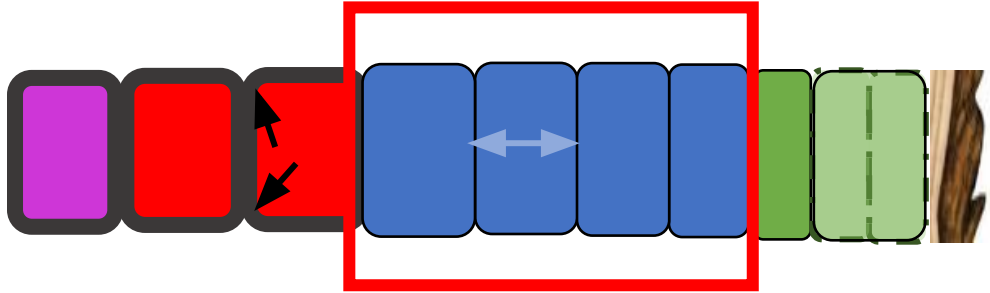
Process-representation: the Cambium

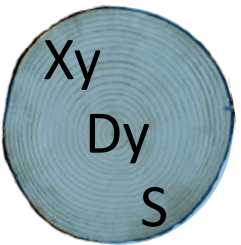
The ability of cells to divide is determined by a “division signal”. Cells can divide only if the local concentration of division signal is higher than a “division threshold”.





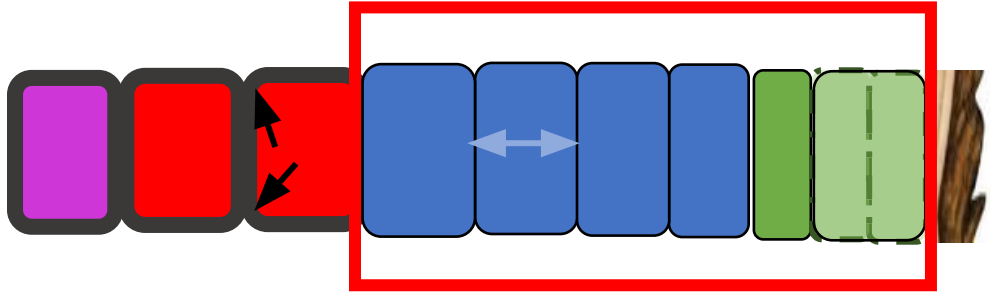
Process-representation: Cell enlargement

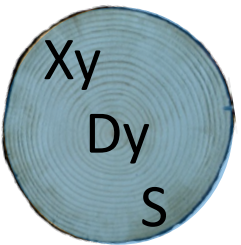




Process-representation: ~~Cell enlargement~~ expansion

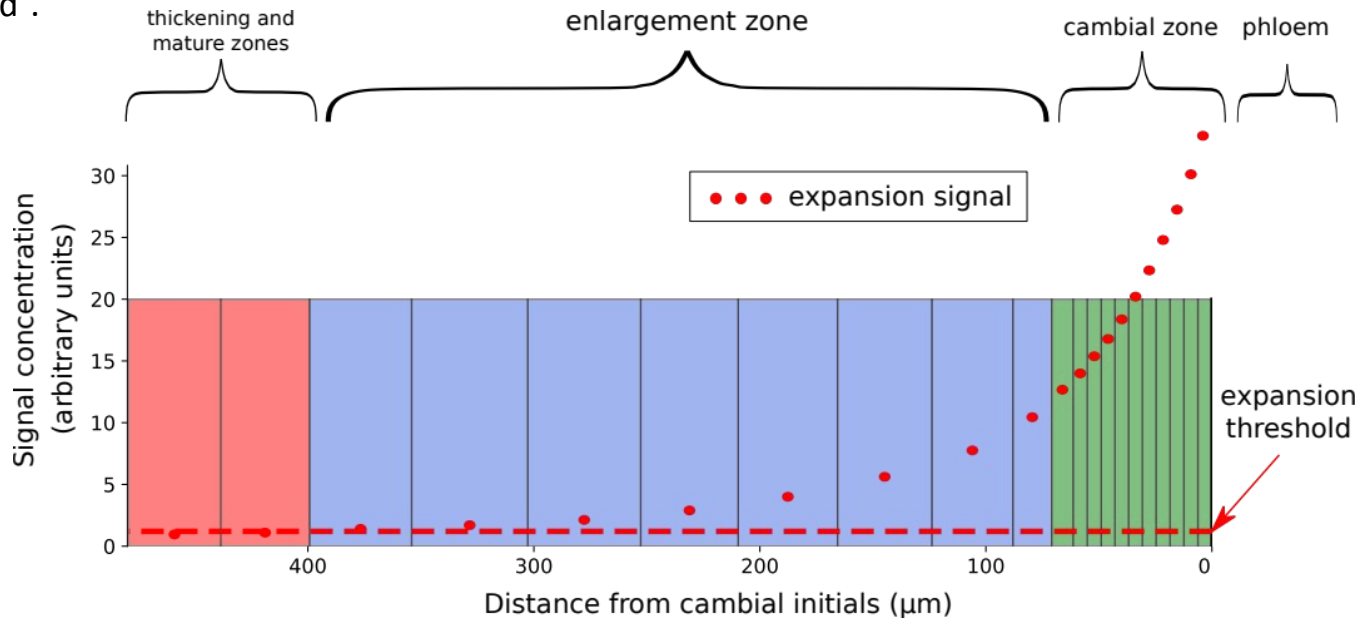
Dividing cells are also expanding!
(no division without expansion)



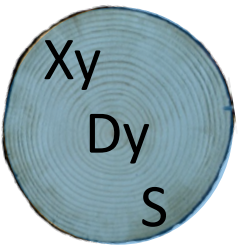


Process-representation: ~~Cell enlargement~~ expansion

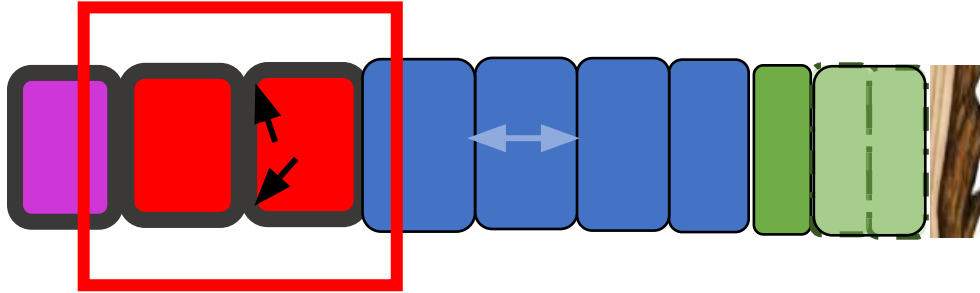
An “expansion signal” determines which cells are expanding, based on an “expansion threshold”.



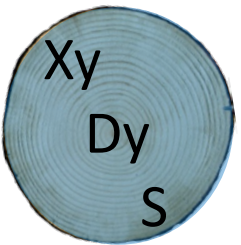
The expansion rate of a cell is proportional to its concentration of expansion signal and inversely proportional to its size.



Process-representation: wall thickening

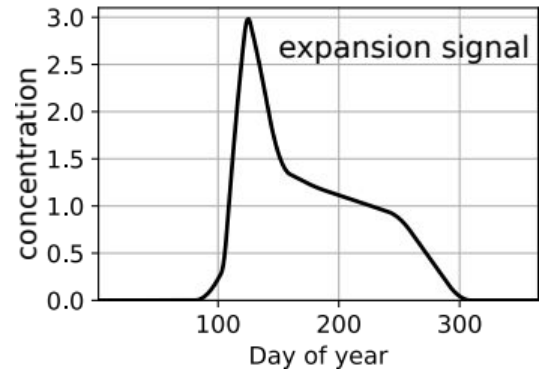
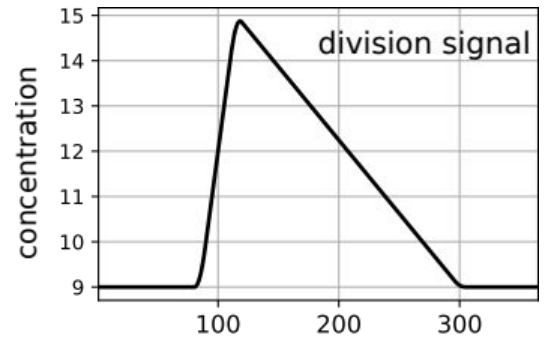


Once a cell stopped enlarging, it can still transport signals, but wall thickening is not modeled.

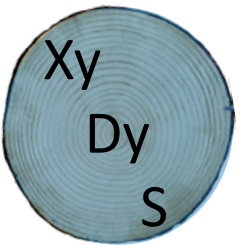


Inputs/forcing

- Biochemical signals (hormones, peptides, ...)
- Imposed boundary concentrations
- Transport processes: diffusion, polar active transport
- Cross-talk between signals
- All settings are saved in JSON files
- Time step for simulation around 1 hour (can be much less for fast-diffusing signals)

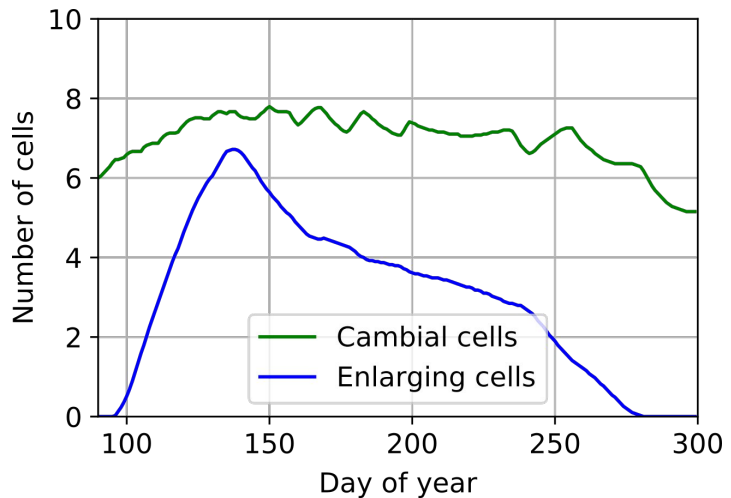
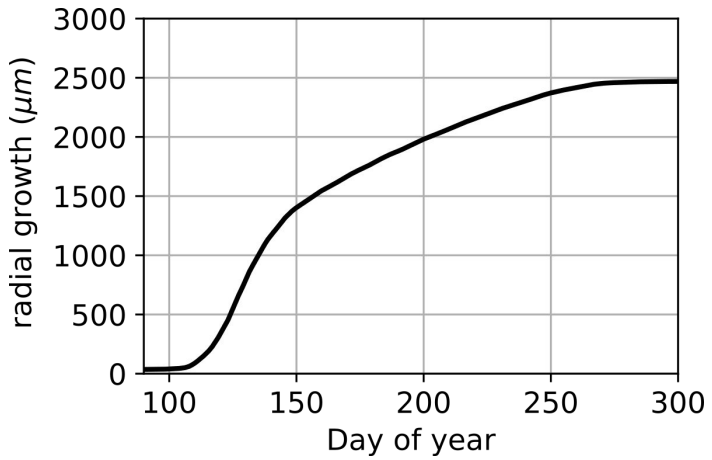


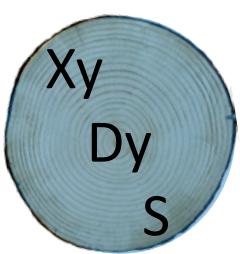
imposed boundary concentrations of the signals



Outputs

- The spatio-temporal evolution of the cell file and the signal concentrations, as a video or a sequence of images.
- Xylem growth curves.
- The evolution of the number of cells in each developmental zone.
- Cell diameters at any time step and the final tracheidogram.

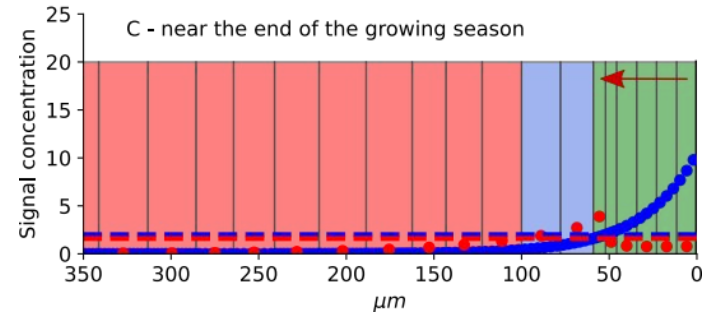
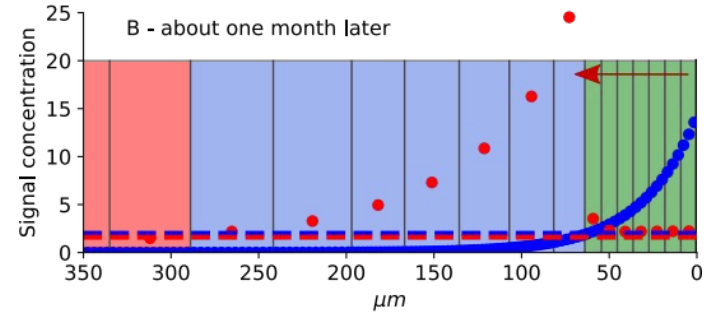
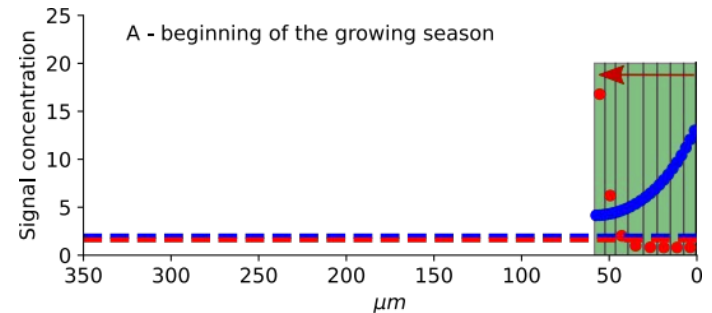
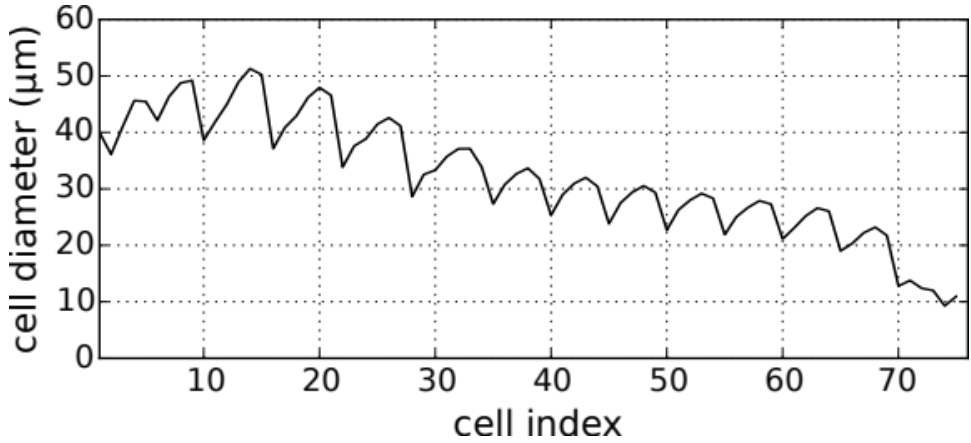


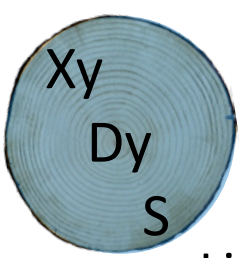


An example: Two-signal model with cross-talk

Hartmann et al. (2021) J. Exp. Bot.

- Division signal: cytokinin (diffusive)
- Expansion signal: auxin (polar active transport toward the xylem)
- Polar auxin transporters (PINs) are synthesized only where cytokinin concentration > division threshold (cross-talk).
- Auxin-dependent PIN synthesis.





Limitations and outlooks

- Limitation: Data on hormone concentrations in the cambium are scarce, and little is known about their cross-talks. Many hypotheses have to be made.
- Outlooks:
 1. Taking temperature into account: Most biochemical processes are affected by temperature, so this effect should be taken into account.
 2. Trying to relate signal concentrations to environmental factors.