Computational model of auxin-CUC interaction in the floral meristem

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Summary

The floral meristem is modeled using a 2D disk of cells that are growing and dividing, based on two previous models, GridAuxin and MassSpringCells. Mechanics are modeled using a mass-spring model where cell walls (springs) are pulling cell wall junctions (masses). Each cell has auxin, CUC, and PIN, that are produced, degraded, and interacting, calculated using a differential equations solver. The model is implemented in C++, and can be run inside the VLab environment¹ and the MorphoDynamX software². The model can be run either one simulation at a time, or batch-run using a python code.

The Model Folder

Within the model folder "MassSpringAuxin":

- "specifications.txt" lists all the files within the folder to be included with the model
- "CellDisk.hpp" and "CellDisk.cpp" are the model source files, and can be edited using a text editor or IDEs such as VS Code.
- "CellDisk.mdxv" can be edited using a text editor, and contain metadata of the model, including which initial condition to use.
- "Init_blank_72cells_2023-09-07.mdxm" is the initial condition used in the model. This can be changed to another MDX mesh file.

Running the model one simulation at a time

- 1. Open the VLab Browser.
- 2. Select the oofs repository.
- 3. Navigate to the model, and double click on the window to open it.
- 4. Right click on the model icon, and select "run". The model would now open in MDX.
- 5. Set the desired parameters, mainly in Process -> Model -> 01 Cell Disk and Process -> Model -> Auxin Gradient Model. If output is desired, set "Run name", "Output directory", and "Output frequency".
- 6. Double-click Process -> Model -> 01 Cell Disk to run it. Click on the stop button to stop when desired.

Running the model in batch mode

- 1. Using a python code, such as the provided "create_run_20231010_demo.py", create a run file, such as the provided "run_20231010.py". The former file specifies the parameter combinations to be tested, while the latter file contains the commands to be fed into MDX.
- 2. Open the model in MDX following steps 1-4 in the previous section.

- 3. Under Process -> Tools -> Python -> Python Script, select the run file created in step 1 ("run_20231010.py"). The model would now run automatically.
- 4. Screenshots are automatically saved in "output directory/run name/Screenshots/*.jpg". Cell complex data are automatically saved in "output directory/run name/CCData/*.txt". The following data are saved in these files: Cell index (CCIndex), x and y coordinates, cell area, and auxin and CUC concentrations. Each row represents a cell.
- 5. In the demo, 5 simulations each of WT, *drmy1*, *cuc1*, and *drmy1 cuc1*, with growth rates 0.4, 0.8, and 1.2 were run, and the results were saved in the directory "20231010". The simulations were named as follows: "Run_CUC Prod_SD Auxin Prod_PIN low CUC_PIN high CUC_Plasticity_Unchanging Noise_sim number_date".

Parsing and analysis of CCData

- 1. The code "Parse_output_2023-10-10_demo.R" parses these data files, identifies auxin maxima, tracks them over time, and summarizes them in "RData_20231010.RData". It also plots how auxin maxima are assigned and tracked. These plots are saved in "output directory/run name/CCData/*.png".
- 2. The data frames in the output RData file can be analyzed as desired. For example, the provided code "Modeling_analysis_2023-10-10_demo.R" reads in the RData file and generates three plots in the "Plots" folder.

References

- 1. Federl, P., and Prusinkiewicz, P. (1999). Virtual laboratory: An interactive software environment for computer graphics. Proc. Comput. Graph. Int. CGI 1999. 10.1109/CGI.1999.777921.
- 2. Strauss, S., Runions, A., Lane, B., Eschweiler, D., Bajpai, N., Trozzi, N., Routier-Kierzkowska, A.L., Yoshida, S., Da Silveira, S.R., Vijayan, A., et al. (2022). Using positional information to provide context for biological image analysis with MorphoGraphX 2.0. eLife *11*, 1–38. 10.7554/eLife.72601.