

A parametric active 4D model for the automatic construction of developmental atlases from confocal images of shoot apical meristems

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Abstract:

Patterning at the shoot apical meristem (SAM) is the emerging result of a complex interplay between genetically defined domains, differential tissue growth processes and highly dynamic hormonal signals, among which auxin, a phytohormone, is as a major player [1]. The progresses in live microscopy acquisition and the development of sensitive and quantitative biosensors [2] offer unprecedented tools to study the quantitative links between signaling input dynamics and their robust translation into organ development. However, to cope with the massive amount of images generated, advanced computational tools are required to make automatic quantification and data analysis possible [3, 4].

In this work, we addressed this issue by developing a pipeline that automatically performs quantification and spatio-temporal registration on time series of multi-channel confocal microscopy images with nuclei-located biosensors. It relies on image analysis methods to detect nuclei on a reference channel, quantify the other signals and perform sequence-wise image registration, but also on computational geometry to detect the epidermal cell layer and estimate curvature and surfacic growth. We then make use of the robust shape dynamics of the SAM to register all the time series into a common spatio-temporal referential. To do so, we propose an original model-based approach that relies on the optimization of a parametric 4D SAM shape model onto the detected nuclei point cloud (Figure1), using an iterative energy minimization process already used on leaf images [5]. Aligning this model allows to project all the data points into a canonical cylindrical referential and to assign them a developmental time index, or in other words to insert them in to a developmental atlas.

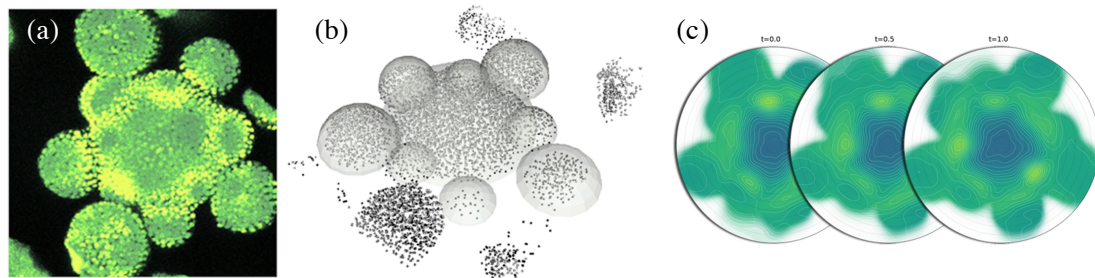


Figure1. From confocal images to epidermis developmental atlas: (a) maximal intensity projection of an auxin sensor (R2D2) confocal image stack, (b) optimized 4D SAM model on the detected nuclei points and (c) three frames of an auxin level atlas of the SAM.

Applying this pipeline on R2D2 auxin biosensor image sequences [2] and focusing on the epidermis field dynamics allows to assess quantitatively and in time the relation between auxin signaling and shape emergence in the SAM on large datasets, and provides a frame to study the joint dynamics of other markers and hormones in a commonly defined referential.

References:

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