

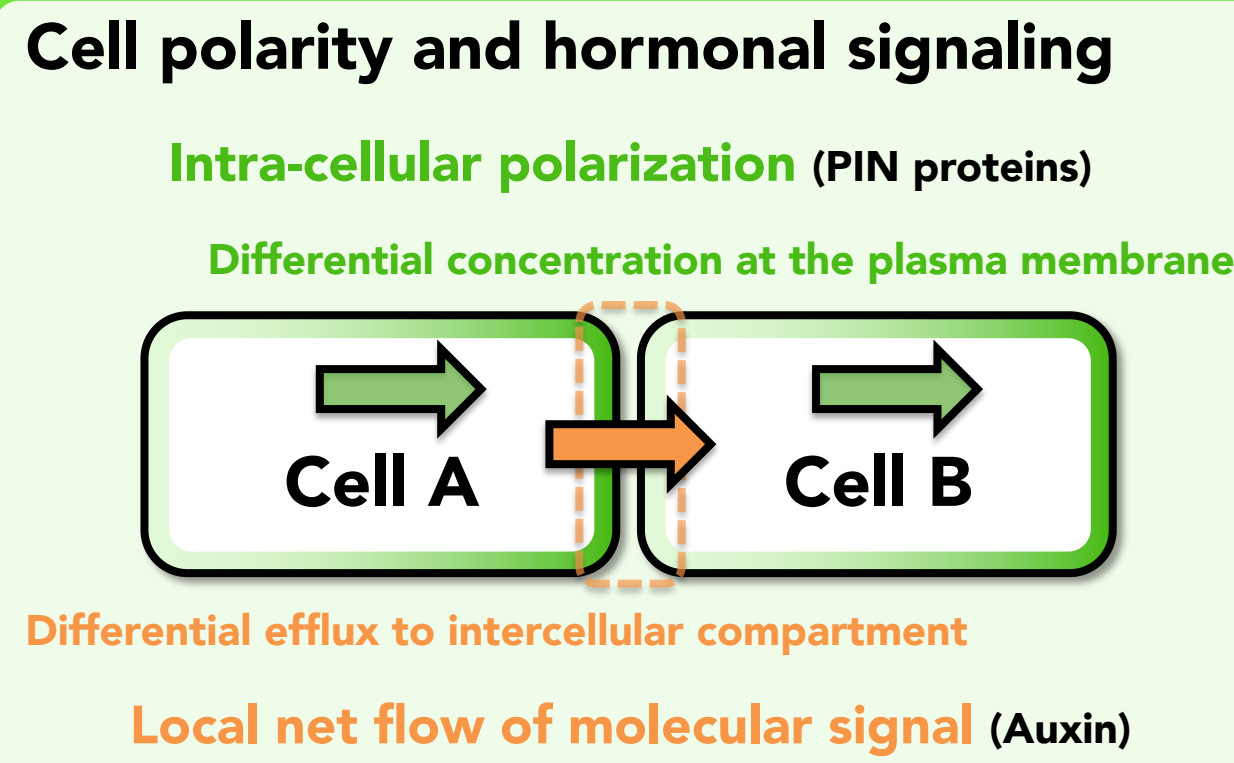
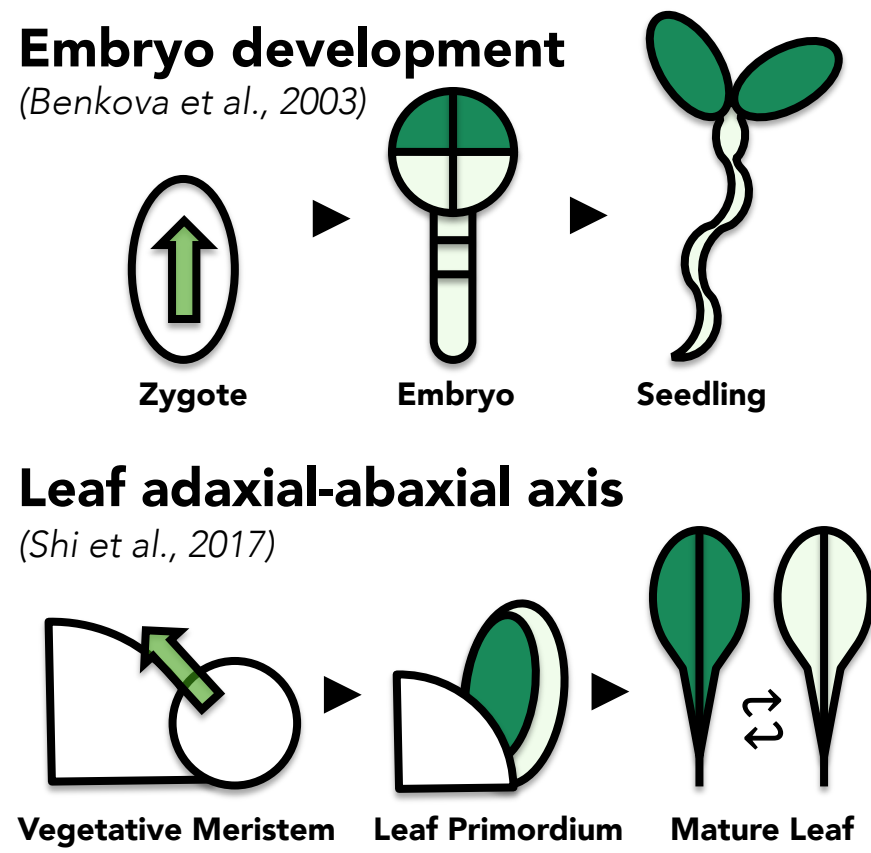
Quantifying cell polarities in confocal images using 3D wall meshes

A computational geometry approach to the estimation of cell-interface and tissue-level polarities in 3D stacks of co-imaged fluorescent transmembrane carriers and cell-wall markers

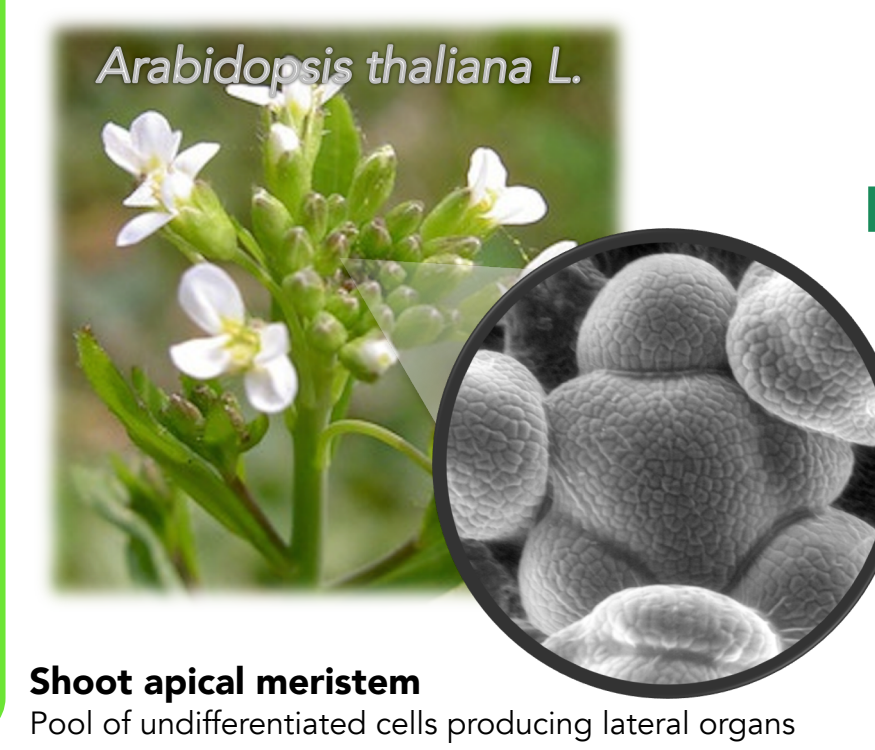
Guillaume CERUTTI [★], Carlos GALVAN-AMPUDIA, Jonathan LEGRAND, Christophe GODIN, Teva VERNOUX

Laboratory for Reproduction and Development of Plants, Université de Lyon, ENS-Lyon, INRA, Inria, CNRS, Lyon, France.

Polarized auxin transport is a key process for the patterning of multicellular plant tissues



Organogenesis at the SAM

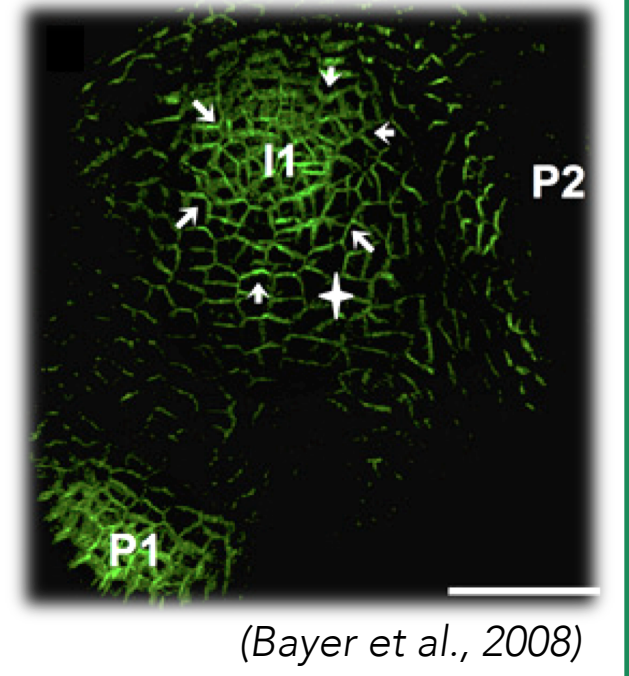


Convergent PIN1 cell polarities

Directional flow of auxin molecules

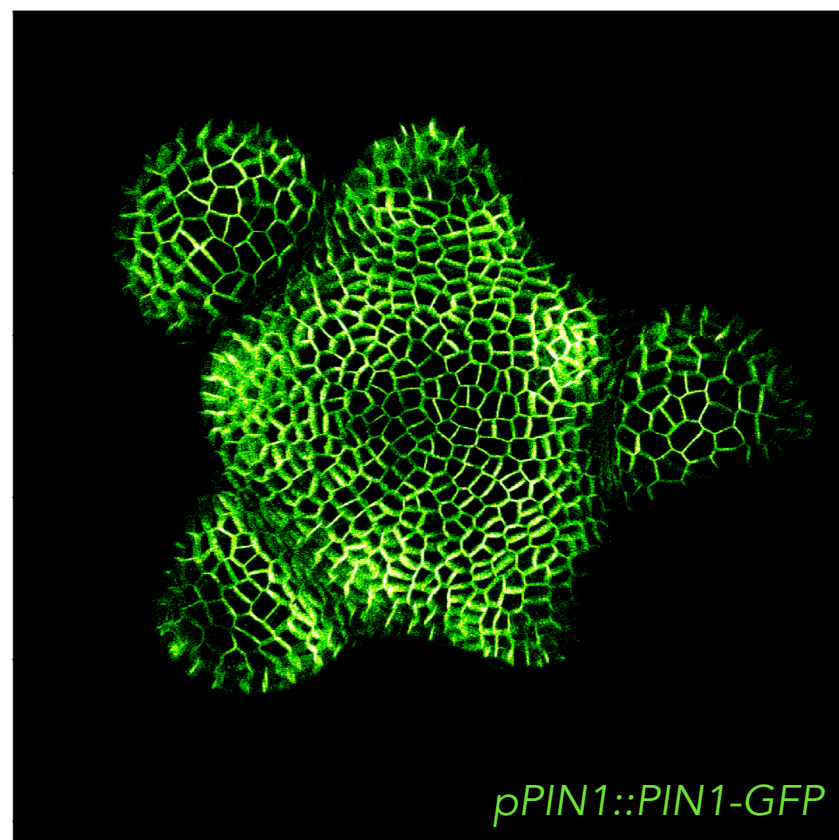
Local peak of signal

Organ initiation at tissue scale



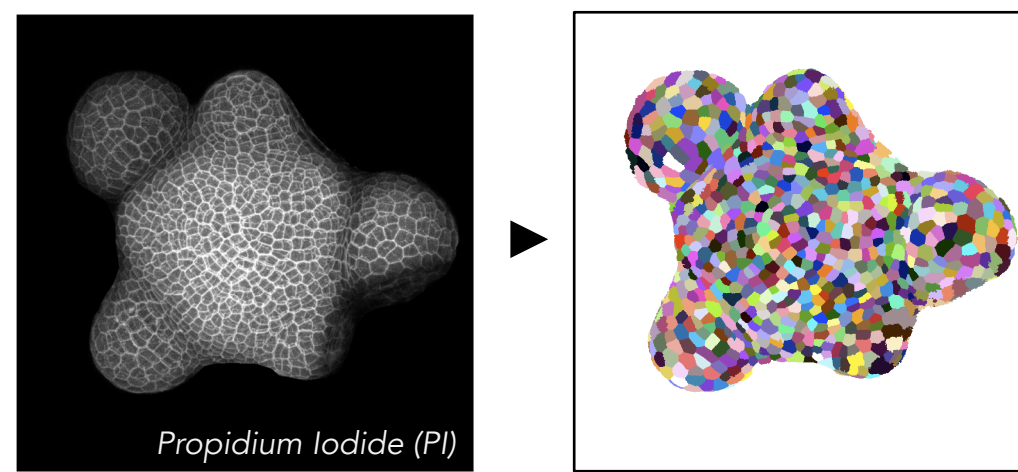
How to quantify PIN1 polarities in the SAM at cellular level?

Live-imaging of SAMs expressing fluorescent PIN1 proteins using confocal microscopy

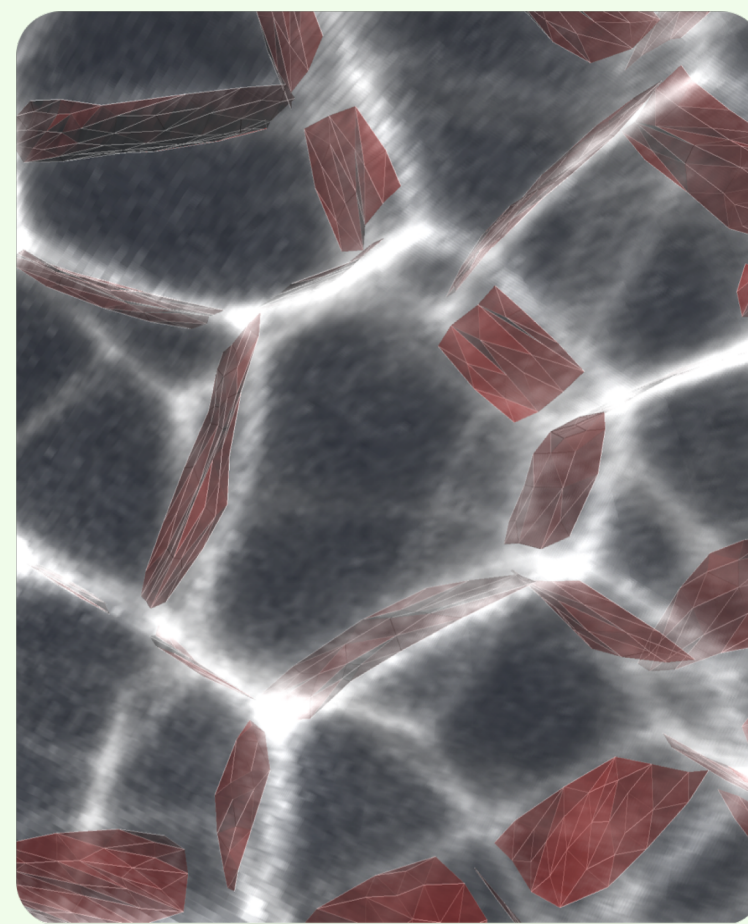


- Resolution cannot separate cell membranes (0.2µm)
- Crescent caused by gradient often used as a clue
- Hard to know which cell the signal belongs to

Co-image a cell wall marker for spatial reference



Extraction of cell wall triangular meshes from 3D segmented image



Labelled 3D confocal image stacks (0.2x0.2x0.6µm voxels)

- 3D seeded watershed segmentation (Fernandez et al., 2010)

Compute a mesh for each anticlinal L1 cell interface

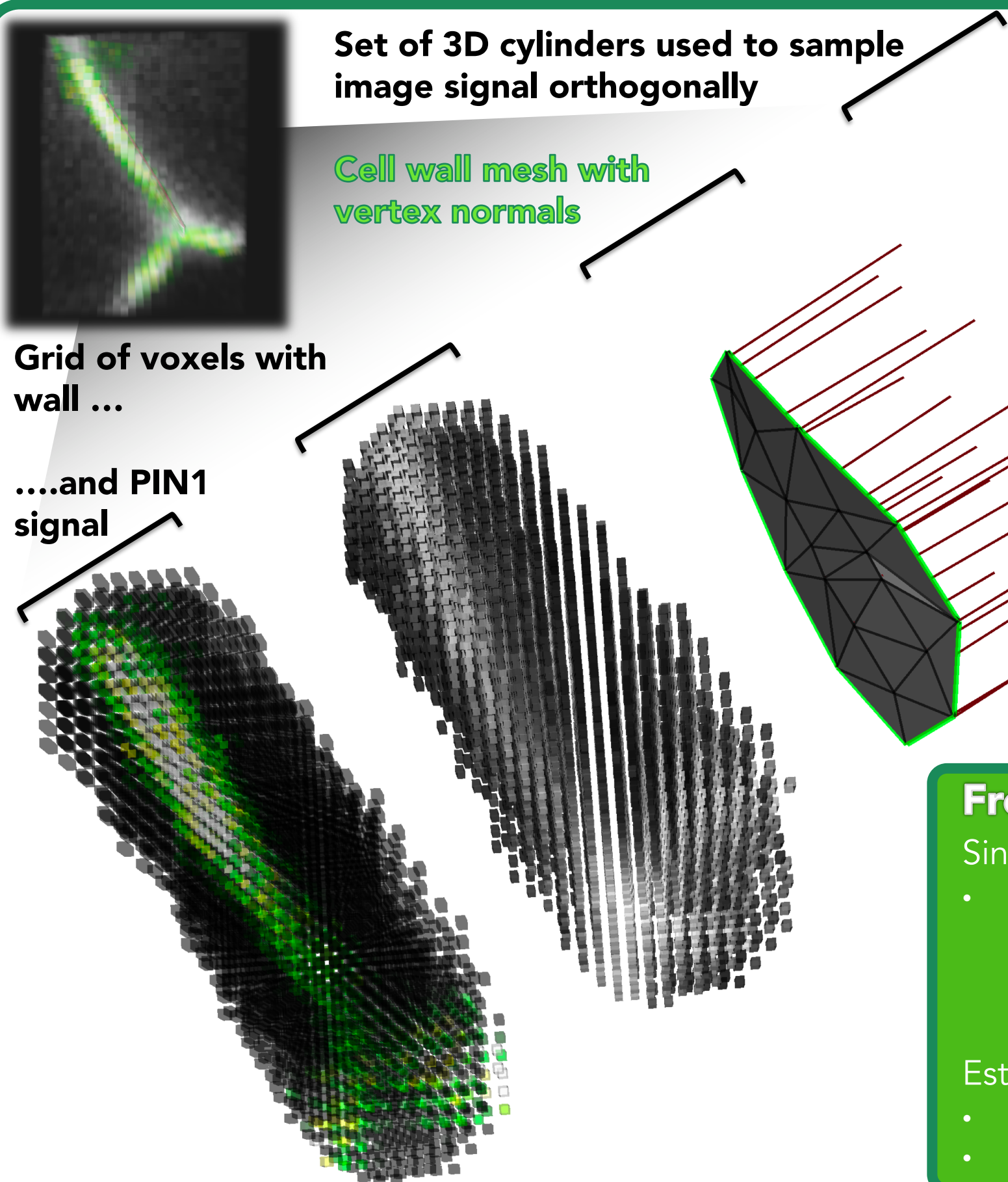
- Marching cubes on every L1 cell (contact with background label)
- For each pair of neighbor cells, keep only common vertices
- Use the triangle subset of the left cell in the label pair
- Apply quadric decimation and isotropic remeshing on wall mesh

Regular surface meshes within the image grid

Estimate normal at each vertex of every wall mesh

- Oriented left to right according to cell label pair

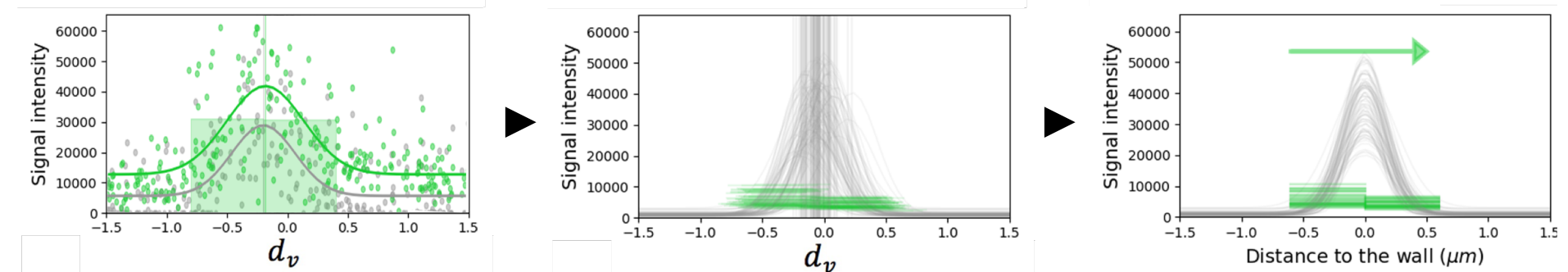
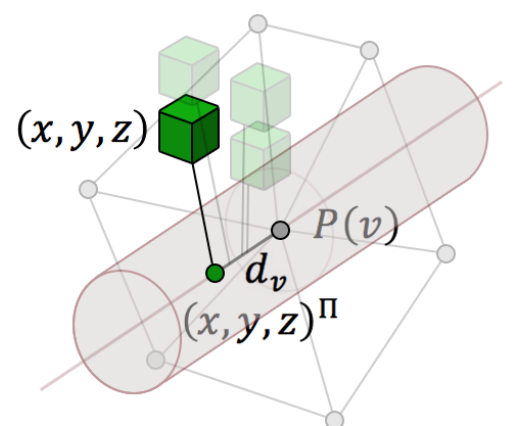
Use wall marker information to quantify accurately PIN1 levels within each cell and estimate local polarity



Are there significantly different PIN1 levels between sides of a cell wall?

At each vertex, 1D projection of image signals on a locally normal axis

- For each vertex \mathbf{v} of the wall mesh (except on contour), cylinder centered on $\mathbf{P}_{\mathbf{v}}$
- Signed abscissa $d_{\mathbf{v}}$ of the orthogonal projection of voxel on the normal vector $\vec{n}_{\mathbf{v}}$
- Distance $r_{\mathbf{v}}$ of the voxel center to its projection up to cylinder radius $r_{\mathbf{v}} < r_{\mathbf{c}} = 1\mu\text{m}$
- Keep only voxels on the 1D axis up to half-cylinder height : $|d_{\mathbf{v}}| < d_{\mathbf{c}} = 1.5\mu\text{m}$
- Wall abscissa d_0 estimated using a Gaussian approximation of membrane signal



Estimate wall-level PIN1 polarity in 3D using the whole set of wall mesh vertex cylinders

- Compute the average intensity on each side of the wall using close voxels : $|d_{\mathbf{v}} - d_0| < d_{\text{max}} = 0.6\mu\text{m}$
- Statistical test on the two PIN1 intensity distributions to decide if they have different means : $\mathbf{PA}_{\mathbf{A}\mathbf{B}} = \begin{cases} 1 & / & 0.5 \\ 0 & & \\ -1 & / & -0.5 \end{cases}$

$$\text{Wall polarity vector : } \overline{\text{PIN1}}_{\mathbf{A}\mathbf{B}} = \mathbf{PA}_{\mathbf{A}\mathbf{B}} |\overline{\text{PIN1}}_{\mathbf{A}\mathbf{B}} - \overline{\text{PIN1}}_{\mathbf{A}\mathbf{B}}| \vec{n}_{\mathbf{A}\mathbf{B}}$$

From wall-level polarities to cell PIN1 polarity and towards tissue-scale polarity maps

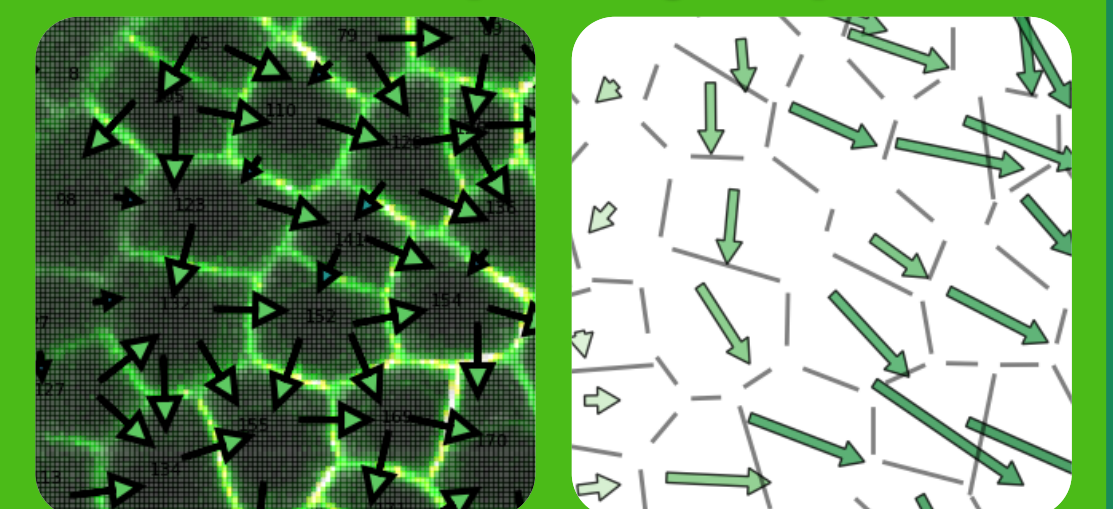
Single polarity vector per cell : weighted average (area) of wall vectors

- Wall PIN1 polarity vectors are the same for cells (A \blacktriangleright B) or (B \blacktriangleright A)

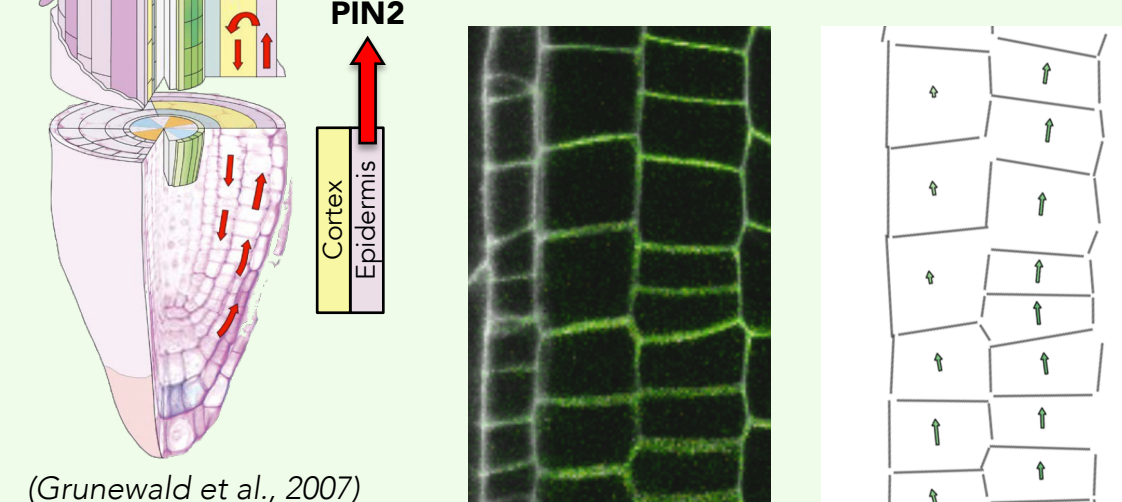
$$\overline{\text{PIN1}}_{\mathbf{A}} = \frac{1}{\sum_{B \in \mathcal{N}(\mathbf{A})} A_{\mathbf{A}\mathbf{B}}} \sum_{B \in \mathcal{N}(\mathbf{A})} A_{\mathbf{A}\mathbf{B}} \overline{\text{PIN1}}_{\mathbf{A}\mathbf{B}}$$

Estimate a tissue-level continuous vector-field of local PIN1 polarity

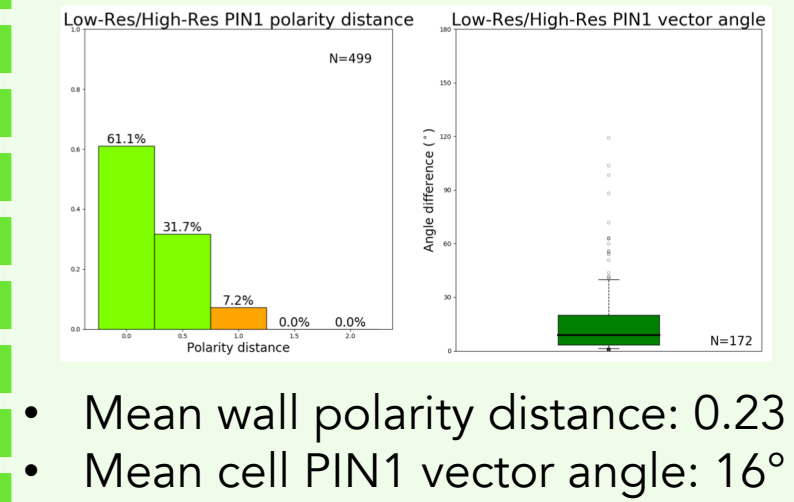
- Distance-weighted average of cell polarity vectors in any point of the space
- When computed on 2D projected L1 plane, allows to derive PIN1 convergence maps



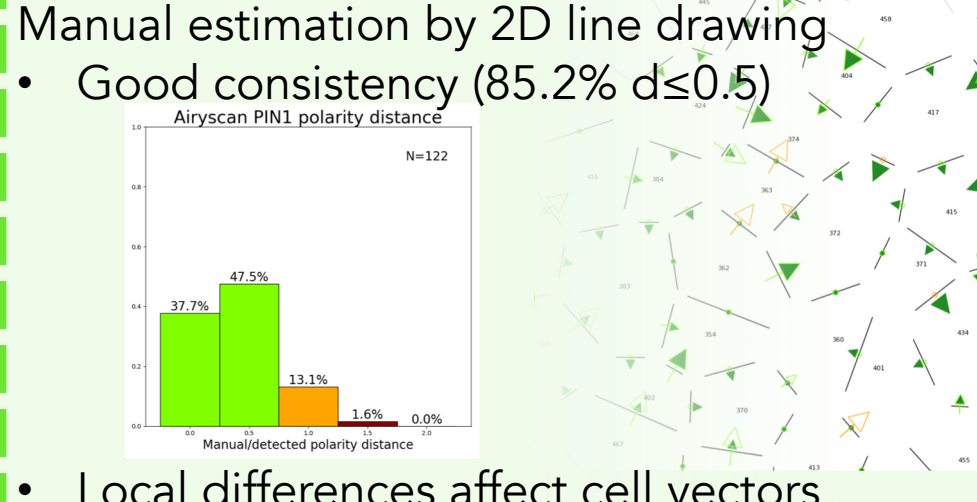
Correct PIN2 polarity in root epidermal cells



Consistent SAM PIN1 polarity at 0.1 and 0.2µm



Comparison to super-resolution techniques : AiryScan (Shi et al., 2017)



Results & Conclusions

Highly consistent estimation of polarities

- Provides reproducible cell-level PIN1 polarity measures
- Same tissue imaged at different resolutions
- Comparable to (manual) methods with super-resolution
- Several individual SAMs show similar patterns (N=16)

A new tool for tissue scale polarity analysis