Analysis of the spatial organisation of maize vascular bundles

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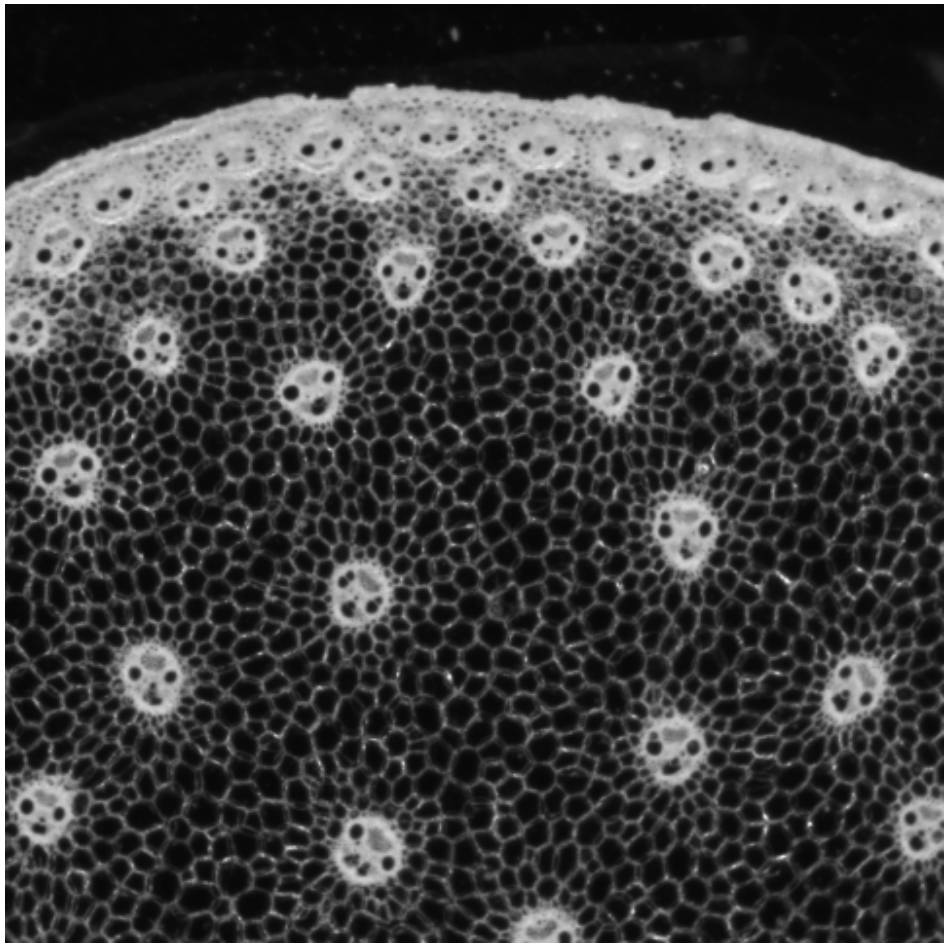
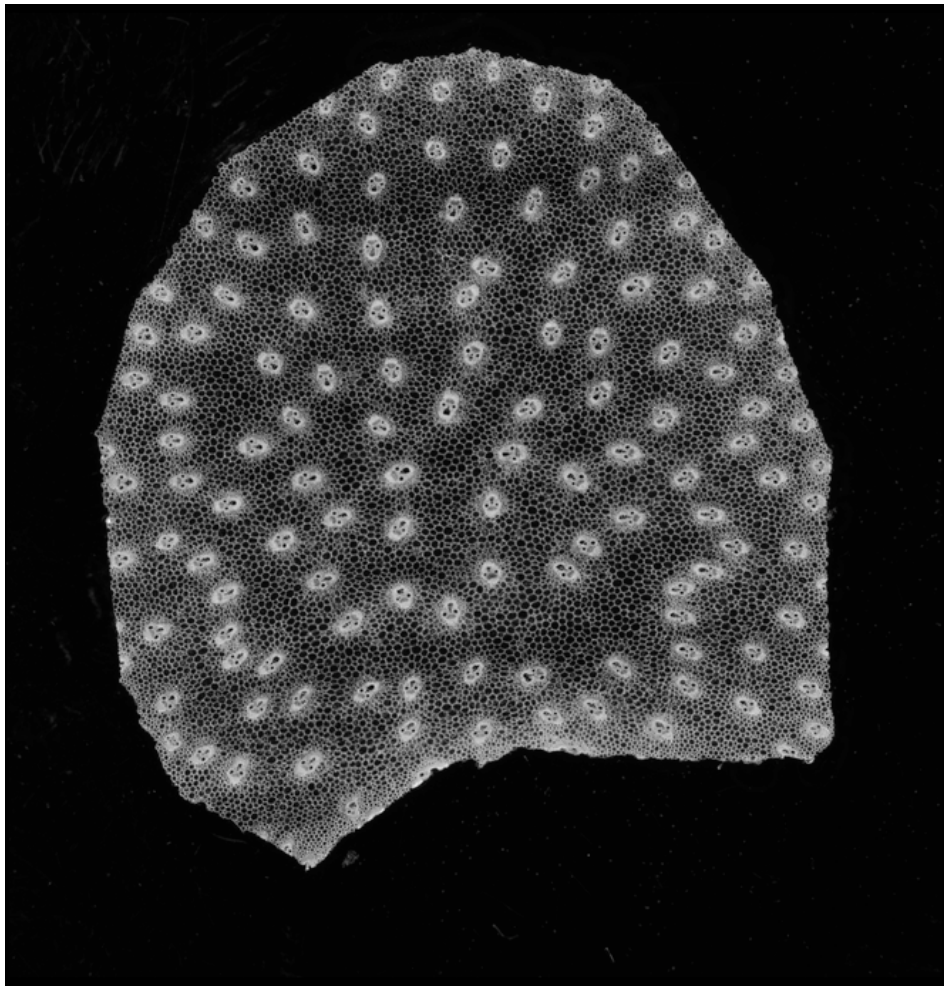
Context: valorisation of agro-resources

Objectives

- Quantify relationships:
  - bio-chemical composition
  - cellular morphology & organisation
  - cell wall degradability
- Quantify histology

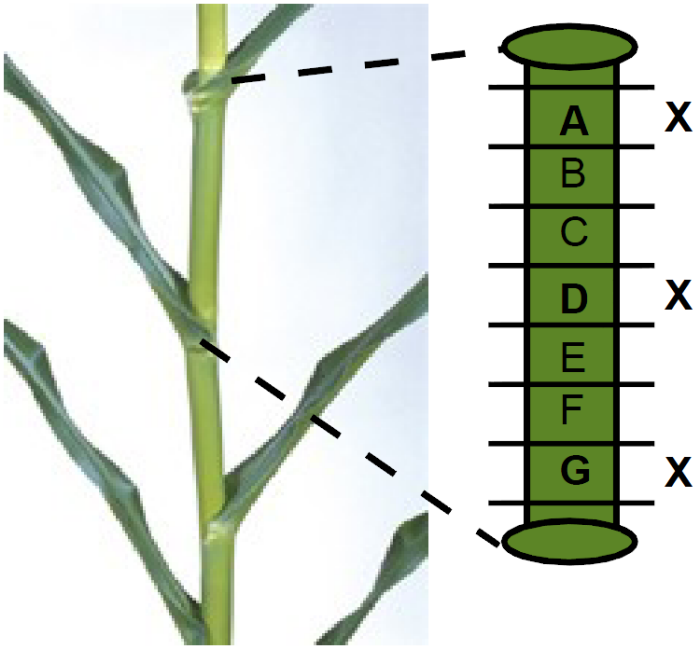


Macroscopy imaging



- BlueBox imagery
  - 4000×4000 pixels^2
  - Resolution $\simeq 3.6$ µm/px
  - field of view: 1.5×1.5 cm^2
- Can observe
  - cells
  - vascular bundles
  - their relative position

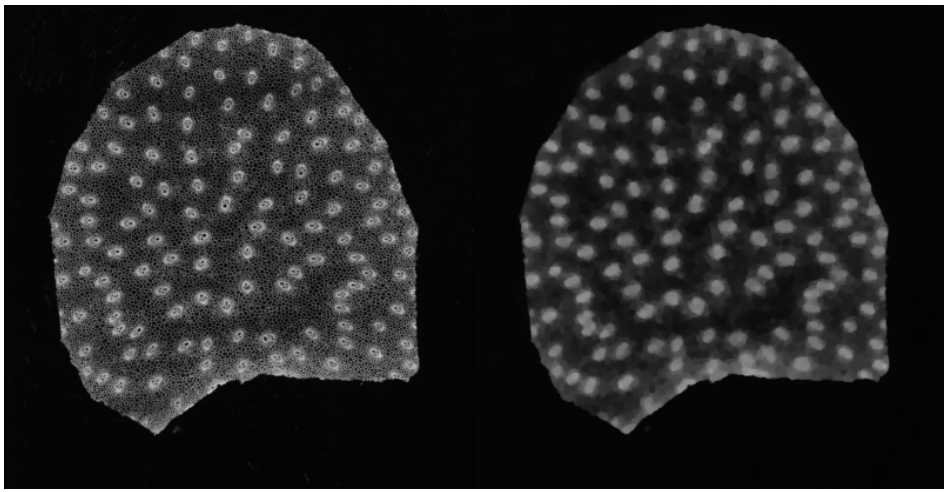
Maize sampling

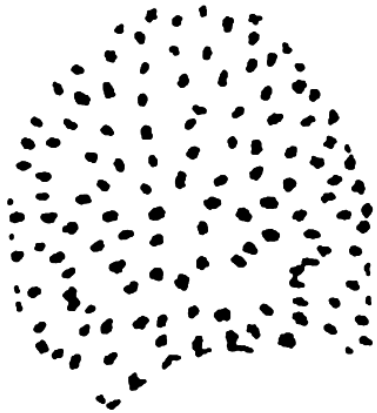


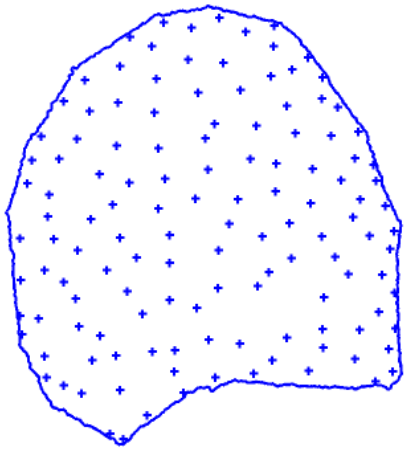
- Sampling:
  - 2 genotypes
  - 8 stems by genotype
  - 3 slabs by stem

Image Processing

- Vascular bundles segmentation
- Contour segmentation and simplification
- Results in a bounded point pattern







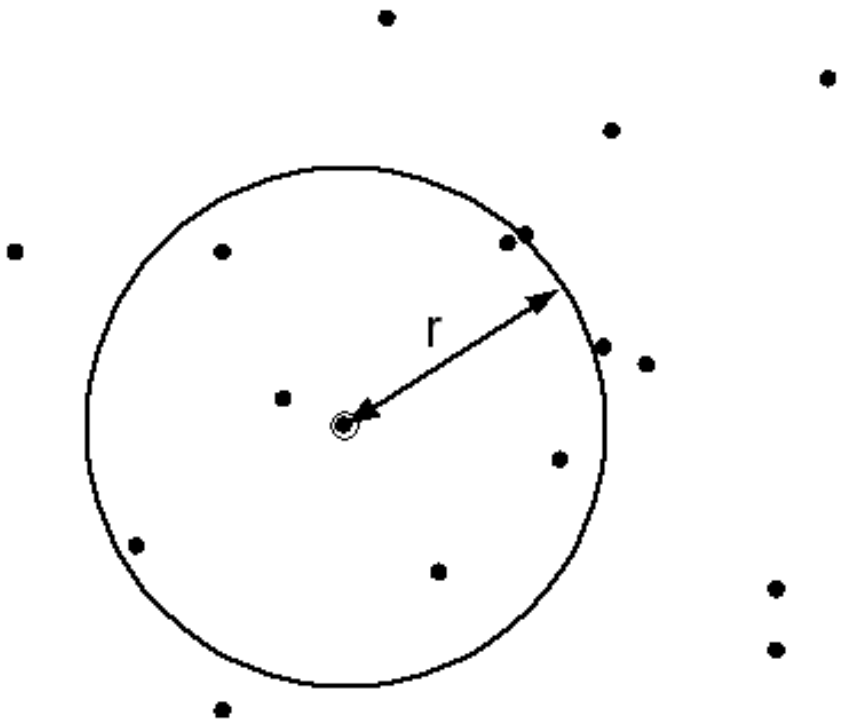
Descriptive functions

- Ripley's K-function

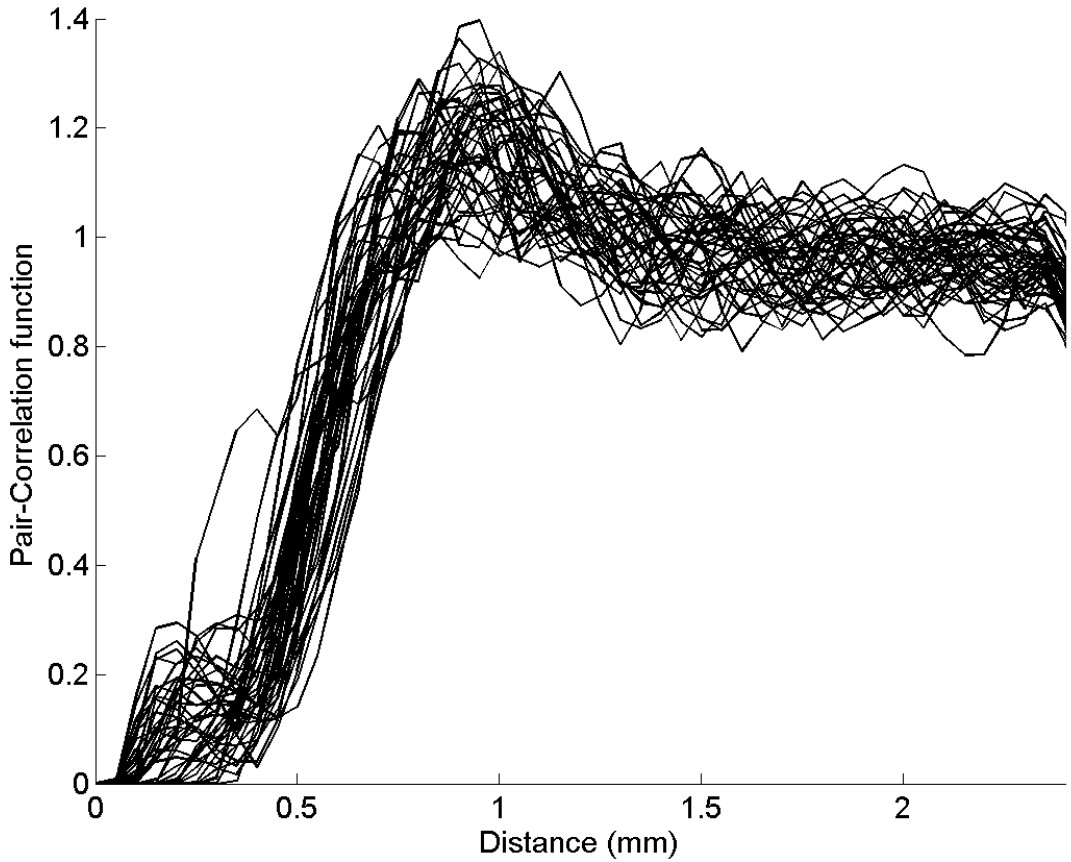
$$K(r) = \frac{\#\{X \setminus x \cap b(x, r)\}}{\lambda}$$

- Pair-correlation function (PCF)

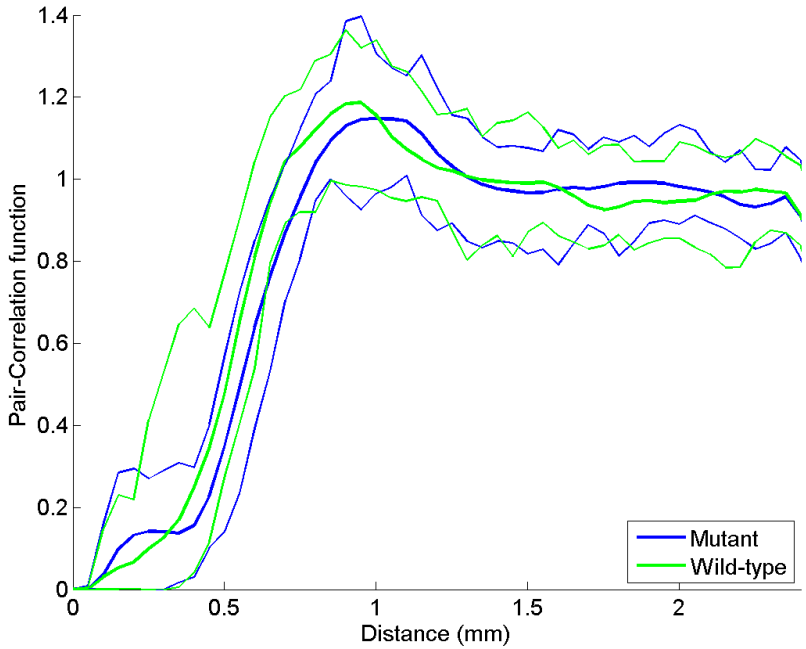
$$g(r) = \frac{K'(r)}{2\pi r}$$

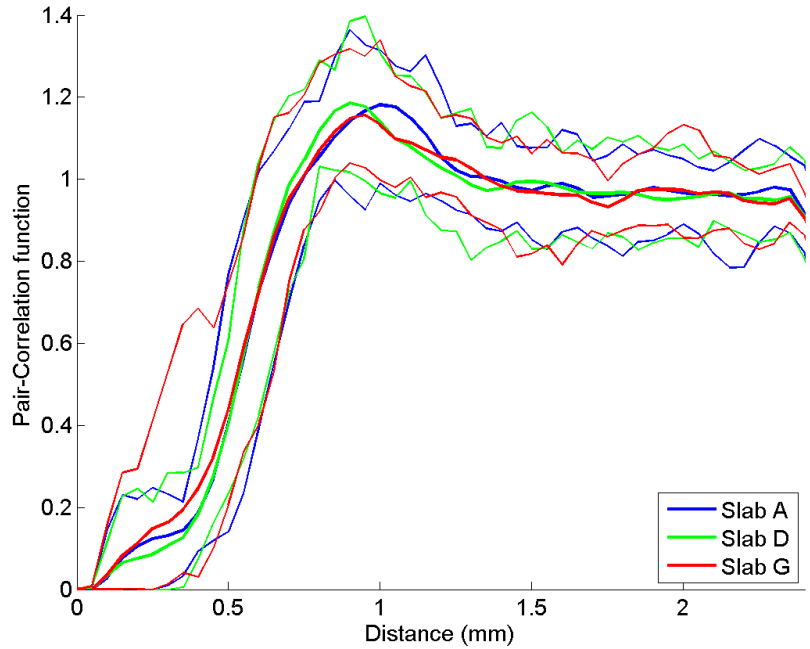


Group-wise analysis



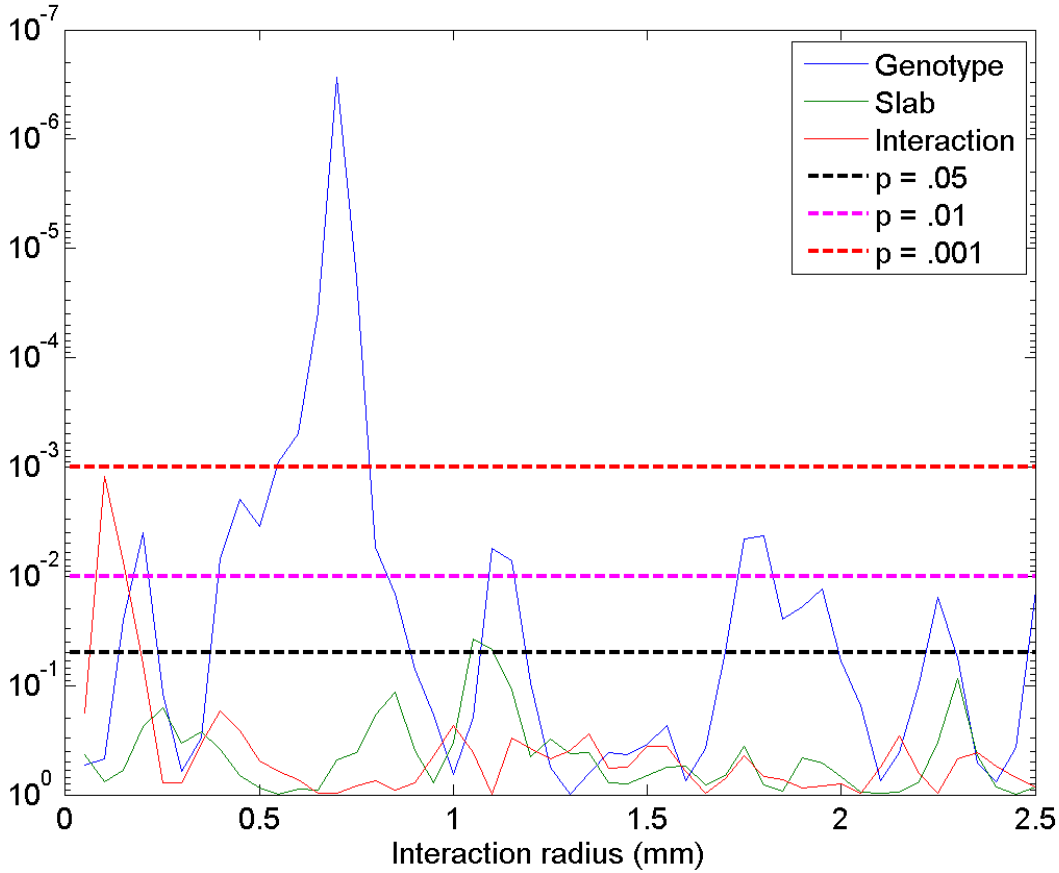
Average by group





Multivariate Analysis of Variance (MANOVA)

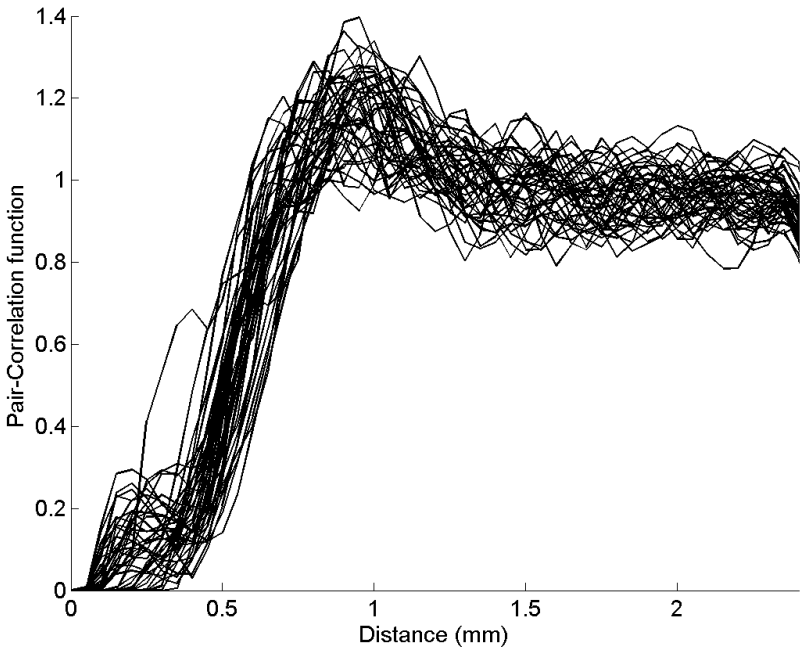
- computation of p-value for each distance, plot -log(p)
- model = genotype + slab + interaction



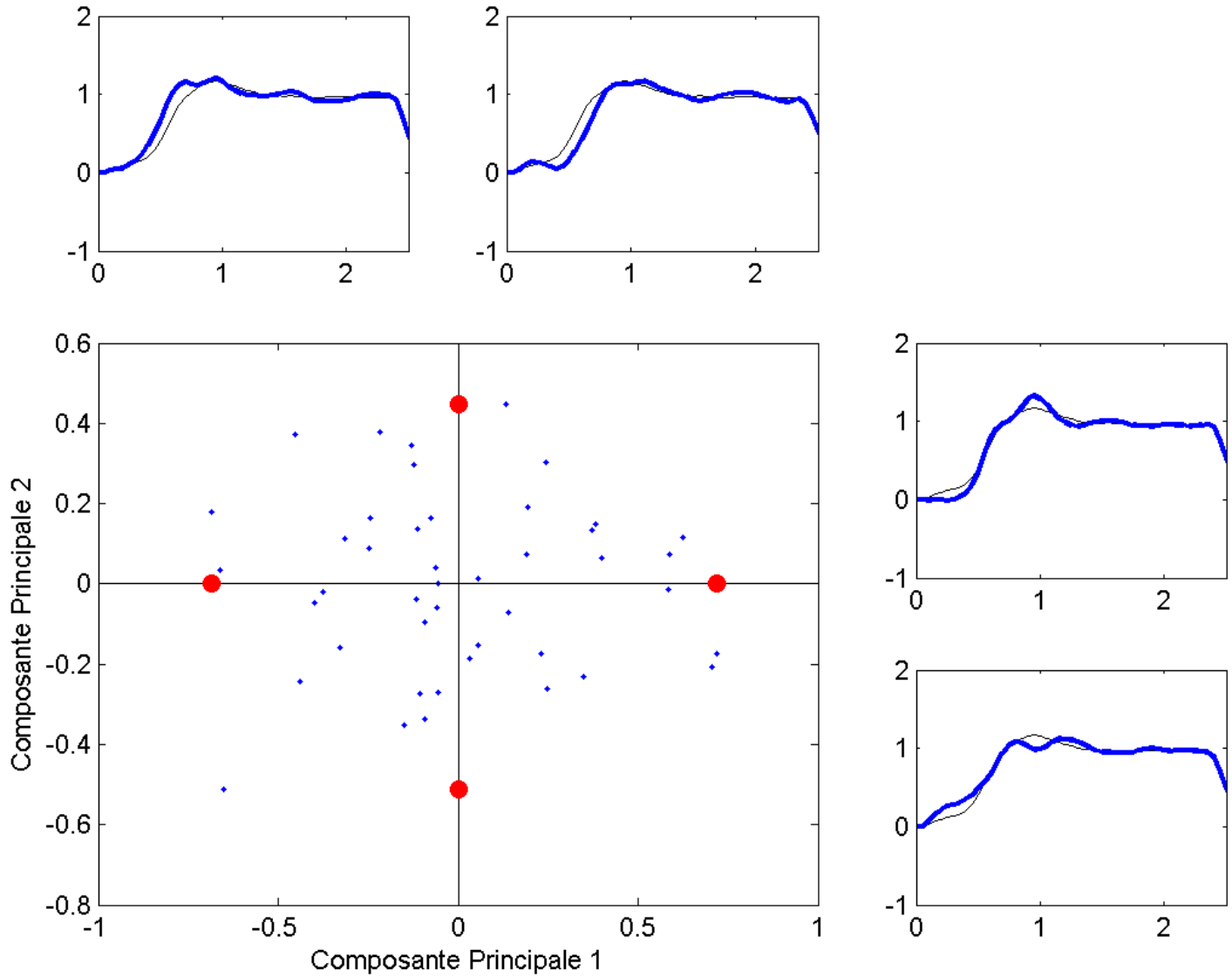
Principal Components Analysis of functions

- each curve is seen as a point in $\mathbb{R}^p$
- analysis of variations around the mean curve
- interpret loadings as curve tendencies

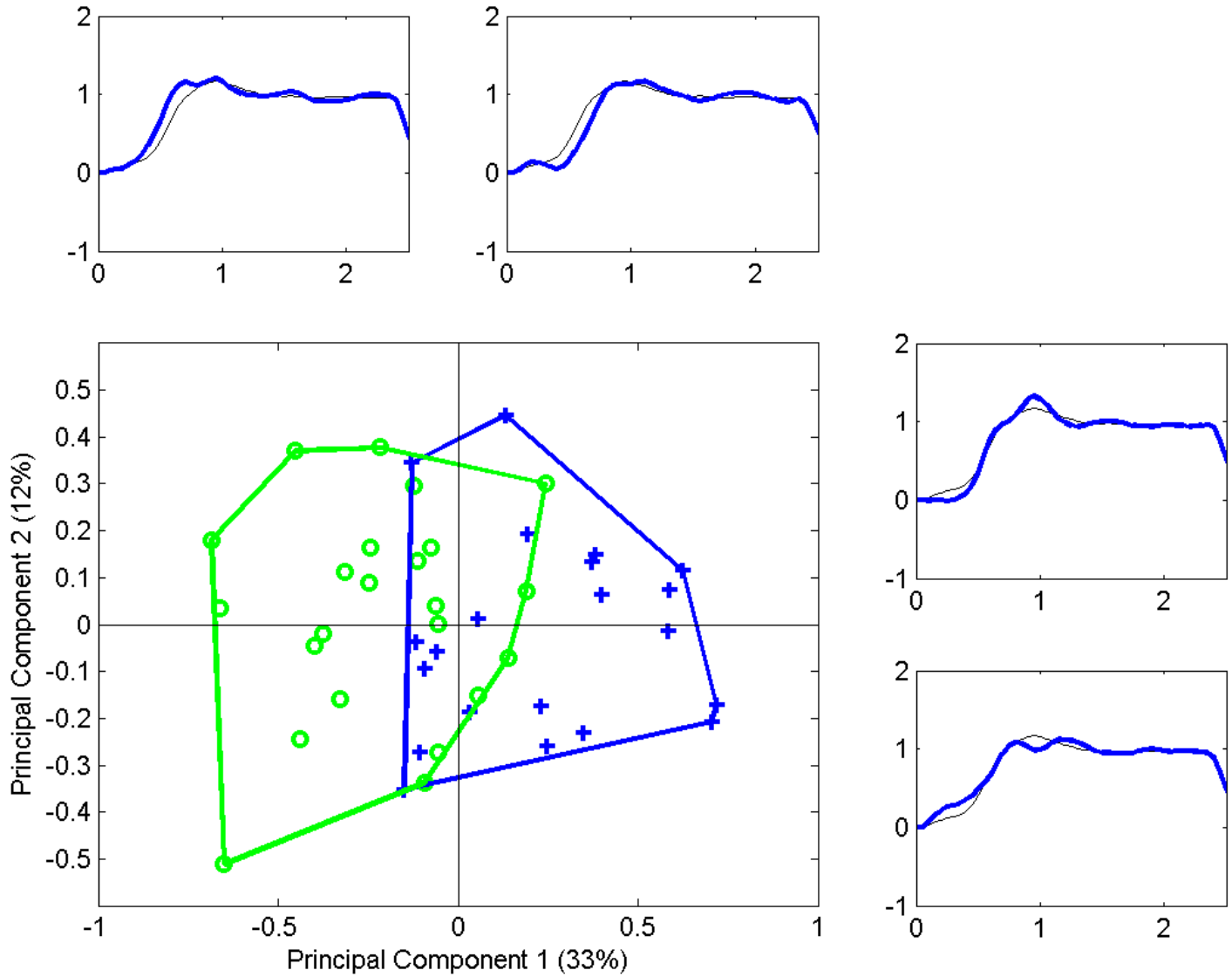
$$\begin{aligned} f_i(r) = & f_0(r) \\ & + c_{i,1} \cdot v_1(r) \\ & + c_{i,2} \cdot v_2(r) \\ & + \dots \end{aligned}$$



Interpretation of eigen vectors

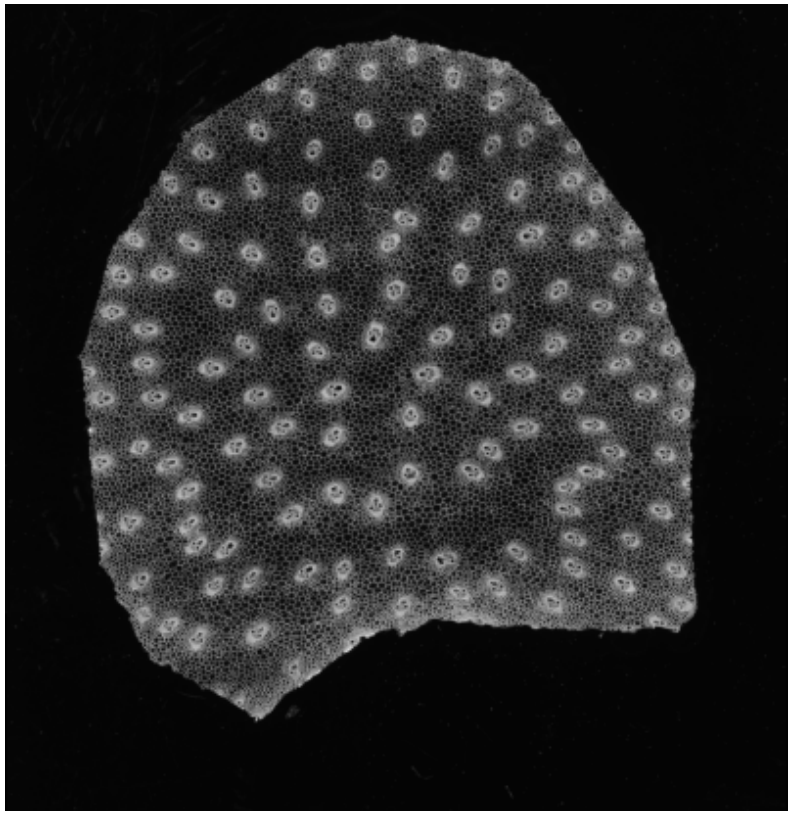


Testing hypotheses

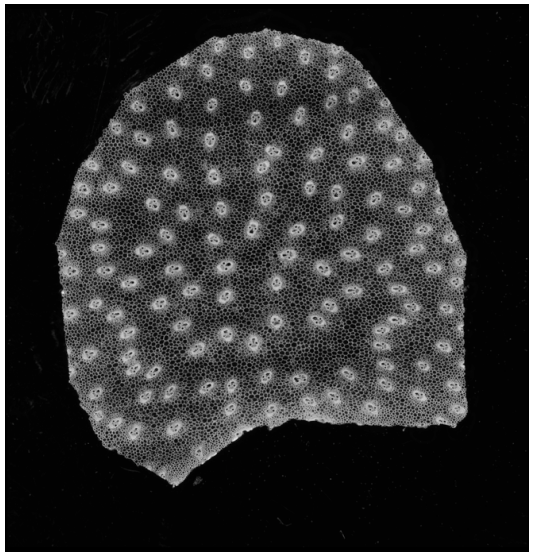
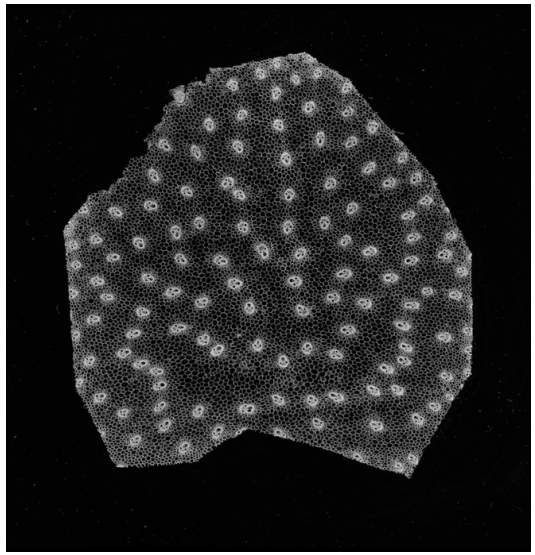
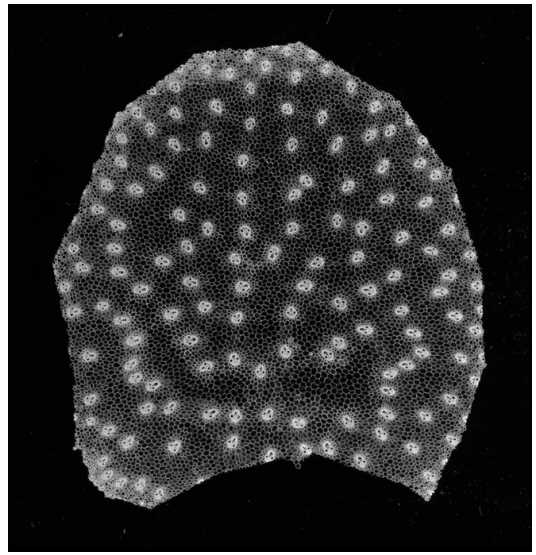
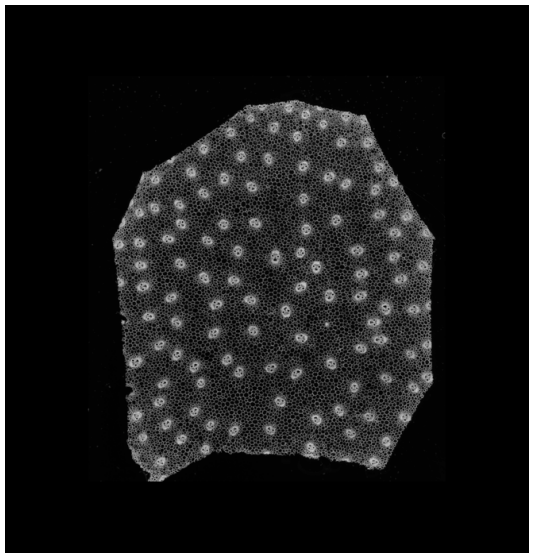
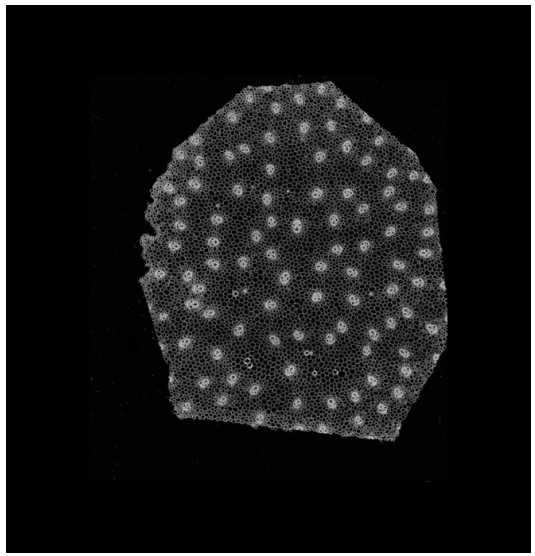
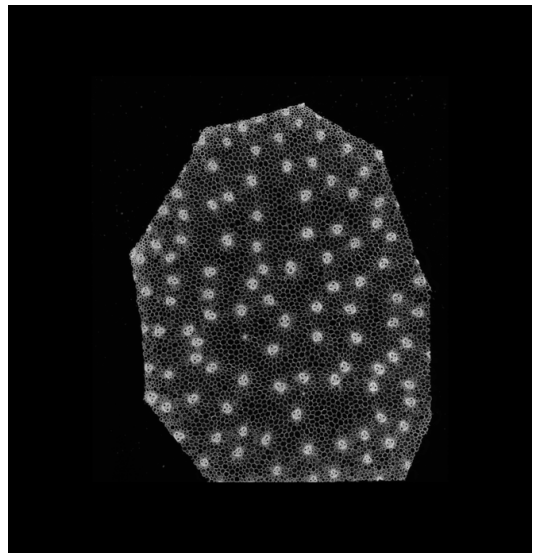


Summary

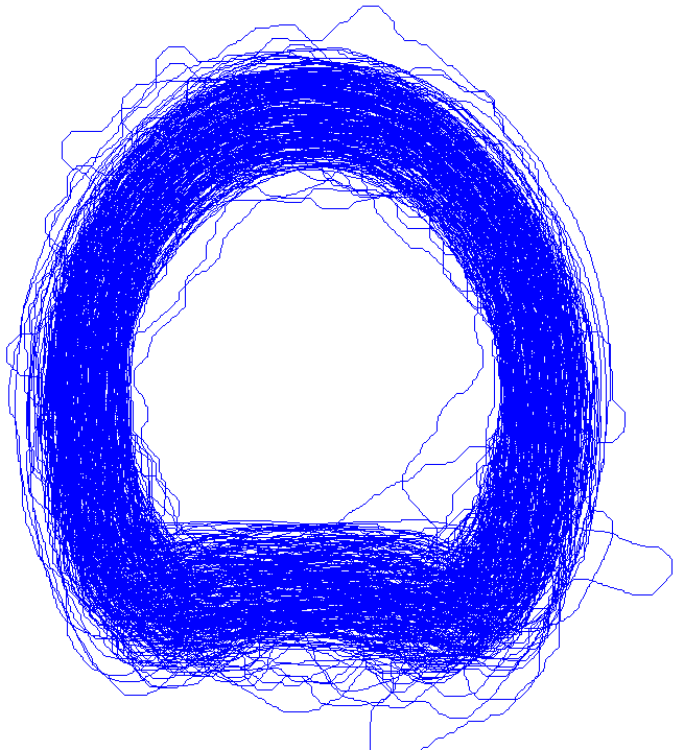
- PCA on PCF
  - allows groupwise analysis
  - synthetic curves
  - detection of differences
- Limits
  - loadings interpretation
  - non homogeneity



Density Estimation

Slab imagery and segmentation



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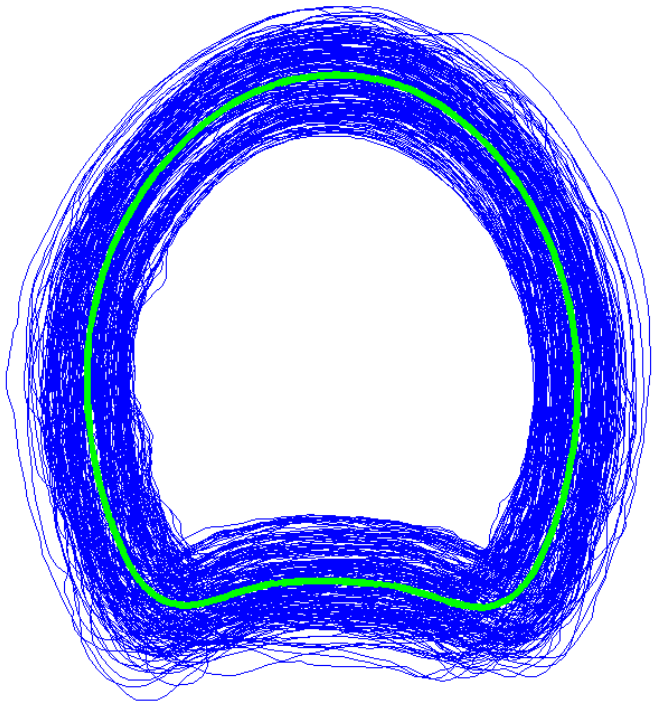
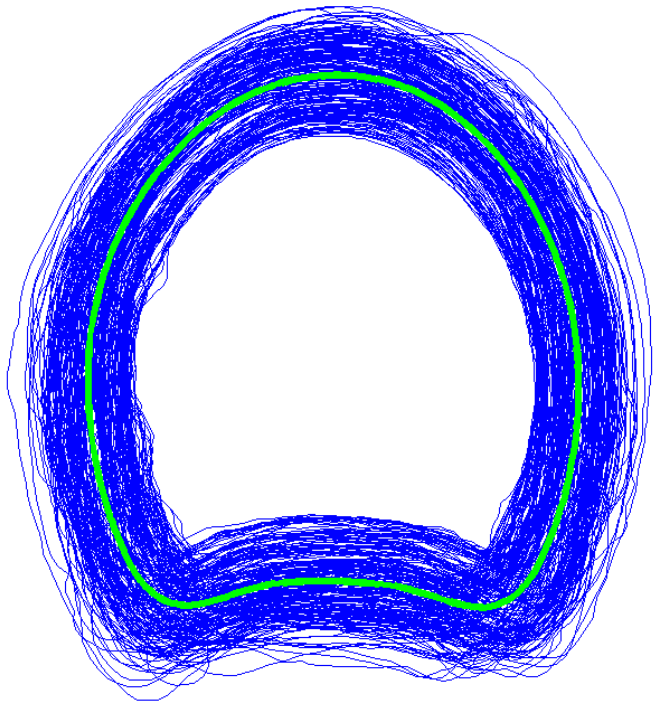
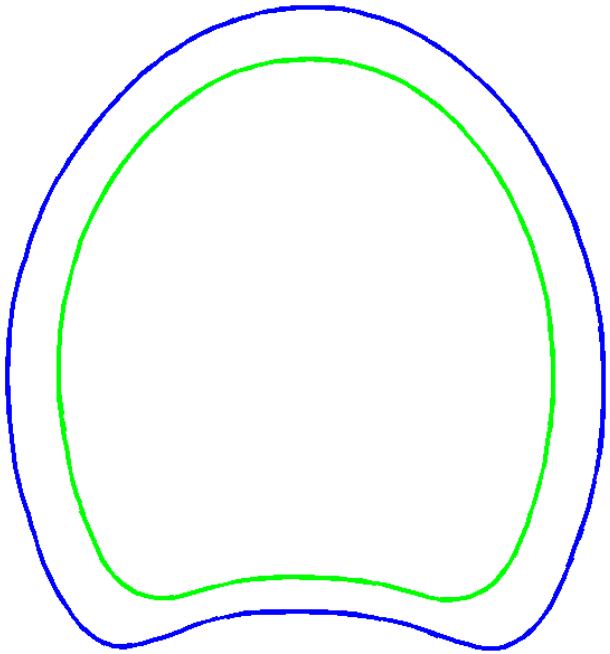


Shape analysis on contours

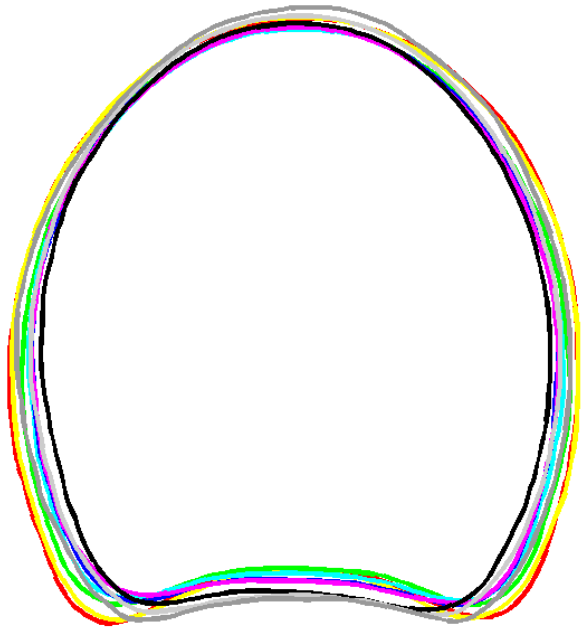
- Apply PCA on contours
- Reference contour + effects:
  - genotype
  - slab
  - stem



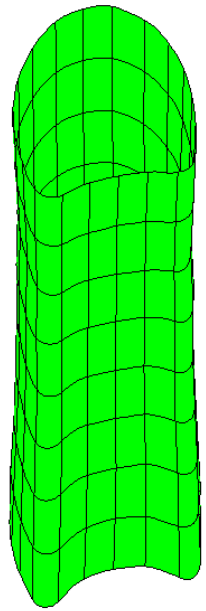
Contour modelling



by genotype

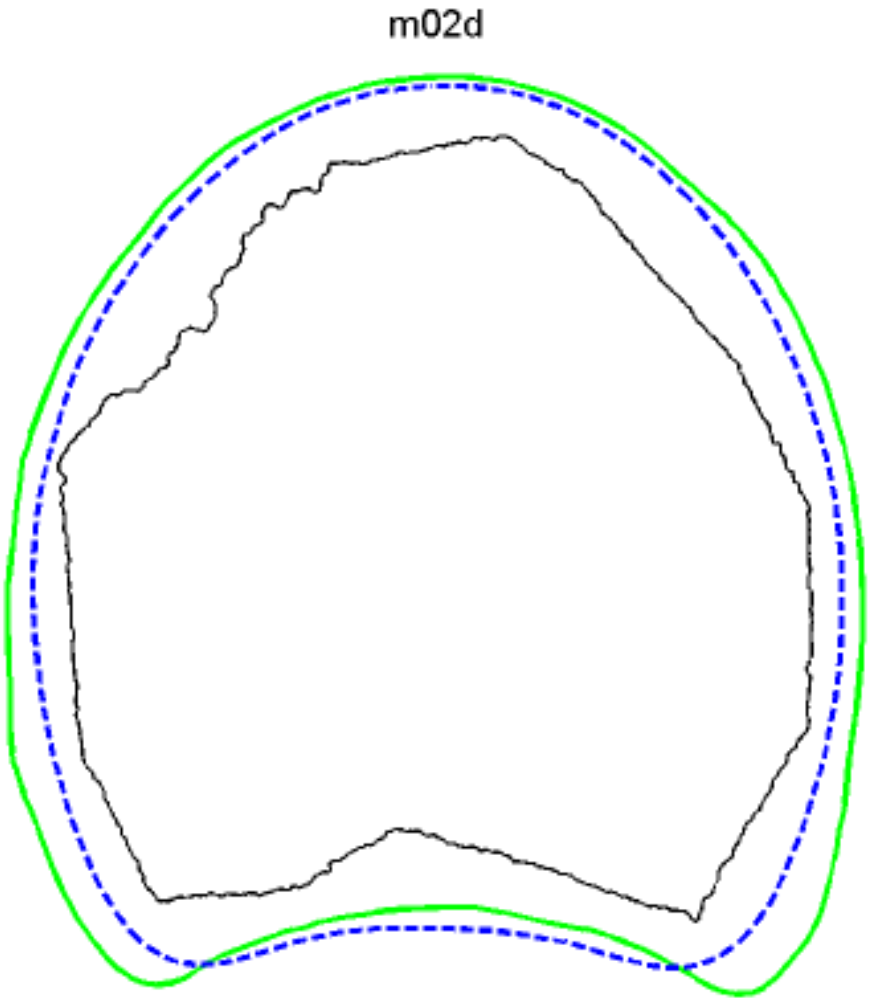


by slab

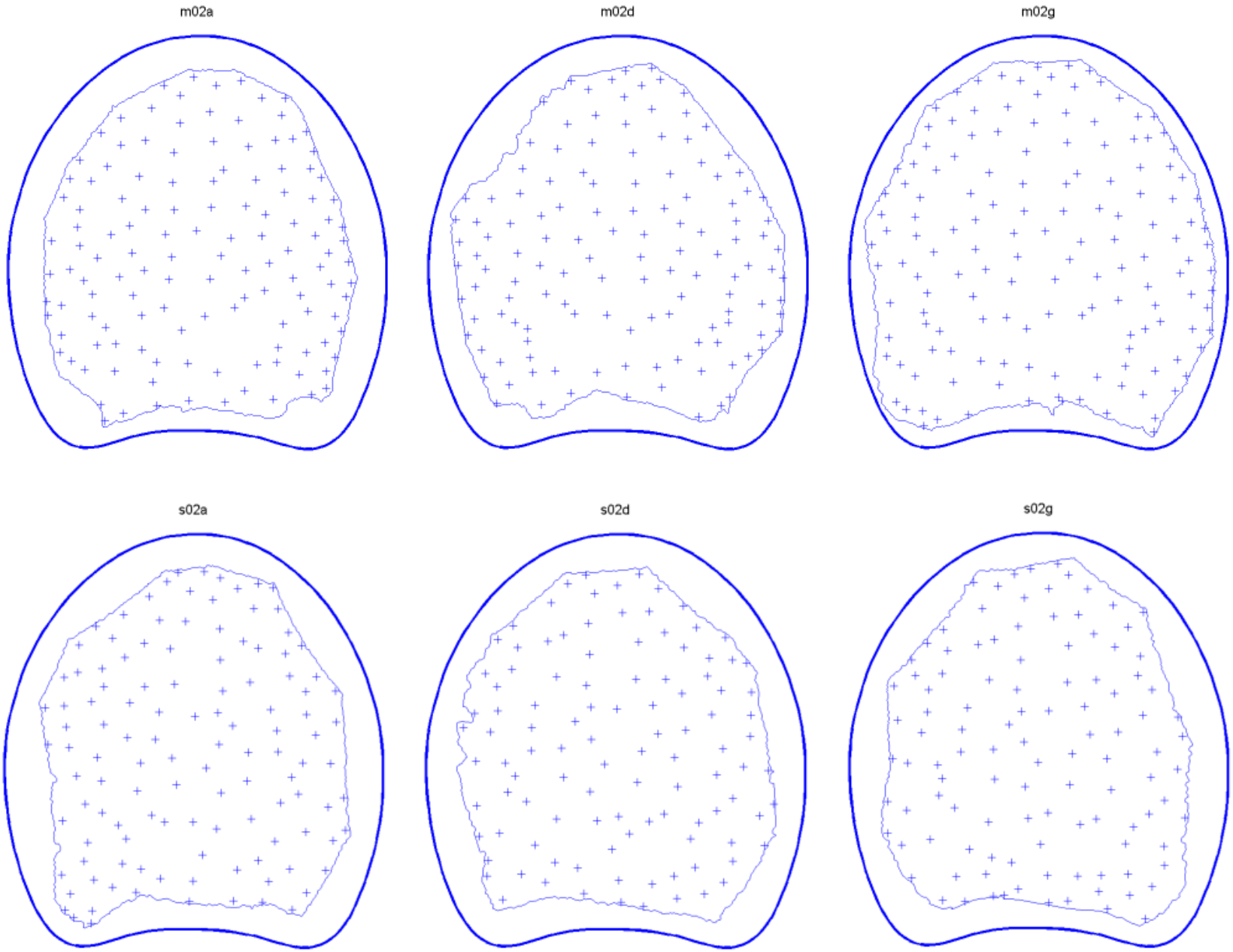


sample stem

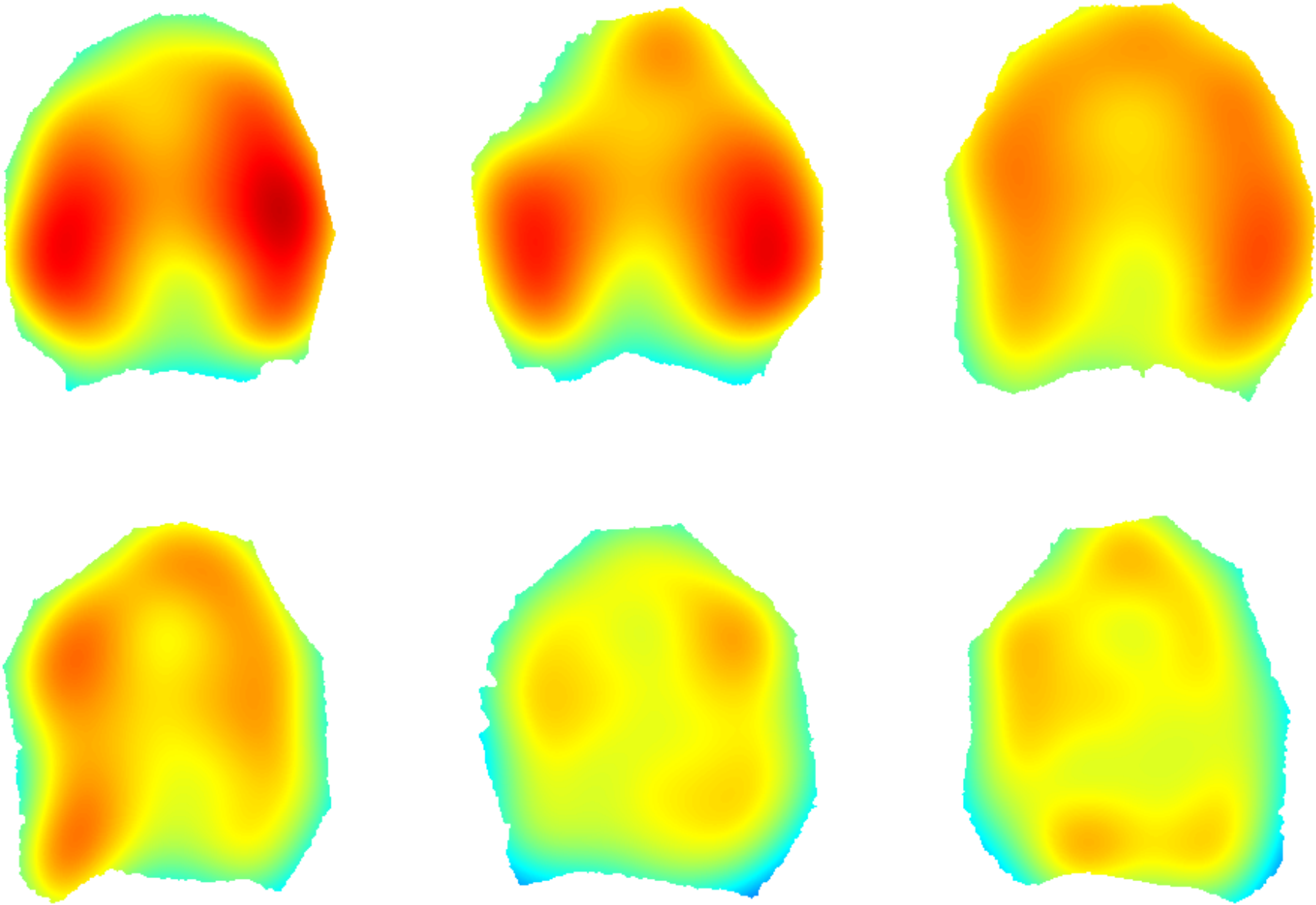
Spatial normalisation



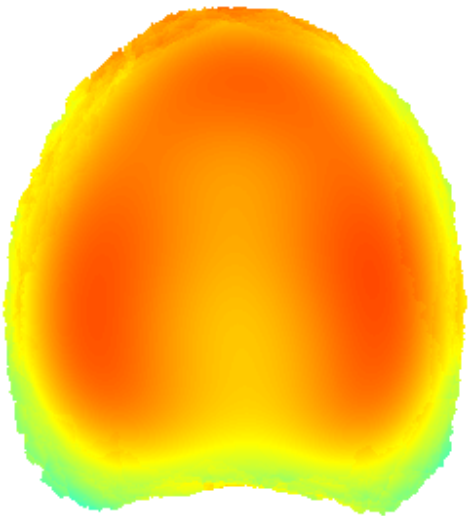
Projection onto reference slab



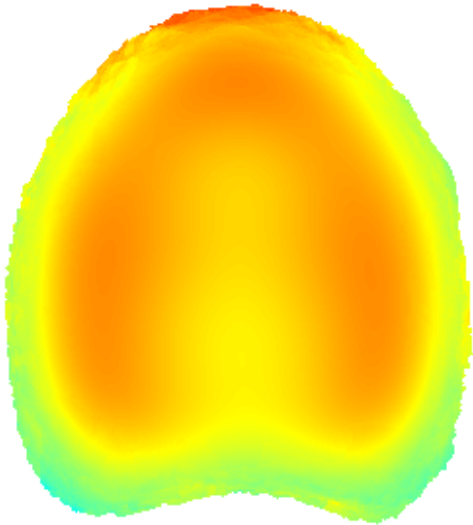
Computation of density maps



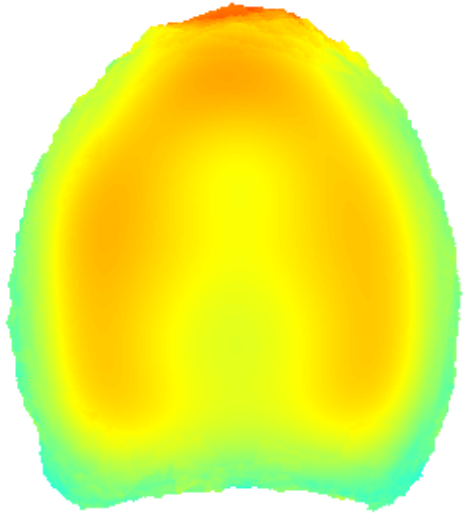
Average densities



Mutant



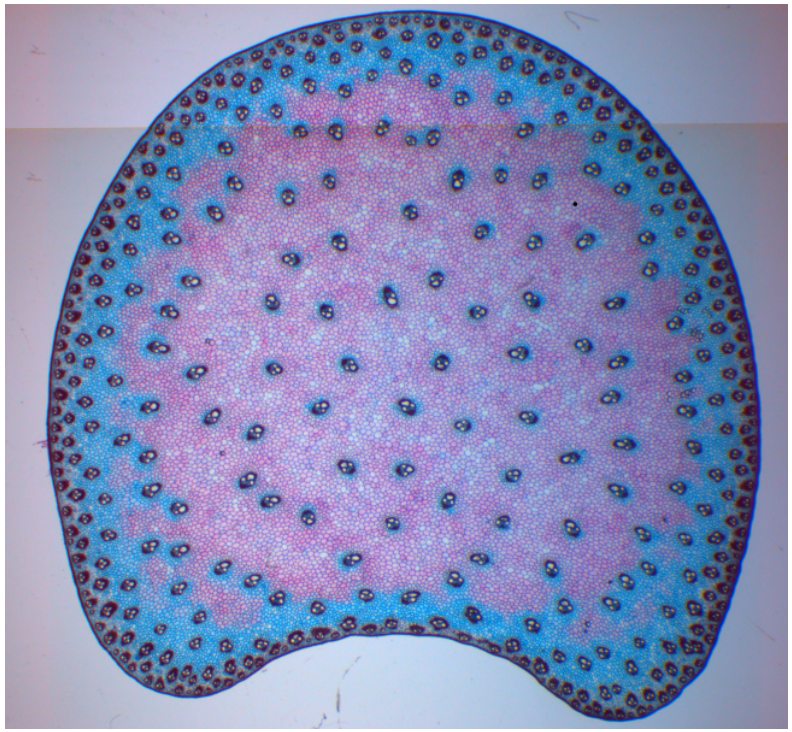
All



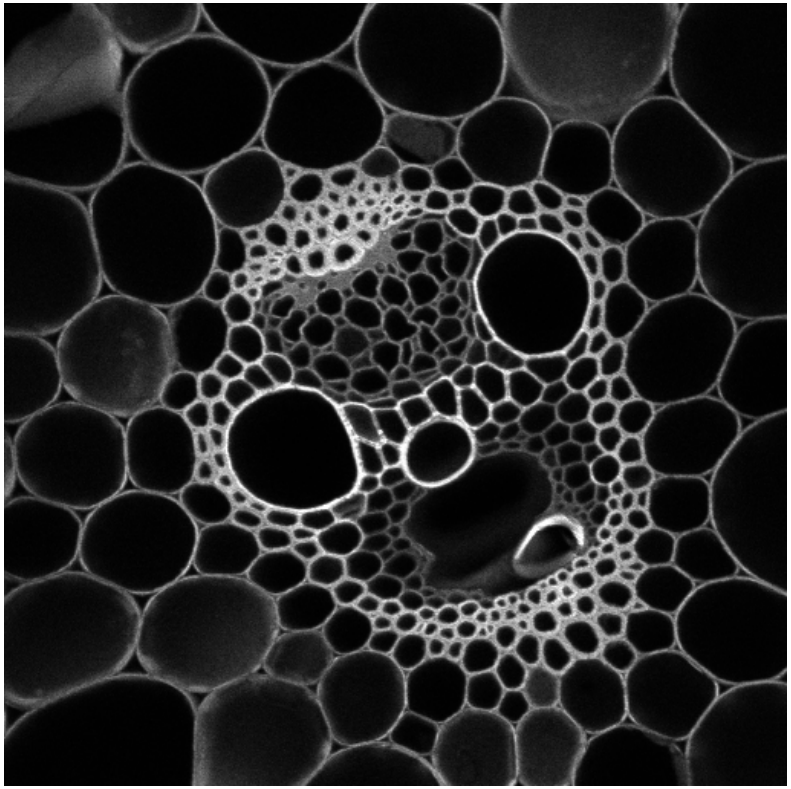
WildType

Perspectives

- non-inhomogeneous estimation of K and PCF
- localisation of functions
- fusion with other acquisitions
- towards stem modelling...



Any questions ?



Synopsis