## Dynamics and robustness of plant form

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What determines the trajectory in the space of shapes?

## Outline

- Average dynamics of leaf contours
-From leaf contour to leaf blade
-Distributions of flower shape


## Leaves in the model plant Arabidopsis thaliana



## It is highly difficult to follow the same living leaf



How to obtain a trajectory in shape space from independent samples?

## Why leaves?

- Source of energy (photosynthesis)
- Diverse shapes: simple, lobed, compound; toothed, untoothed
- Shape ~ paleoclimates?



Greenwood, New Phytol 2005

Some of the previous approaches for leaves

## Landmarks <br> + PCA

Klingenberg
J Evol Biol 2012


Langlade et al. PNAS 2005
Discretised contour + PCA

Fourier modes + PCA

Chitwood et al.
Plant Physiol 2012



Little investigation of developmental trajectories

## Combining landmarks and contours to analyse leaf morphogenesis

Collect a large number of samples ( $\sim 300$ )


## Identifying landmarks

- Basis, 2 points: expert
- Leaf tip: distance from basis
- Sinuses: curvature
- Tooth tips: curvature or symmetry

- Identifying primary sinuses: iterative tests based on angles (one parameter: limit angle)



## Registration and reparametrisation

Contours $\mathbf{f}_{i}(s), i \in\{0, \ldots, n\}, s \in\left[0, s_{i, \omega}\right]$
Landmarks $\left\{s_{i, \alpha}\right\}, \alpha \in\{0, \ldots, \omega\}$ with $s_{i, 0}=0$


- Co-reparametrisation:
- Co-reparametrisation:
$\varphi_{i}:\left[0, s_{i, \omega}\right] \rightarrow[0,1]$ piecewise affine, such that $\varphi_{i}\left(s_{i, \alpha}\right)=\frac{\left\langle s_{i, \alpha}\right\rangle_{i}}{\left\langle s_{i, \omega}\right\rangle_{i}}$

Co-parametrised contours: $g_{i}=f_{i} \circ \varphi_{i}$

- Co-registration

Minimise the distance between contours modulo rotation-translation $\left(\mathrm{R}_{i}\right)$ and scaling $\left(\rho_{i}\right)$ :

$$
\mathcal{E}\left(\left\{\rho_{i}, \mathrm{R}_{i}\right\}\right)=\sum_{i>j} \int_{0}^{1} \mathrm{~d} \tilde{s}\left(\rho_{i} \mathrm{R}_{i} \mathbf{g}_{i}(\tilde{s})-\rho_{j} \mathrm{R}_{j} \mathbf{g}_{j}(\tilde{s})\right)^{2}
$$

solved through iterated Procustes transformations to an averaged contour

- Outcome:

Registered contours/landmarks $\mathrm{R}_{i} \mathbf{f}_{i}(s)$, to keep size information

## Contours+ landmarks



Leaf tip vs. no landmark


## Contours+

 landmarks

Contours+ landmarks


## Developmental trajectories



## Developmental trajectories

$\rho$

Sliding average (Gaussian kernel)

+ quantification of leaf shape / teeth


## Developmental trajectories



+ quantification of leaf shape / teeth


## Comparison wild-type / mutant



## From leaf contours to leaf blade

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Conformal maps: transformations that keep the same angles In 2 D , the contours define all the transformation!

## Applying conformal maps to leaves

## Approach:

- Observe growing leaves
- Quantify contours and predict growth assuming conformal map (Schwartz-Christoffle)
- Quantify growth in the lamina
- Compare 'predicted' and measured growth



Good 'prediction' of displacements


Prediction of smoothed growth distribution

## Robustness of form

## Shape and size are robust in spite of internal and external perturbations



Bilateral symmetry

Shape and size are robust in spite of internal and external perturbations


Flower size in Arabidopsis varies by about 5\%

The sepal as a model system

abaxial sepal


## Genetic screen for variability:

Individual plants in which sepals are variable in size
flowers from a single WT plant

flowers from the single vos / plant

## Genetic screen for variability:

Individual plants in which sepals are variable in size

WT sepals

vos / mutant sepals


## Towards a 3D analysis



- Image in 3D (confocal microscopy)
-Binary images (supports) of many sepals
-Distance = overlap between supports
-Co-registration
- Probabilistic sepal


## Summary

-Combining landmarks and contours to analyse leaf shape during morphogenesis
-Contours give all information for 2D isotropically growing systems
-Work in progress: variability of contours, 3D shape

Biot et al. Development 2016
Alim et al. Phys. Biol. 2016
Hong et al. Dev Cell 2016
Mollier et al. in progress

