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# Statistical spatio-temporal atlas of gene expression patterns during organ growth

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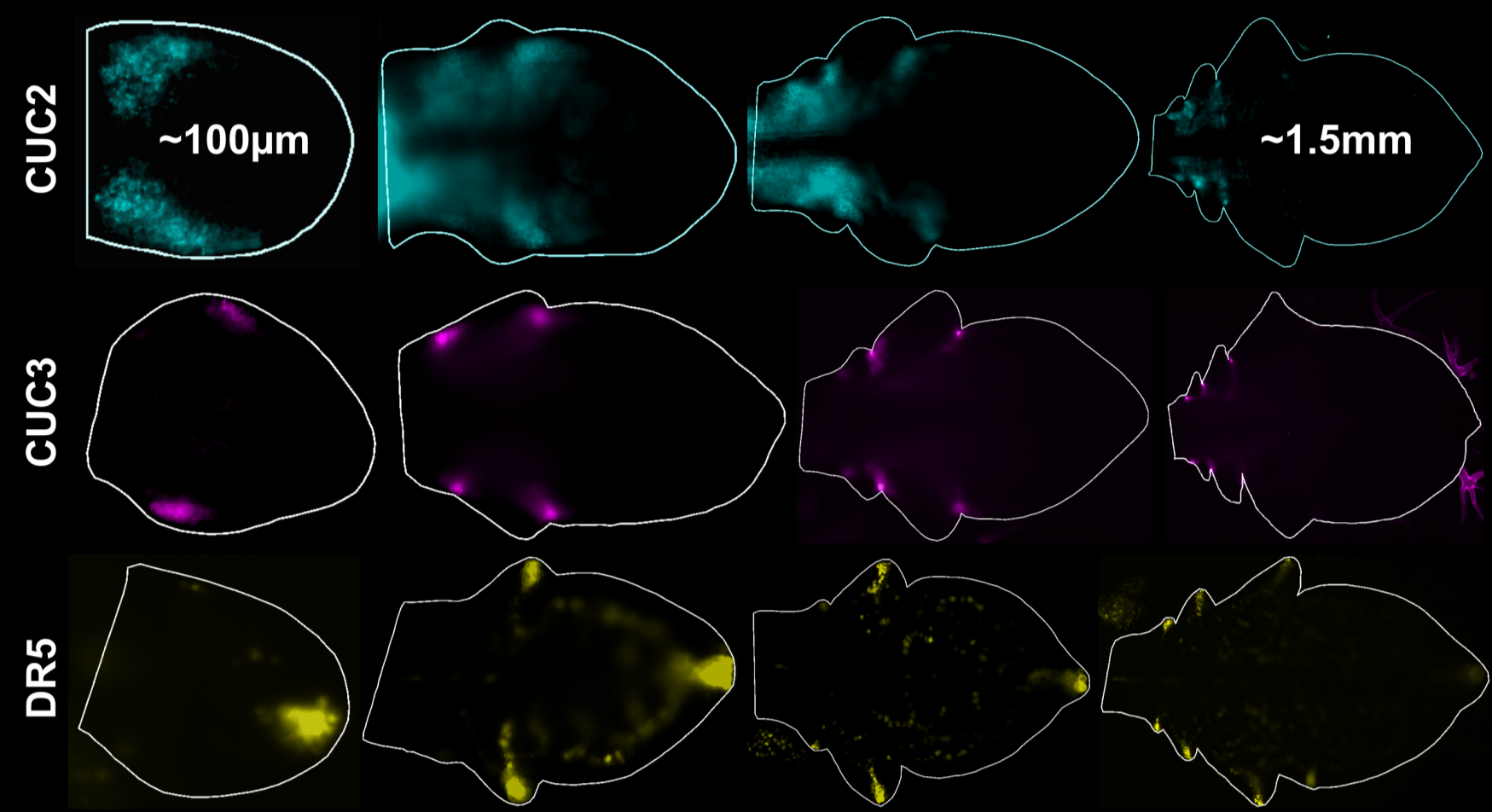
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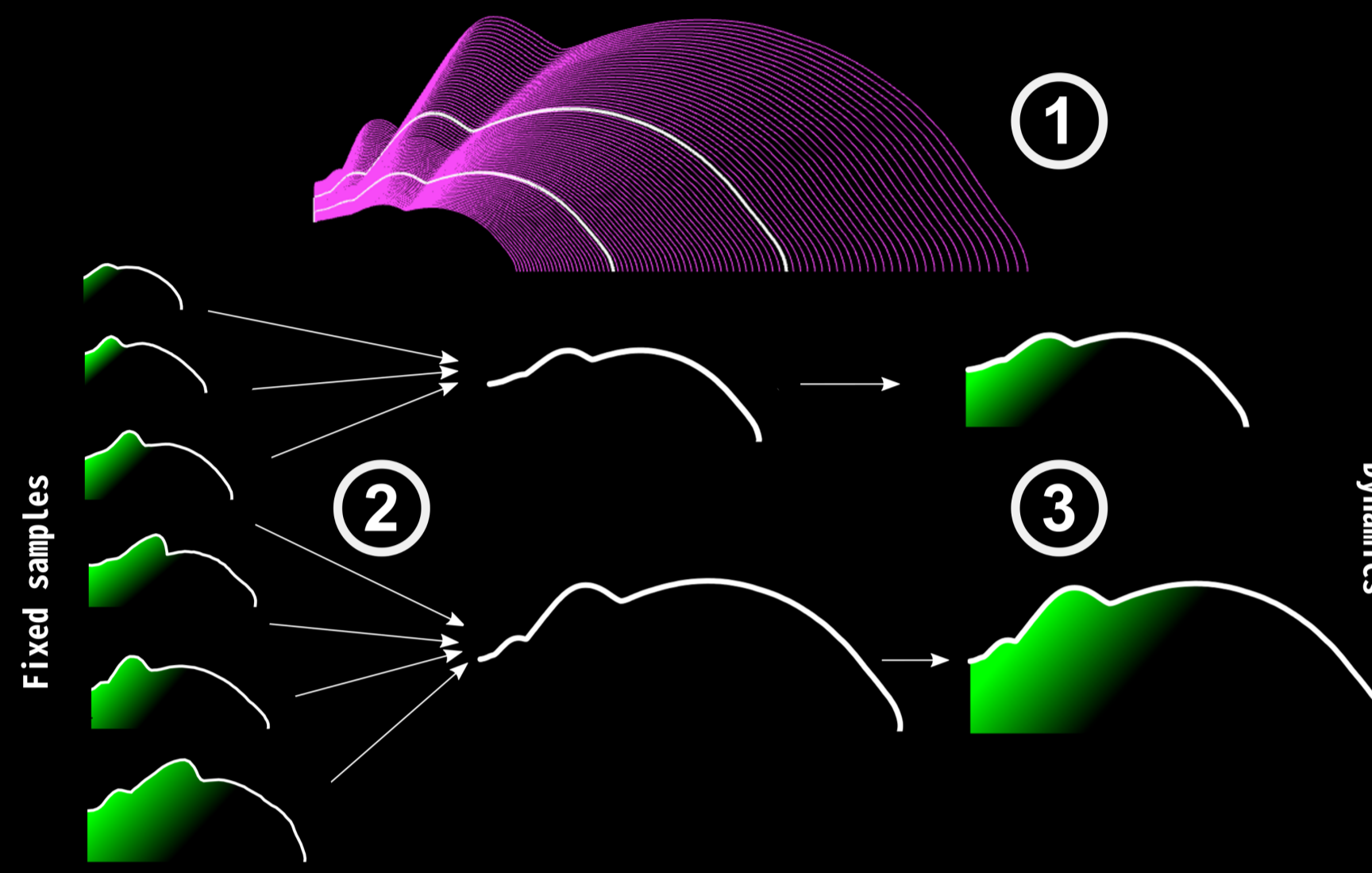
Development of living organisms is a multiscale complex choreography that requires spatio-temporal coordination of expression of genes involved in cell division, expansion, differentiation and migration. Fluorescent markers and microscopy imaging reveal 2D and 3D gene expression patterns in tissues but it is difficult to follow spatio-temporal dynamics of gene expression. In deed acquisition of live images all along growth implies severe technical challenges, also linked to rapid changes of both organ shape and size. As an alternative to time-lapse imaging, we reason that we can exploit series of static, standard images sampled at different developmental stages on different individuals to infer with high precision the continuous dynamics of gene expression in an evolving, growing shape. Our goal is to set-up a statistical methodology and its computational implementation to build spatio-temporal statistical atlases of gene expression patterns in growing organs.

## Visualizing gene expression patterns



Our goal is to reconstruct signal dynamics from still data

## Overall strategy

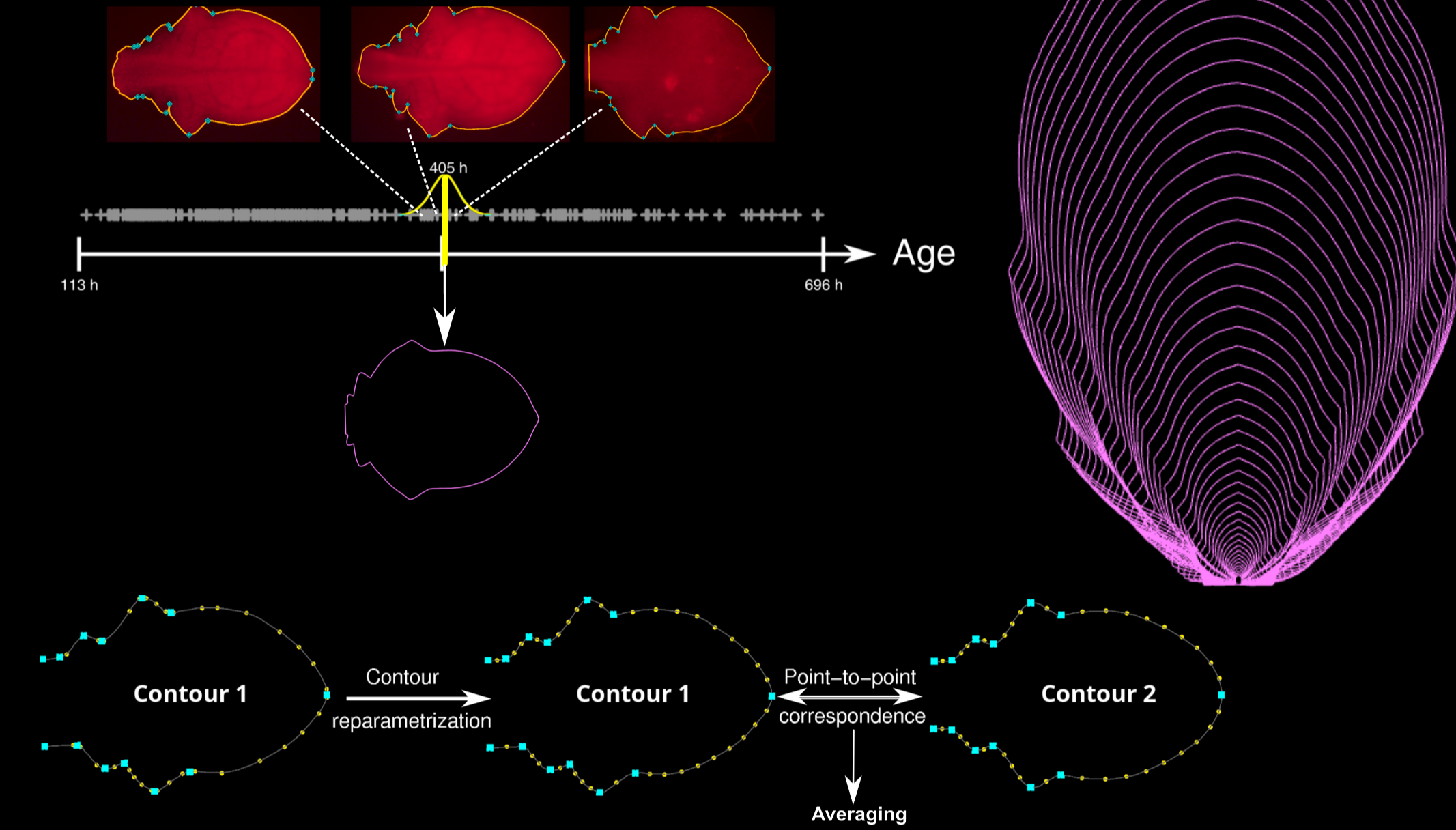


1. Spatio-temporal referent framework: growth trajectory
2. Signal spatial normalization: projection into the reference
3. Signal averaging: built of the signal dynamics

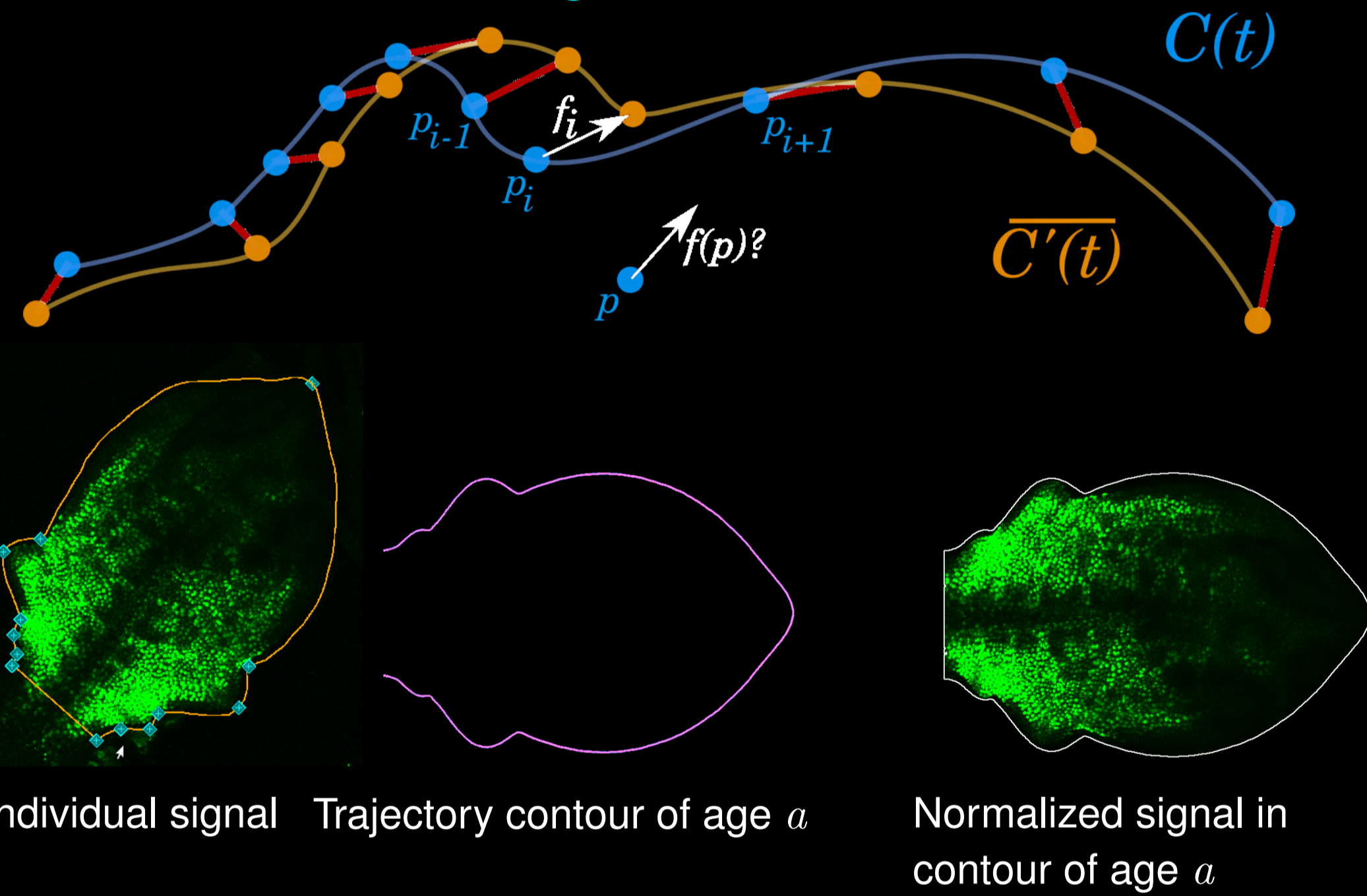
## Computing a referent framework

MorphoLeaf software, Biot et al., 2016

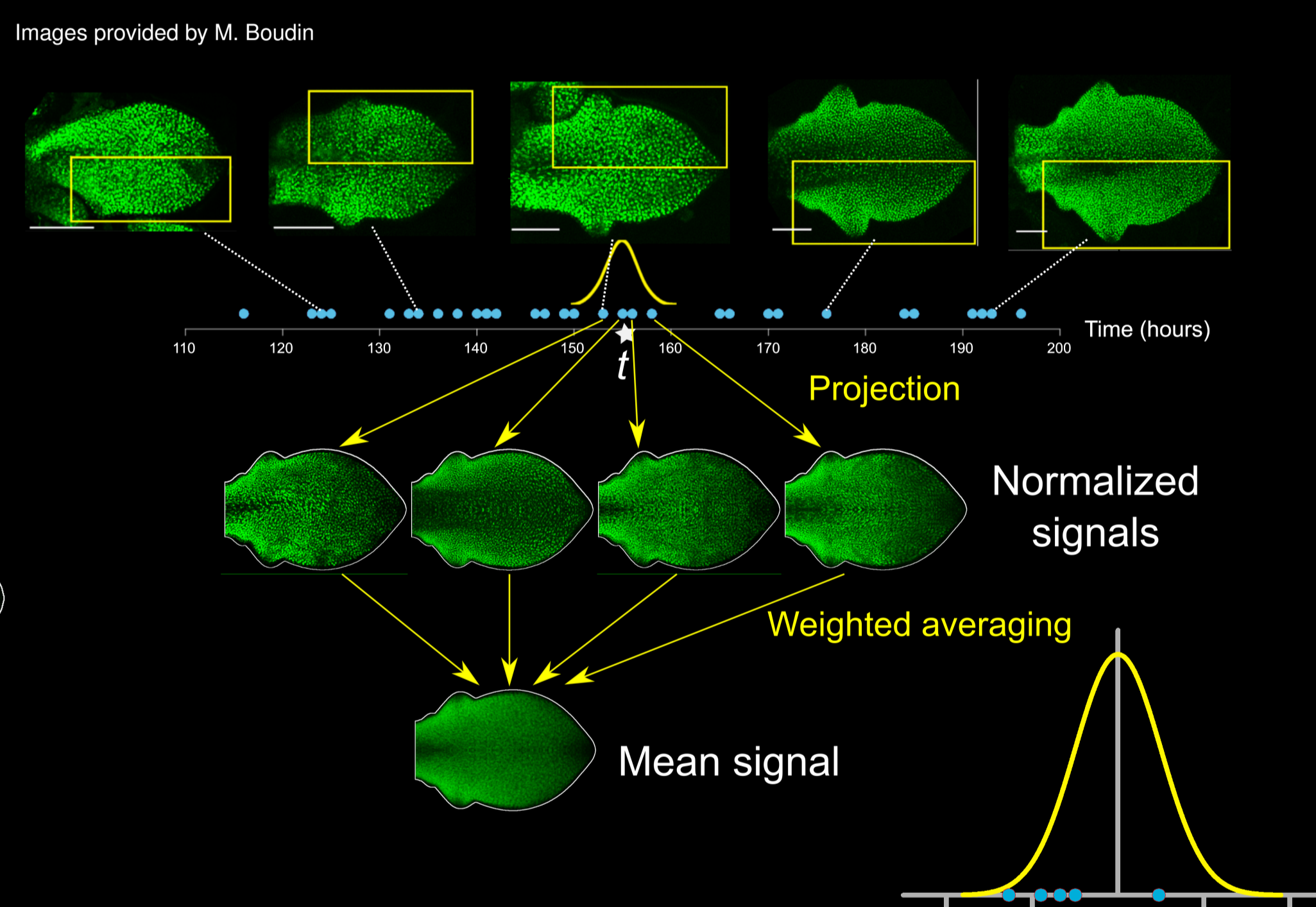
MorphoLeaf software, Biot et al., 2016



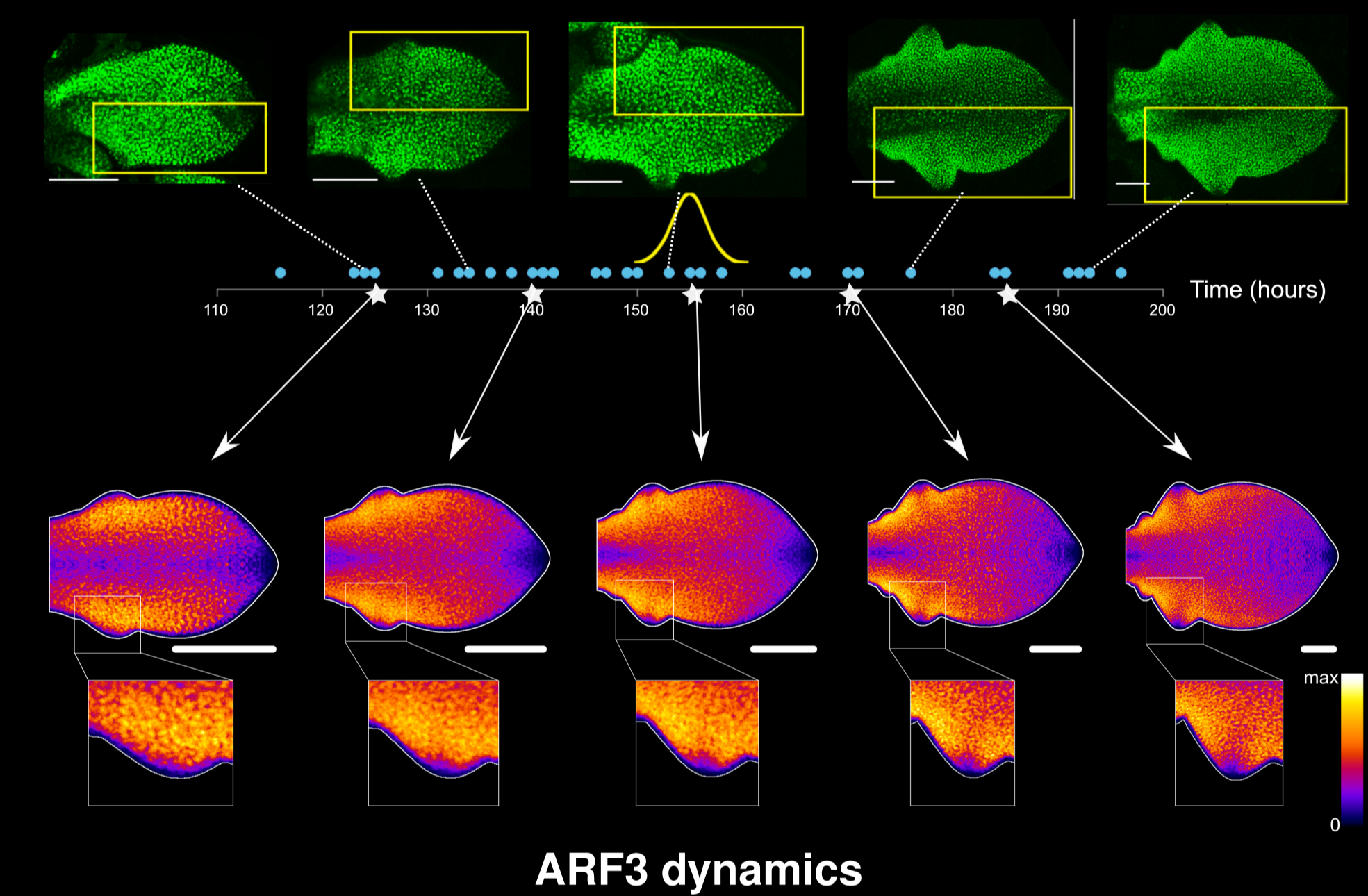
## Individual signal normalization



## Average signal dynamics



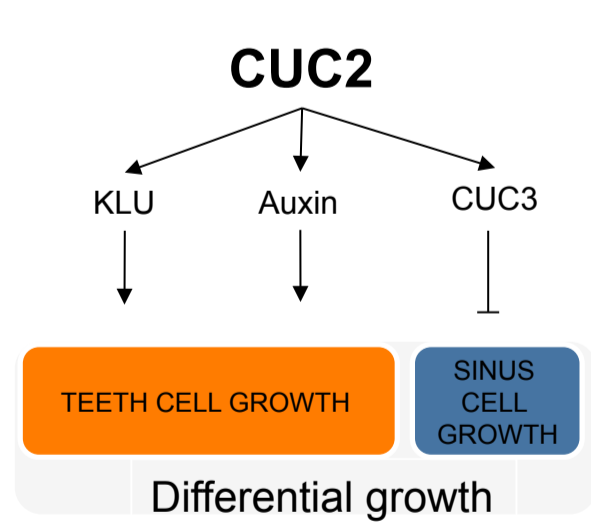
## Average signal dynamics



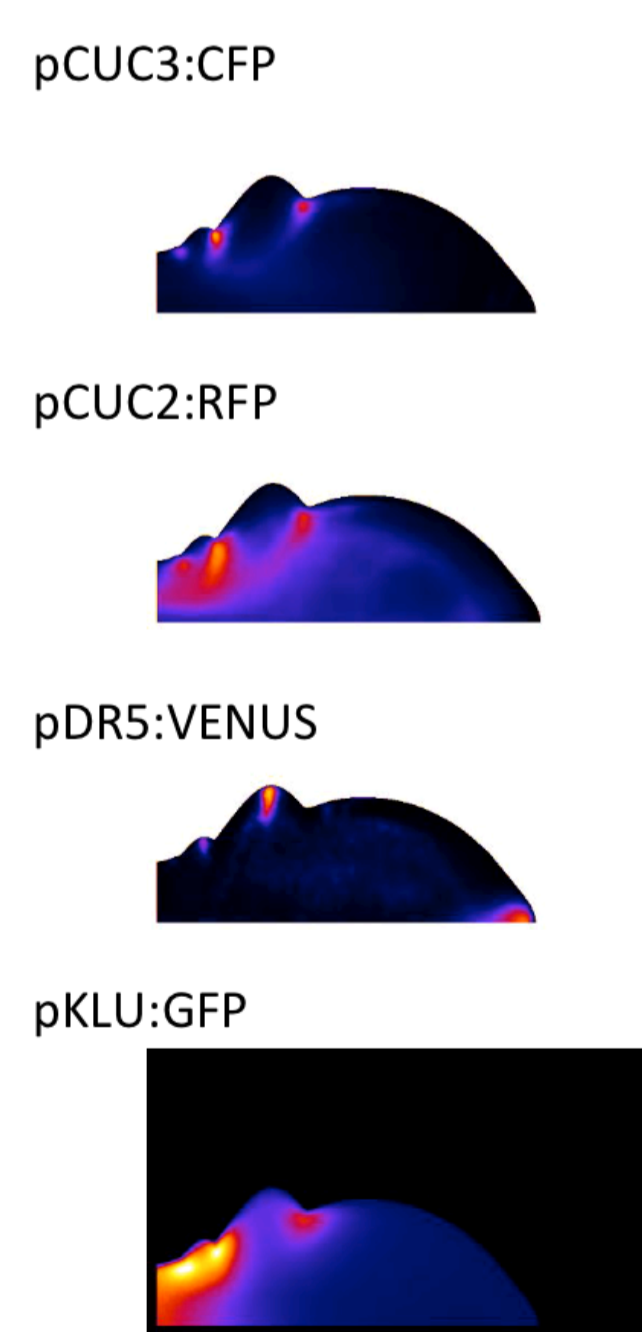
## RESULTS

CUC2 control leaf shape through different molecular relay

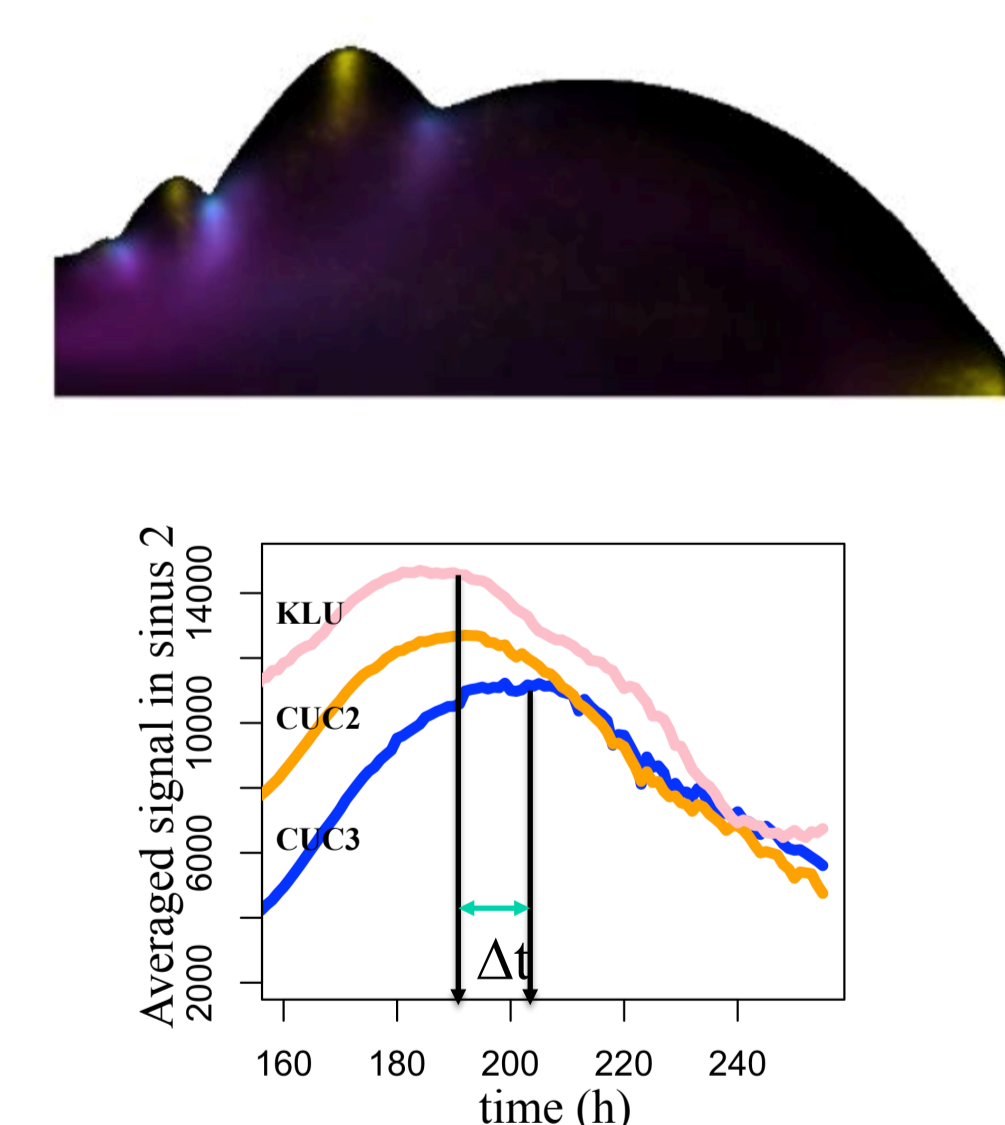
(Maugarny-Calès et al., 2019)



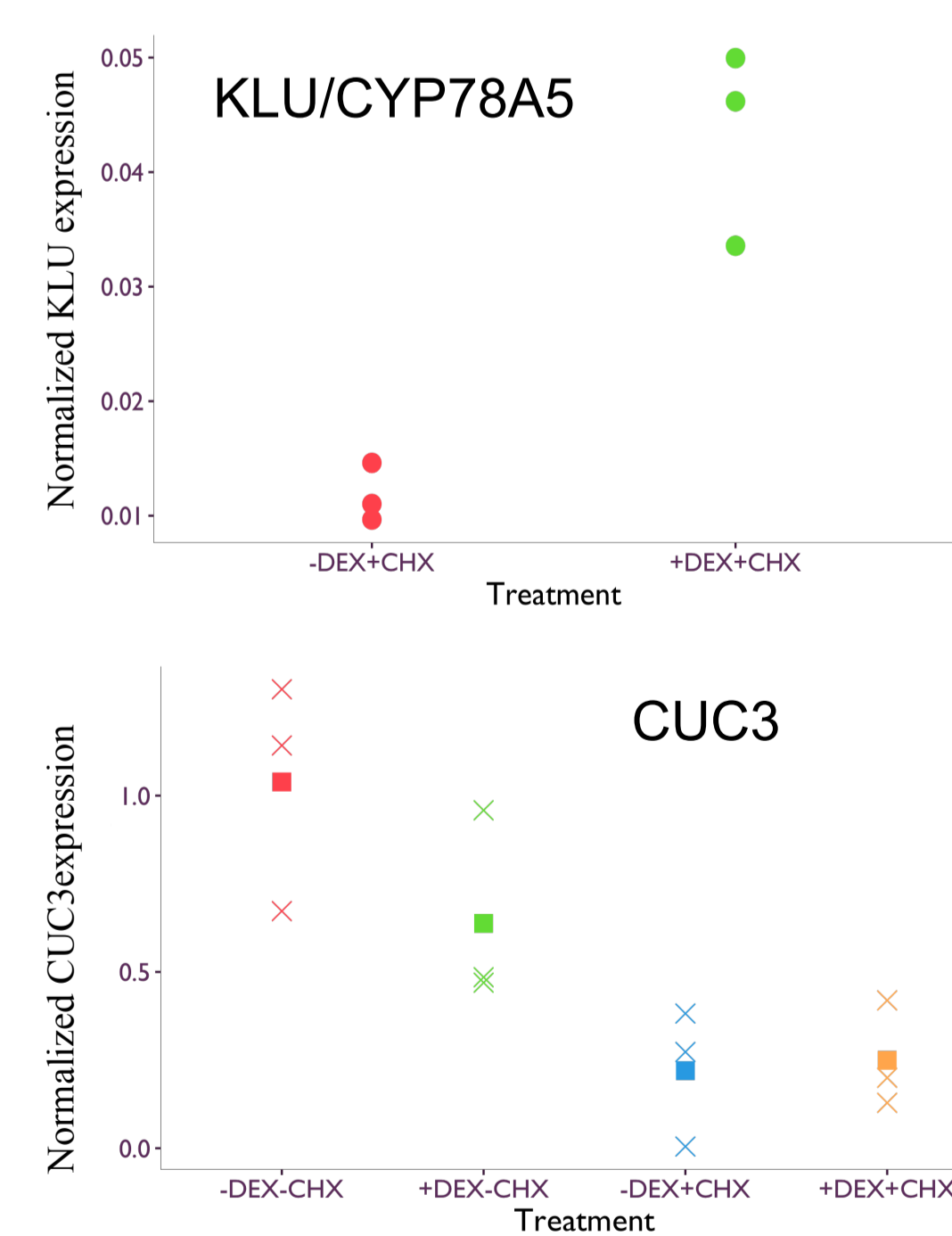
- Dynamic expression map over 6 days of leaf growth (141 hours).
- The leaf is growing from 100µm to over 1mm long (10x).
- Averaging ≈150-200 half leaves images per reporter line with a good size-distribution.



CUC2 CUC3 DR5:VENUS



CUC3 expression dynamic is delayed compared to CUC2 and KLU expression dynamics



## CONCLUSION :

- We developed a method to quantify the spatio-temporal dynamics of gene expression in a 2D, fast growing organ over several days. This statistical method is based on reporter genes and does not require challenging live-imaging methodologies.
- As a proof of concept, we used this methodology to analyze the Gene Regulatory Network of leaf shape development.

## References

- Biot E et al (2016). *Development* 143: 3417-3428
- Maugarny-Calès A et al (2019) *PLoS Genetic* 15:e1007913
- Oughou M et al (2019). *IEEE ISBI'2019* e8759188

## Acknowledgements

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