TRICHOME PATTERN FORMATION:

COMPUTATIONAL EXPLORATION OF THE ROBUSTNESS AND MECHANISTIC INFLUENCES OF THE TURING MECHANISM

Toquinha-O. Bergmann¹, Hanne Bechtle², Jonas Pleyer¹, Dr. Martin Hülskamp², Dr. Christian Fleck¹

¹Freiburg Center for Data Analysis and Modeling, University Freiburg, ²Botanical Institute, Biocenter, Cologne University

Introduction

Trichome Phenotypes Col-0 gli mm gli try

Fig. 1: Col-0 wildtype and three patterning mutants. Leaf three is depicted exemplarily.

Model system

- 2D point pattern Easily observable model
- Different patterning proteins and their functions identified
- Not essential proteins

Reaction-Diffusion System

 $\begin{array}{lll} \partial \tau [GL1]_{j} \; = \; \sigma_{0} - \lambda_{0} \; [GL1]_{j} + \beta_{-} [AC]_{j} - \beta_{0} [GL1]_{j} [GL3]_{j} \\ \partial \tau [GL3]_{j} \; = \; \sigma_{1} - \lambda_{1} \; [GL3]_{j} + \beta_{-} [AC]_{j} - \beta_{0} [GL1]_{j} [GL3]_{j} - \beta_{1} [GL3]_{j} [TRY]_{j} + \alpha_{1} [AC]_{j}^{2} \\ \partial \tau [TRY]_{j} \; = \; \sigma_{2} - \lambda_{2} [TRY]_{j} & - \beta_{1} [GL3]_{j} [TRY]_{j} + \alpha_{2} [AC]_{j}^{2} + \delta \langle [TRY]_{j} \rangle \\ \partial \tau [AC]_{j} \; = \; - \lambda_{3} \; \; [AC]_{j} - \beta_{-} [AC]_{j} + \beta_{0} [GL1]_{j} [GL3]_{j} \end{array}$

Fig. 3: System of discretized and coupled ordinary differential equations describing the time evolution of GL1, GL3, TRY and the active complex (AC). Where <[TRY]> defines the passive transport of TRY.

Exploring interaction networks

- Using reaction-diffusion principles to model and simulate protein interactions - Turing mechanism
- Investigating how different proteins might interact to form phenotype
- Reproducing genotype-phenotype relationships

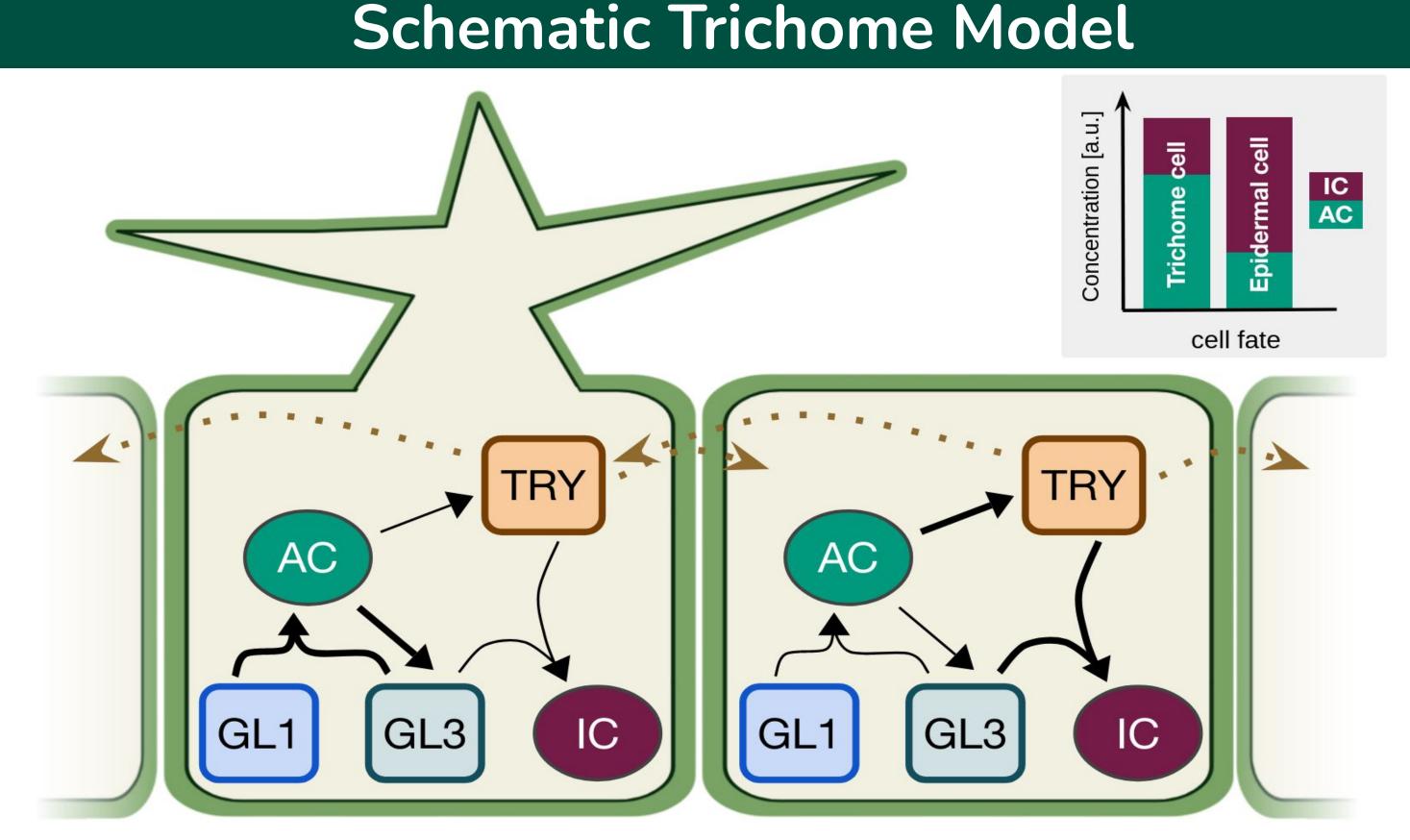


Fig. 2: An Activation-Inhibition-Model for Trichome Patterning in Arabidopsis. With GL1 and GL3 forming an Activation-Complex (AC) activating GL3 and TRY. With GL3 and TRY forming an Inhibition-Complex (IC). AC/IC ratio determines cell fate.

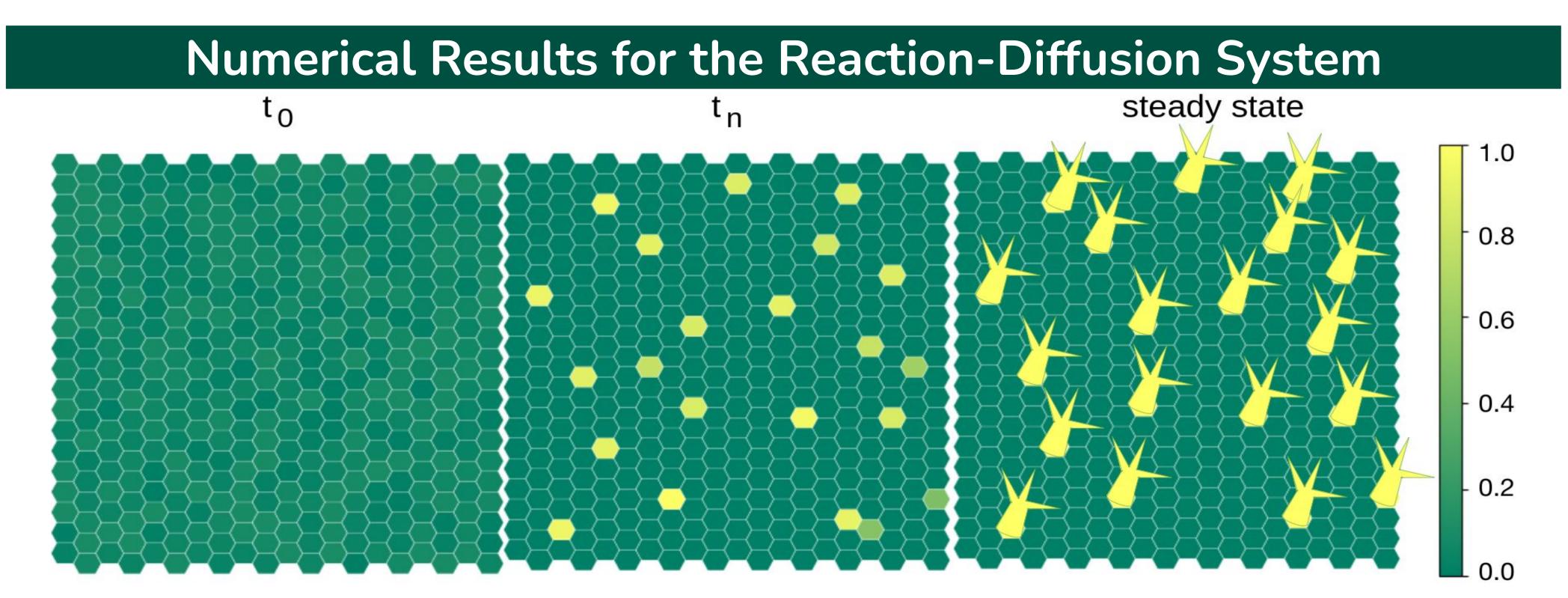


Fig. 4: Visualization of the numerical integration of the reaction-diffusion system. Cells are assumed to be organized on a hexagonal grid. Shown are initial homogeneous (left), intermediate (middle) and steady (right) states. The colors indicate the concentration of AC, which has been normalized to a value between 0 and 1.

Parameter Space Analysis of Bulk Data

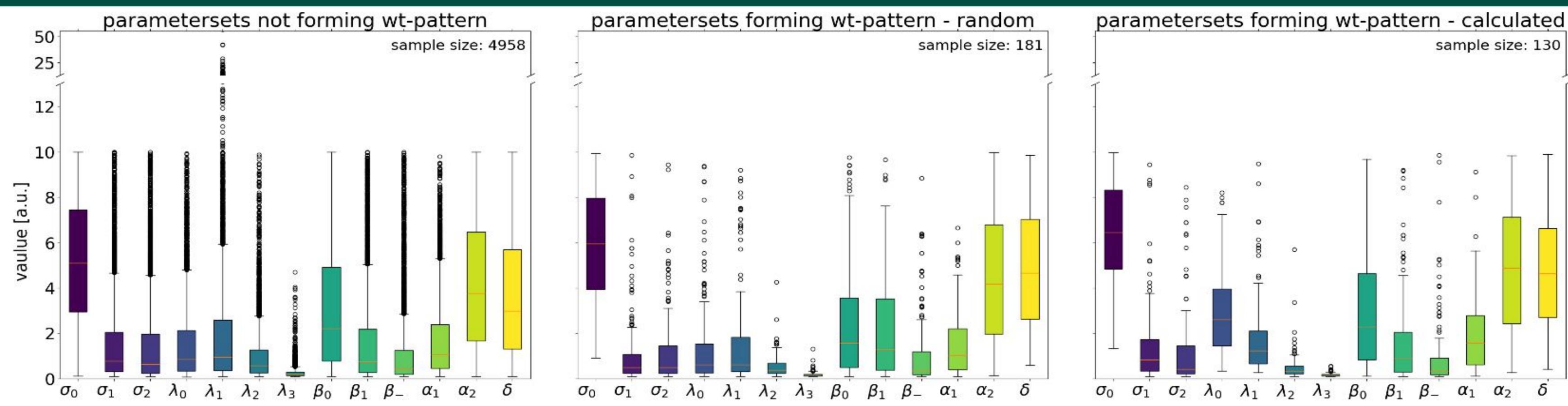


Fig. 5: Distribution of parameters in Turing space (parameter-sets that can form patterns according to Turing mechanism). Parameters in Turing space without wild-type pattern (left), parameters with wild-type pattern (centre and right), of which randomly drawn (centre) and calculated from stabilization data (right).

Further Research Questions

- How do the mechanical interactions influence the pattern?
- How do different cell shapes affect the resulting pattern?
- How does the tissue grow after the pattern has stabilized?
- Which processes drive intercalation the initial pattern has formed?
- → Need dynamic and flexible model

Dynamic Simulation Output Discrepancy of the content of the con

Fig. 6: Freely motile vertex-shaped cell model with Reaction Diffusion System between adjacent cells.

Puzzle-Shaped Epidermal Cells

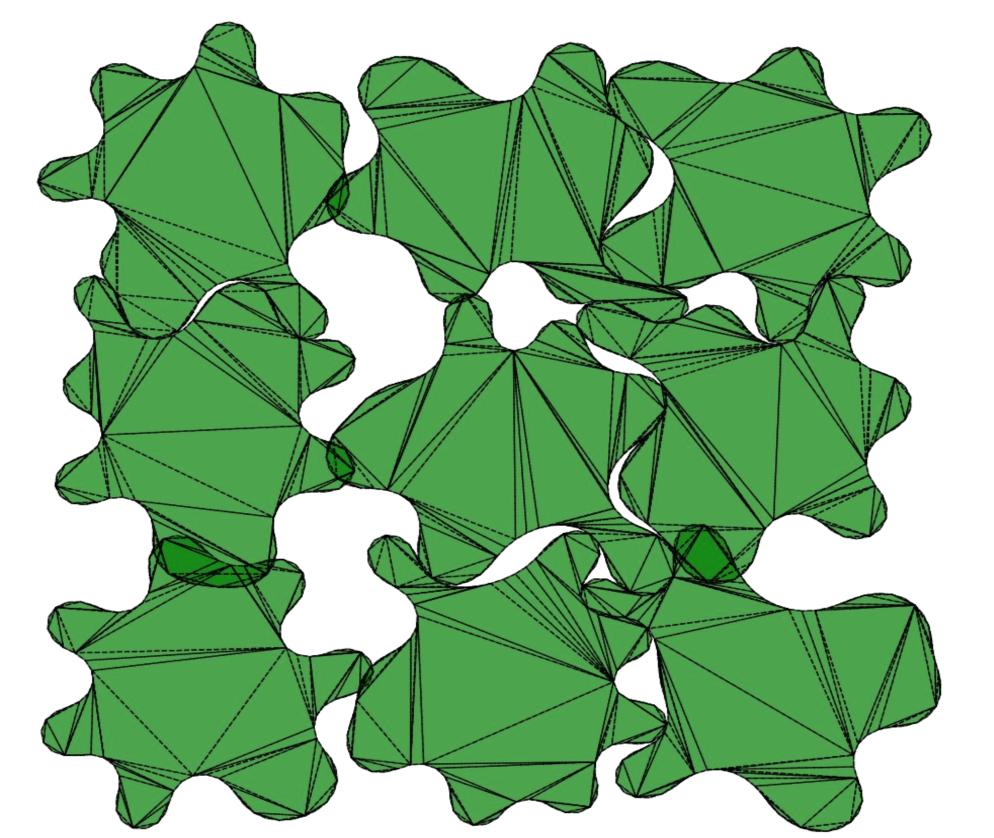


Fig 7: Experimental model of Puzzle-shaped epidermal cells, modeled by triangulated multi-vertex agents.

cellular_@aza

- Agent-Based Model (ABM)
- Treat cells individually
- Mechanistic rules
- Low-parametric
- Flexible in Model design
- Greater variability of cell shapes

cellular-raza.com



universitätfreiburg