

# Signaling in Multicellular Models of Plant Development

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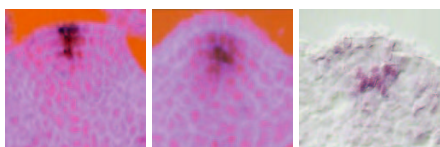
The **Shoot Apical Meristem (SAM)** of plants is the biological target for a mathematical model of multicellular organisms. The model is implemented *in Silico*, and simulations of the dynamical time development are performed.

## The Shoot Apical Meristem (SAM) of *Arabidopsis*

- Source of aboveground part of plant
- Small (about  $10^3$  cells)
- Genes important for the development identified

### Expression Patterns

- CLAVATA3 (CLV3): stem cell marker
- CLAVATA1 (CLV1): receptor kinase
- WUSCHEL (WUS): homeodomain, transcription factor

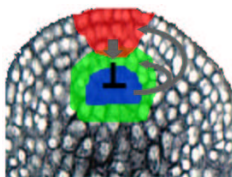


CLV3, CLV1 and WUS expressions.

### Interactions

Gene interactions are identified by *loss-of-function* and *promoter::gene* mutant experiments.

- WUS induces CLV1 and CLV3 expression
- CLV1 and CLV3 act in a network repressing WUS expression



The interactions between **CLV3**, **CLV1** and **WUS** regulates the development of the SAM, and thereby the complete plant.

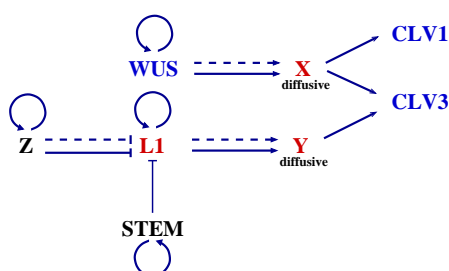
### Acknowledgements

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## The SAM Model Network

How can WUS regulate CLV3 when the expression domains don't overlap?



A partly hypothesized network. **X** is suggested by experiments, but unknown. **L1** and **Y** have genes with analogous expression patterns (ATML1 and ACR4).

## The Generic Model

Essential parts of a developmental system are introduced in a mathematical model.

- Cell Growth
- Cell Cycle/Proliferation
- Mechanical Cell Interactions
- Gene Regulatory Network (GRN)
- Molecular Transport

## The GRN-Equations

$$\tau_a \dot{v}_a^{(i)} = g(u_a^{(i)} + h_a) - \lambda_a v_a^{(i)}$$

where

$$u_a^{(i)} = \sum_b T_{ab} v_b^{(i)} + \sum_j \Lambda_{ij} (\hat{T}_{ab} v_b^{(j)} + \sum_{bc} \tilde{T}_{ac}^{(1)} \tilde{T}_{cb}^{(2)} v_b^{(j)} v_c^{(i)}),$$

$v$  - set of protein concentrations

$T$  - intracellular interactions

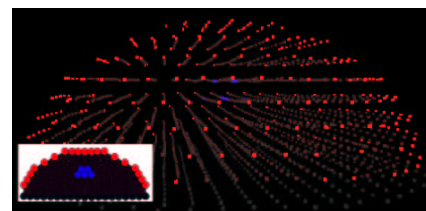
$\hat{T}, \tilde{T}^{(1)}, \tilde{T}^{(2)}$  - intercellular interactions

$g(x)$  - a sigmoidal function

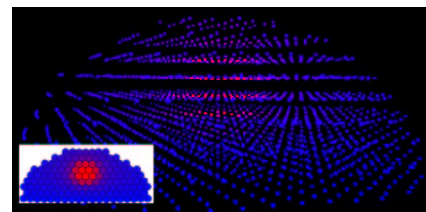
$\lambda, \tau, \Lambda, h$  - parameters

## Simulation Results

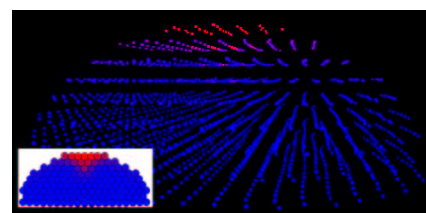
Simulation of a nongrowing SAM of 1765 cells. The final (stable) expression levels are shown.



The **WUS** expression region is an initial condition. **L1** is expressed only in the surface layer



**CLV1** expression surrounds the **WUS** domain.



**CLV3** is expressed at the apex.

## Simulation Comments

- No growth/WUS repression
- Parameters tuned by hand (no data)
- New hypotheses
- "Correct" expression patterns with few initial conditions

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