## Modelling Root Growth with Hormone Gradients

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#### Table of Contents

- Extracellular Systems
  - Root Structure
  - Hormones
  - Model

- 2 Intracellular Systems
  - Microtubule Organization
  - Model

#### Structure

The root is composed of *three distinct regions*:

- Differentiation Zone (DZ): Cells stop growing and develop specialized function. Differentiation occurs when cells reach a certain size (Pavelescu et al., 2018).
- Elongation Zone (EZ): Rapid growth, minimal division.
- Meristematic Zone (MZ): Rapid division, minimal growth.

#### Brassinosteroid and Auxin

**Brassinosteroid** (BR) induces cell *growth*. Higher levels of BR are found far from the root tip in the elongation zone.

**Auxin** induces cell *division*. Higher levels of auxin are found near the root tip in the meristematic zone.

### Modelling BR and Auxin

We model BR and Auxin using a Logistic Function:

$$B(x) = \frac{1}{1 + e^{a(x-m)}}$$

$$A(x) = 1 - B(x)$$

- x denotes the distance from the top of the root.
- a sets the size of the transition region.
- m sets the boundary between the EZ and MZ.

#### Discretization

We built the model by considering discrete time intervals  $\Delta t$ . The growth of a cell over  $\Delta t$  is

$$G(x, \Delta t) = B(x) \cdot \Delta t$$

The probability of a cell dividing in  $\Delta t$  is

$$P(x, \Delta t) = A(x) \cdot \Delta t$$

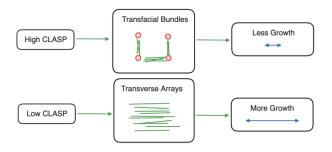
To check for division, we generate a random  $p \in [0,1]$ . If  $p < P(x, \Delta t)$ , the cell splits into two cells of half the size.

#### Model

Link

## Microtubule Organization

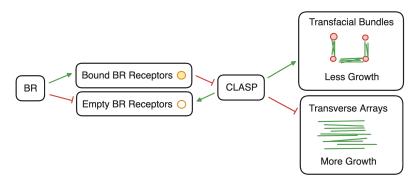
**Microtubules** (MTs) are a thread-like polymer that supports the cytoskeleton of a cell. **CLASP** controls how MTs are arranged.



\* This is a simplification of agent-based simulations.

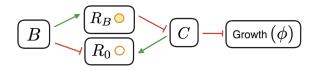
#### BR, MTs, and CLASP

**BR** binds to receptors on the membrane. When **CLASP** is high, the cell begins to produce new receptors.



Our goal is to find the growth  $(\phi)$  as a function of BR (B).

### Representing MTs with DEs



We used a system of differential equations to model the relationship between BR (B), CLASP (C), and receptors  $(R_0, R_B)$ .

$$\begin{cases} C' = s - t(1 + uR_B)C \\ R'_0 = v(1 + wC) - k_{\text{in}}^0 R_0 - k_{\text{on}} BR_0 + k_{\text{off}} R_B \\ R'_B = k_{\text{on}} BR_0 - k_{\text{in}}^B R_B - k_{\text{off}} R_B \end{cases}$$

# Finding $\phi$

Then, we represent the organization of the MTs as  $\phi(B)$ . This function is a simplification of work from Ambrose et al., 2011.

$$\phi(B) = \frac{C_m^n}{C_m^n + C(B)^n}$$

- $\phi = 0$  represents high levels of TFBs (low growth).
- $\phi = 1$  represents transverse arrays (high growth).

We are still missing C(B), but we have a trick!

### Time Scale Analysis

We assume that extracellular processes take place on a much longer time scale than intracellular ones. This means each cell will quickly settle into a steady state, so

$$\begin{cases} C' = 0 \\ R'_0 = 0 \\ R'_B = 0 \end{cases}$$

Here is the steady state solution. Now we have  $\phi(B)$ !

#### Model

Link