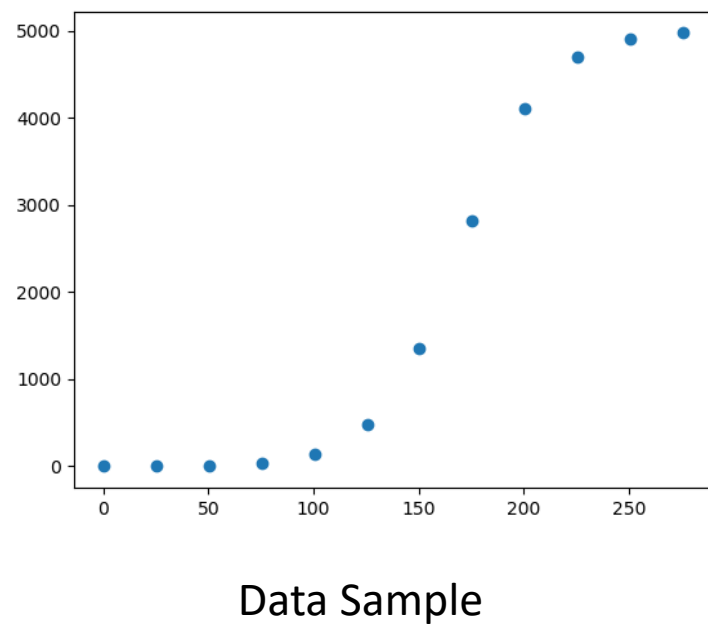


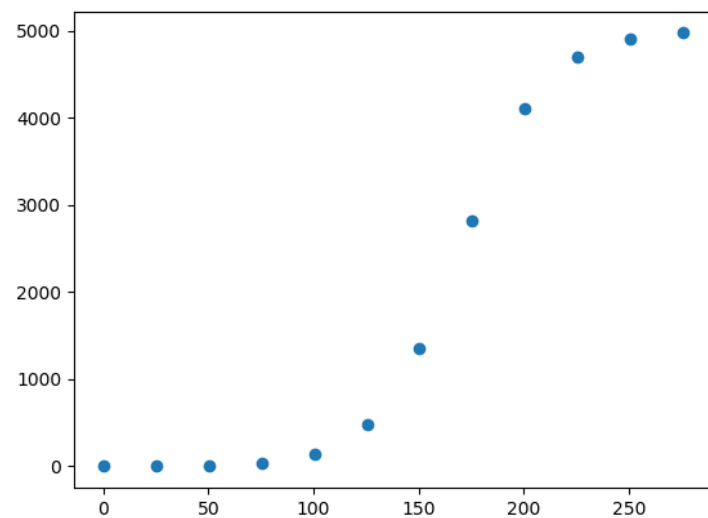
PFE 8

Palubicki

Data Models

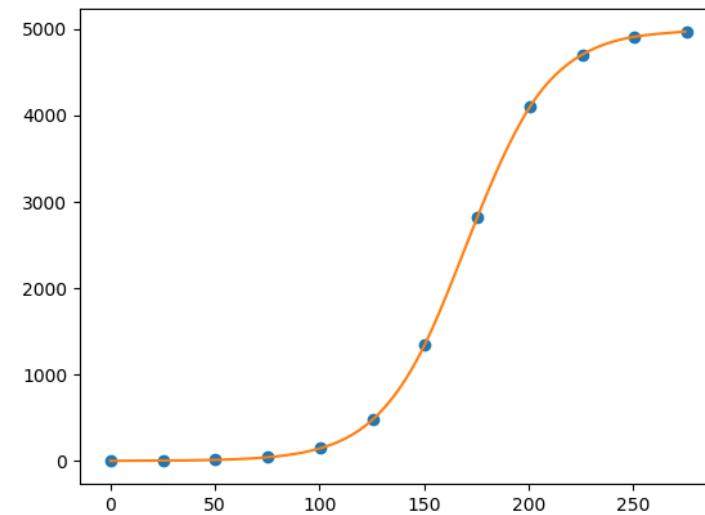


Data Models

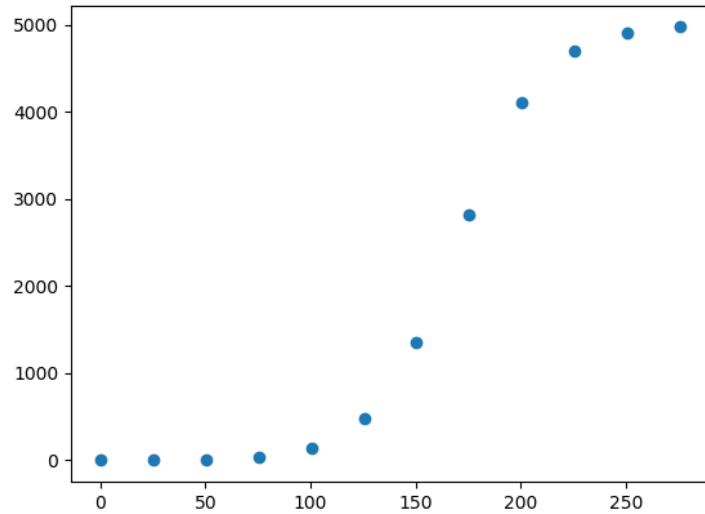


Data Sample

Interpolation



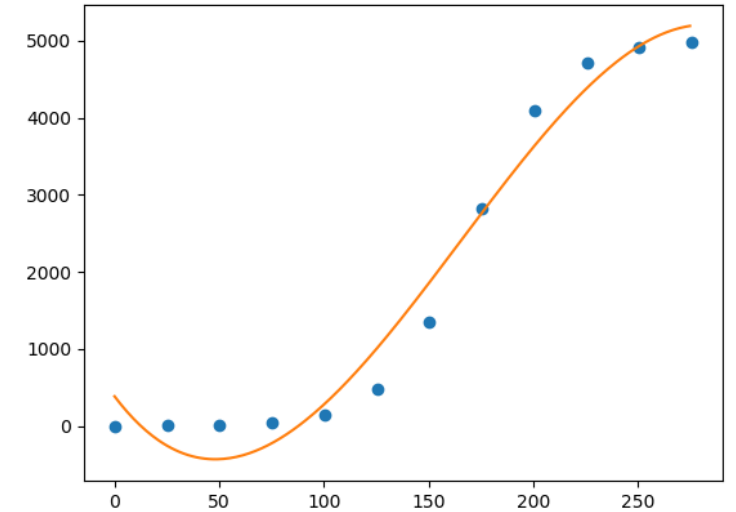
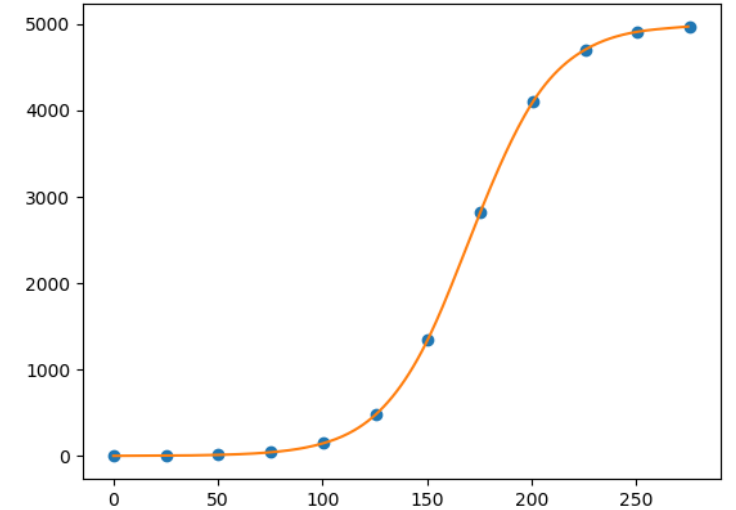
Data Models



Data Sample

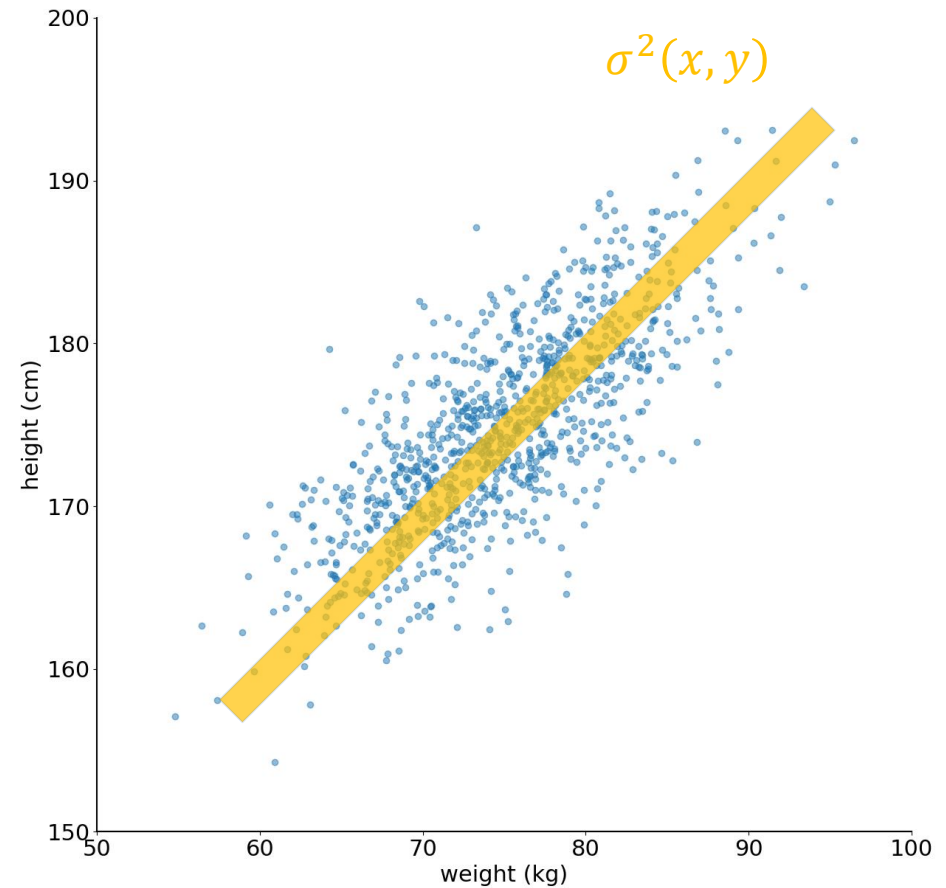
Interpolation

Approximation



Covariance

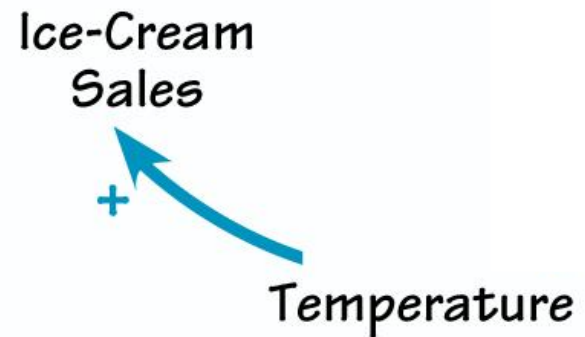
- Quantify correlations between variables
- E.g. Weight is correlated with height



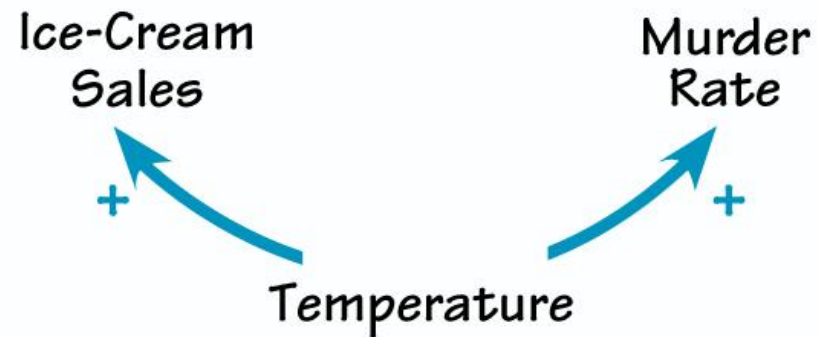
Causality vs. Correlation

- Causality is an **abstraction** that indicates how the world progresses.
- What causes to go from one state to another.
- It is an expressive method to describe patterns and essentially what we would like to extract from a good data model.

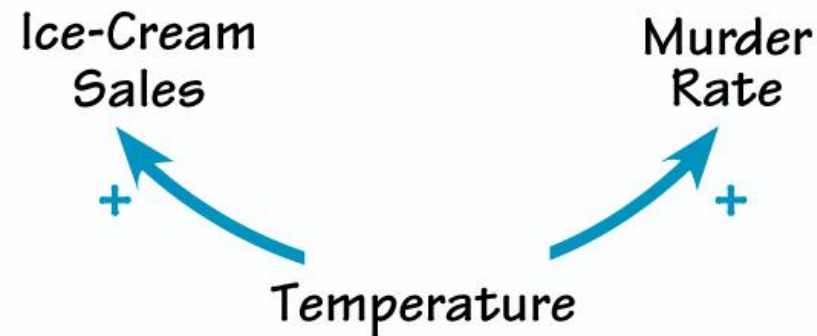
Causality vs. Correlation



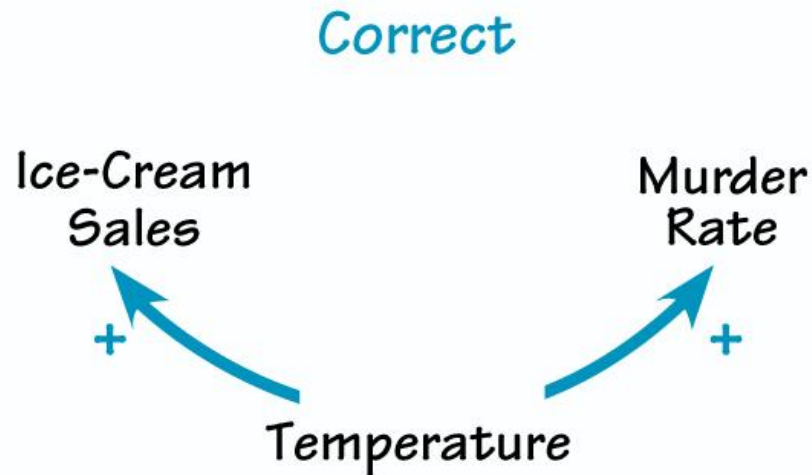
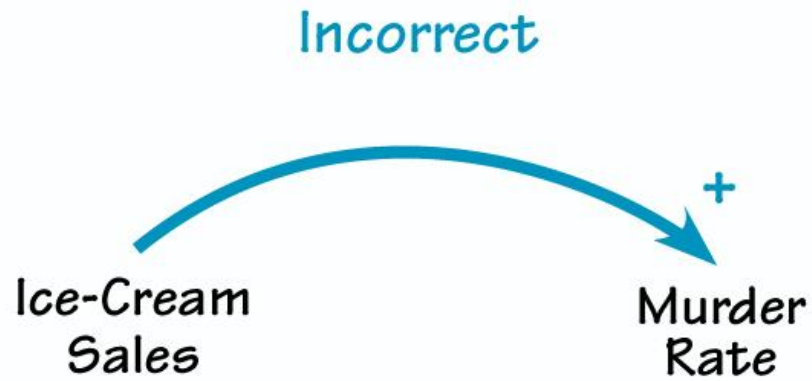
Causality vs. Correlation



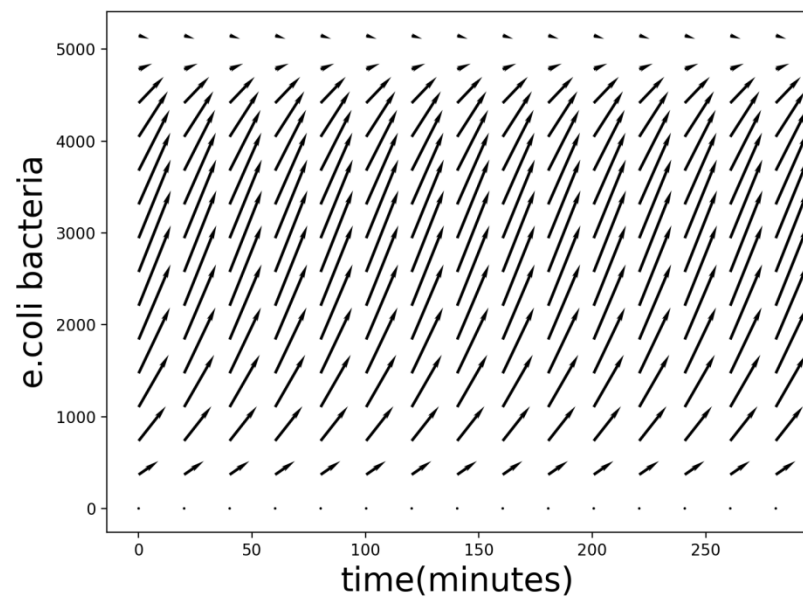
Causality vs. Correlation



Causality vs. Correlation

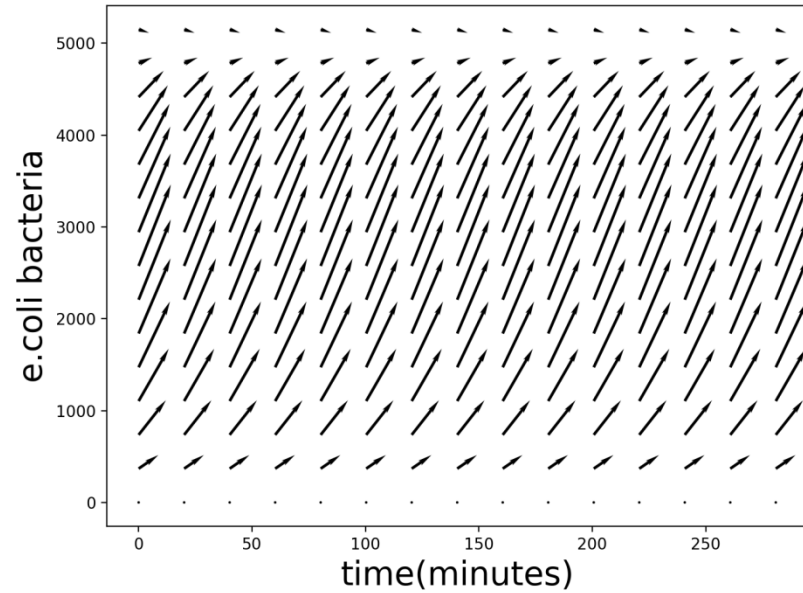


Differential Equations

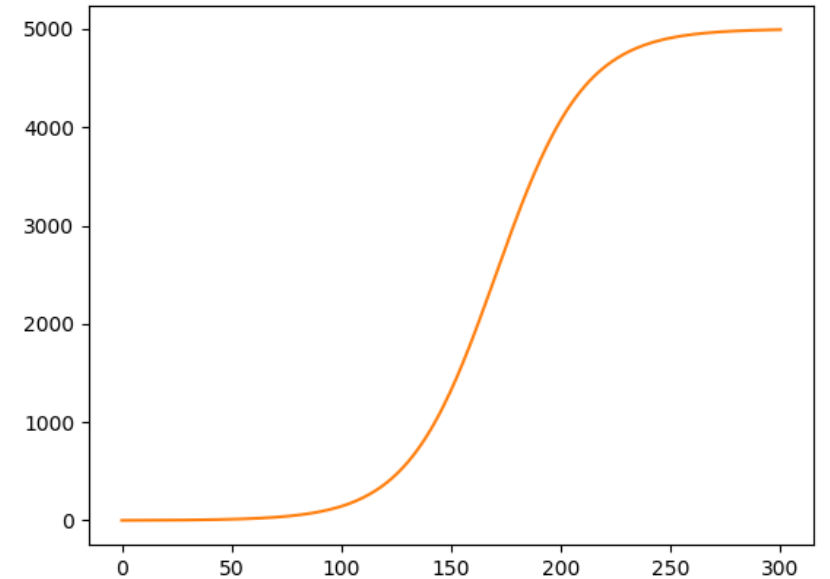


Differential
Equations

Differential Equations

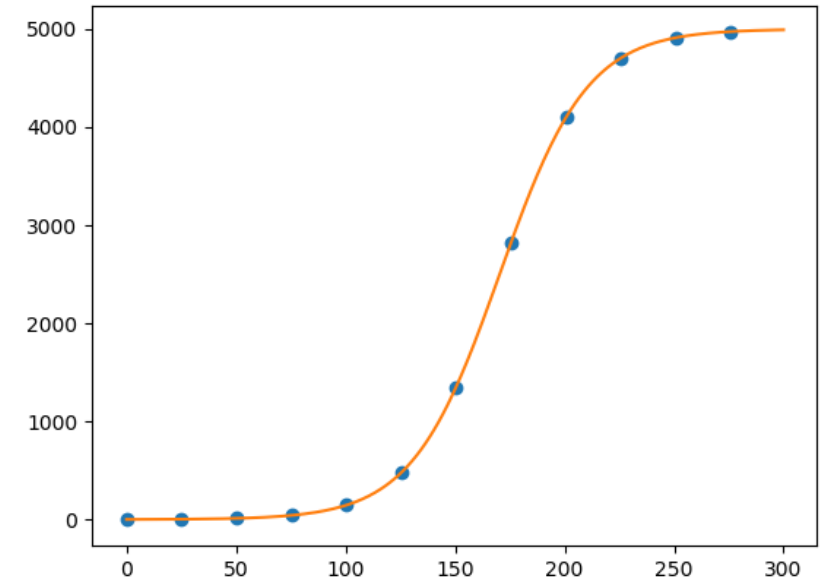
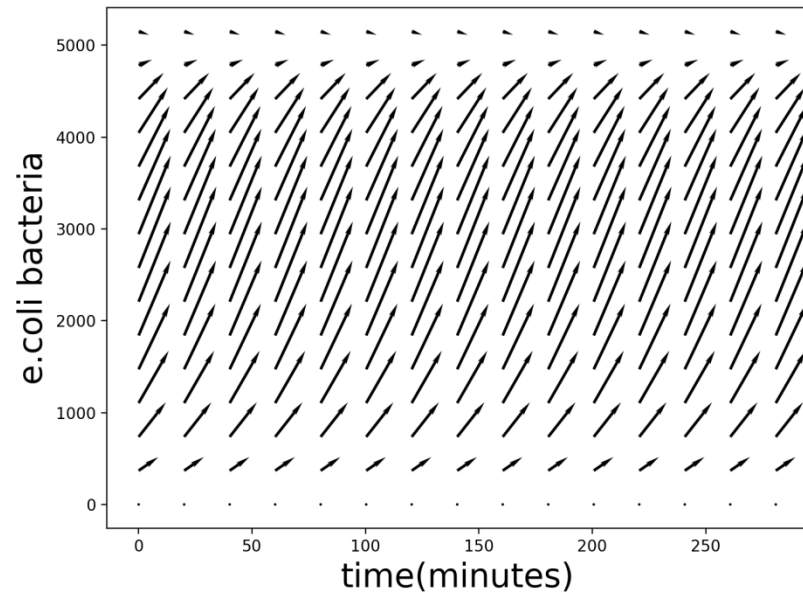


Differential
Equations



Model

Differential Equations



Explicit causality

Population growth depends on whole population size but limited by food availability

Model

Can be evaluated with experimental data

SIR Model

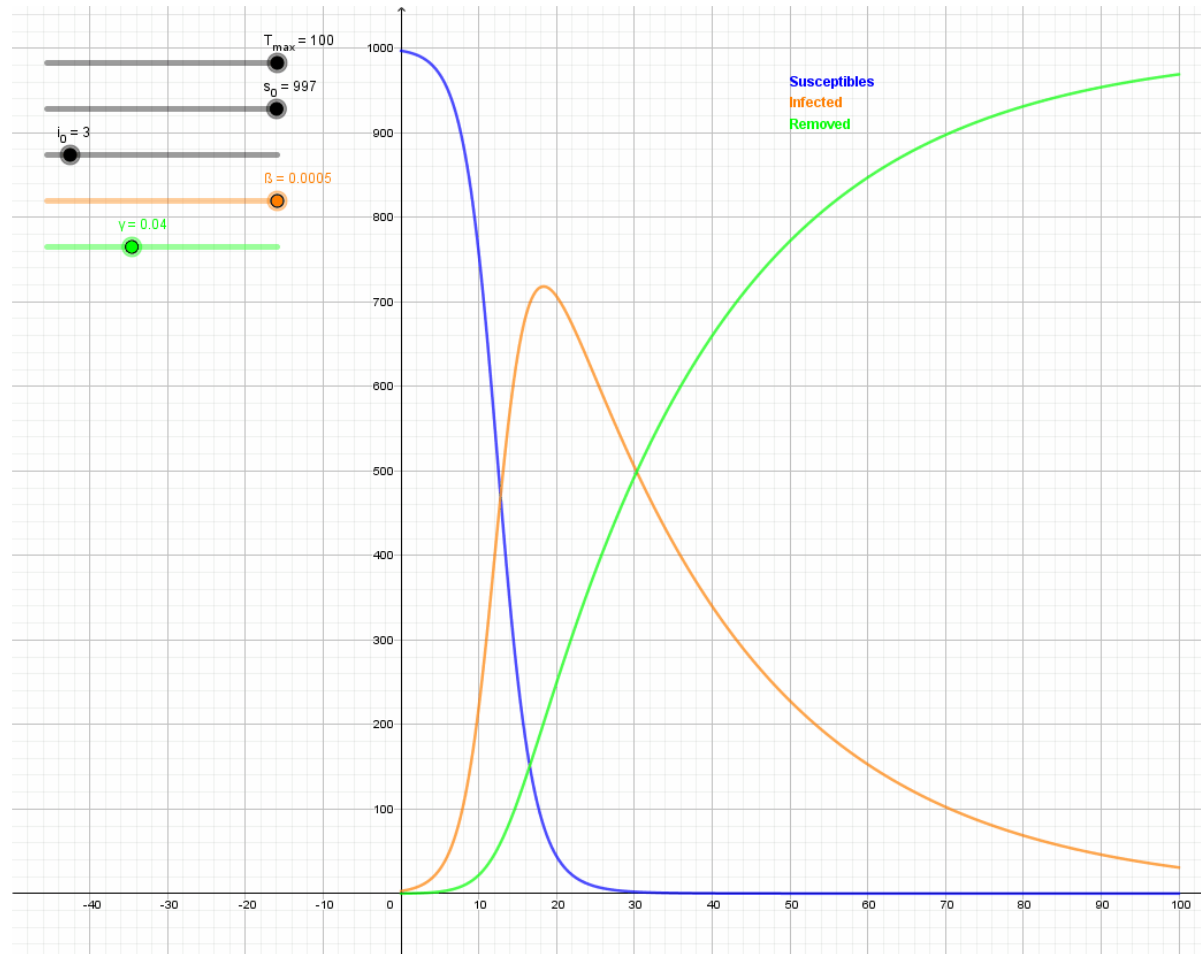
- **N**: total population
- **S(t)**: number of people susceptible on day t
- **I(t)**: number of people infected on day t
- **R(t)**: number of people recovered on day t
- **β**: expected amount of people an infected person infects per day
- **D**: number of days an infected person has and can spread the disease
- **γ**: the proportion of infected recovering per day ($\gamma = 1/D$)

$$\begin{aligned}\frac{dS}{dt} &= -\beta \cdot I \cdot \frac{S}{N} \\ \frac{dI}{dt} &= \beta \cdot I \cdot \frac{S}{N} - \gamma \cdot I \\ \frac{dR}{dt} &= \gamma \cdot I\end{aligned}$$

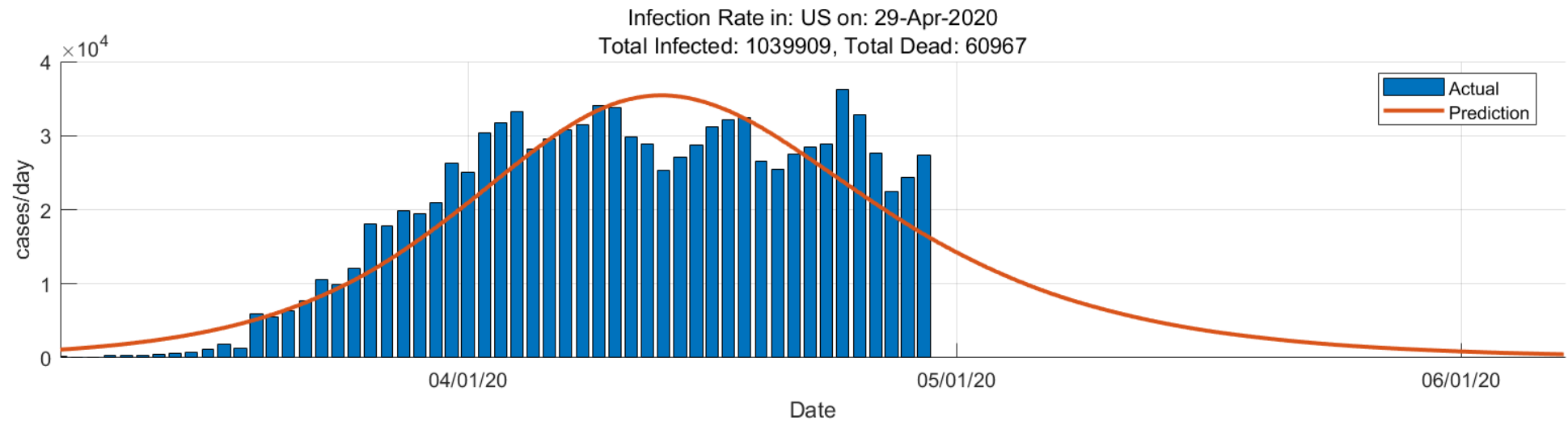
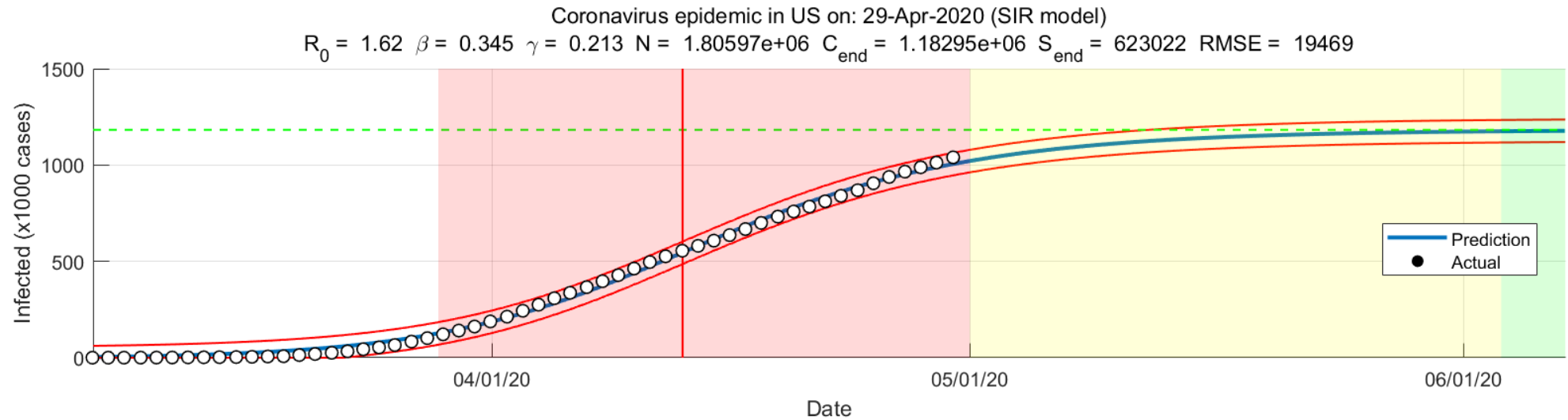
$$\frac{dS}{dt} + \frac{dI}{dt} + \frac{dR}{dt} = 0,$$

$$S(t) + I(t) + R(t) = \text{constant} = N,$$

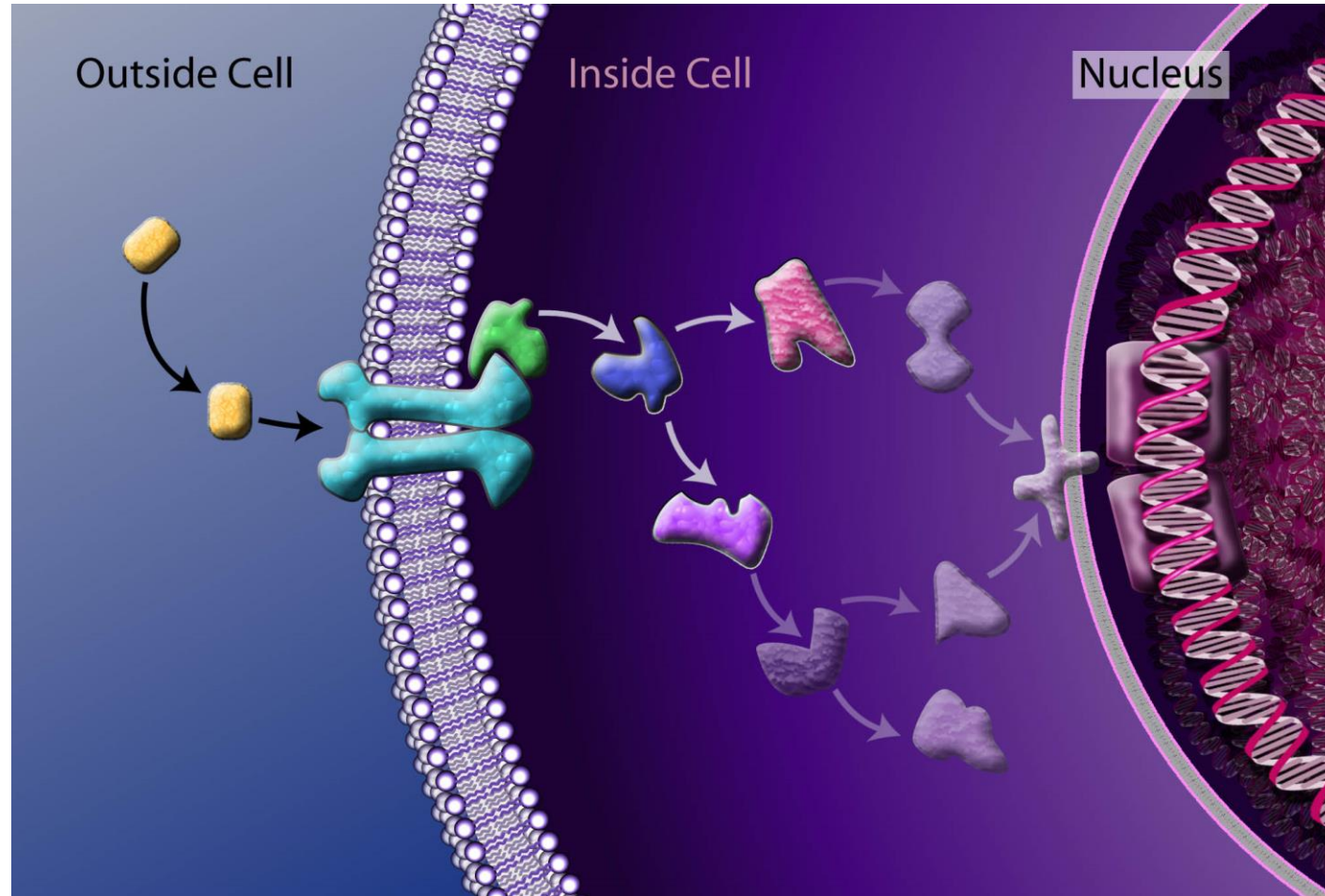
SIR Model Parameter Space Exploration



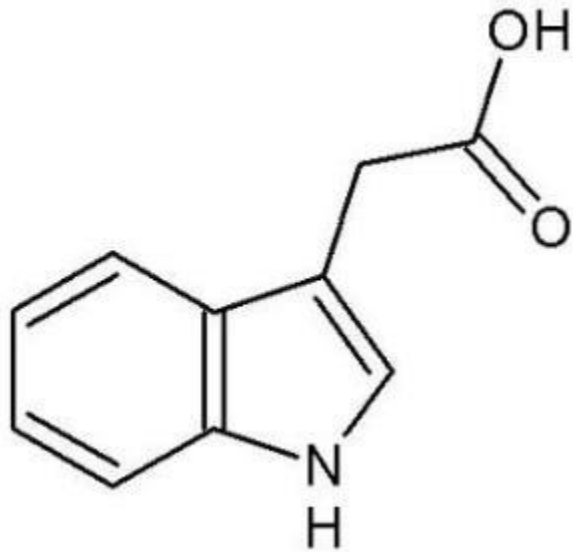
SIR Model Prediction



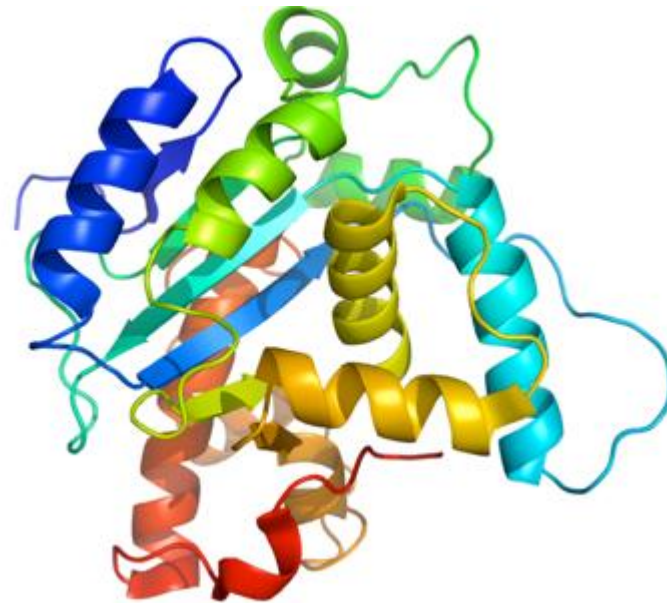
Information processing in organisms



Signals

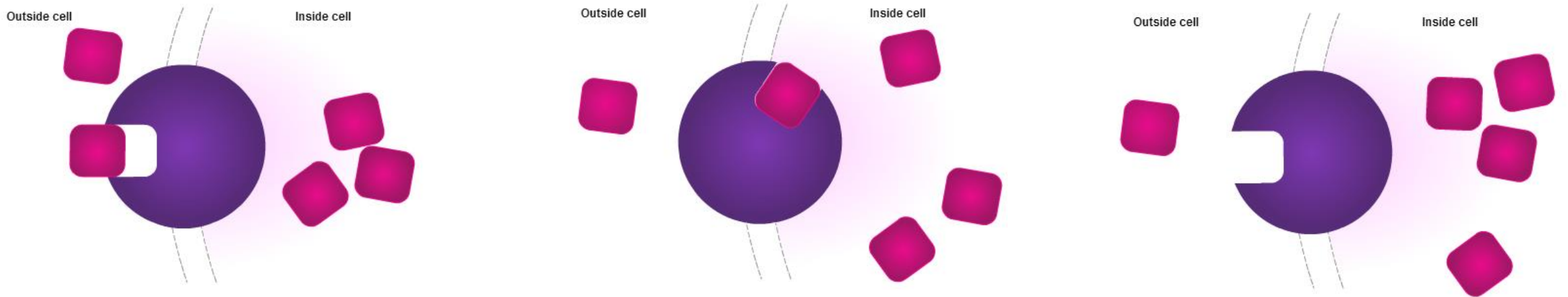


Hormones

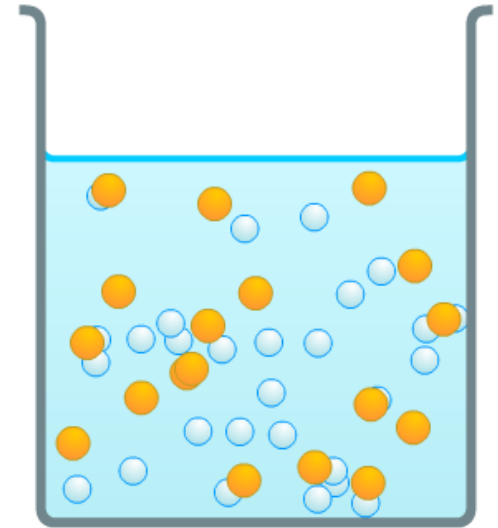
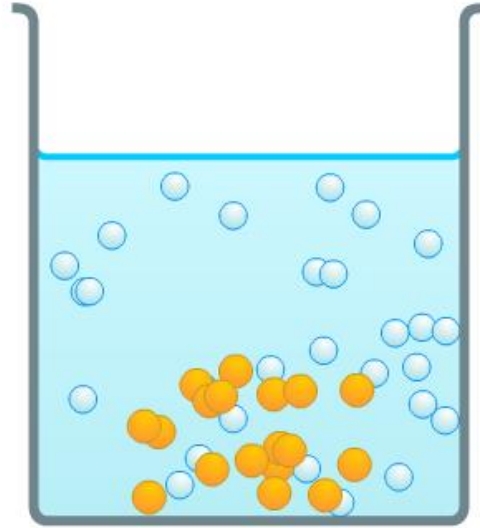
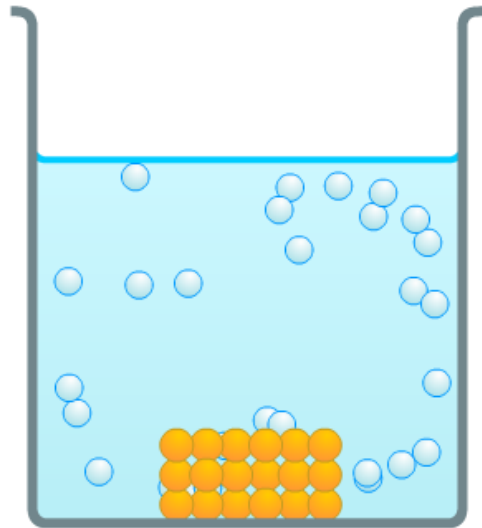


Proteins

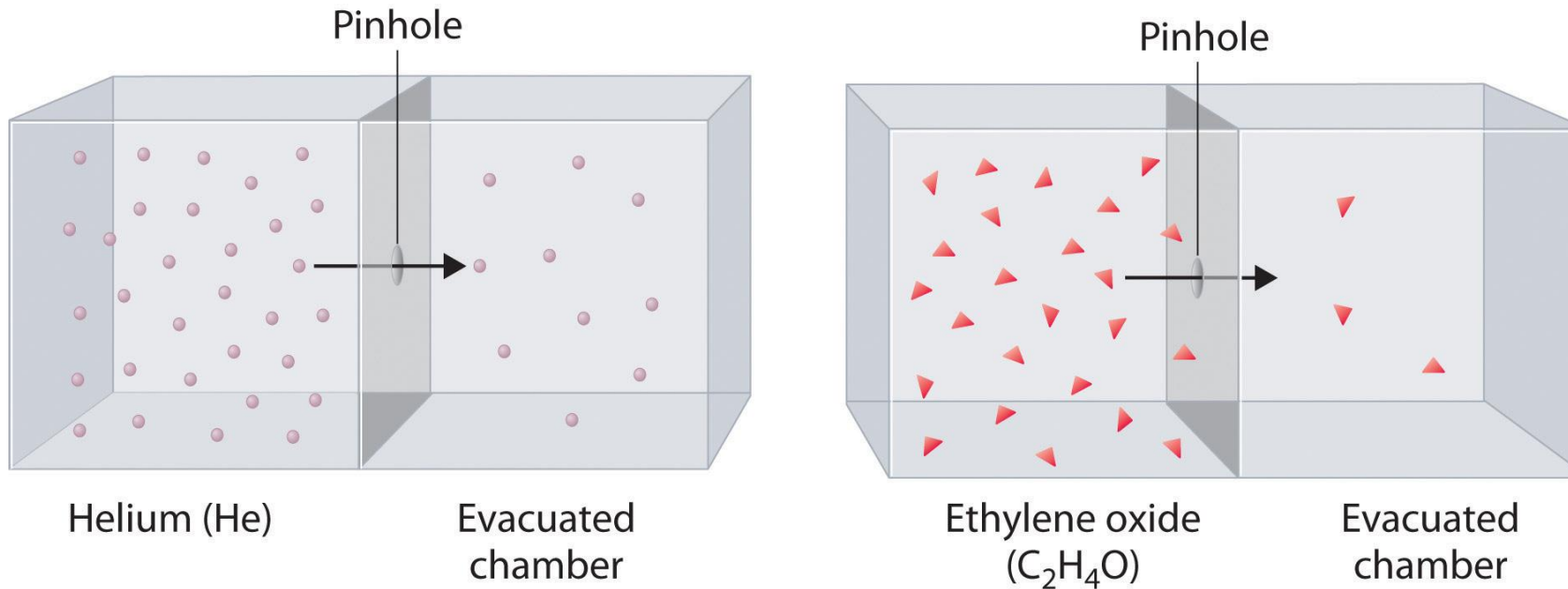
Active/Passive transport



Diffusion

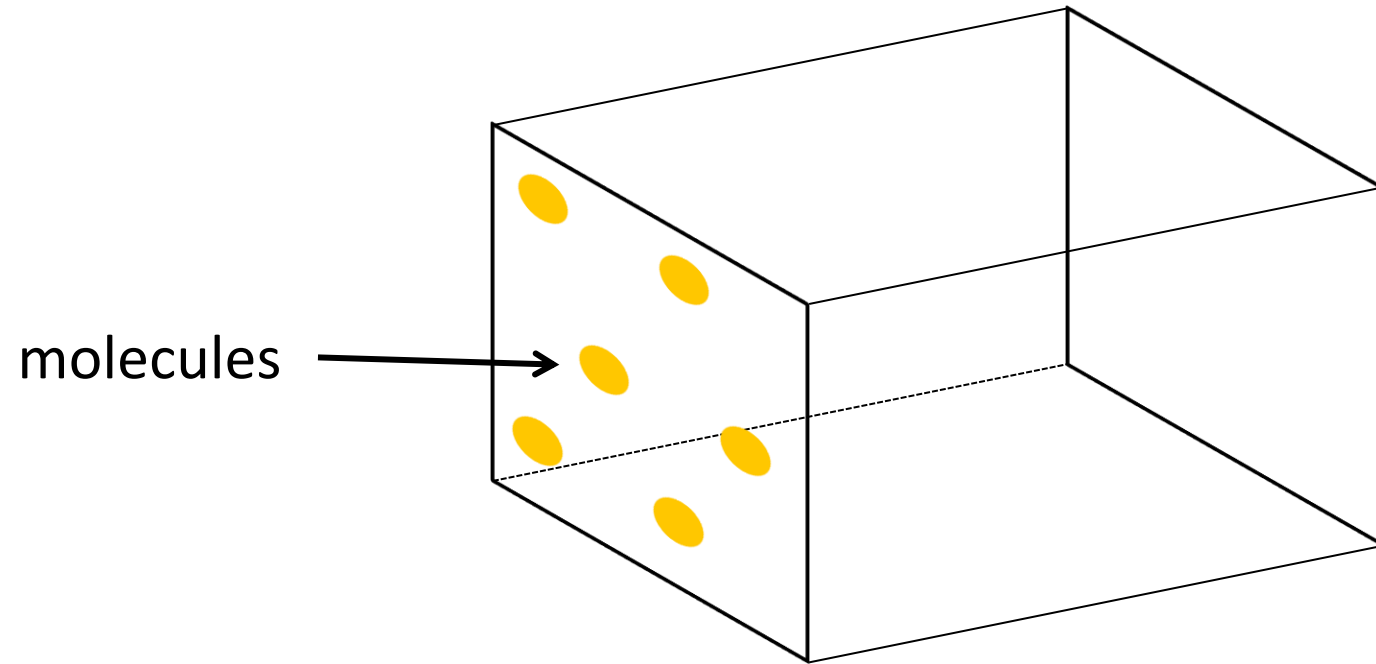


Grahams Law

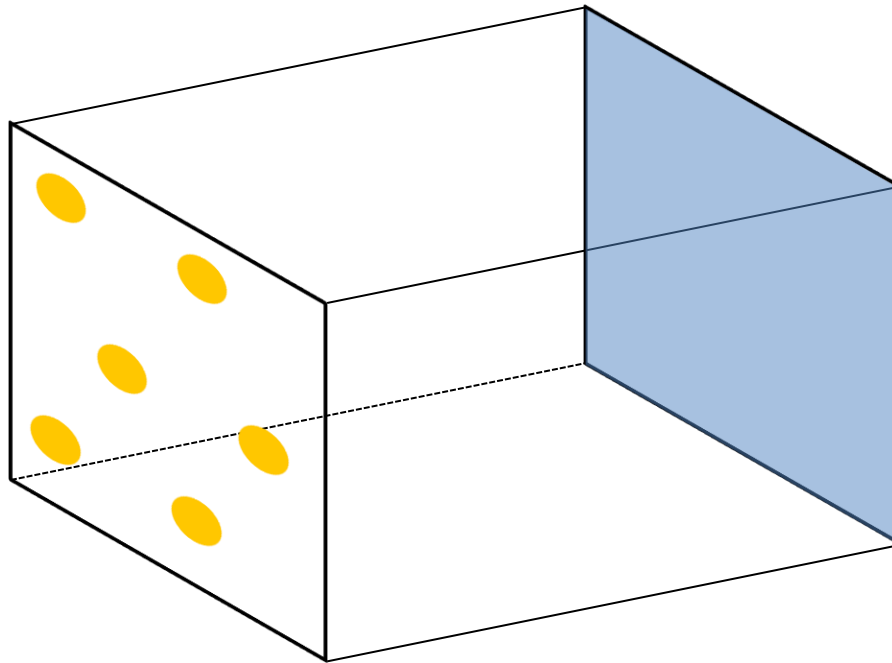


$$\frac{Rate_A}{Rate_B} = \sqrt{\frac{Molar\ Mass_B}{Molar\ Mass_A}}$$

Diffusion



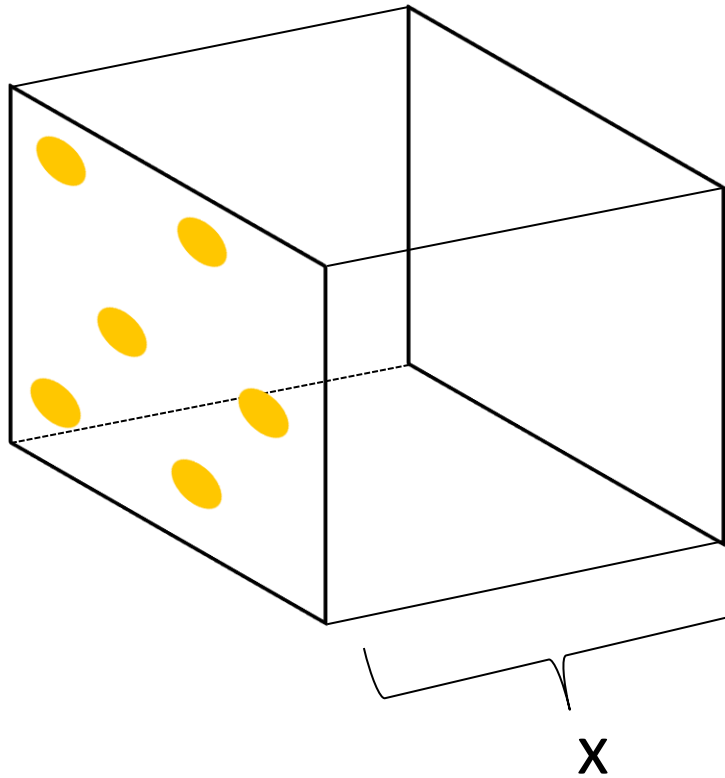
Diffusion



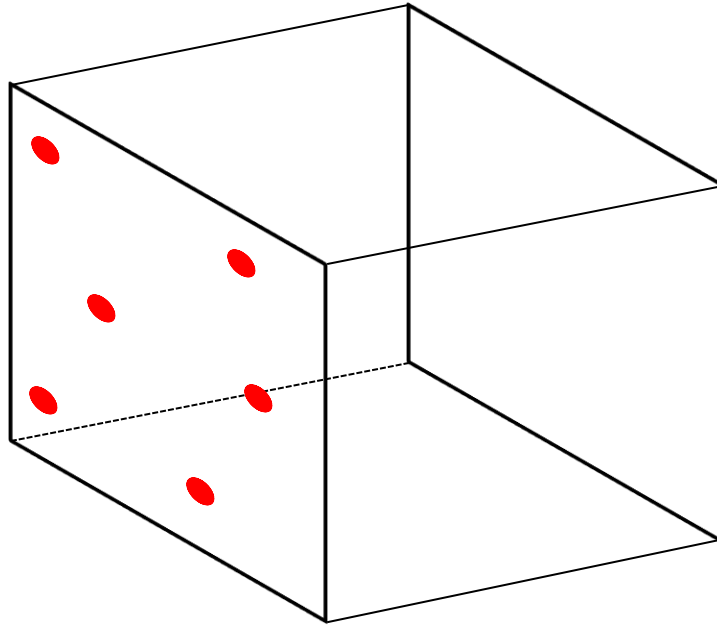
What parameters influence how many molecules move from the front side of the cube to the backside?

Diffusion

Distance x

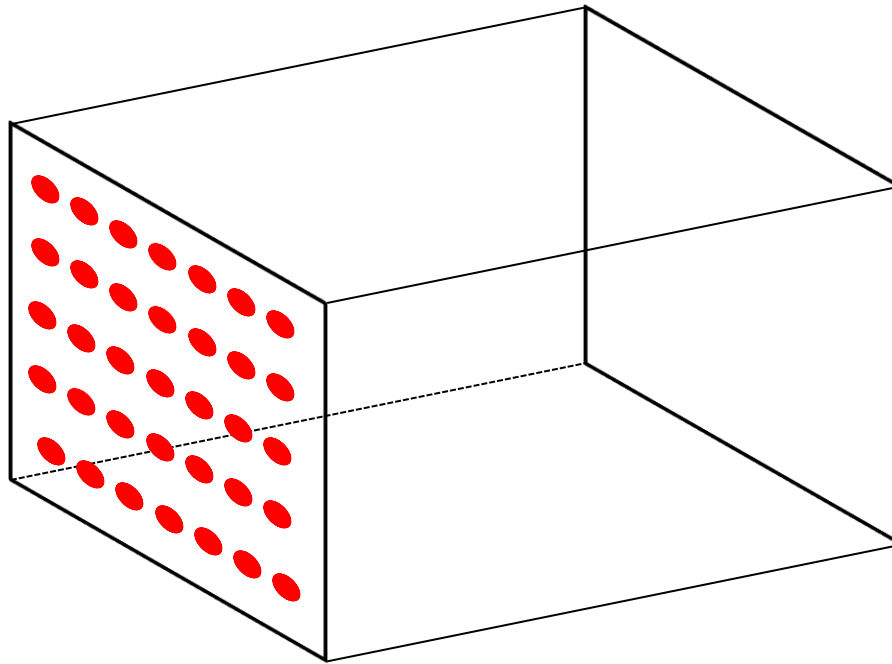


Diffusion



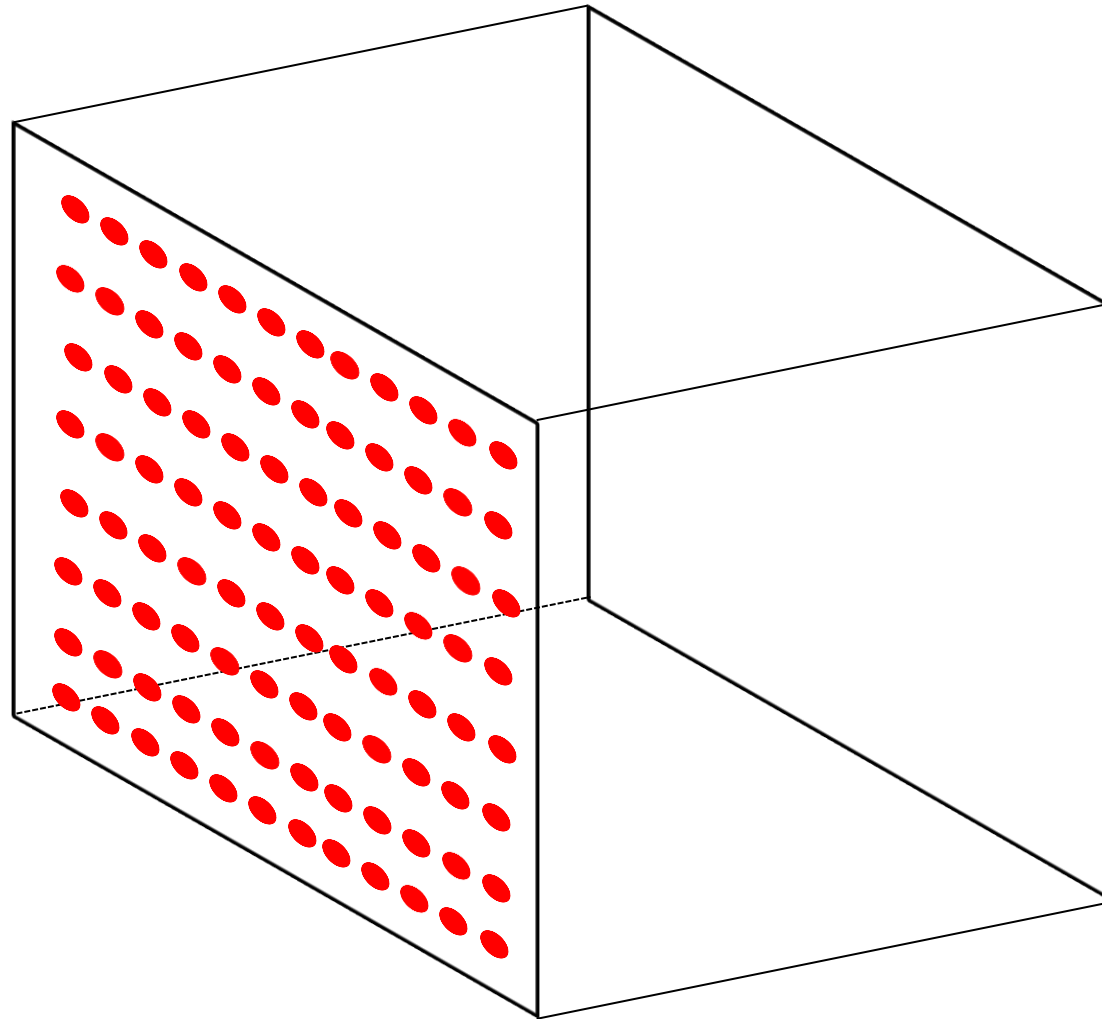
"Molar mass" D
(diffusion coefficient)

Diffusion



Density
(concentration) c

Diffusion



Area A

Ficks First Law

The rate of
change of
molecules over
time

$$\dot{V} = \frac{(c_1 - c_2) \cdot A \cdot D}{x}$$

Ficks First Law

$$\dot{V} = \frac{(c_1 - c_2) \cdot A \cdot D}{x}$$

$$\frac{\dot{V}}{A} = \frac{(c_1 - c_2)}{x} D$$

Ficks First Law

$$\dot{V} = \frac{(c_1 - c_2) \cdot A \cdot D}{x}$$

$$\frac{\dot{V}}{A} = \frac{(c_1 - c_2)}{x} D$$

Flux

Gradient

Ficks First Law

$$\dot{V} = \frac{(c_1 - c_2) \cdot A \cdot D}{x}$$

$$\frac{\dot{V}}{A} = -D \nabla c$$

Flux

Gradient

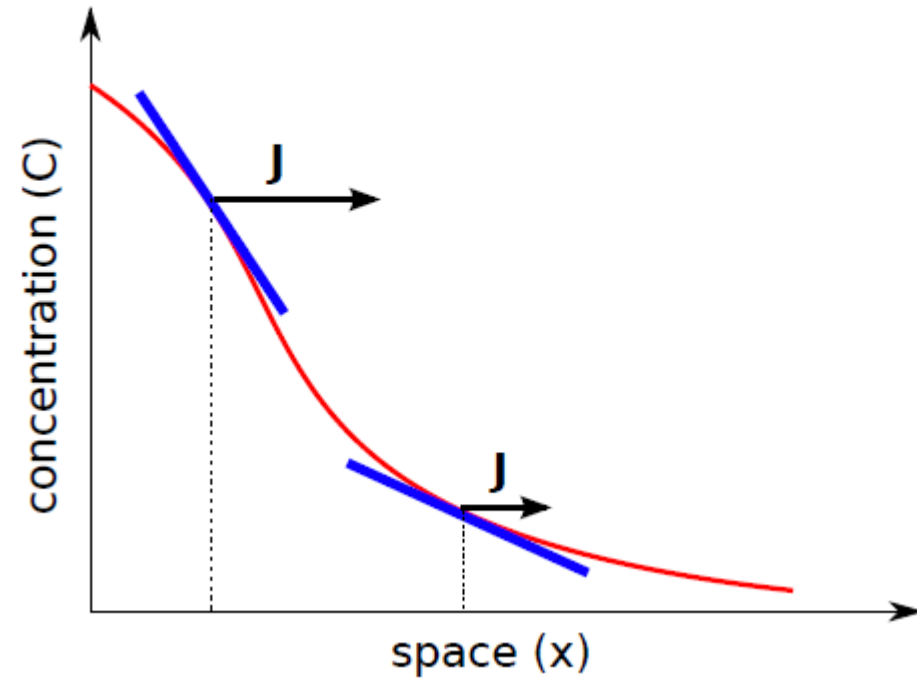
Ficks First Law

$$\dot{V} = \frac{(c_1 - c_2) \cdot A \cdot D}{x}$$

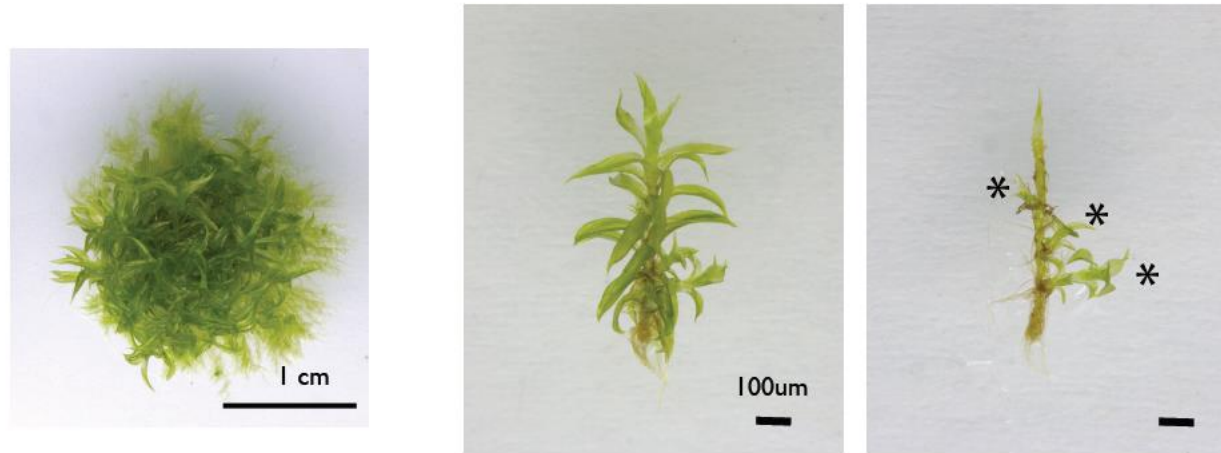
$$J = -D \nabla c$$

Flux

Gradient



Modeling Example: how is lateral branching controlled in *Physcomitrella patens*?



Coudert et al. Three ancient hormonal cues co-ordinate shoot branching in a moss. eLife 2015

Independent evolution of lateral branching



liverwort



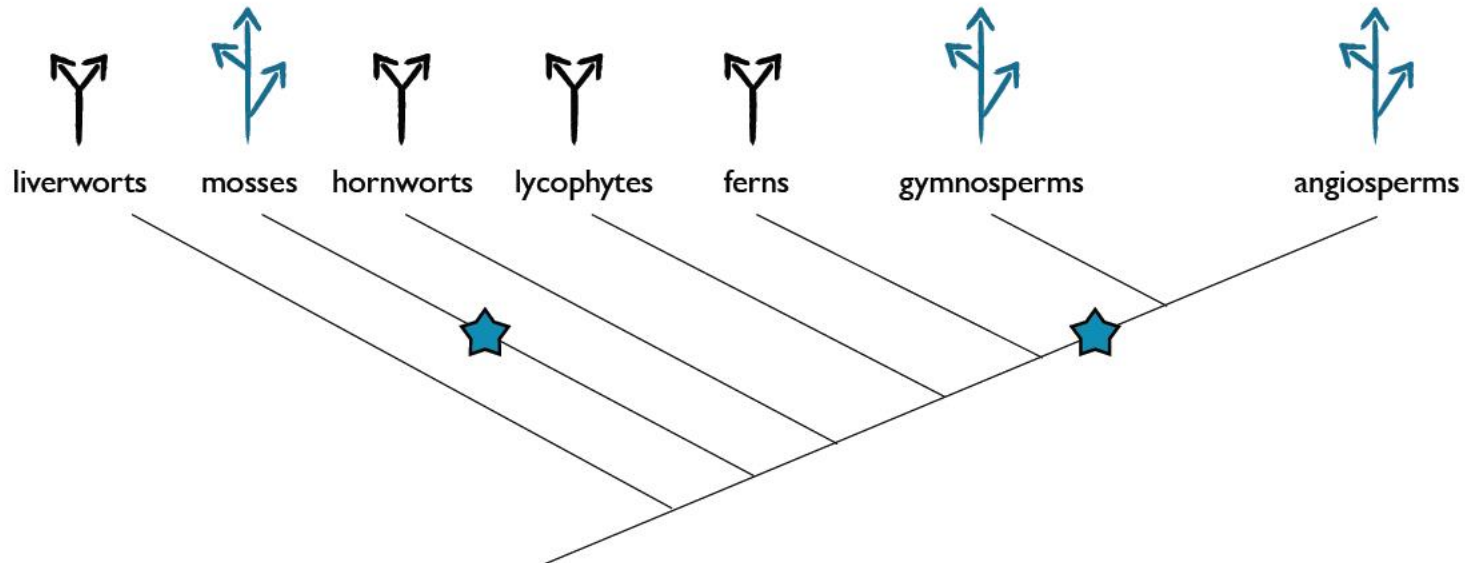
moss



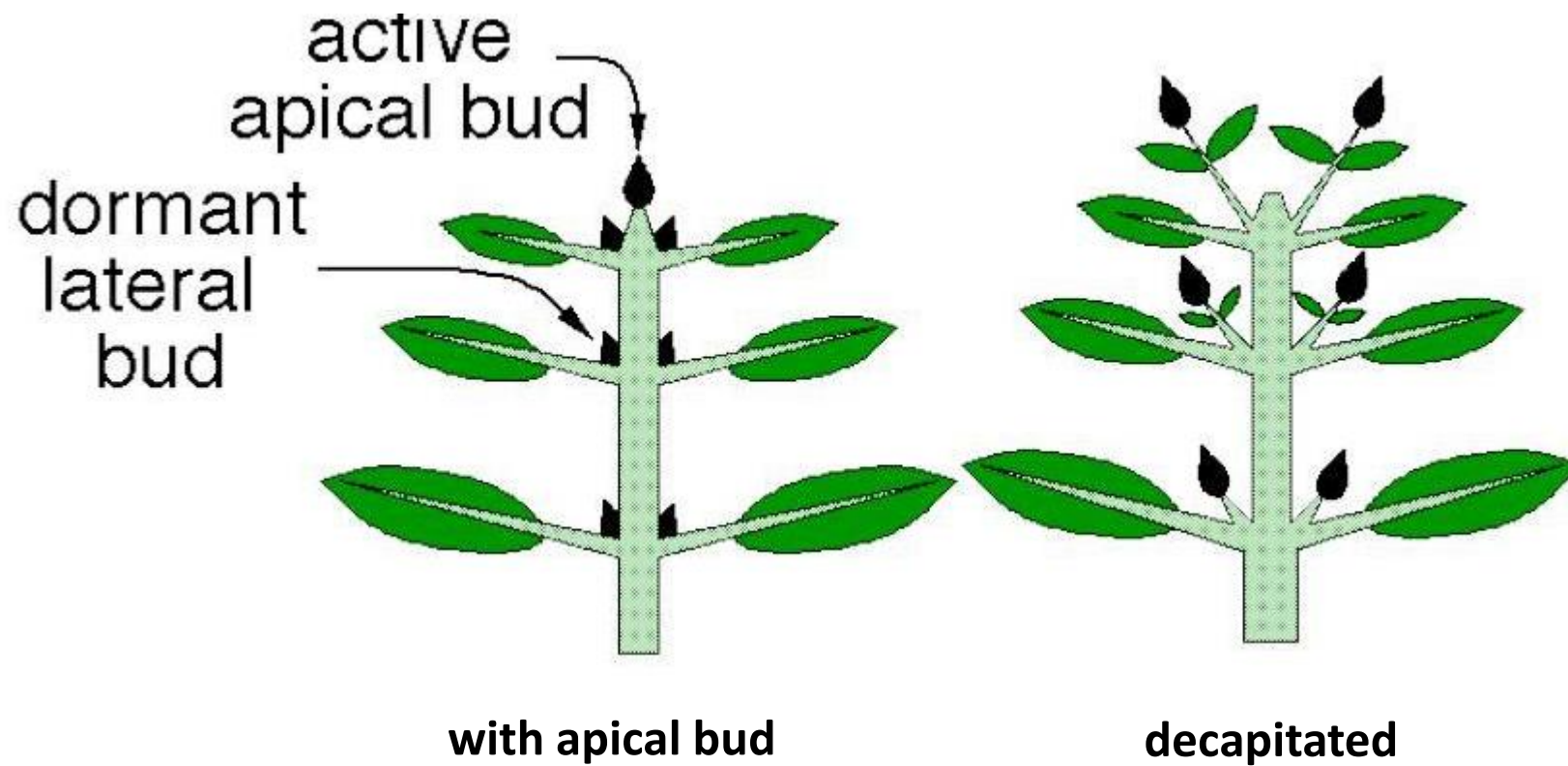
lycophyte



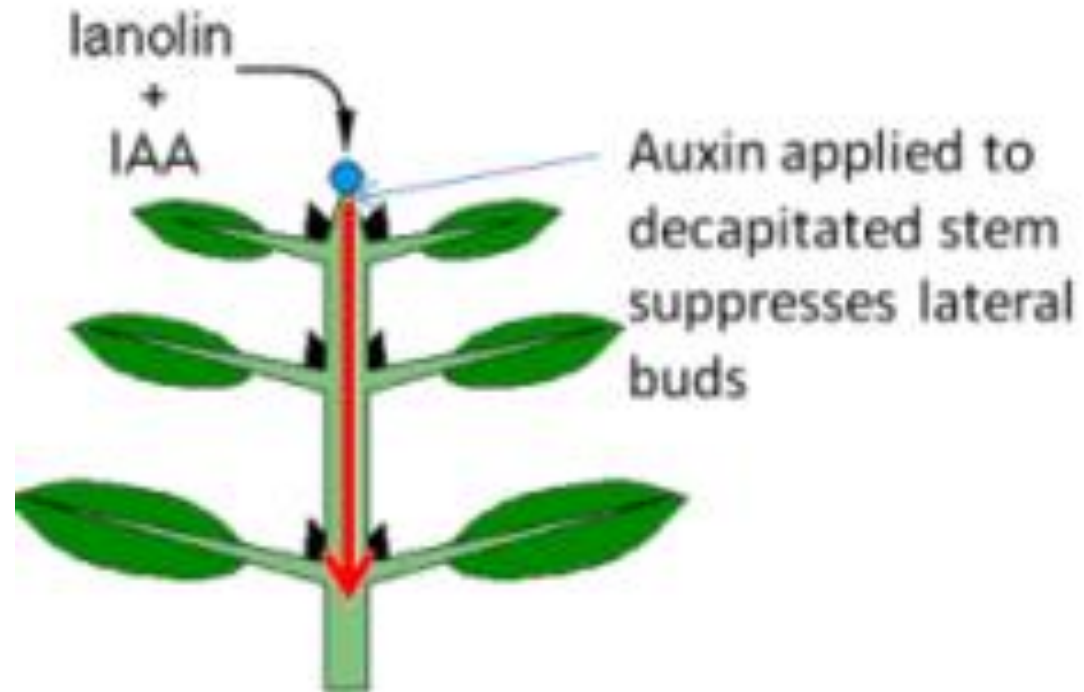
angiosperm



Apical Dominance



Auxin suppresses lateral buds



Apical dominance in moss

Decapitation experiment
performed in the moss
Splachnum ampullaceum

Treatment	Percent- age of bud reactiva- tion
Intact	0
Decapitated + water	84
Decapitated + IAA (1 mgm./ml.)	0

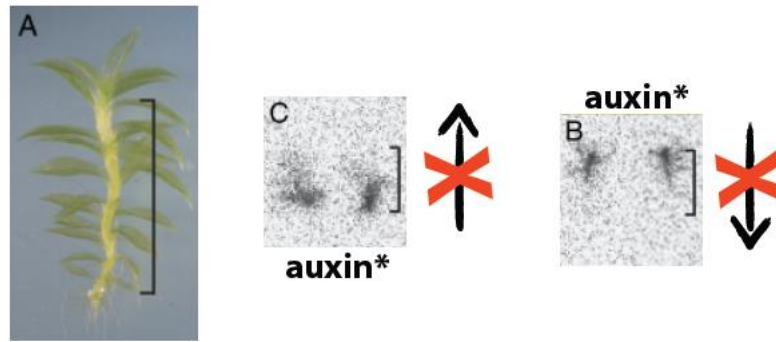
von Maltzhan et al., Nature 1959

Apical dominance in moss

Decapitation experiment
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Splachnum ampullaceum

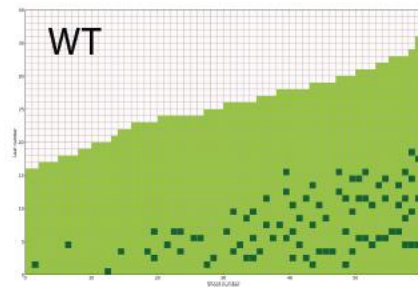
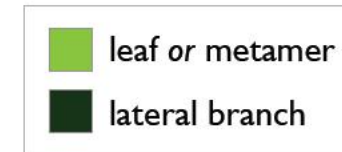
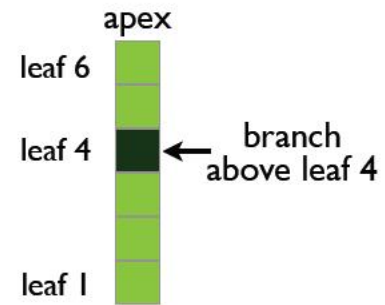
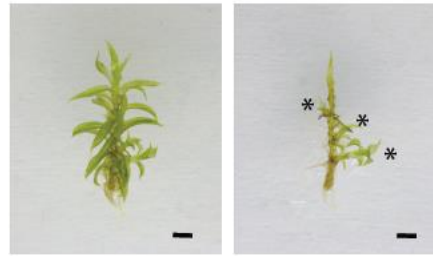
Treatment	Percent- age of bud reactiva- tion
Intact	0
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von Maltzhan et al., Nature 1959

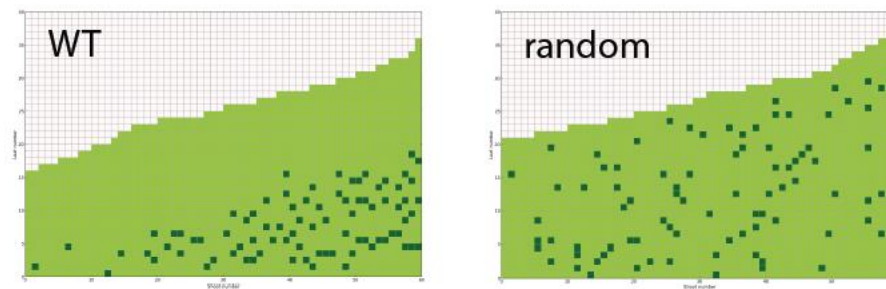
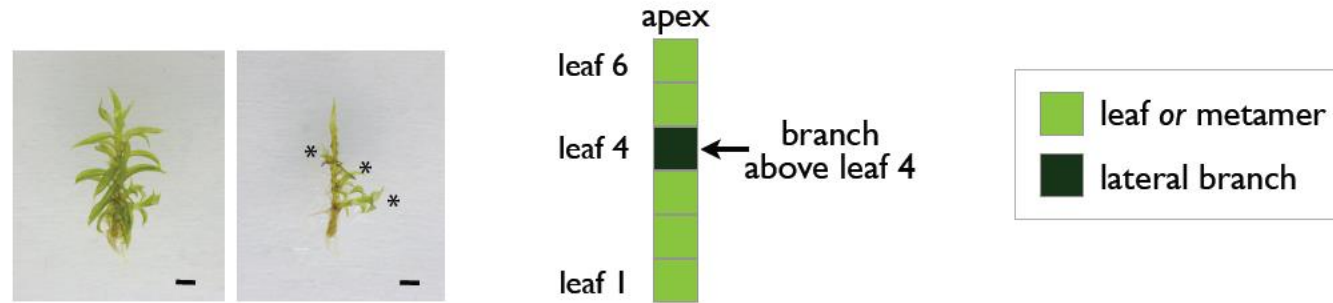


Fujita et al., Evol. Dev. 2008

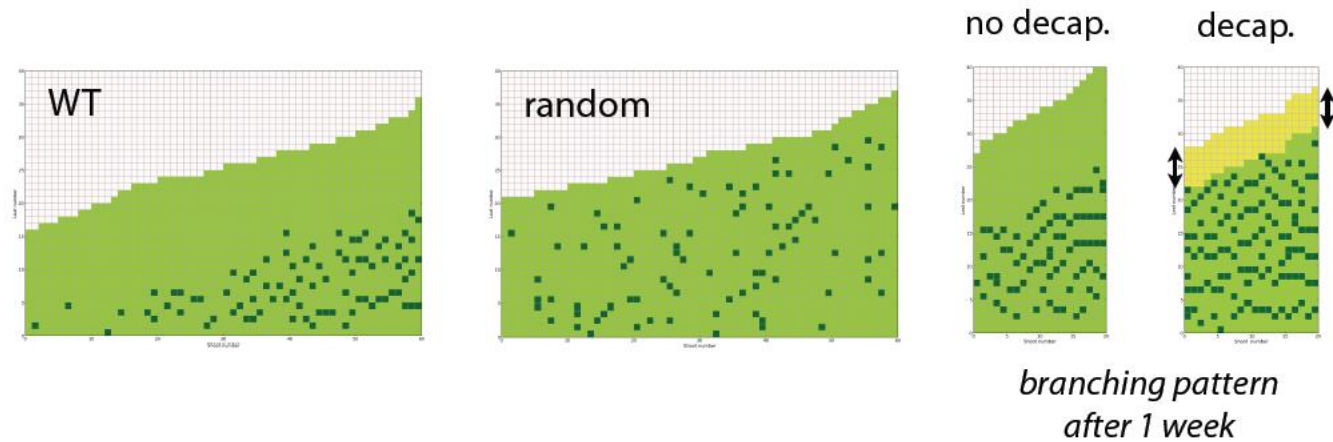
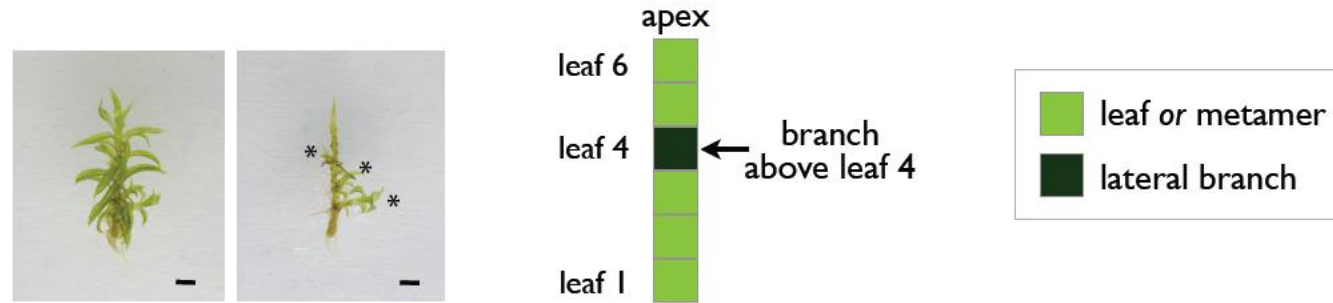
Branching inhibited by the apex



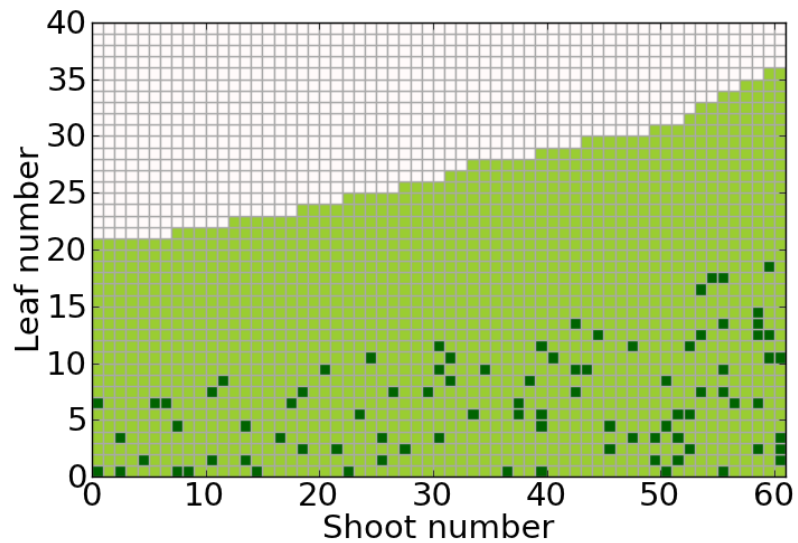
Branching inhibited by the apex



Branching inhibited by the apex

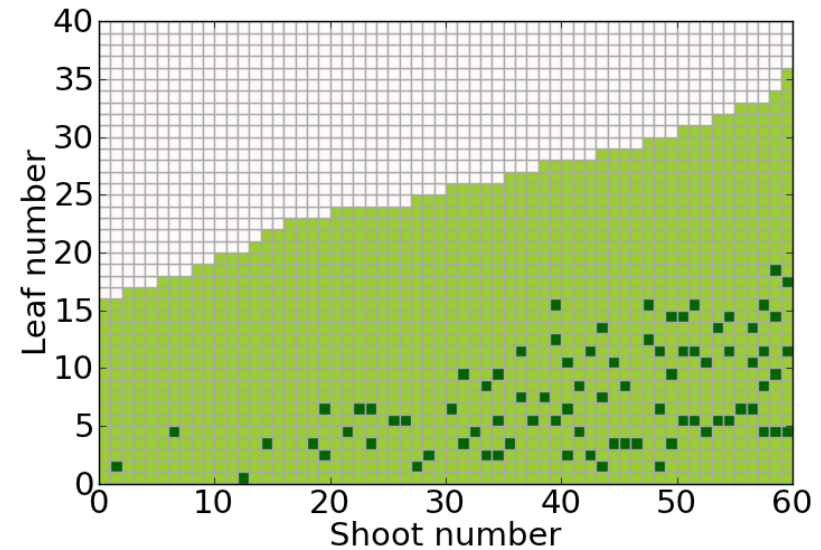


Average distance between branches



Random model:

Ave. distance between neighbors: 3.13

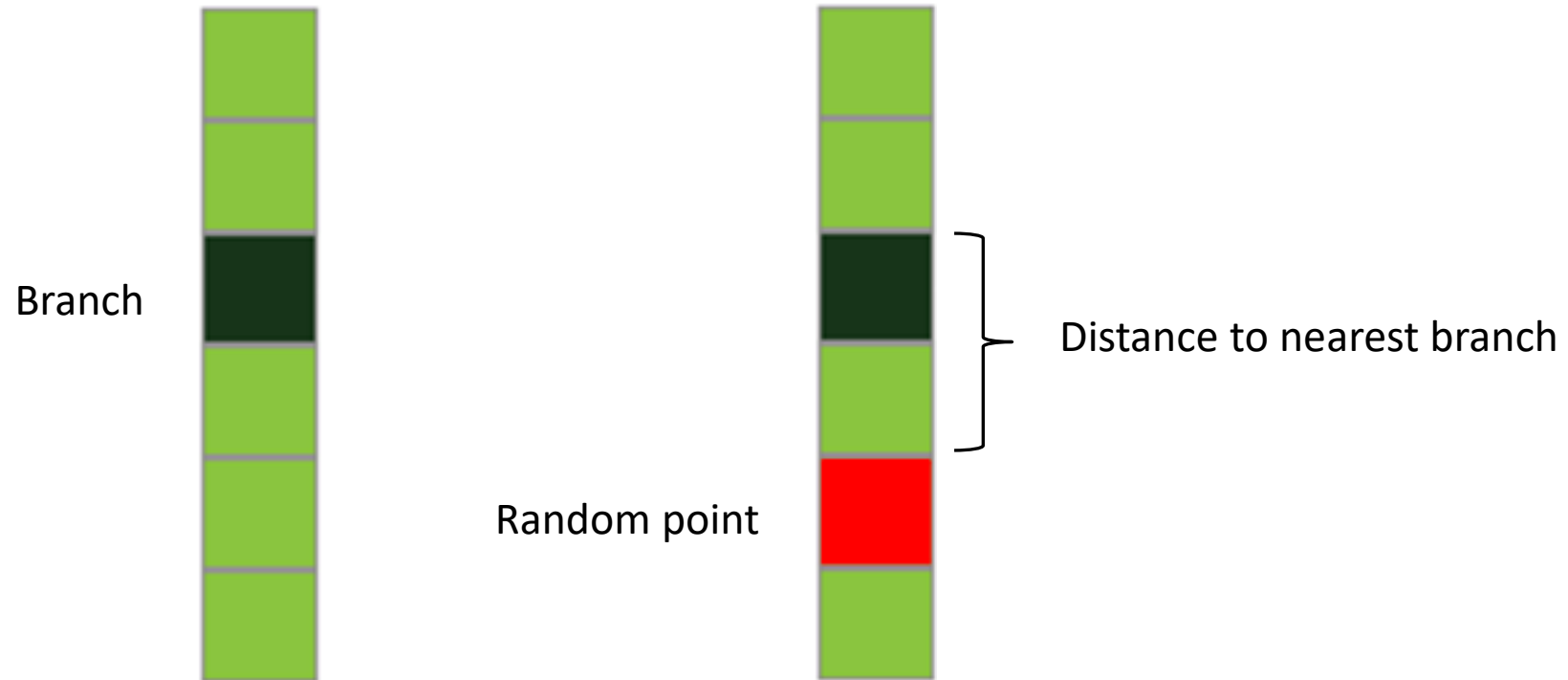


Wild-type:

Ave. distance between neighbors: 4.48

Branch distribution is over-dispersed?

- Calculate minimum distance of random points in the branching zone to real branches



Branch distribution is over-dispersed

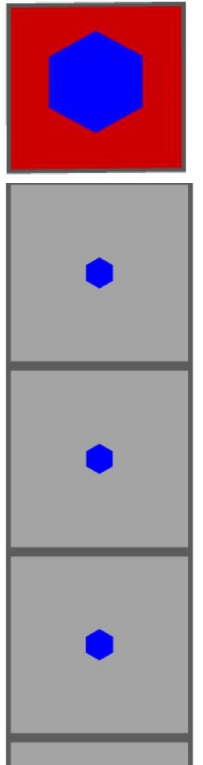
- Calculate Hopkins index:

$$H = \frac{\langle \min_i (\|x - b_i\|) \rangle_x}{\langle \min_i (\|b_j - b_i\|) \rangle_j}$$

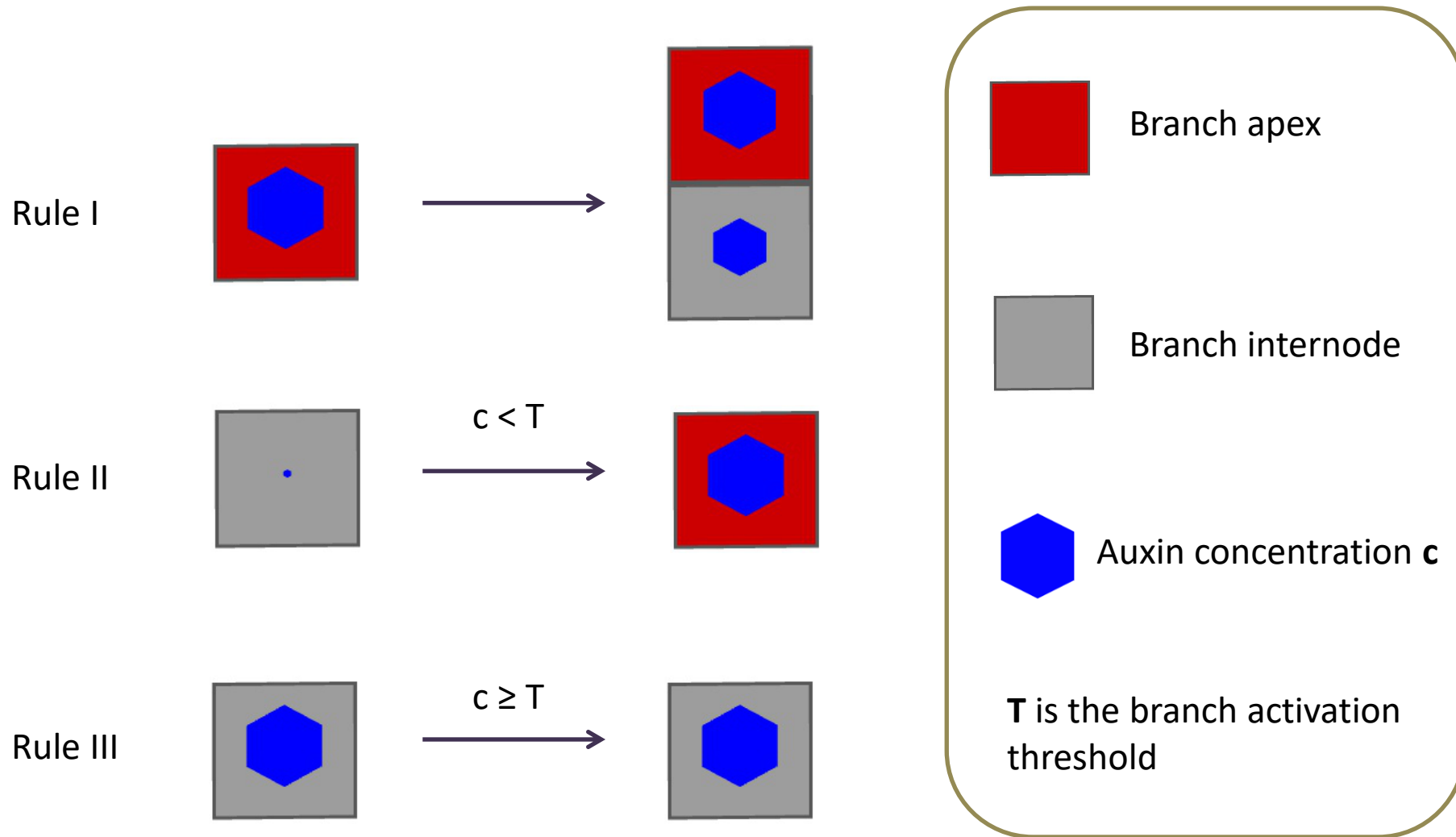
Wild-type data Hopkins Index: **0.81** ($\sigma = 0.09$)

Moss Branching Model

- Biologically
 - Apices are sources of auxin production that produce further metamers
 - Branch initiation is controlled by auxin concentration
 - How is auxin moving through the moss shoot?
- Mathematically
 - Represent mosses as a set of connected compartments
 - Each compartment expresses the local concentration of auxin

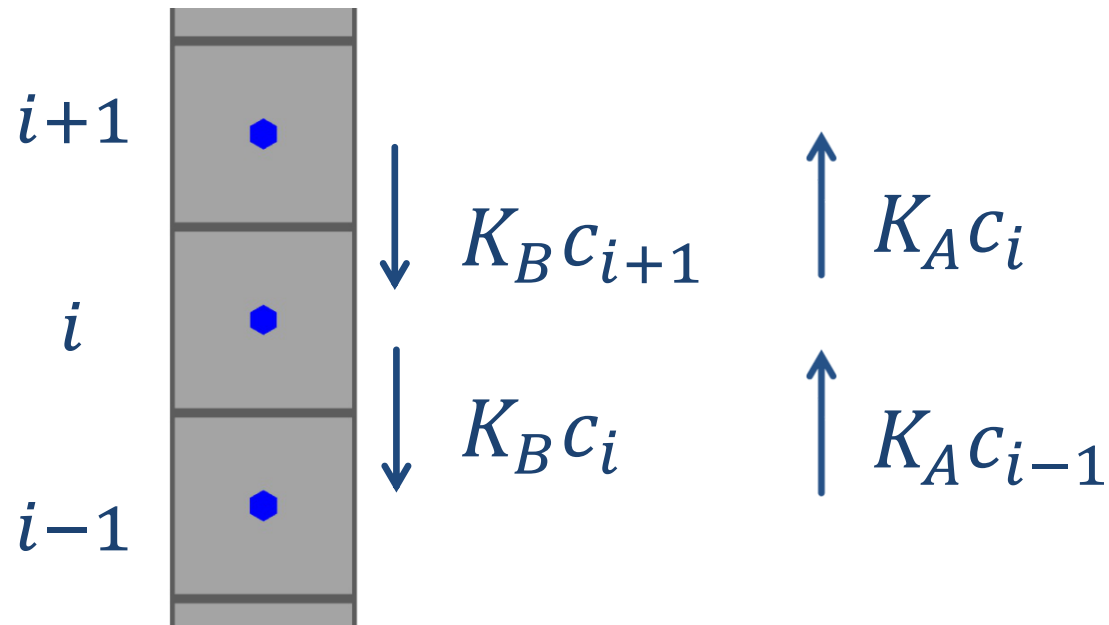


Development in the Moss Branching Model



Directional movement of auxin in the moss branching model

$$\frac{dc_i}{dt} = K_B(c_{i+1} - c_i) + K_A(c_{i-1} - c_i) - v c_i$$

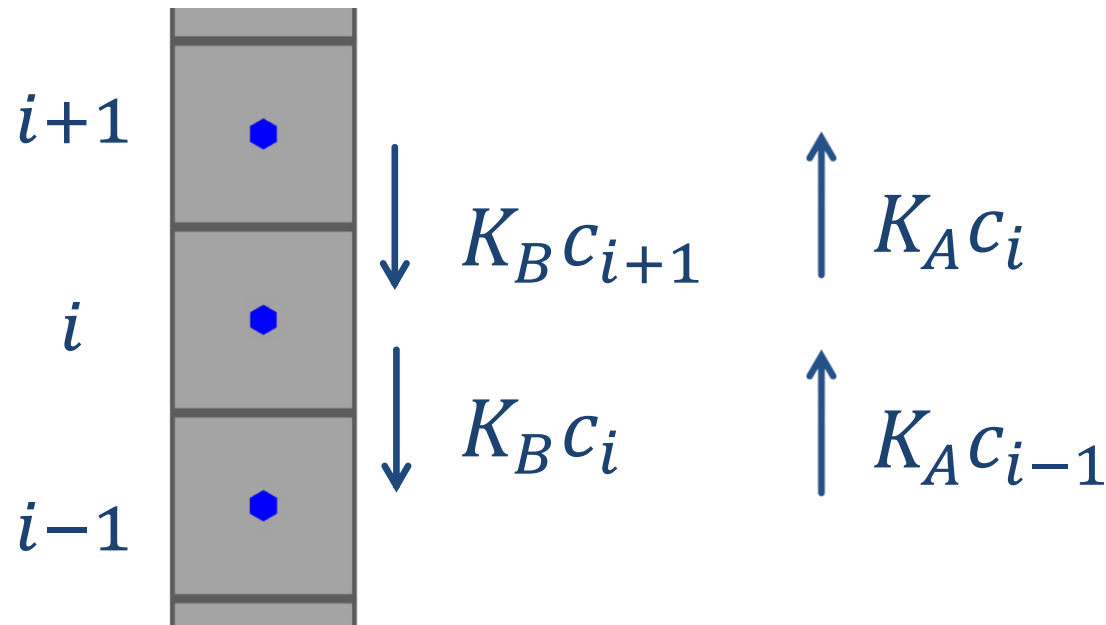


Directional movement of auxin in the moss branching model

$$\frac{dc_i}{dt} = K_B(c_{i+1} - c_i) + K_A(c_{i-1} - c_i) - vc_i$$

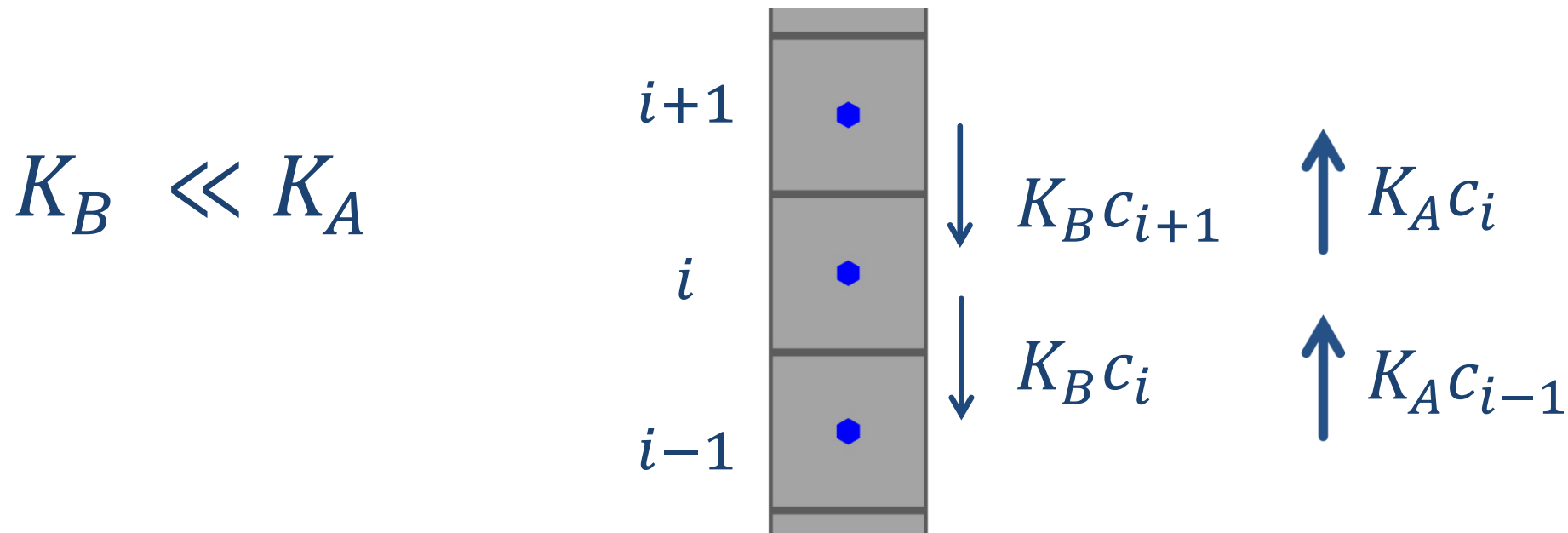
$$K_B \approx K_A$$

Diffusion



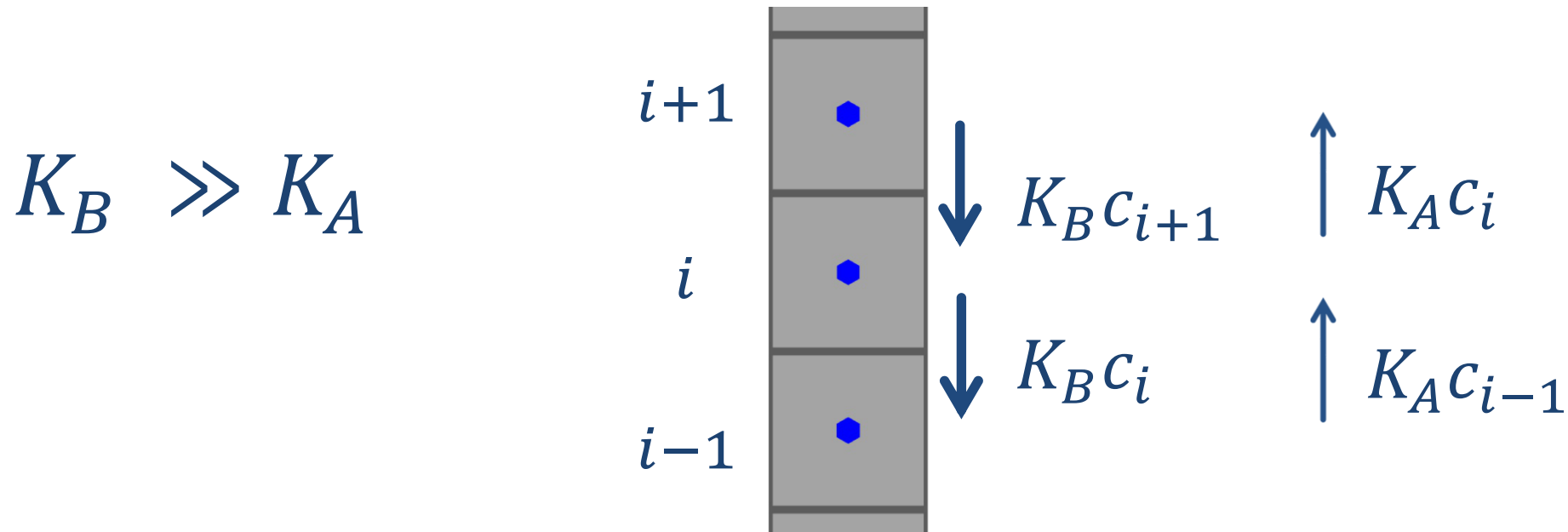
Directional movement of auxin in the moss branching model

$$\frac{dc_i}{dt} = K_B(c_{i+1} - c_i) + K_A(c_{i-1} - c_i) - vc_i$$



Directional movement of auxin in the moss branching model

$$\frac{dc_i}{dt} = K_B(c_{i+1} - c_i) + K_A(c_{i-1} - c_i) - vc_i$$



Input Parameters

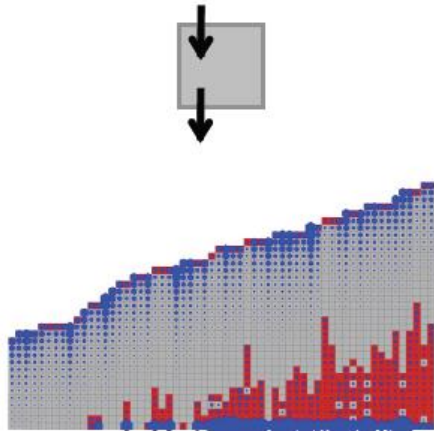
- H_{apex} is the target auxin concentration of the terminal apex (stochastic parameter)
- H is the target auxin concentration of lateral apices (stochastic parameter)
- T is the branching threshold (stochastic parameter)
- ν is the auxin concentration decay rate
- K_A and K_B determine the rate of directional auxin transport

Development and Auxin Transport



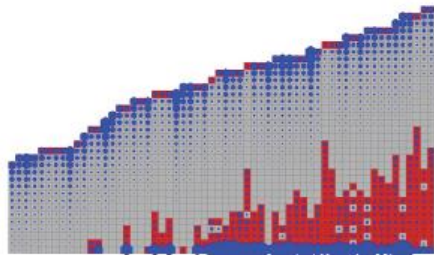
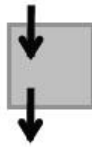
Directional movement of auxin

basipetal
auxin transport

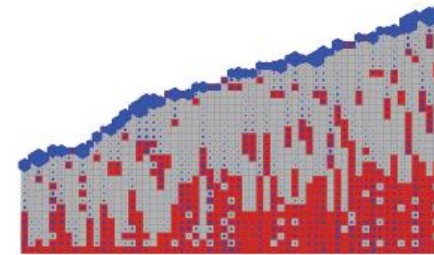
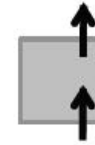


Directional movement of auxin

basipetal
auxin transport

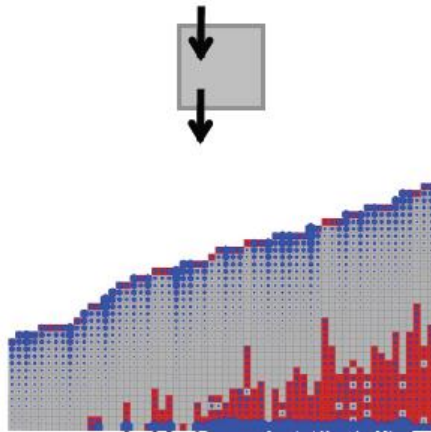


acropetal
auxin transport

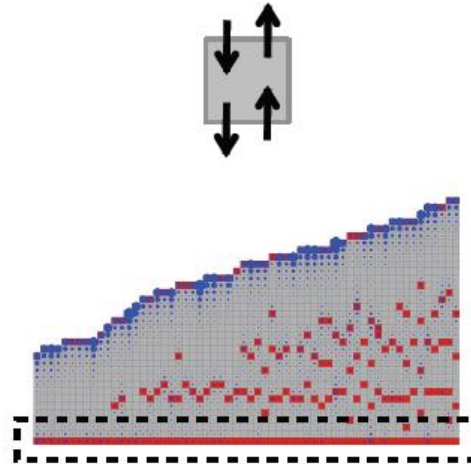


Directional movement of auxin

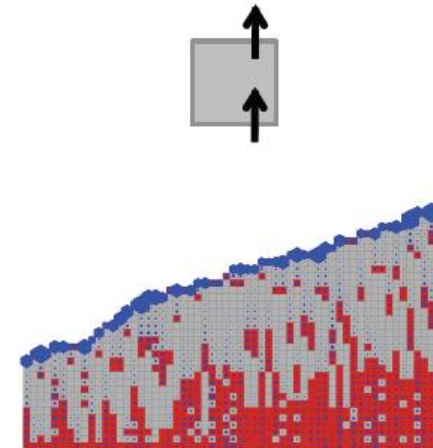
basipetal
auxin transport



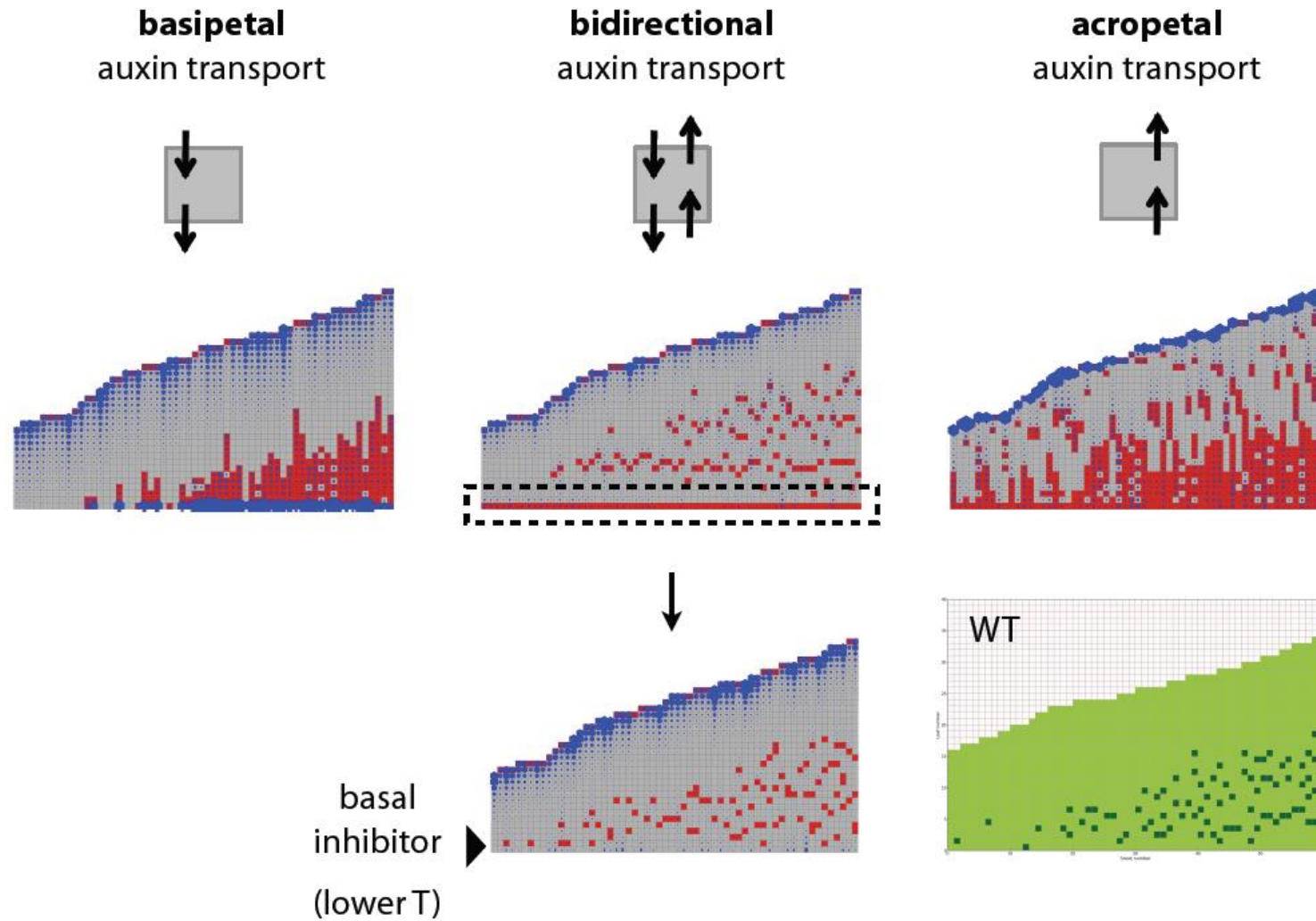
bidirectional
auxin transport



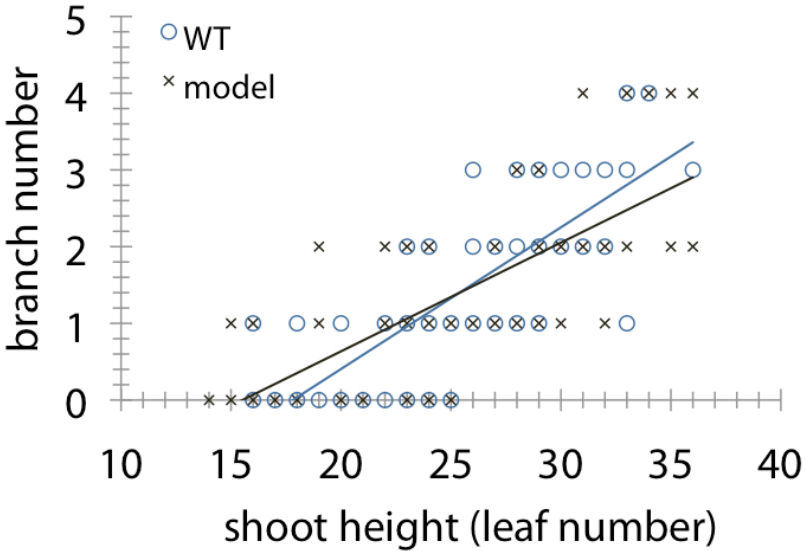
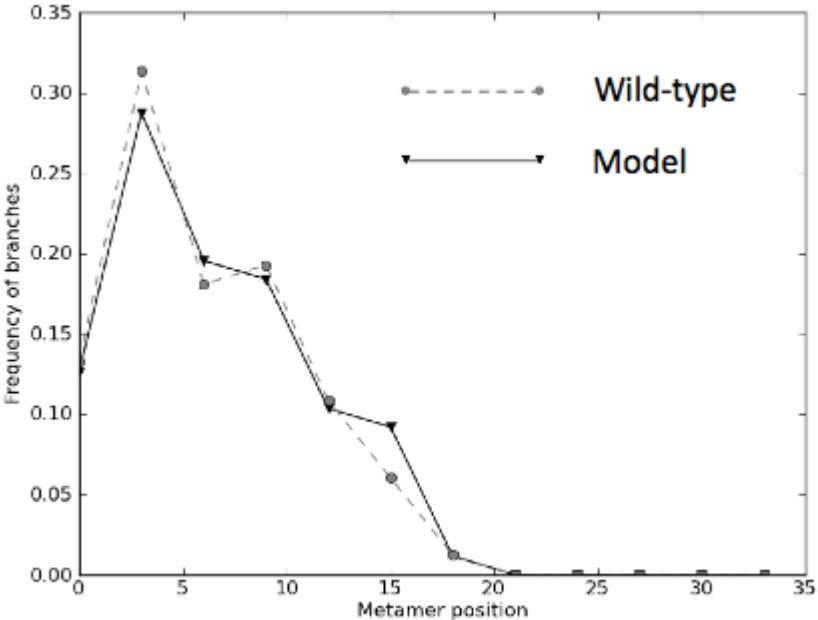
acropetal
auxin transport



Bidirectional transport model captures real data

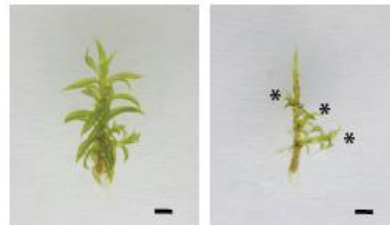
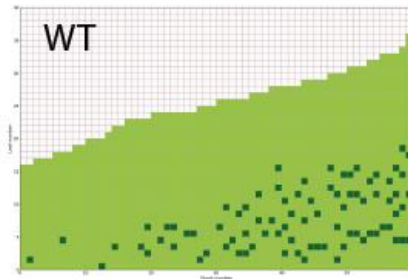
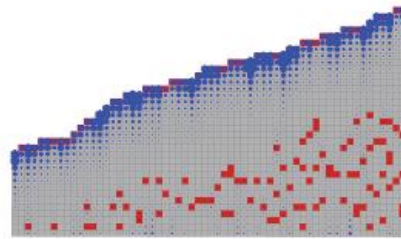


Quantitative analysis: bidirectional model



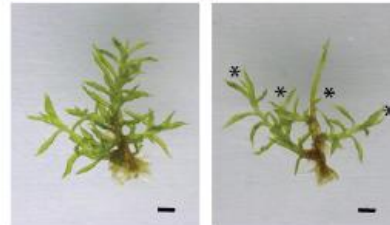
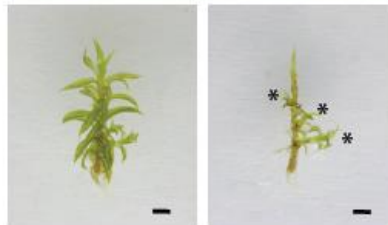
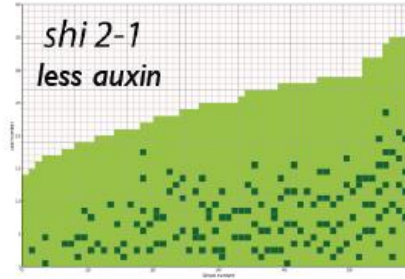
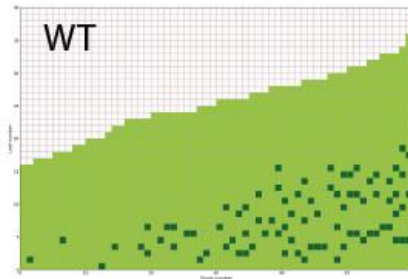
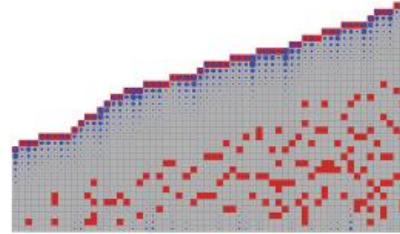
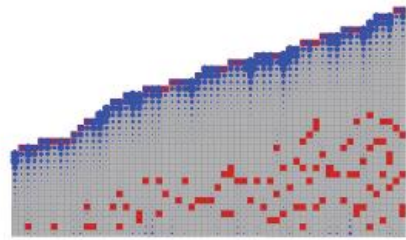
	Model	Wild-type
Branch number	87	83
Distance between branches	4.46	4.48
Apical inhibition zone	18.0	17.9

Branching patterns in altered auxin level mutants

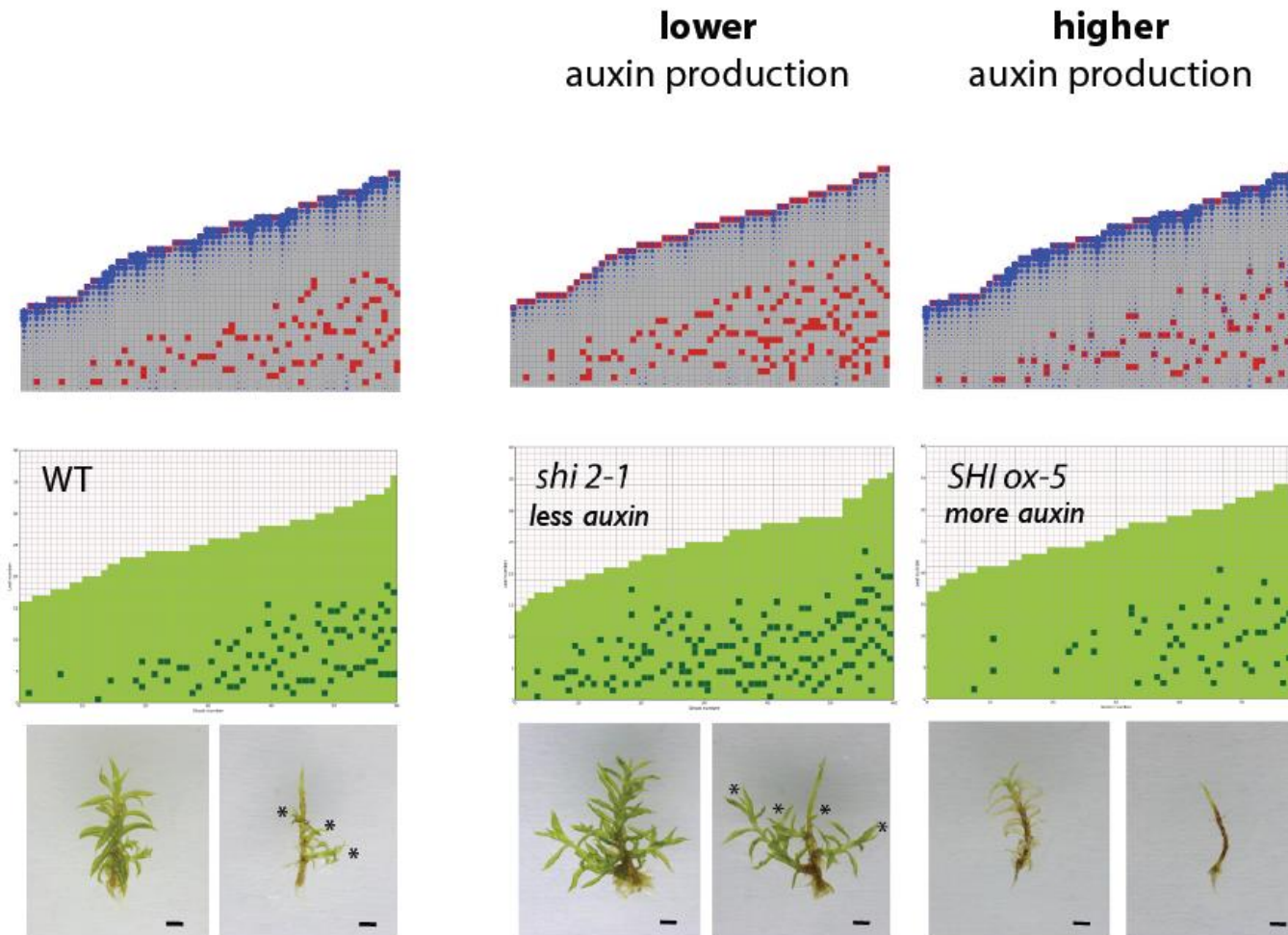


Branching patterns in altered auxin level mutants

lower
auxin production

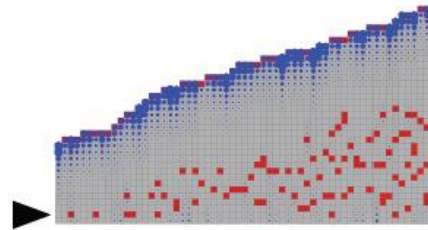


Branching patterns in altered auxin level mutants

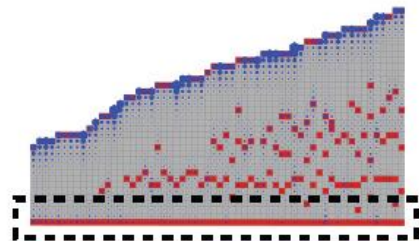


Strigolactone deficient mutant

WT with basal inhibitor
lower basal threshold

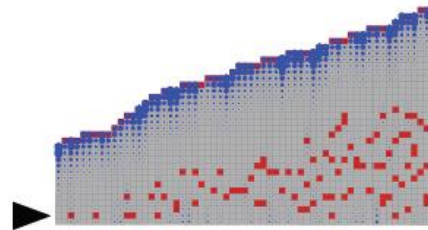


WT without basal inhibitor

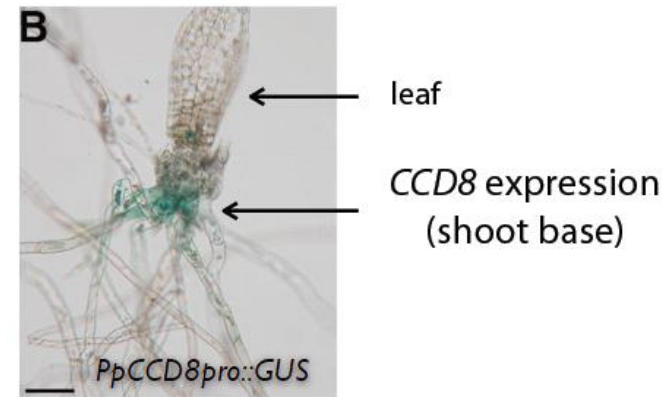
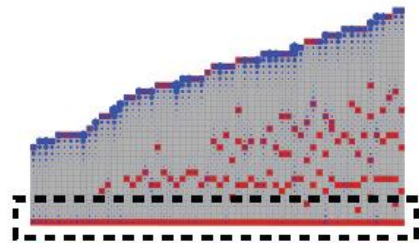


Strigolactone deficient mutant

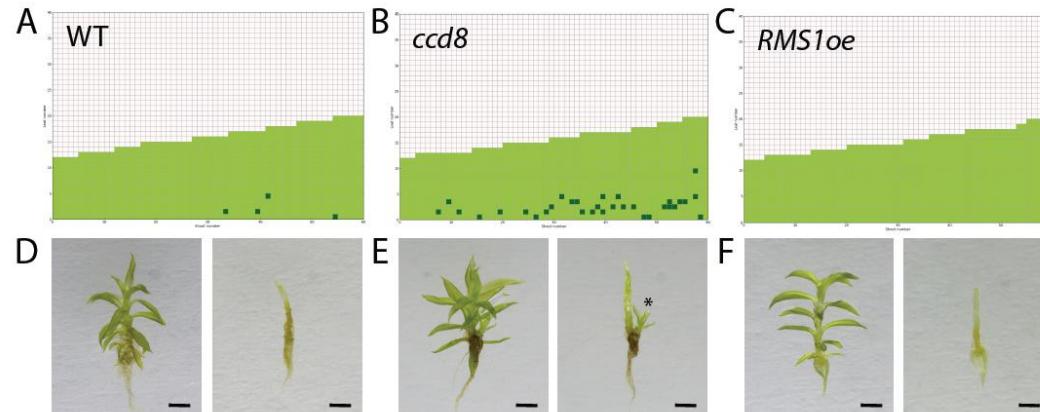
WT with basal inhibitor
lower basal threshold



WT without basal inhibitor

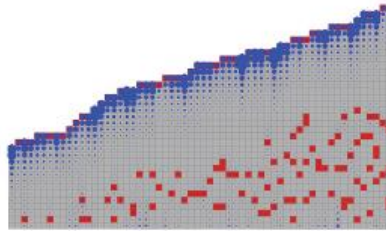


Proust et al., Development 2011

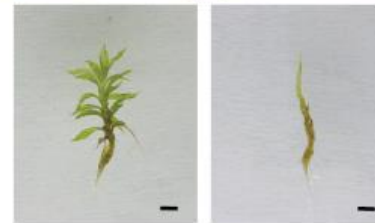
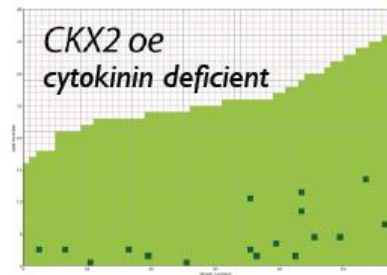
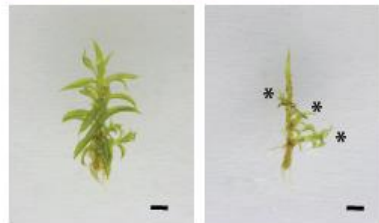
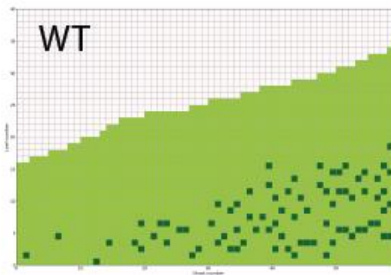
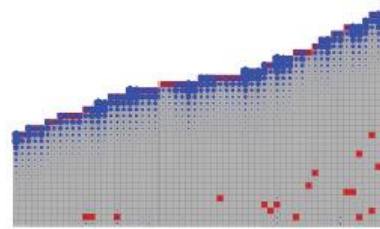


Cytokinin deficient mutant

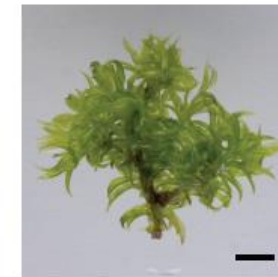
with basal inhibitor
lower basal threshold



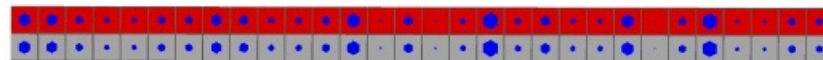
lower global threshold



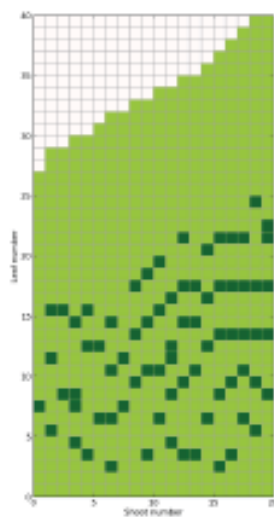
cytokinin over-producer



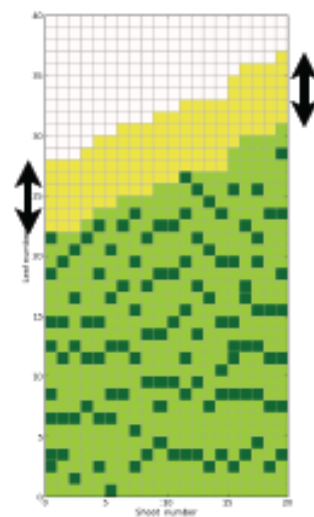
Decapitation simulation



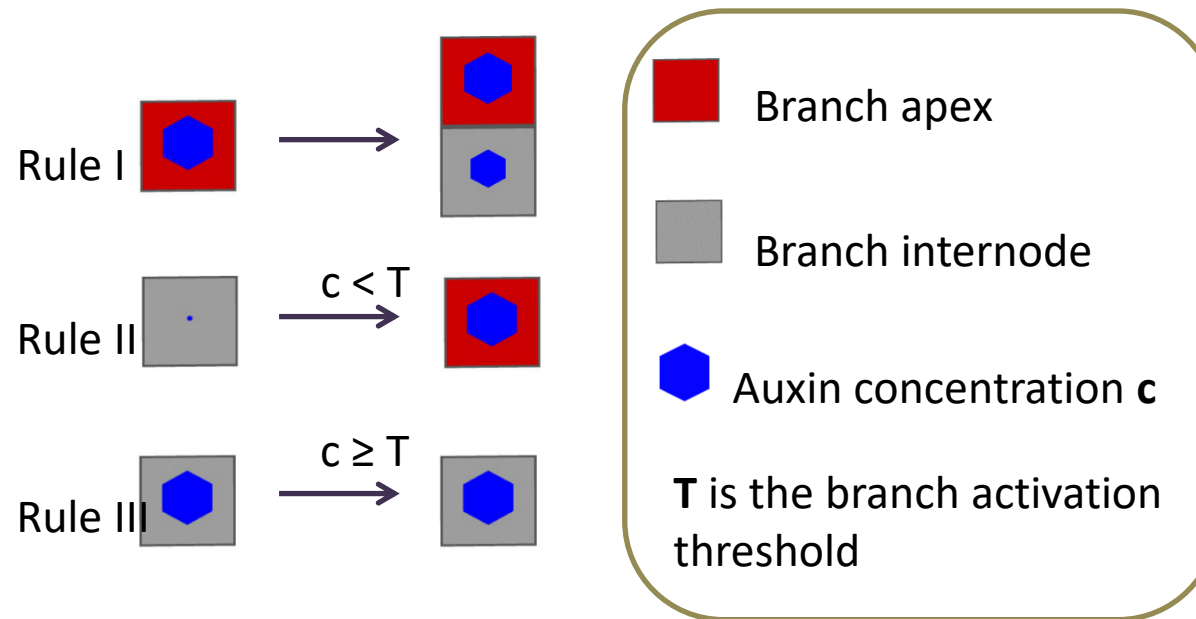
no decap.



decap.



*branching pattern
after 1 week*

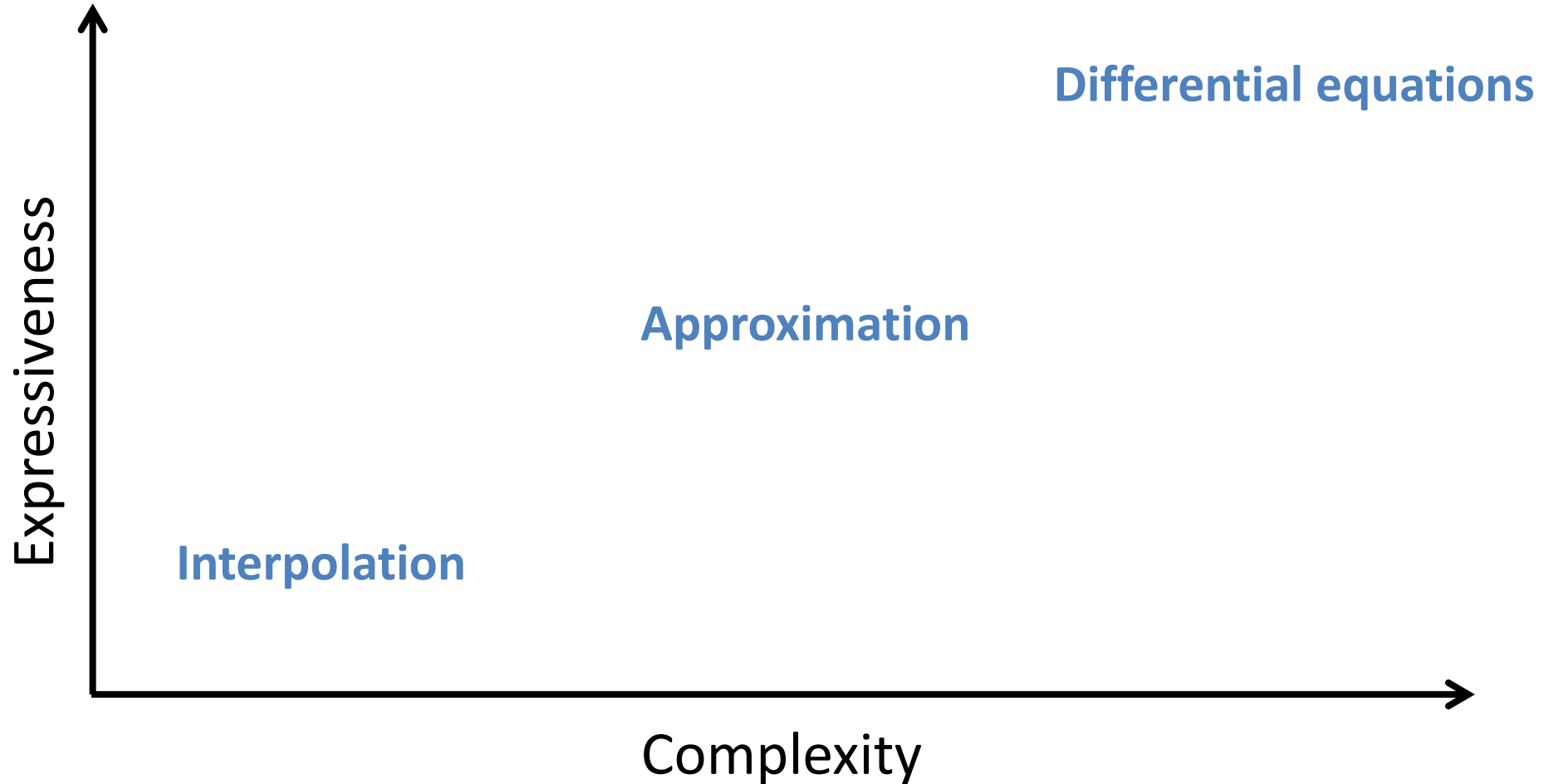


$$\frac{dc_i}{dt} = K_B(c_{i+1} - c_i) + K_A(c_{i-1} - c_i) - \nu c_i$$

Causality

- Parameter space of simple model captures branching patterns of mutant and transgenic lines:
 - Denser branching at low auxin levels
 - Sparser branching at high auxin levels
 - **Local** and **global thresholds** of branching capture effects of **cytokinin** and **strigolactones**
- Auxin, cytokinin and strigolactones control major aspects of branching patterns in *Physcomitrella patens*

Data Models



Group Presentation 25th May during lecture

- Present an example of a diffusion model from any topic (max 10 minutes, slides, topics must be unique, 3 people). The example must have a python implementation associated with it that you include and describe in the presentation. Explain the python libraries used, the diffusion model and the results.
- https://docs.google.com/spreadsheets/d/1HnV9assGZBdS1AaV_JTCz2LXRKe0TH0cFdyWYaMSDRc/edit?usp=sharing