

Combining morphodynamics, hormone signaling, and cell differentiation in computational models

Young scientist school on *Bioinformatics and Systems Biology*
Novosibirsk, 28-29 June, 2010

Henrik Jönsson
Computational Biology & Biological Physics



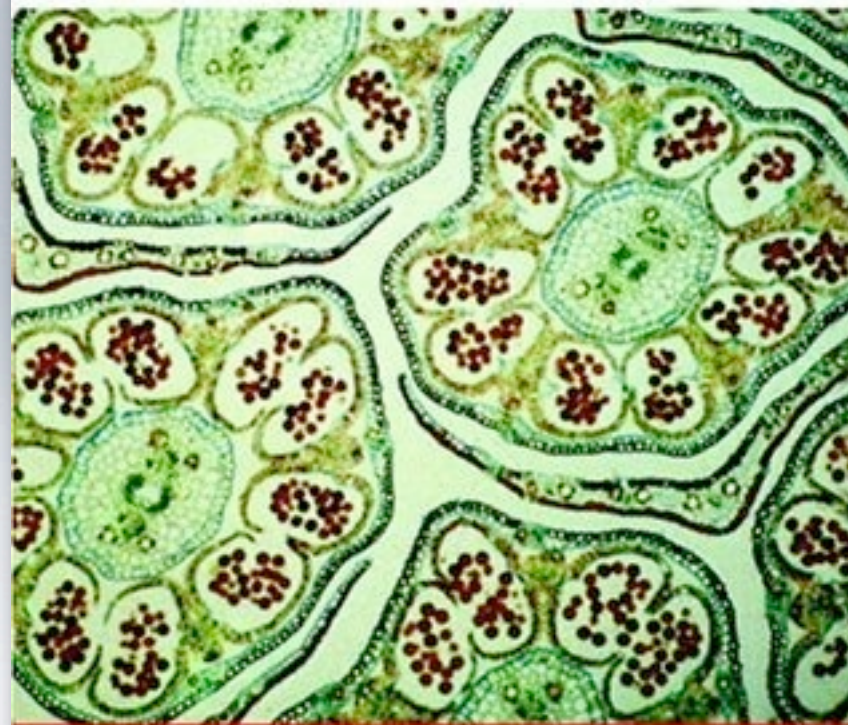
LUND UNIVERSITY

what is life?

what is life?

What is Life?
with *Mind and Matter*
and *Autobiographical*
Sketches

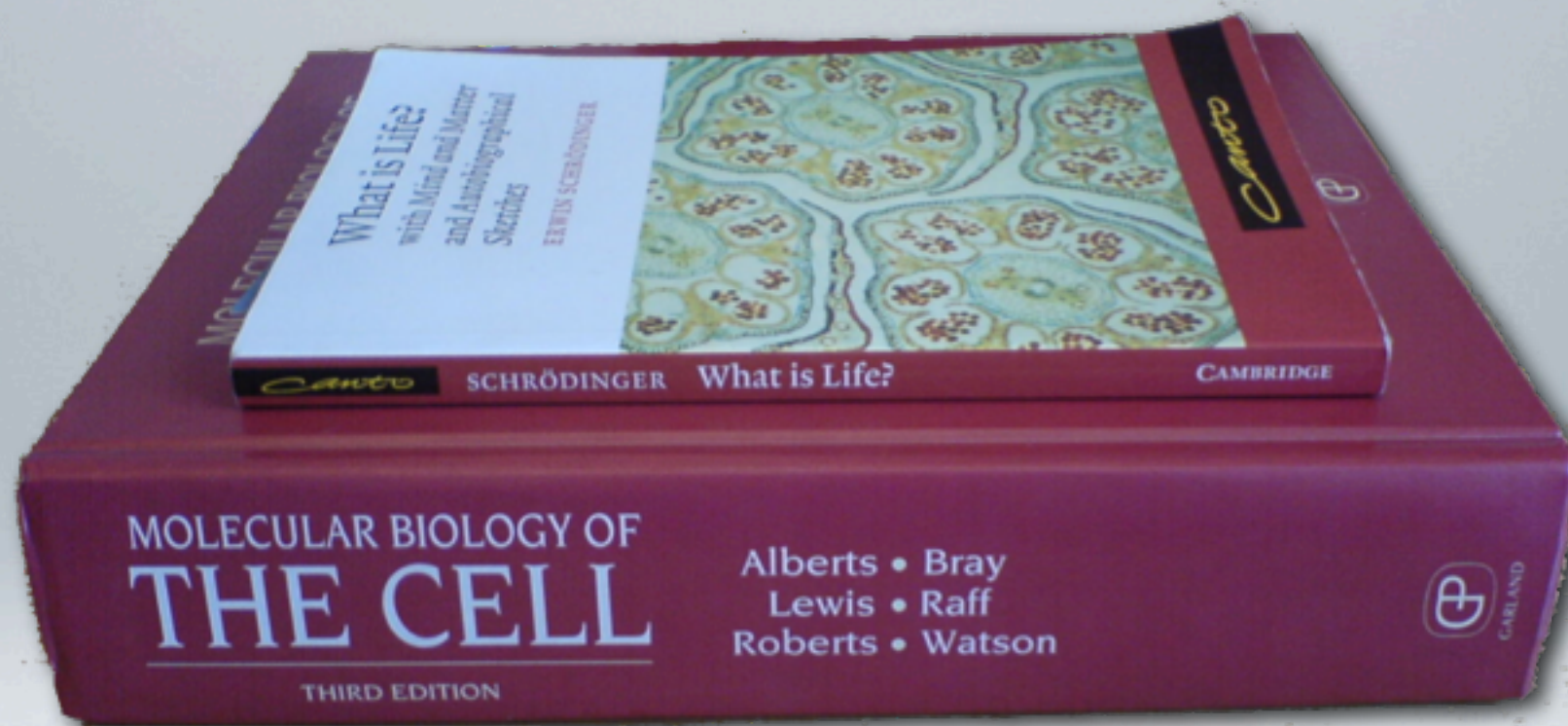
ERWIN SCHRÖDINGER



Canto

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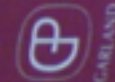
what is life?



MOLECULAR BIOLOGY OF
THE CELL

THIRD EDITION

Alberts • Bray
Lewis • Raff
Roberts • Watson



GARLAND

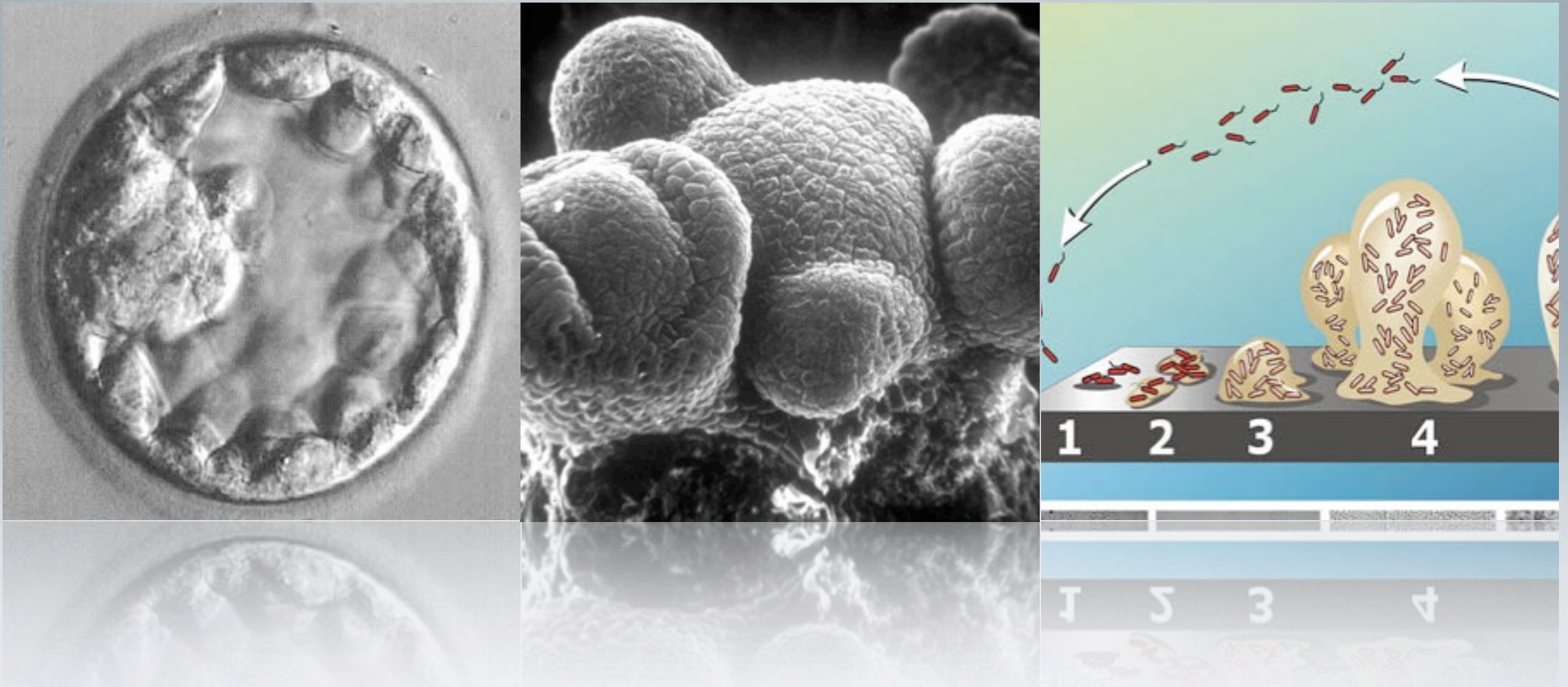
THIRD EDITION
THE CELL
MOLECULAR BIOLOGY OF

Roberts • Watson
Lewis • Raff
Alberts • Bray



GARLAND

the problem



How can differentiation and morphogenesis be regulated in an correlated fashion in multicellular systems?

Plants vs animals



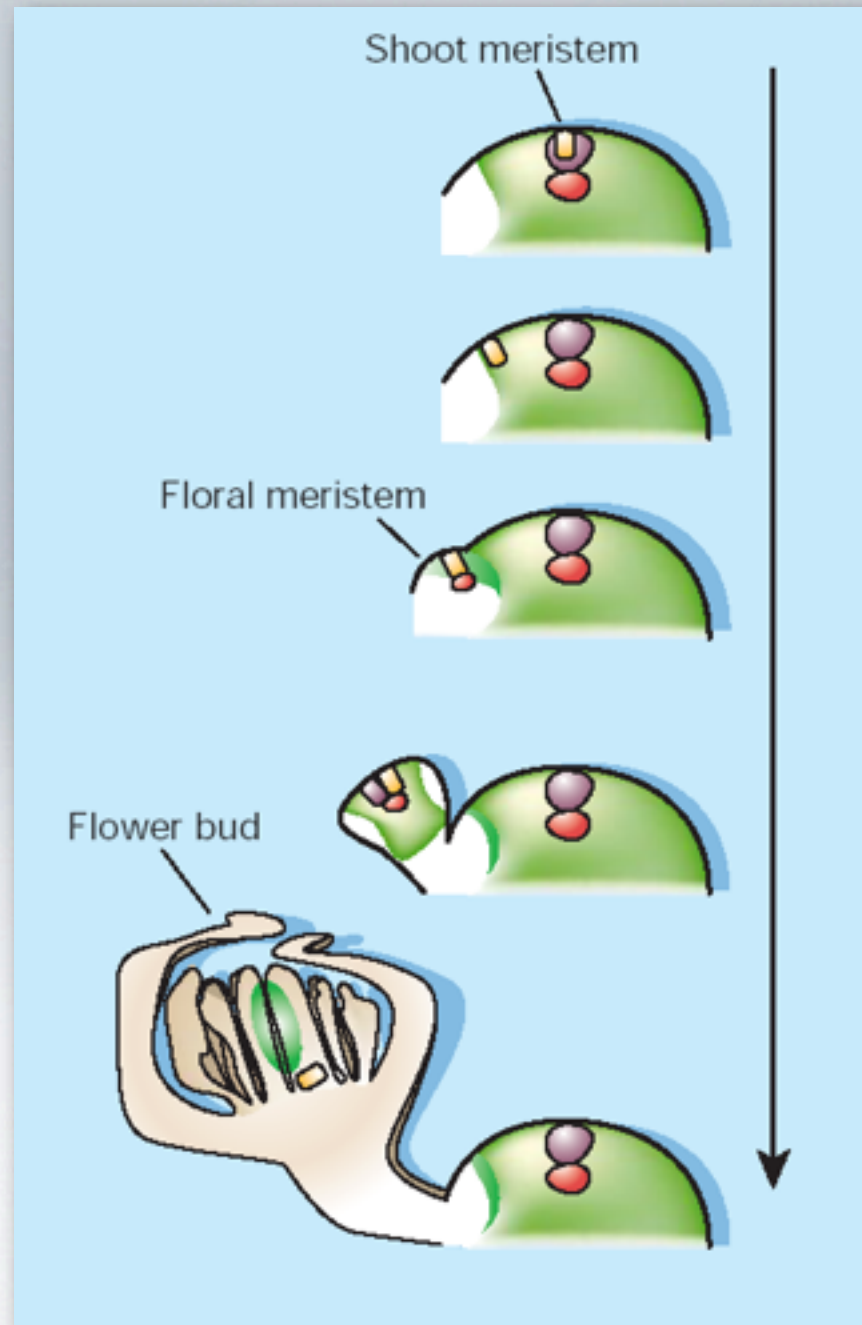
Plants vs animals



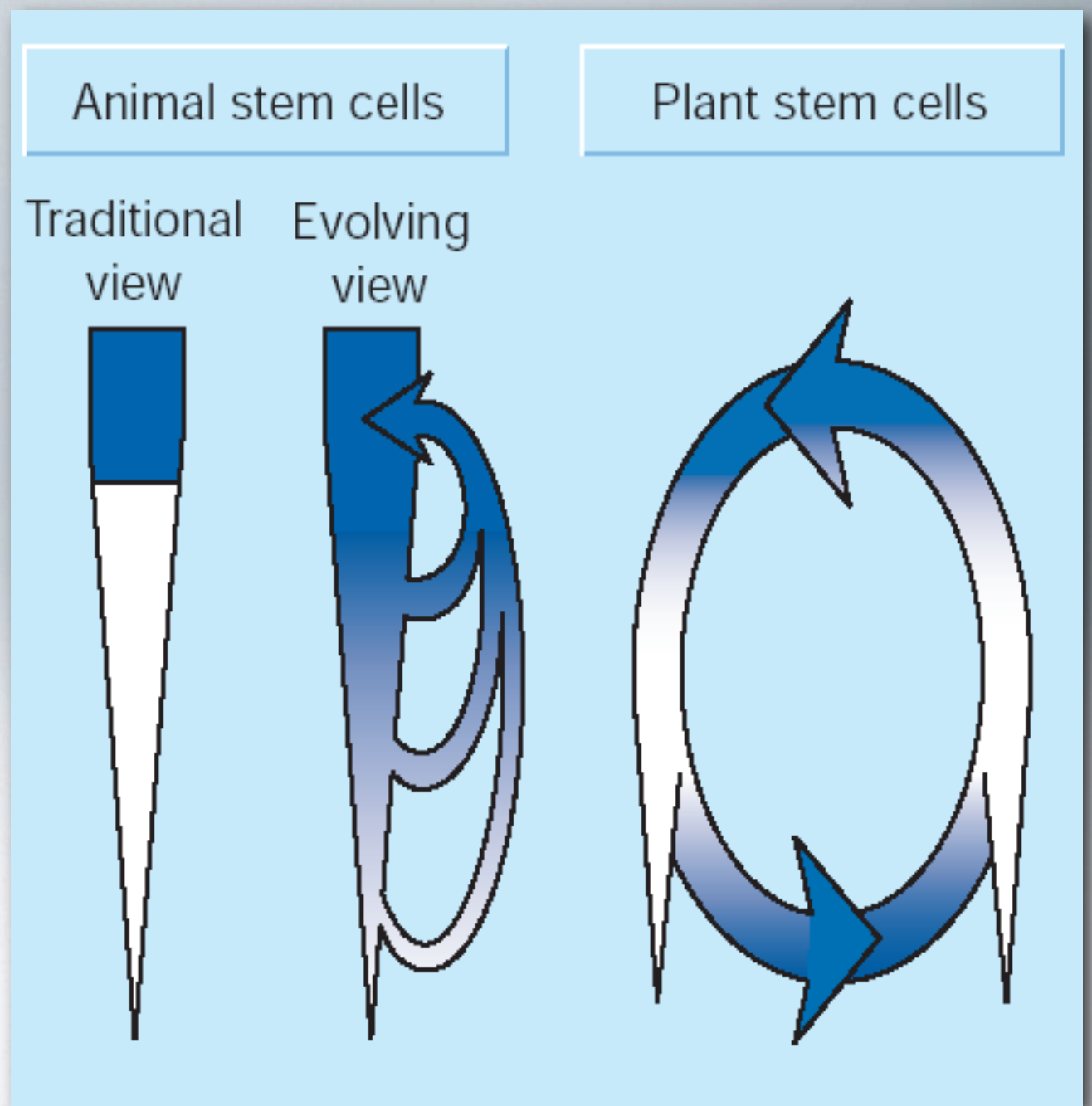
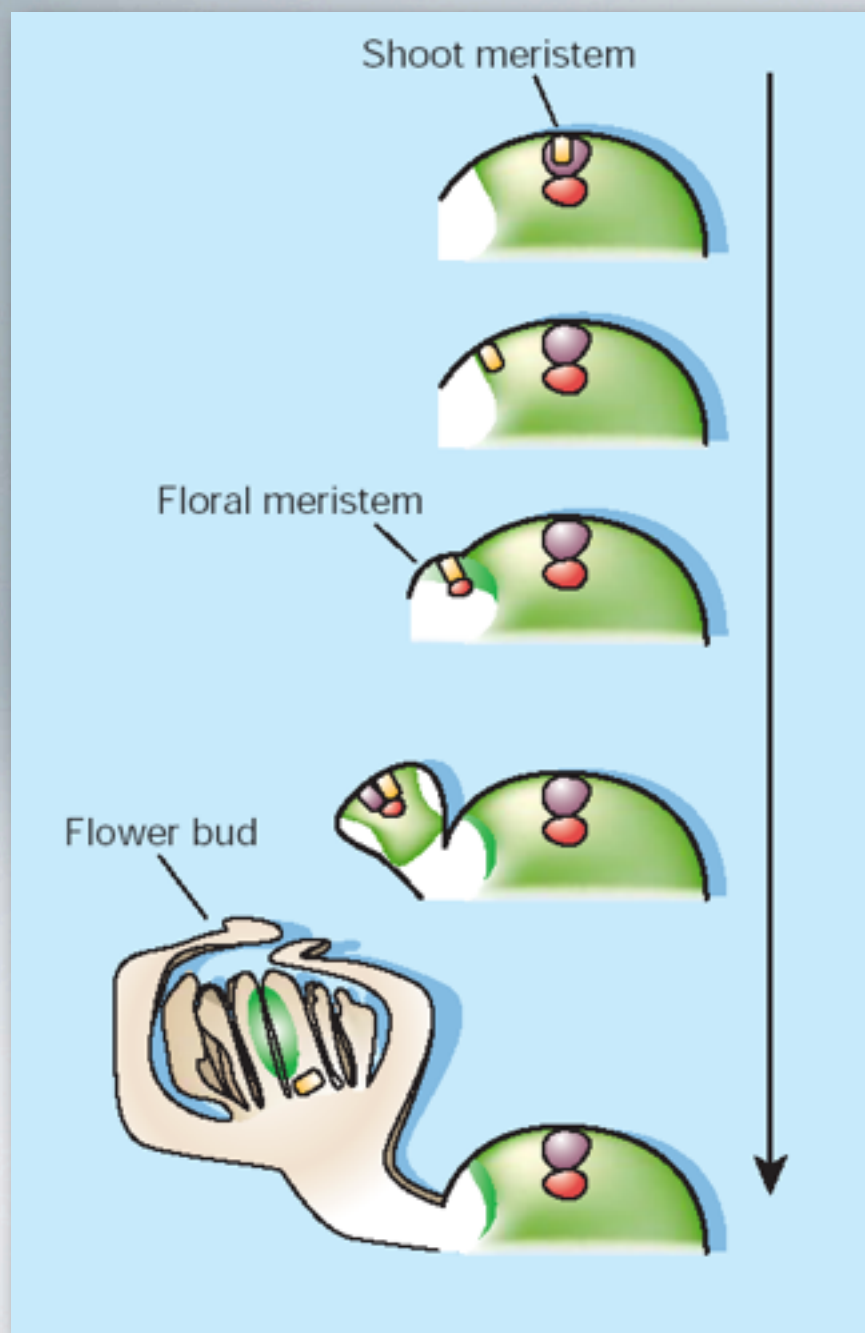
Plants vs animals



Robustness and plasticity



Robustness and plasticity

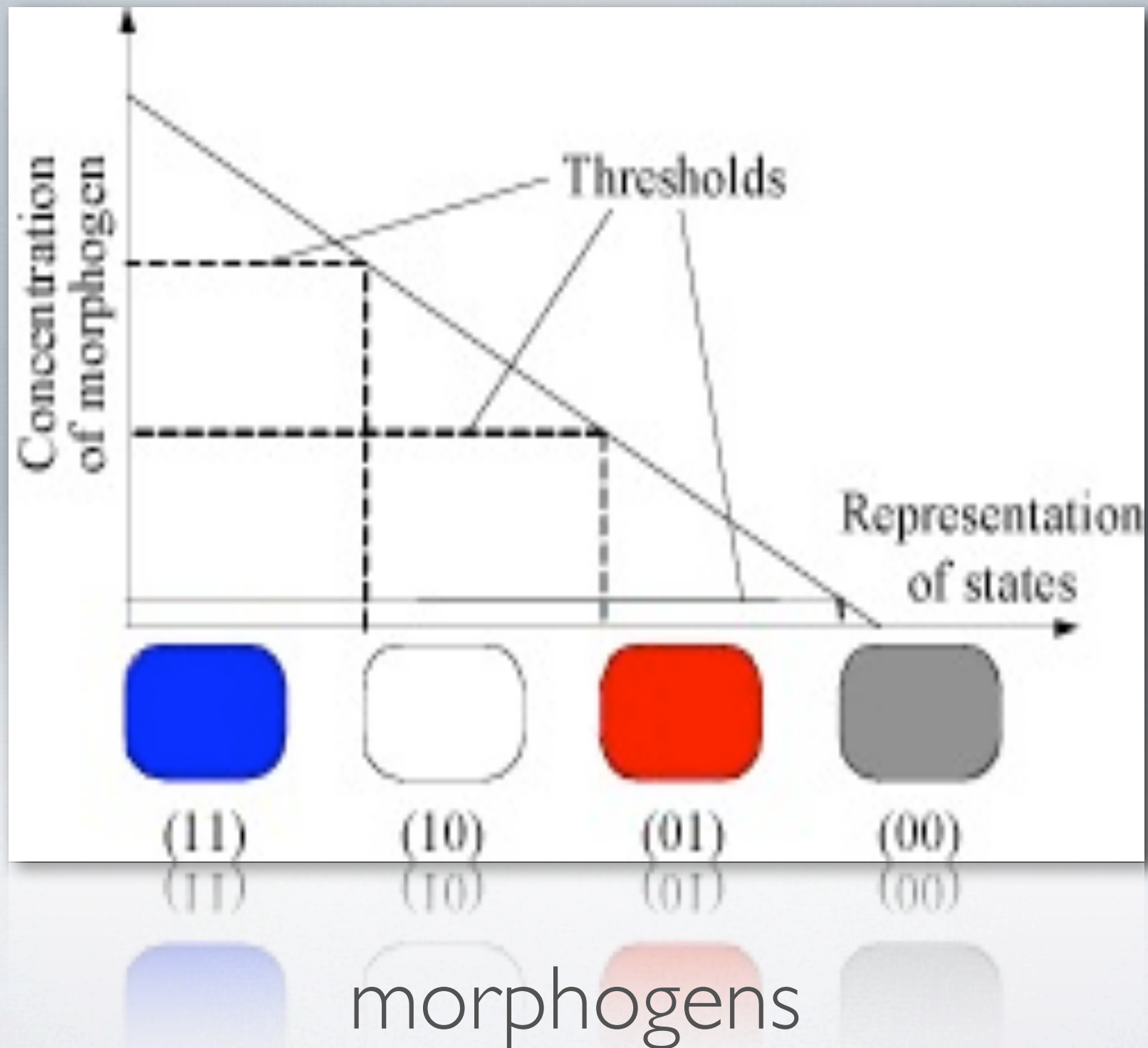


pattern generation

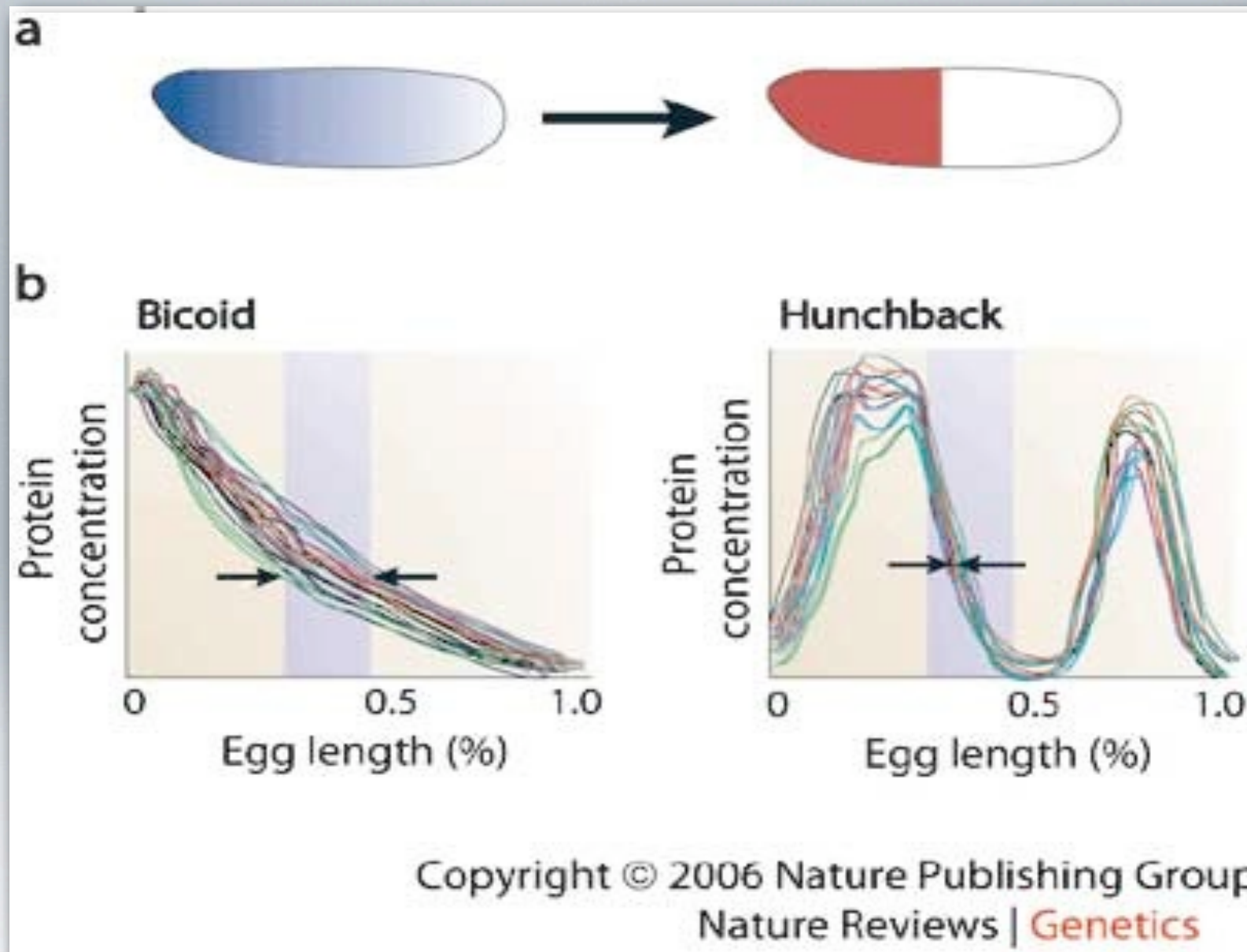
pattern generation

growth and mechanics in next talk...

pattern generation



pattern generation



morphogens

spontaneous pattern generation

spontaneous pattern generation

A Turing

spontaneous pattern generation

THE CHEMICAL BASIS OF MORPHOGENESIS

By A. M. TURING, F.R.S. *University of Manchester*

(*Received 9 November 1951—Revised 15 March 1952*)

It is suggested that a system of chemical substances, called morphogens, reacting together and diffusing through a tissue, is adequate to account for the main phenomena of morphogenesis. Such a system, although it may originally be quite homogeneous, may later develop a pattern or structure due to an instability of the homogeneous equilibrium, which is triggered off by random disturbances. Such reaction-diffusion systems are considered in some detail in the case of an isolated ring of cells, a mathematically convenient, though biologically unusual system.

A Turing

spontaneous pattern generation

reactions + diffusion

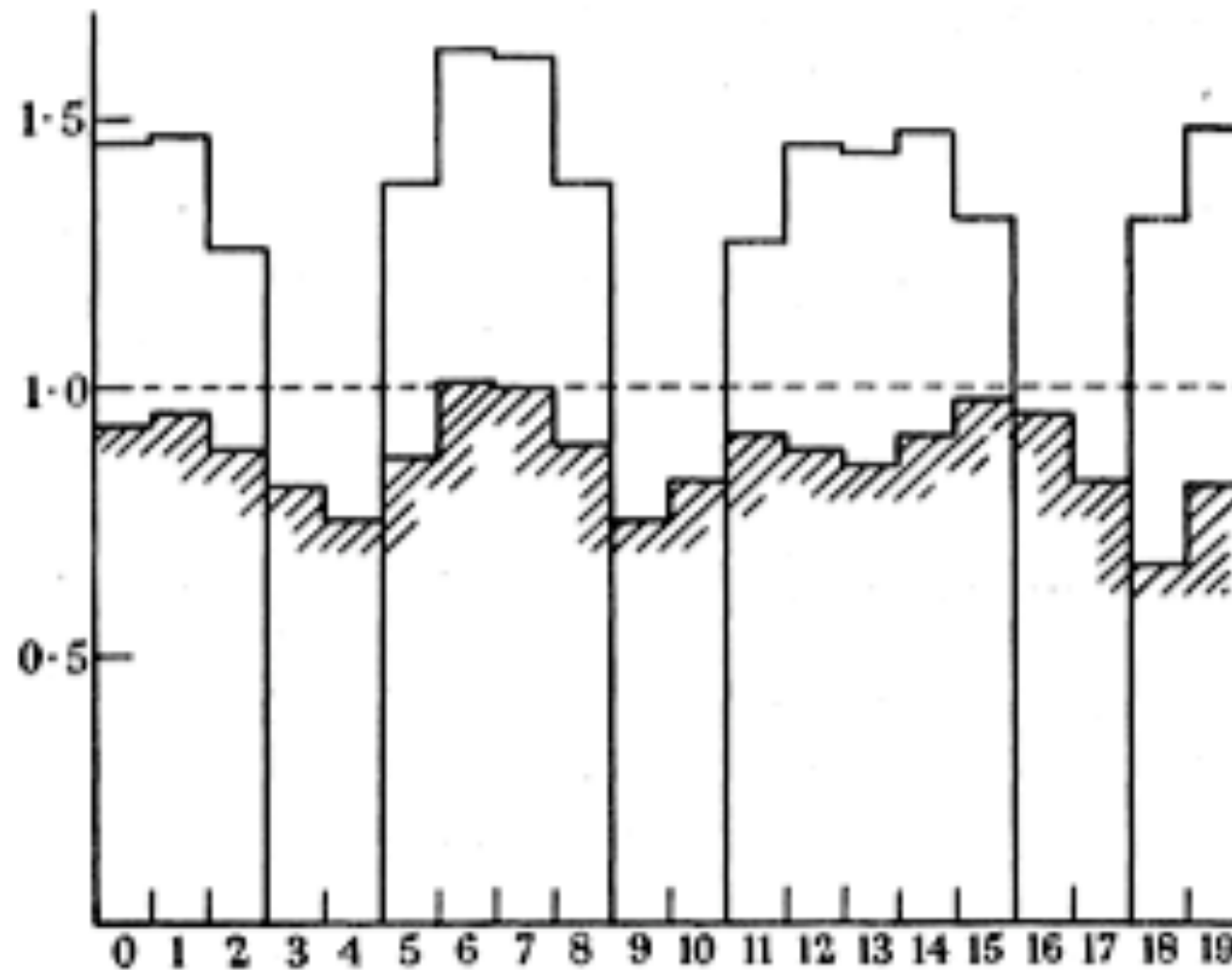
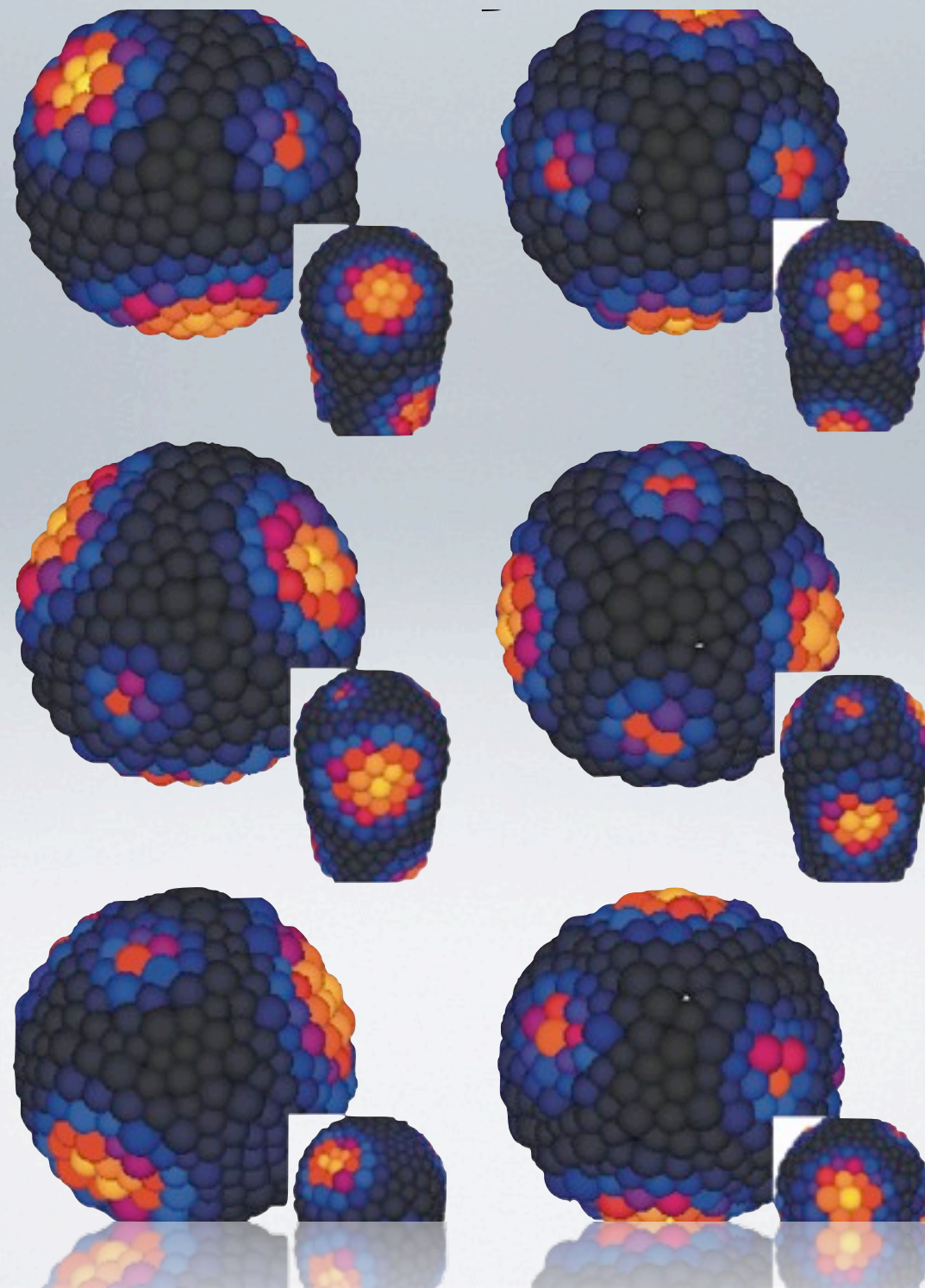


FIGURE 3. Concentrations of Y in the development of the first specimen (taken from table 1).
----- original homogeneous equilibrium; // // // // incipient pattern; ——— final equilibrium.

A Turing

spontaneous pattern generation

regulated transport

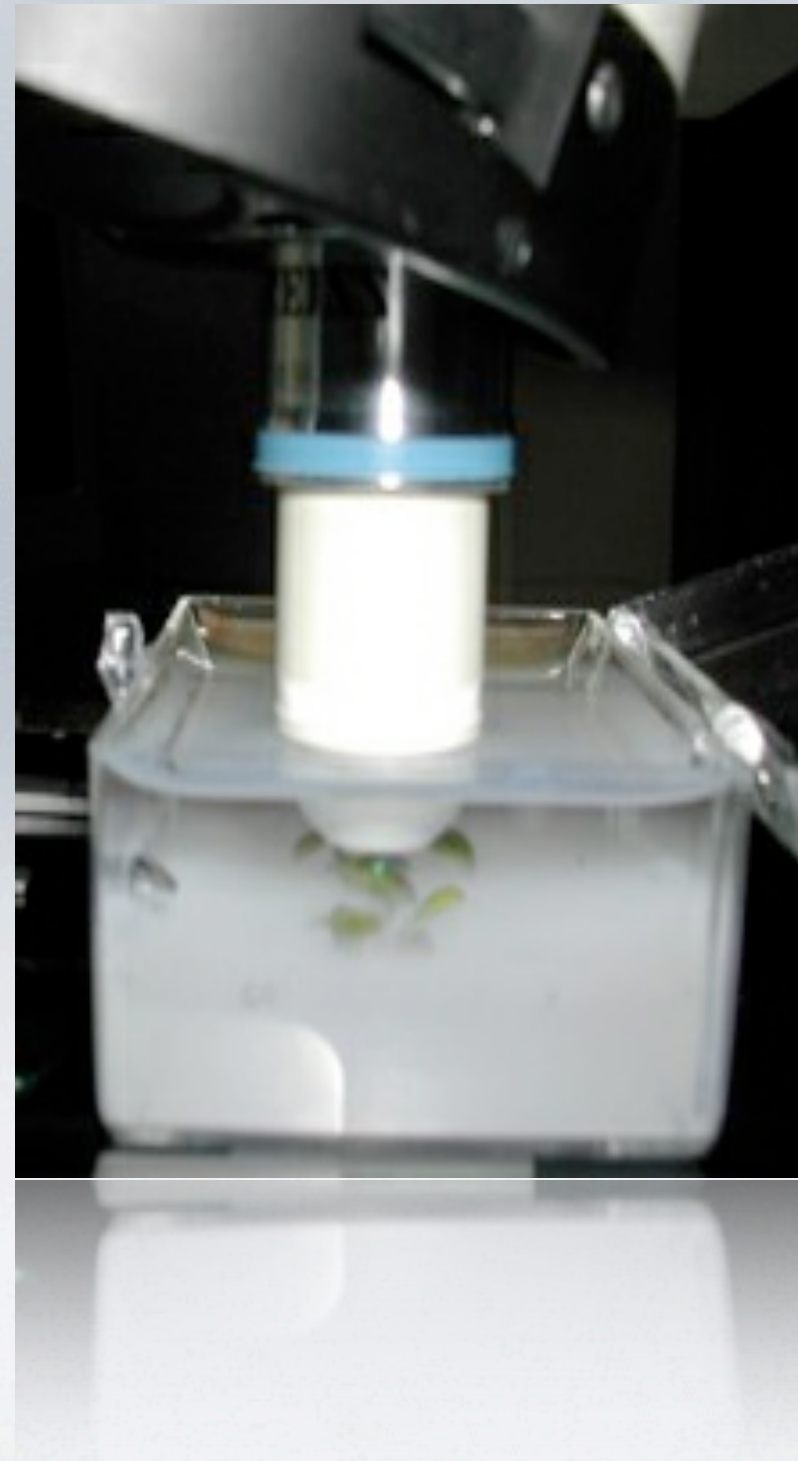
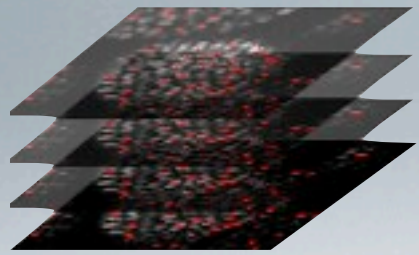


data

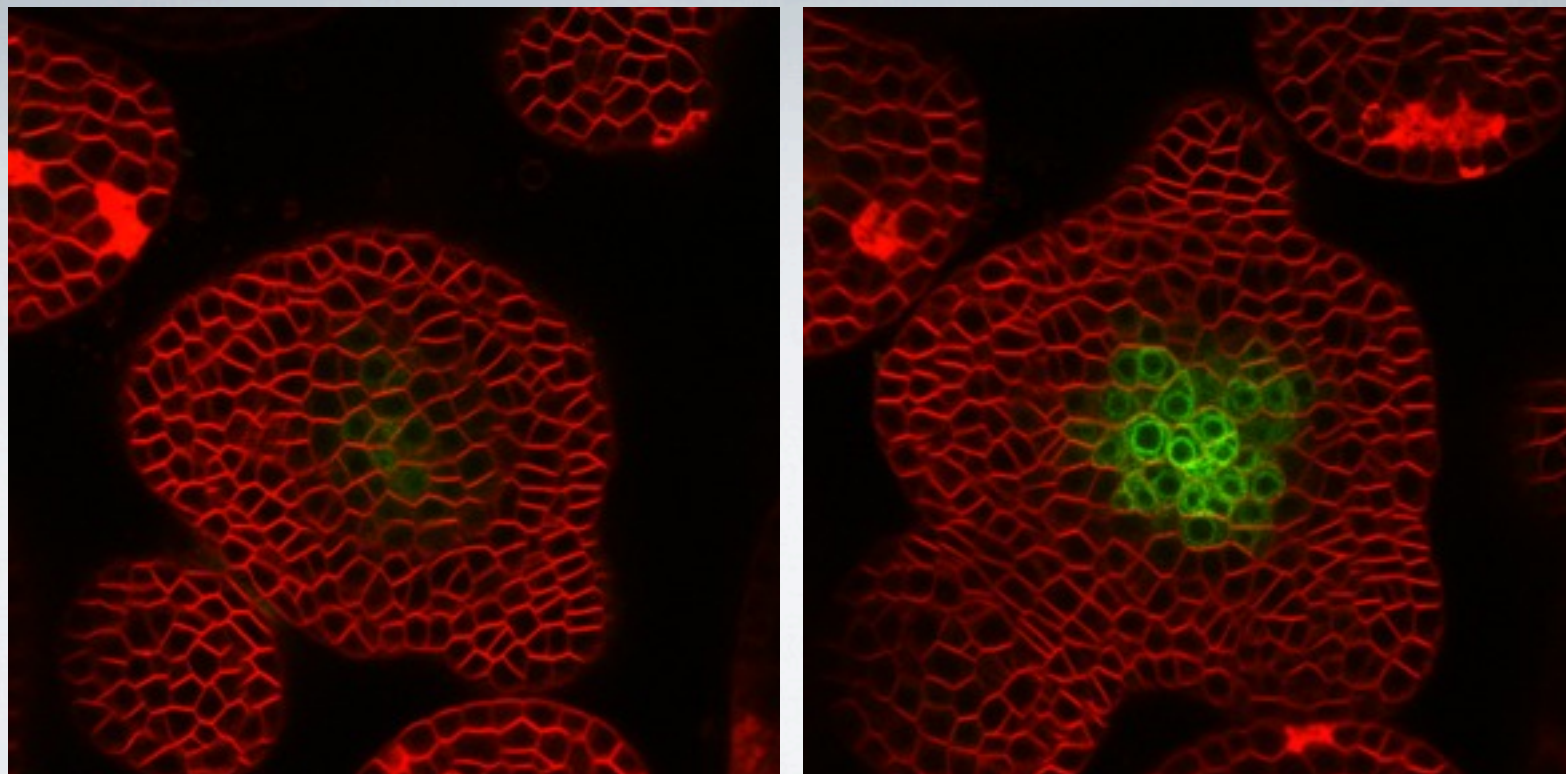
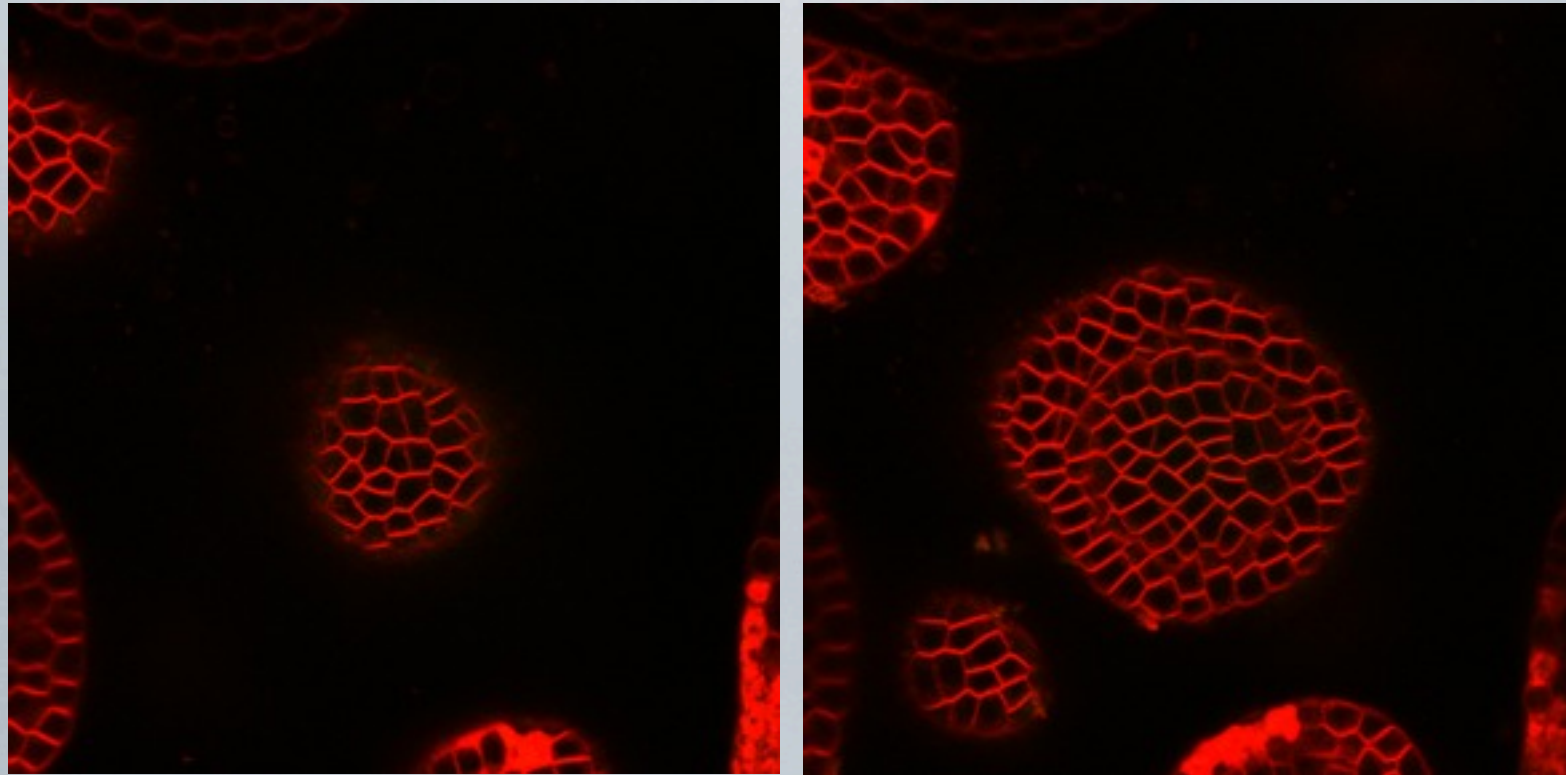
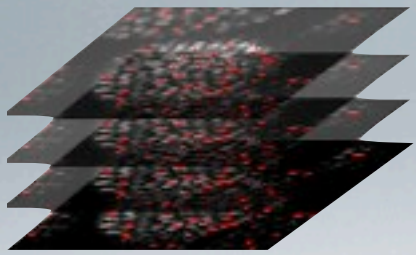
data



data

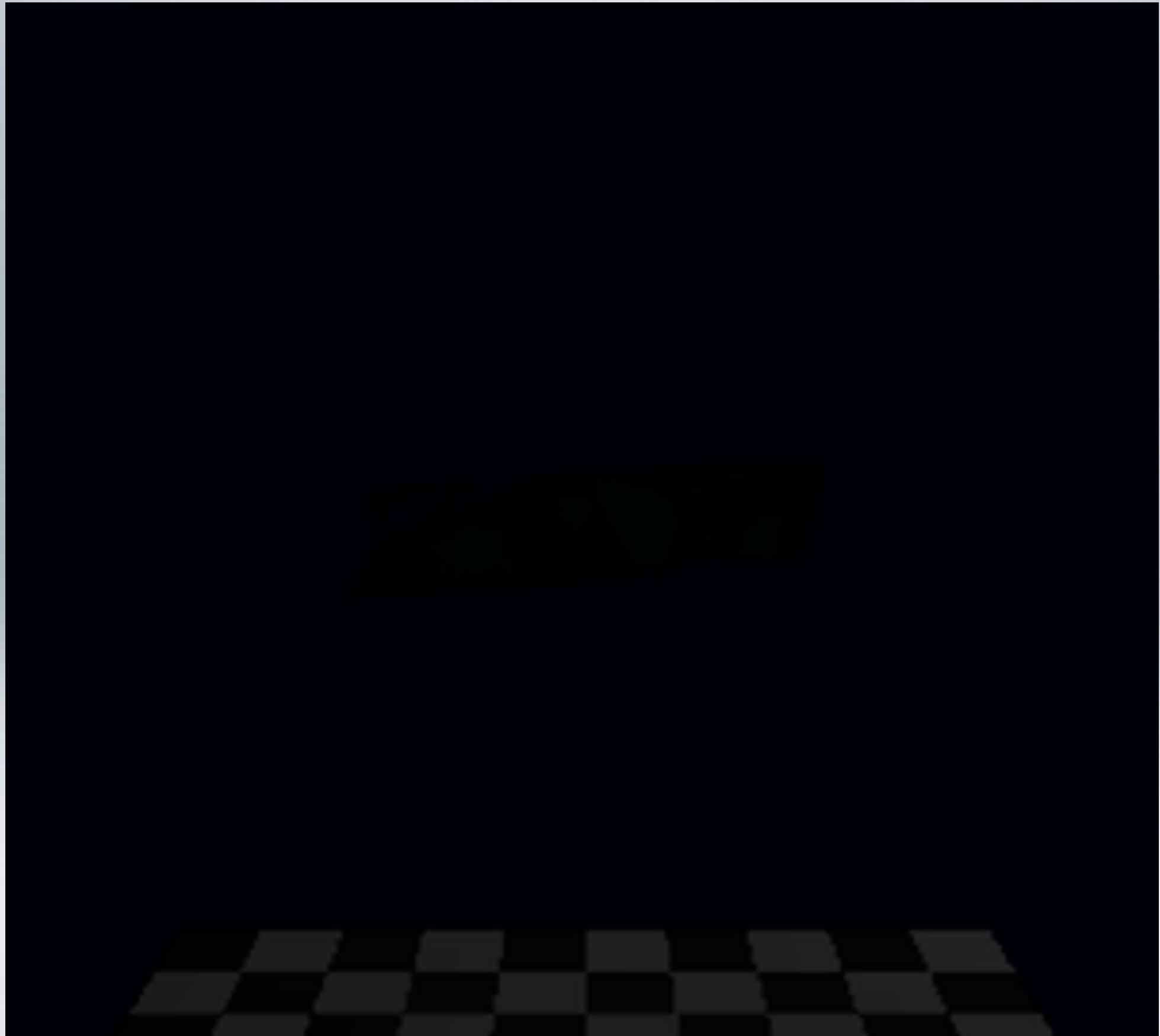


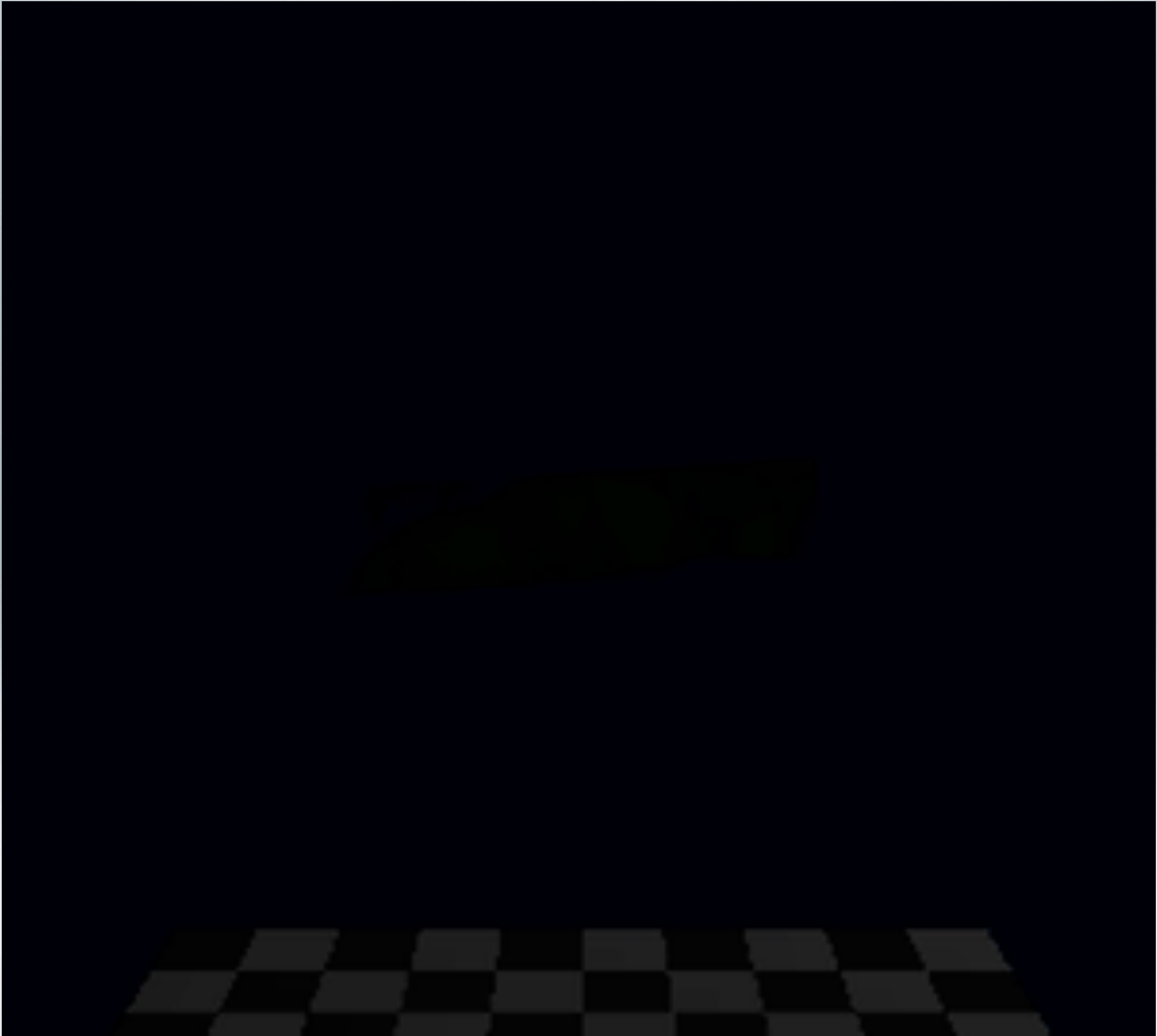
data



Venu Reddy

WUS::GFP





What is science?

What is science?

“eine wissenschaft, aber nicht wissenschaft”

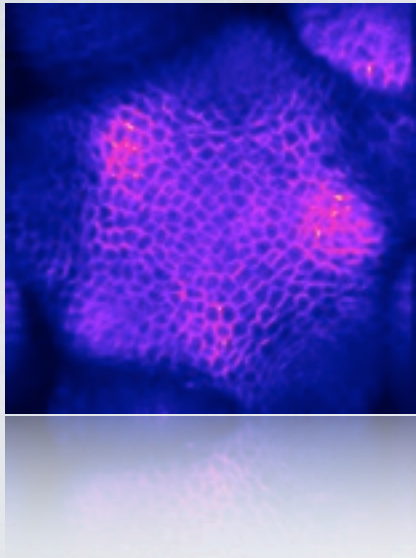
What is science?

“eine wissenschaft, aber nicht wissenschaft”

Immanuel Kant

The criterion of true science lay in its relation to mathematics...

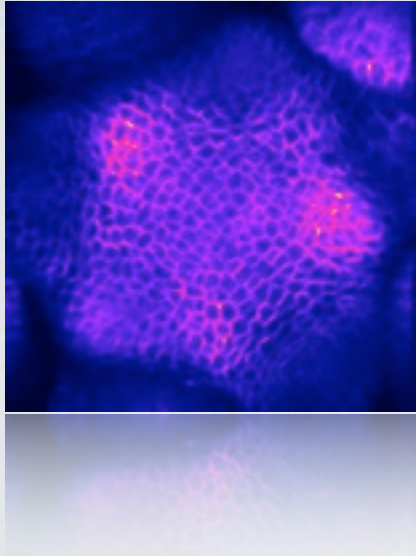
the method



experiment

hypotheses

the method



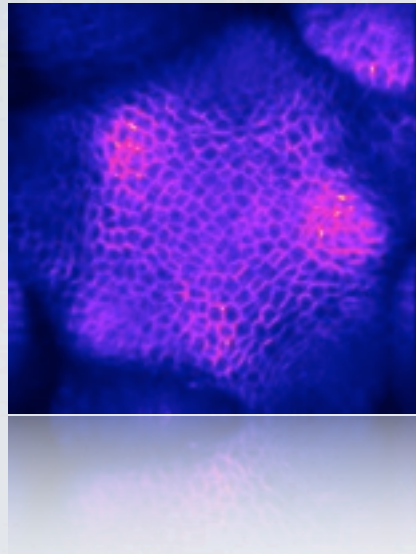
experiment

hypotheses

mathematical
models



the method

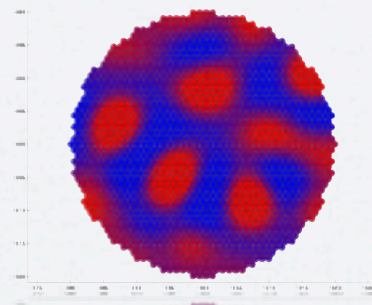


experiment

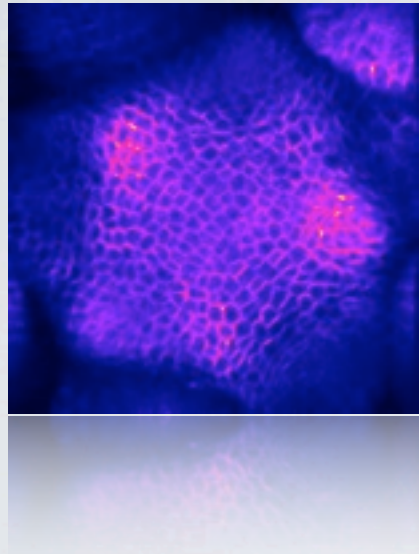
hypotheses

mathematical
models

computer simulations



the method

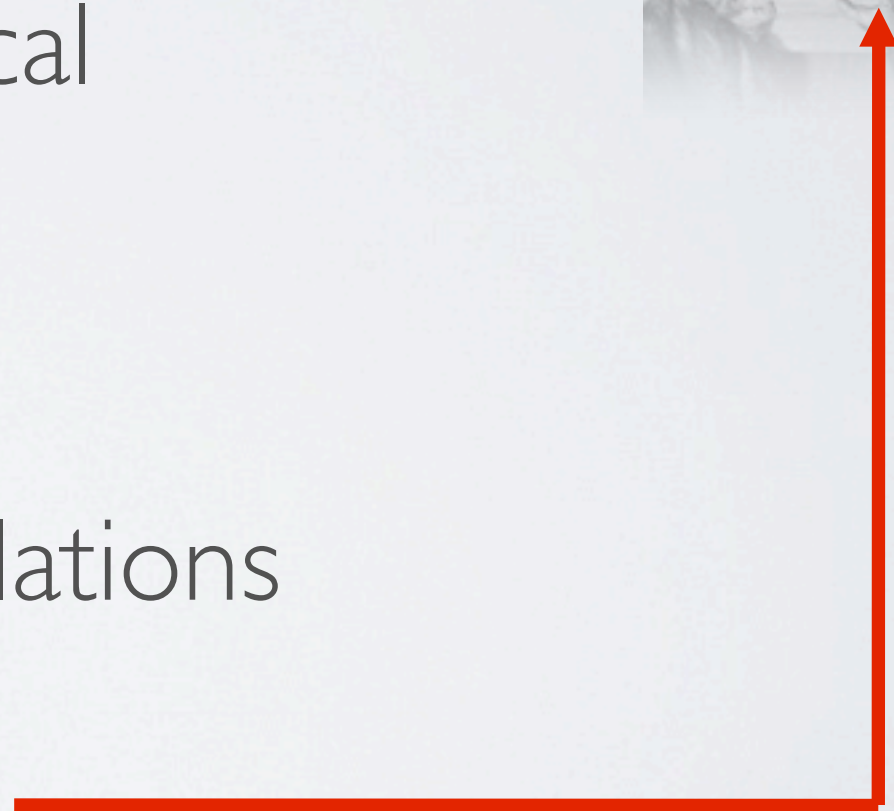
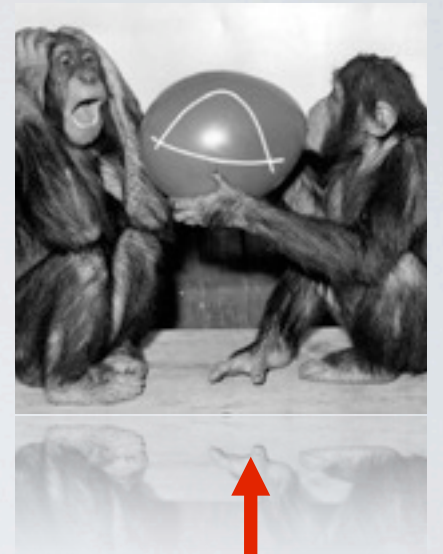
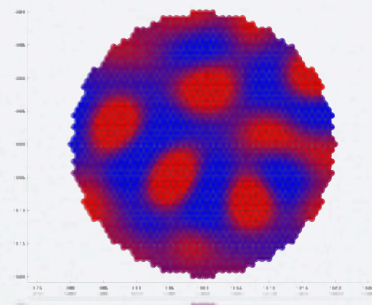


experiment

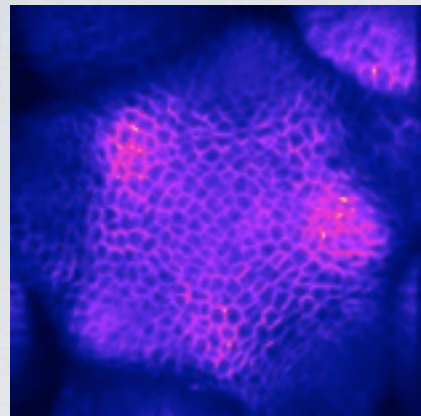
hypotheses

mathematical
models

computer simulations



the method



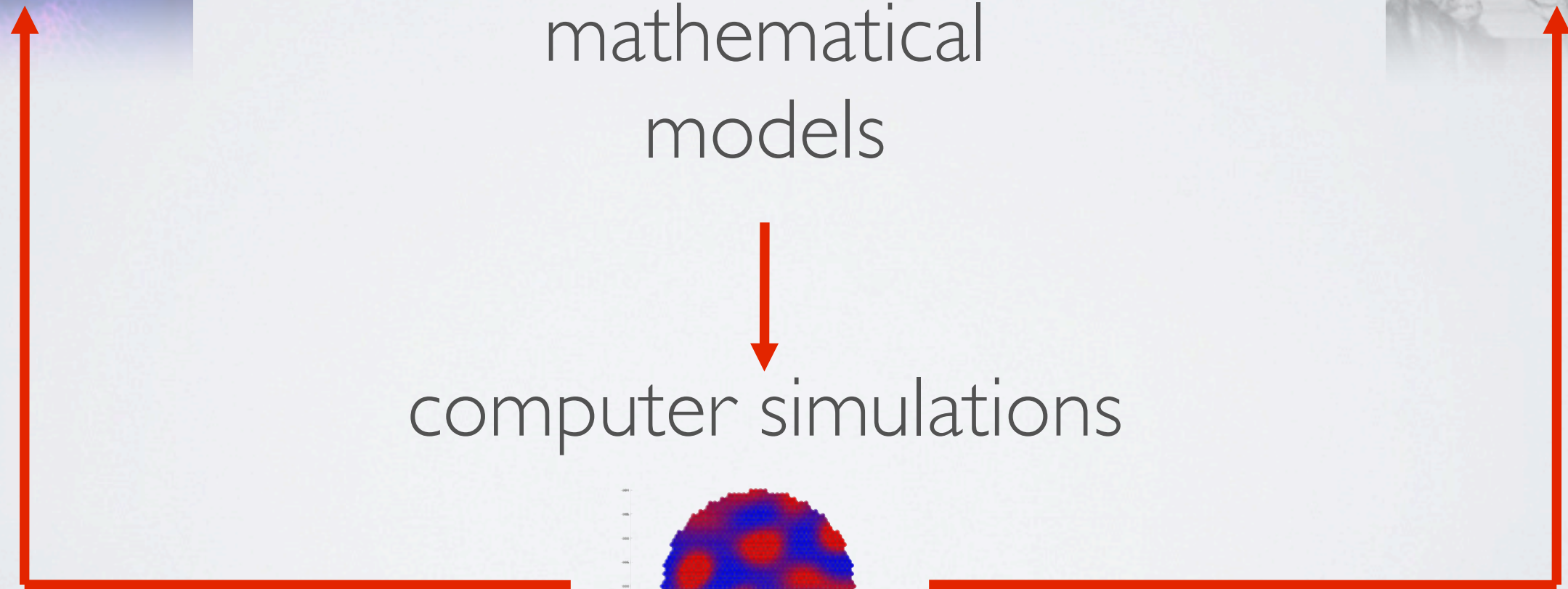
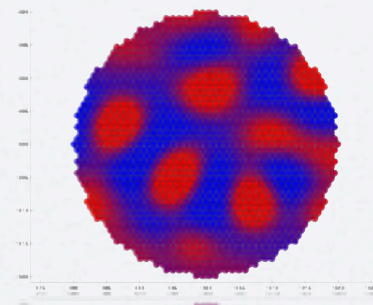
experiment

hypotheses



mathematical models

computer simulations



can this be automatized?

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- use imaging data for generating dynamic templates

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- use imaging data for generating dynamic templates
- define (differential equation) models in the computer

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- model predictions to propose new experiments

can this be automatized?

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all steps in the computer

image segmentation

image segmentation

COncocal STack ANalyZer Application
COSTANZA

image segmentation

The screenshot shows the ImageJ software interface. The main window displays a microscope image of a cluster of cells. The 'Results' table is open, showing the following data:

Cell id	x	y	z	Boa volume	Mean cell intensity
0	203.0	6.0	0.0	48.0	35.20834
1	241.0	23.0	1.0	146.0	38.863003
2	4.0	124.0	0.0	88.0	37.59091
3	133.0	129.0	3.0	1341.0	78.858406
4	108.0	128.0	4.0	956.0	75.50288
5	90.0	134.0	3.0	953.0	80.15304
6	125.0	138.0	2.0	92.0	63.163036
7	117.0	142.0	2.0	230.0	66.85656
8	105.0	146.0	2.0	662.0	74.47864
9	144.0	141.0	3.0	856.0	67.75192
10	122.0	150.0	6.0	1025.0	73.01044
11	113.0	155.0	2.0	266.0	86.81951
12	17.0	173.0	0.0	102.0	36.31372
13	9.0	207.0	0.0	64.0	39.984383
14	231.0	218.0	0.0	10.0	33.2
15	243.0	219.0	0.0	82.0	35.987797
16	10.0	219.0	0.0	72.0	35.708332
17	255.0	229.0	0.0	61.0	41.24591
18	239.0	235.0	0.0	125.0	34.967995
19	241.0	231.0	0.0	26.0	38.653854

The 'Wand (tracing) tool' dialog is open, showing the following options:

Input options:

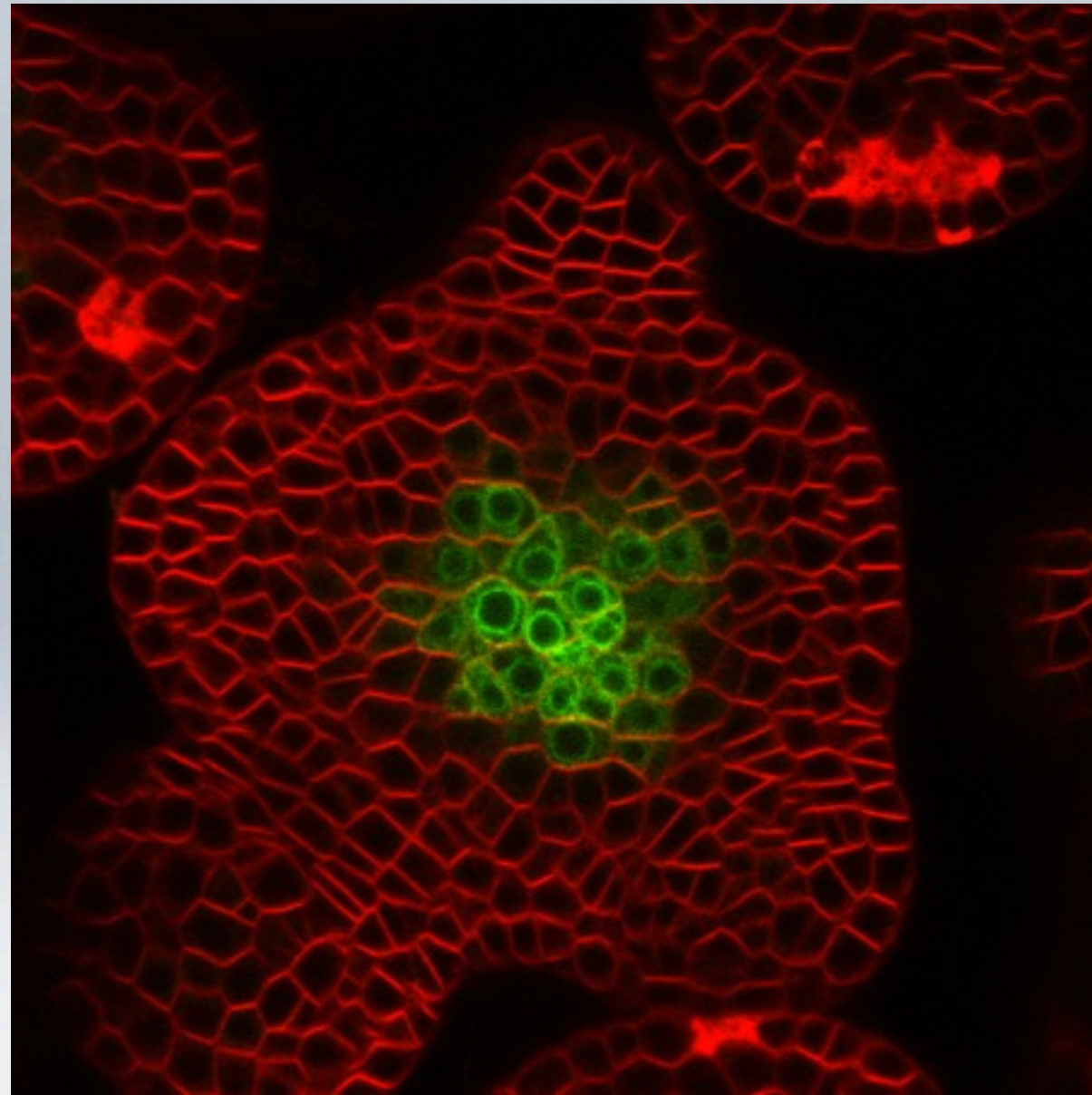
- Use secondary stack to measure intensity level

Output options:

- Mark cell centers.
- Display basins of attractions (BOA).
- Display basins of attractions according to mask
- Display internal working stack.

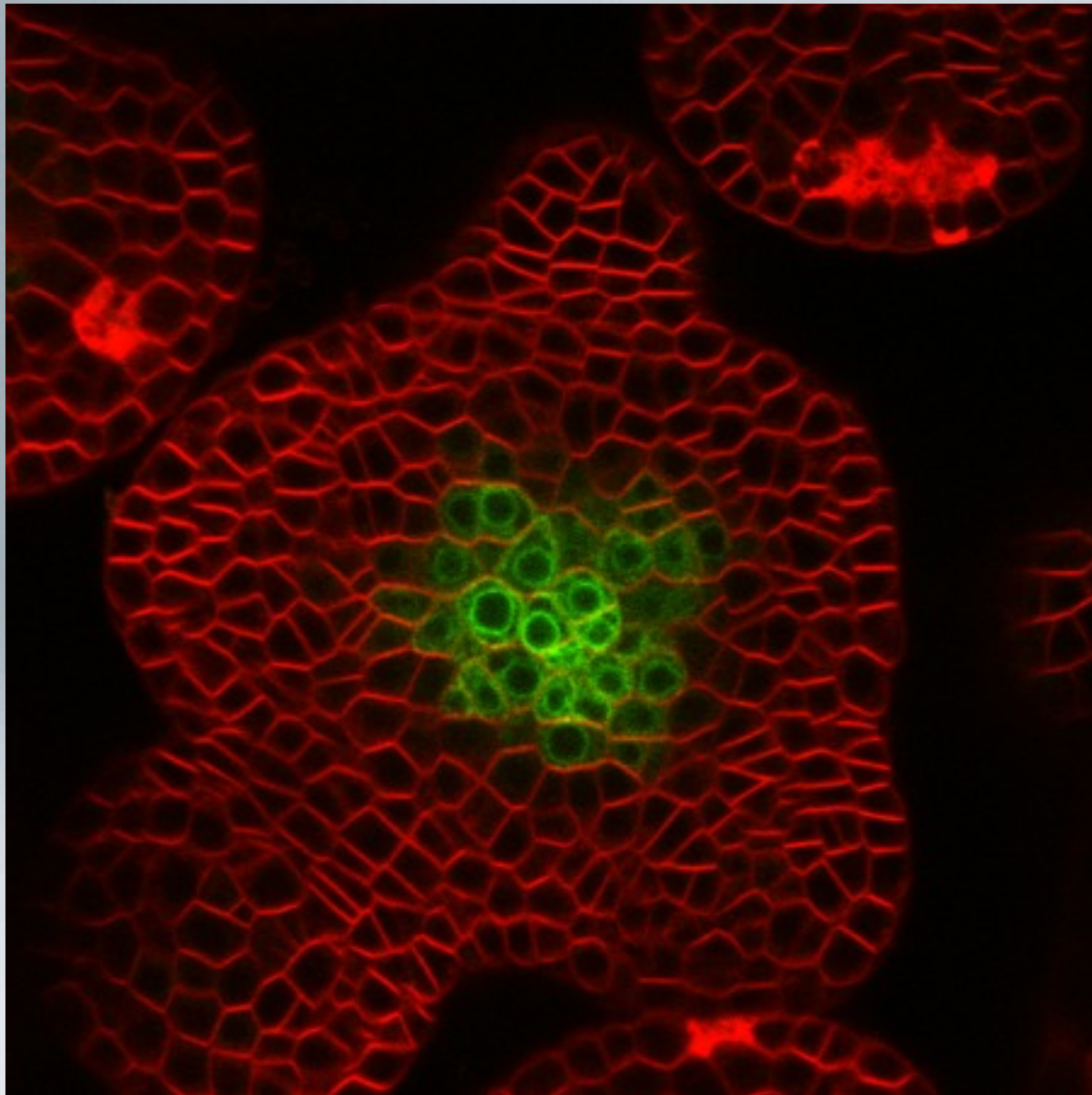
The 'Preview' window shows a microscope image of a cluster of cells.

Quantitative measures from image



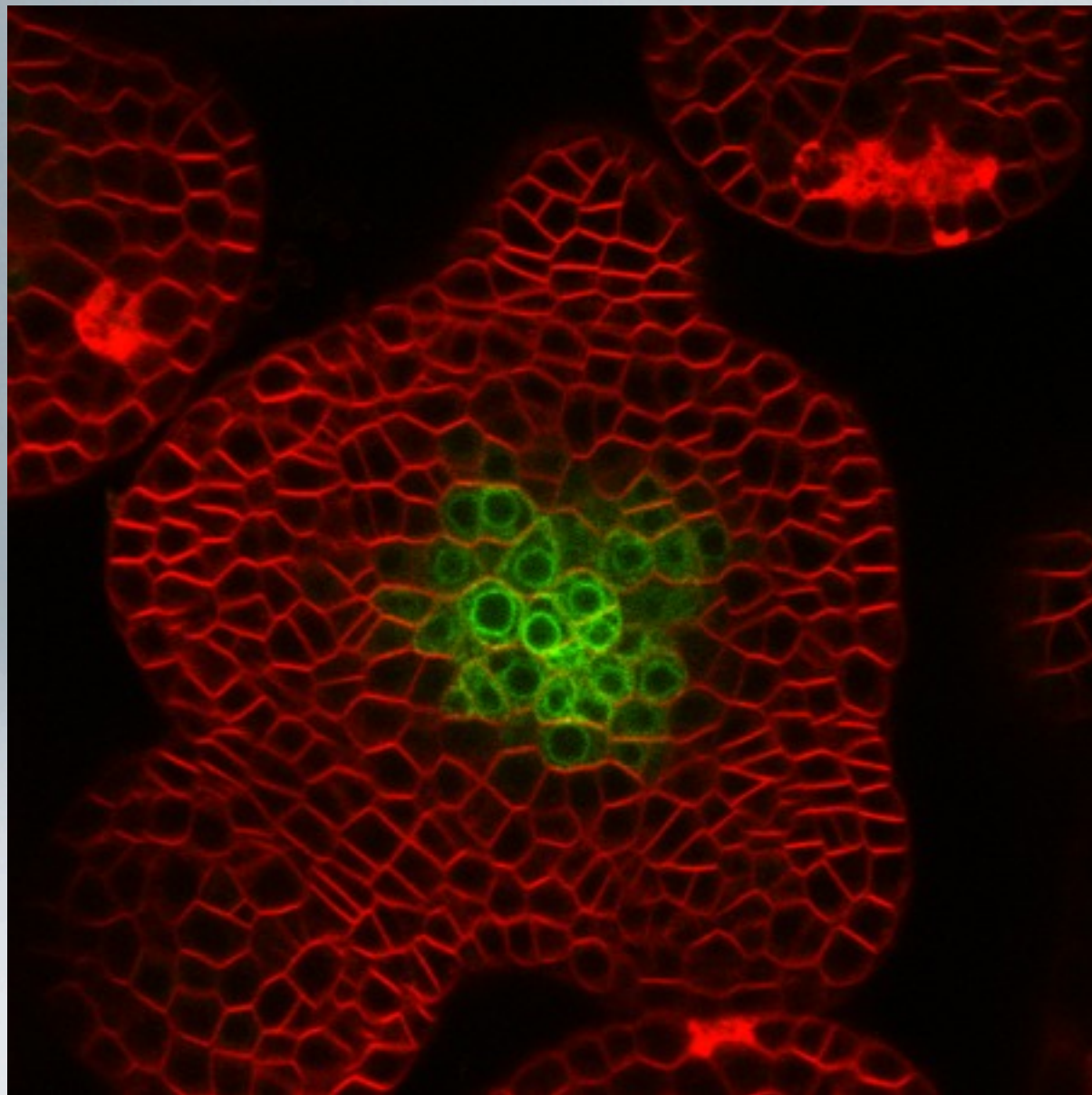
Green WUS::GFP
Red membrane stain

Quantitative measures from image

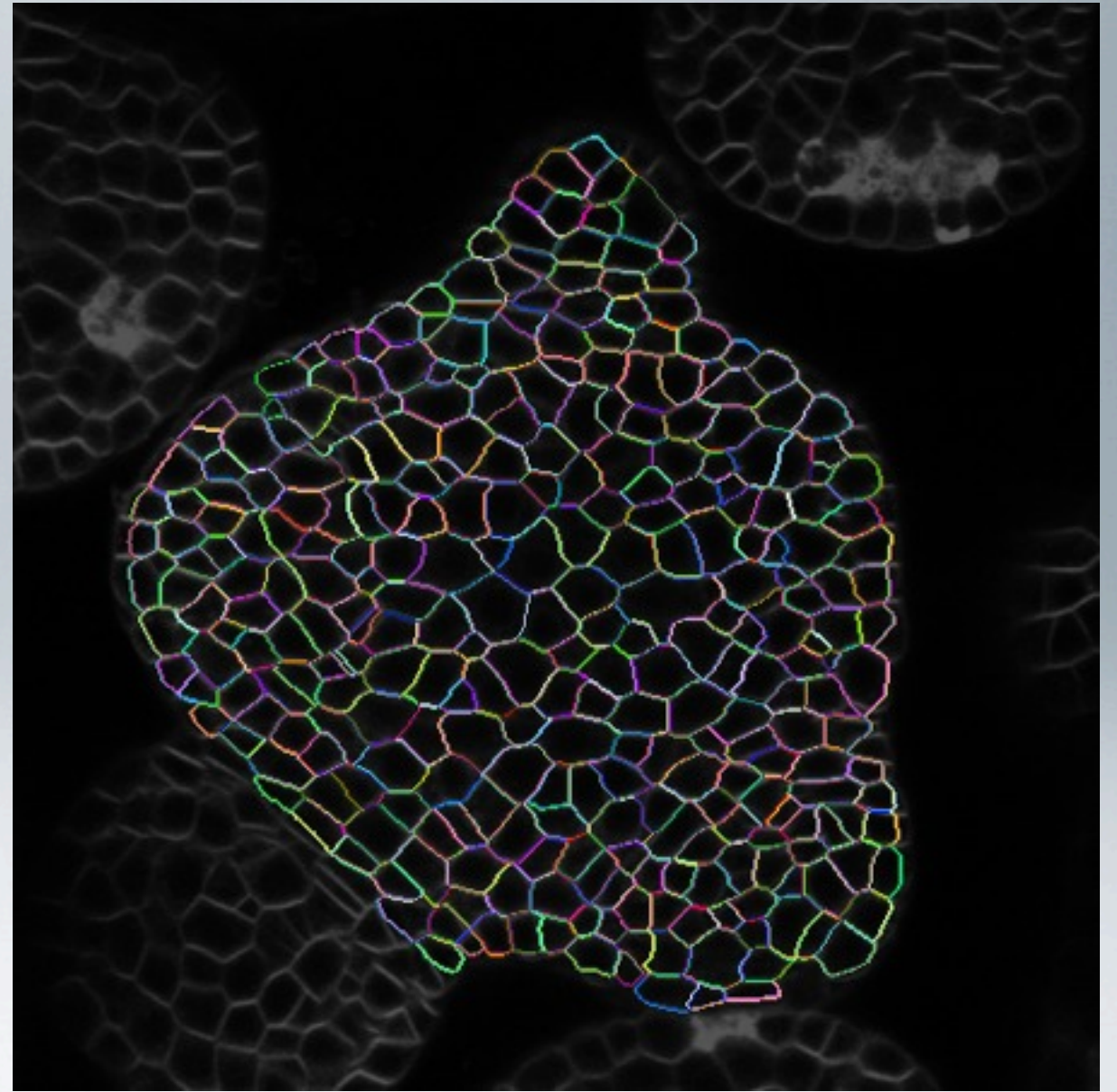


Green WUS::GFP
Red membrane stain

Quantitative measures from image

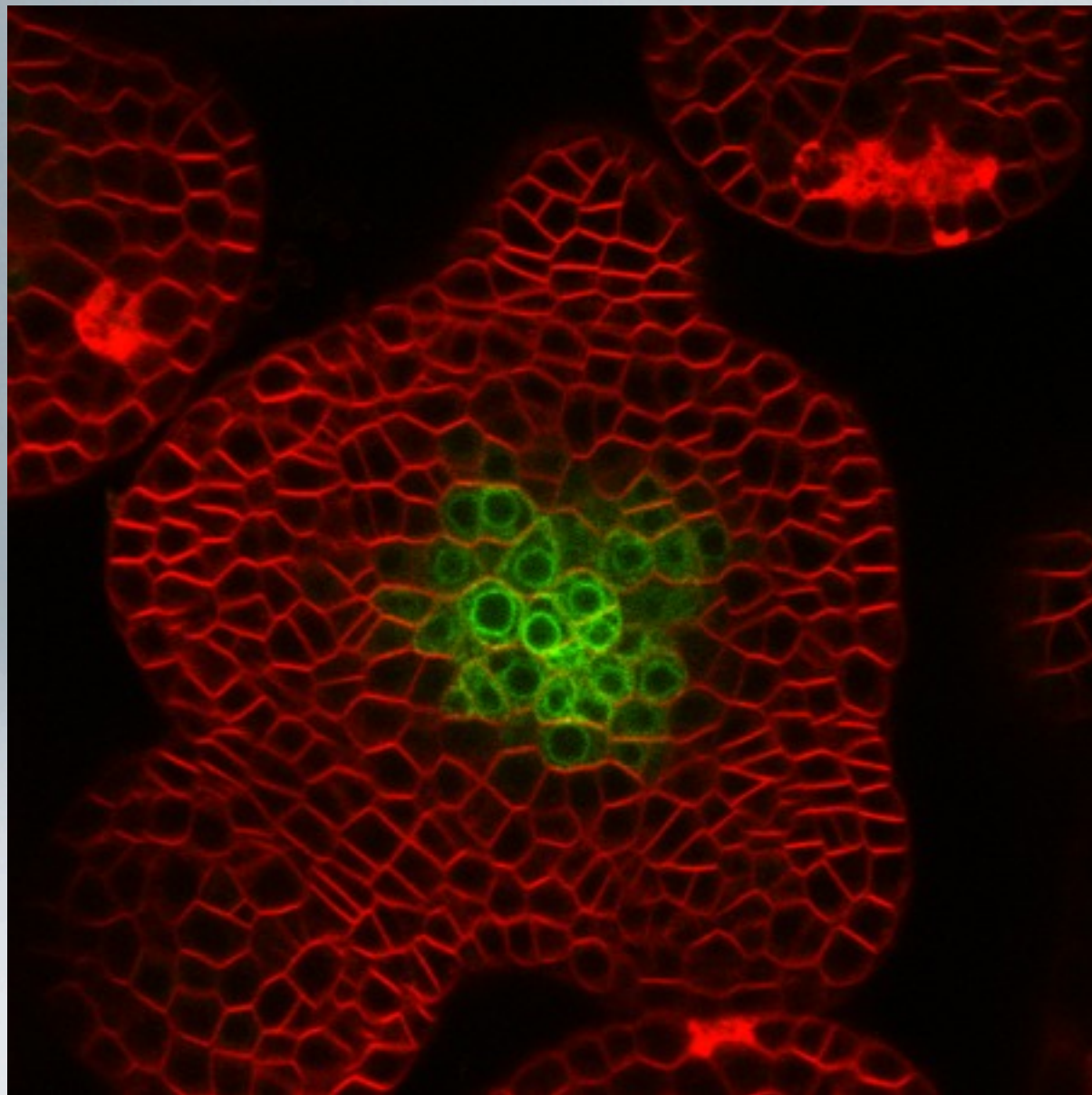


Green WUS::GFP
Red membrane stain

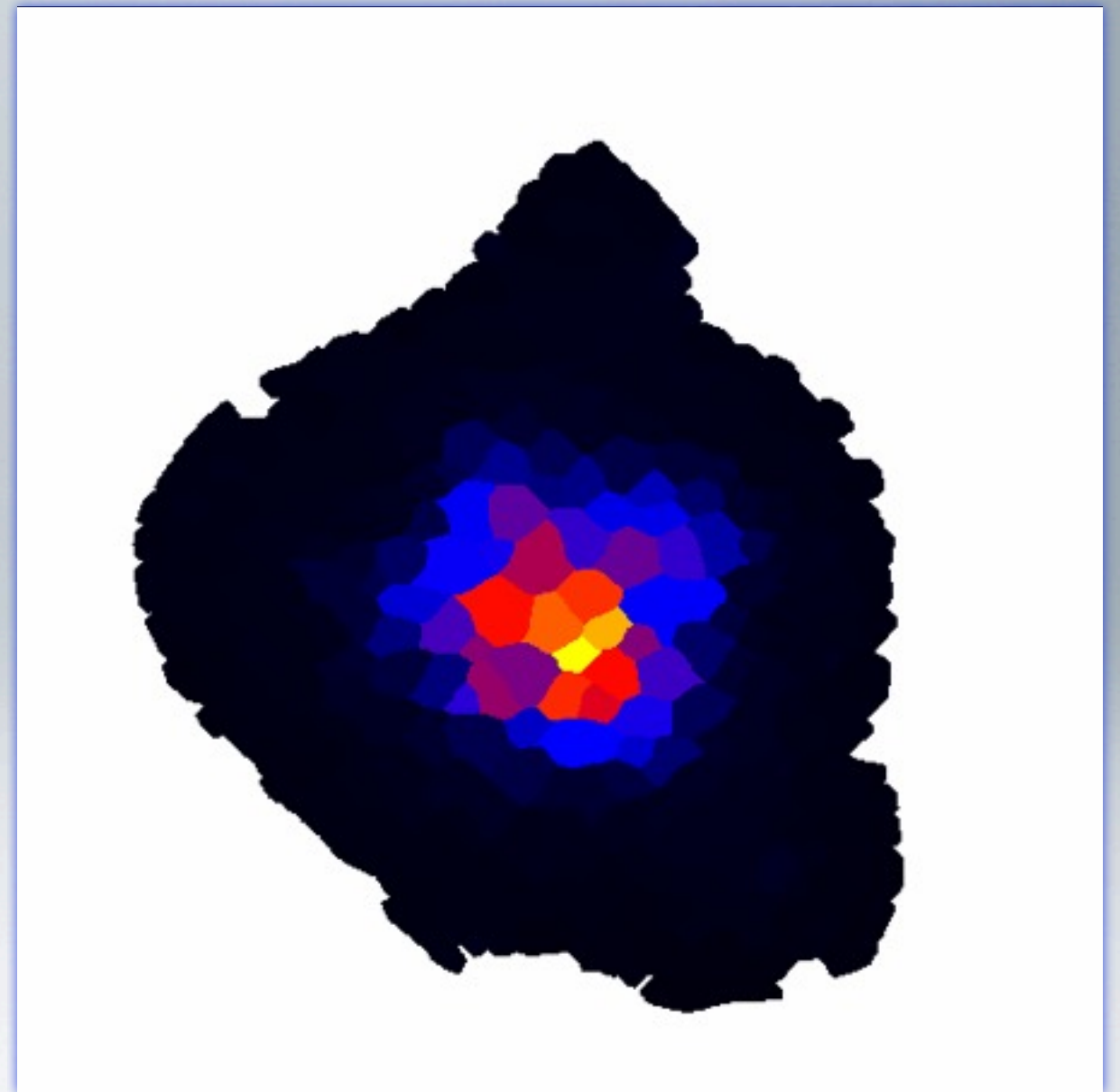


segment cells

Quantitative measures from image



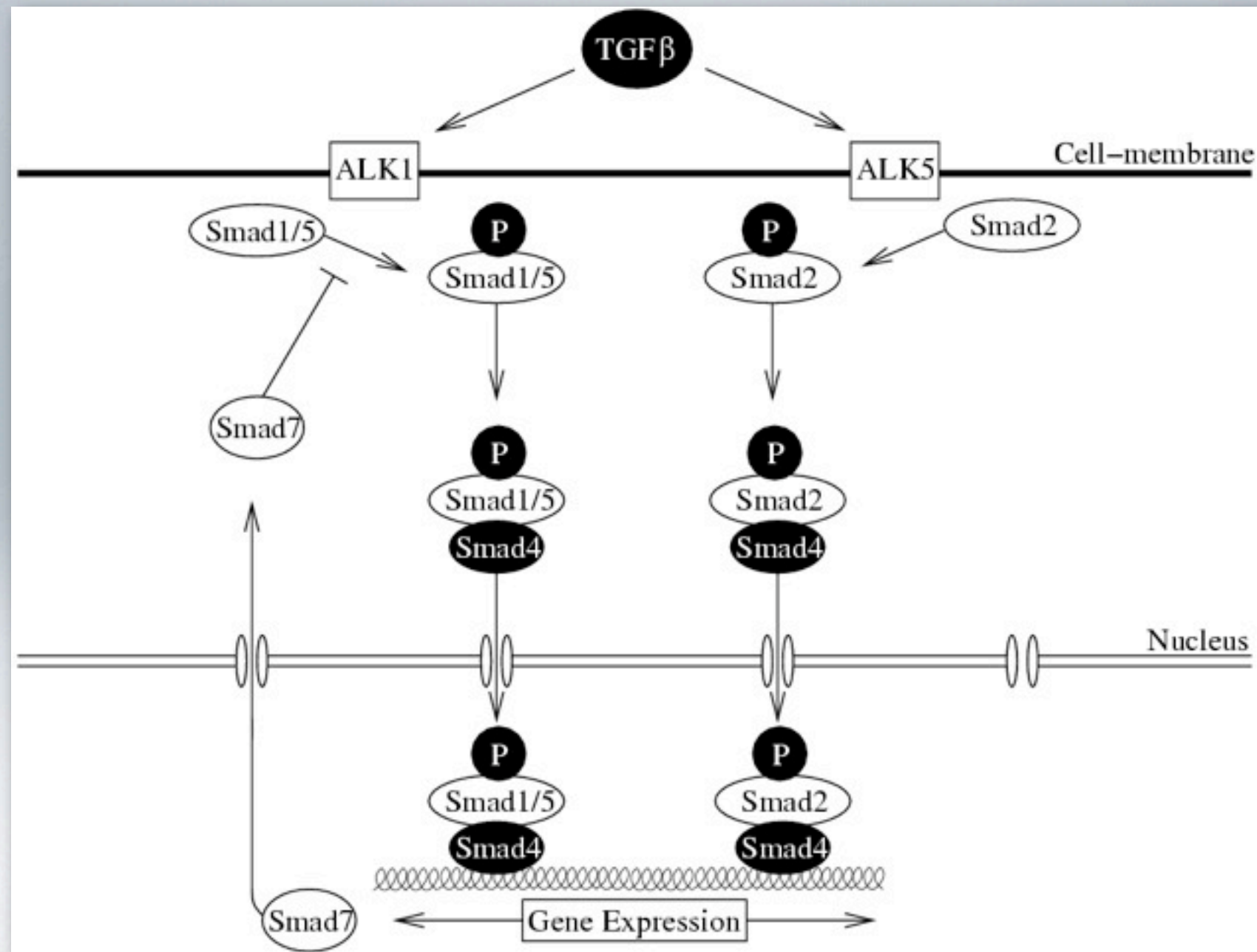
Green WUS::GFP
Red membrane stain



WUS "concentration"

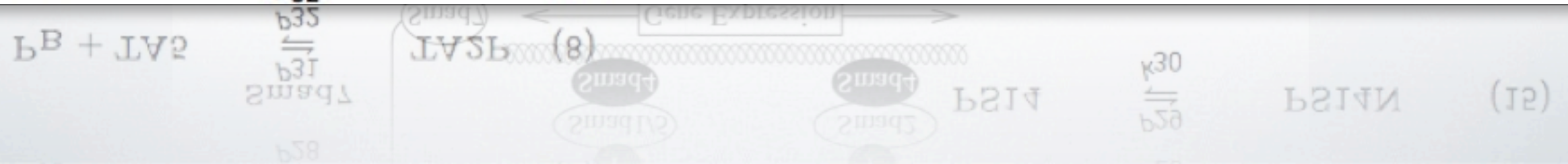
model definitions

model definitions



model definitions

	\emptyset	$\xrightleftharpoons[p_0 p_1]{p_0}$	ALK1 (1)		\emptyset	$\xrightleftharpoons[p_2 p_3]{p_2}$	Smad1 (9)
	\emptyset	$\xrightleftharpoons[p_4 p_5]{p_4}$	Smad4 (2)		\emptyset	$\xrightleftharpoons[p_6 p_7]{p_6}$	Smad2 (10)
	\emptyset	$\xrightleftharpoons[p_8 p_9]{p_8}$	ALK5 (3)		\emptyset	$\xrightleftharpoons[p_{10}]{PS14N (p_{11}, p_{12})}$	Smad7 (11)
TGF β + ALK1		$\xrightleftharpoons[p_{14}]{p_{13}}$	TA1 (4)			$\xrightleftharpoons[p_{17}]{TA1 (p_{15}, p_{16})}$	PSmad1 (12)
PSmad1 + Smad4		$\xrightleftharpoons[p_{19}]{p_{18}}$	PS14 (5)	Smad1			
TGF β + ALK5		$\xrightleftharpoons[p_{21}]{p_{20}}$	TA5 (6)	Smad2		$\xrightleftharpoons[p_{24}]{TA5 (p_{22}, p_{23})}$	PSmad2 (13)
P_A + TA1	Smad7	$\xrightleftharpoons[p_{28}]{p_{27}}$	TA1P (7)	PSmad2 + Smad4		$\xrightleftharpoons[p_{26}]{p_{25}}$	PS24 (14)
P_B + TA5	Smad7	$\xrightleftharpoons[p_{32}]{p_{31}}$	TA2P (8)	PS14		$\xrightleftharpoons[k_{30}]{p_{29}}$	PS14N (15)

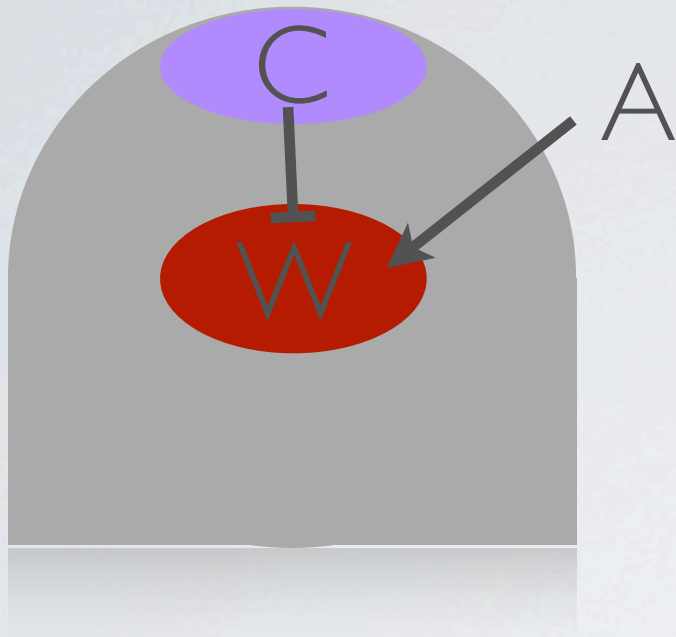


model definitions

mass action dynamics

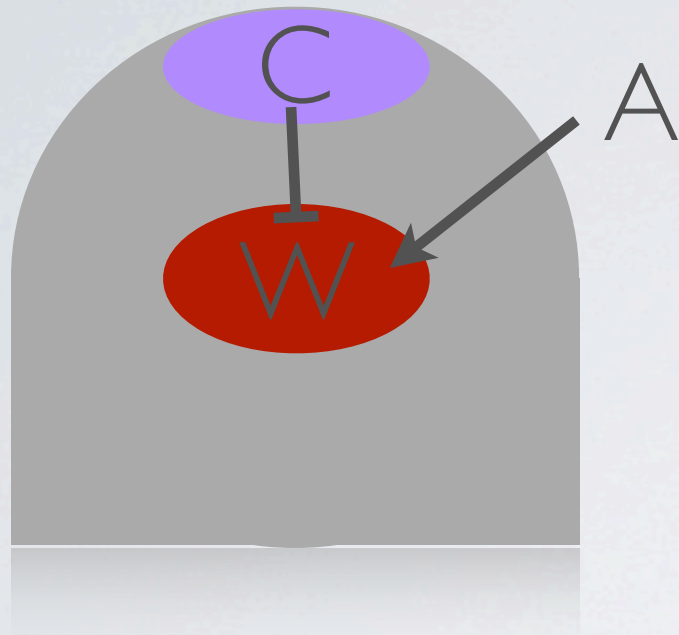
$$\begin{aligned}
 \frac{dA_1}{dt} &= p_0(1 - p_1 A_1) - p_{13} T_\beta A_1 + p_{14} T_1 \\
 \frac{dS_1}{dt} &= p_2(1 - p_3 S_1) - \frac{p_{15} T_1 S_1}{p_{16} + S_1} + p_{17} P_1 \\
 \frac{dS_4}{dt} &= p_4(1 - p_5 S_4) - p_{18} P_1 S_4 + p_{19} P_{14} - \\
 &\quad p_{25} P_2 S_4 + p_{26} P_{24} \\
 \frac{dS_2}{dt} &= p_6(1 - p_7 S_2) - \frac{p_{22} T_1 S_2}{p_{23} + S_2} + p_{24} P_2 \\
 \frac{dA_5}{dt} &= p_8(1 - p_9 A_5) - p_{20} T_\beta A_5 + p_{21} T_5 \\
 \frac{dS_7}{dt} &= \frac{p_{11} P_{14}}{p_{12} + P_{14}} - p_{10} S_7 \\
 \frac{dP_1}{dt} &= \frac{p_{15} T_1 S_1}{p_{16} + S_1} - p_{17} P_1 - p_{18} P_1 S_4 + p_{19} P_{14} \\
 \frac{dP_{14}}{dt} &= p_{18} P_1 S_4 - p_{19} P_{14} - p_{29} P_{14} + p_{30} P_{14N} \\
 \frac{dP_{14N}}{dt} &= p_{29} P_{14} - p_{30} P_{14N} \\
 \frac{dP_2}{dt} &= \frac{p_{22} T_1 S_2}{p_{23} + S_2} - p_{24} P_2 - p_{25} P_2 S_4 + k_{17} P_{26} \\
 \frac{dP_{24}}{dt} &= p_{25} P_2 S_4 - p_{26} P_{24} \\
 \frac{dT_1}{dt} &= p_{13} T_\beta A_1 - p_{14} T_1 - \\
 &\quad p_{27} S_7 P_{P1} T_1 + p_{28} T_{1P} \\
 \frac{dT_5}{dt} &= p_{20} T_\beta A_5 - p_{21} T_5 - \\
 &\quad p_{31} S_7 P_{P2} T_5 + p_{32} T_{5P} \\
 \frac{dP_A}{dt} &= -p_{27} S_7 P_A T_1 + p_{28} T_{1P} \\
 \frac{dP_B}{dt} &= -p_{31} S_7 P_B T_1 + p_{32} T_{1P} \\
 \frac{dT_{1P}}{dt} &= p_{27} S_7 P_A T_1 - p_{28} T_{1P} \\
 \frac{dT_{5P}}{dt} &= p_{31} S_7 P_B T_5 - p_{32} T_{5P}
 \end{aligned}$$

model definitions



$$\frac{d[W]}{dt} = \frac{V_{max} K_C^n [A]^n}{(K_C^n + [C]^n)(K_A^n + [A]^n)} - k[W]$$

model definitions



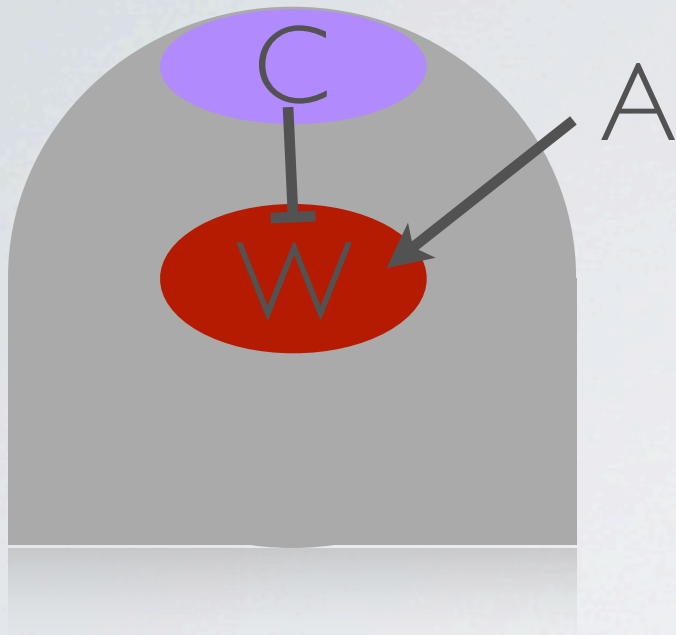
transcription

degradation

$$\frac{d[W]}{dt} = \frac{V_{max} K_C^n [A]^n}{(K_C^n + [C]^n)(K_A^n + [A]^n)} - k[W]$$

The equation is annotated with two red arrows: one pointing from the word 'transcription' to the numerator of the fraction, and another pointing from the word 'degradation' to the subtraction term $-k[W]$.

model definitions



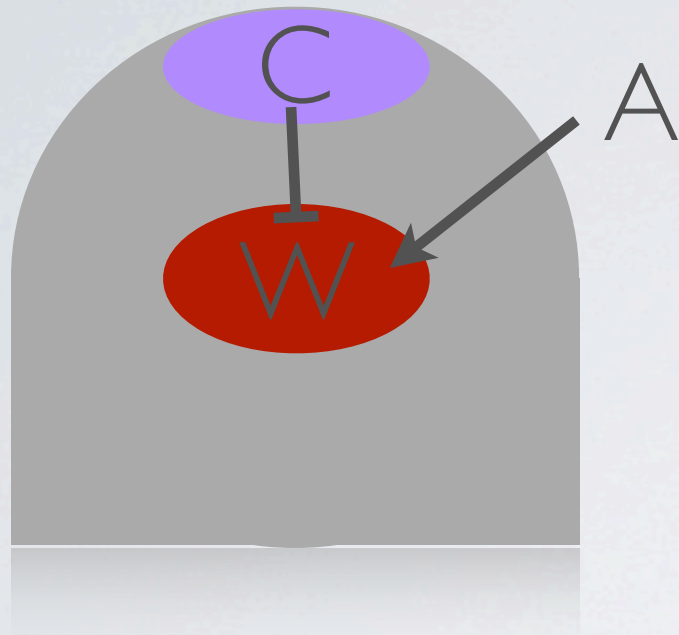
transcription

degradation

$$\frac{d[W]}{dt} = \frac{V_{max} K_C^n [A]^n}{(K_C^n + [C]^n)(K_A^n + [A]^n)} - k[W]$$

$$\frac{d[Ws]}{dt} = k_1[W] - k_2[Ws] + D\nabla^2[Ws]$$

model definitions



transcription

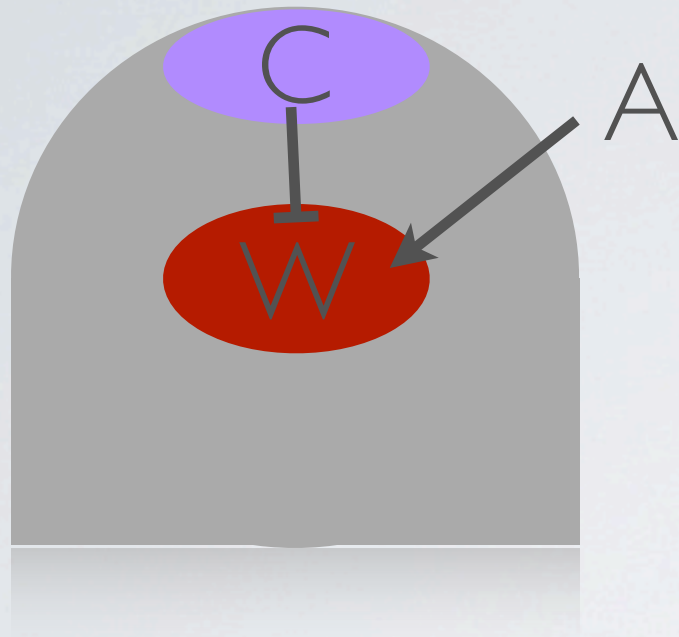
degradation

$$\frac{d[W]}{dt} = \frac{V_{max} K_C^n [A]^n}{(K_C^n + [C]^n)(K_A^n + [A]^n)} - k[W]$$

$$\frac{d[Ws]}{dt} = k_1[W] - k_2[Ws] + D\nabla^2[Ws]$$

diffusion

model definitions



transcription

degradation

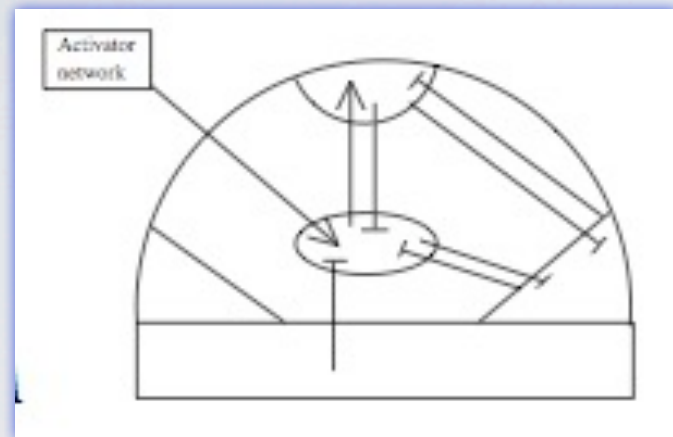
$$\frac{d[W]}{dt} = \frac{V_{max} K_C^n [A]^n}{(K_C^n + [C]^n)(K_A^n + [A]^n)} - k[W]$$

$$\frac{d[Ws]}{dt} = k_1[W] - k_2[Ws] + D\nabla^2[Ws]$$

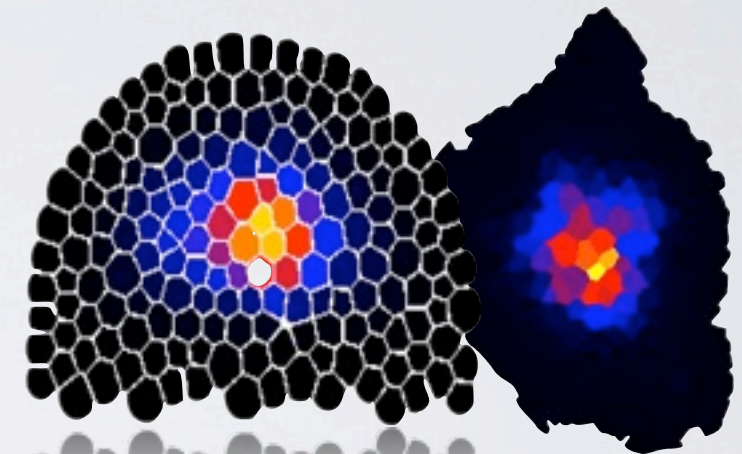
protein?

diffusion

computational approach



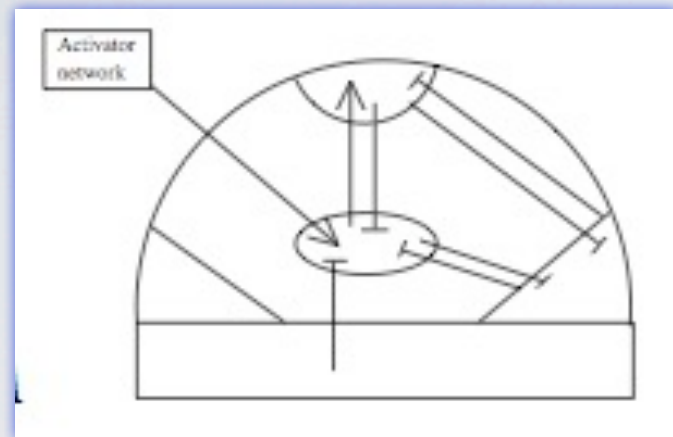
Model(s)



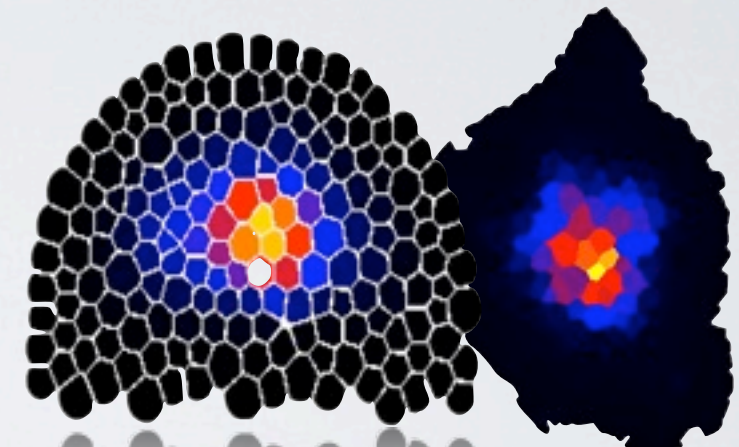
Data



computational approach



Model(s)



Data

predictive models VS parameter fitting

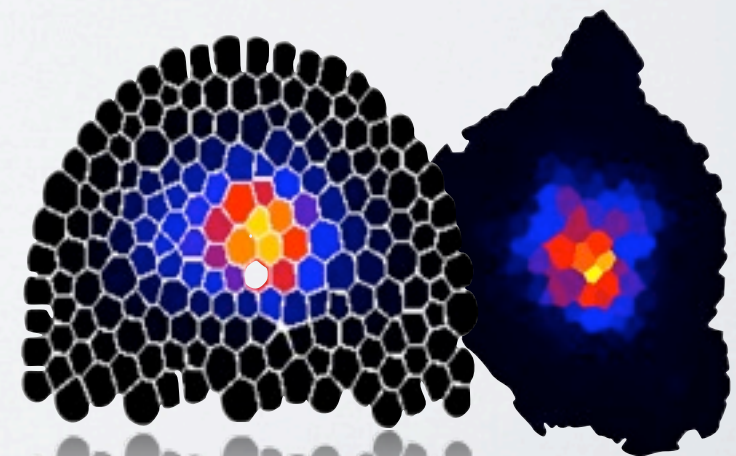
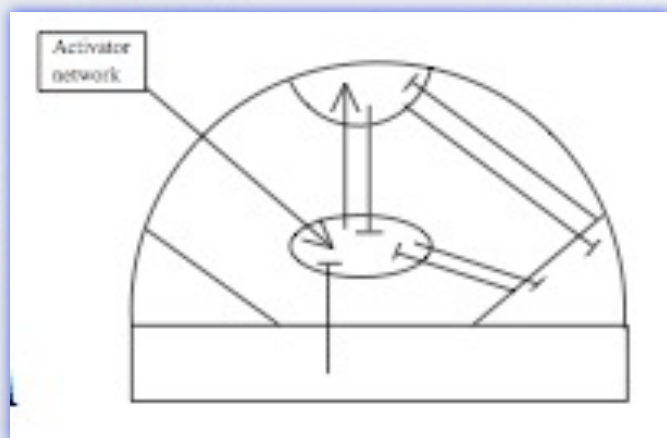
computational approach



Model(s)



Data



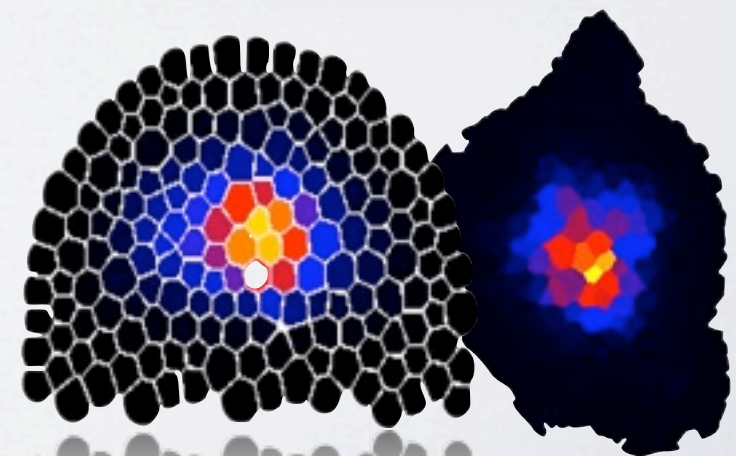
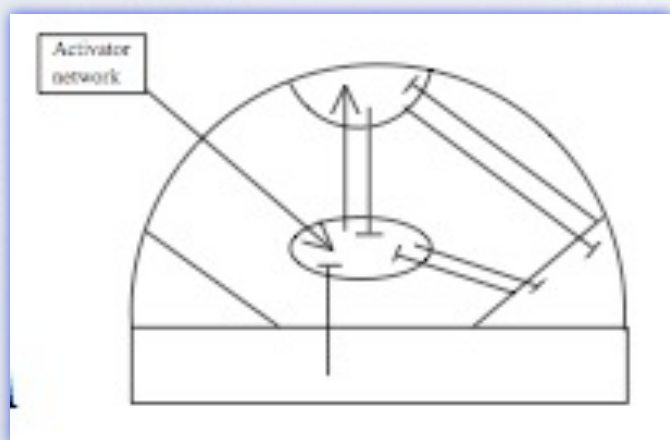
computational approach



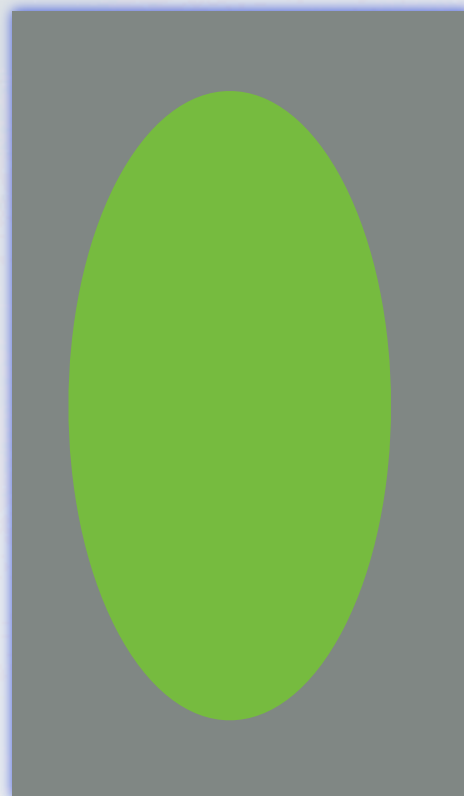
Model(s)



Data



computational approach

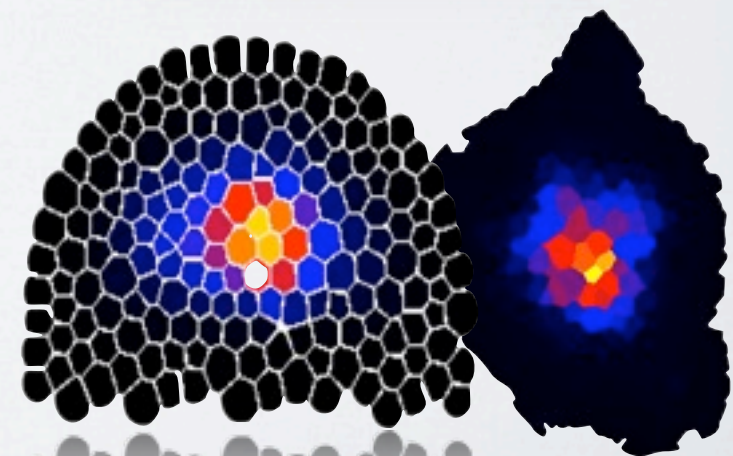
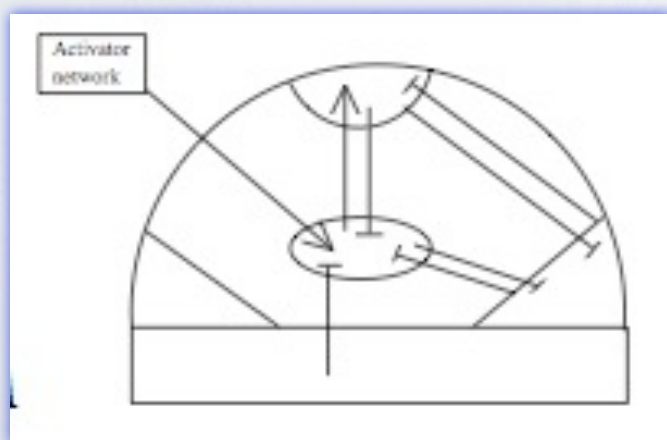


Model(s)

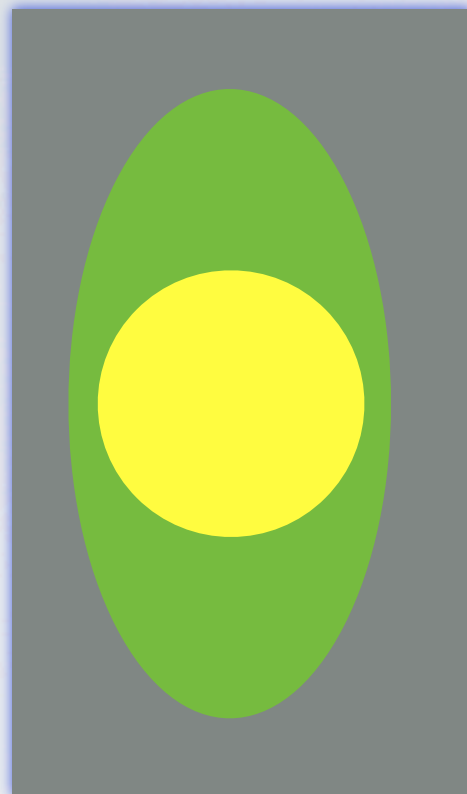
optimize / train



Data



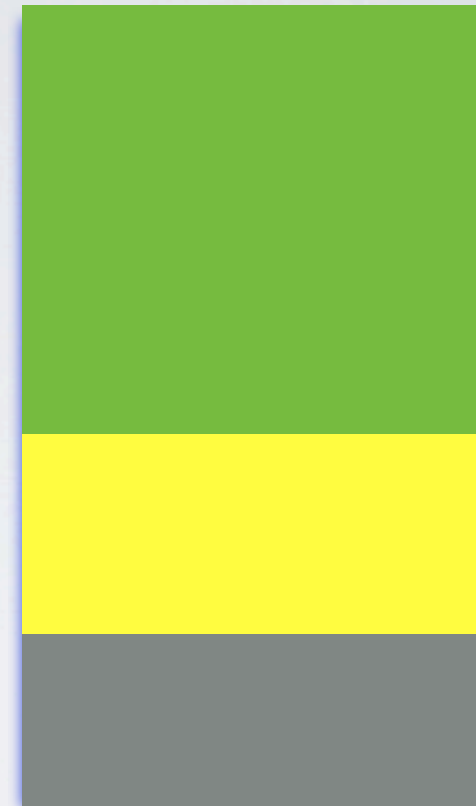
computational approach



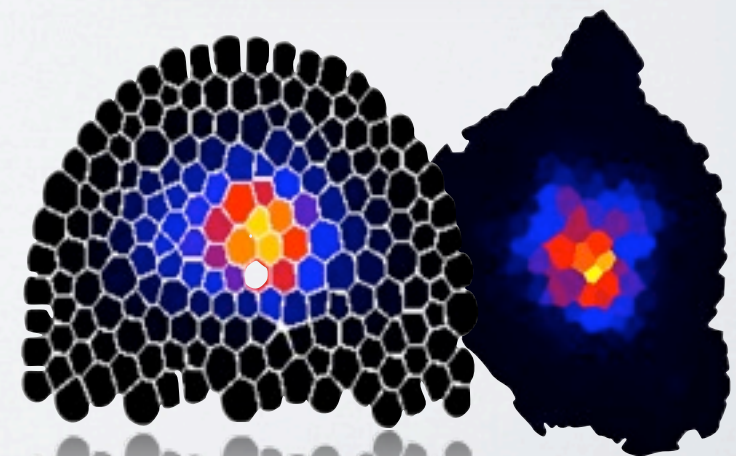
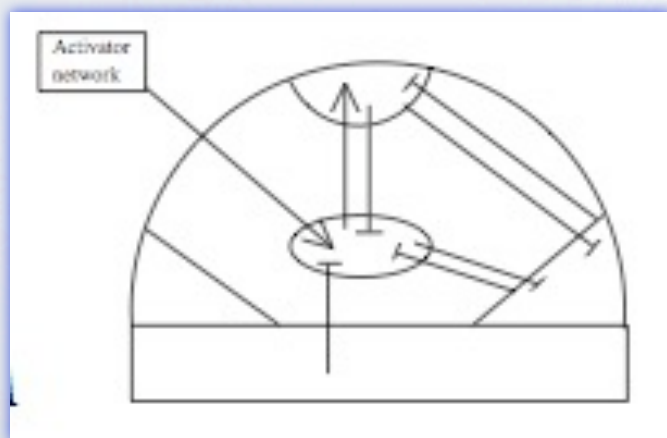
Model(s)

optimize / train

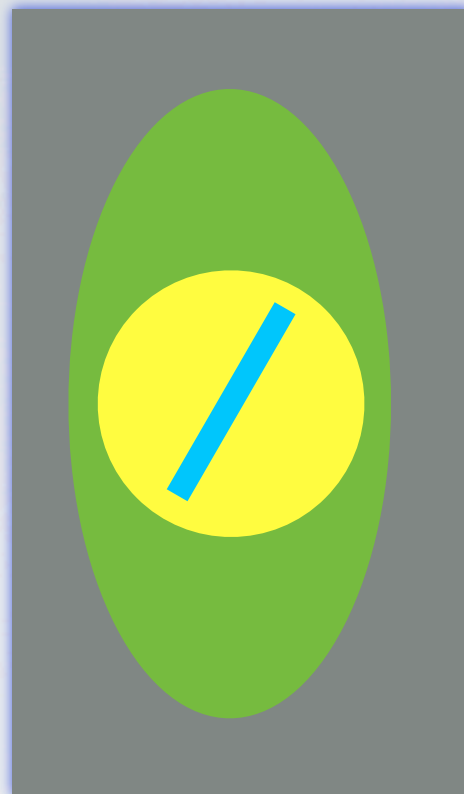
filter / test



Data



computational approach



Model(s)

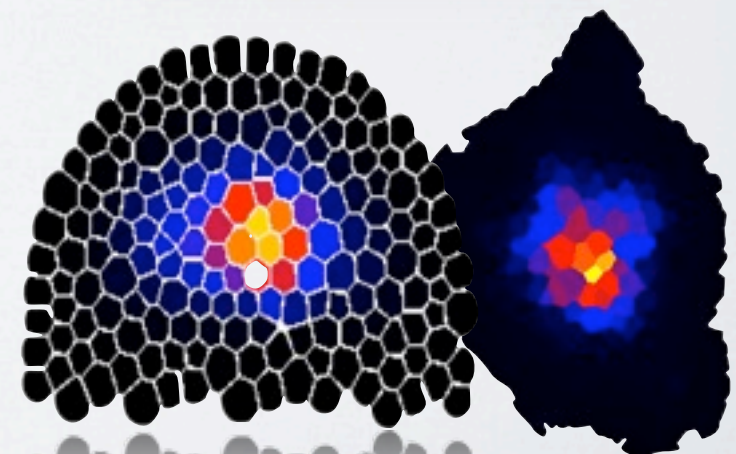
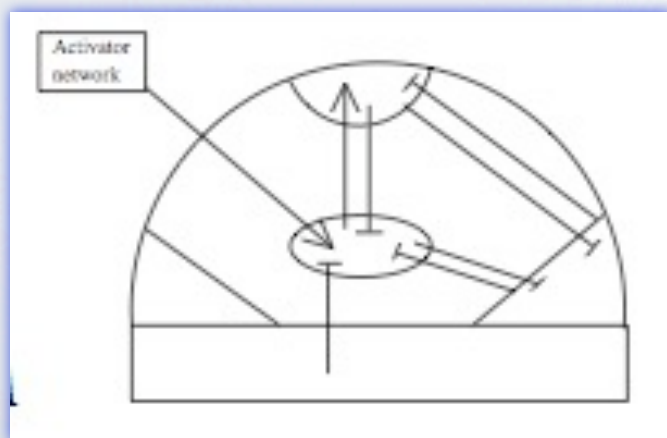
optimize / train

filter / test

analyze / validate



Data



computer modeling

computer modeling

...computer manipulation of a mathematical model...

(Leopold and Hall 1966)

computer modeling



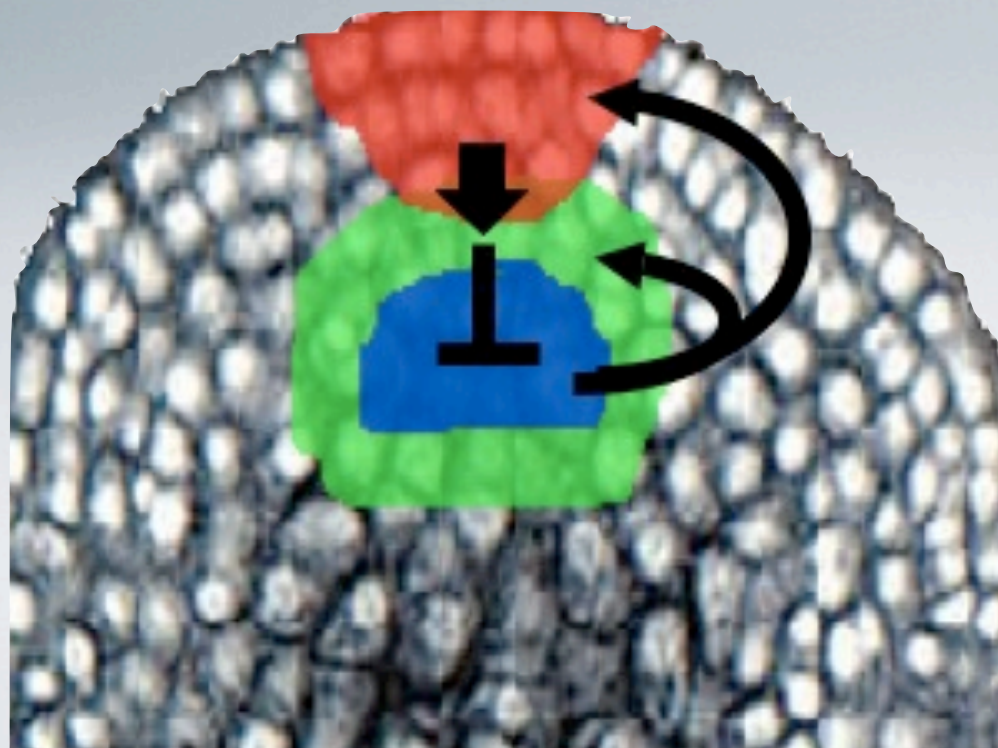
...com

odel...

stem cell regulation

stem cell regulation

- CLV3 marks stem cells and WUS 'defines' an organizing center

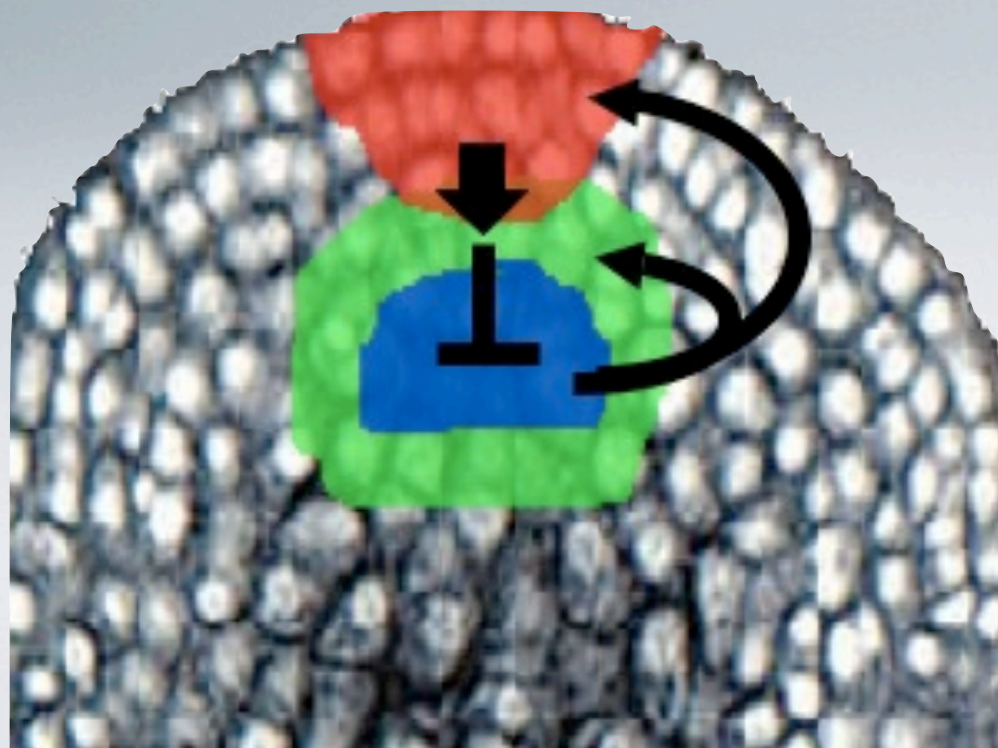


- CLV3 extracellular peptide
- CLV1 receptor
- WUS transcription factor



stem cell regulation

- CLV3 marks stem cells and WUS 'defines' an organizing center
- WUS activates CLV3 (stem cells)

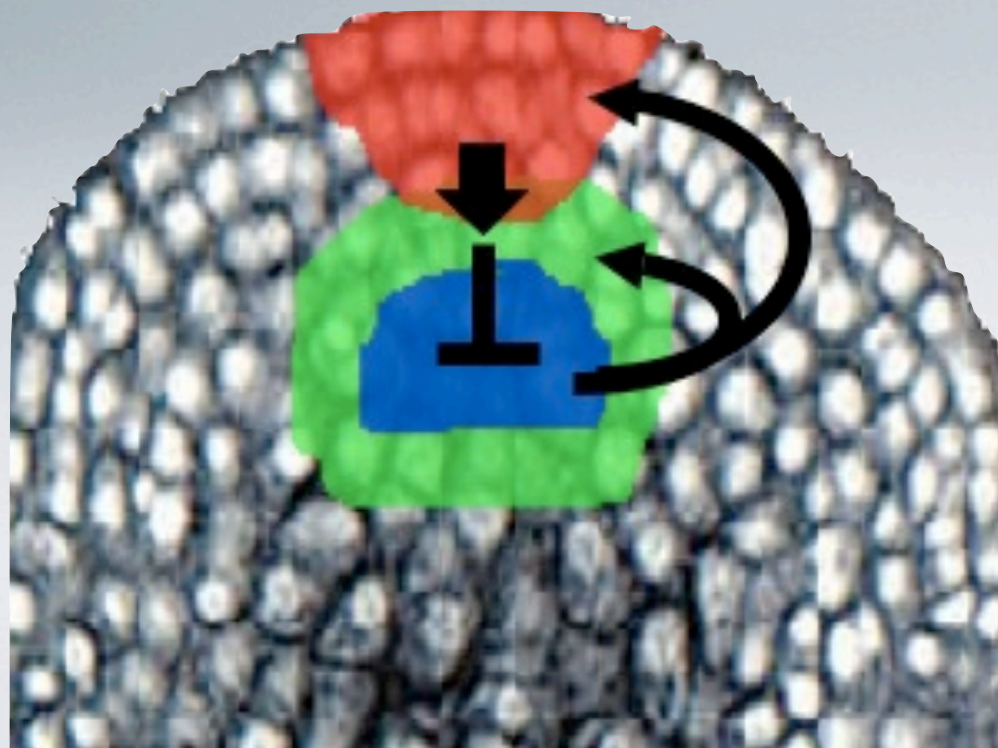


- CLV3 extracellular peptide
- CLV1 receptor
- WUS transcription factor



stem cell regulation

- CLV3 marks stem cells and WUS 'defines' an organizing center
- WUS activates CLV3 (stem cells)
- CLV3/CLV1 network repress WUS



- CLV3 extracellular peptide
- CLV1 receptor
- WUS transcription factor



What activates WUS?

What activates WUS?

How is the CLV3 to WUS signal mediated?

What activates WUS?

How is the WUS to CLV3 signal mediated?

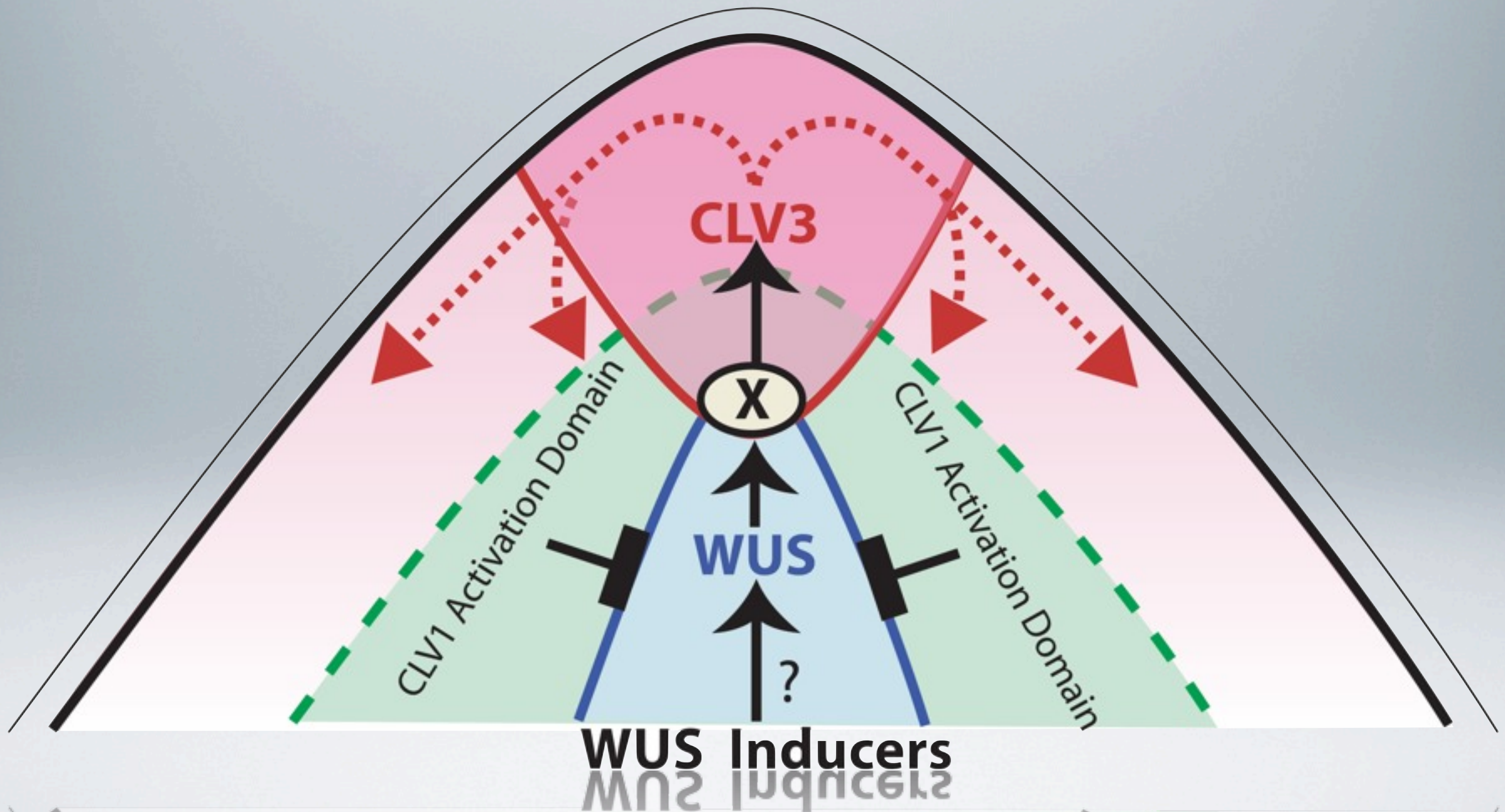
How is the CLV3 to WUS signal mediated?

What activates WUS?

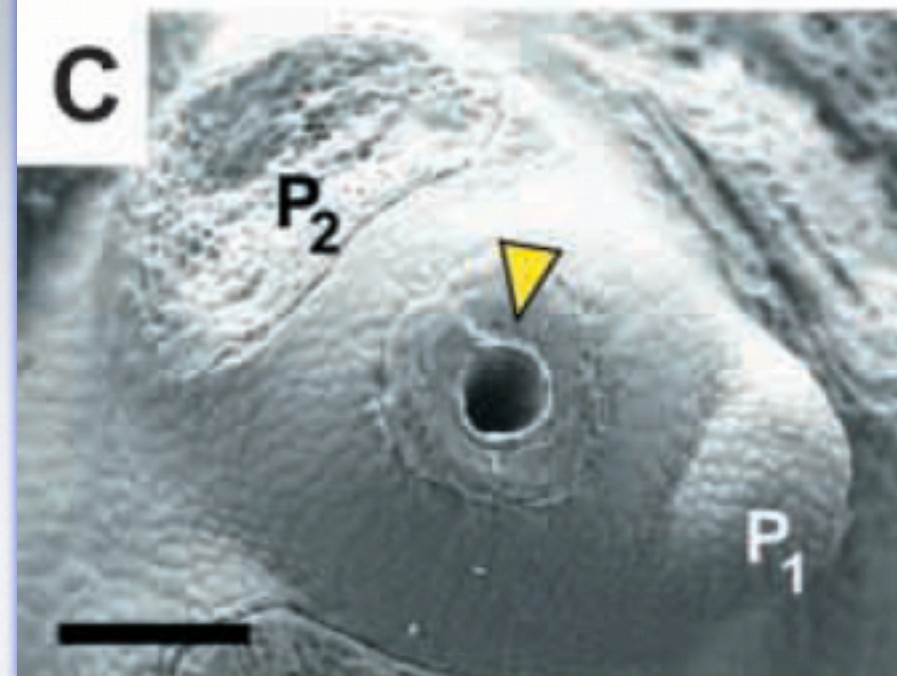
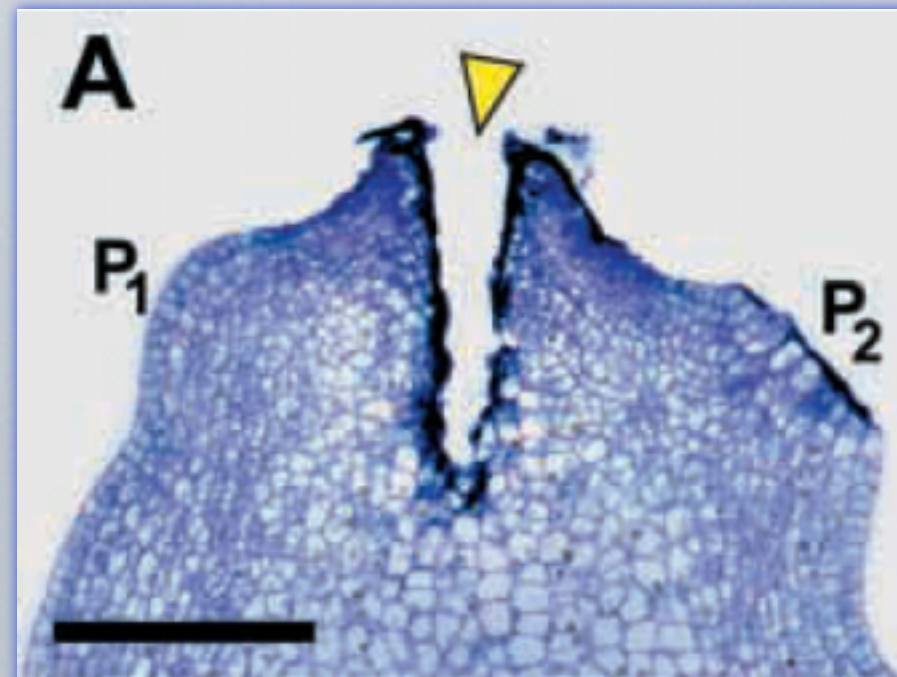
How is the WUS to CLV3 signal mediated?

How is the CLV3 to WUS signal mediated?

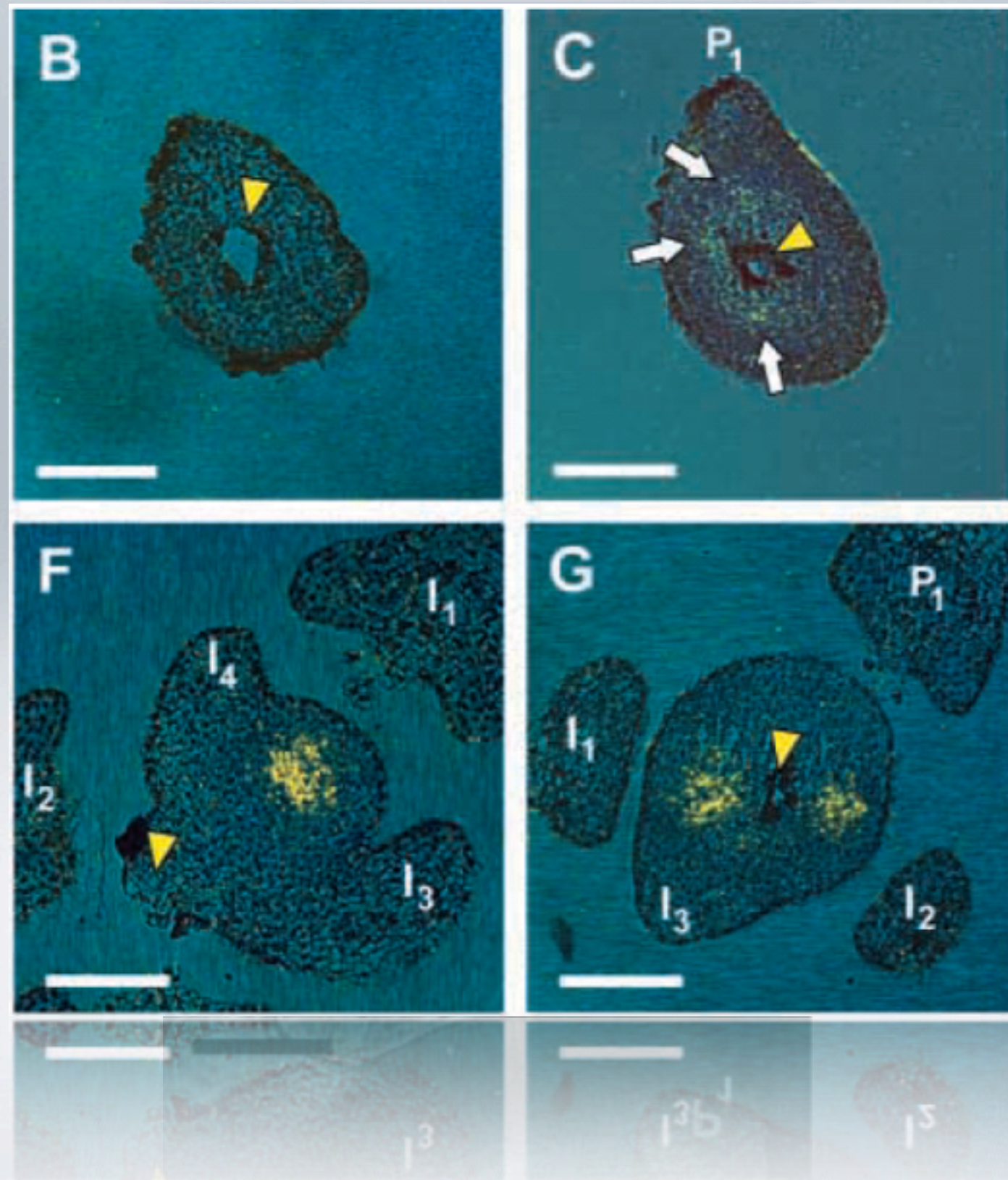
What activates WUS?



Laser ablation experiment

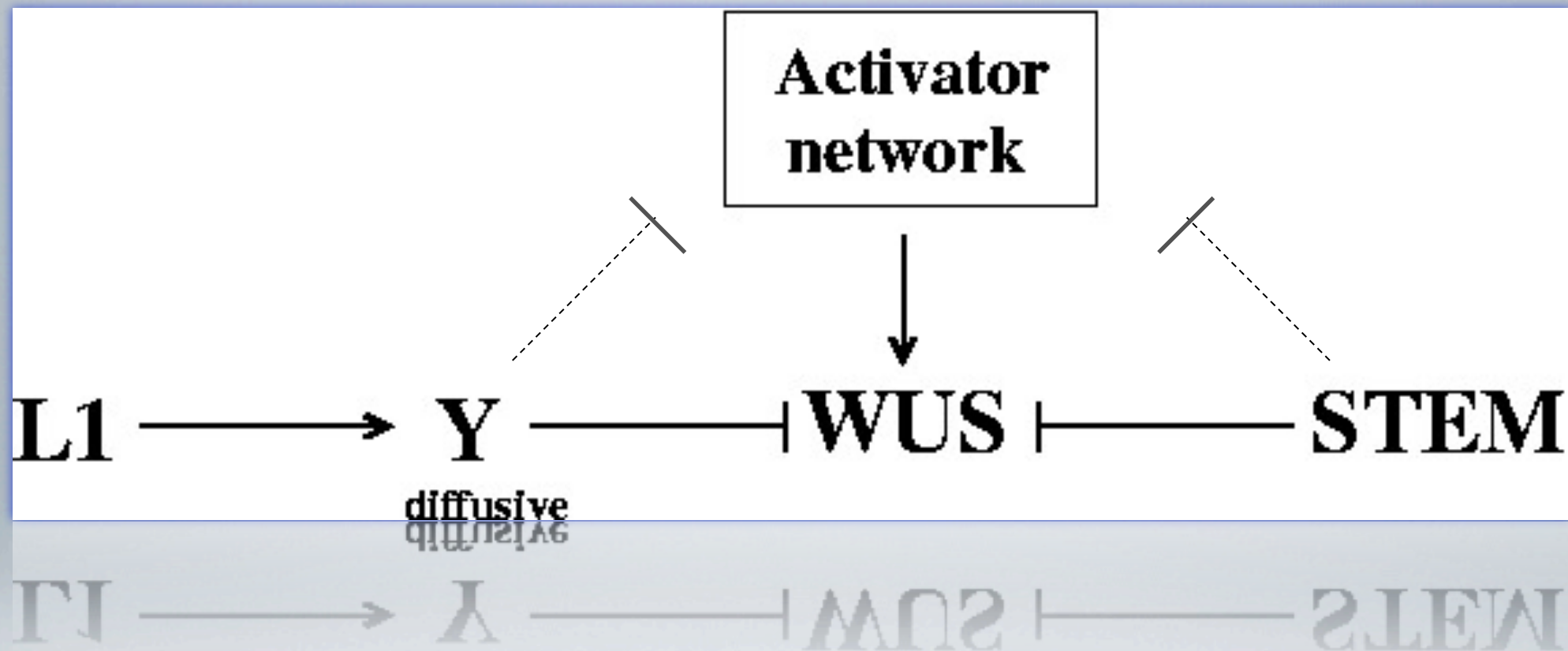


Laser ablation experiment

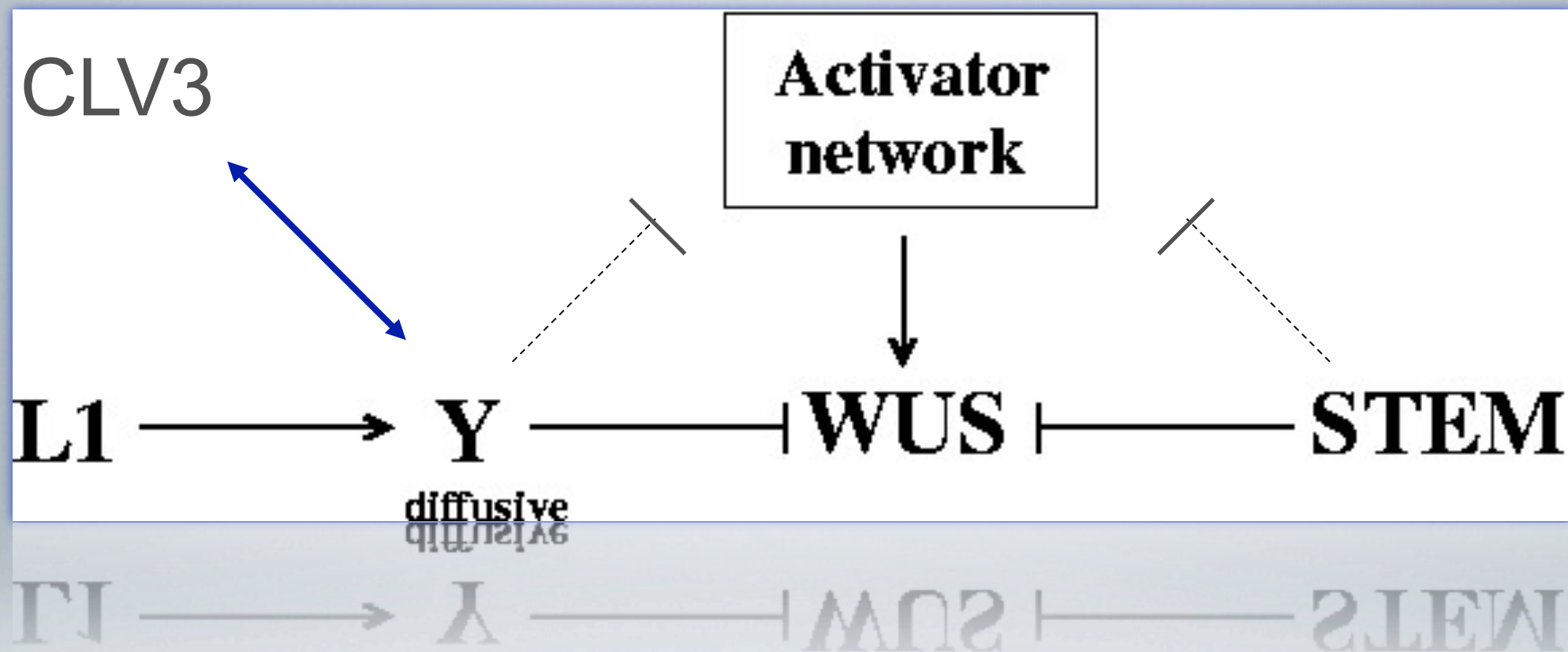


WUS
expression

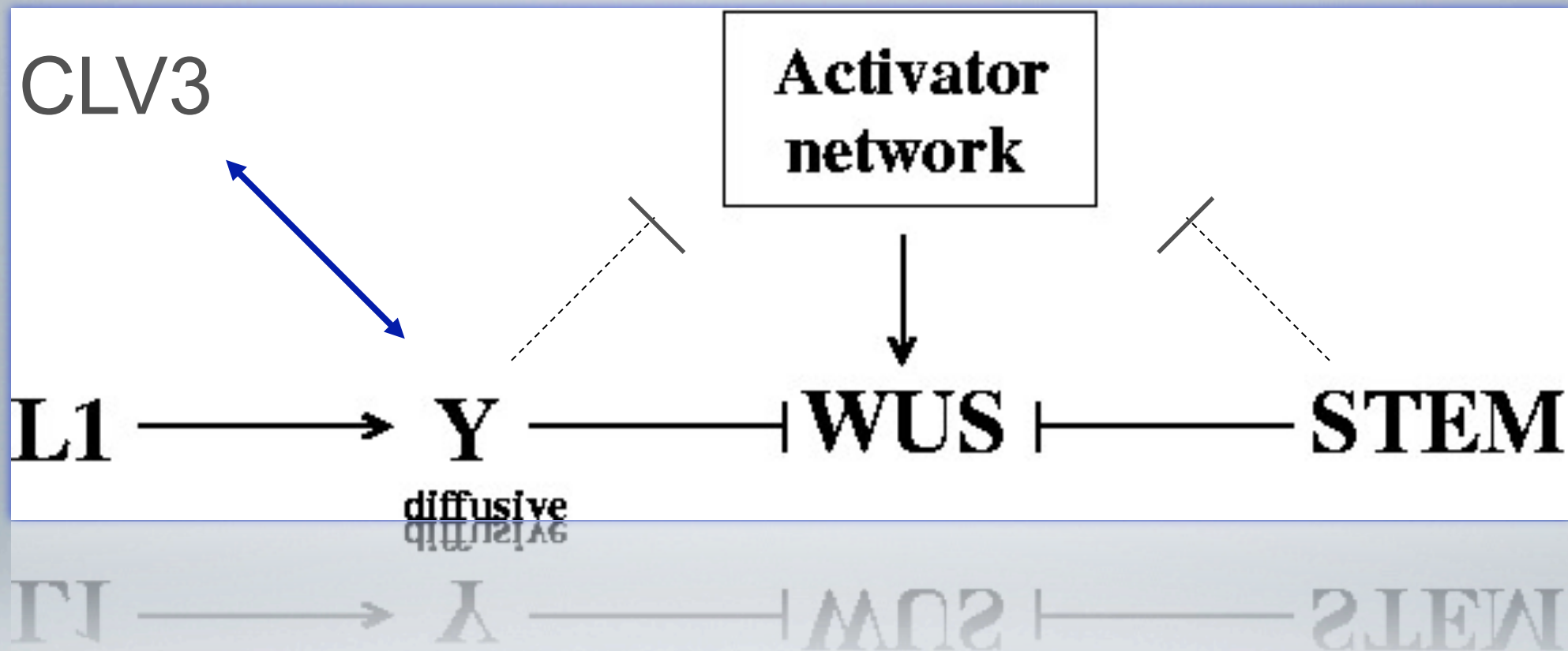
WUS network



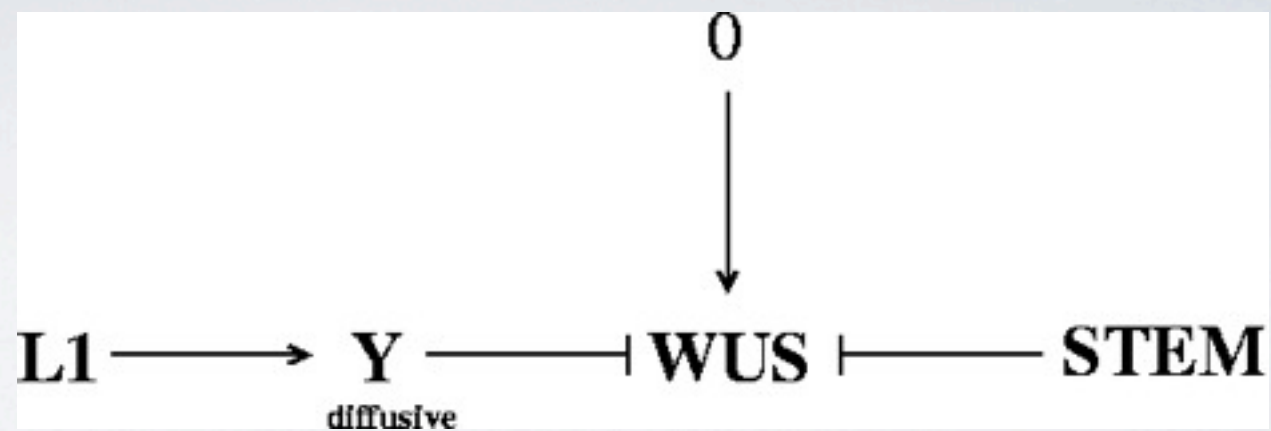
WUS network



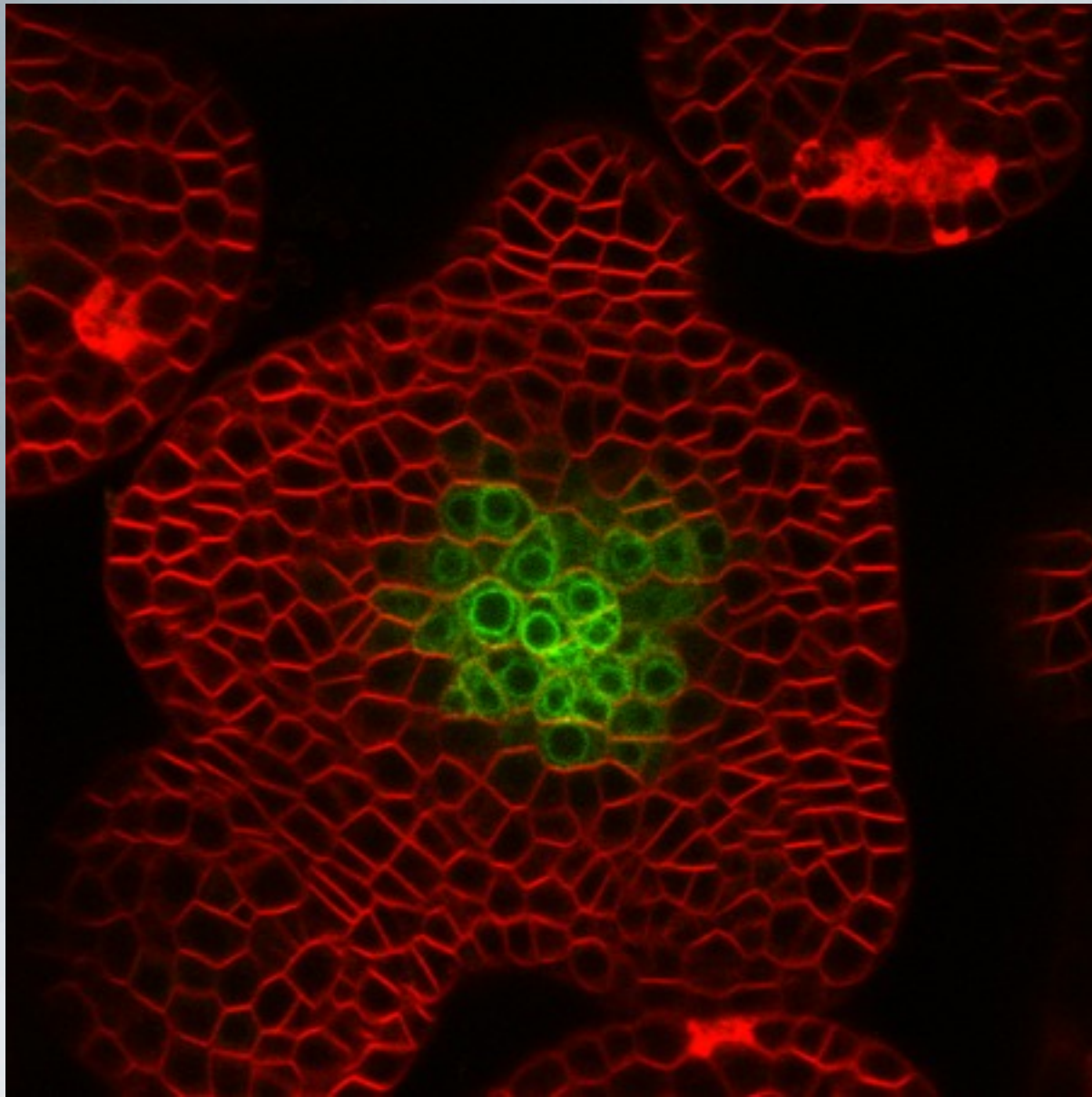
WUS network



Comparison network

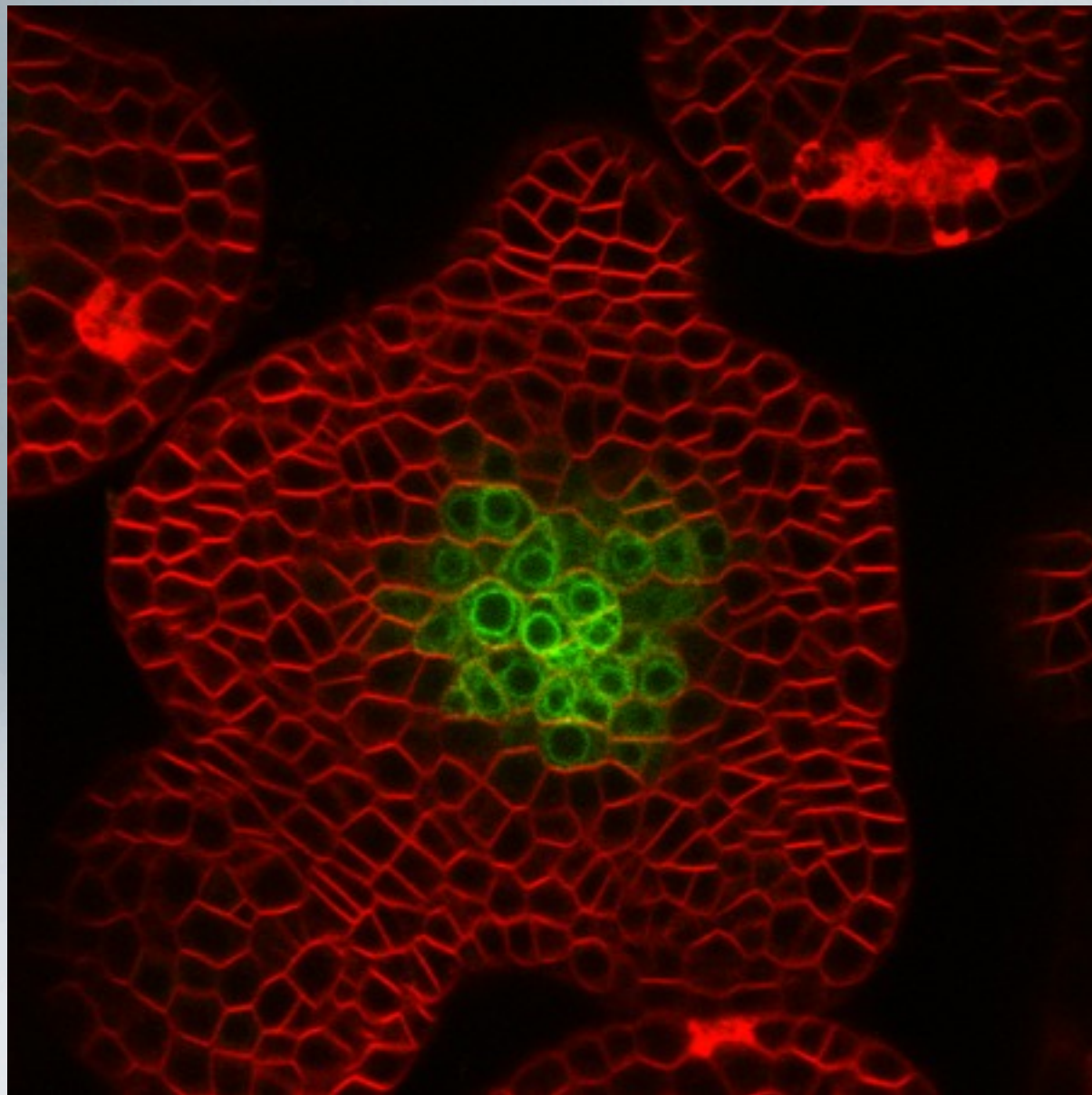


Quantitative measures from image

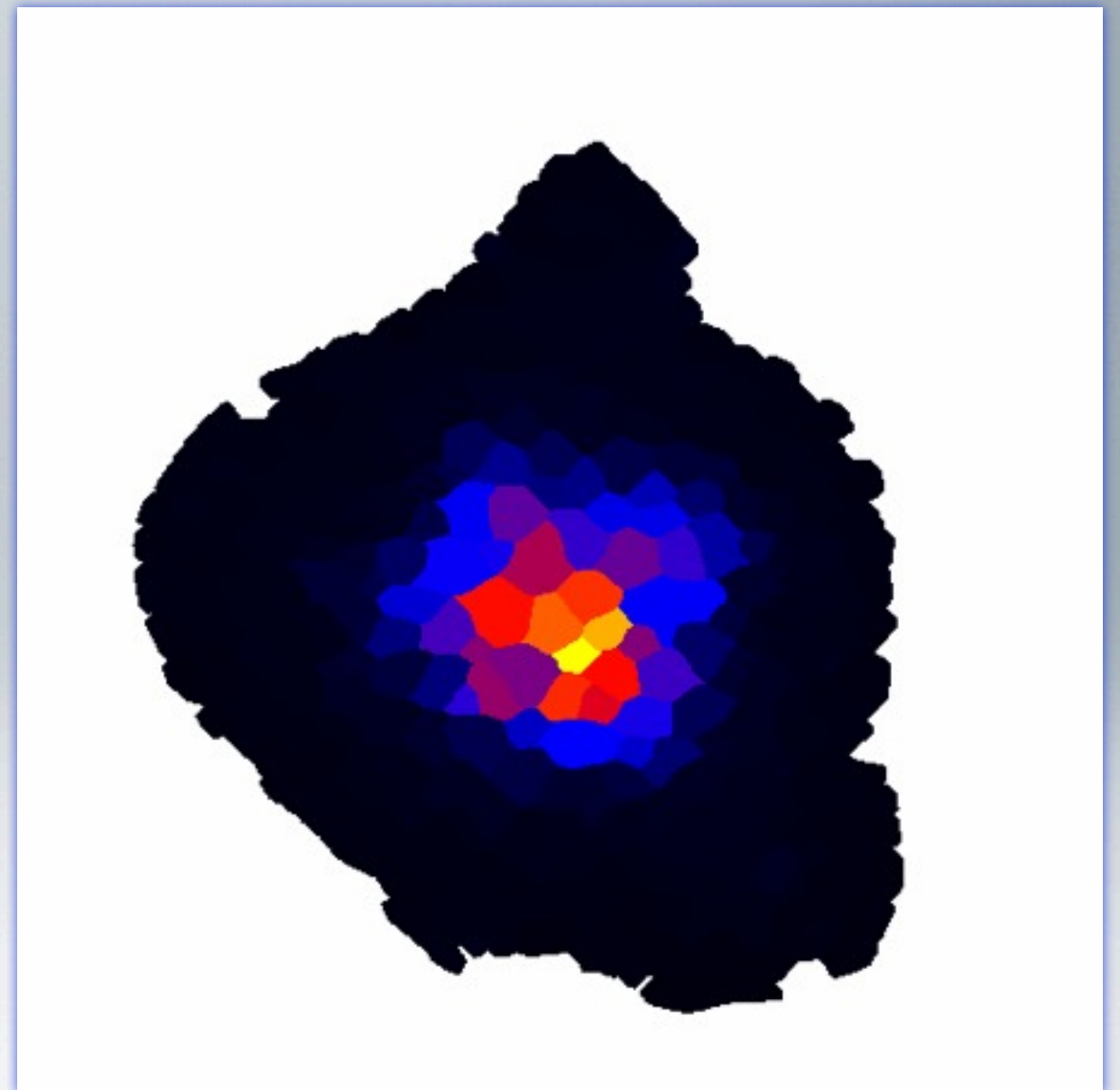


Green WUS::GFP
Red membrane stain

Quantitative measures from image



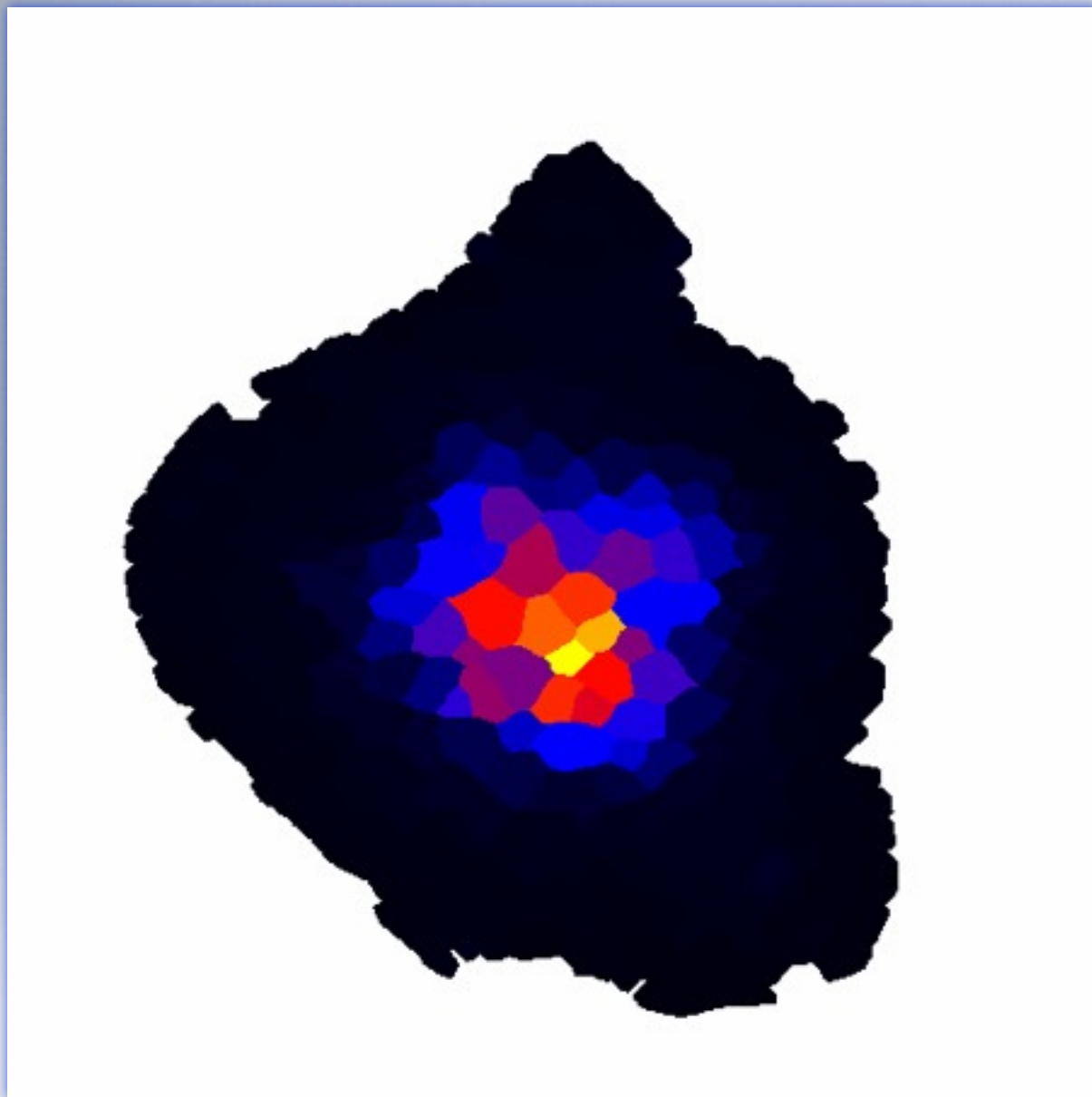
Green WUS::GFP
Red membrane stain



WUS "concentration"

WUS network simulation

Cell volumes, wall areas, and neighbors from template

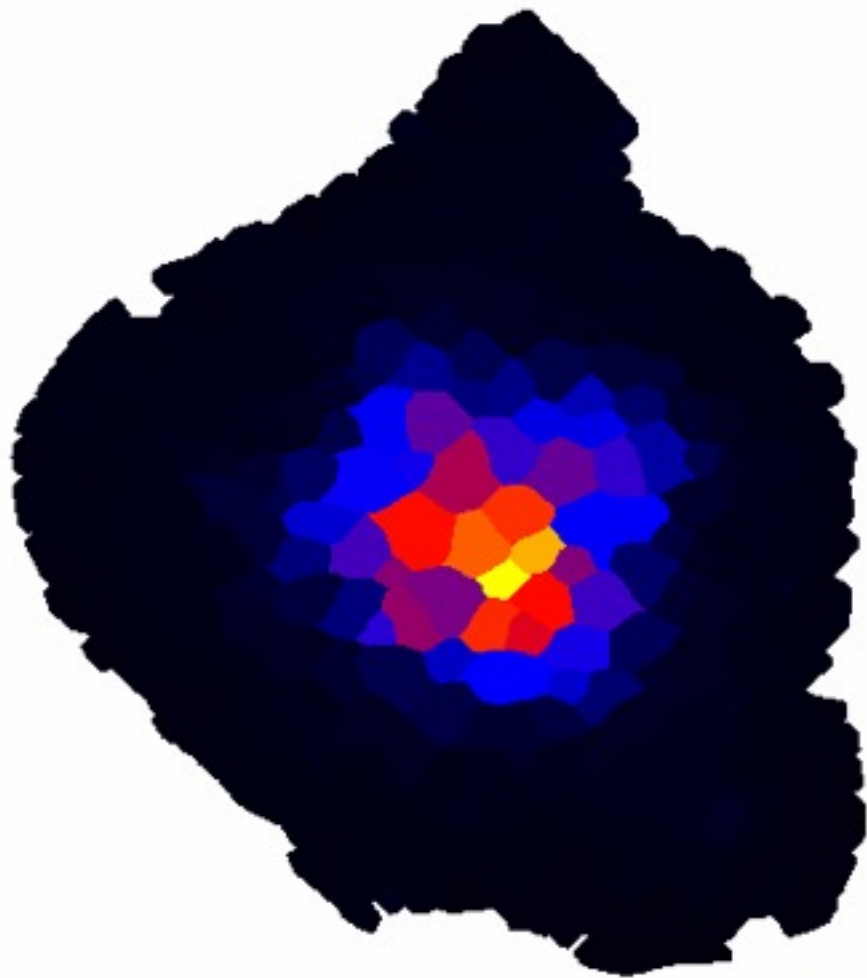


Template

Simulation

WUS network simulation

Cell volumes, wall areas, and neighbors from template

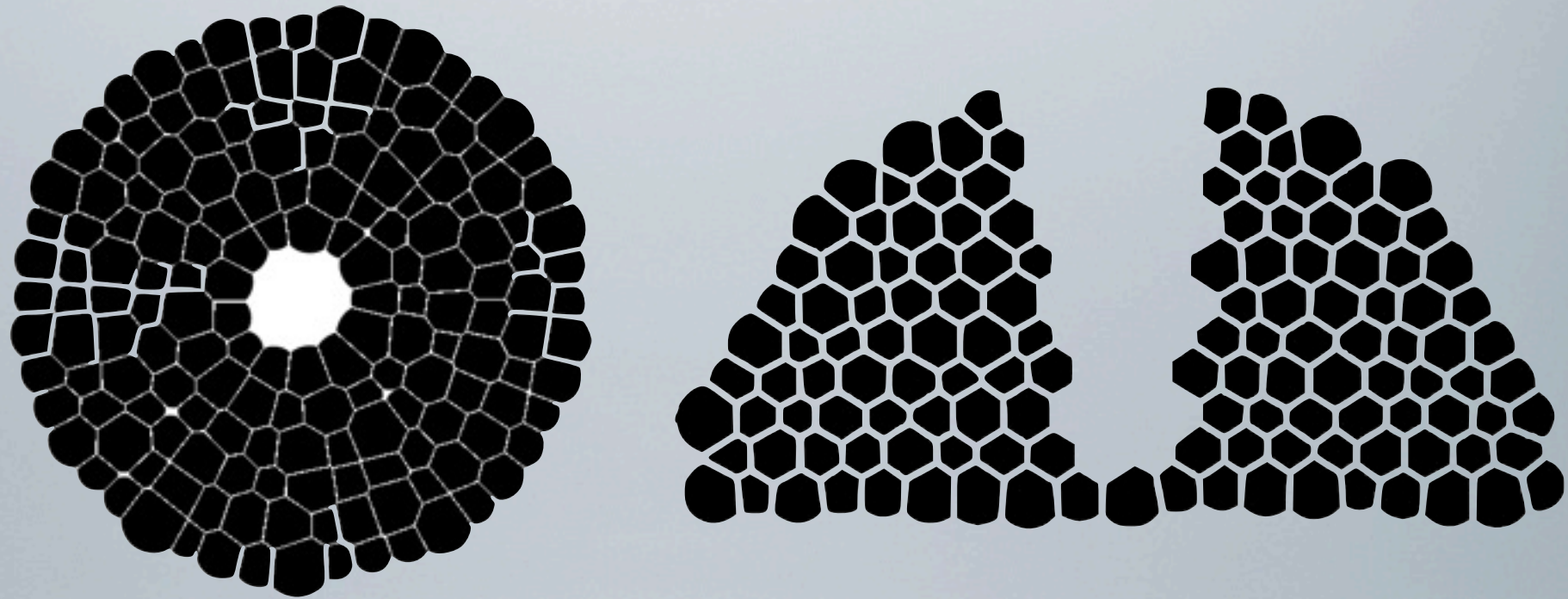


Template

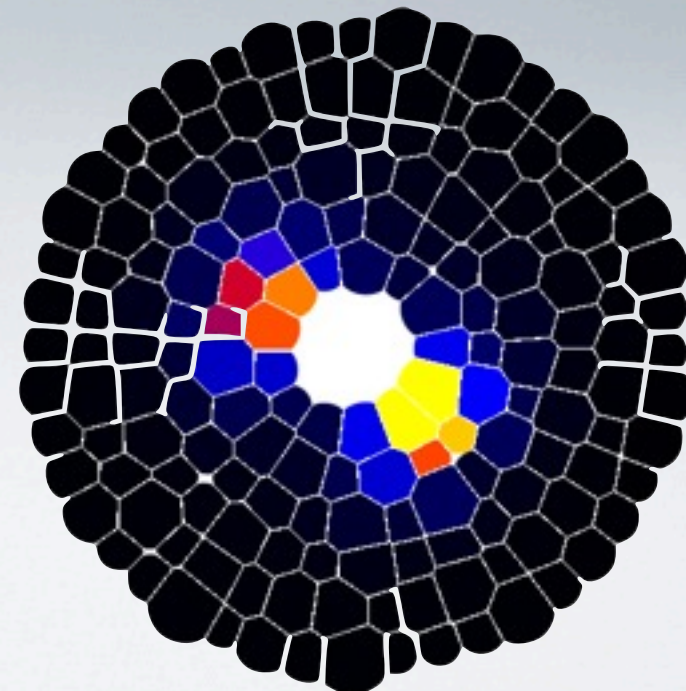
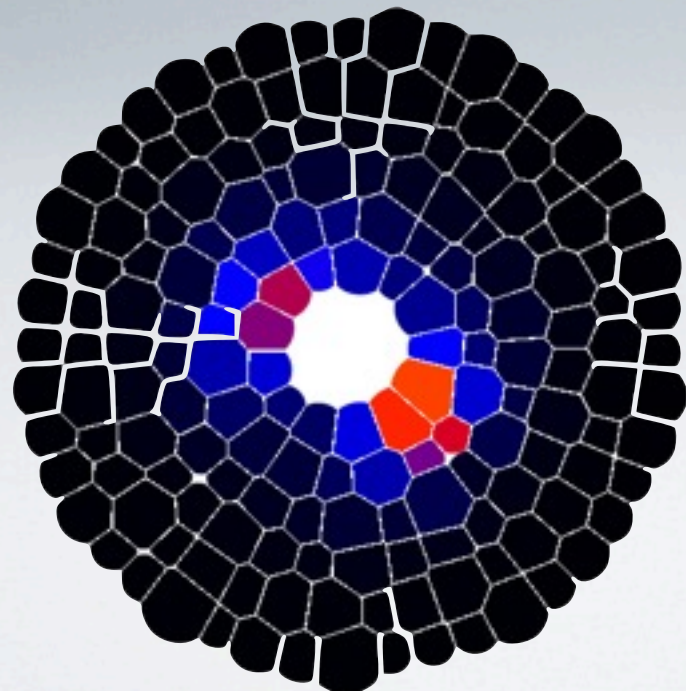
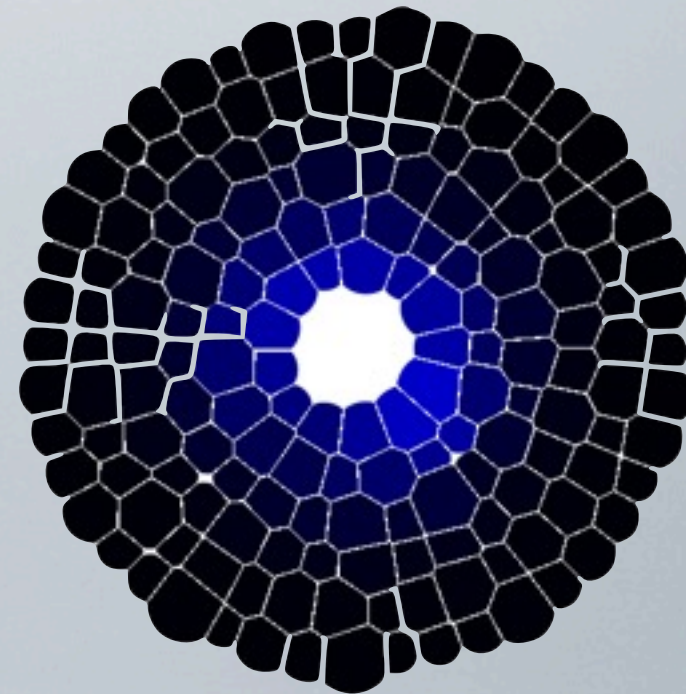
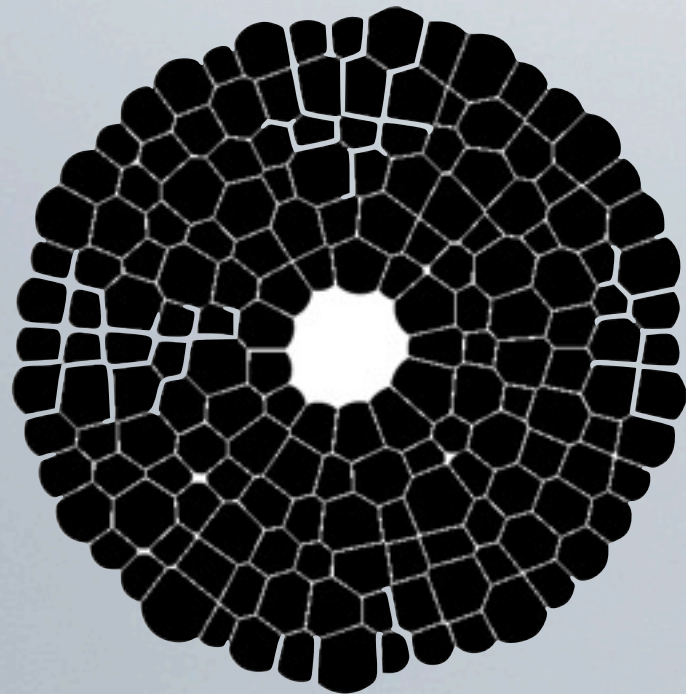


Simulation

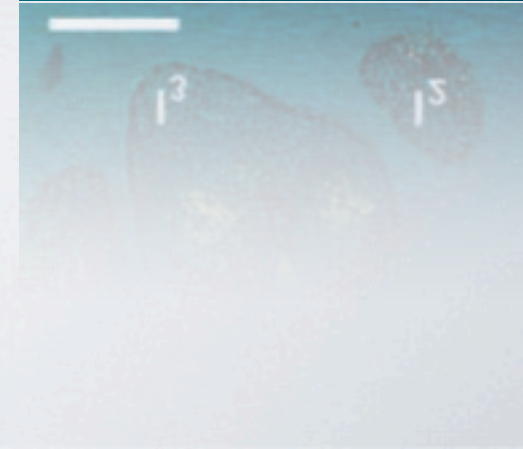
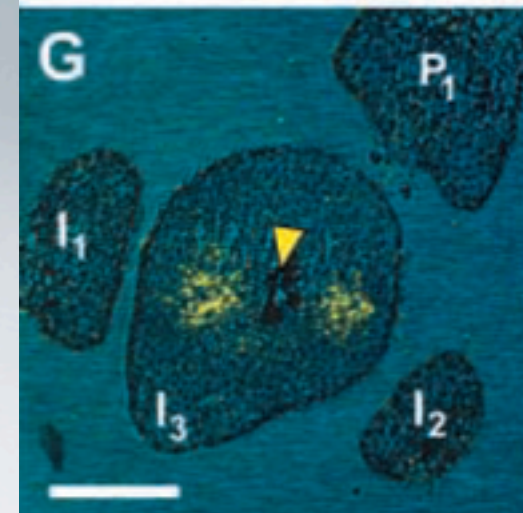
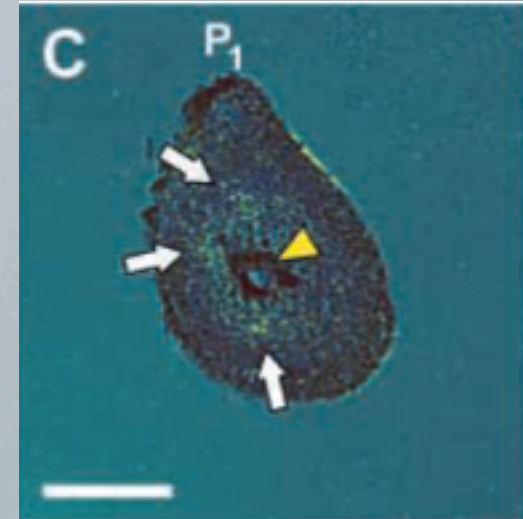
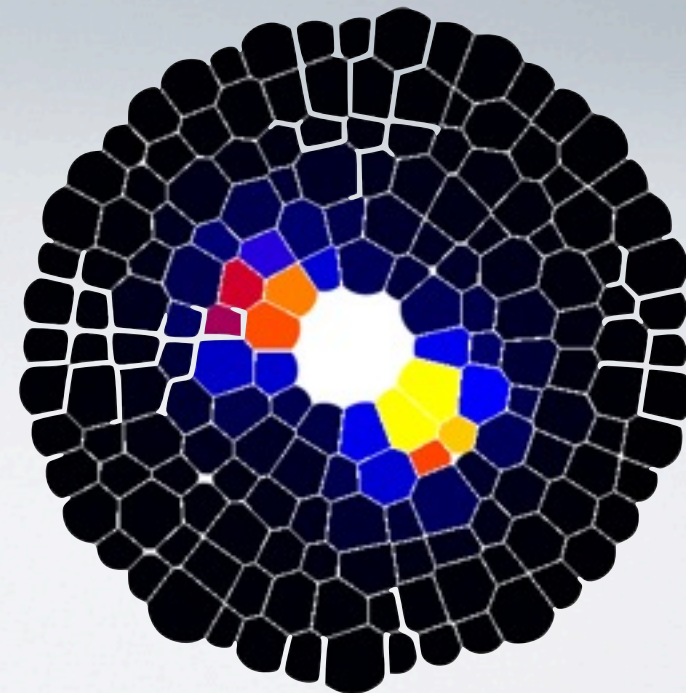
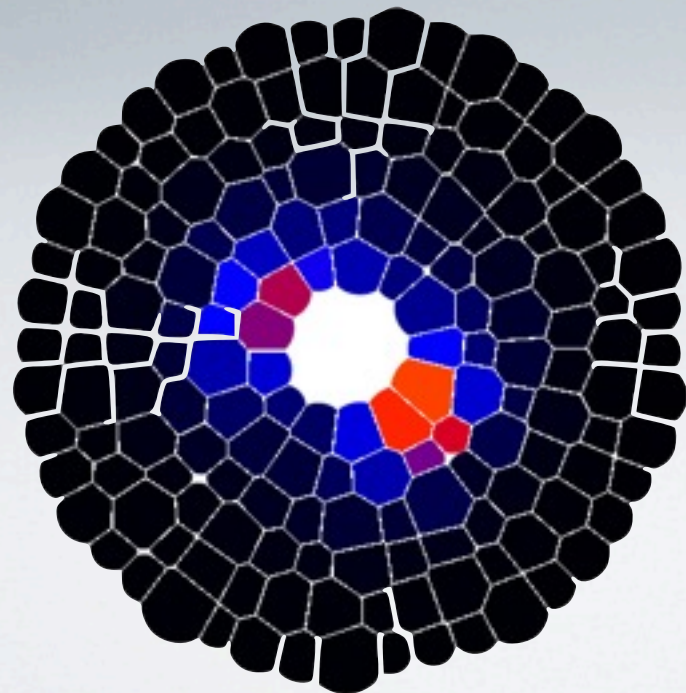
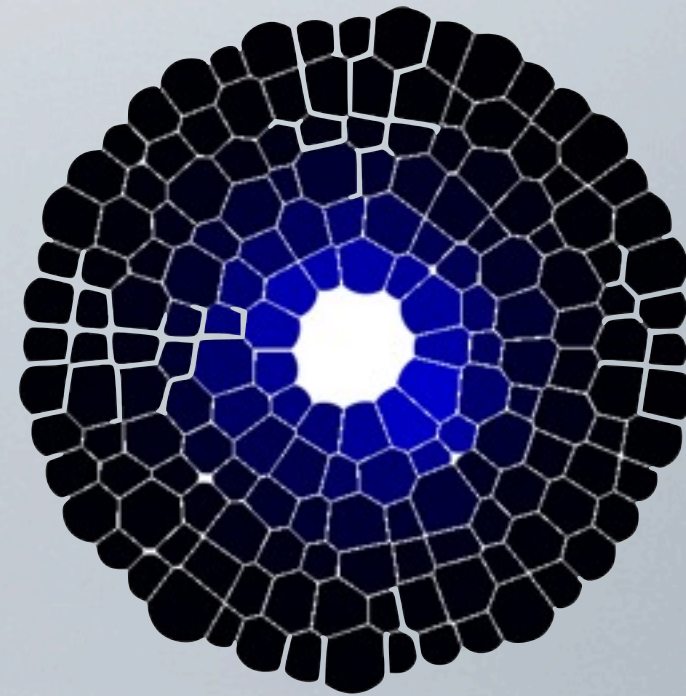
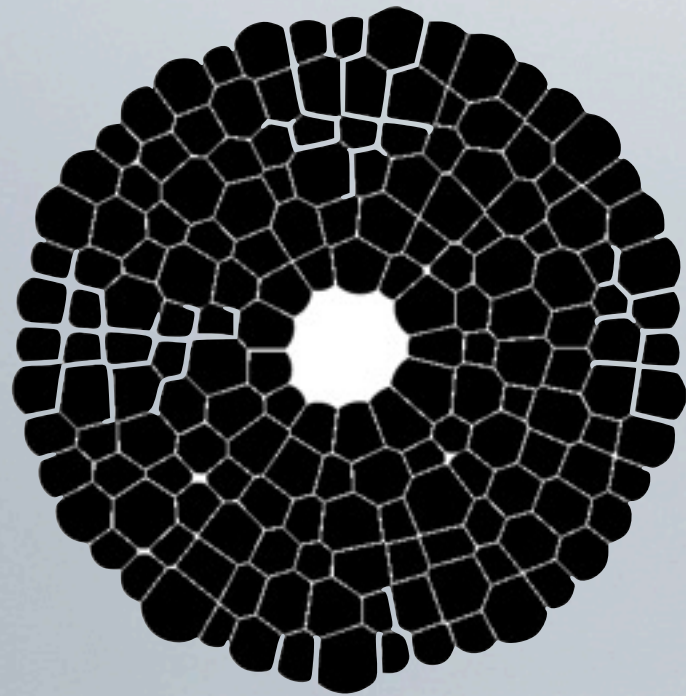
Laser ablation simulation



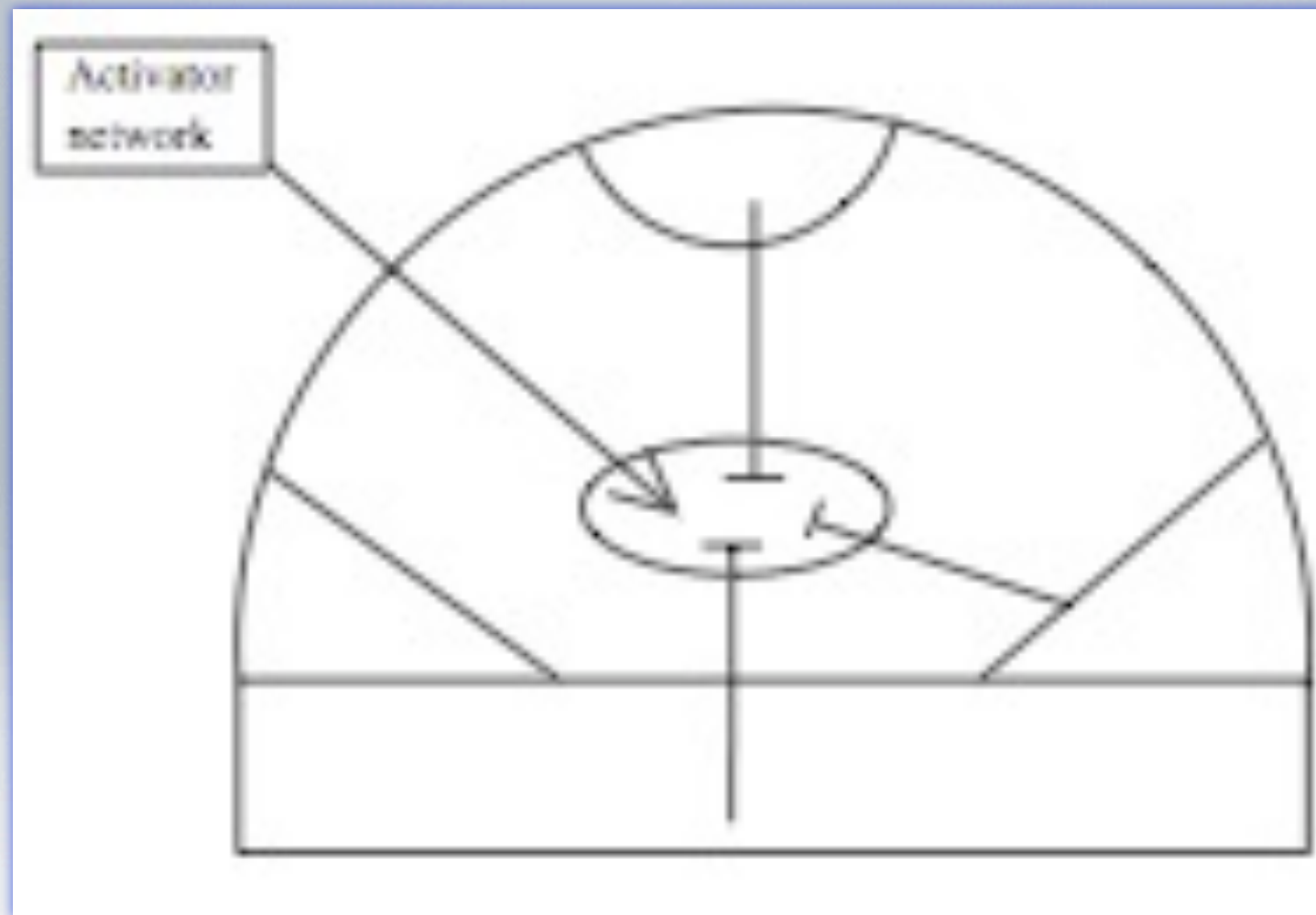
Laser ablation simulation



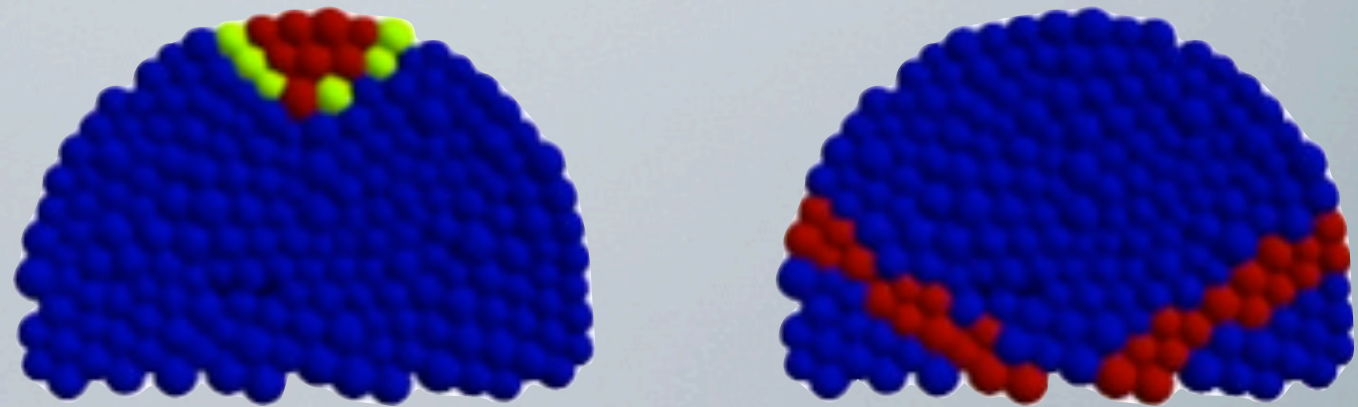
Laser ablation simulation



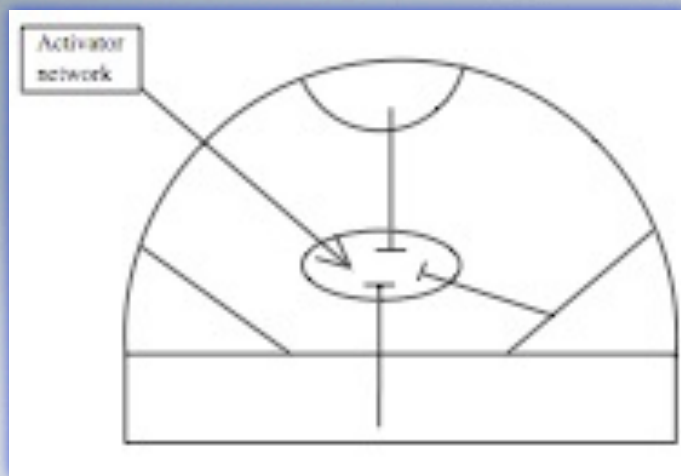
CLV3 based WUS repression



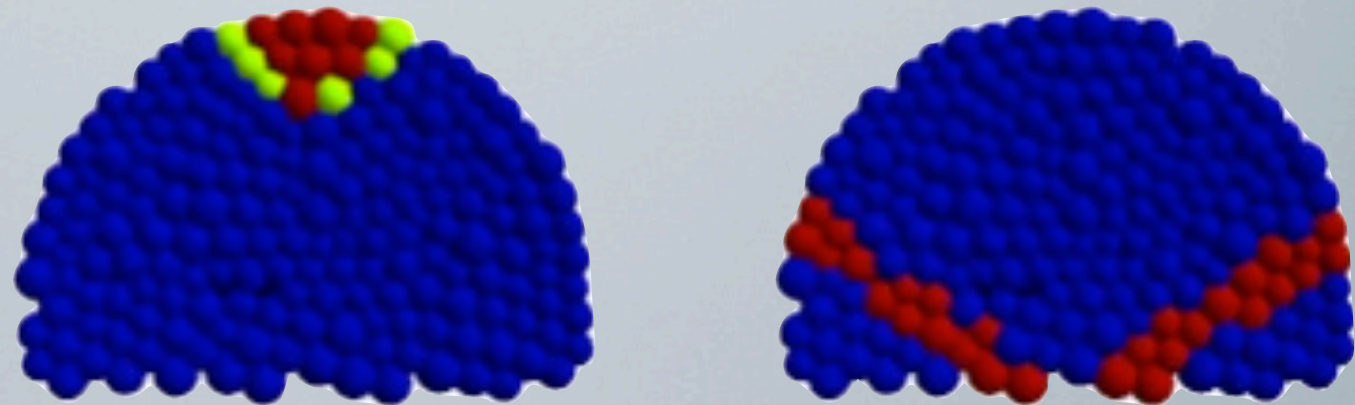
CLV3 based WUS repression



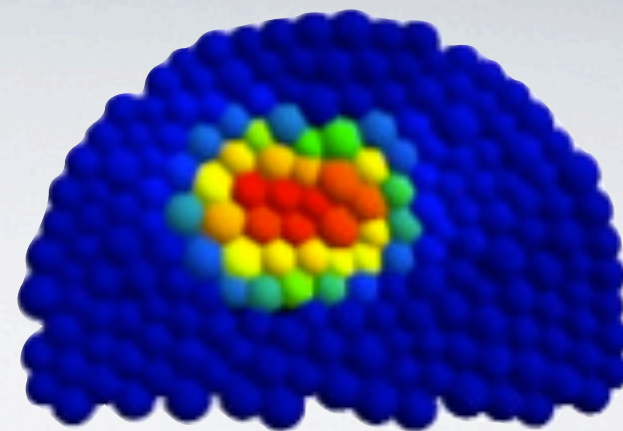
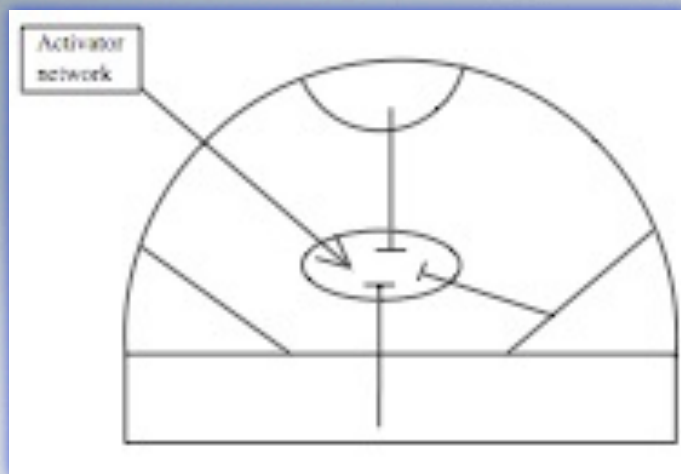
CLV3 + PZ repressors static



CLV3 based WUS repression

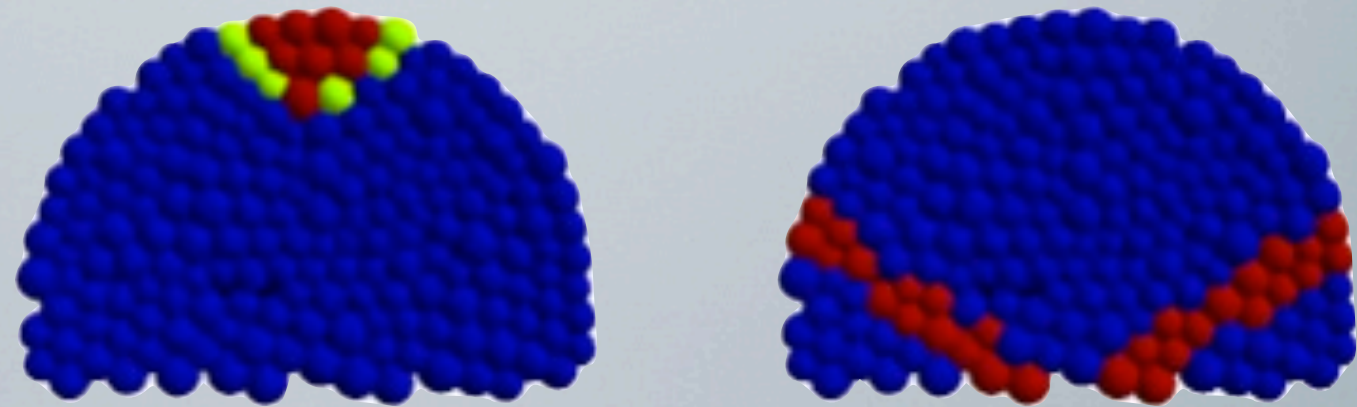


CLV3 + PZ repressors static

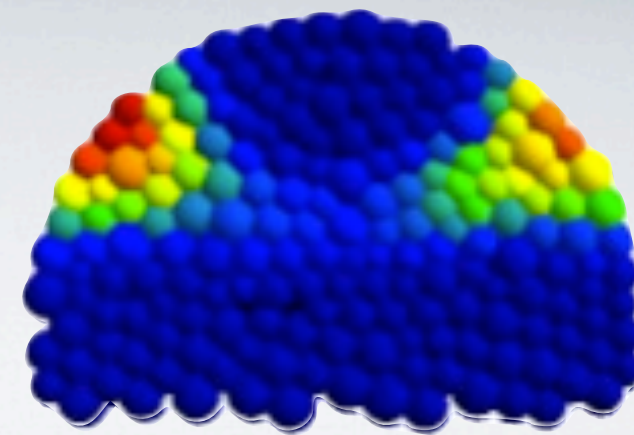
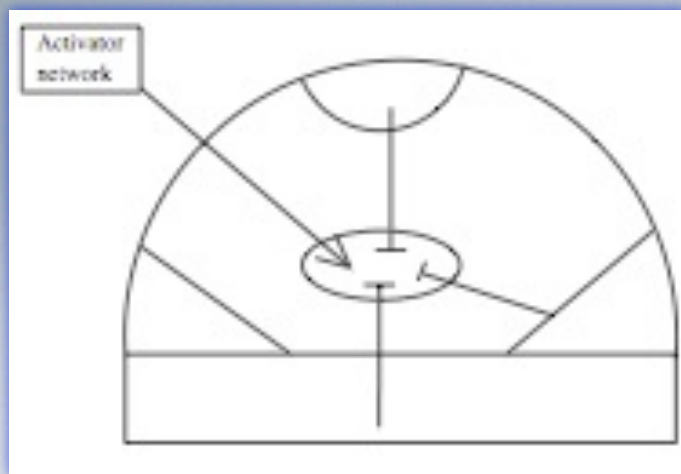


WUS

CLV3 based WUS repression



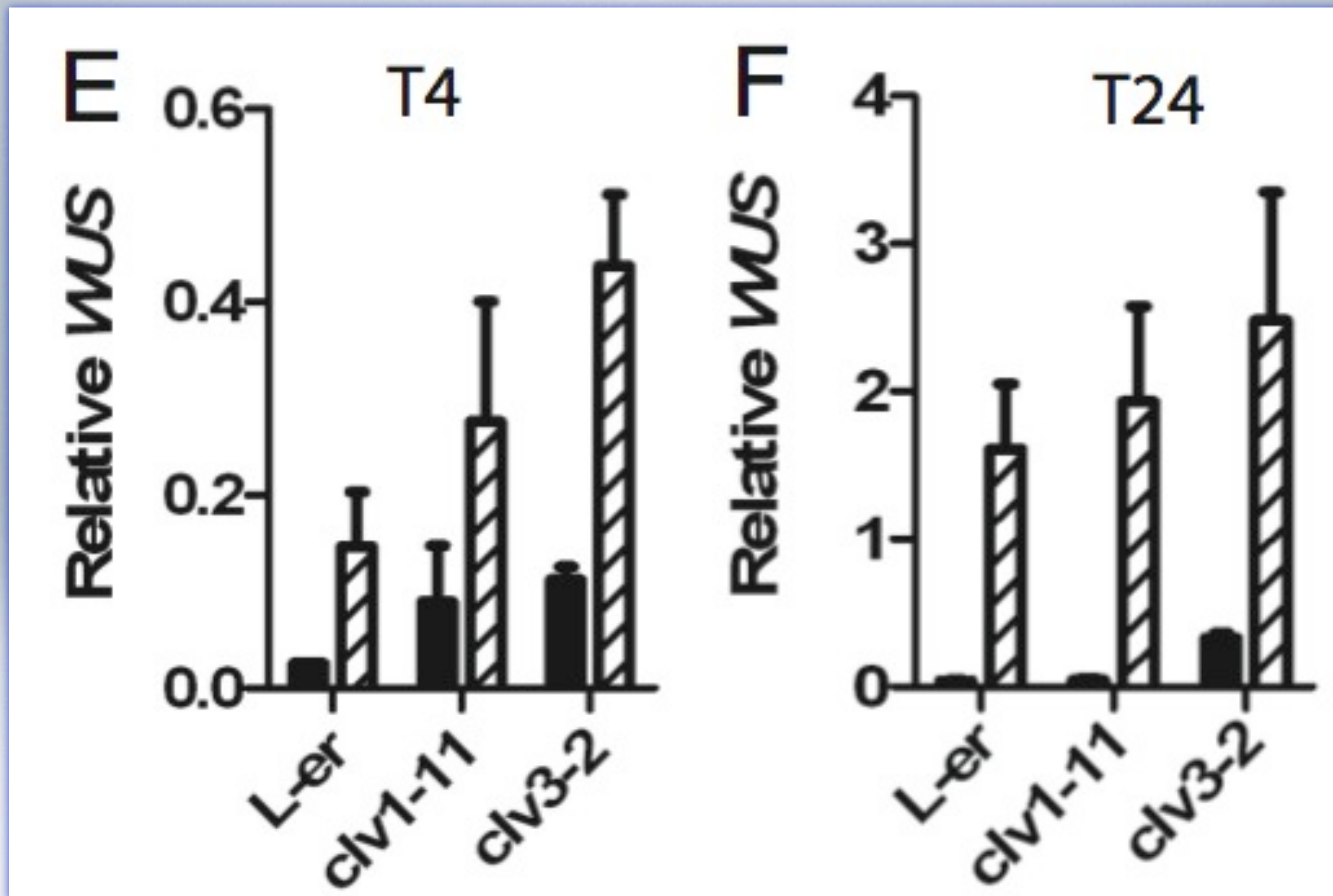
CLV3 + PZ repressors static



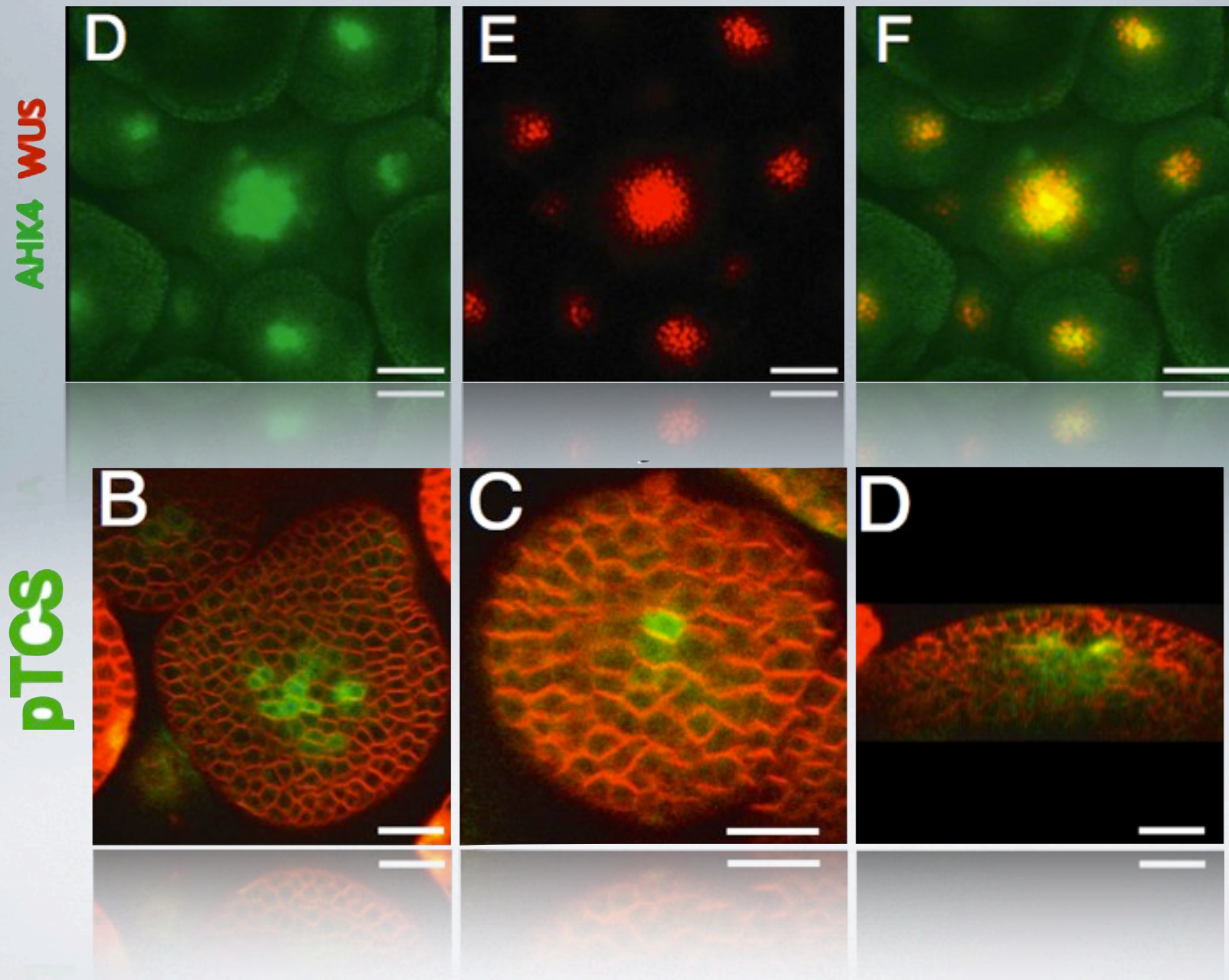
Activator
needed!

WUS

Cytokinin activator?

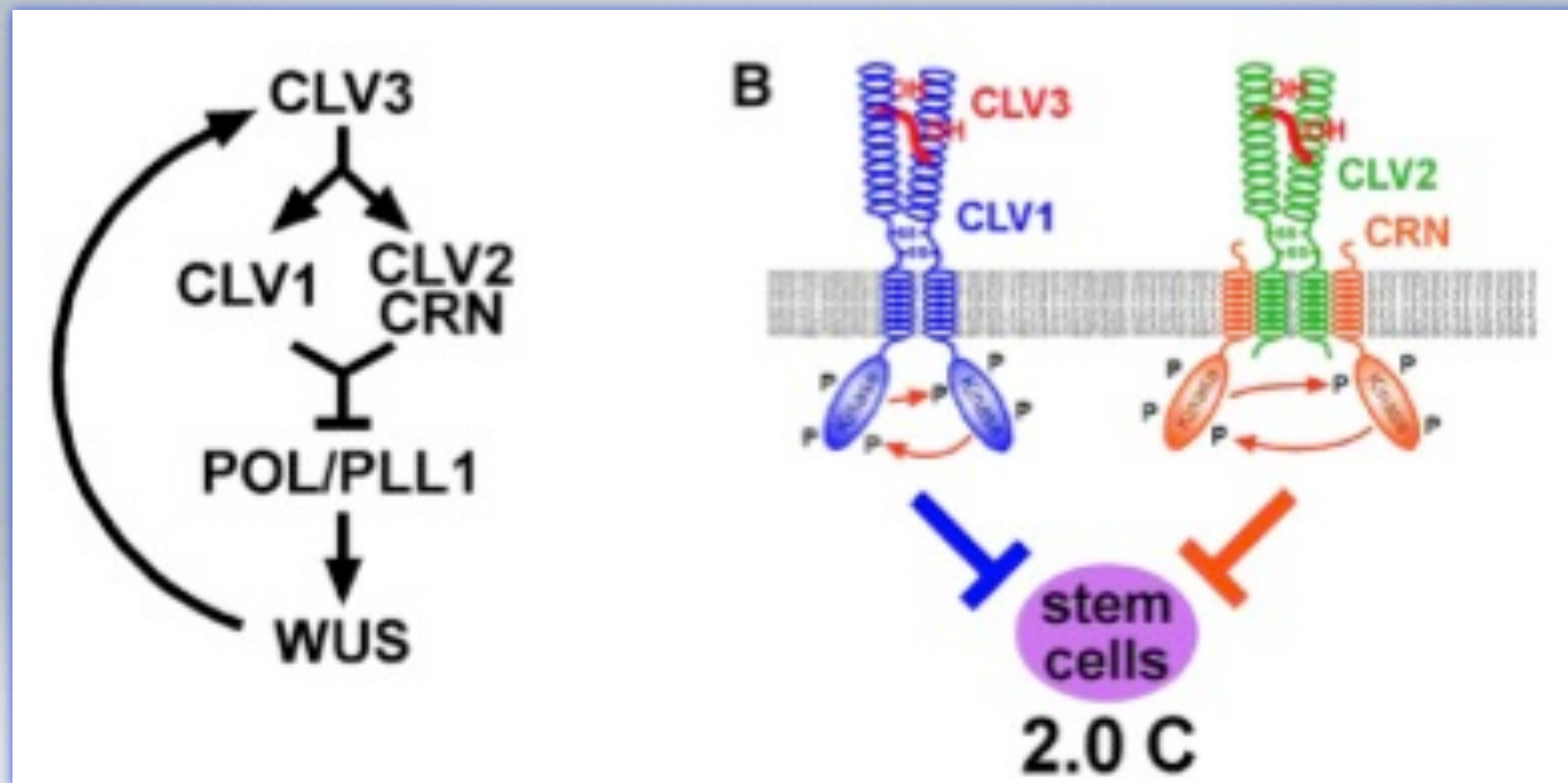


Cytokinin activator?

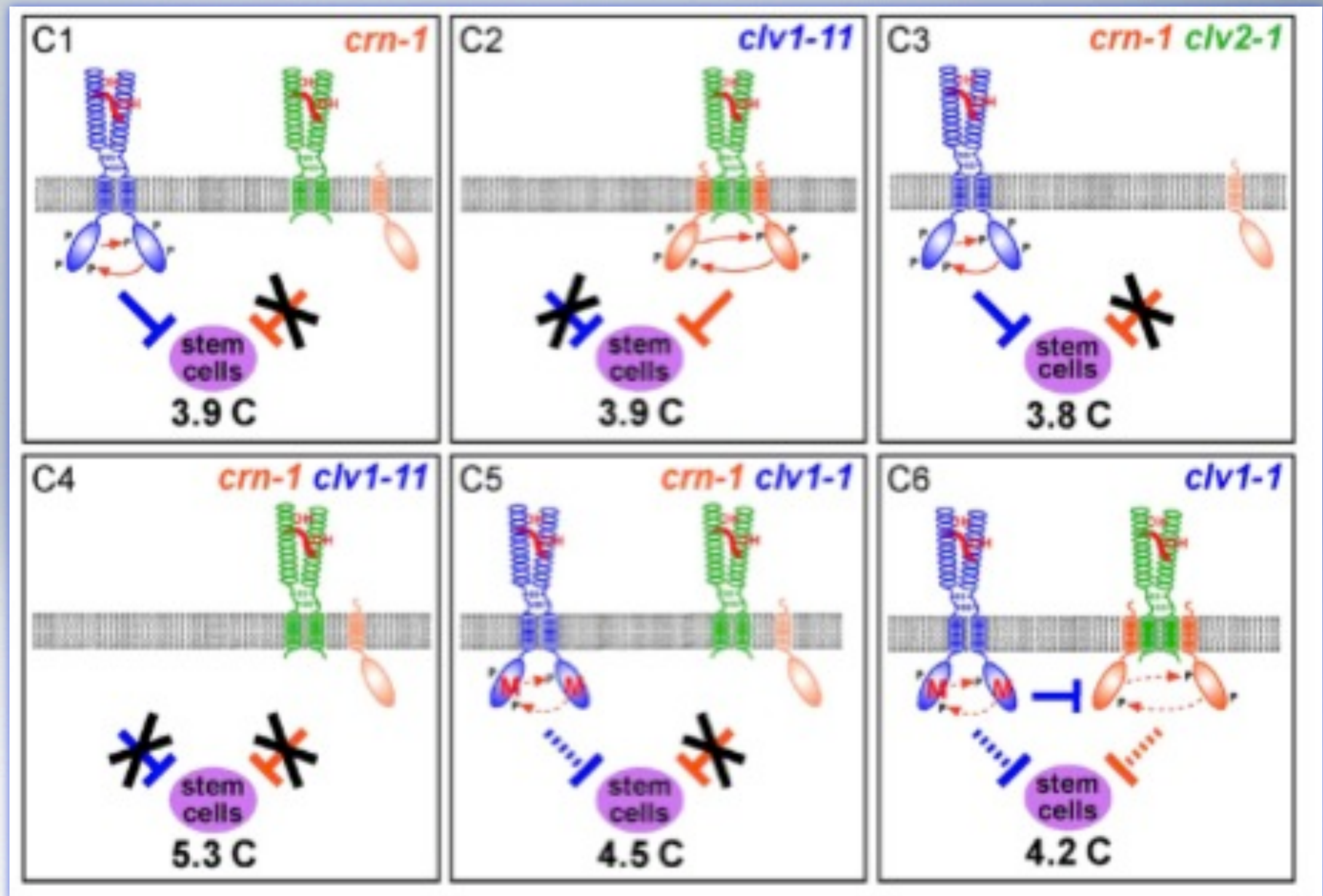
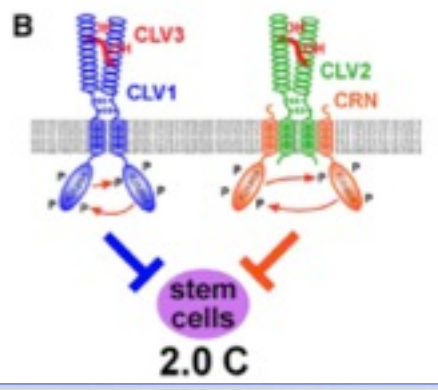
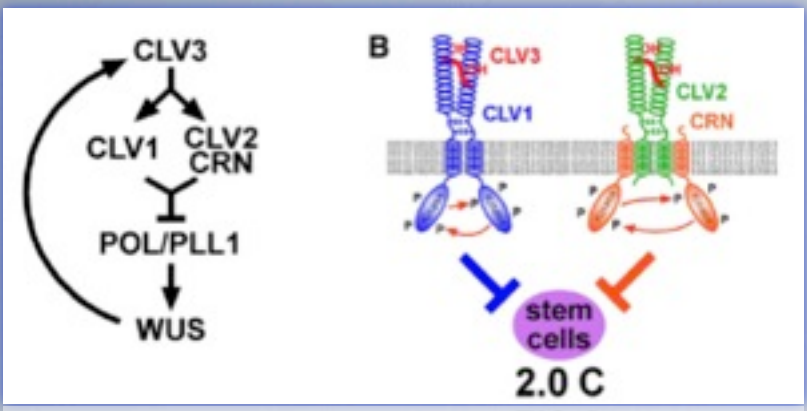


How is the CLV3 to WVUS signal mediated?

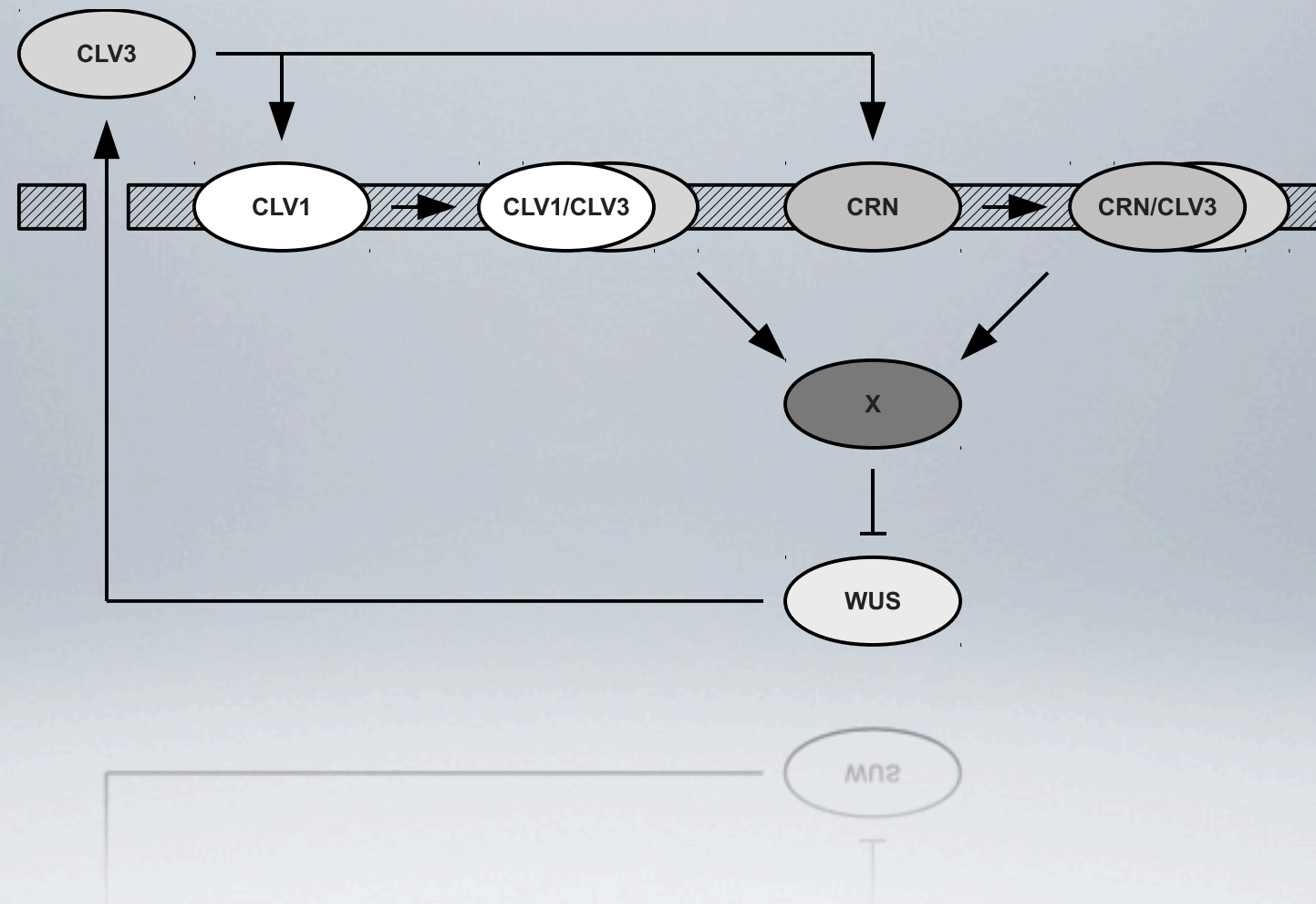
How is the CLV3 to WUS signal mediated?



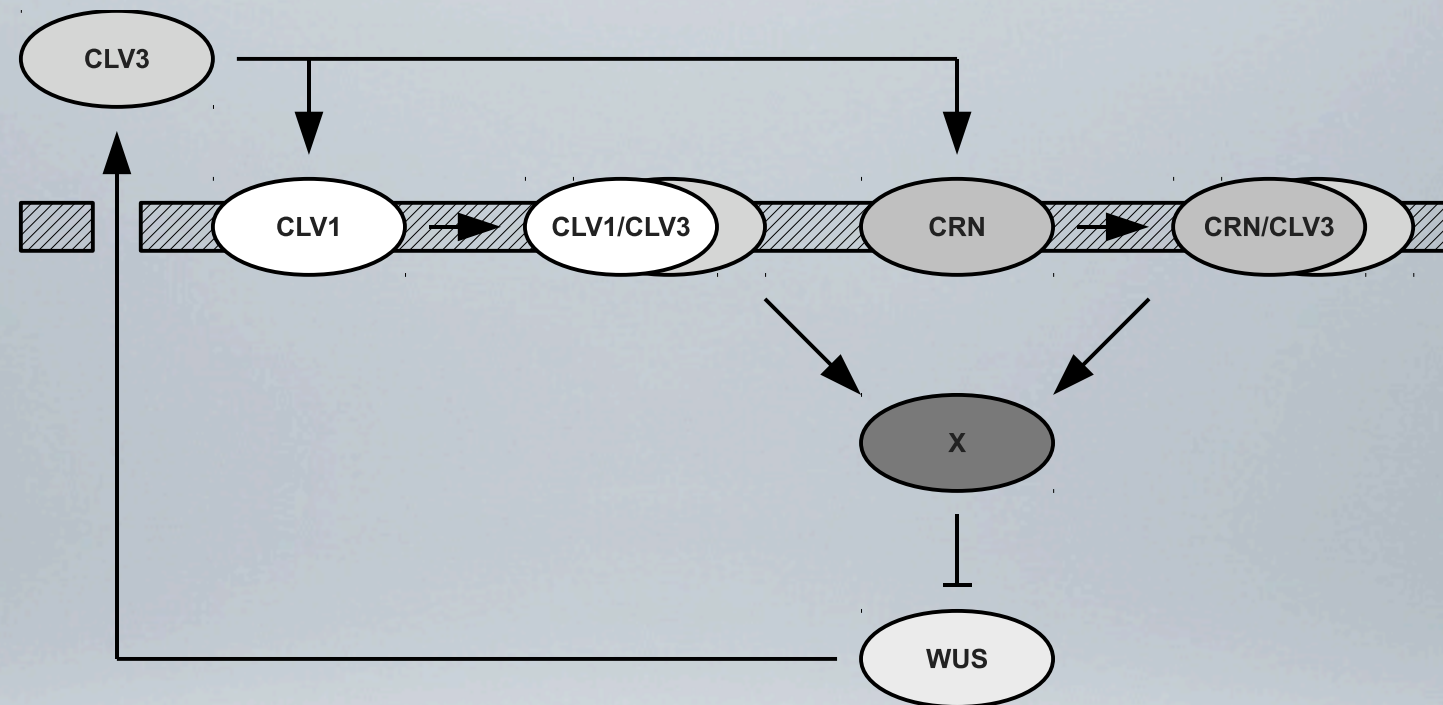
How can *clv1* non-null mutants have stronger phenotypes than a *clv1* null mutant?



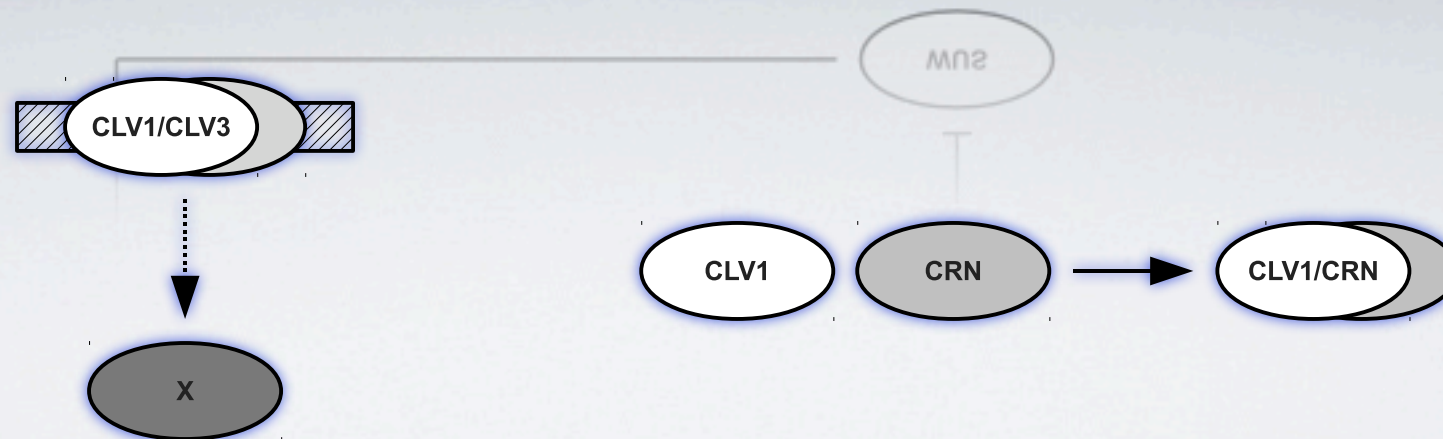
Can differences in mutant implementation alter wild type predictions?



Can differences in mutant implementation alter wild type predictions?



clv1-1
(non-null)



loss-of-signal

interference

Finding predictive models

Finding predictive models

- Optimize towards wt and 4 single mutants

Finding predictive models

- Optimize towards wt and 4 single mutants
- Test with two double mutants

WT comparison

hypotheses for mutant compared with mutant free models

biological predictions

biological predictions

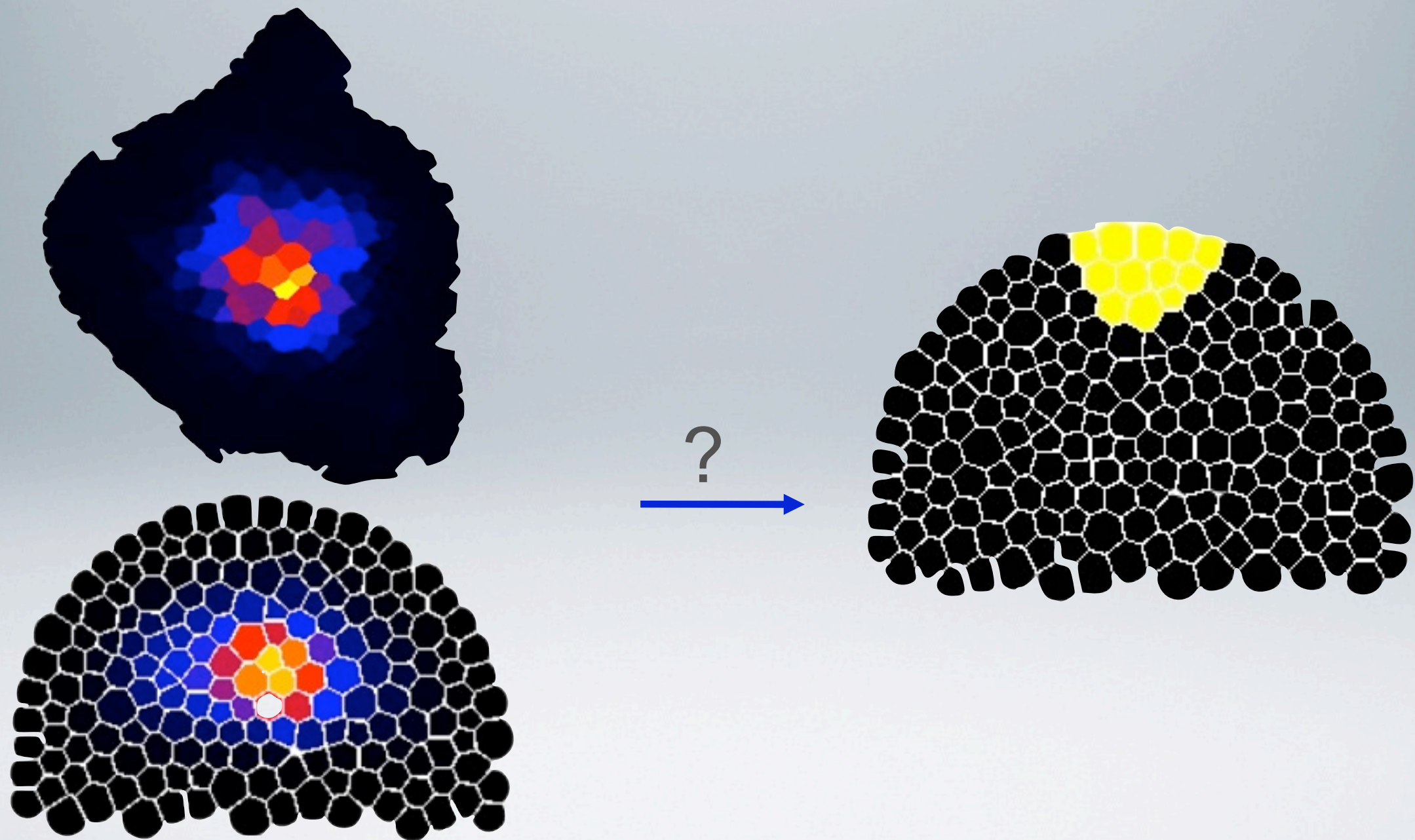
- Loss-of-signal mutant uses CLV3 sequestration and requires CLV1-CLV3 internalization

biological predictions

- Loss-of-signal mutant uses CLV3 sequestration and requires CLV1-CLV3 internalization
- Interference model leads to abundance of receptors

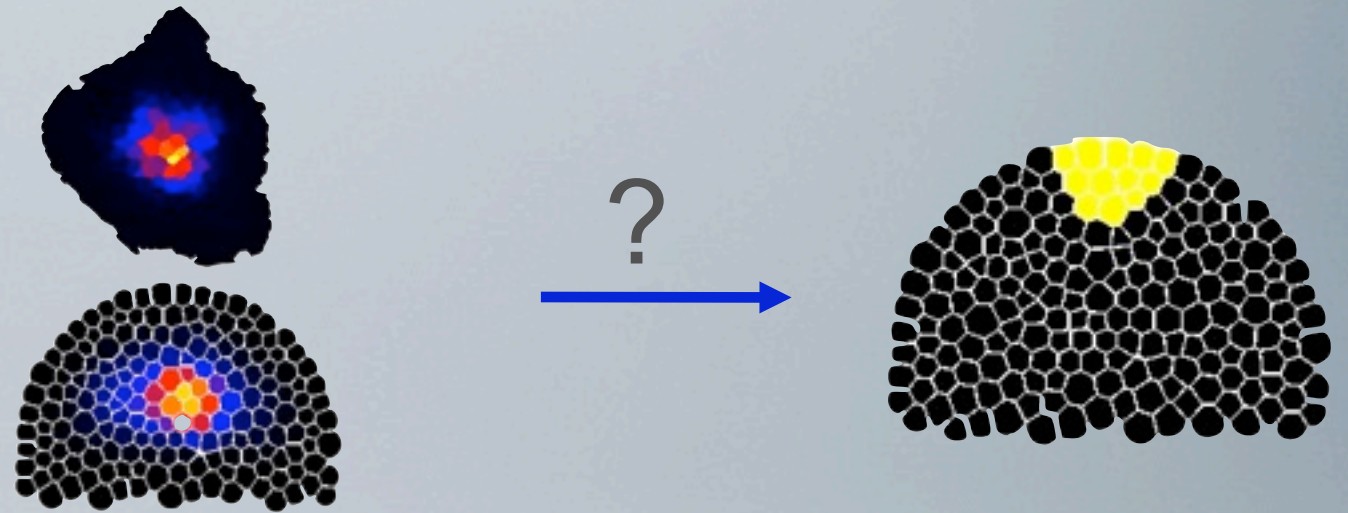
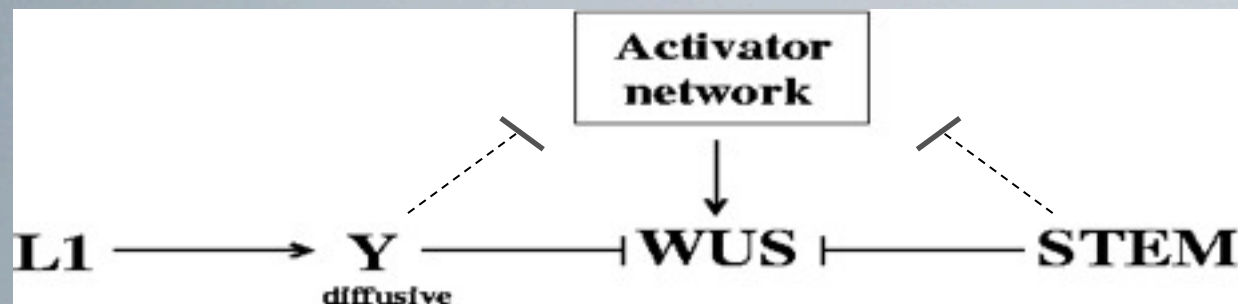
How is the WUS to CLV3 signal mediated?

How is the WUS to CLV3 signal mediated?



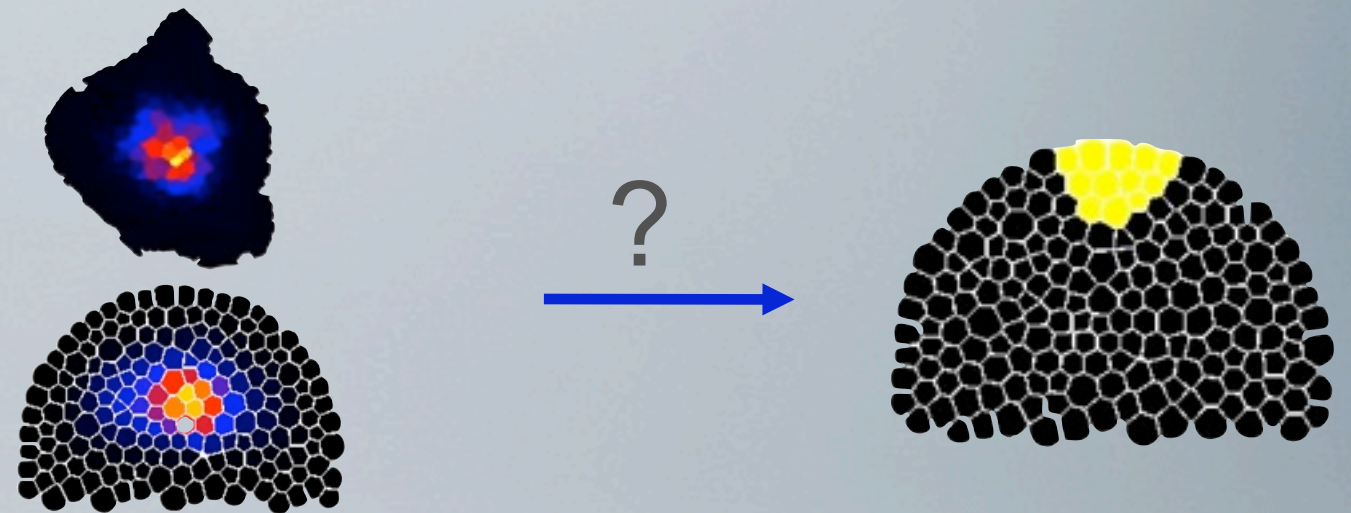
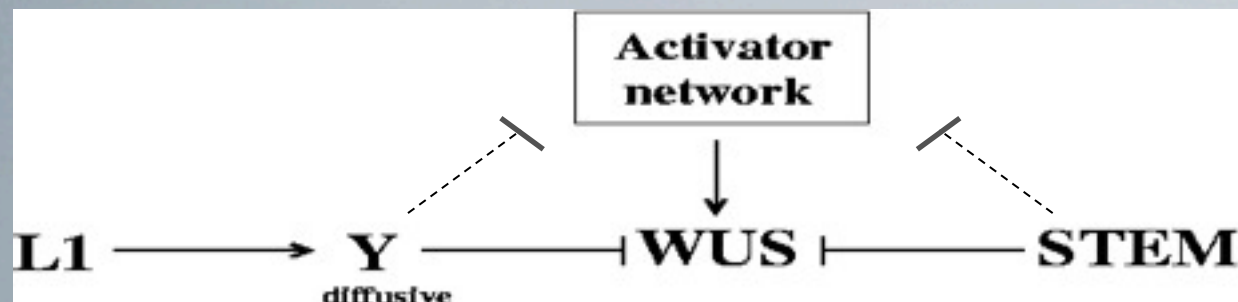
Parameter optimization: from WUS

WUS model from Jönsson et al (2005)

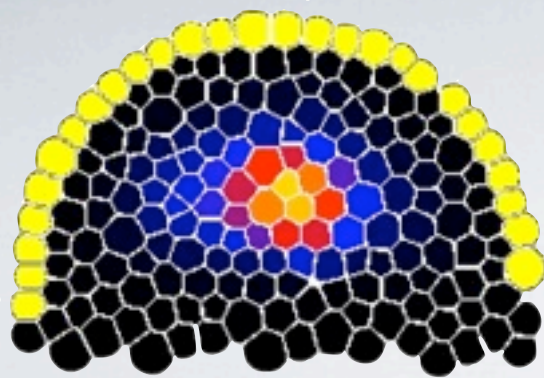


Parameter optimization: from WUS

WUS model from Jönsson et al (2005)

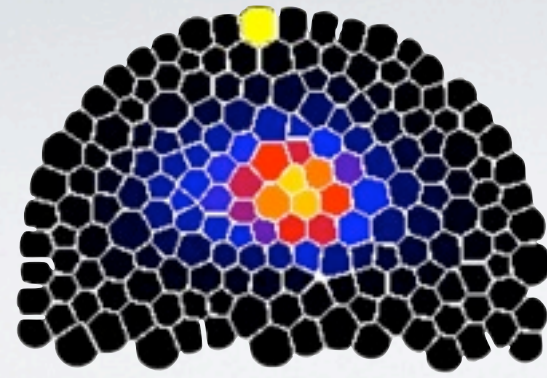


‘Optimize’ hypotheses for WUS \rightarrow CLV3

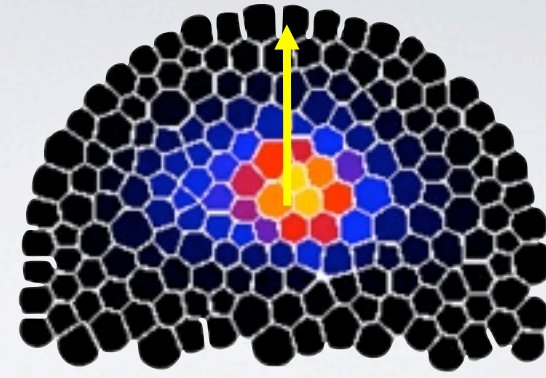


WUS + LI

Jönsson et al (2003)

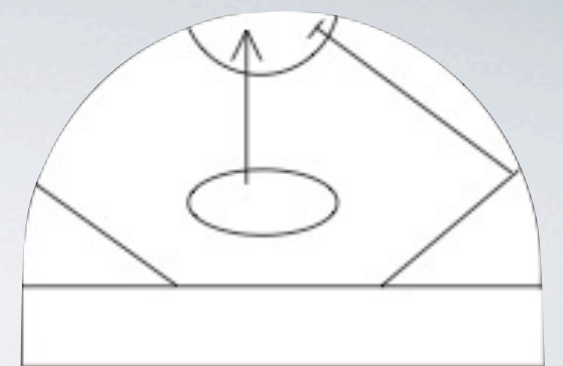


WUS+apical



WUS

directional



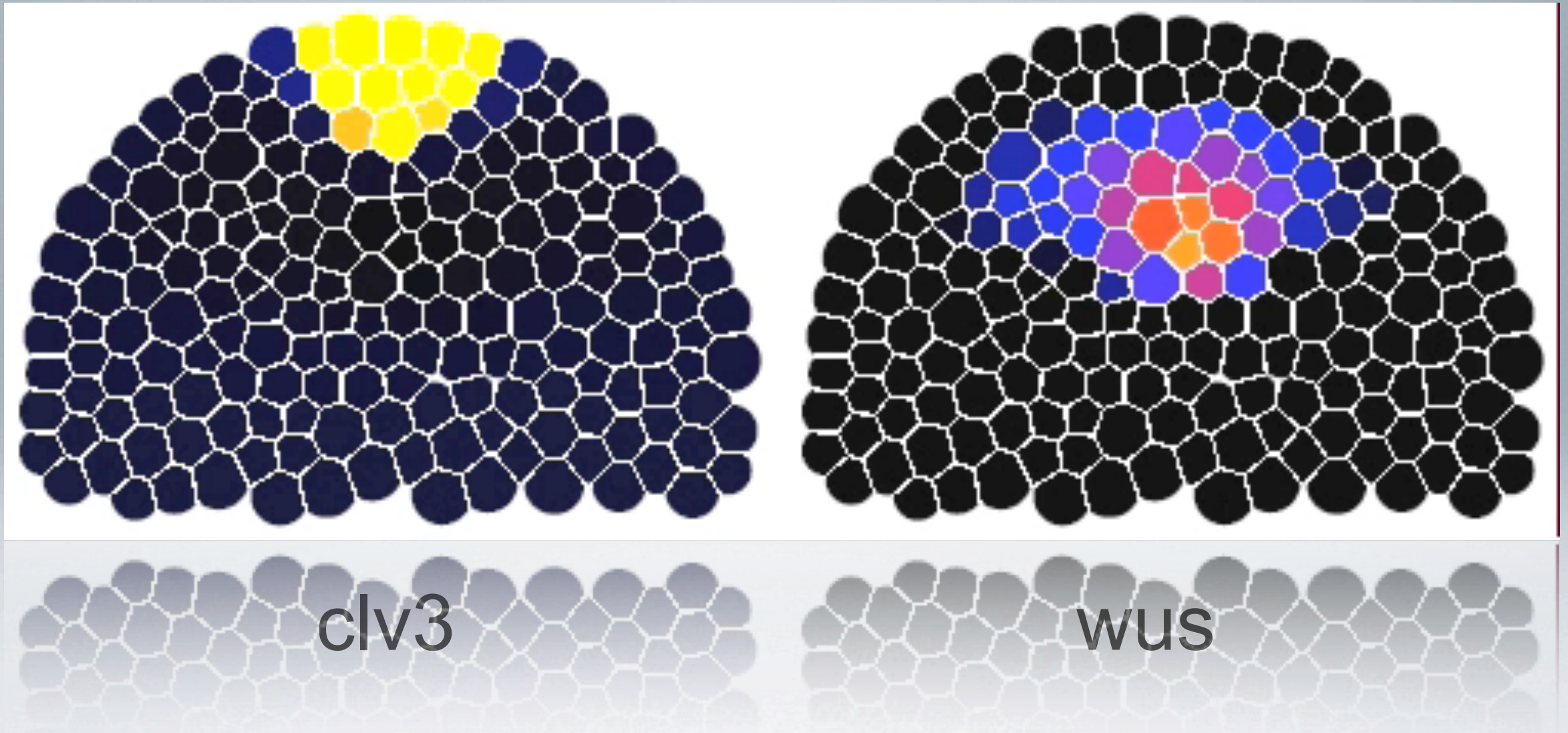
WUS + PZ

CLV3 expression domain optimization

clv3

wus

CLV3 expression domain optimization



Thank you!

<http://www.thep.lu.se/~henrik/>

The computable plant
Elliot Meyerowitz
Marcus Heisler
Venu Reddy

Bruce Shapiro
Eric Mjolsness

Sarah Engman
Jeremy Gruel
Pawel Krupinski
Pontus Melke
Patrik Sahlin
Christopher Sturk
(Computational Biology
& Biological Physics
Lund University)

Thank you!

<http://www.thep.lu.se/~henrik/>

The computable plant
Elliot Meyerowitz
Marcus Heisler
Venu Reddy

Bruce Shapiro
Eric Mjolsness



Sarah Engman
Jeremy Gruel
Pawel Krupinski
Pontus Melke
Patrik Sahlin
Christopher Sturk
(Computational Biology
& Biological Physics
Lund University)