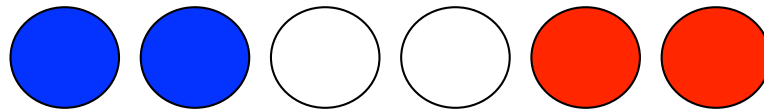
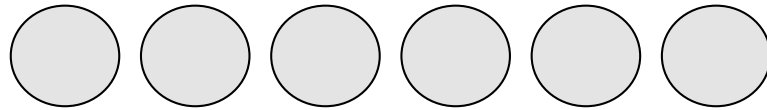


The Problem: Pattern Formation

Homogenous Progenitor Population



C_1



C_2



C_3

Different Differentiated Cell Types

The Problem: Pattern Formation

Different cell types = different gene expression profiles

Therefore problem is:

How is differential spatial pattern of gene expression controlled?

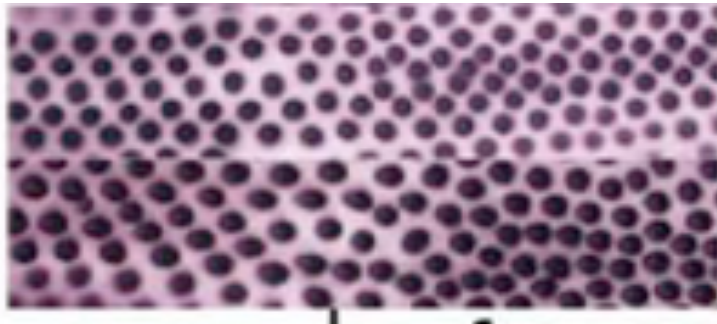
Requirement:

A symmetry breaking event to provide a spatial polarization

A mechanism to convert polarized signal to discrete regions of differential gene expression

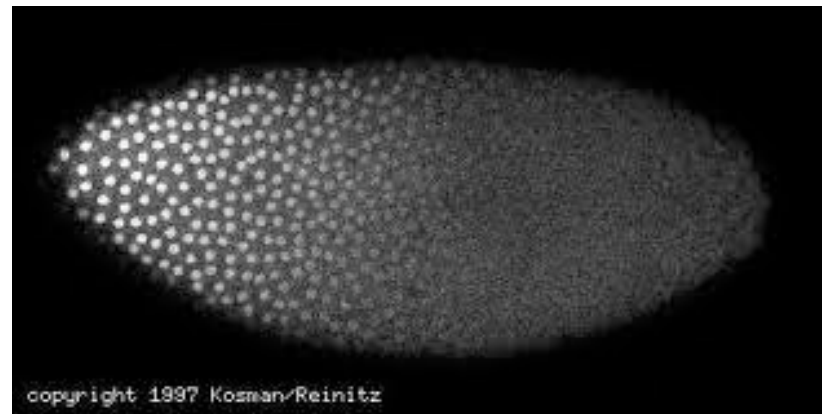
Strategies of Pattern Formation

Oscillations –
cell intrinsic
e.g. Somitogenesis

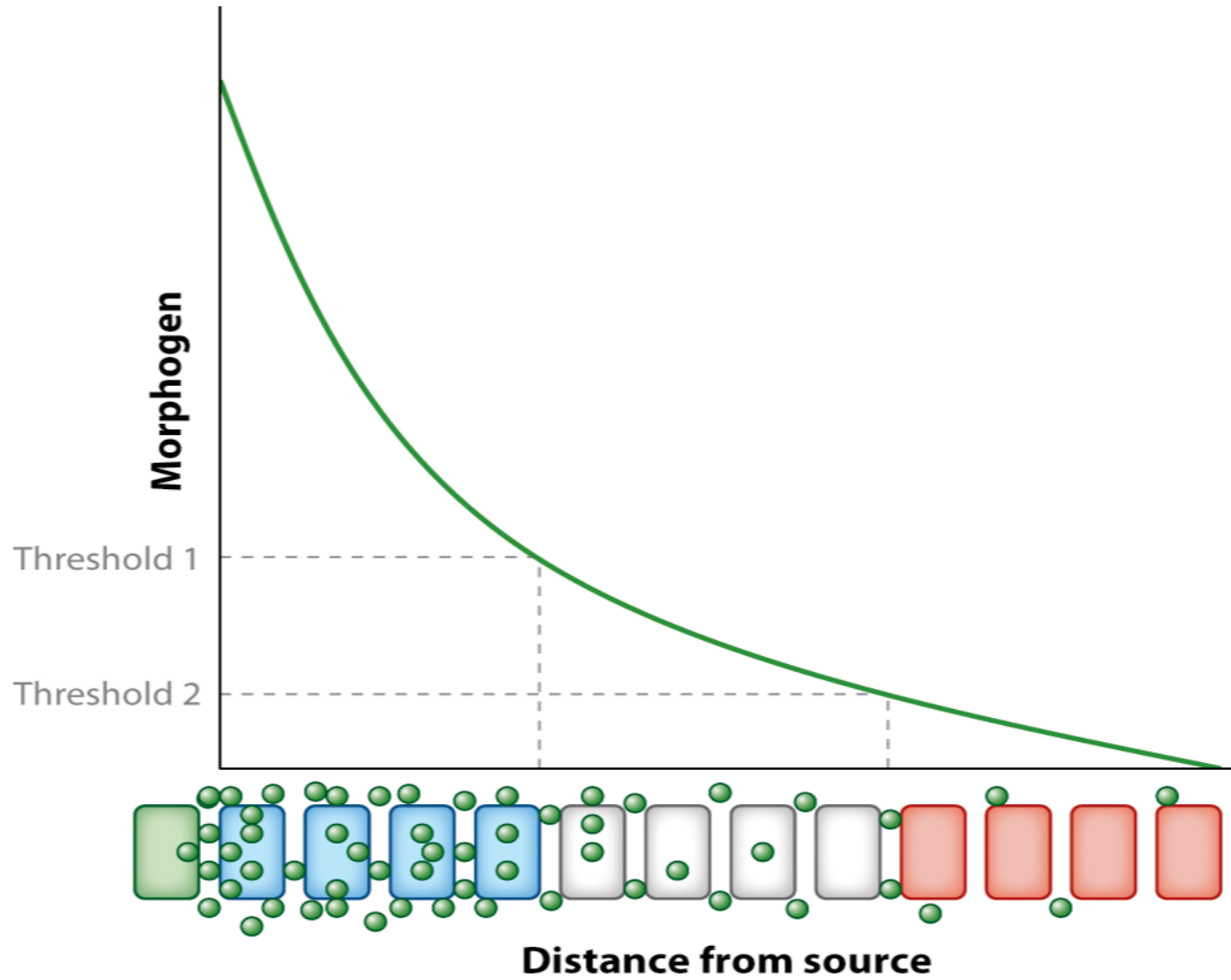


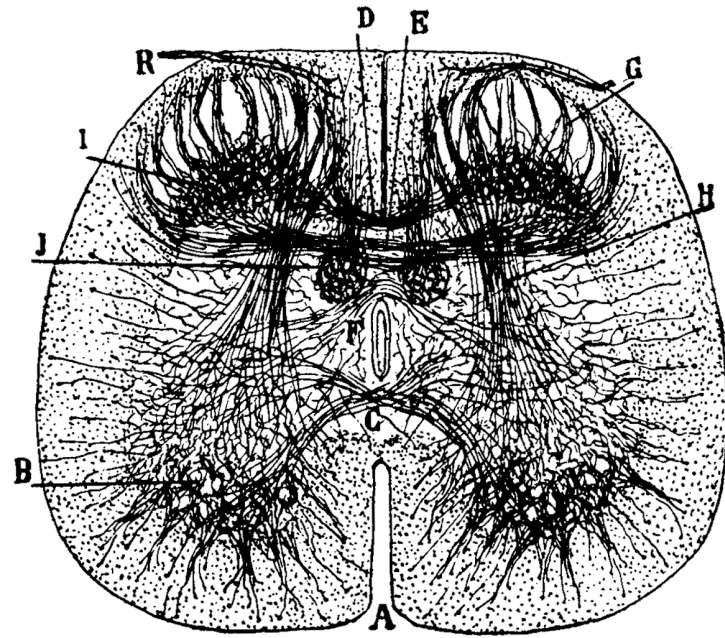
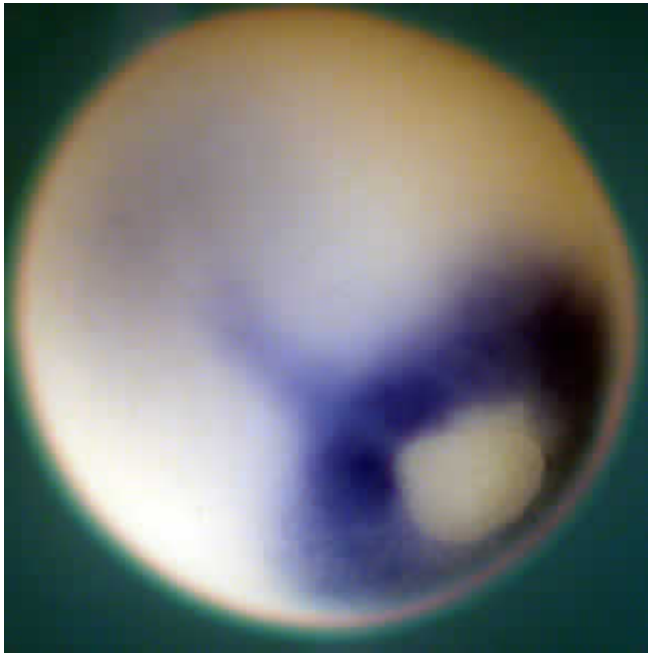
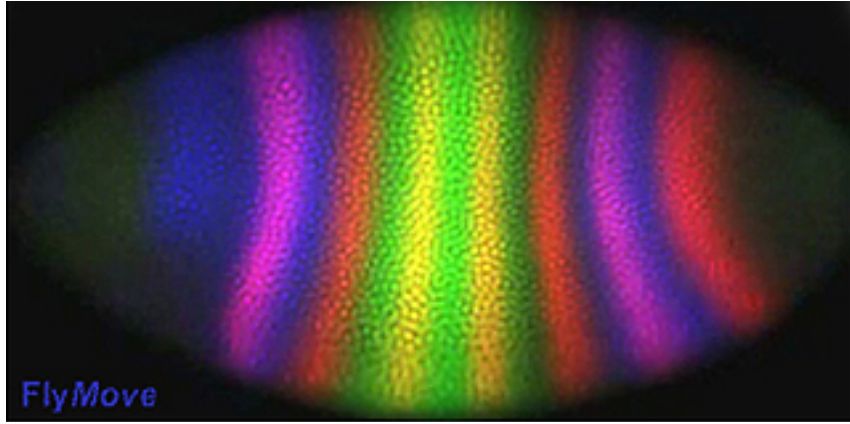
Local Cell-Cell Interactions –
self organizing
e.g. Notch-Delta signaling

Morphogens –
Isn't self organizing
But long range

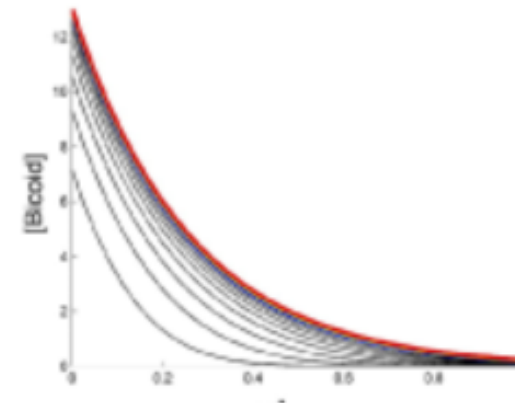
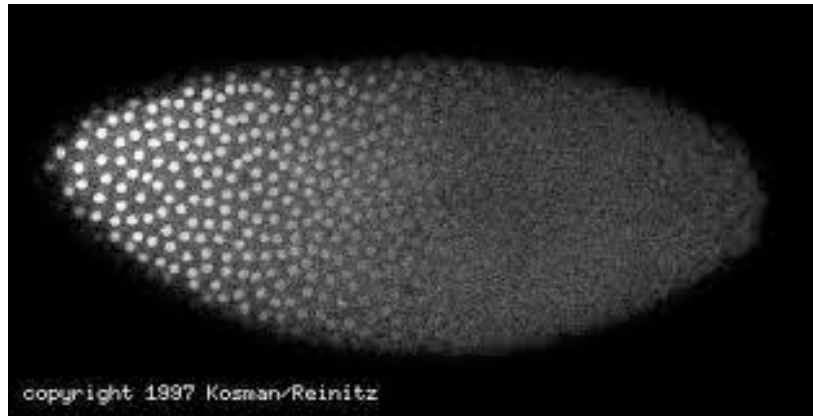


MORPHOGEN GRADIENTS

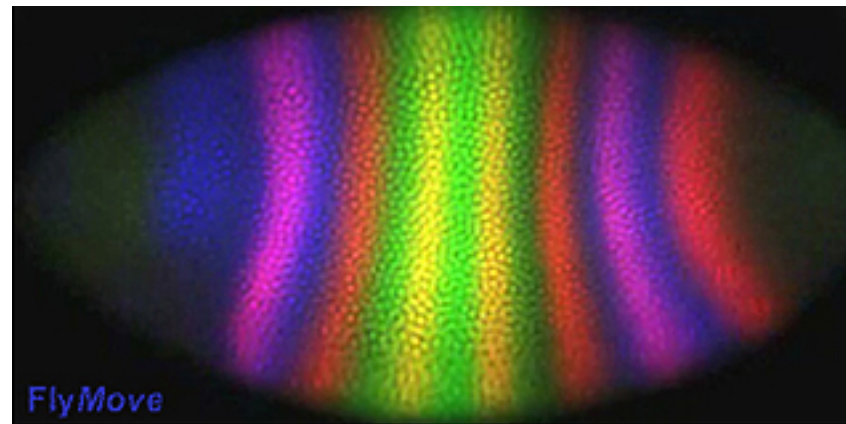




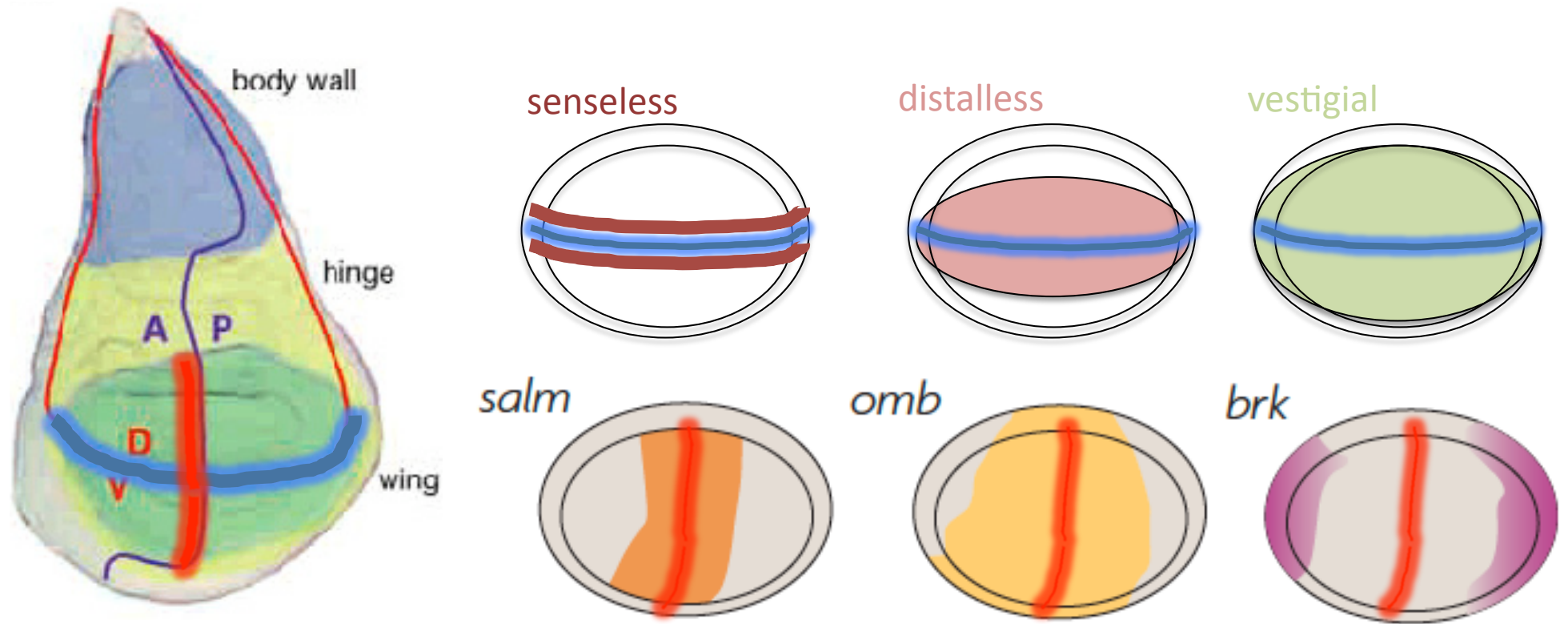
The early *Drosophila* embryo is a syncytium



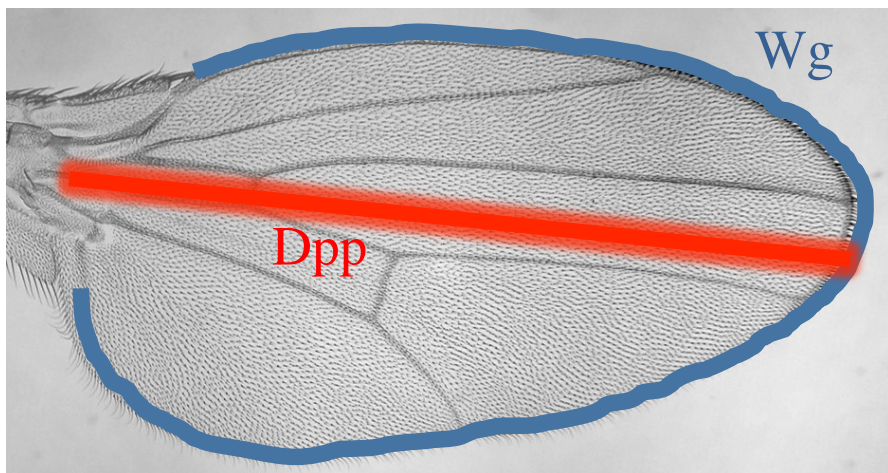
Grimm O et al. Development 2010;137:2253-2264



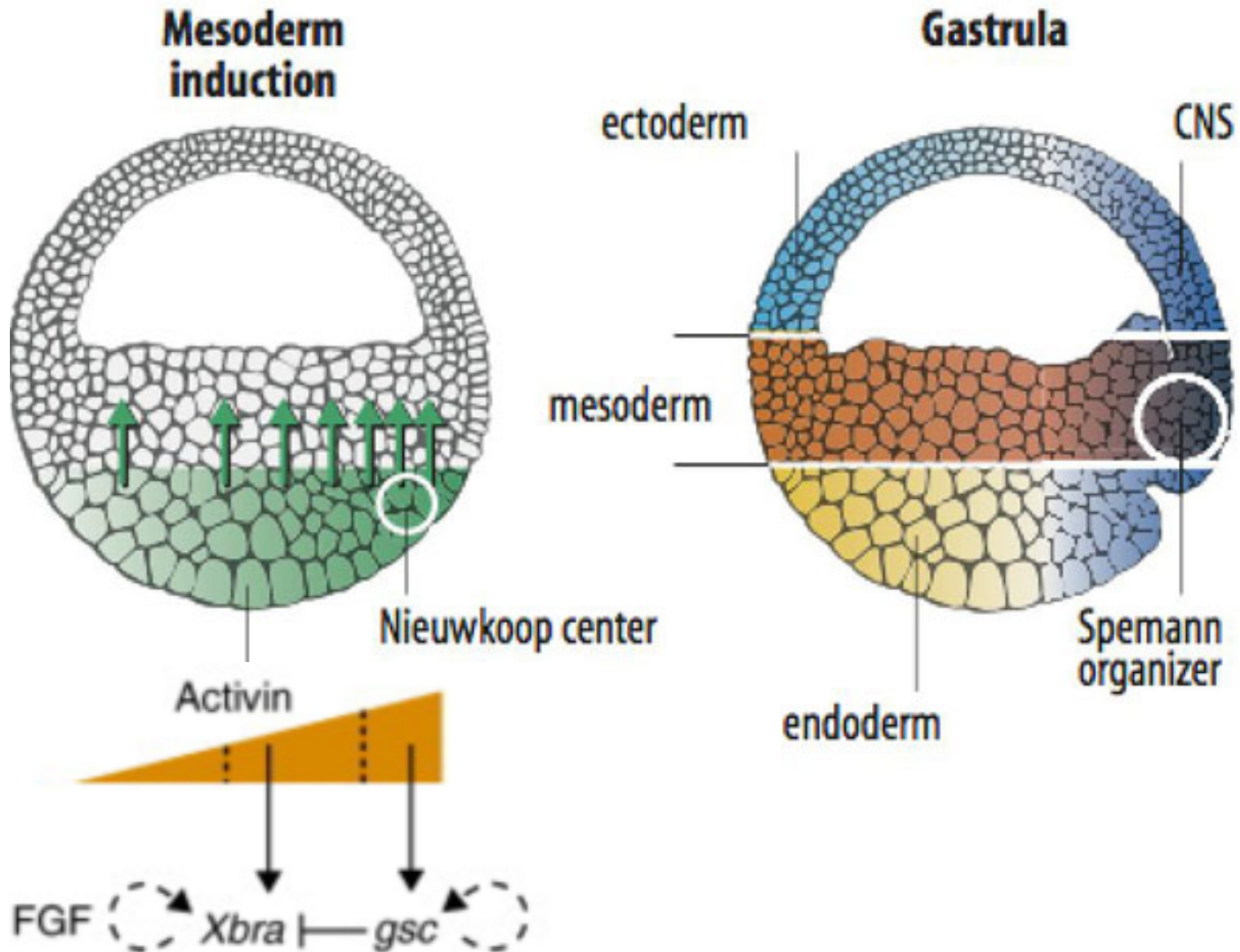
Wingless and Dpp in wing imaginal discs



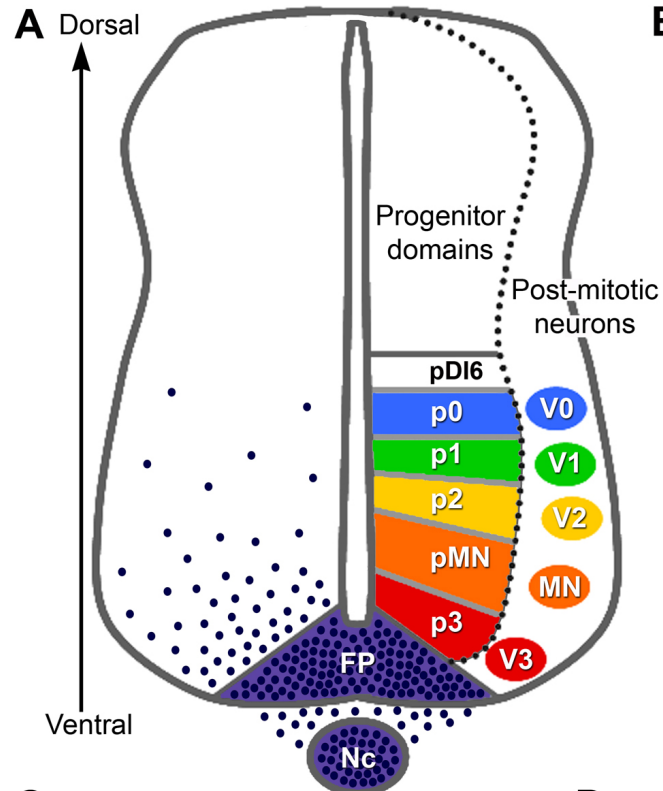
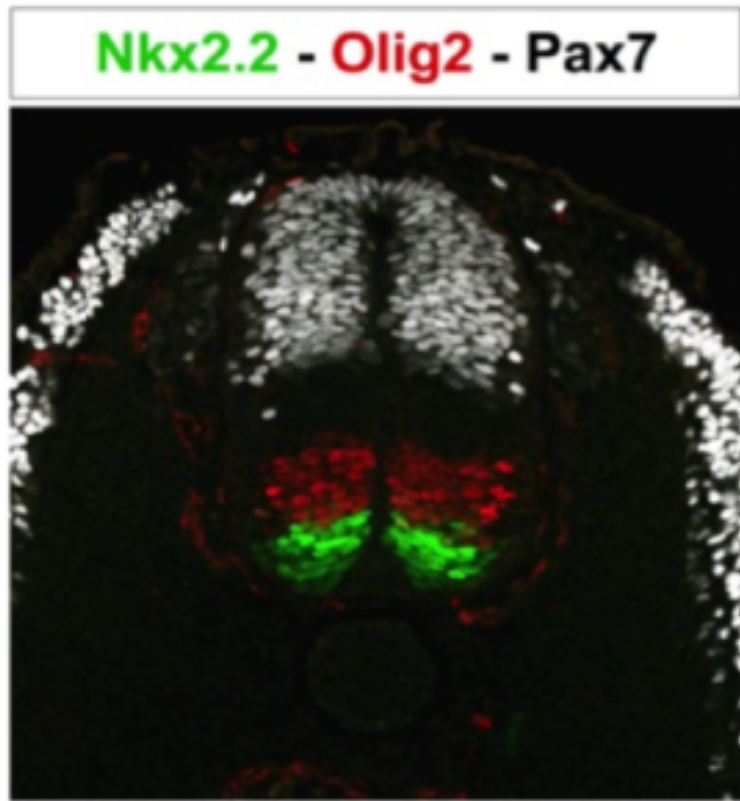
Adapted from Affolter and Basler



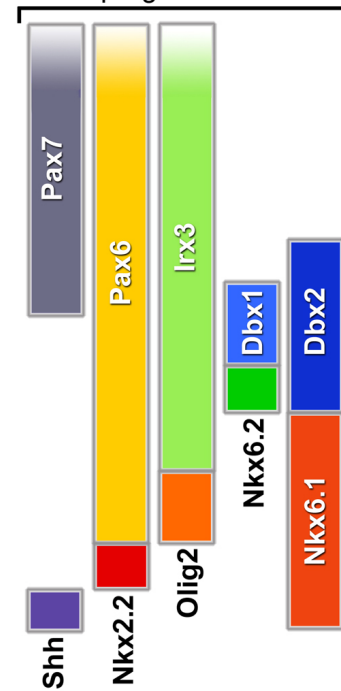
Graded signal transduction: Mesoderm



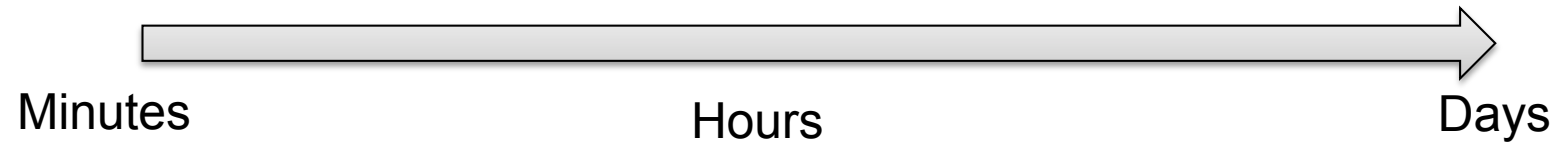
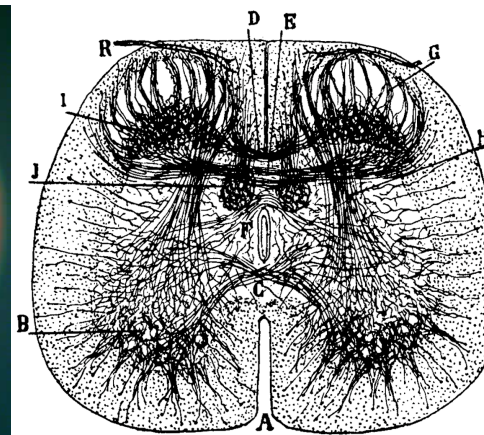
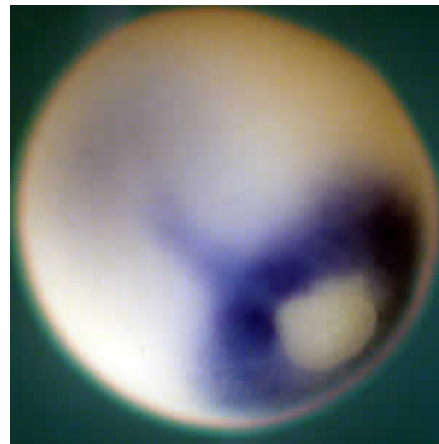
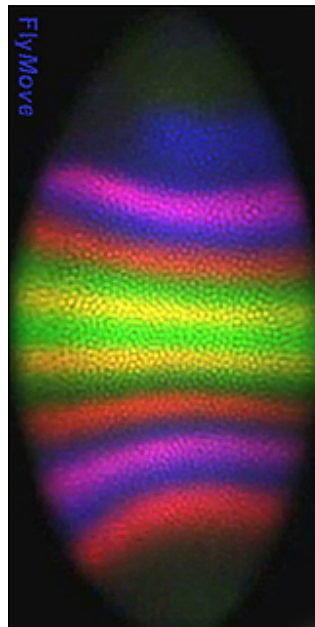
Neural patterning



B Profiles of expression of TFs in progenitor cells



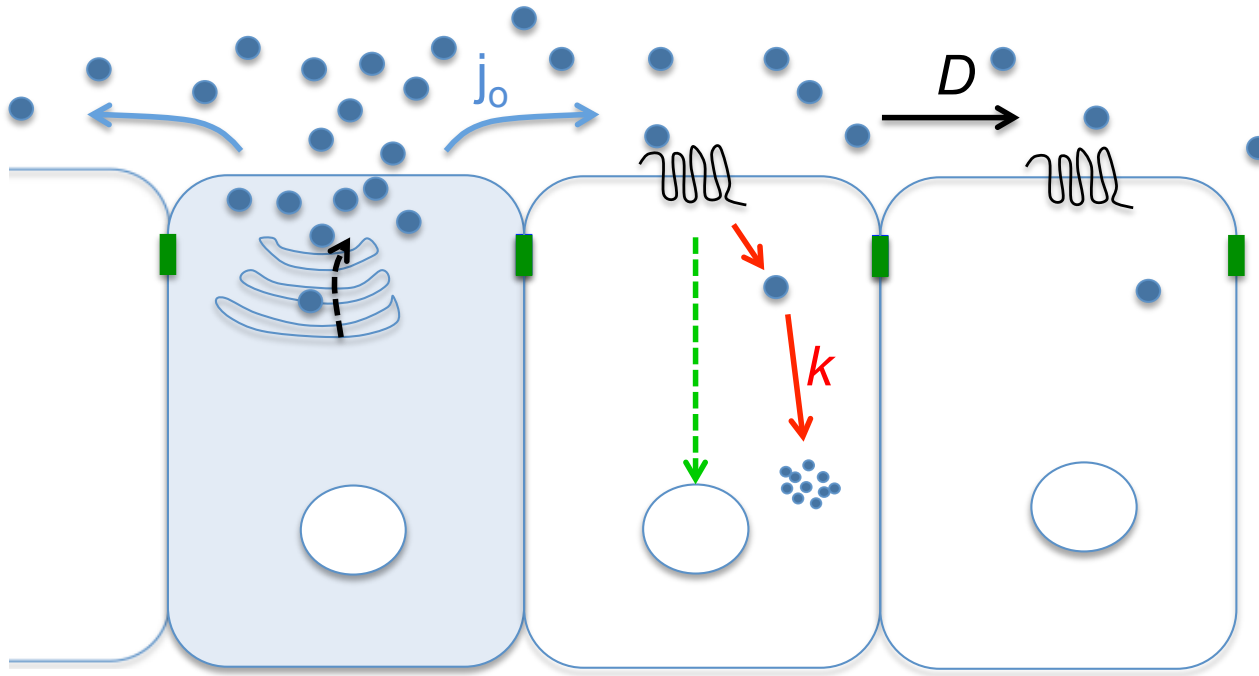
Different time scales of patterning



Morphogens:

- Identification – what and where
- Formation - intercellular transmission
- Perception - signal transduction
- Interpretation - convert to discrete responses

Establishing a morphogen gradient



-Current j_0 [molecules/(($\mu\text{m s}$))] at the source boundary
= Rate of secretion

-Uniform degradation with a rate k (s^{-1})
= Extracellular protease + Lysosomal targeting

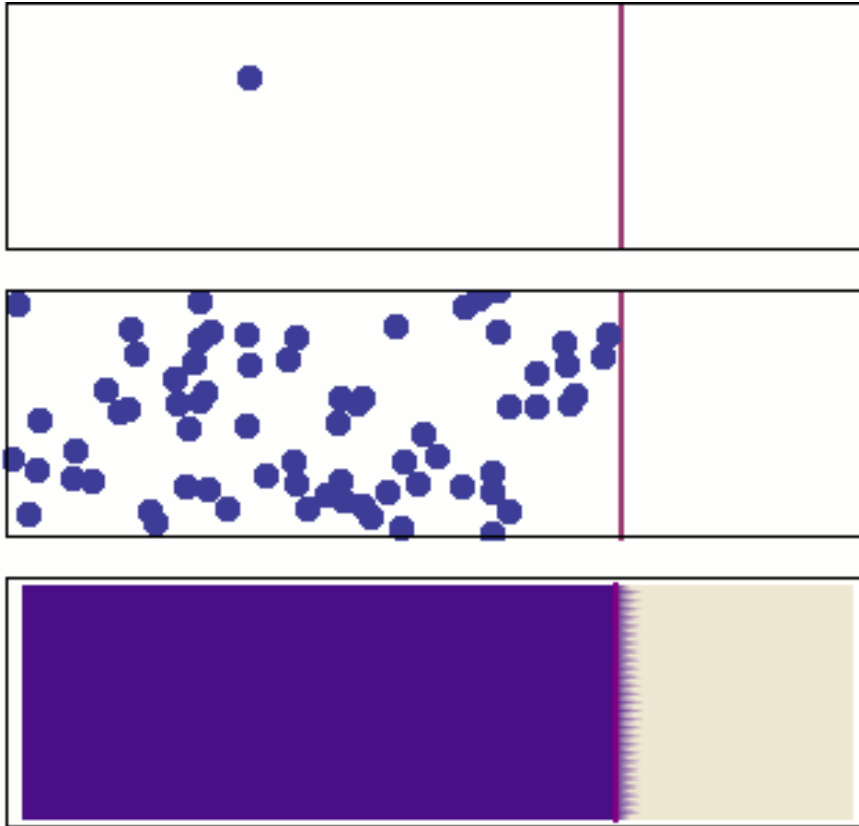
-Effective diffusion coefficient D (mm^2/s).
= Diffusion or any random walk process

$$\frac{\partial C}{\partial t} = j_0(x) + D \frac{\partial^2 C}{\partial x^2} - kC$$

Steady state solution $C = C_0 e^{-x/\lambda}$

$$\text{where } c_0 = \frac{j_0}{\sqrt{Dk}} \text{ and } \lambda = \sqrt{\frac{D}{k}}$$

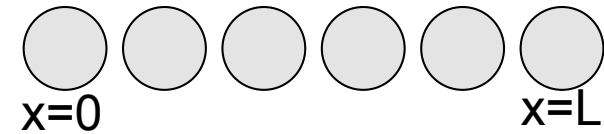
Diffusion: molecules undertake random walk. Move from regions of high concentration to regions of low concentration, with rate proportional to the concentration gradient (spatial derivative). Results in a flux, J .



$$J = -D \frac{\partial C}{\partial x}$$

<https://upload.wikimedia.org/wikipedia/commons/4/4d/DiffusionMicroMacro.gif>

Initial conditions: $t=0$
 $C=0$ for all x
 $C(x,0)=0$



Boundary conditions:

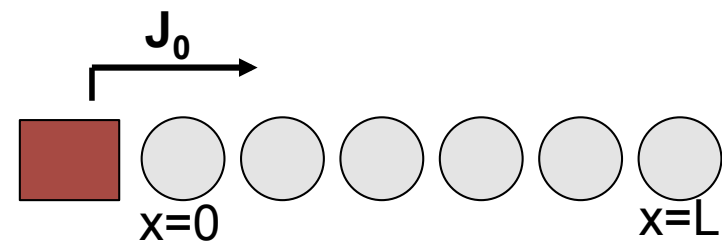
Morphogen produced at $x=0$ at constant rate $=J_0$ 'Flux'

Flux caused by concentration difference and diffusion counteracts:

$$J = -D \frac{\partial C}{\partial x}$$

$$D \frac{\partial C}{\partial x} \Big|_{x=0} = -J_0$$

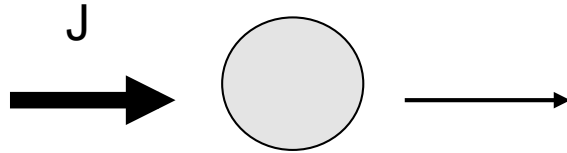
Morphogen is 0 at the end of the tissue ($x=L$)



$$D \frac{\partial C}{\partial x} \Big|_{x=L} = 0$$

DIFFUSION

Prior to steady state concentration is changing over **time** at a location. Indicates that there must be a difference in flux in to and out of every **location**



$$\frac{\partial C}{\partial t} = - \frac{\partial J}{\partial X}$$

Continuity equation: no molecules are lost or gained across the tissue

Flux caused by concentration difference and diffusion counteracts it

$$J = -D \frac{\partial C}{\partial X}$$

Substitute for J

$$\frac{\partial C}{\partial t} = - \frac{\partial}{\partial X} \left(-D \frac{\partial C}{\partial X} \right) = D \frac{\partial^2 C}{\partial X^2}$$

DEGRADATION

Take simple case where morphogen is degraded at a constant rate:

$$\frac{\partial C}{\partial t} = -kC \quad \text{k is rate of degradation}$$

Put diffusion and degradation together

$$\frac{\partial C}{\partial t} = D \frac{\partial^2 C}{\partial x^2} - kC$$

STEADY STATE

At ss there is no change in concentration at a position

$$\frac{\partial C}{\partial t} = 0$$

$$\frac{\partial C}{\partial t} = D \frac{\partial^2 C}{\partial x^2} - kC = 0$$

$$D \frac{\partial^2 C}{\partial x^2} = kC$$

Spread of morphogen balanced by degradation

$$\frac{\partial^2 C}{\partial x^2} = \frac{k}{D} C$$

Second order derivative. Solution is proportional to conc. Parameters and concentration are positive therefore look for a solution that gives only positive

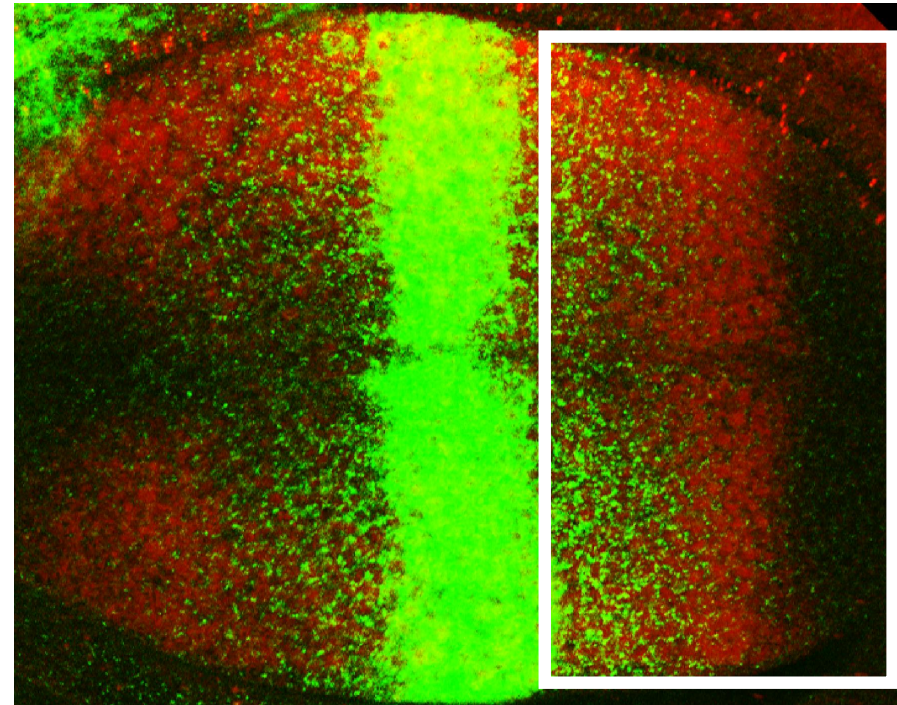
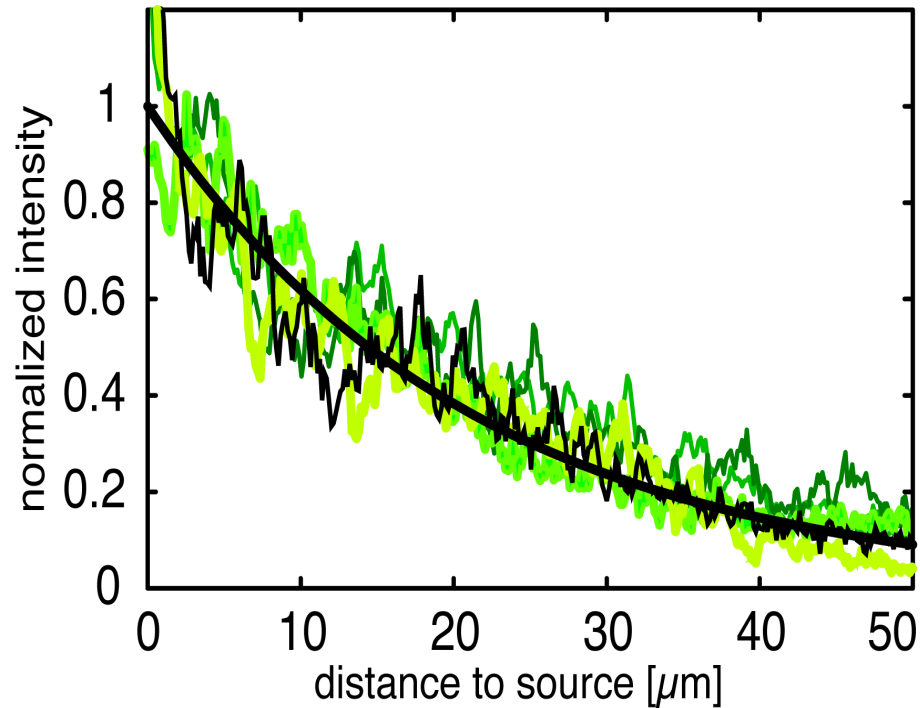
$$C = C_0 e^{-x/\lambda}$$

$$C_0 = \frac{J_0}{\sqrt{Dk}}$$

$$\lambda = \sqrt{\frac{D}{k}}$$

Dpp gradient in the wing imaginal disc

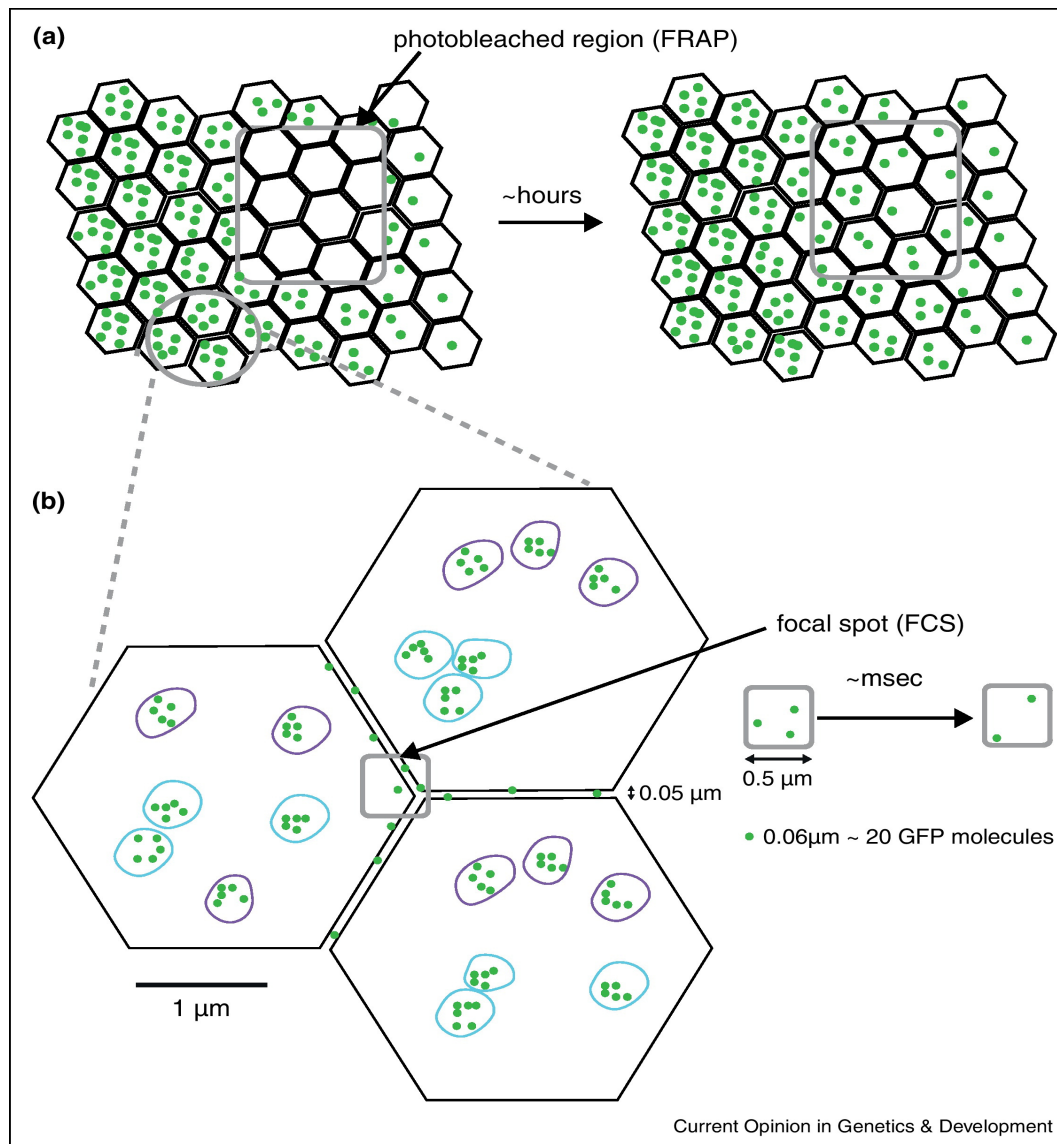
Dpp-GFP
Sal



$$C = C_0 e^{-x/\lambda}$$

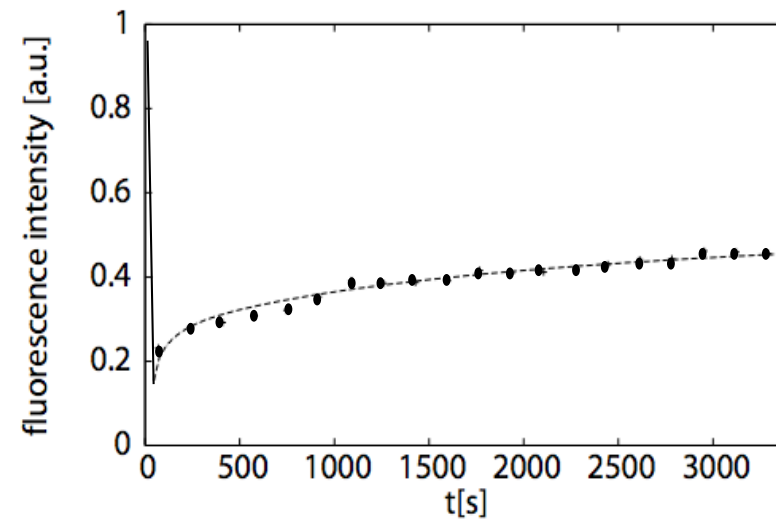
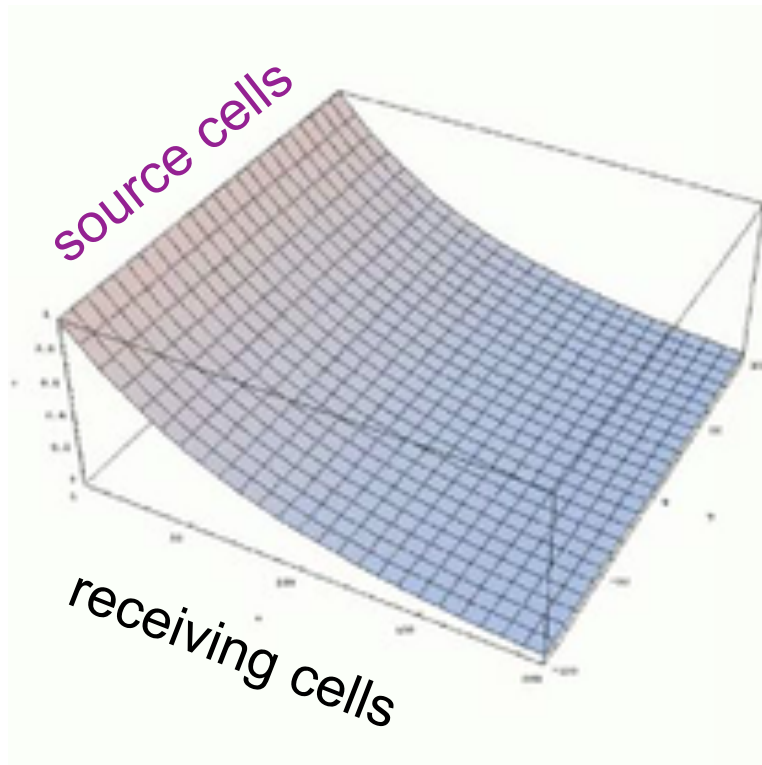
$$c_0 = \frac{j_0}{\sqrt{Dk}} \quad \lambda = \sqrt{\frac{D}{k}}$$

Techniques to measure gradient kinetics



FRAP

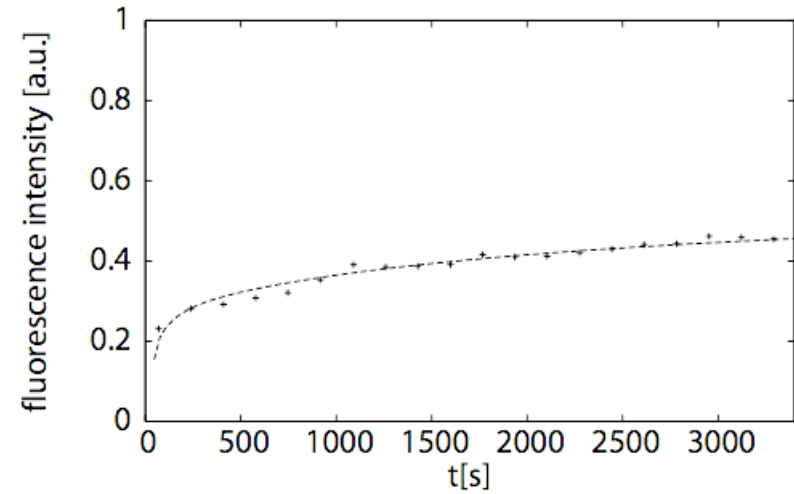
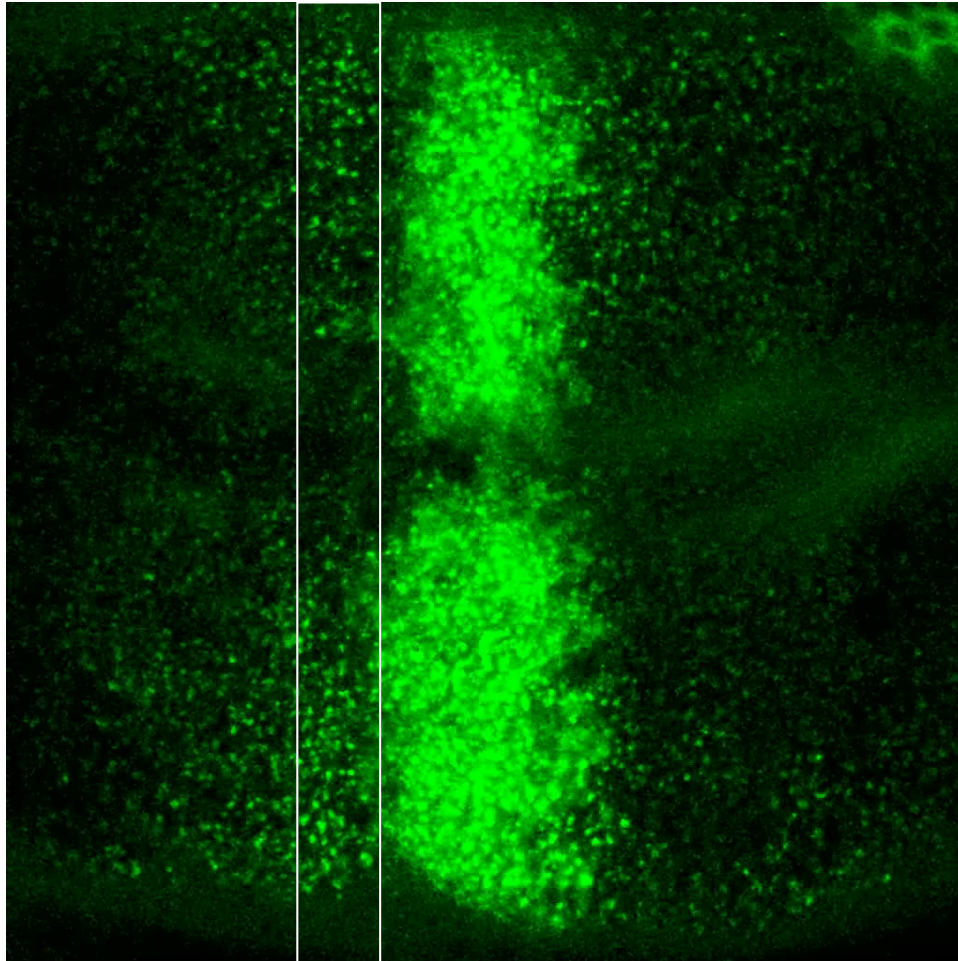
(Fluorescence Recovery After Photobleaching)



$$\frac{\partial C}{\partial t} = j_0(x) + D \frac{\partial^2 C}{\partial x^2} - kC$$

D, k, J0

FRAP of GFP-Dpp



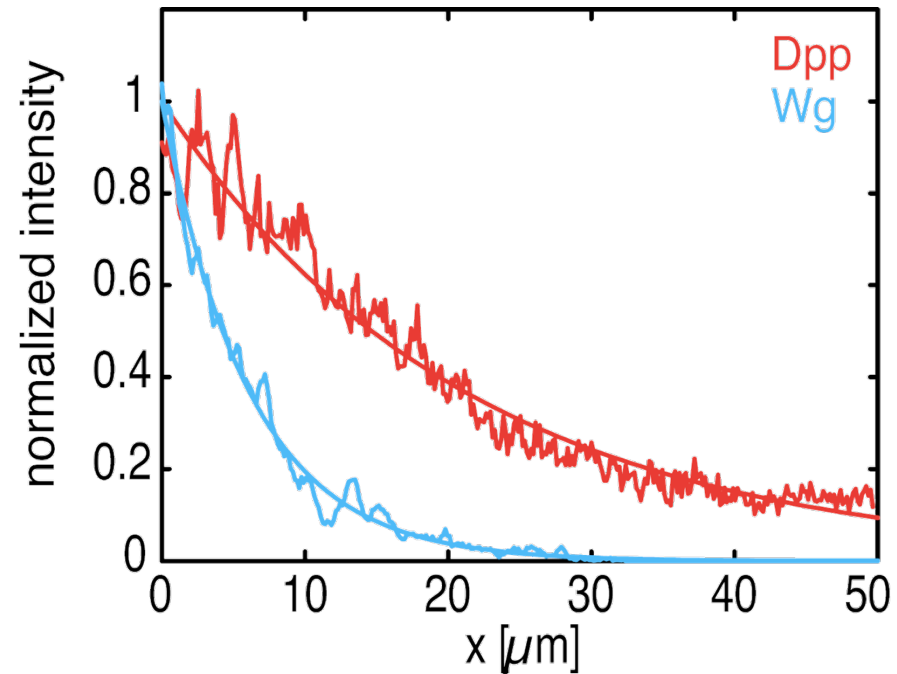
$$D = 0.10 \mu\text{m}^2/\text{s} \pm 0.05$$

$$k = 0.000252 \text{ s}^{-1} \pm 0.0001$$

$$\nu = 2.69 \text{ molecules/s} \times \text{cell} \pm 1.58$$

gradient profile results from specific kinetic behavior

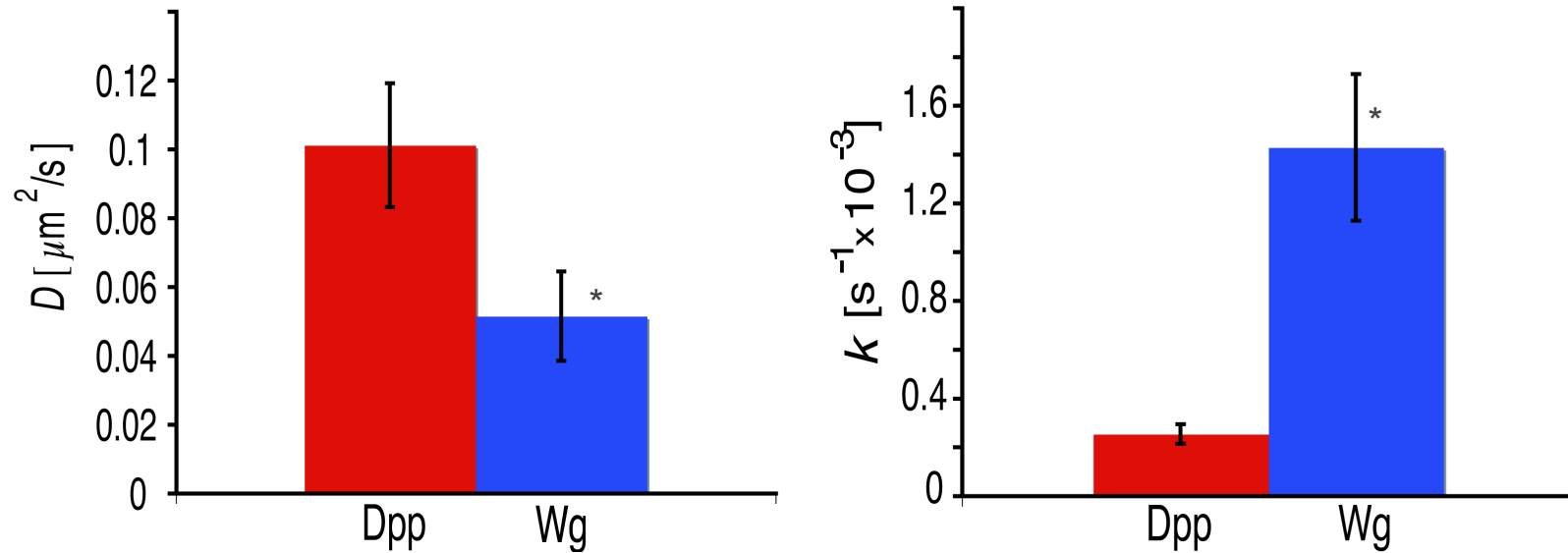
D, k, ν, ψ



$$\text{decay length } \lambda = \sqrt{\frac{D}{k}}$$

Dpp 20.2 μm ± 5.7 (SD), n = 26
Wg 5.8 μm ± 2.04 (SD), n=12

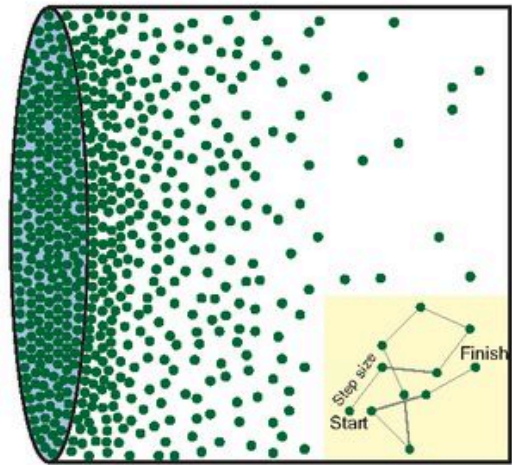
kinetics of the Dpp vs the Wg gradient



$$\lambda = \sqrt{\frac{D}{k}}$$

DIFFUSION + DEGRADATION

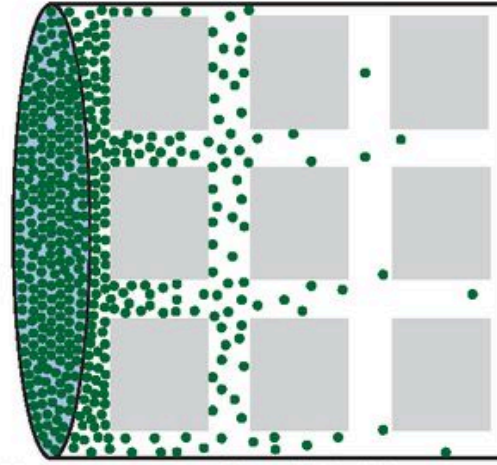
B Free diffusion



Ship (source)
with
drunken sailors
(morphogen)

City
(target field)

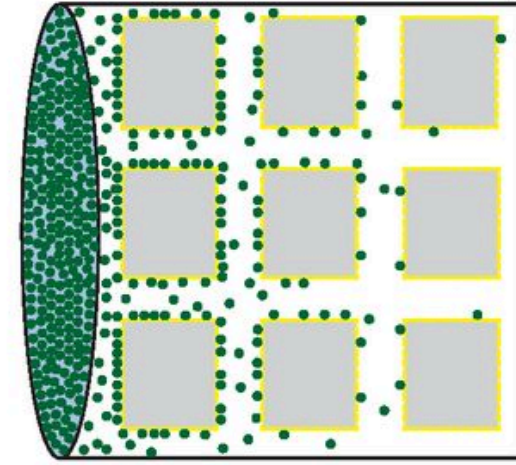
**C Hindered diffusion:
tortuosity**



Ship (source)
with
drunken sailors
(morphogen)

City with buildings
(target field with cells)

**D Hindered diffusion:
tortuosity + transient binding**

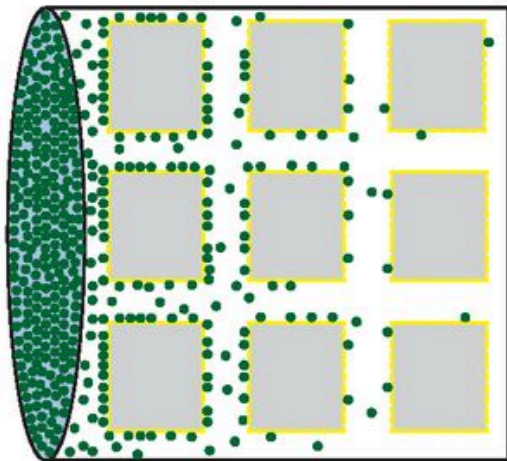


Ship (source)
with
drunken sailors
(morphogen)

City with buildings and pubs
(target field
with cells and
negative diffusion regulators)

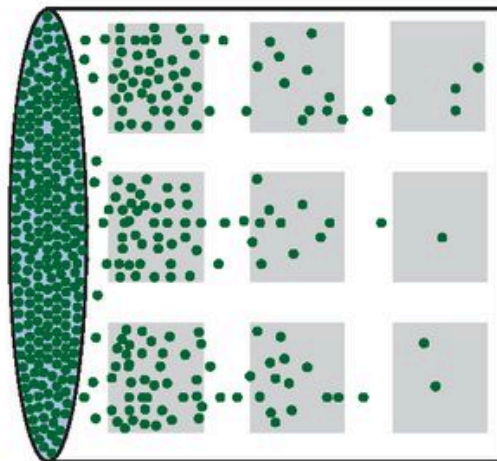
Route of movement

**D Hindered diffusion:
tortuosity + transient binding**



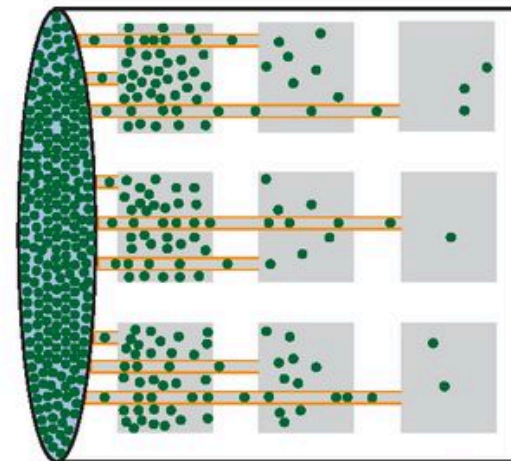
Ship (source) with drunken sailors (morphogen) City with buildings and pubs (target field with cells and negative diffusion regulators)

G Transcytosis



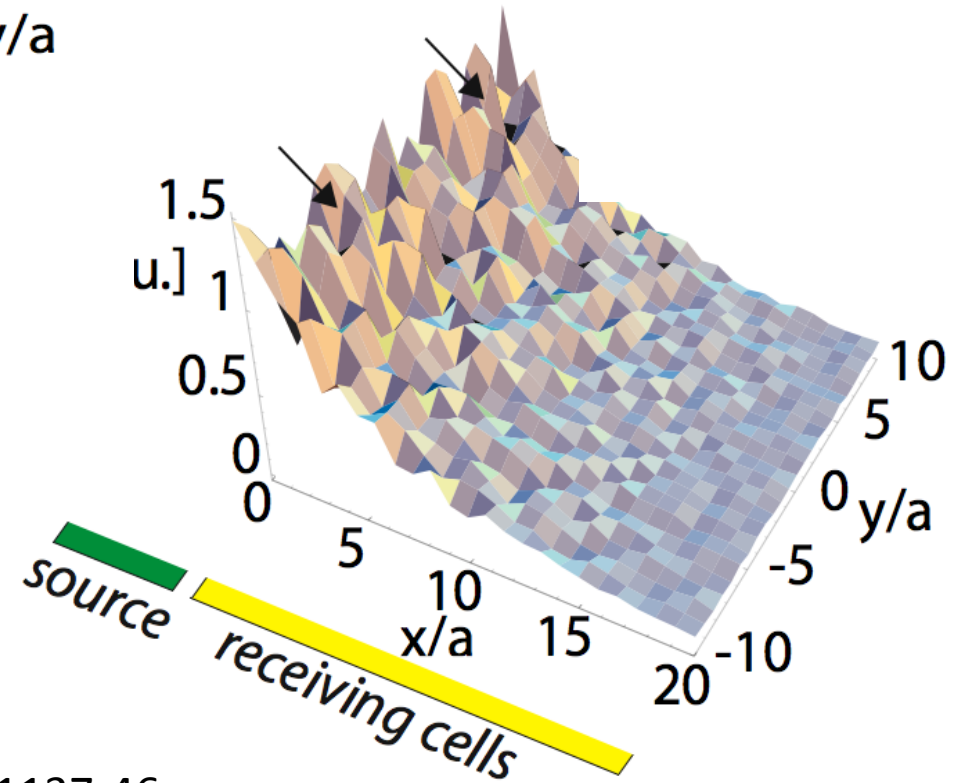
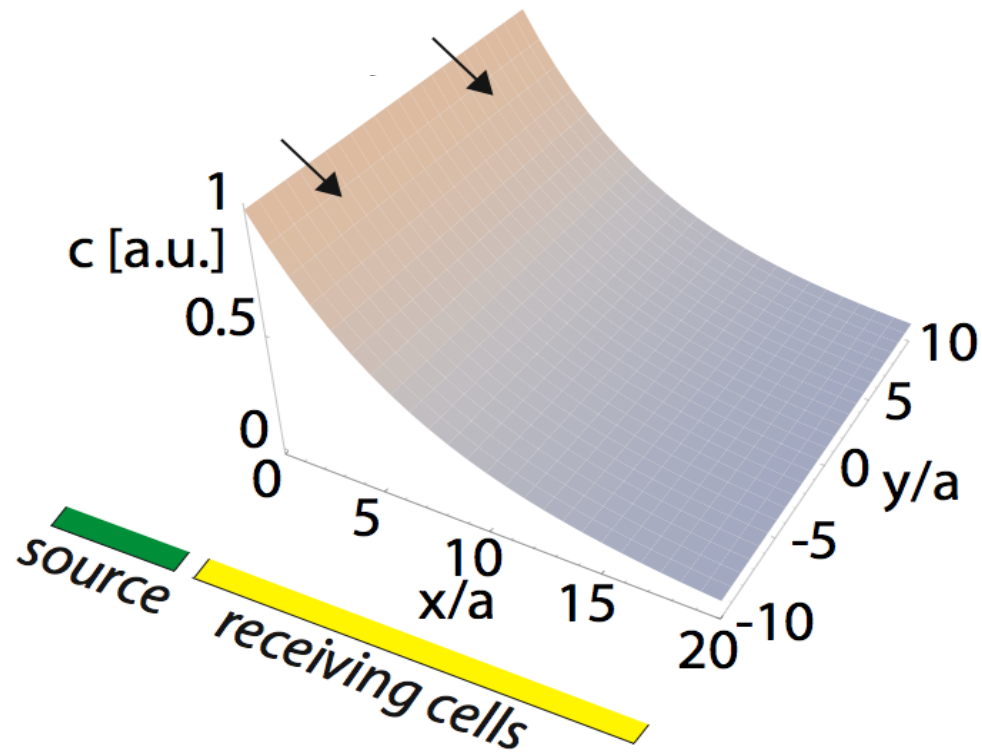
Ship (source) with drunken sailors (morphogen) City with buildings (target field with cells)

H Cytonemes



Ship (source) with drunken sailors (morphogen) City with buildings and subway (target field with cells and cytonemes)

Noise



Morphogens:

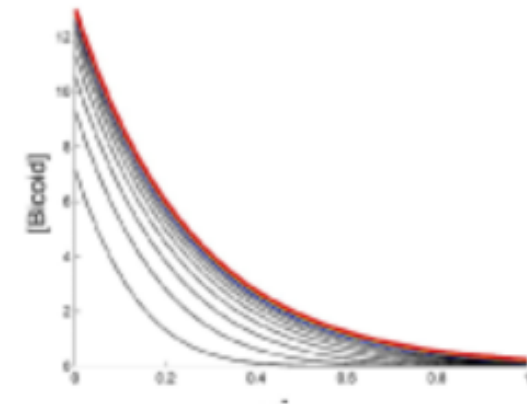
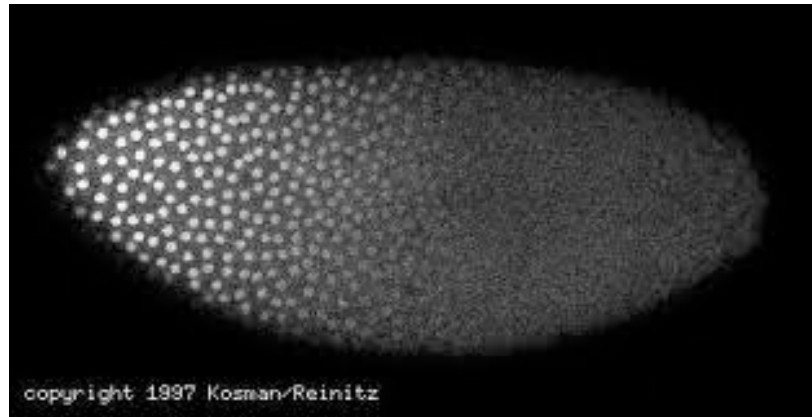
- Identification – what and where
- Formation - intercellular transmission
- Perception - signal transduction
- Interpretation - convert to discrete responses

Morphogen Interpretation

- How does the signaling pathway transform the extracellular ligand?
- How is differential gene expression encoded in cis-regulatory elements?
- What role does the transcriptional network play in producing discrete spatial patterns of gene expression?
- How does cell proliferation and tissue growth affect gradient interpretation?

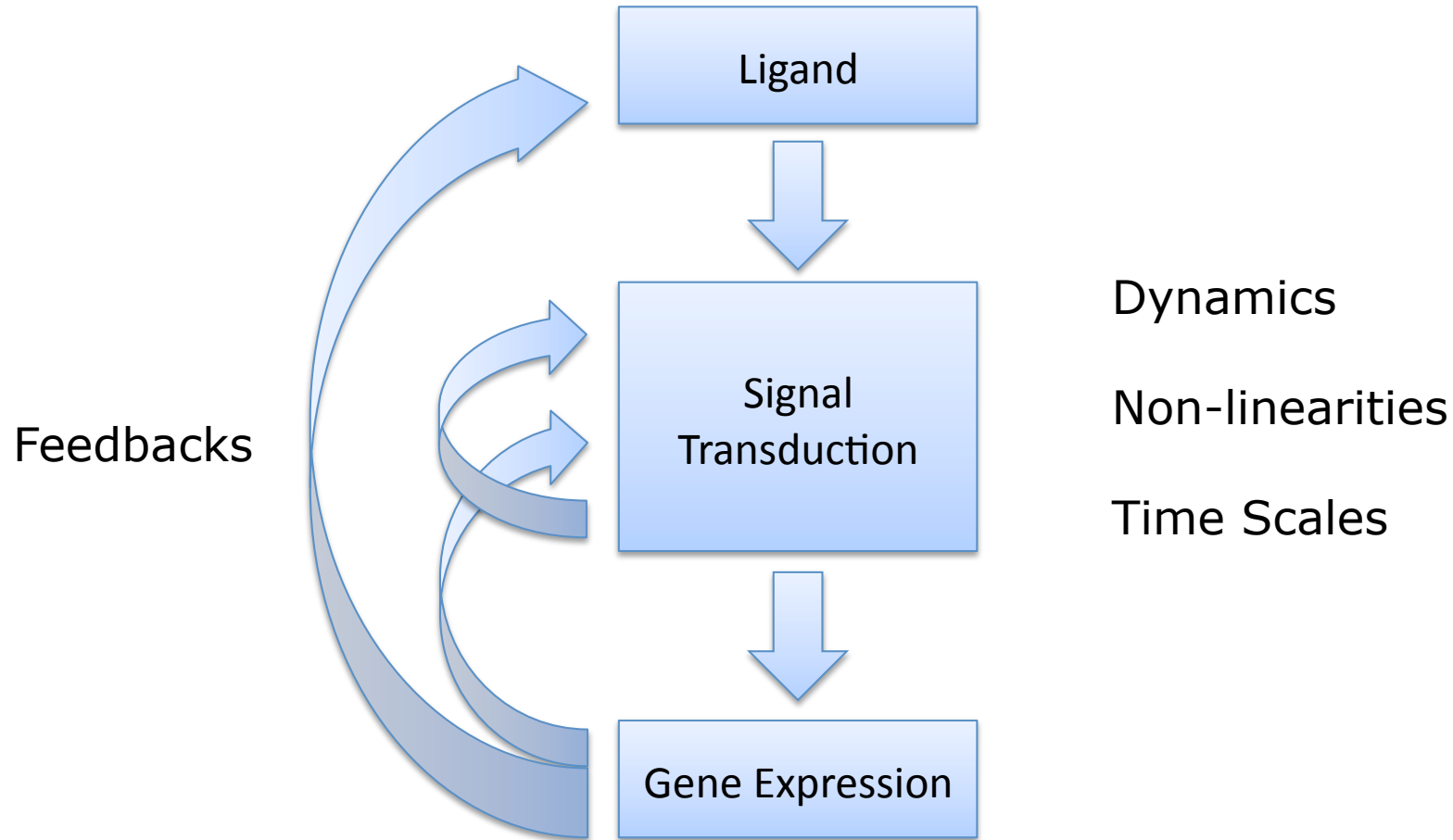
'Direct' Morphogens

BICOID



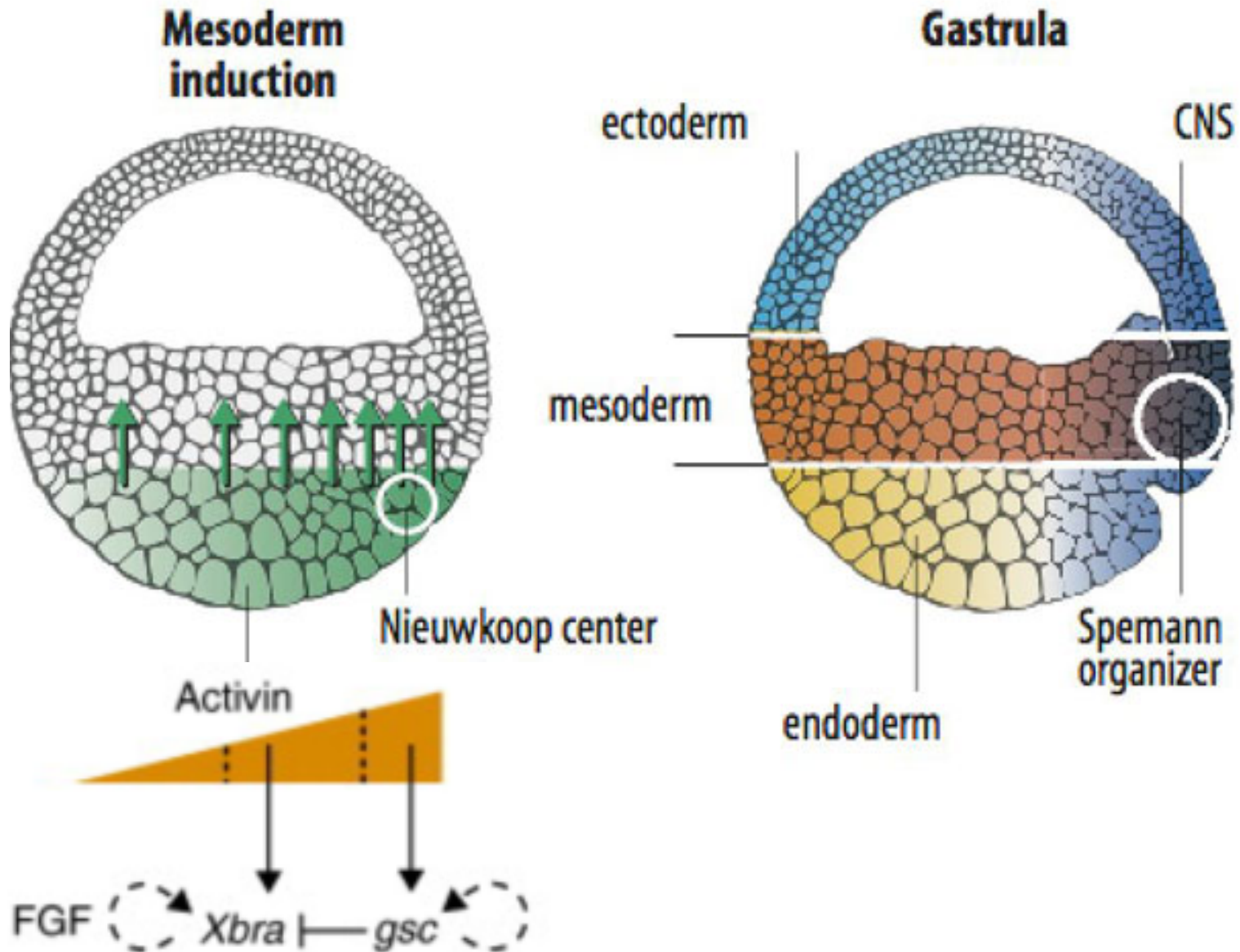
Grimm O et al. Development 2010;137:2253-2264

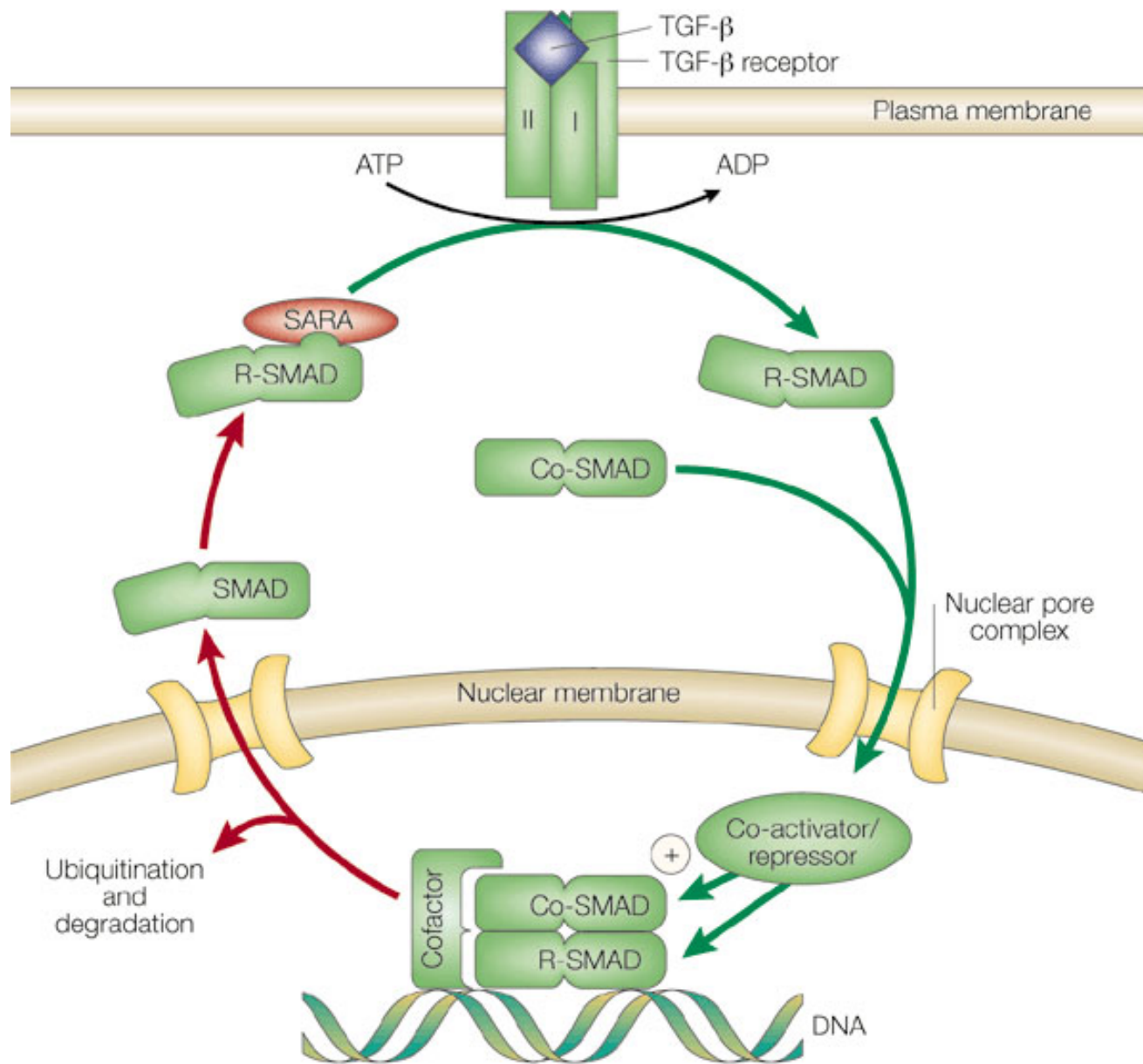
Signal Transduction



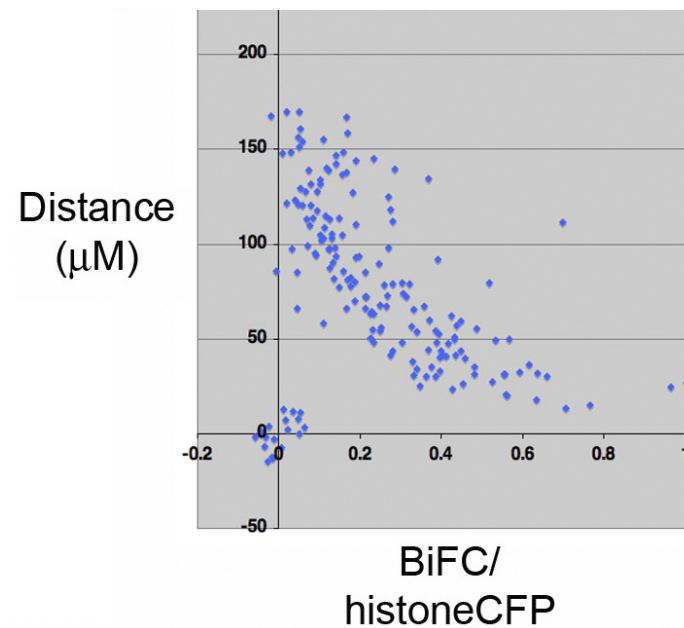
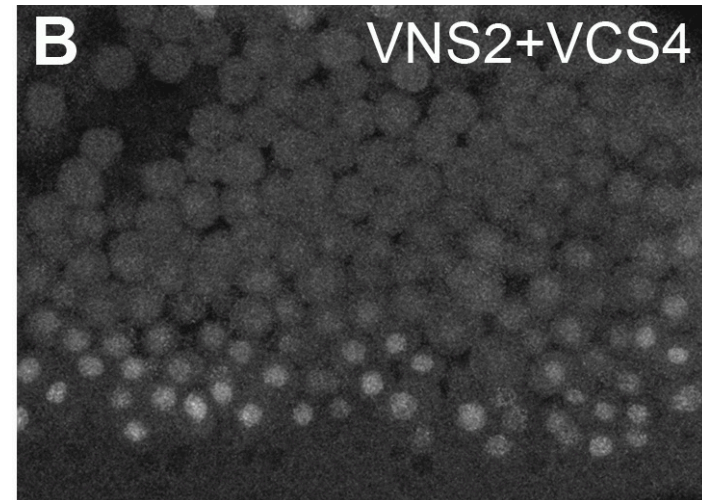
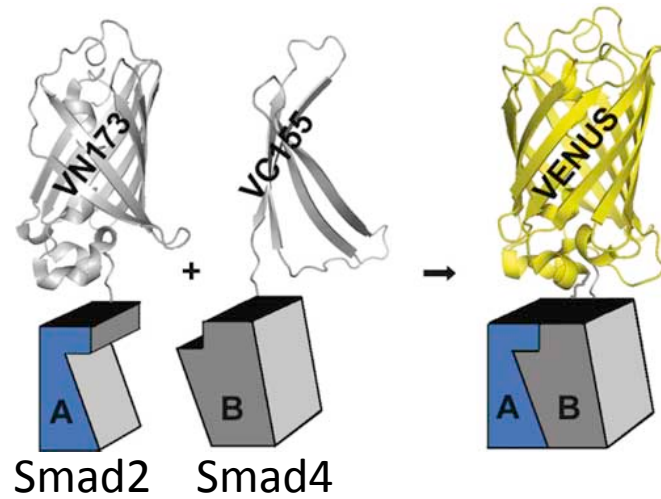
- Sensors and reporters – single cell, time resolved data
- Mechanistic models – interpret experimental observations

Graded signal transduction: Mesoderm



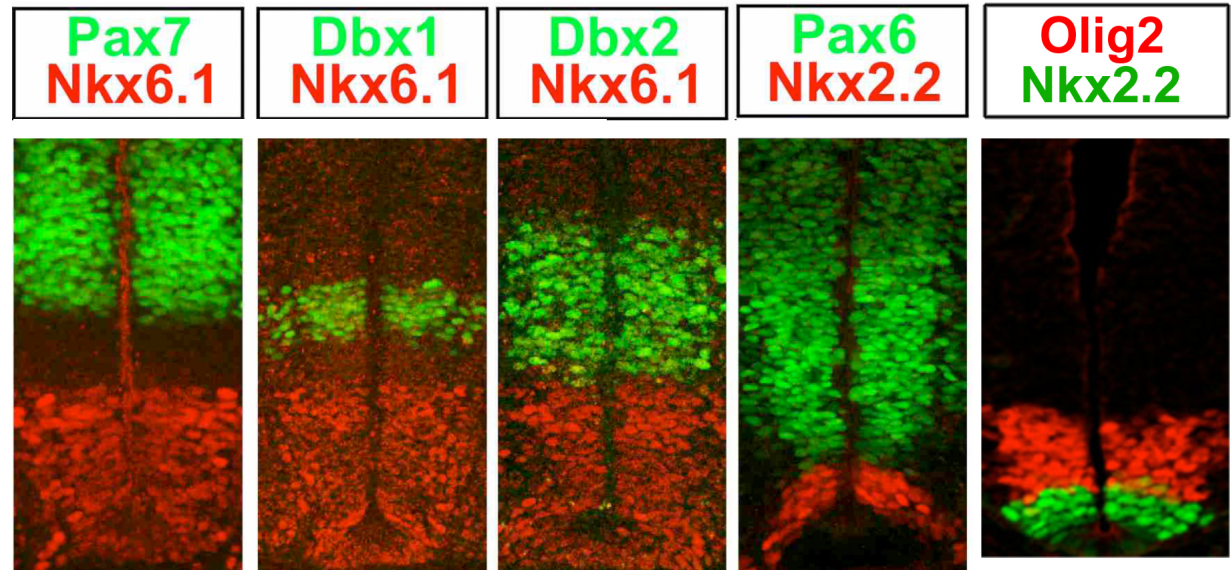
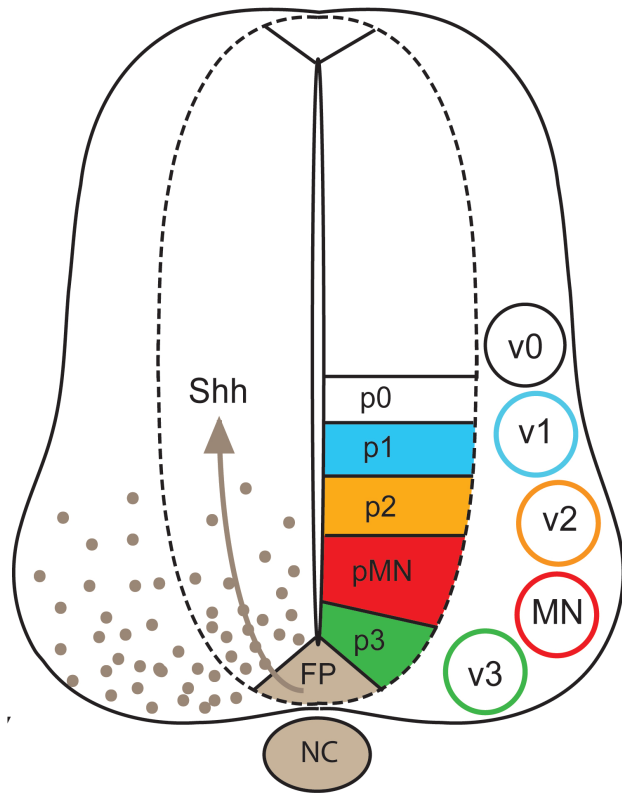


SMAD activity sensors

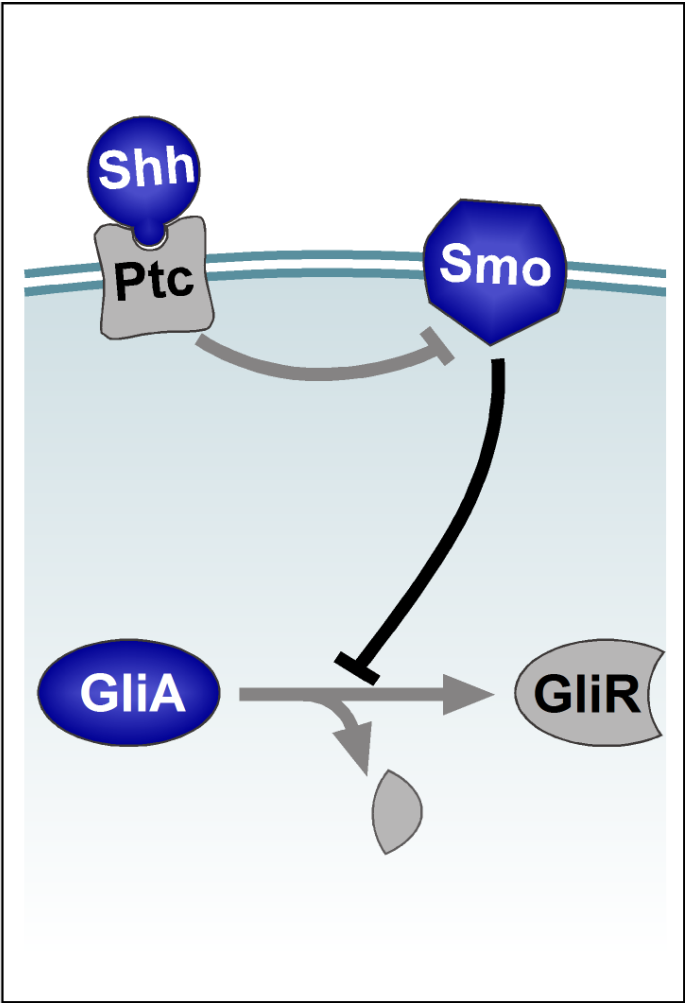
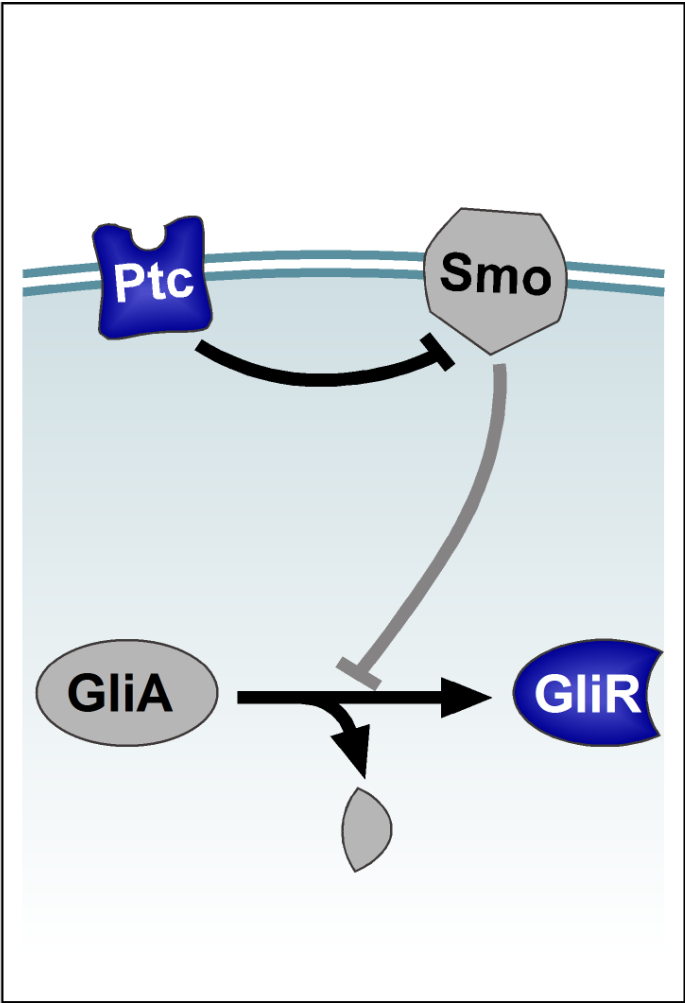


Harvey SA, Smith JC (2009) PLoS Biol 7(5): e1000101. doi:10.1371/journal.pbio.1000101

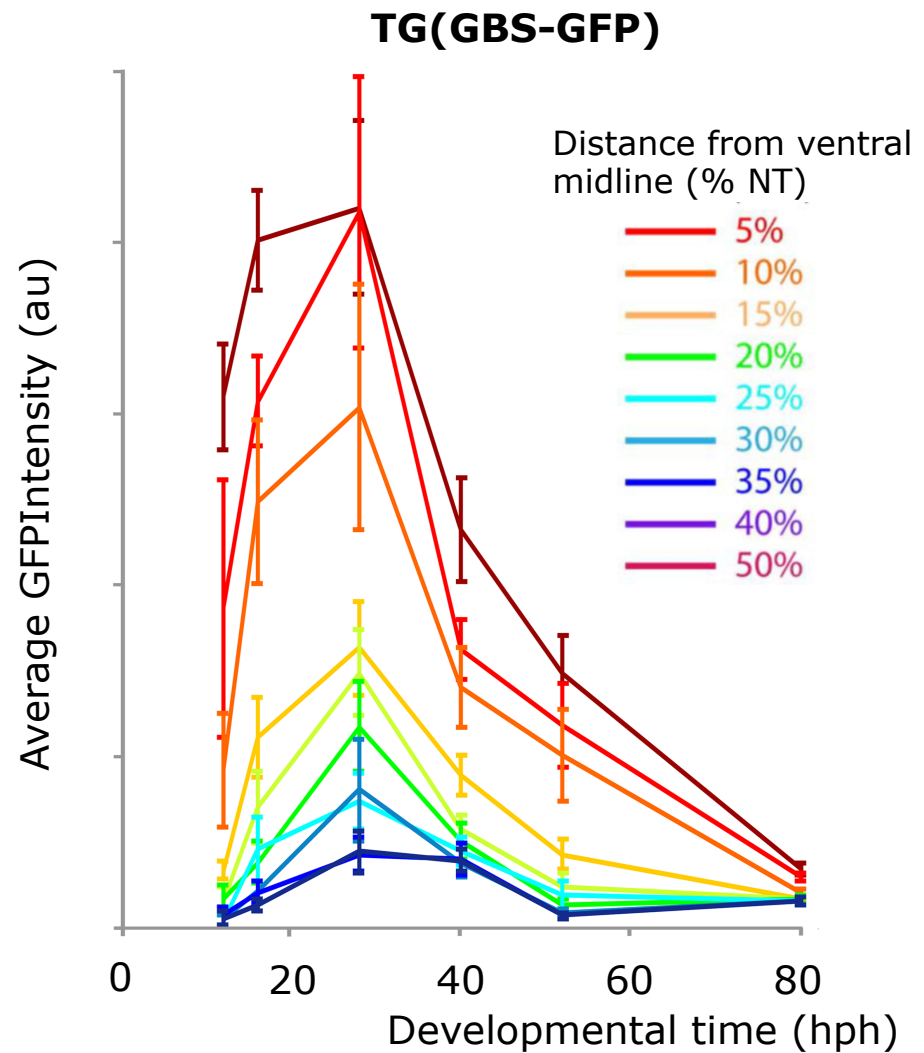
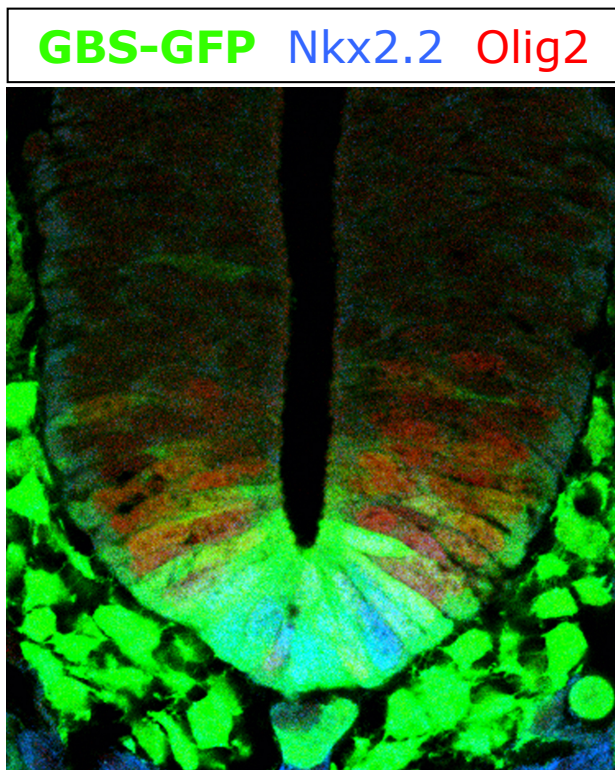
Shh signalling patterns neural progenitors



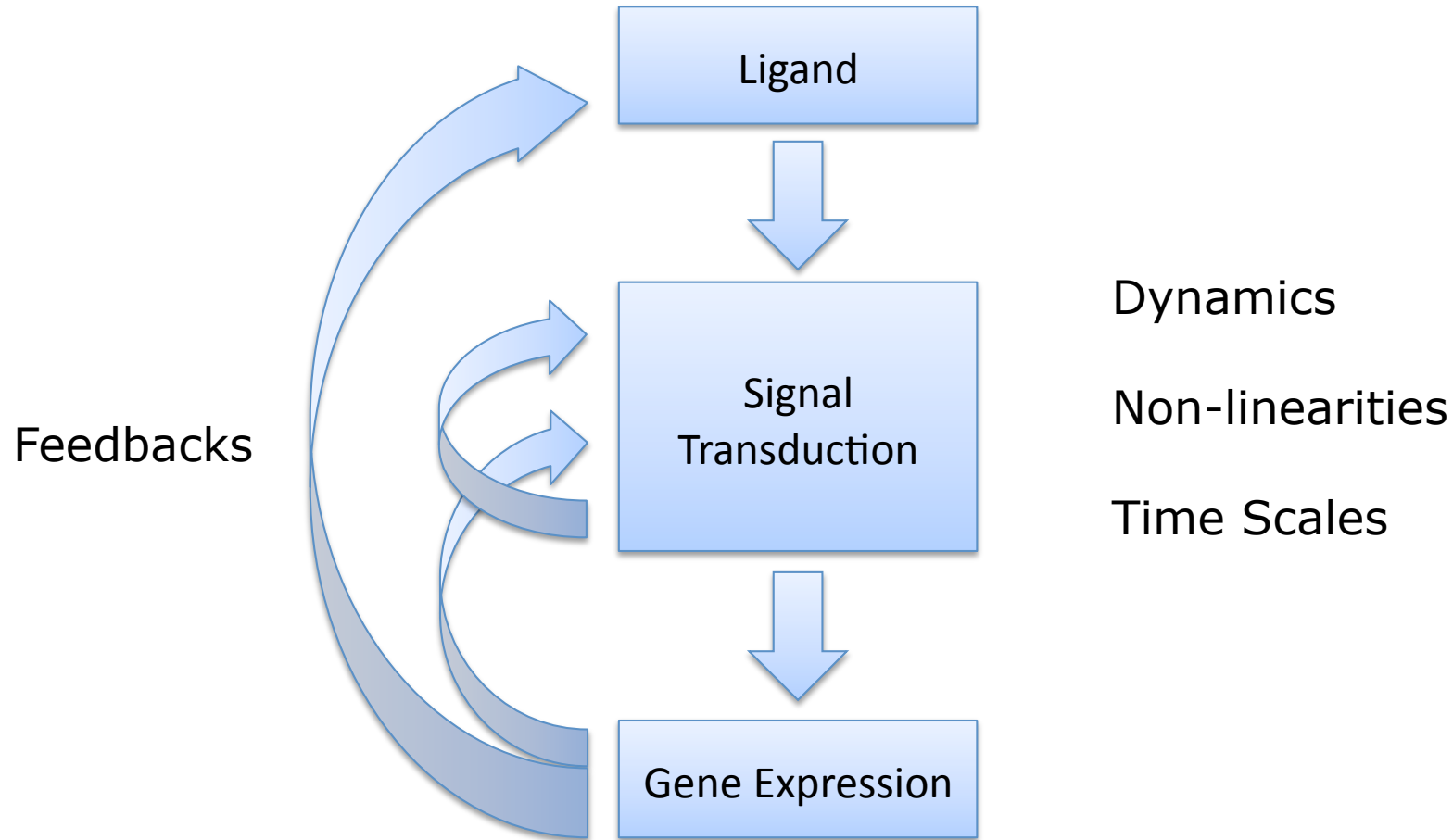
Intracellular communication



Gli activity is dynamic



Signal Transduction

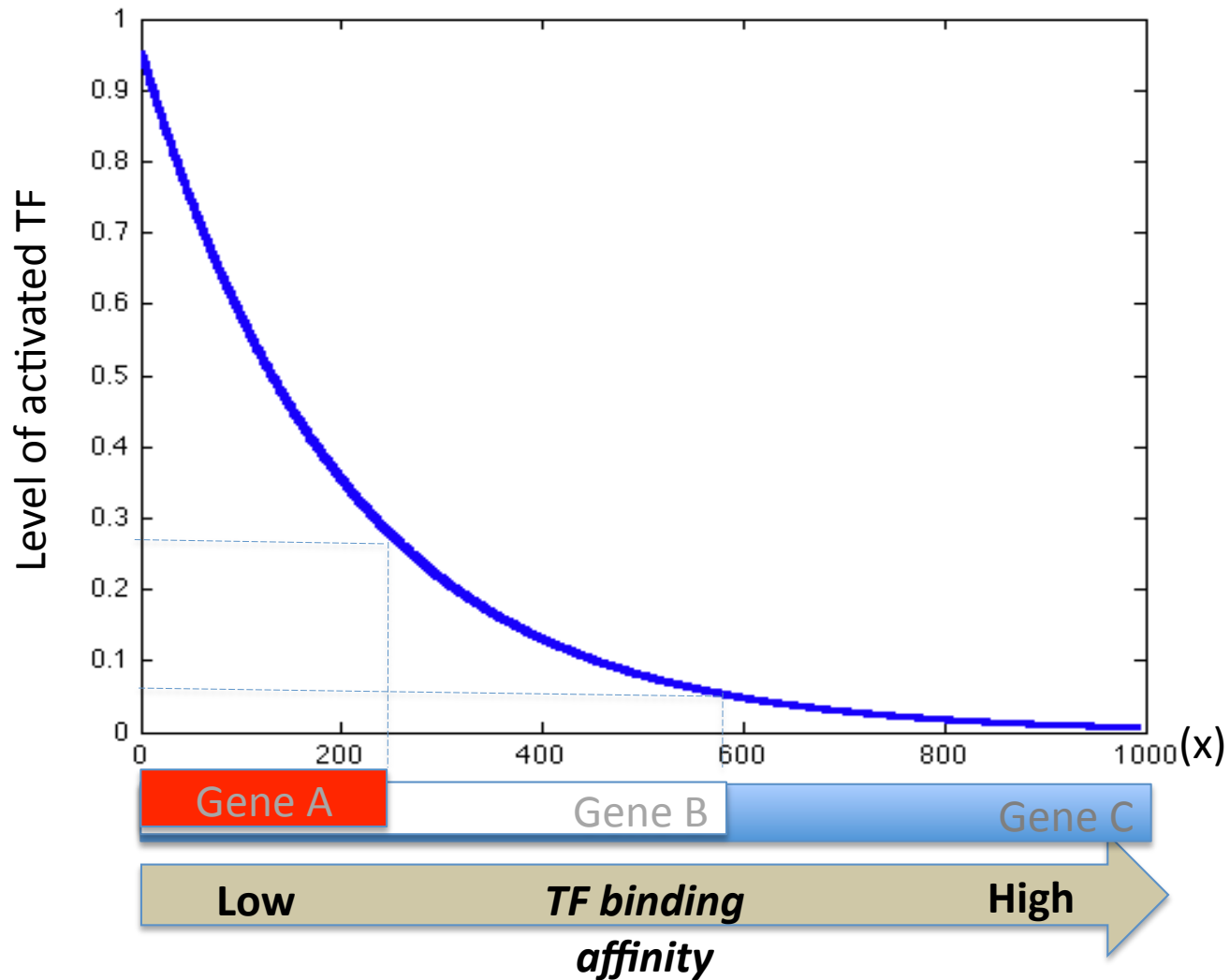


- Sensors and reporters – single cell, time resolved data
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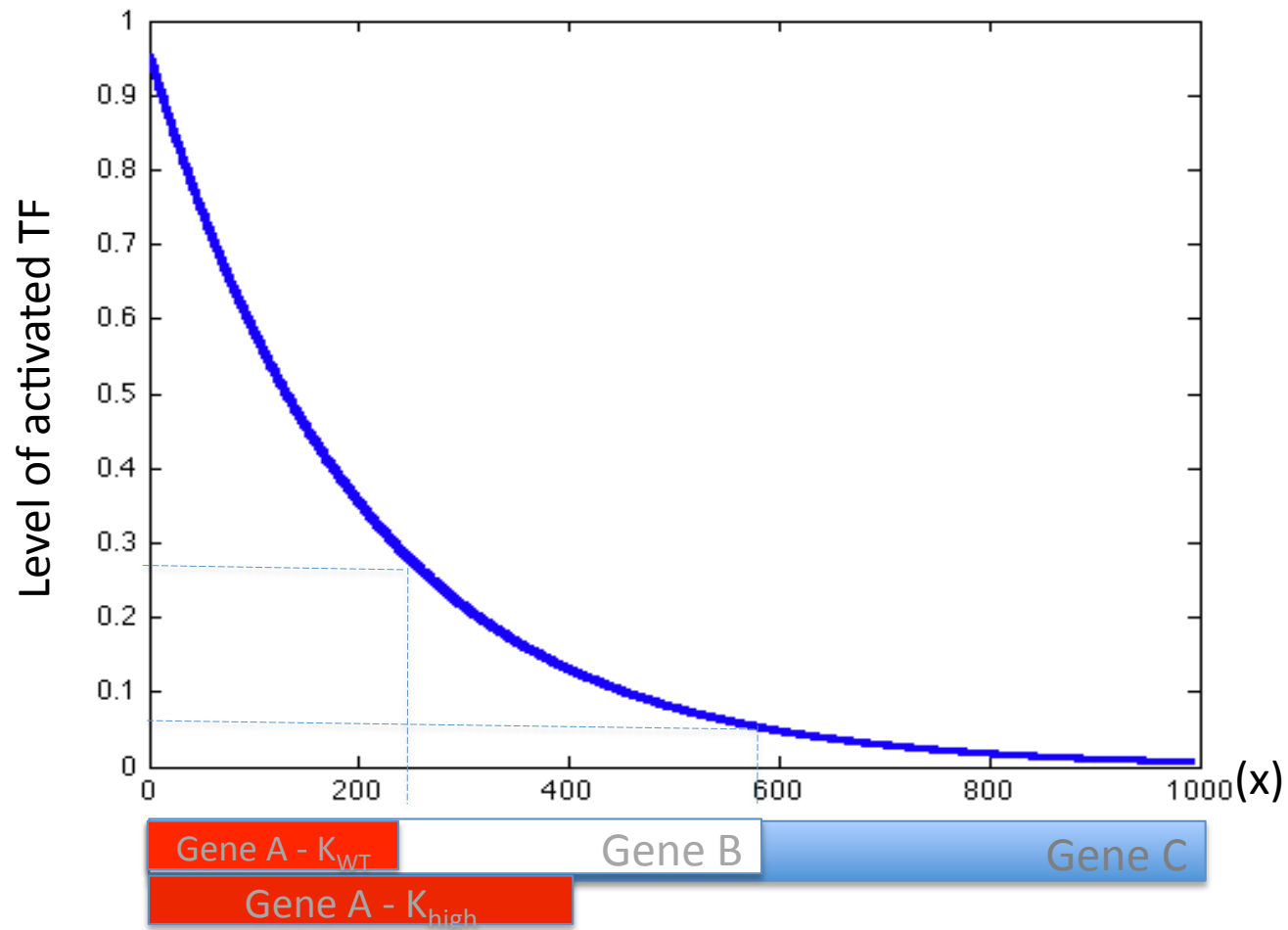
Morphogen Interpretation

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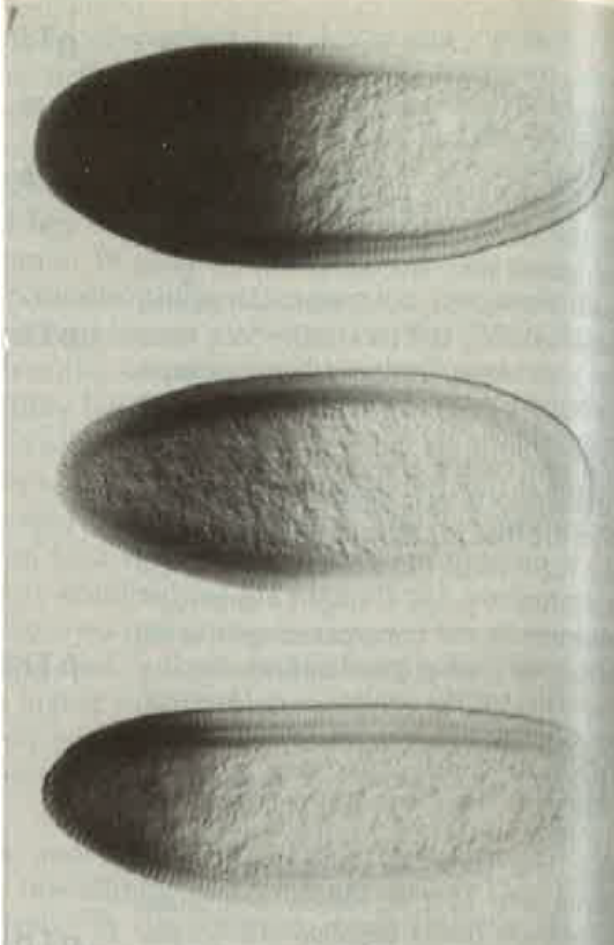
Affinity threshold model



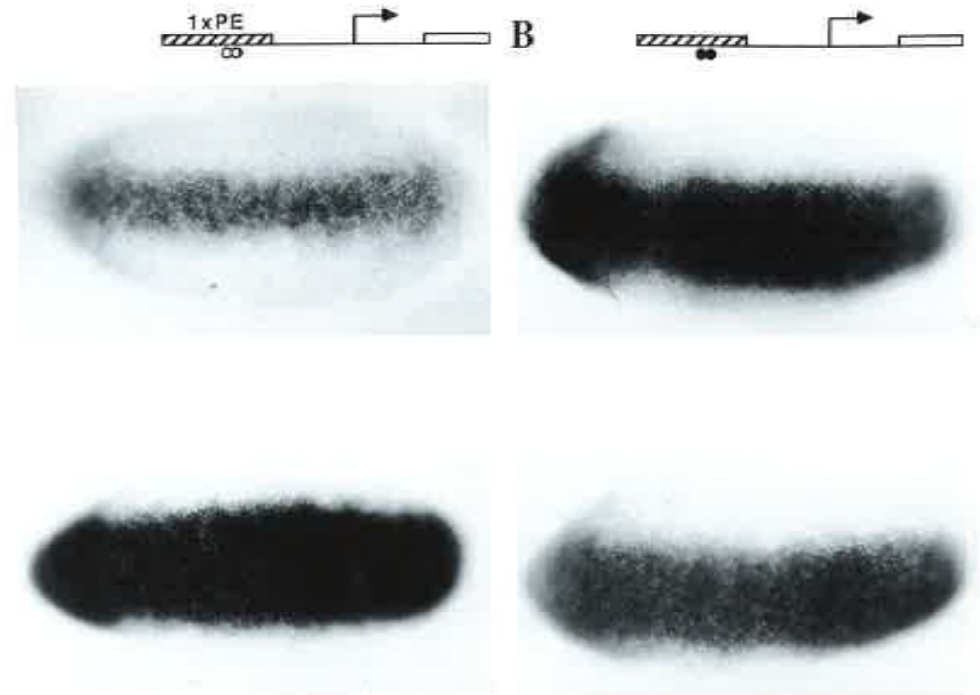
Affinity threshold model



Support for A-T model

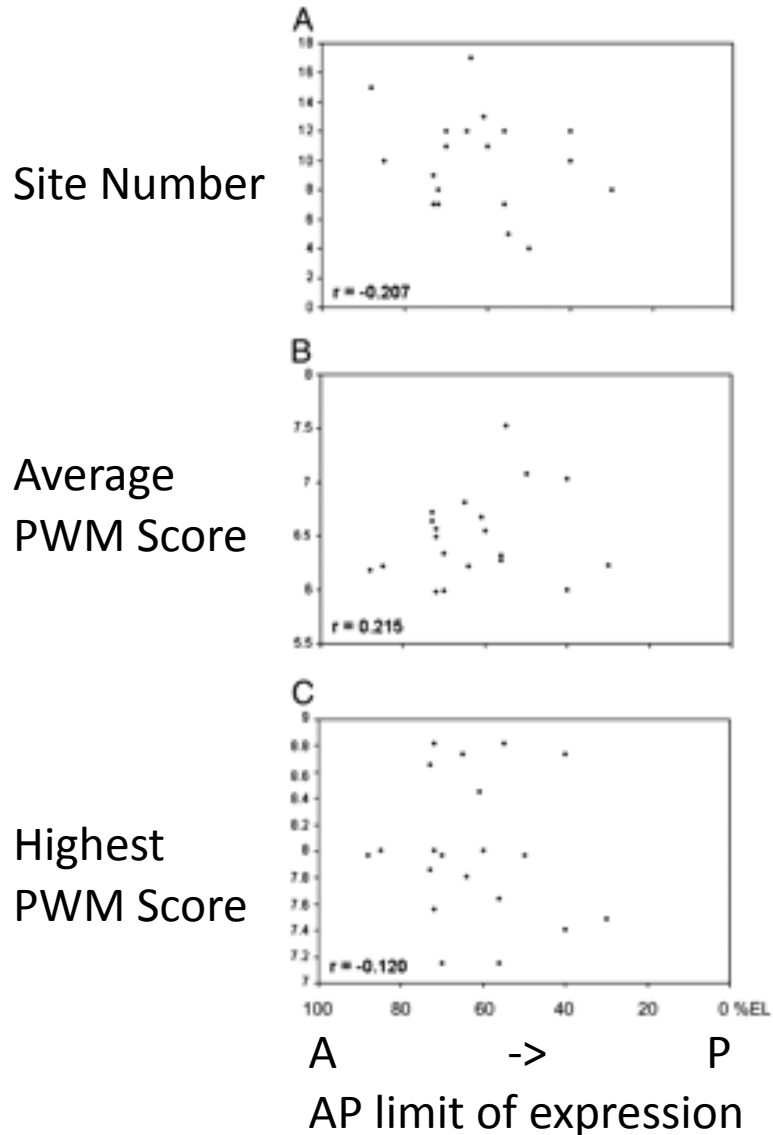


Nature (1989) **340**, 363 – 367 W
WOLFGANG DRIEVER,
GUDRUN THOMA & CHRISTIANE NÜSSLEIN-VOLHARD



Cell (1993) 72:741–752
Jin Jiang and Michael Levine

Challenges to A-T model

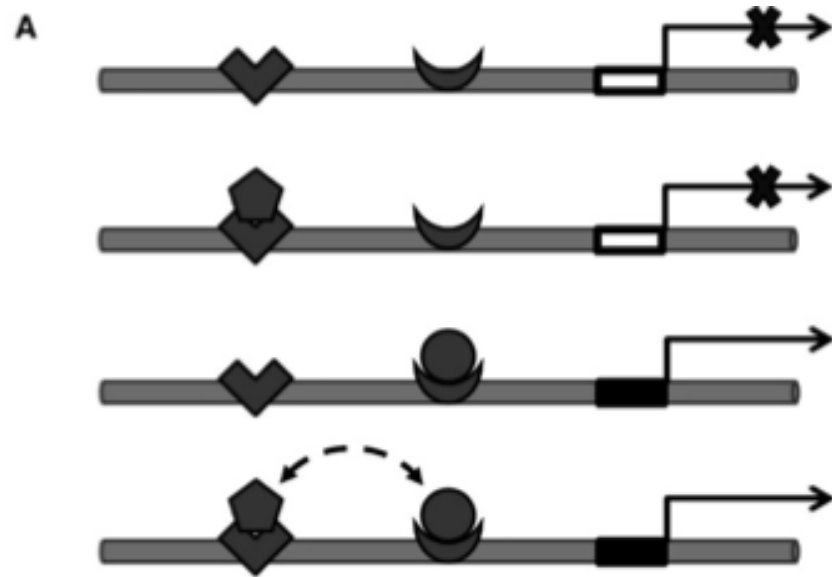


Comparison of the expression profile and Bcd binding sites of 21 genes

No correlation

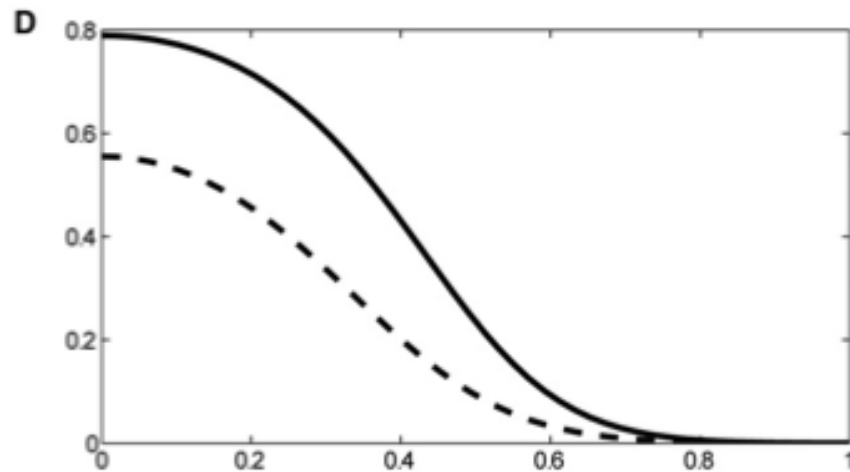
Ochoa-Espinosa et al (2005) *Proceedings of the National Academy of Sciences* 102: 4960–4965

Uniformly expressed factors influence gene expression



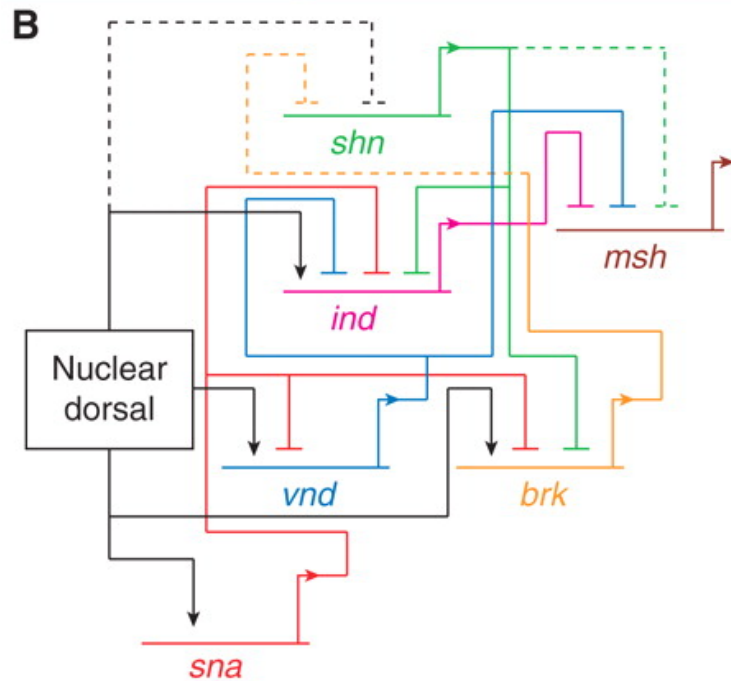
A spatially uniformly expressed TF (zelda) can coop with Morphogen TF (dorsal) to promote gene expression.

Decorrelates morphogen TF binding affinity from response



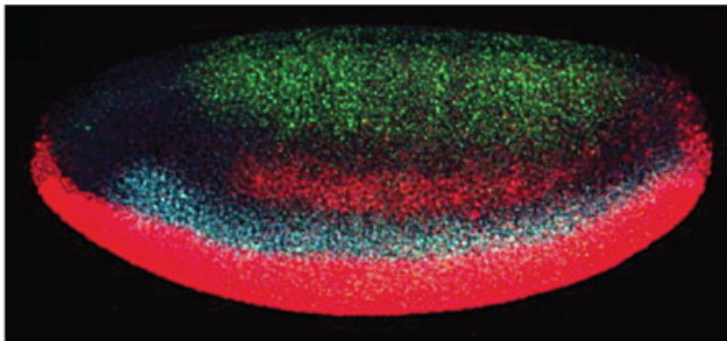
Kanodia et al (2012) *Biophysical Journal* 102: 427-433.

Morphogen target genes are also TFs

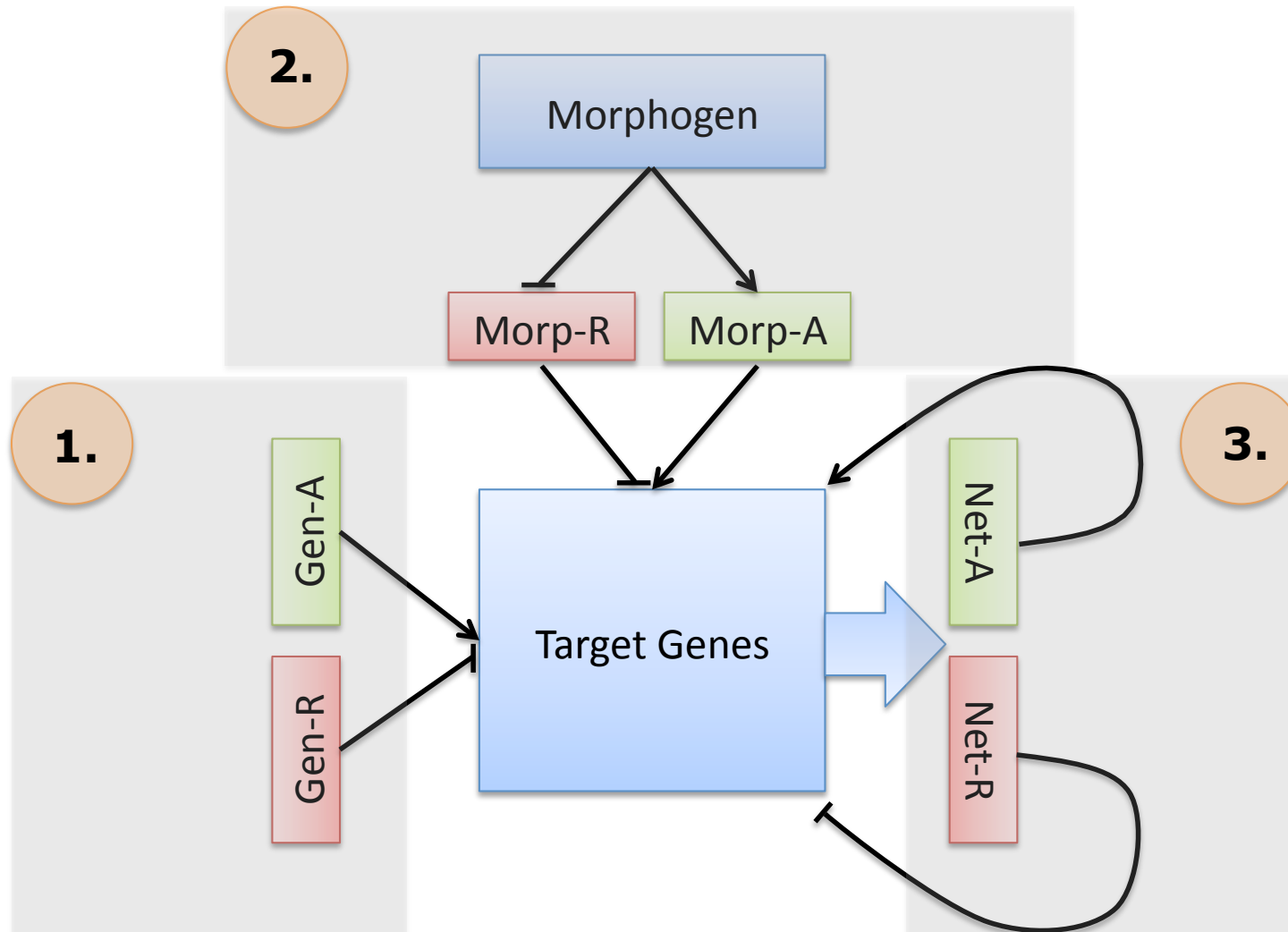


Regulation of Dorsal target genes involves positive and negative interactions between targets

Levine, Stathopoulos and many others



Three Components to Gene Regulation



Morphogen Interpretation

- How does the signaling pathway transform the extracellular ligand?
- How is differential gene expression encoded in cis-regulatory elements?
- **What role does the transcriptional network play in producing discrete spatial patterns of gene expression?**
- How does cell proliferation and tissue growth affect gradient interpretation?

Theoretical Analyses

Development 137, 2385-2395 (2010) doi:10.1242/dev.048033
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Predicting embryonic patterning using mutual entropy fitness and in silico evolution

Paul François* and Eric D. Siggia

Molecular Systems Biology 6; Article number 425; doi:10.1038/msb.2010.74

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An atlas of gene regulatory networks reveals multiple three-gene mechanisms for interpreting morphogen gradients

James Cotterell^{1,2} and James Sharpe^{1,3,*}

Predicting embryonic patterning using mutual entropy fitness and in silico evolution

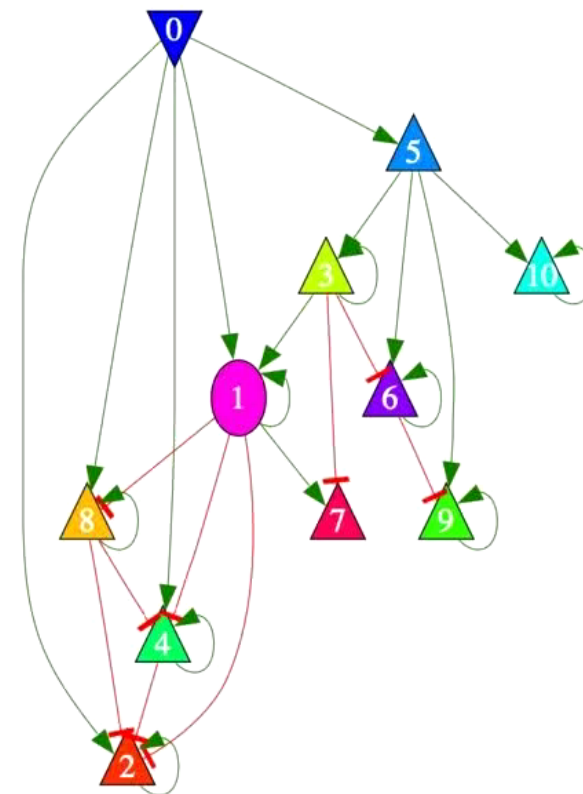
Paul François* and Eric D. Siggia

- In silico evolution of a txn network that patterns (in 1D) a tissue exposed to:
 - A static gradient that disappears before the end of development
 - A gradient that slides across the tissue

Dynamics of the network topology displayed on Fig. 3C

Network is under control of a morphogen gradient (blue dotted), time is developmental time

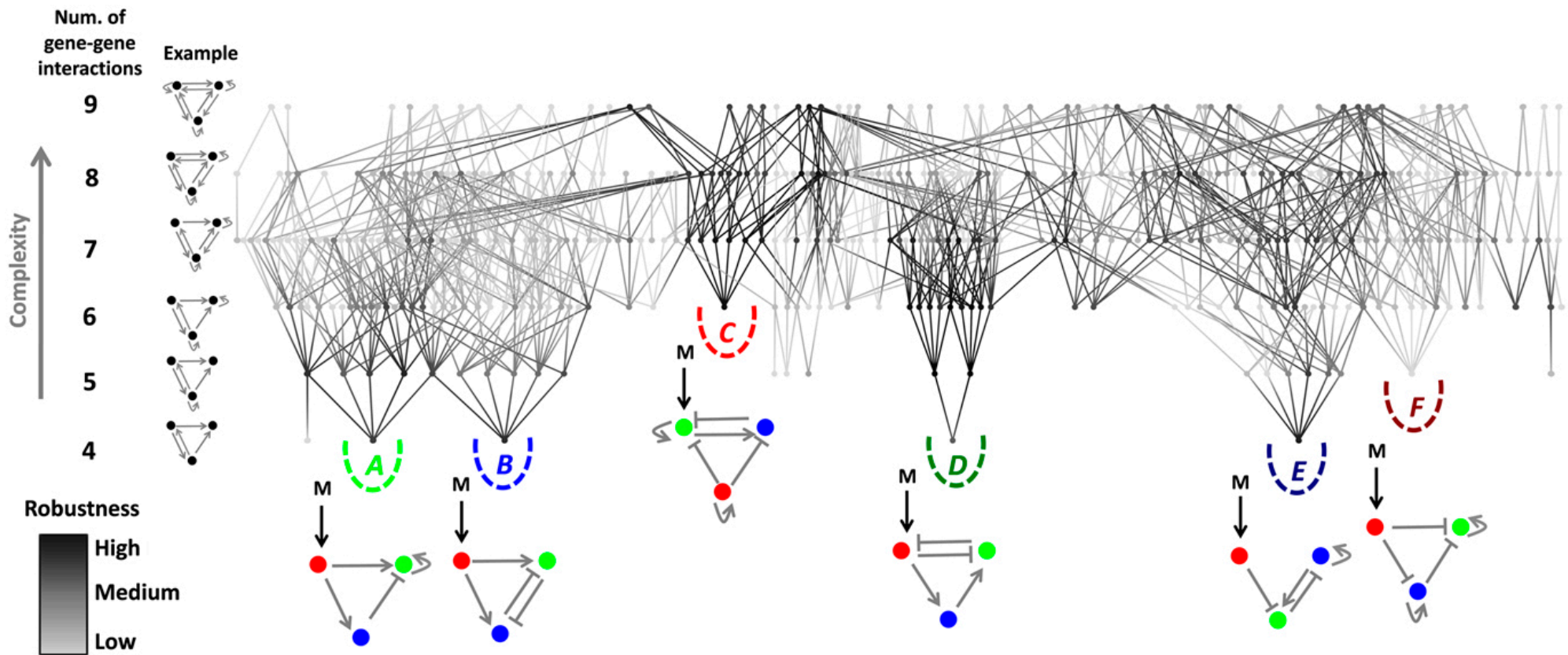
P. François, E. Siggia
pfrancois@rockefeller.edu



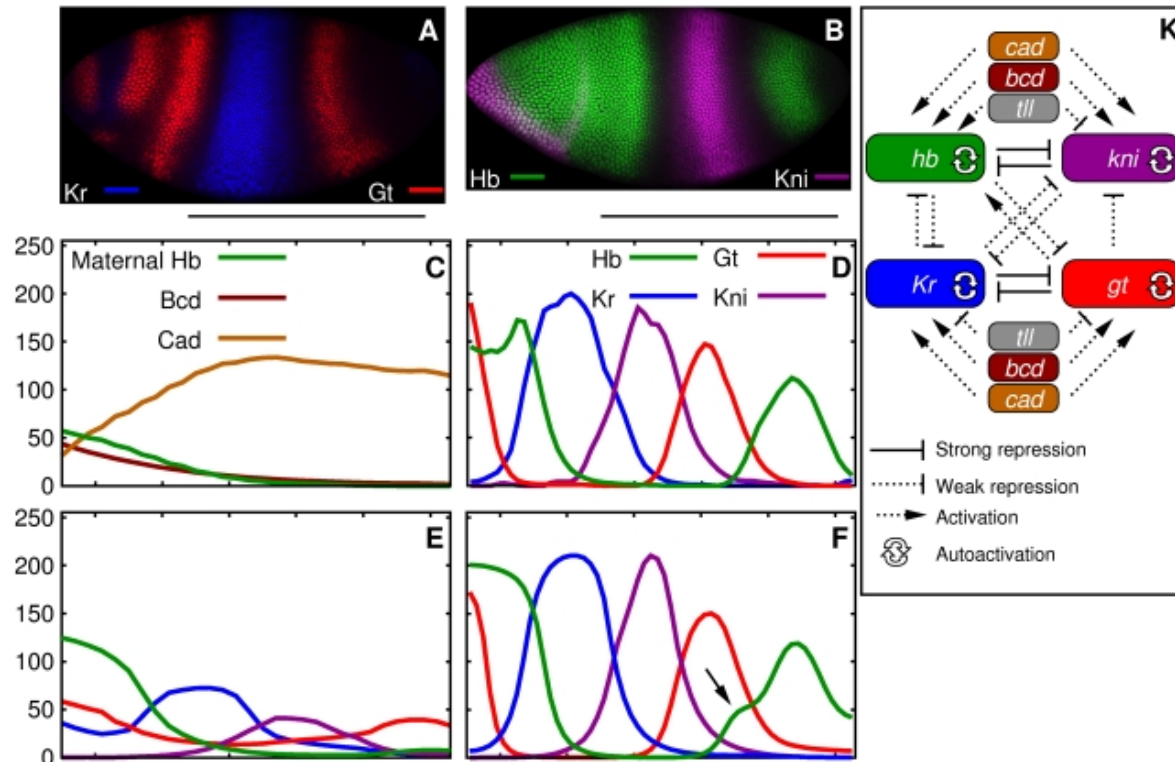
An atlas of gene regulatory networks reveals multiple three-gene mechanisms for interpreting morphogen gradients

James Cotterell^{1,2} and James Sharpe^{1,3,*}

- Simulated an 'atlas' of 3 gene networks regulated by a graded input.
- Identified all networks that gave a 'morphogen' – stripe – output
- Classified these networks into ~6 distinct mechanisms



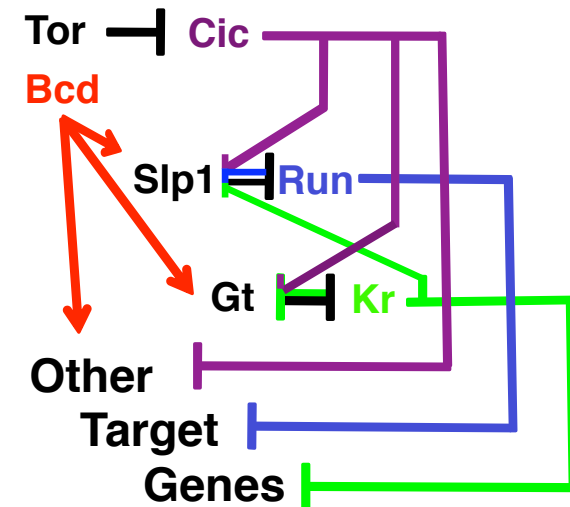
Real World Examples



Reinitz and colleagues

Jaeger et al (2004) *Nature* 430: 368–371

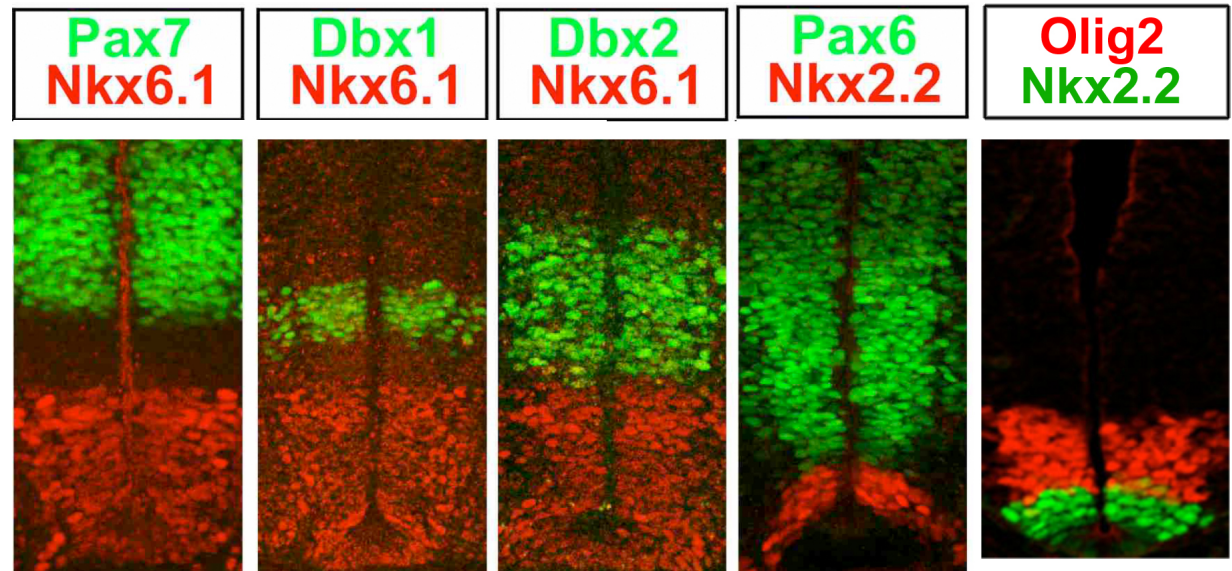
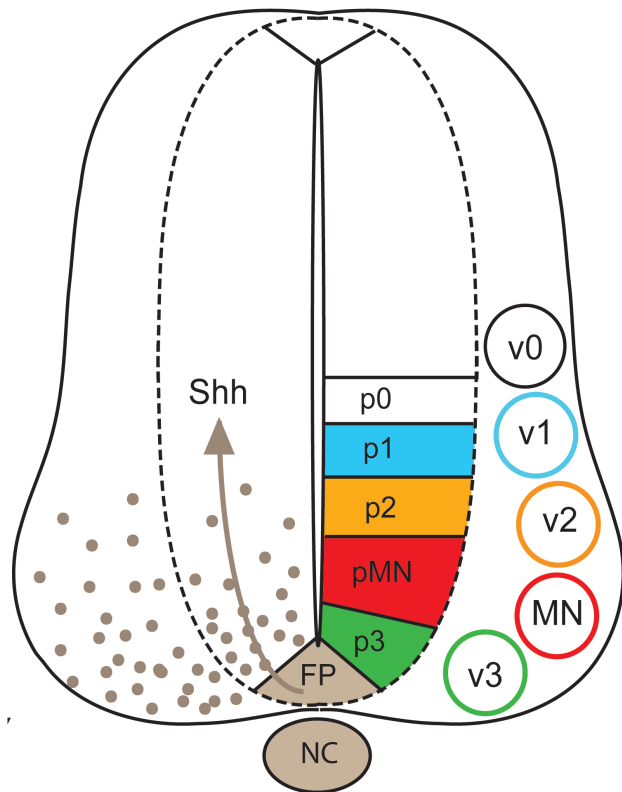
Manu et al. *PLoS Biology* 7: e1000049



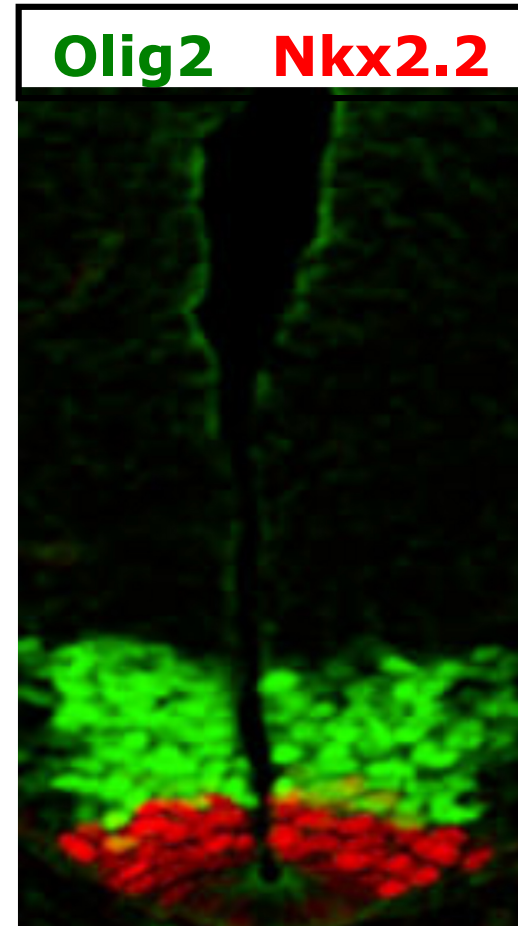
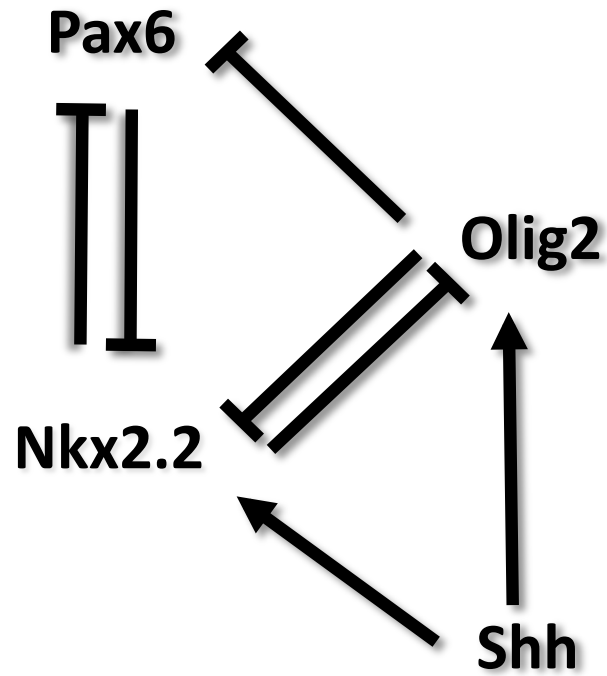
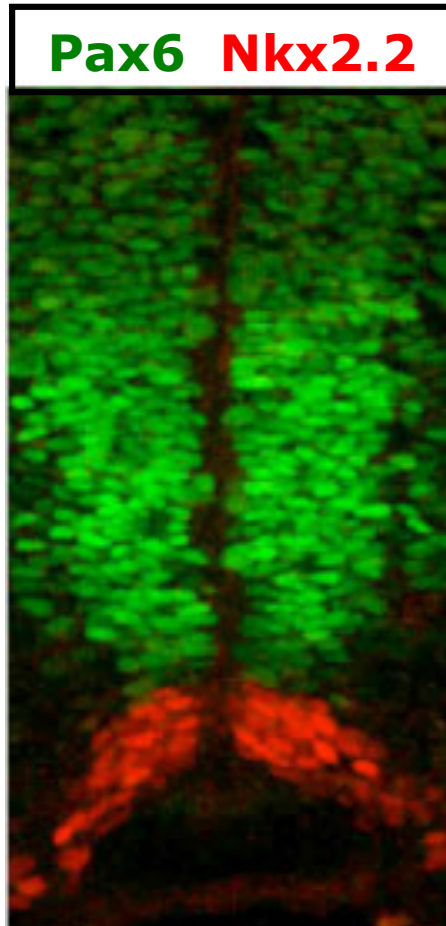
Small and colleagues

Chen et al (2012) *Cell* 149: 618–629

Shh signalling patterns progenitors

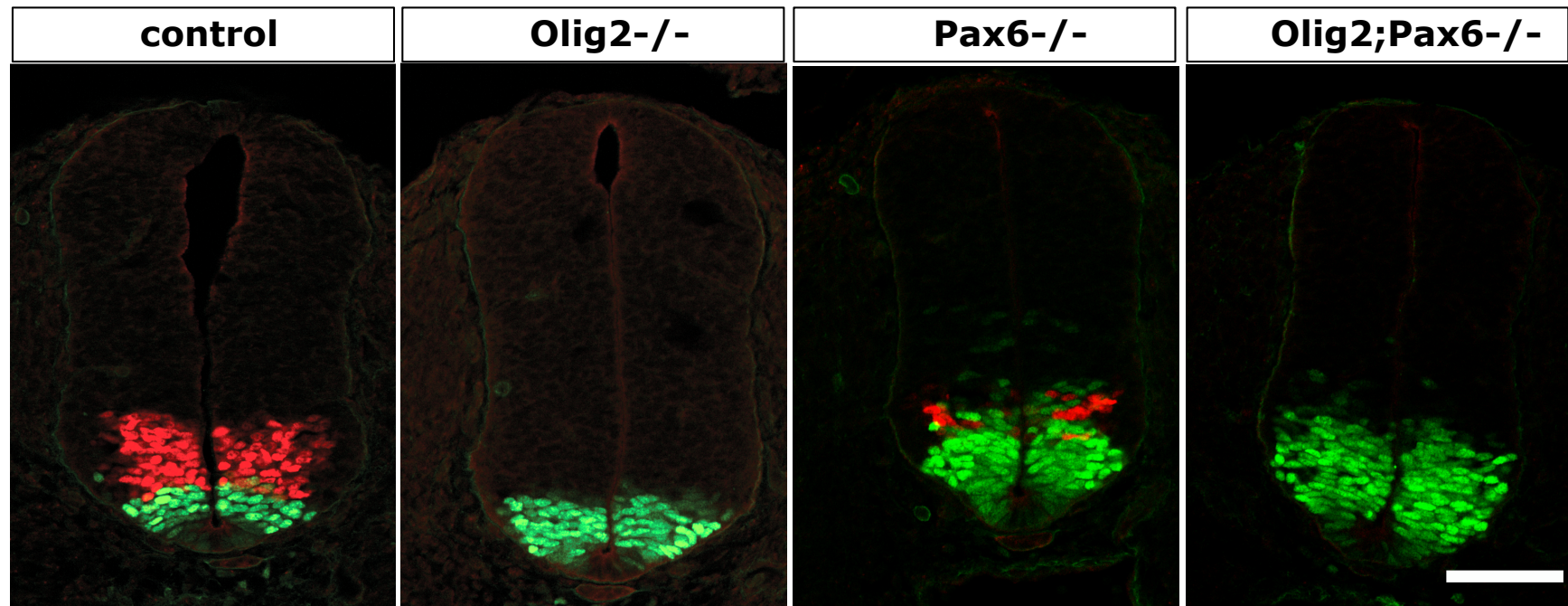


A transcriptional circuit for morphogen interpretation

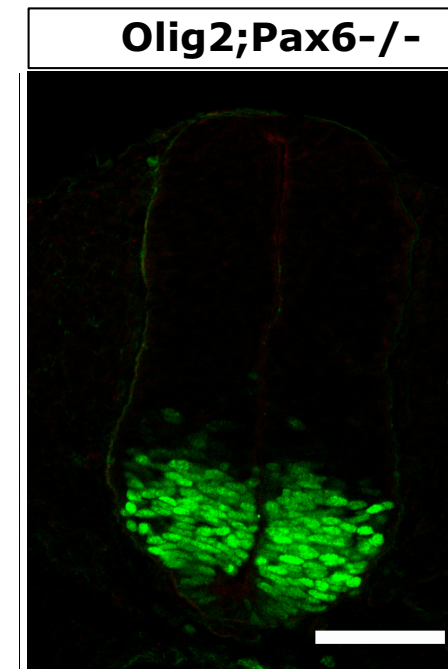
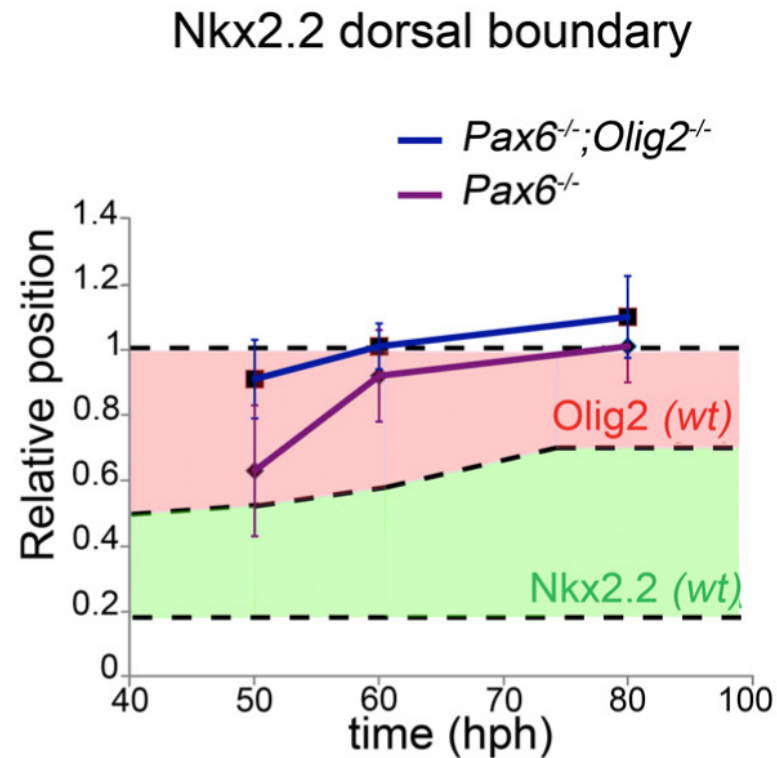
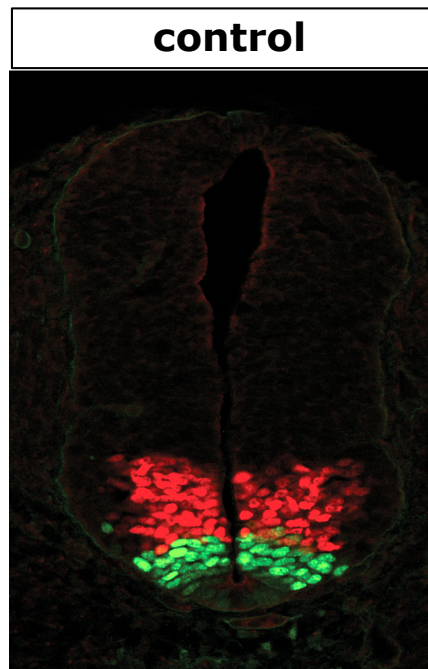


Pax6 and Olig2 repress Nkx2.2

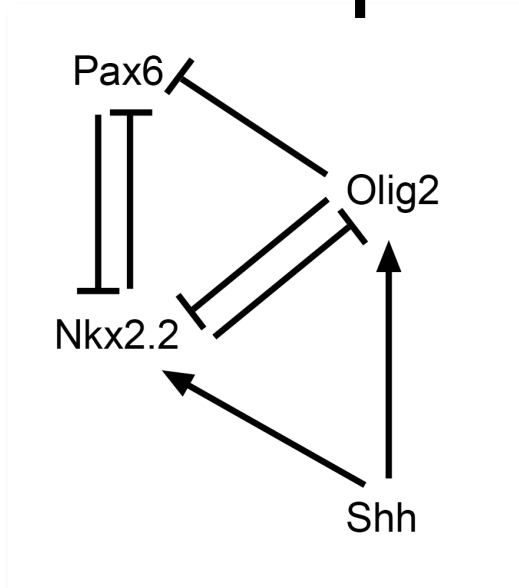
Olig2 **Nkx2.2**



Network generates morphogen response



Network generates morphogen response



$$\frac{dP}{dt} = \frac{\alpha}{1 + \left(\frac{N}{N_{critP}}\right)^{h1} + \left(\frac{O}{O_{critP}}\right)^{h2}} - k_1 P$$

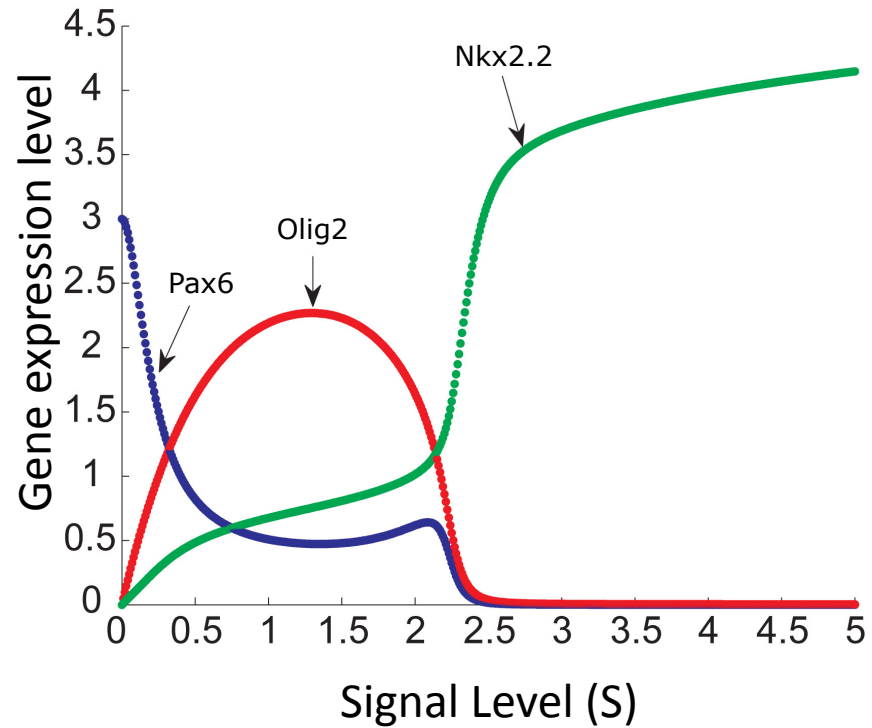
Pax6 (P)

$$\frac{dO}{dt} = \frac{\beta S}{1+S} \times \frac{1}{1 + \left(\frac{N}{N_{critO}}\right)^{h3}} - k_2 O$$

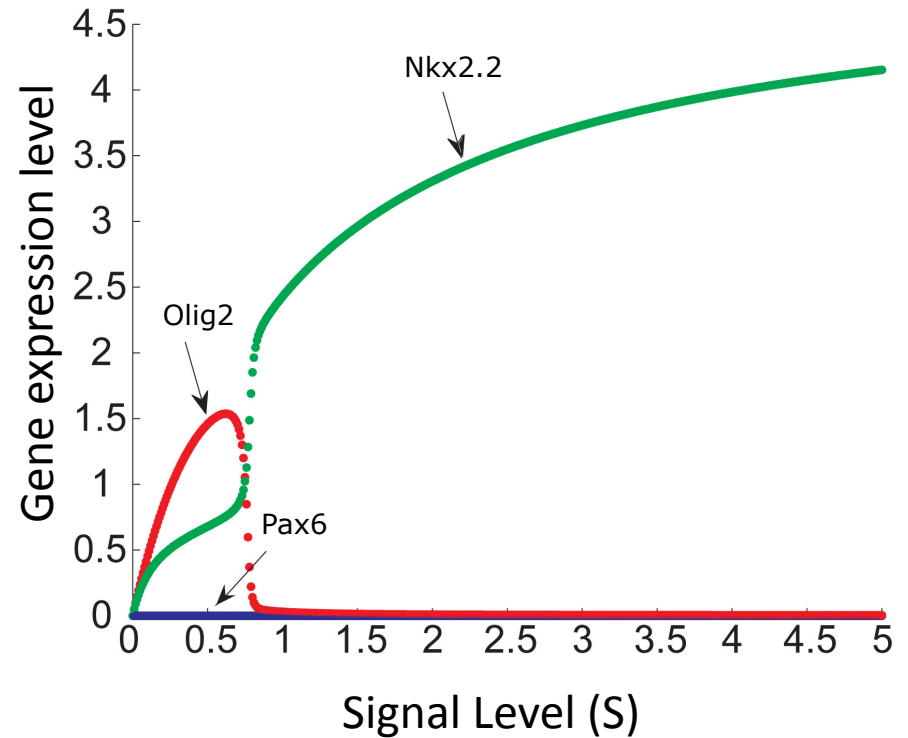
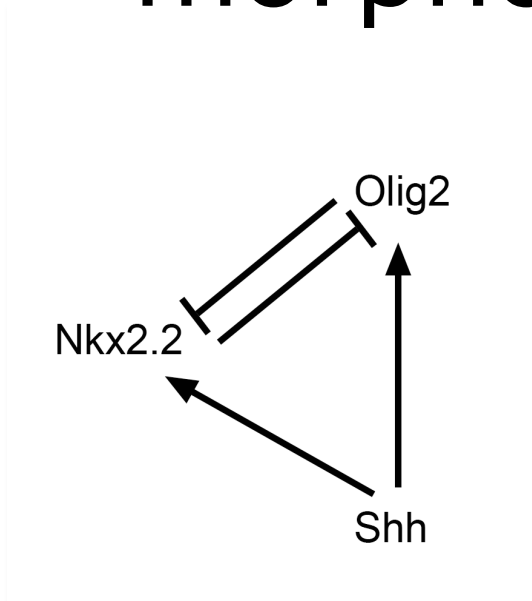
Olig2 (O)

$$\frac{dN}{dt} = \frac{\gamma S}{1+S} \times \frac{1}{1 + \left(\frac{O}{O_{critN}}\right)^{h4} + \left(\frac{P}{P_{critN}}\right)^{h5}} - k_3 N$$

Nkx2.2 (N)



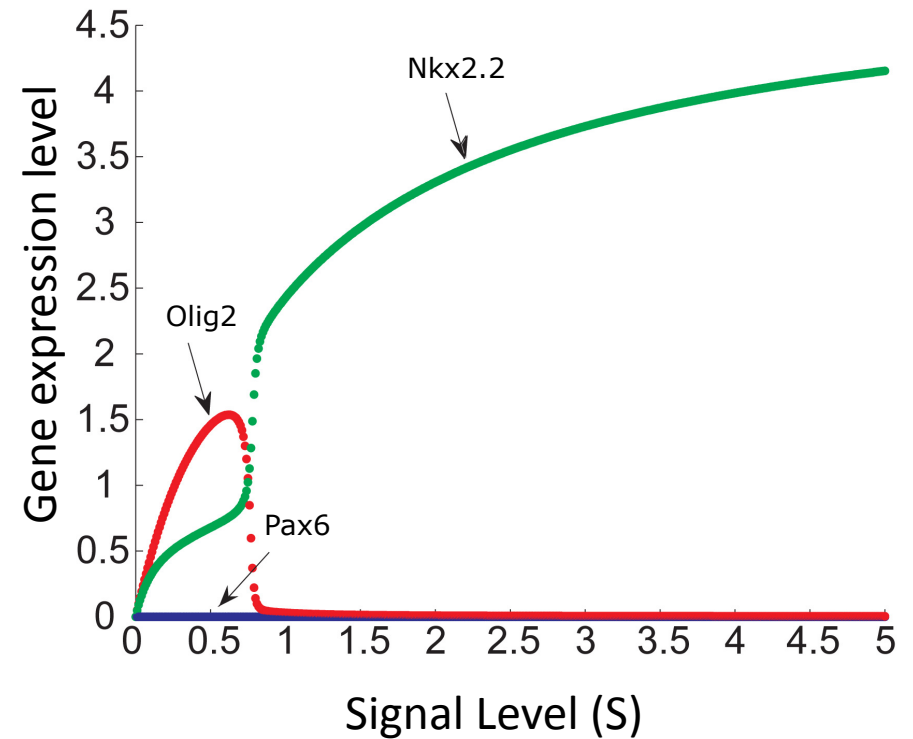
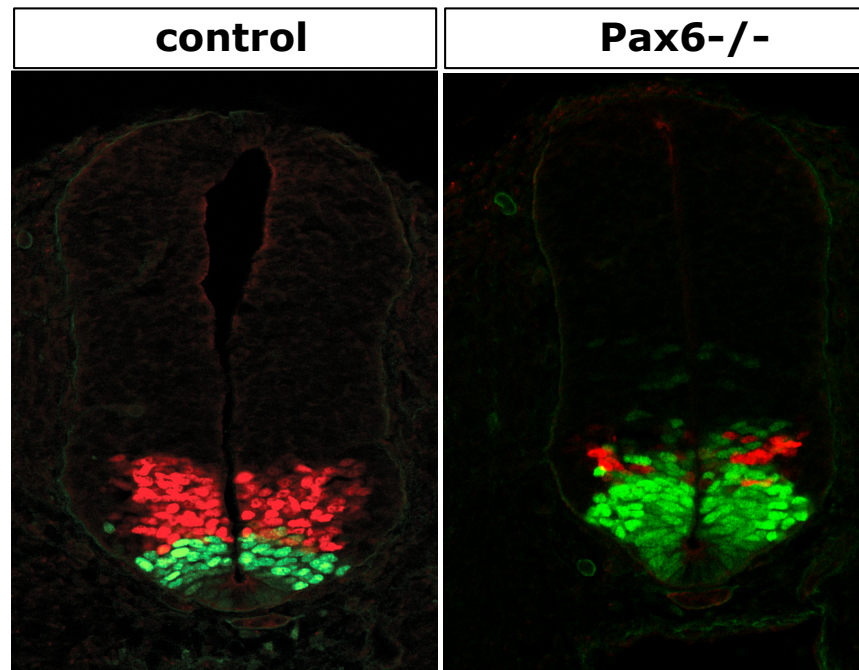
Network generates morphogen response



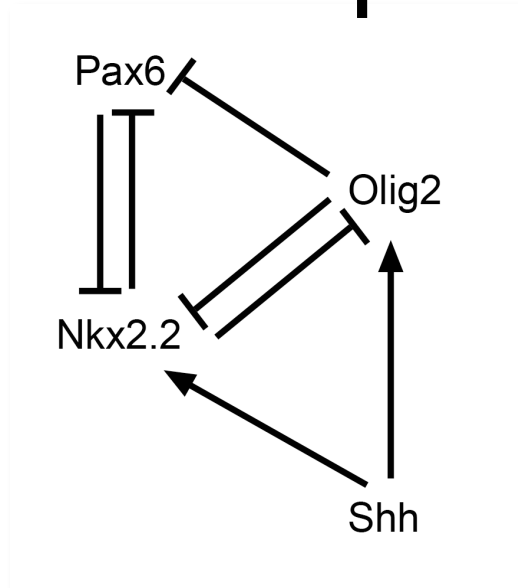
$$\frac{dO}{dt} = \frac{\beta S}{1+S} \times \frac{1}{1 + \left(\frac{N}{N_{critO}}\right)^{h3}} - k_2 O \quad \text{Olig2 (O)}$$

$$\frac{dN}{dt} = \frac{\gamma S}{1+S} \times \frac{1}{1 + \left(\frac{O}{O_{critN}}\right)^{h4} + \left(\frac{P}{P_{critN}}\right)^{h5}} - k_3 N \quad \text{Nkx2.2 (N)}$$

Network generates morphogen response



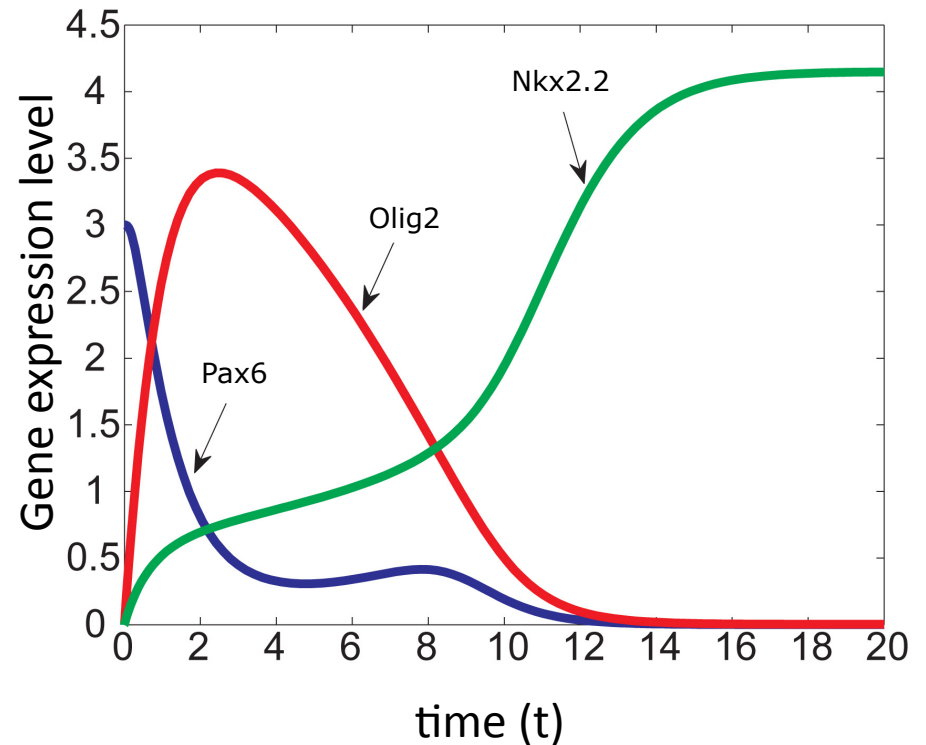
Network generates morphogen response



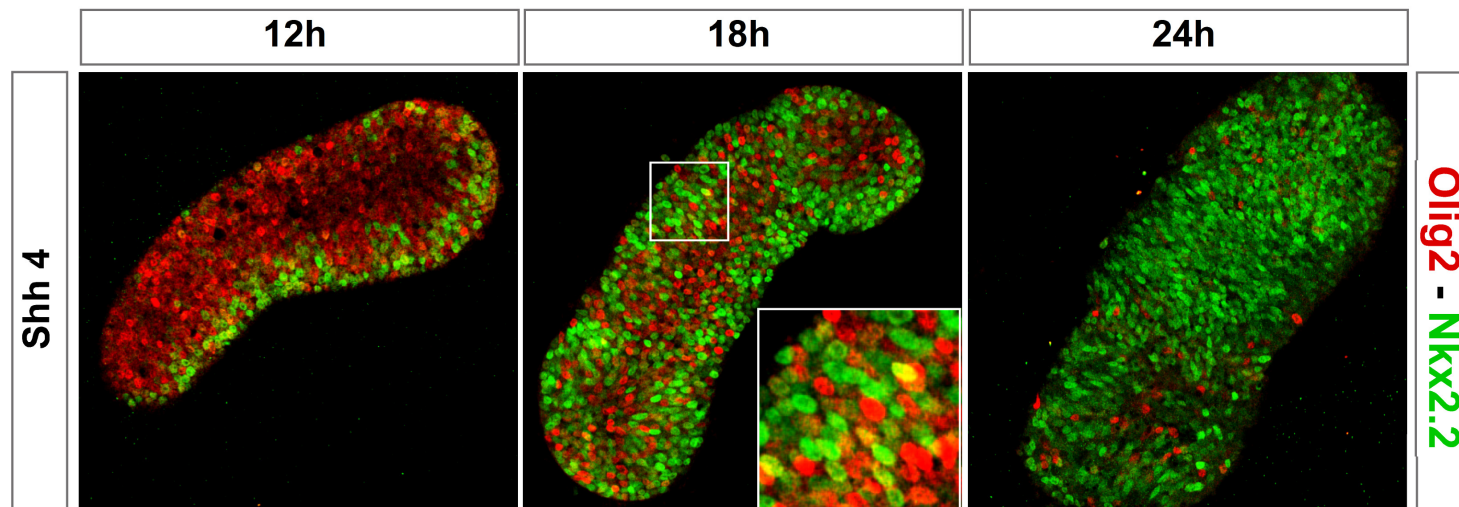
$$\frac{dP}{dt} = \frac{\alpha}{1 + \left(\frac{N}{N_{critP}}\right)^{h1} + \left(\frac{O}{O_{critP}}\right)^{h2}} - k_1 P \quad \text{Pax6 (P)}$$

$$\frac{dO}{dt} = \frac{\beta S}{1+S} \times \frac{1}{1 + \left(\frac{N}{N_{critO}}\right)^{h3}} - k_2 O \quad \text{Olig2 (O)}$$

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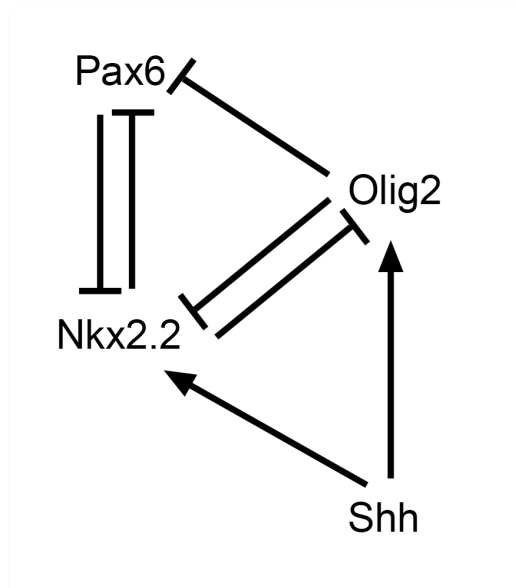


Duration of signalling influences pattern



number of cells

Network confers hysteresis on Nkx2.2



$$\frac{dP}{dt} = \frac{\alpha}{1 + \left(\frac{N}{N_{critP}}\right)^{h1} + \left(\frac{O}{O_{critP}}\right)^{h2}} - k_1 P$$

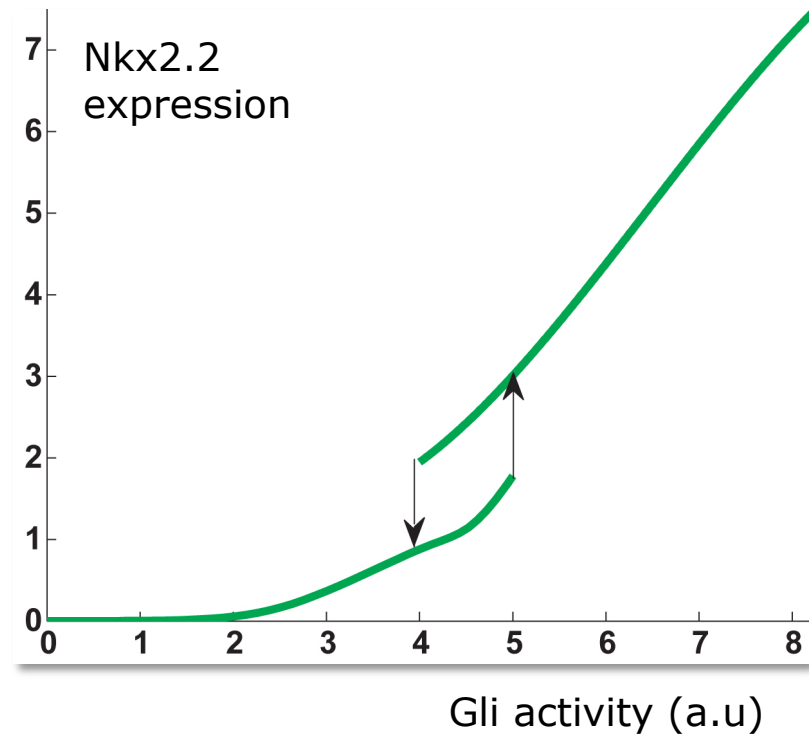
Pax6 (P)

$$\frac{dO}{dt} = \frac{\beta S}{1+S} \times \frac{1}{1 + \left(\frac{N}{N_{critO}}\right)^{h3}} - k_2 O$$

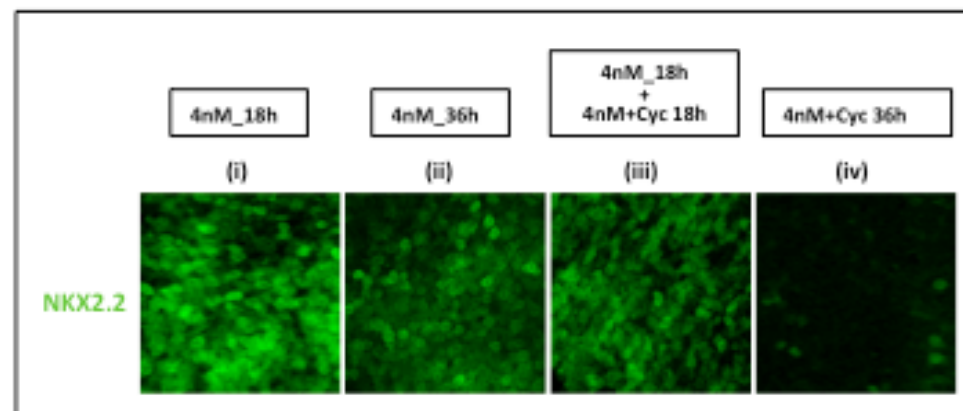
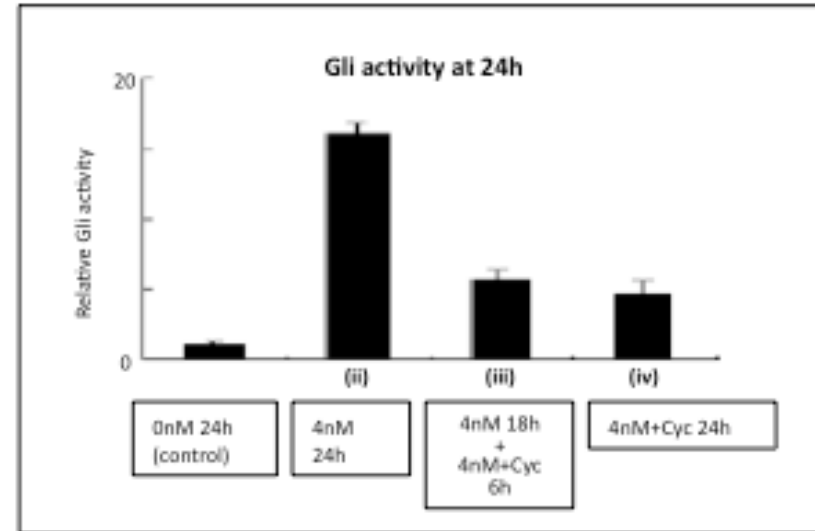
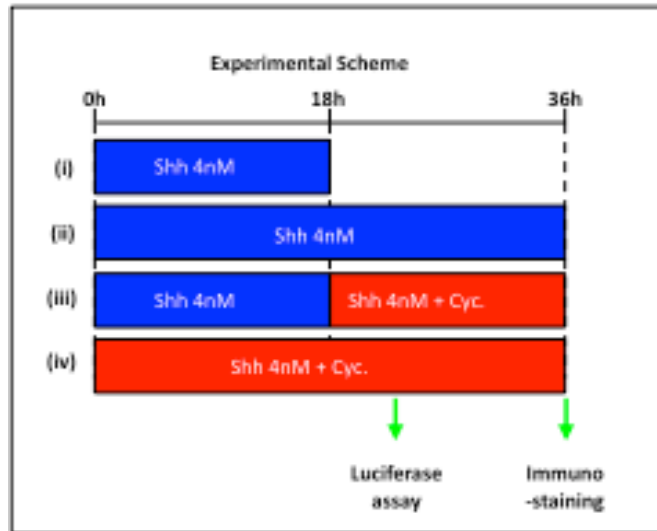
Olig2 (O)

$$\frac{dN}{dt} = \frac{\gamma S}{1+S} \times \frac{1}{1 + \left(\frac{O}{O_{critN}}\right)^{h4} + \left(\frac{P}{P_{critN}}\right)^{h5}} - k_3 N$$

Nkx2.2 (N)



Network confers hysteresis on Nkx2.2



A transcriptional circuit for morphogen interpretation

