

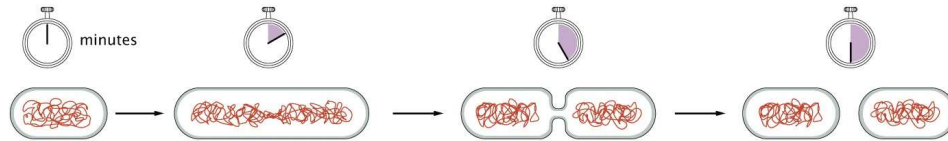
Quantitative principles in biological systems

7. Morphogenesis and information theory

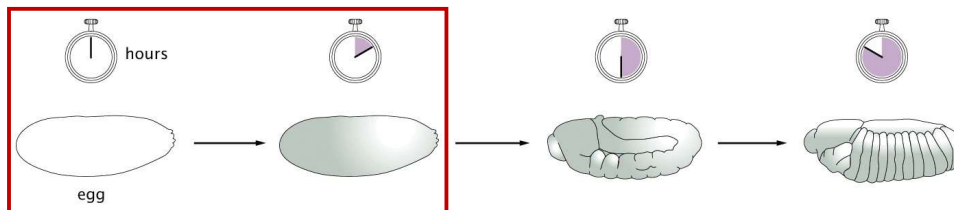
Spring 2026

Review

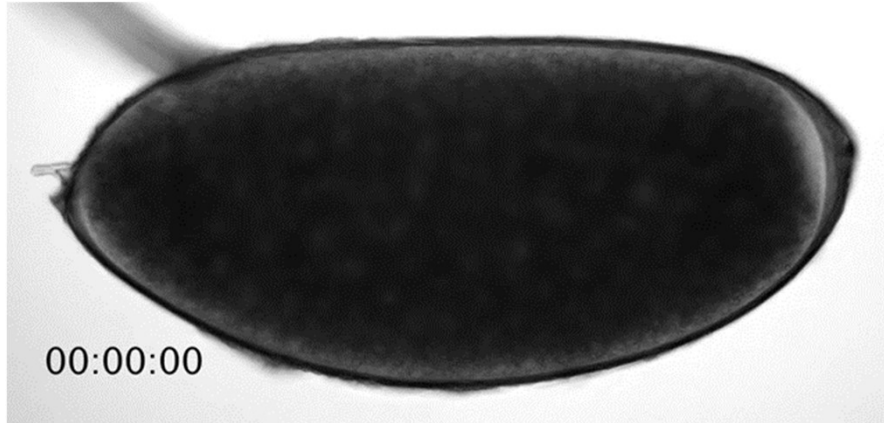
Bacterial cell division



Early development of *Drosophila*

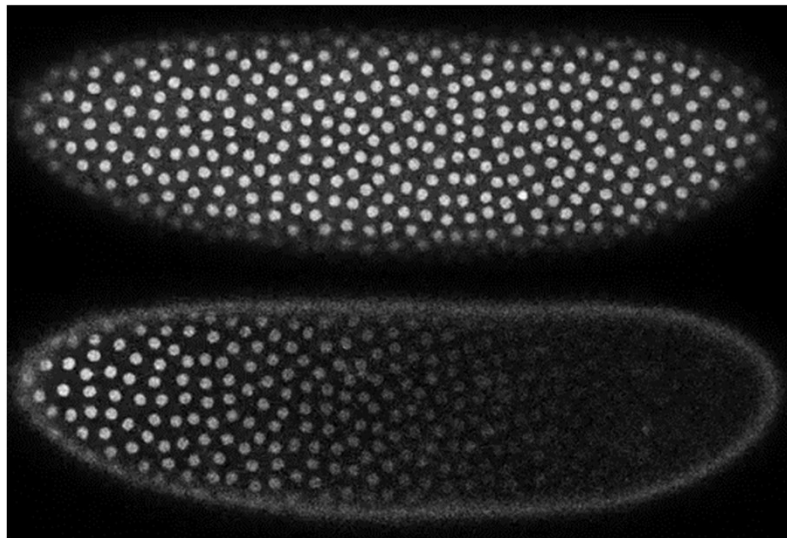


Fruit fly embryogenesis will be our model system for **representing information**.



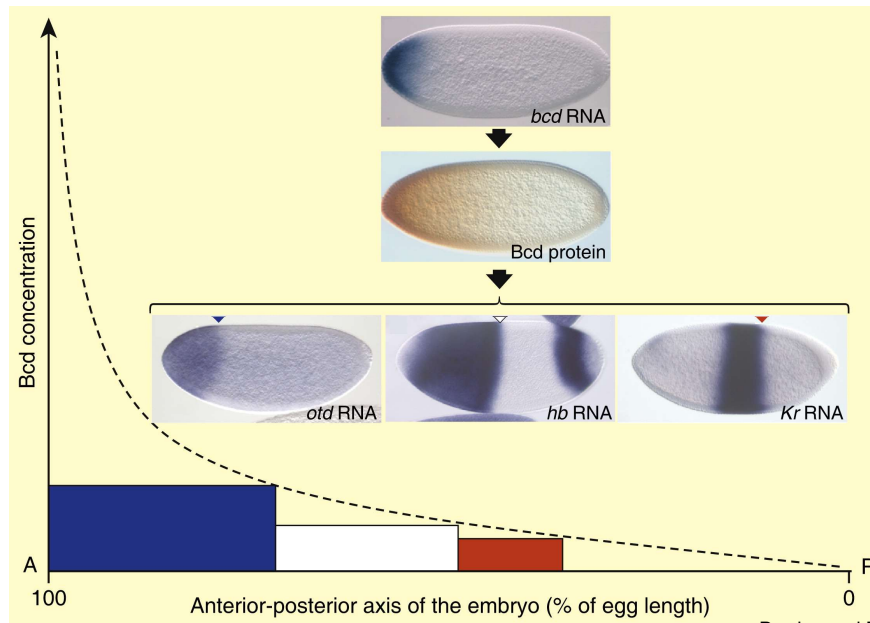
Thomas Gregor lab

Fruit fly embryogenesis will be our model system for **representing information**.



Thomas Gregor lab

Maternal inputs lead to morphogen gradients.



Reaction diffusion

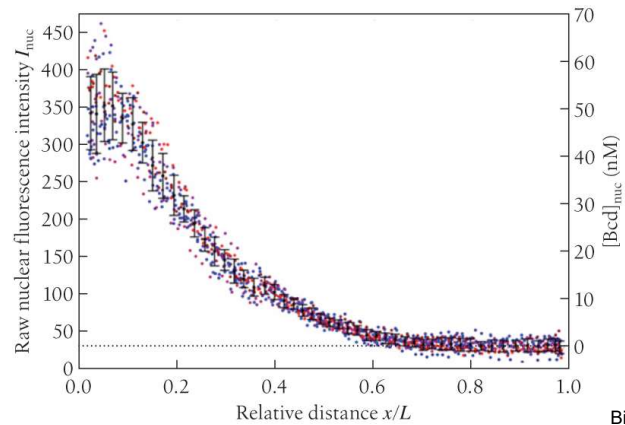
$$\frac{\partial c(x, t)}{\partial t} = D \frac{\partial^2 c(x, t)}{\partial x^2} - \frac{1}{\tau} c(x, t)$$

$$c(x) = \frac{R\tau}{\lambda} e^{-x/\lambda}$$

$$-D \frac{\partial c(x, t)}{\partial x} \Big|_{x=0} = R$$

$$\lambda = \sqrt{D\tau}$$

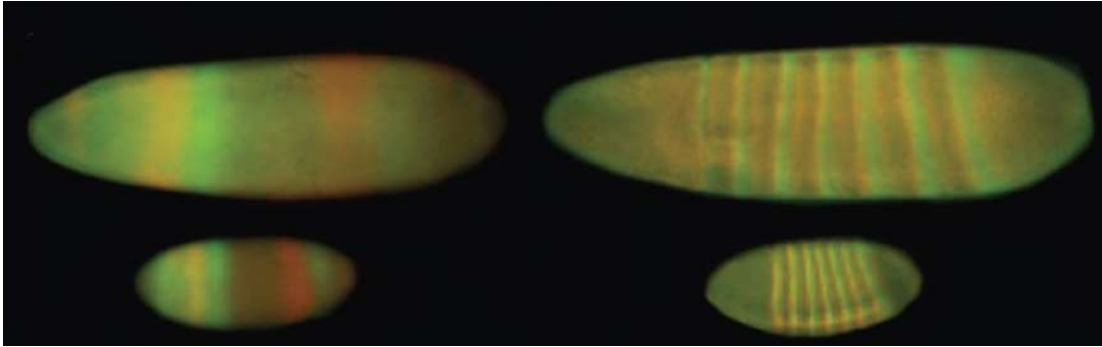
$$\frac{\partial c(x, t)}{\partial x} \Big|_{x=L} = 0$$



Reaction diffusion – No scaling? Not robust?

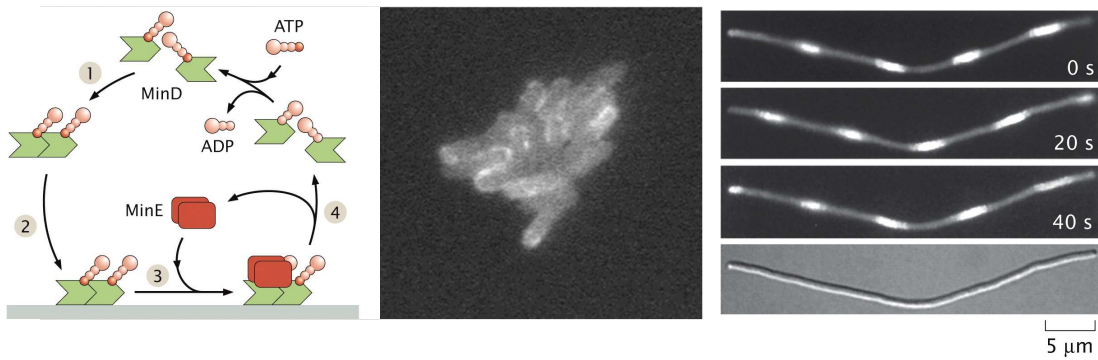
$$\frac{\partial c(x, t)}{\partial t} = D \frac{\partial^2 c(x, t)}{\partial x^2} - \frac{1}{\tau} c(x, t) \quad c(x) = \frac{R\tau}{\lambda} e^{-x/\lambda}$$

$$\lambda = \sqrt{D\tau}$$



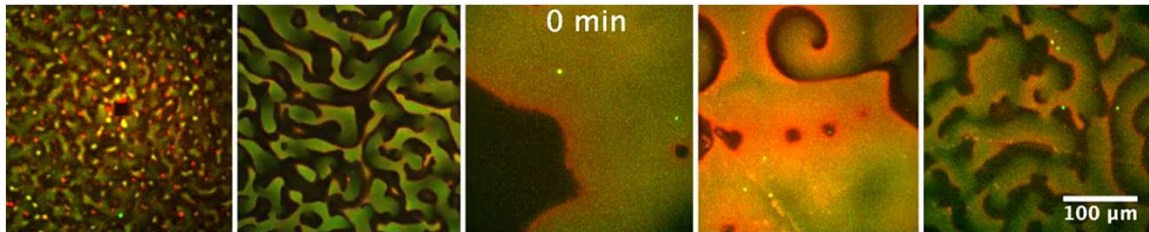
Bialek

Detour: The Min system oscillates to determine division site.



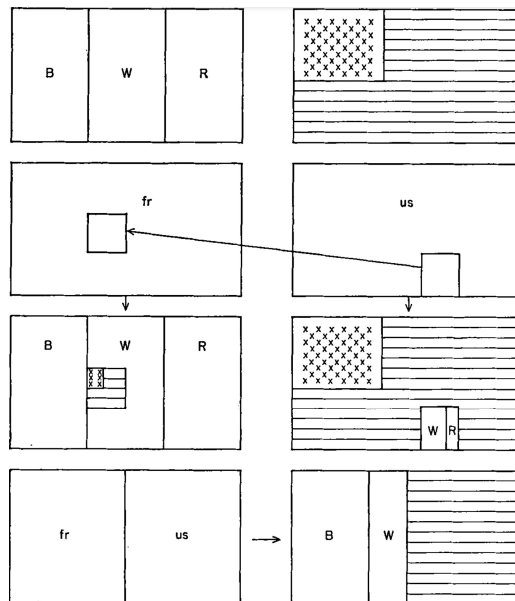
Fabai Wu et al. *Nat Nanotechnol* (2015)
Phillips et al

Detour: Min system in vitro forms different classes of patterns.



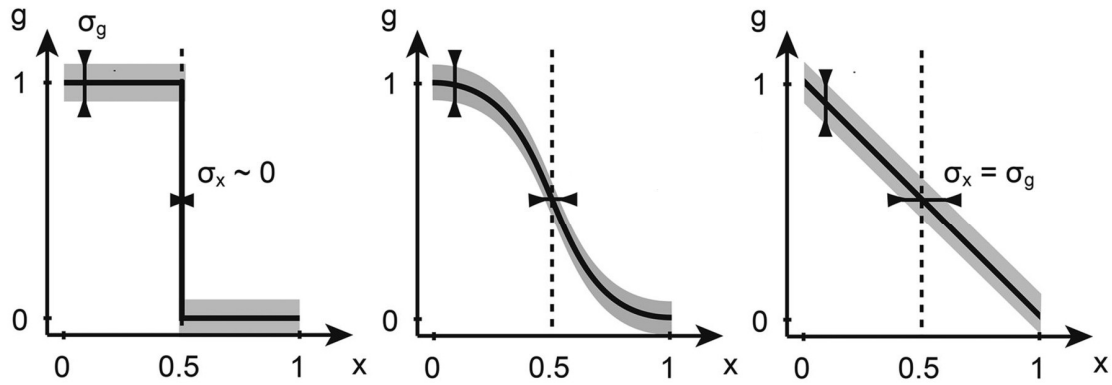
Brauns et al. *Nat Commun* (2021)

“Positional information”



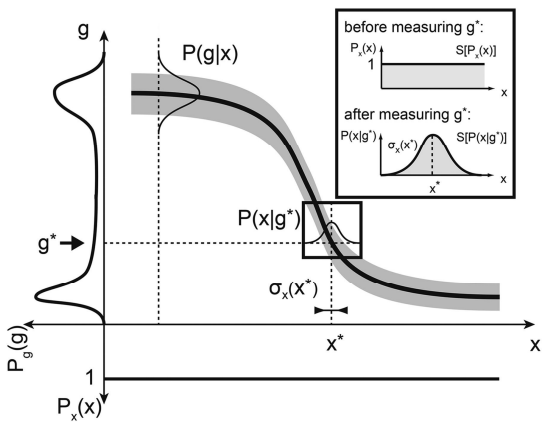
Wolpert. *J Theoret Biol* (1969)

Positional information



Tkacik et al. *Genetics* (2015)

Information theory

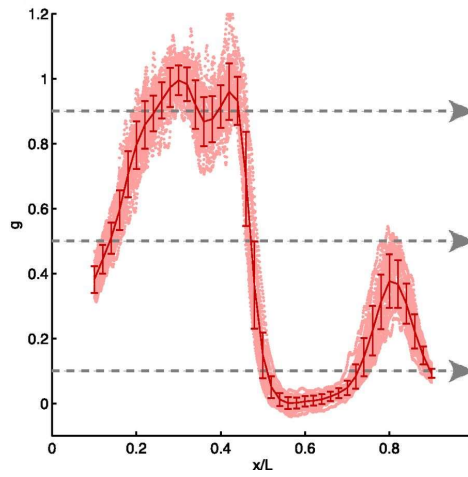
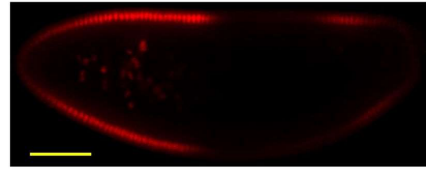
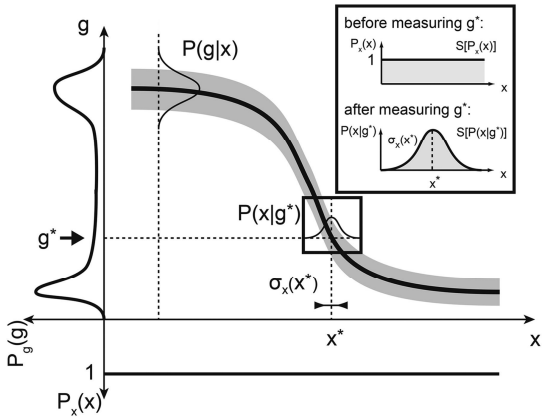


$$I(g, x) = S(p(x)) - S(p(x|g))$$

$$S(p(x)) = - \sum_x p(x) \log p(x)$$

Tkacik et al. *Genetics* (2015)

Information theory

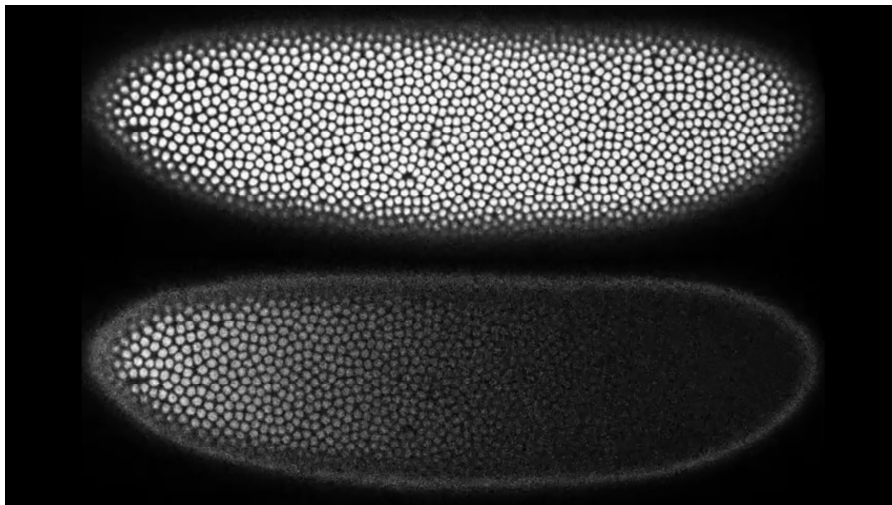


$$I(g, x) = S(p(x)) - S(p(x|g))$$

$$S(p(x)) = - \sum_x p(x) \log p(x)$$

Dubuis et al. PNAS (2013)

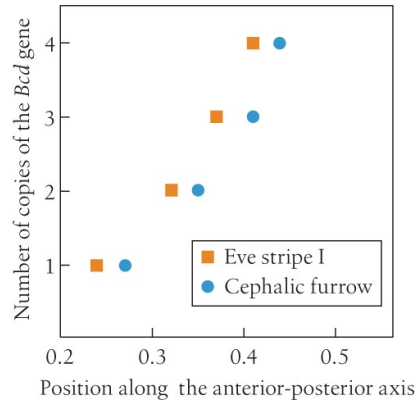
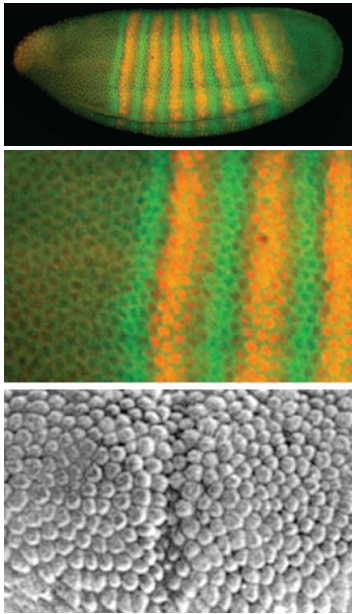
Positional error



≈ 60 cells $\rightarrow \approx 6$ bits to specify every cell

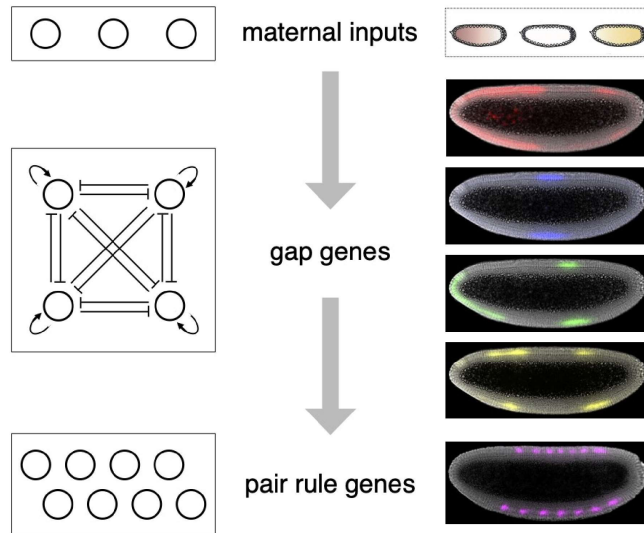
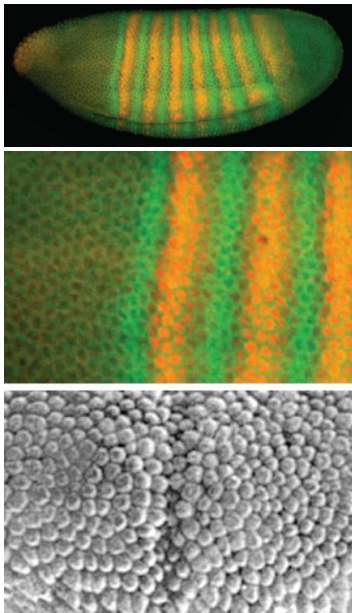
Thomas Gregor lab

Maternal inputs → gap genes → pair rule genes → body plan → positional error



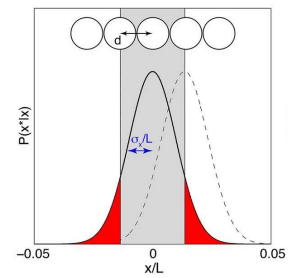
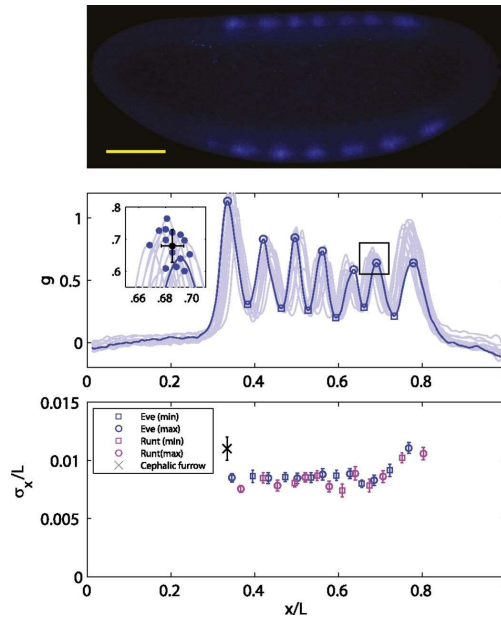
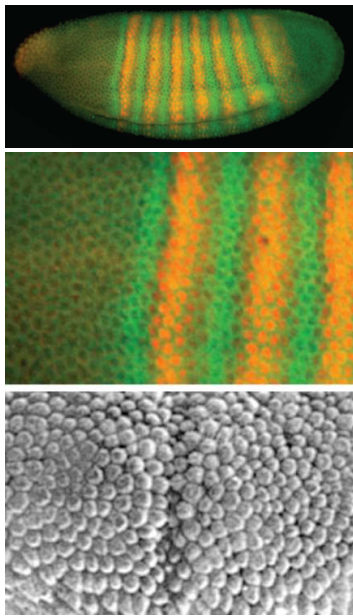
Bialek

Maternal inputs → gap genes → pair rule genes → body plan → positional error



Bialek

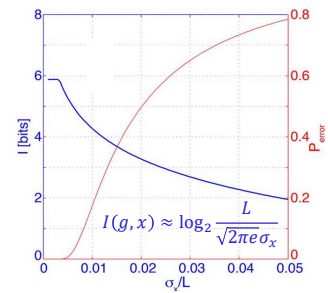
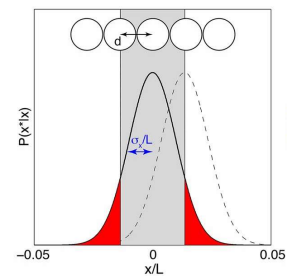
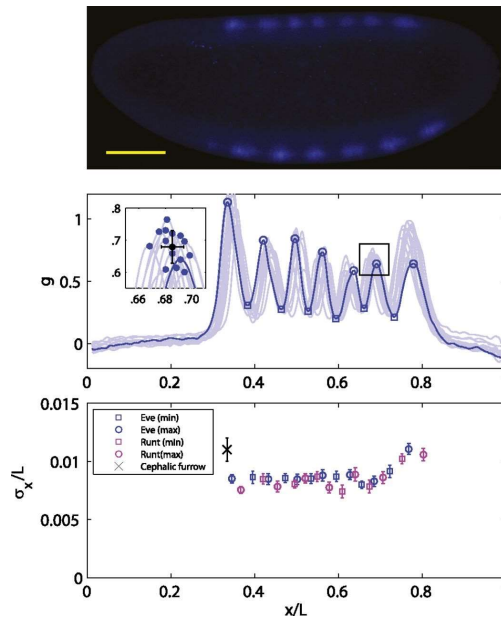
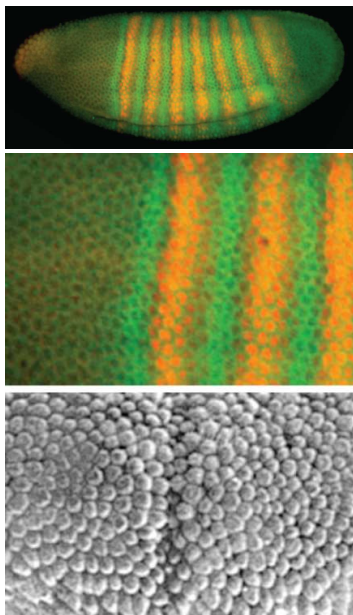
Maternal inputs → gap genes → pair rule genes → body plan → positional error



≈ 1% positional error

Dubuis et al. PNAS (2013)

Maternal inputs → gap genes → pair rule genes → body plan → positional error

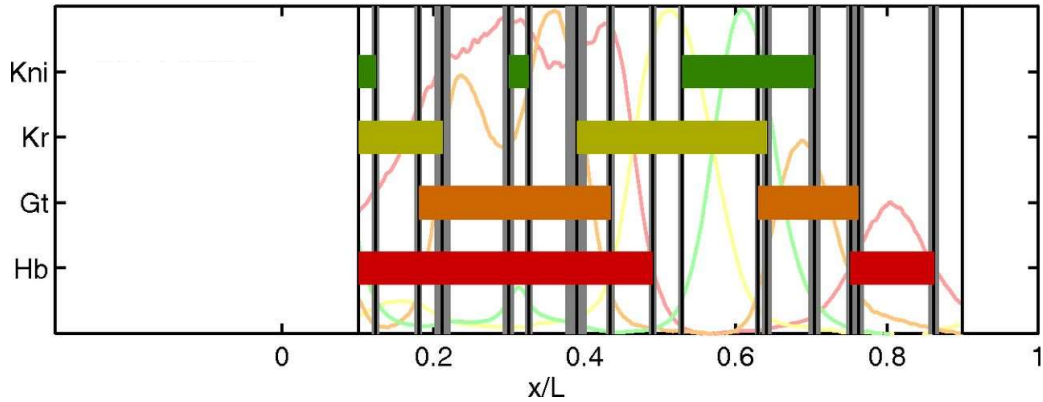


Dubuis et al. PNAS (2013)

How many bits of information?

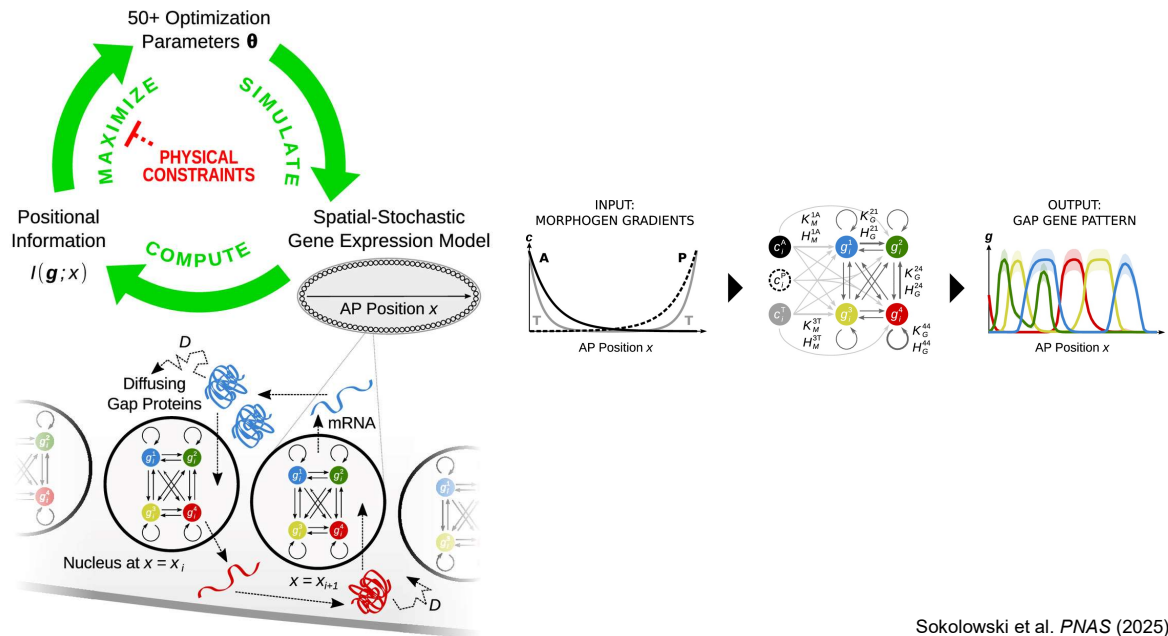
```

1 0 0 0 1 0 0 0 0 1 1 1 0 0 0 0
1 1 1 0 0 0 1 1 1 1 1 0 0 0 0 0
0 0 1 1 1 1 1 0 0 0 1 1 1 1 0 0
1 1 1 1 1 1 1 0 0 0 0 0 1 1 0 0
    
```

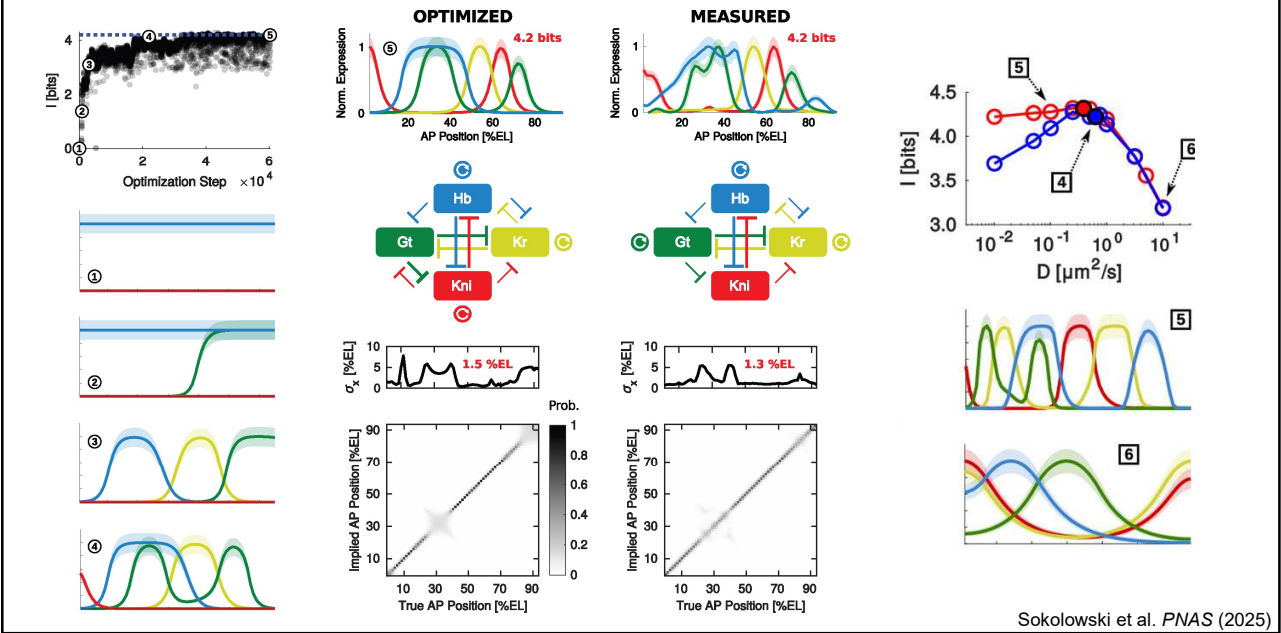


Dubuis et al. *PNAS* (2013)

Maximizing positional information predicts gap gene profiles without parameters.



Maximizing positional information predicts gap gene profiles without parameters.



Maximizing positional information predicts gap gene profiles without parameters.

