

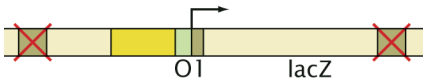
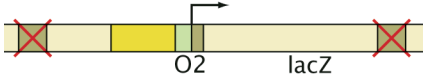
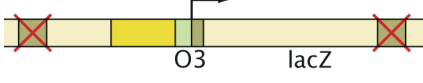
# BE/APH161 – PHYSICAL BIOLOGY OF THE CELL

**Rob Phillips**

Applied Physics and Bioengineering  
California Institute of Technology

# CONFRONTING THEORY AND EXPERIMENT: A SIMPLE CASE

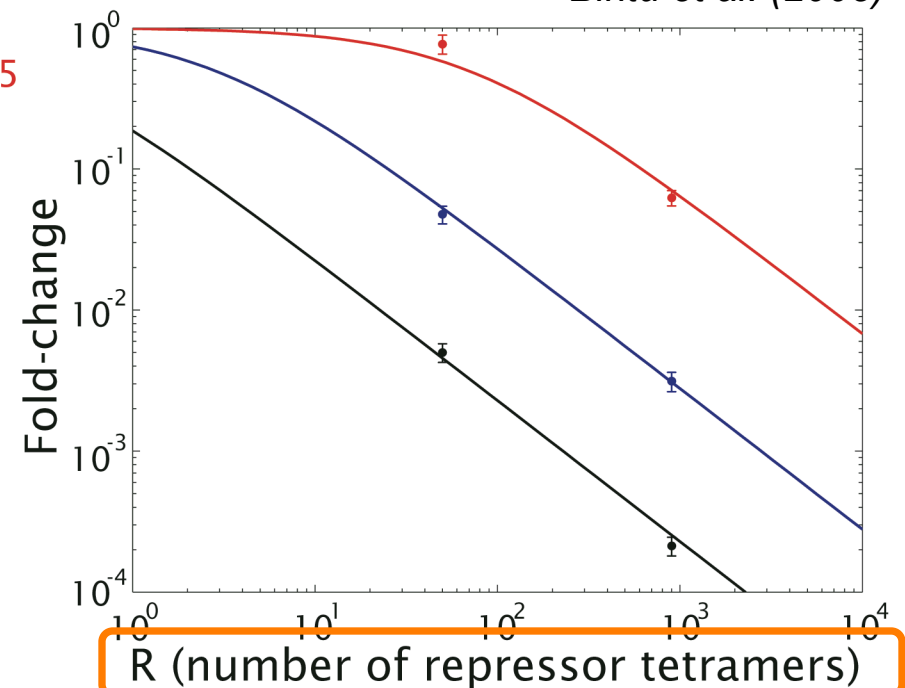
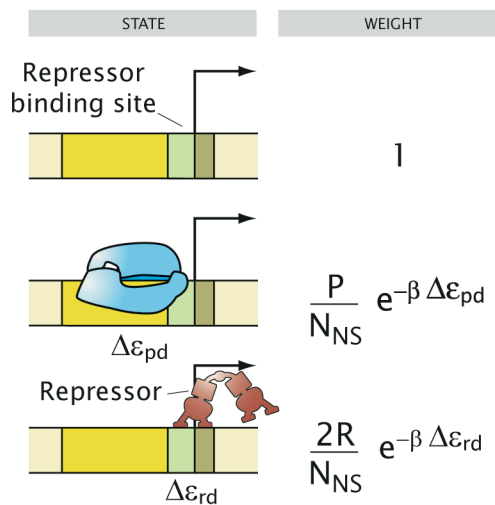
$$\text{fold change} = \left(1 + \frac{R}{N} e^{-\beta \Delta \epsilon}\right)^{-1}$$

	Fold-change	Number of repressors	$\Delta \epsilon_{rd}$ ( $k_B T$ )
	$5 \times 10^{-3}$	$2.1 \times 10^{-4}$	-16.2
	0.048	$3.1 \times 10^{-3}$	-13.7
	0.77	0.063	-10.5

Oehler et al. (1994)

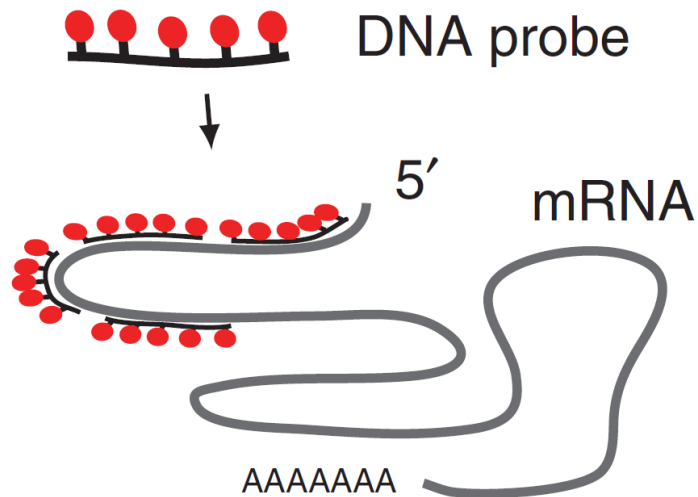
Becker et al. (2005)  
Vilar and Leibler (2003)

Bintu et al. (2005)

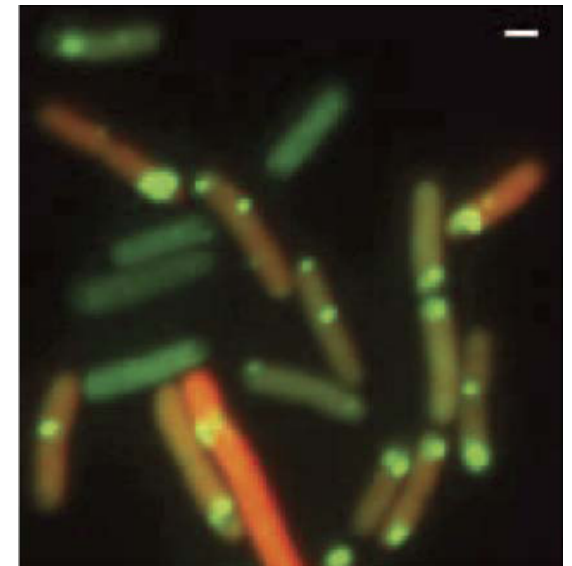
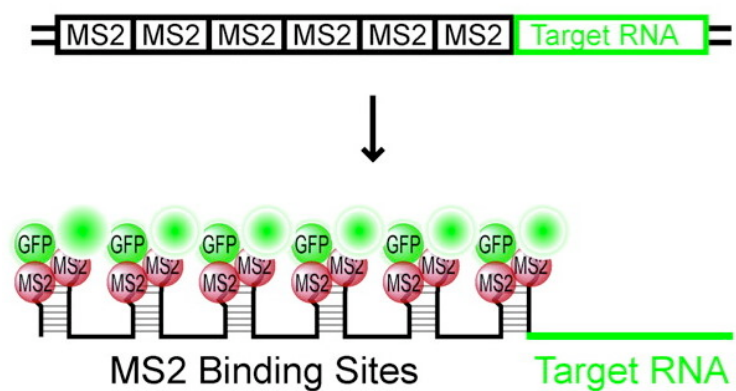


# COUNTING MESSENGER RNAs IN CELLS

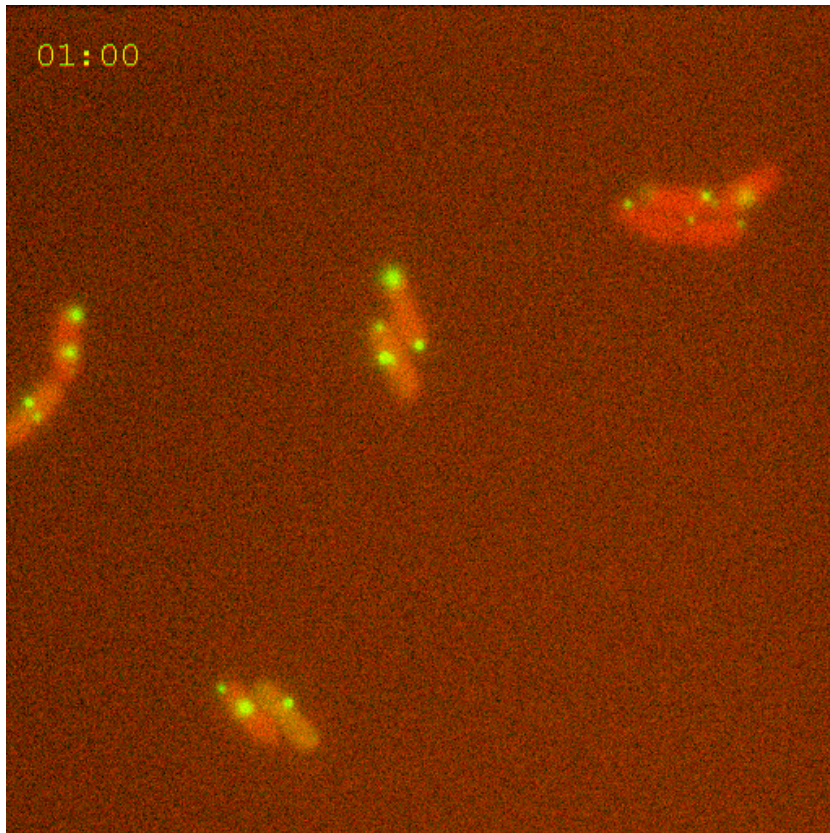
- *Fixed cells*  
*Zenklusen et al. '08*



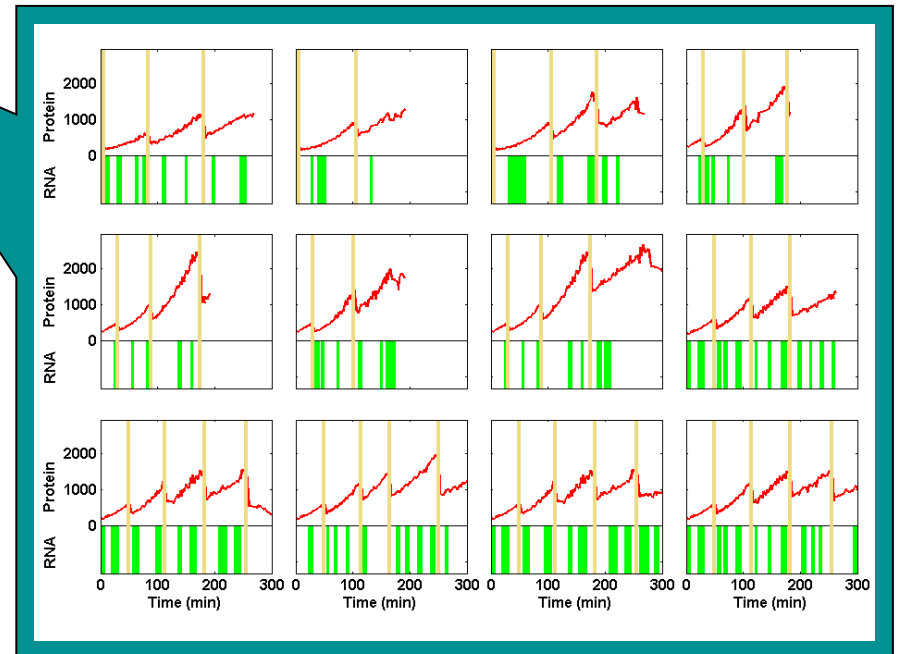
- *Live cells*  
*Golding et al. '05*

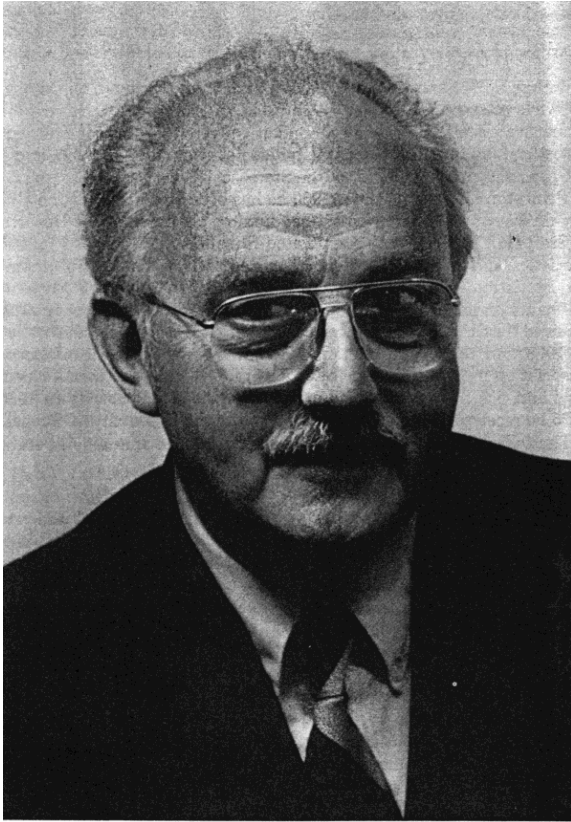


# INFORMATION PROCESSING IN LIVING CELLS: BEYOND FIRST APPROXIMATIONS



Ido Golding



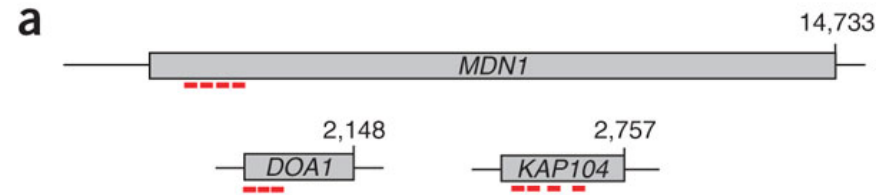


George E. P. Box

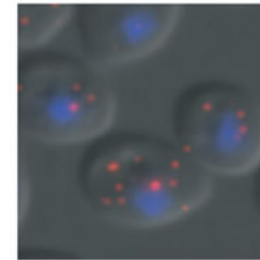
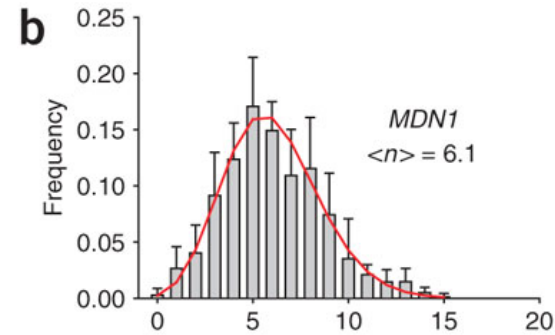
## ON THE USEFULNESS OF MODELS

*"It should be remembered that just as the Declaration of Independence promises the **pursuit** of happiness rather than happiness itself, so the iterative scientific model building process offers only the pursuit of the perfect model. For even when we feel we have carried the model building process to a conclusion, some new initiative may make further improvement possible. **Fortunately to be useful a model does not have to be perfect.**" George Box*

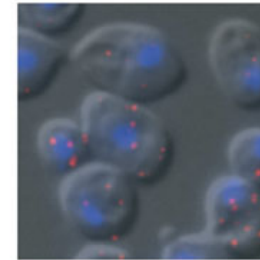
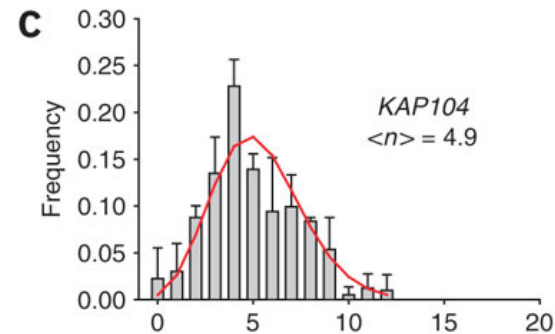
# RNA DISTRIBUTION IN YEAST



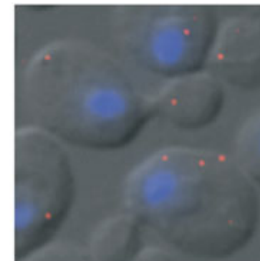
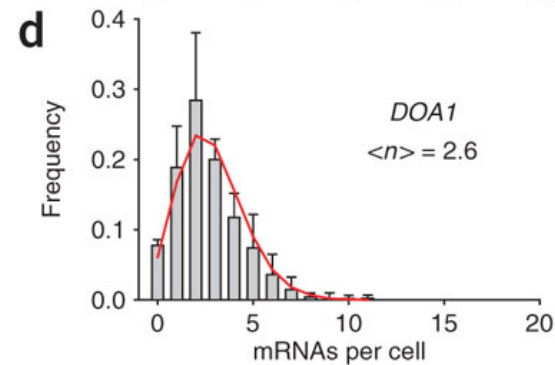
Zenklusen *et al.* '08



*MDN1* mRNA DAPI



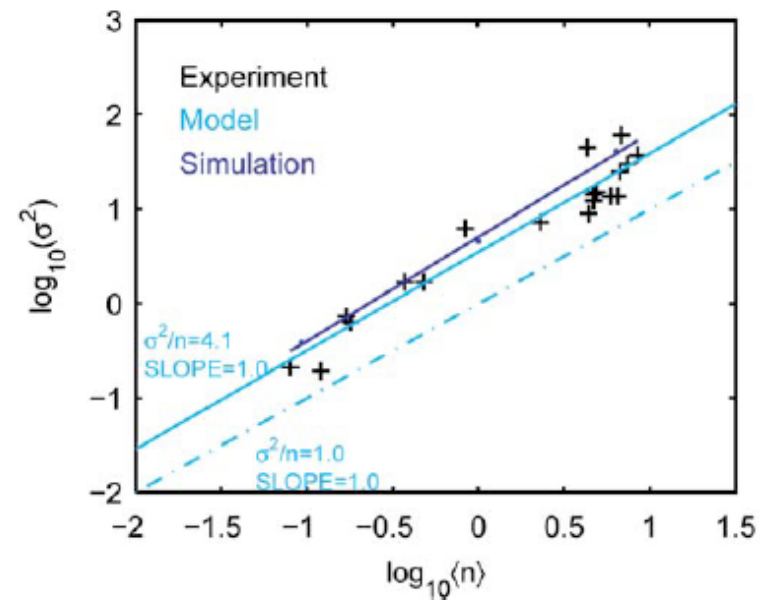
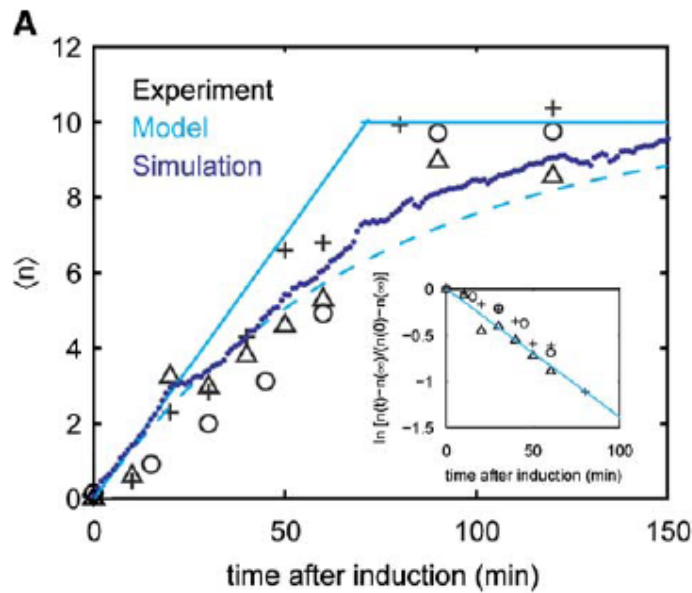
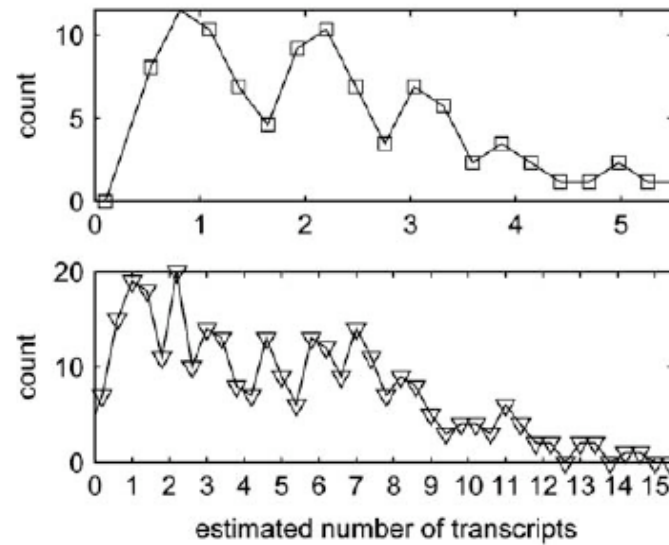
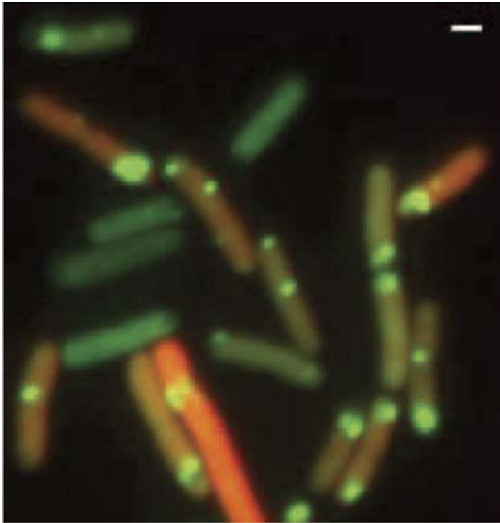
*KAP104* mRNA DAPI



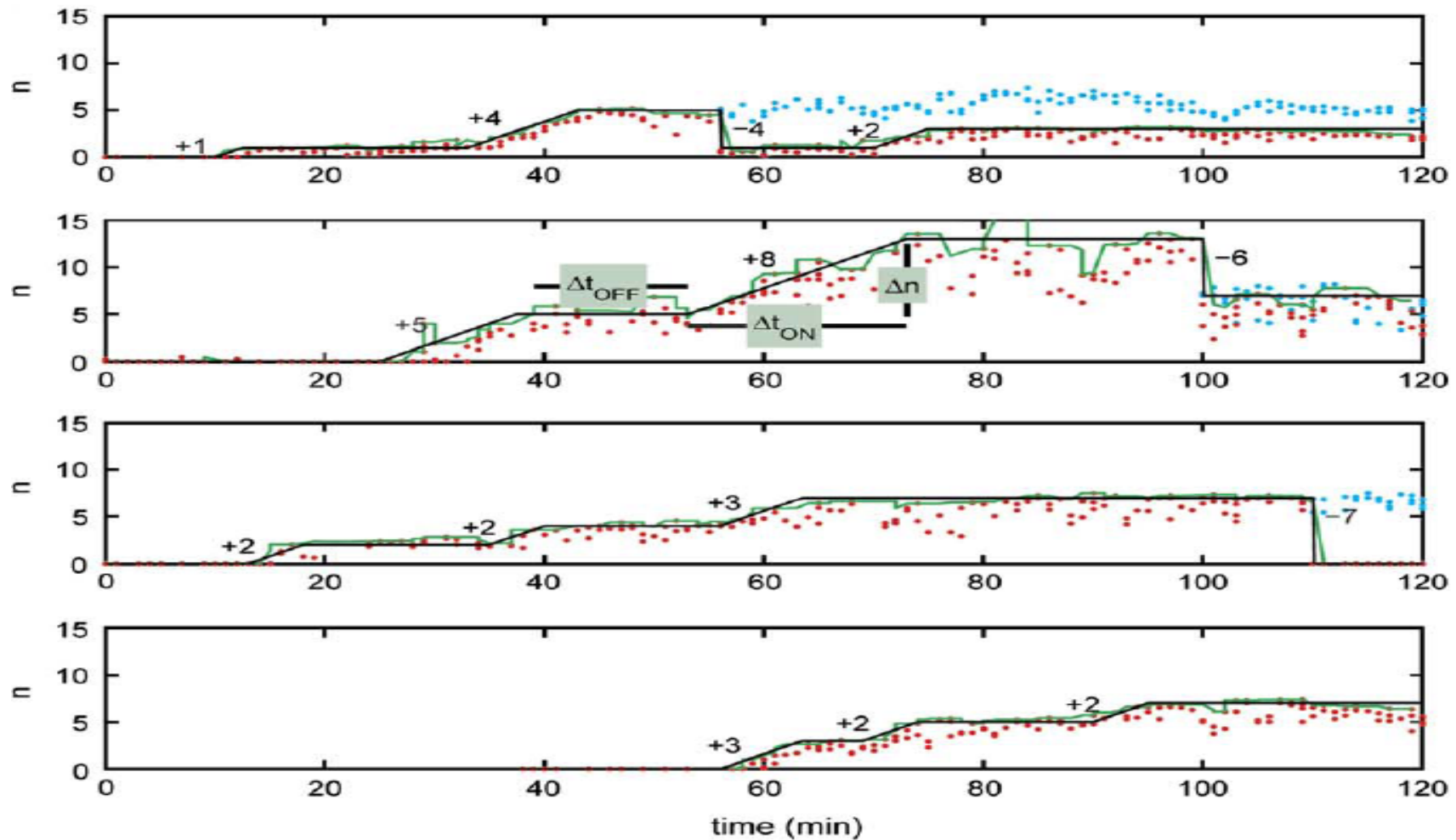
*DOA1* mRNA DAPI

# MRNA PRODUCTION IN *E. COLI*

*Golding et al. '05*

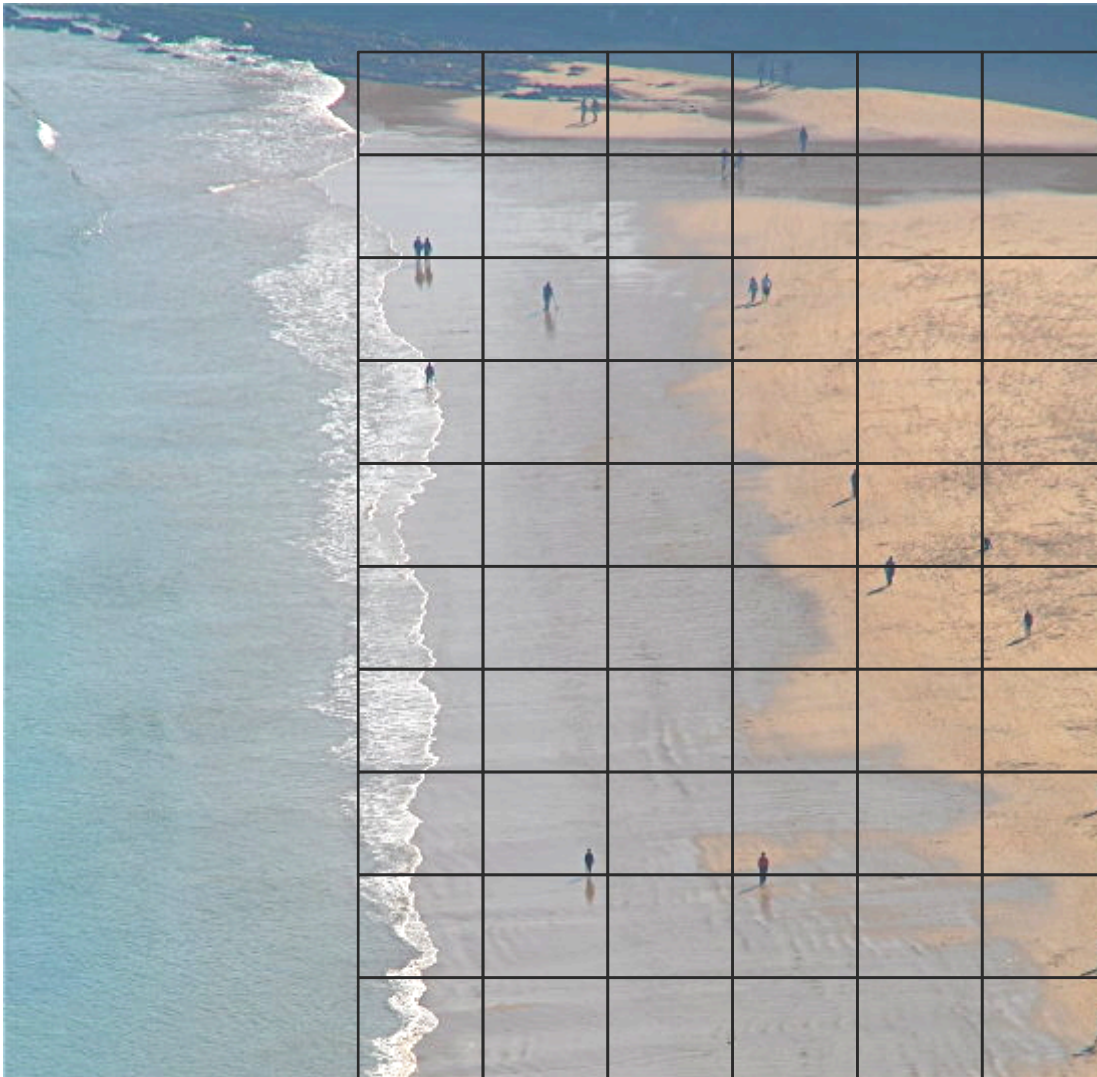


# MRNA PRODUCTION HAPPENS IN BURSTS





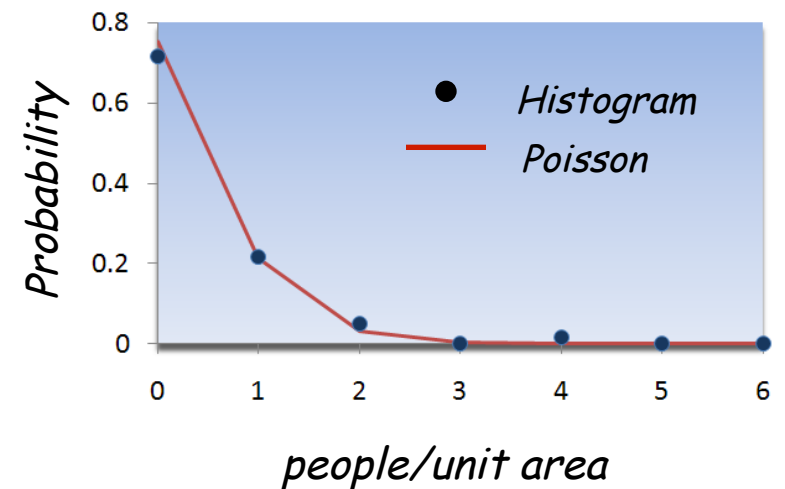
# THE POISSON DISTRIBUTION



What is the distribution of people per square?

$$P(m) = \frac{e^{-\mu} \mu^m}{m!}$$

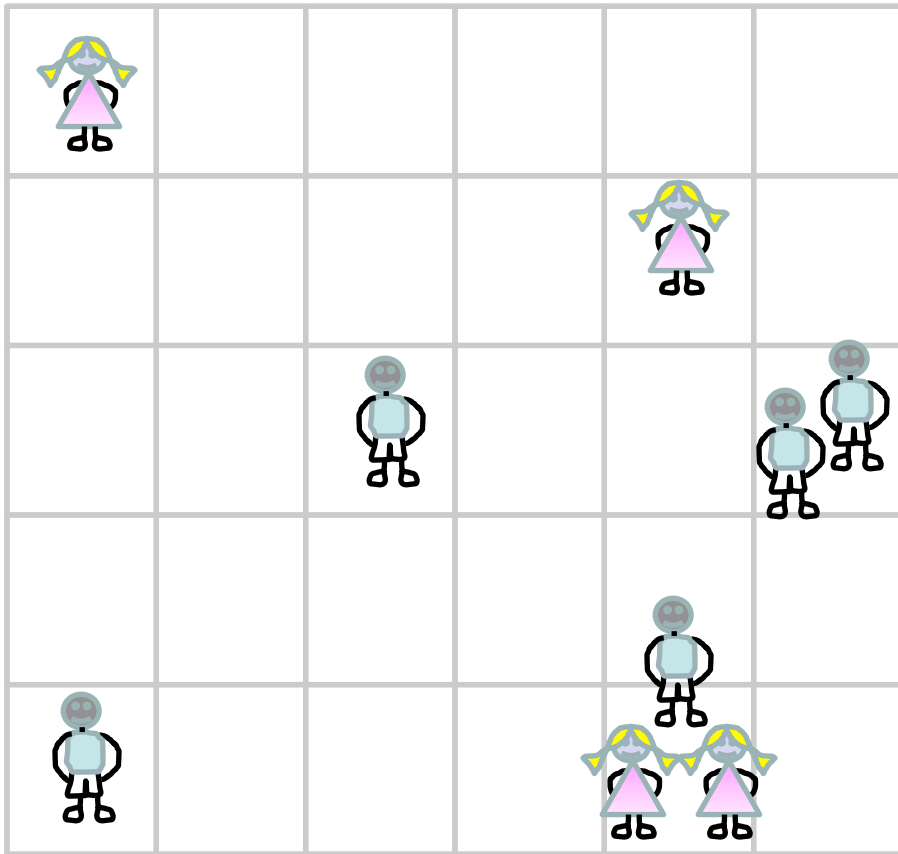
$$\mu = \frac{23 \text{ people}}{60 \text{ squares}} = 0.36$$



(thanks to Al Sanchez and Jane Kondev)

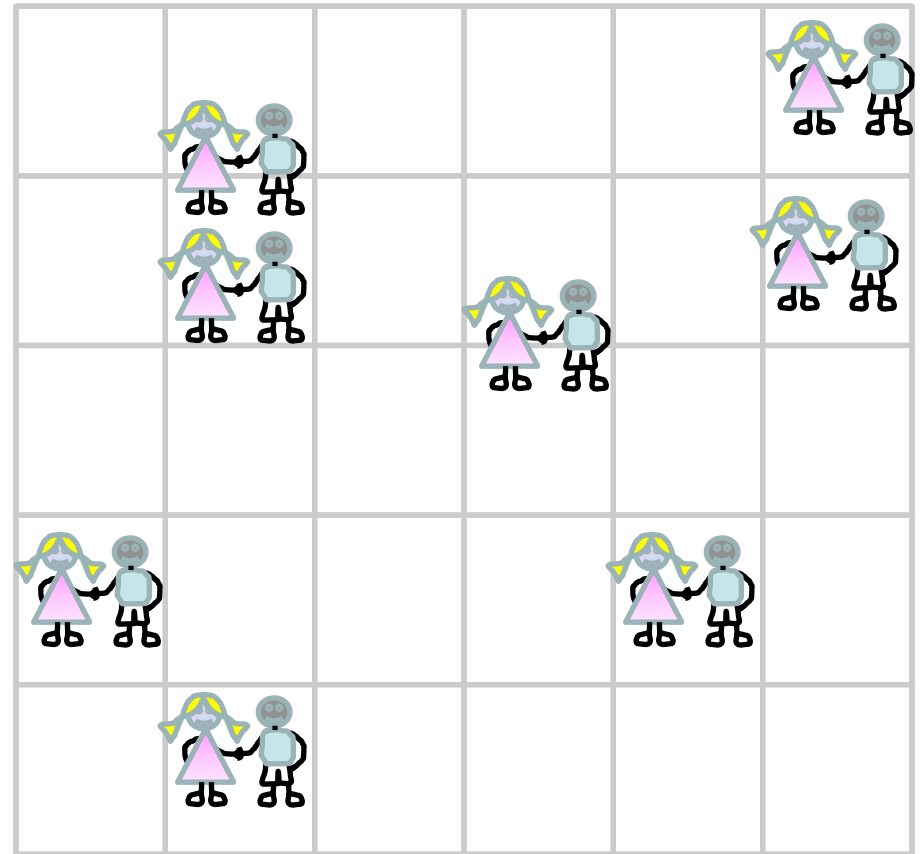
# INTERACTIONS CAN CHANGE THE DISTRIBUTION

*Independent singles: Poisson distribution of people*



$$\text{var}(P) = \lambda P$$

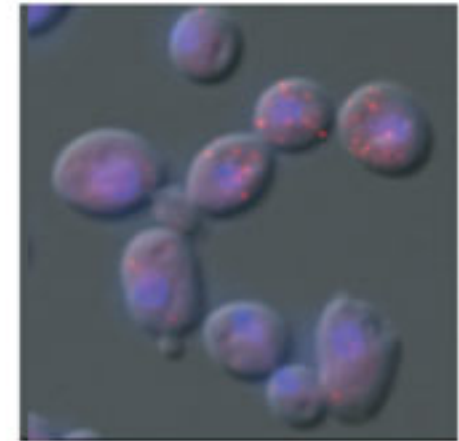
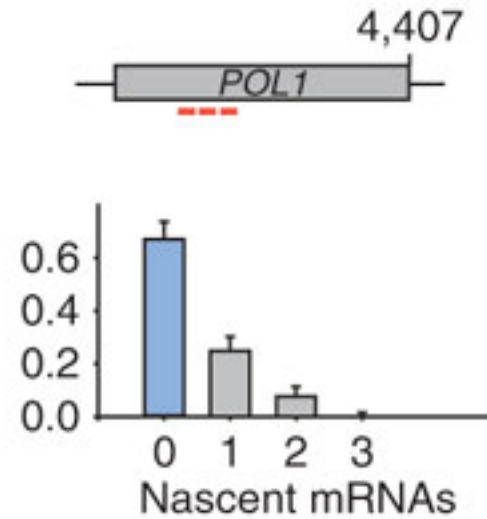
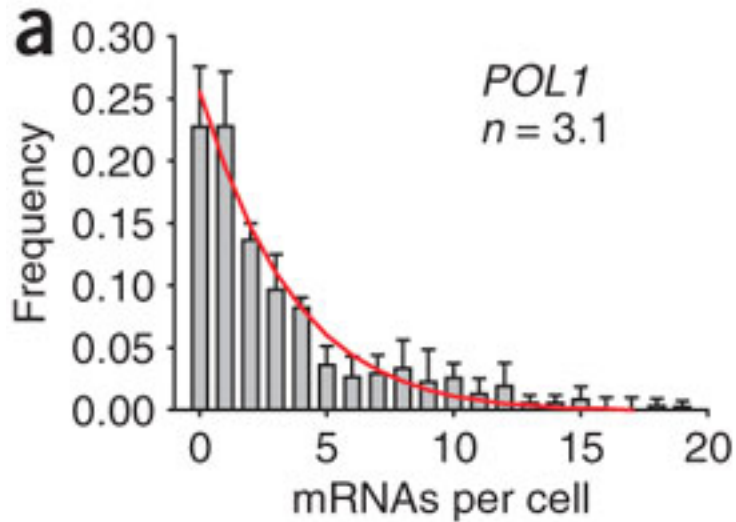
*Valentine's Day: Poisson distribution of couples*



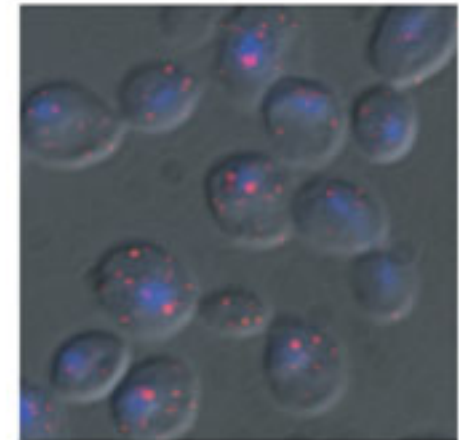
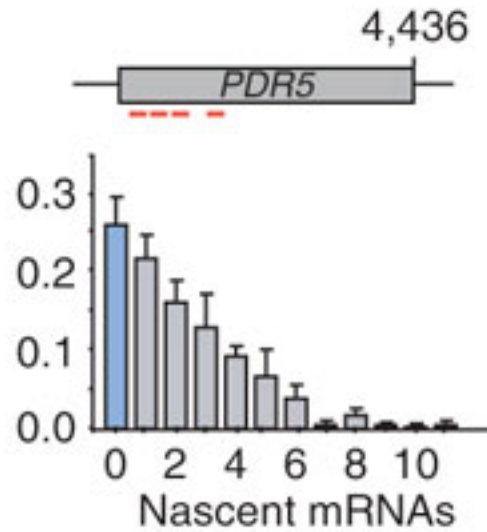
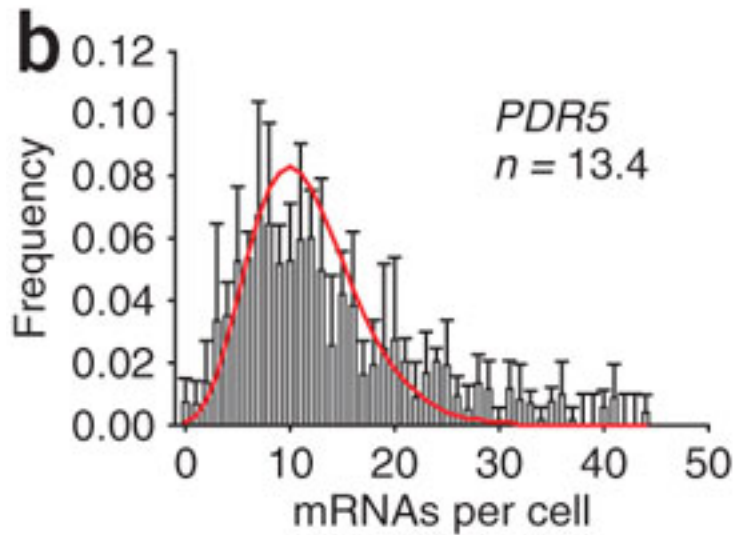
$$\text{var}(P) = 2 \lambda P$$

# NOT POISSON

Zenklusen et al. '08

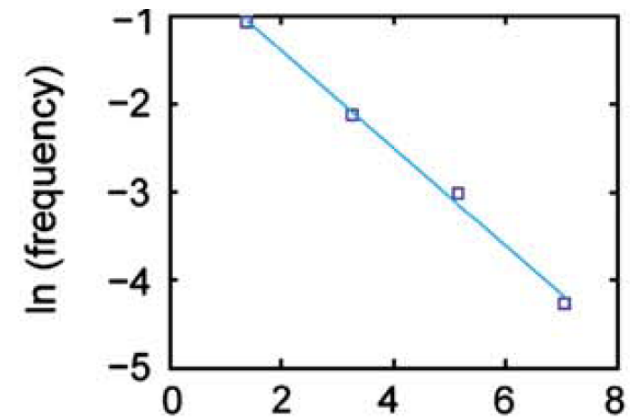
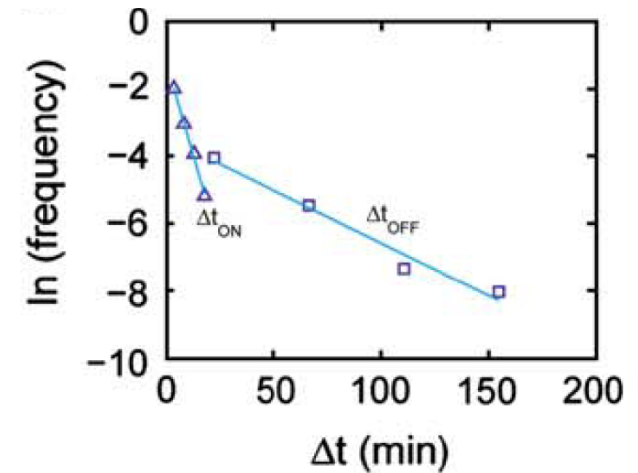
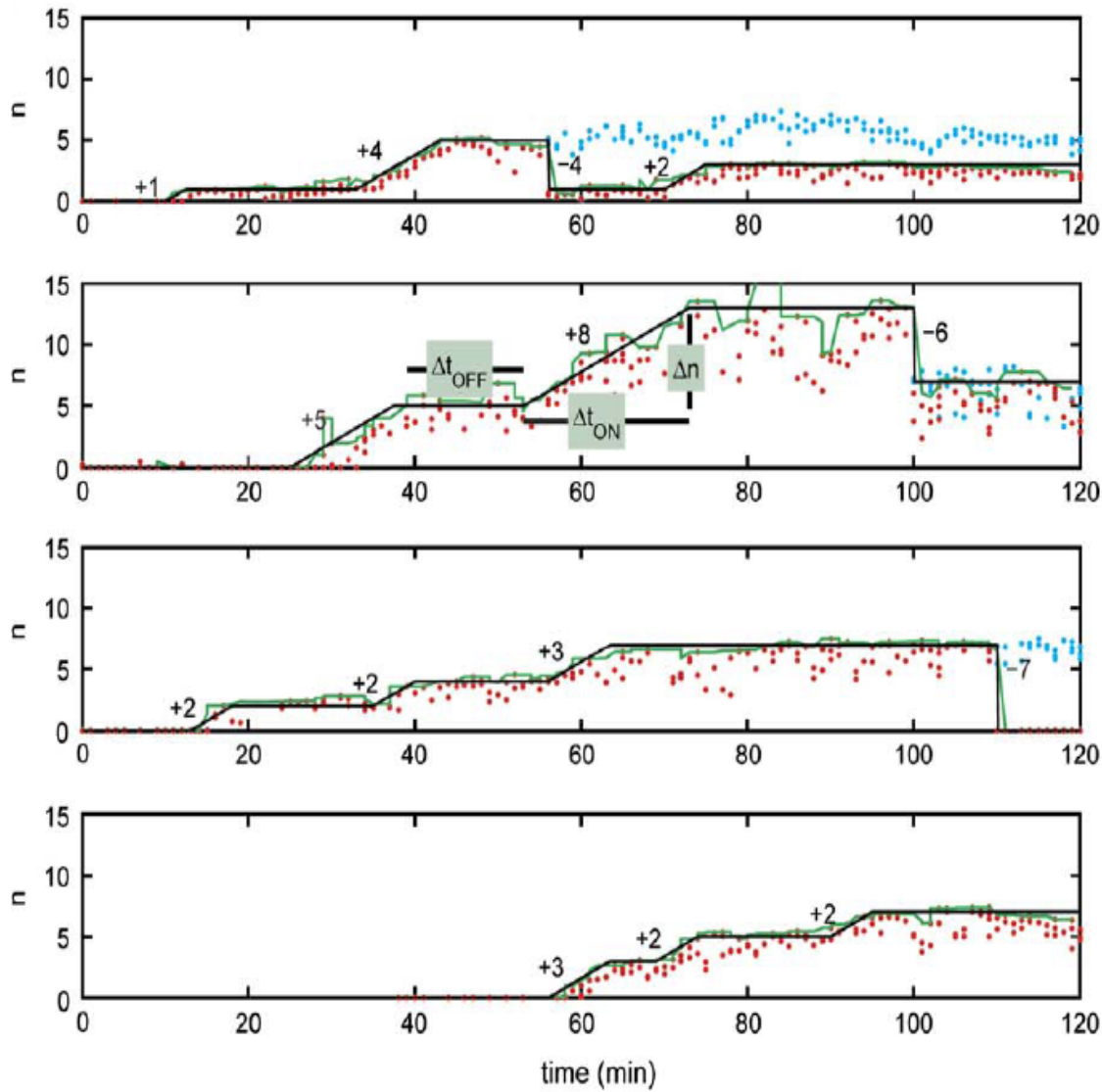


*POL1* mRNA DAPI



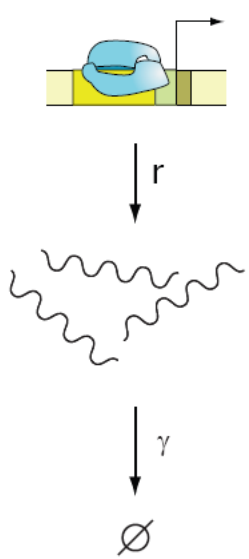
*PDR5* mRNA DAPI

# MRNA PRODUCTION OCCURS IN BURSTS



*What is the origin of transcriptional bursts?*

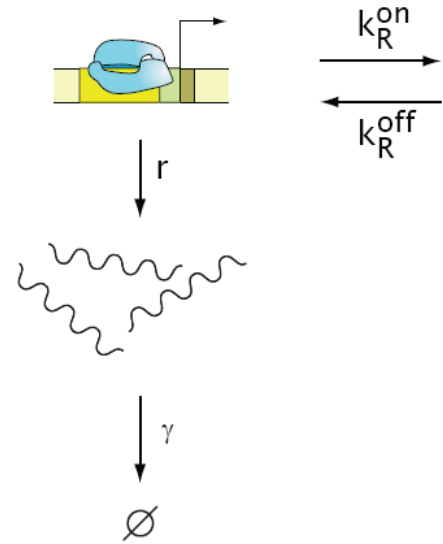
# TWO-STATE PROMOTER



Master equation for a two state promoter

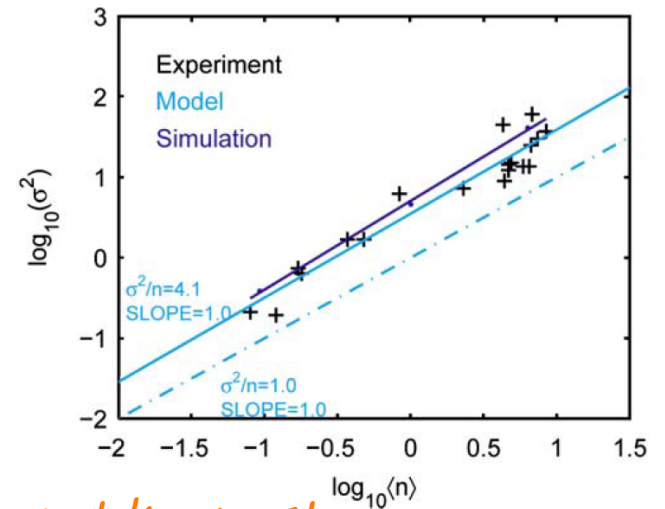
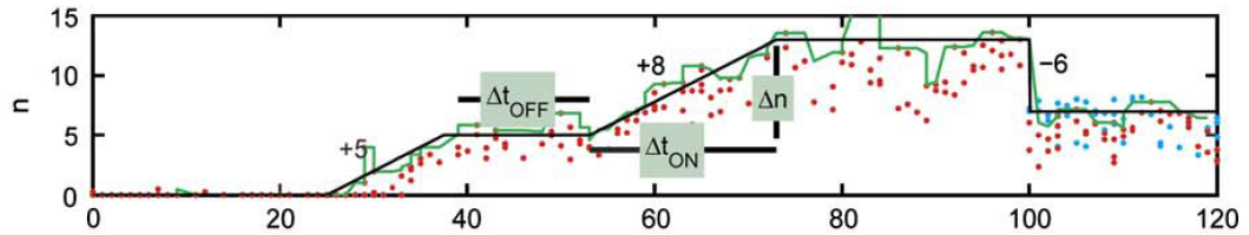
TRAJECTORY	PROMOTER STATE	mRNA STATE	WEIGHT
<p>Repressor binding site</p>	1 $\longrightarrow$ 2	m	$k_R^{\text{on}} \Delta t$
	2 $\longrightarrow$ 1	m	$k_R^{\text{off}} \Delta t$
<p>mRNA</p>	2 $\longrightarrow$ 1	m $\longrightarrow$ m+1	$r \Delta t$
<p>mRNA</p>	1 or 2	m $\longrightarrow$ m-1	$\gamma \Delta t$

# TWO-STATE PROMOTER



At full induction

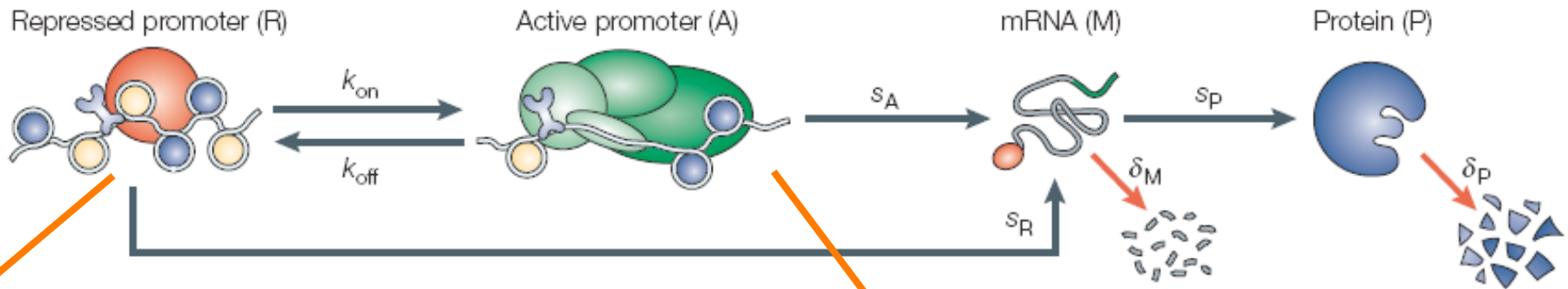
- $k_{on} = 1/(6 \text{ min})$
- $k_{off} = 1/(36 \text{ min})$
- $r = 1/(2.5 \text{ min})$



*Prediction: For the scaling to hold,  $k_{off}$ , not  $k_{on}$ , must be the rate that changes with induction.*

# STOCHASTIC MODEL OF TRANSCRIPTION

*Kepler and Elston '02*



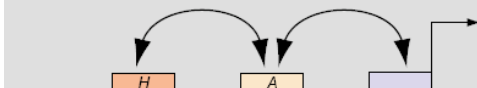
1. Simple repressor



2. Simple activator



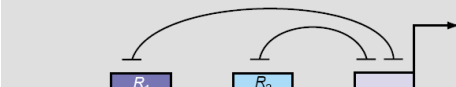
3. Activator recruited by a helper (H)



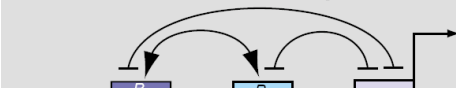
4. Repressor recruited by a helper (H)



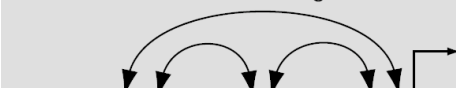
5. Dual repressors



6. Dual repressors interacting



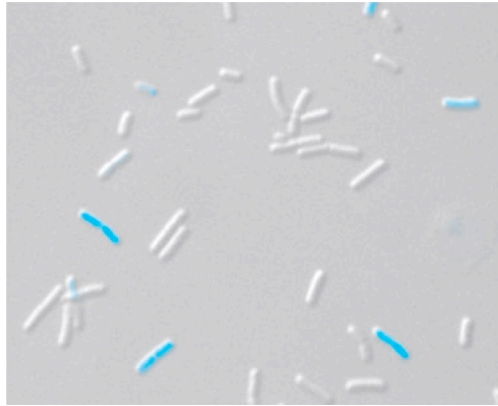
7. Dual activators interacting



*Generalize to arbitrary number of promoter states with different transcription rates.*

# PHENOTYPIC CONSEQUENCES OF NOISE

Maamar, Raj, and Dubnau '07

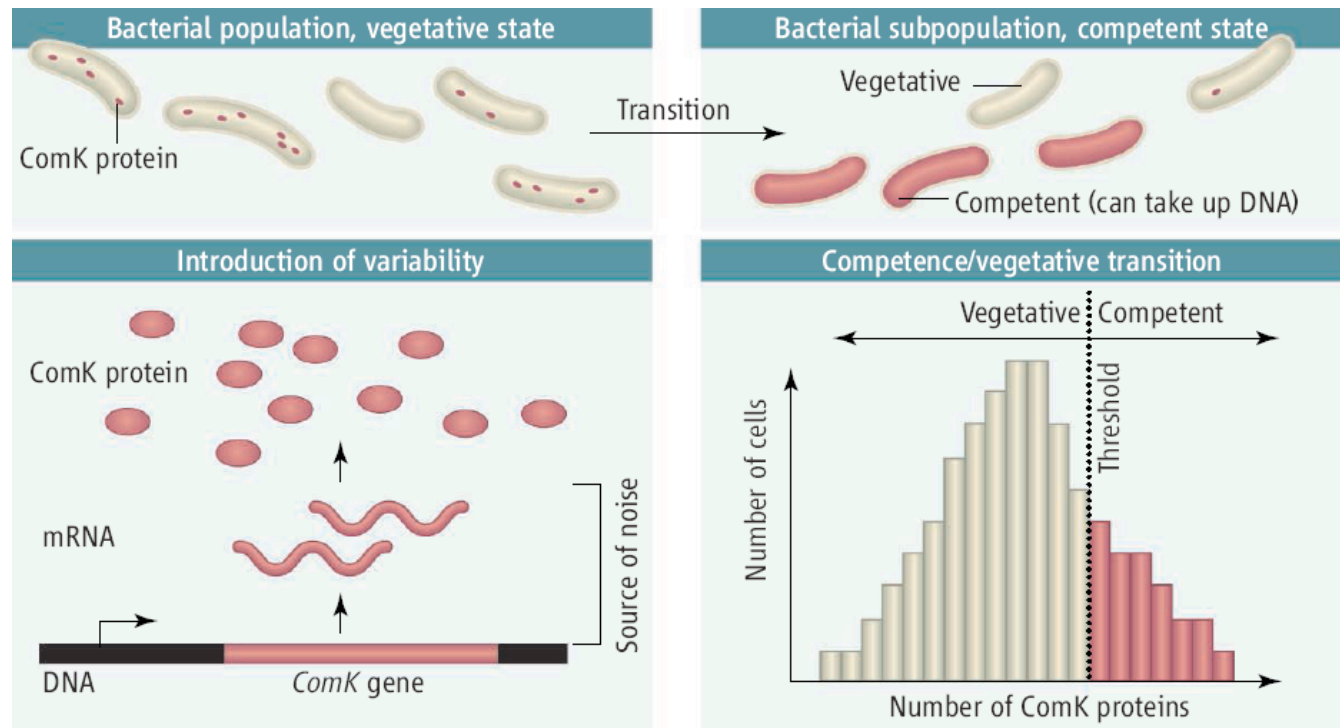


High noise



Low noise

*Amount of noise in expression of a single gene determines the number of competent cells in a population.*

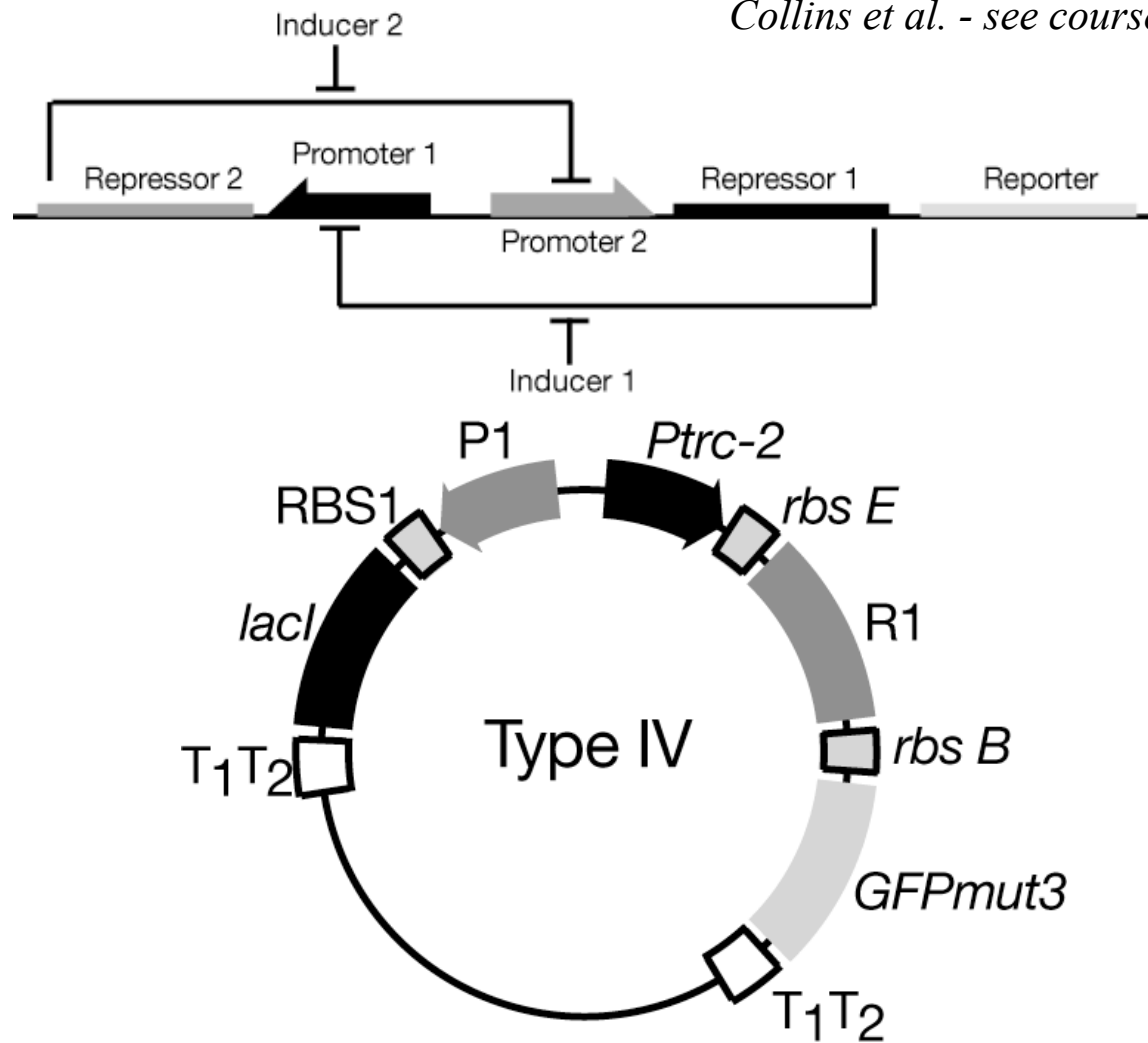


Mettetal and van Oudernaaden '07

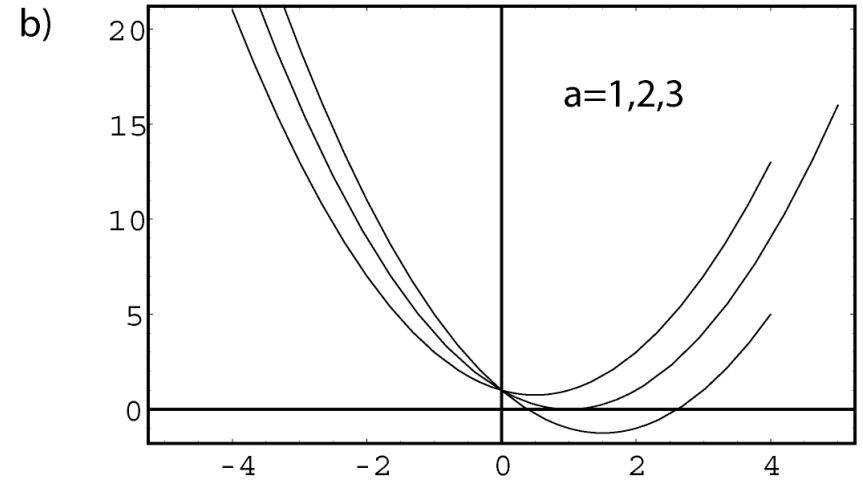
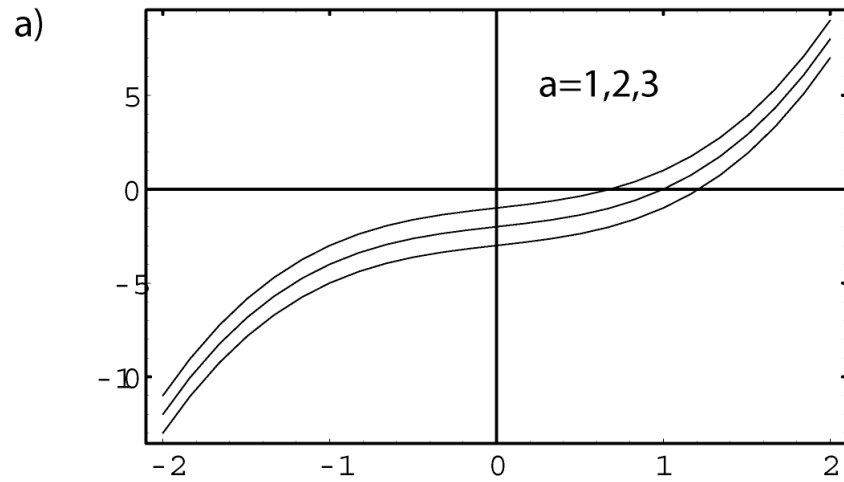


# SYNTHETIC GENETIC SWITCH

*Collins et al. - see course website*

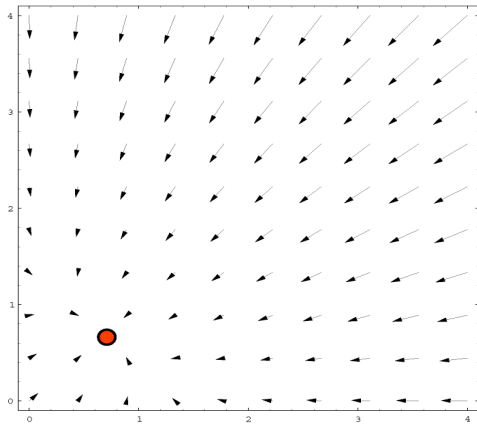


# STABLE SOLUTIONS

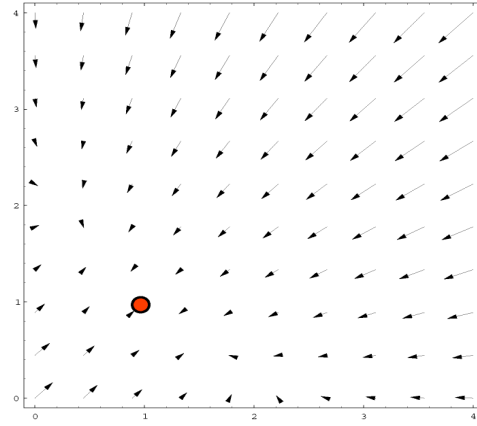


# PHASE PORTRAIT FOR THE SWITCH

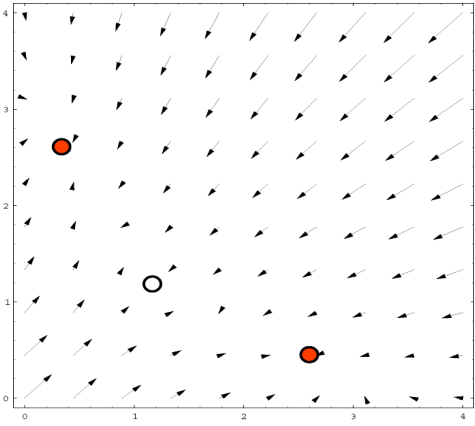
a)



b)

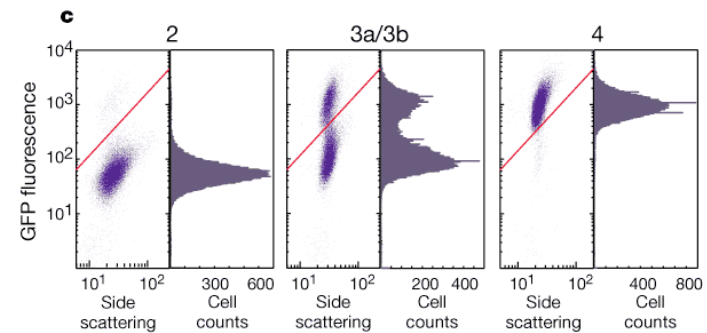
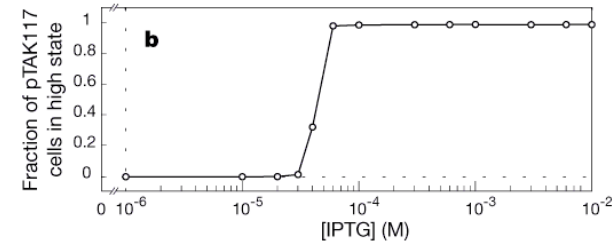
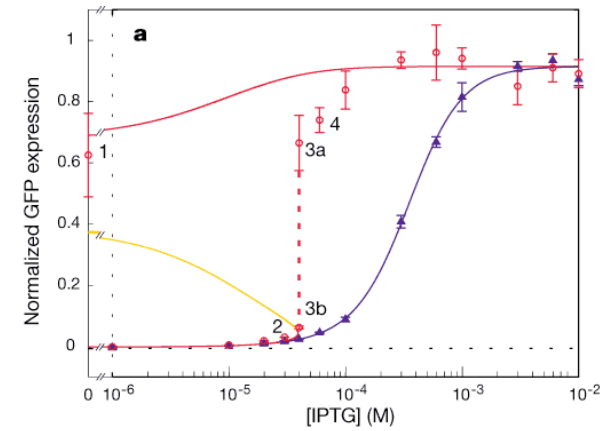
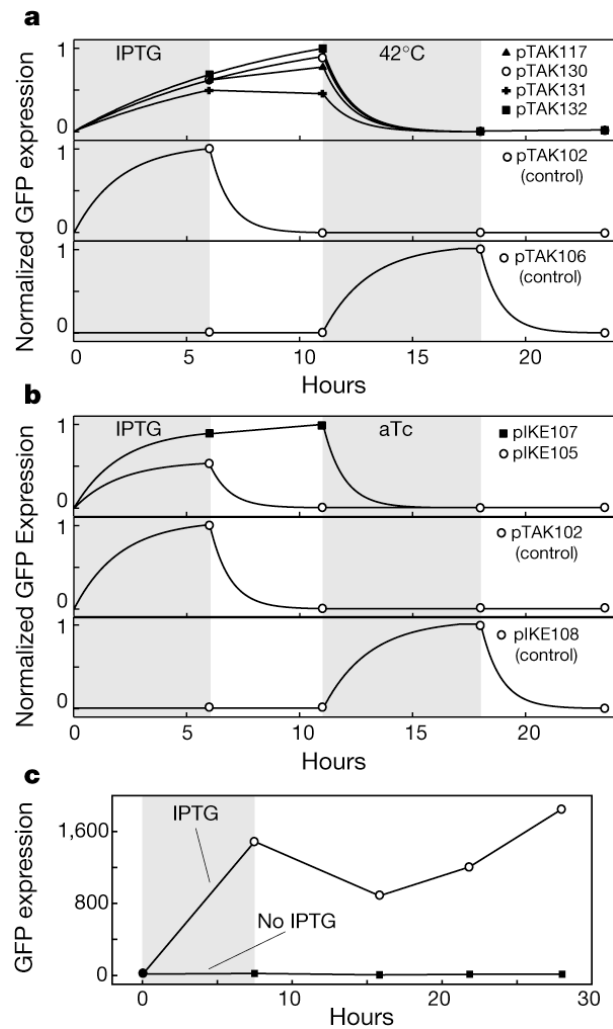


c)



# SYNTHETIC GENETIC SWITCH

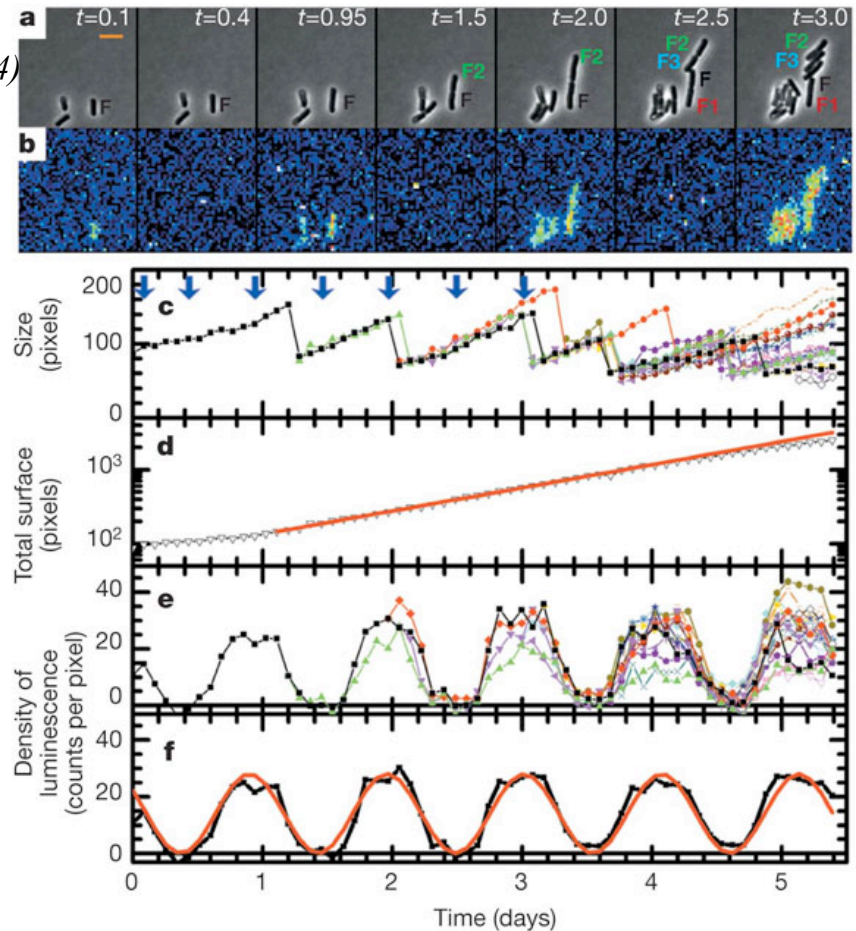
*Collins et al. - see course website*



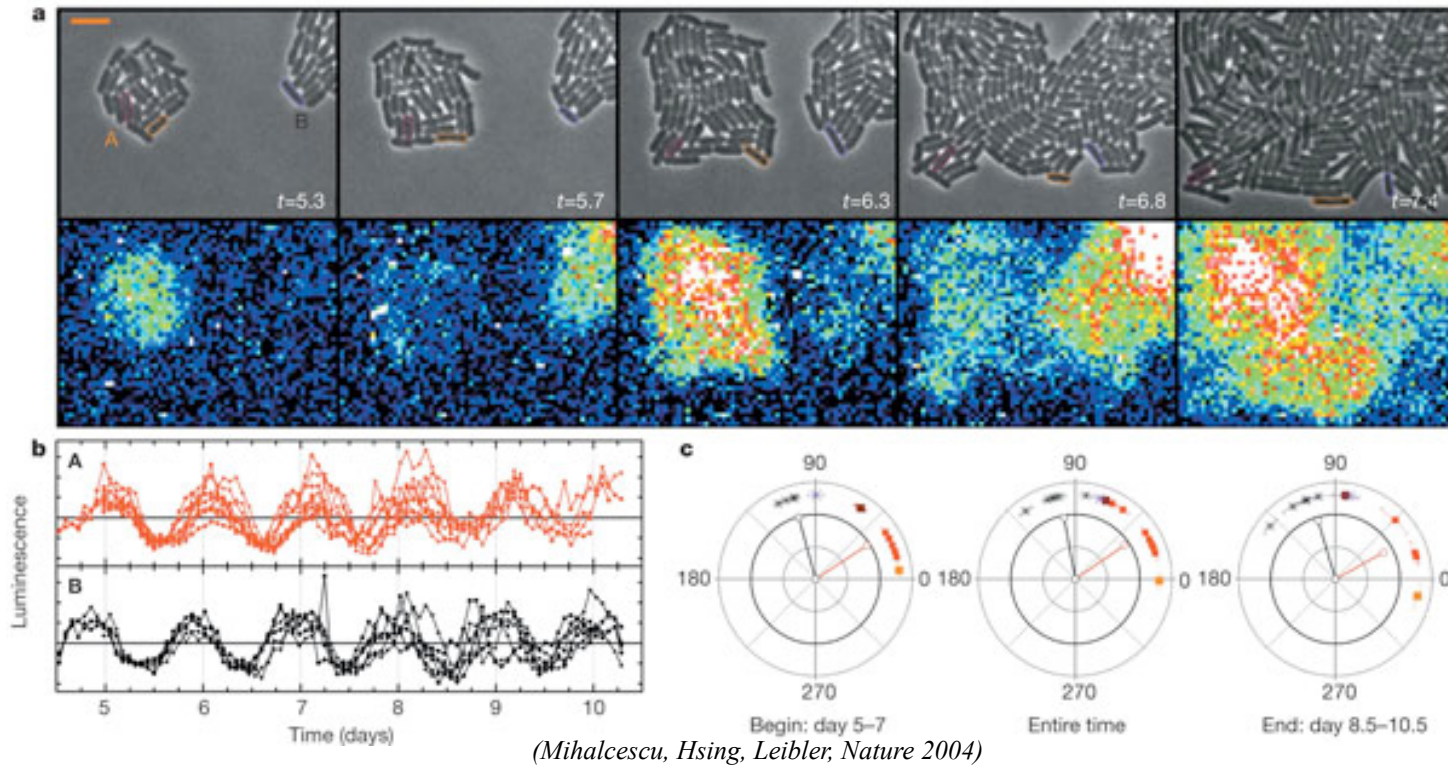
# GENE EXPRESSION IN CYANOBACTERIA

(Mihalcescu, Hsing, Leibler, Nature 2004)

*a*, Snapshots of phase-contrast image showing cell *F* and its progeny and *b*, related bioluminescence image at different times *t* (given in days, a 24 h period of time) from the beginning of the measurement. Pixels in the bioluminescence images were binned 3 times 3 (pseudo-colour, where red is high signal intensity and blue is low signal intensity). Scale bar, 5 microm. *c*, The size of the cell *F* and all its progeny as a function of time measured from the phase-contrast images (non-binned pixels). The arrows point to the time where the snapshots in (*a*) and (*b*) were taken. *d*, The total number of pixels occupied by *F* and its all progeny versus time (black line) plotted in a logarithmic scale. The red line is the corresponding exponential growth fit: total size (*t*) = initial size times  $2t/\tau$  with  $\tau = 23.04 \pm 0.17$  h. *e*, Density of bioluminescence for the same cell and all its progeny versus time. *f*, The average density of bioluminescence versus time (black line) and its fit (red line) with:  $\text{left fence}(t)\text{right fence} = B + A \cos(2\pi t/T_0 + \phi_0)$ . The resulting period is  $T_0 = 25.4 \pm 0.12$  h, the initial phase  $\phi_0 = 52 \pm 2.8^\circ$ , the amplitude  $A = 12.9 \pm 0.3$  counts per pixel and the offset  $B = 14.8 \pm 0.3$  counts per pixel.

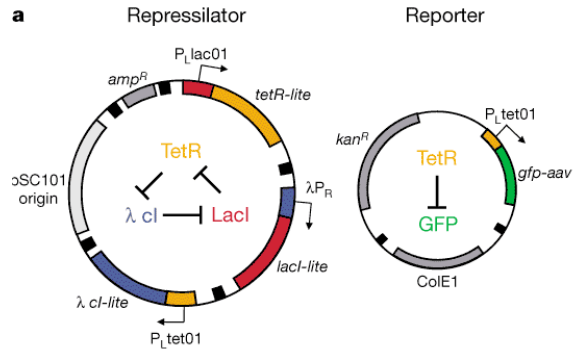


# GENE EXPRESSION IN CYANOBACTERIA

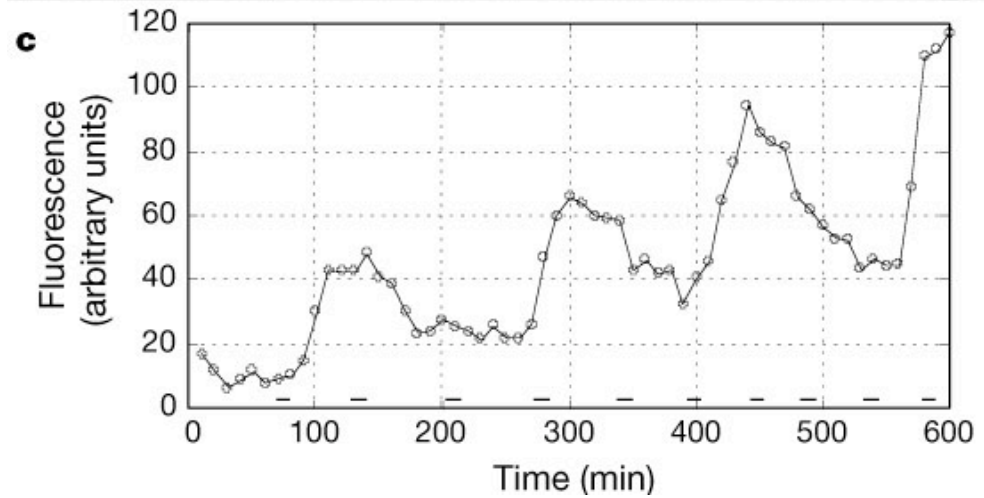
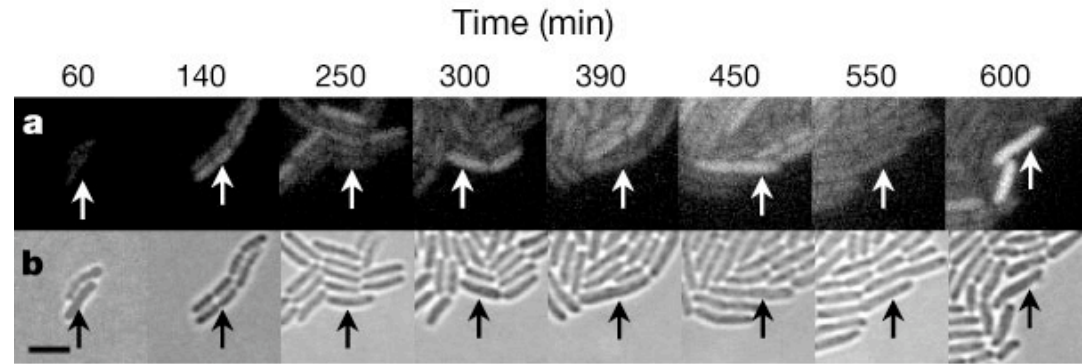
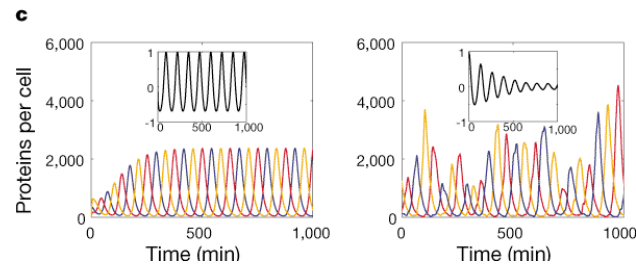
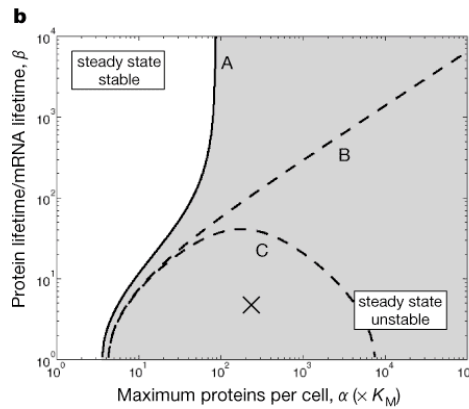


*a*, Upper part shows the phase-contrast snapshots of colonies A and B; lower part shows the related bioluminescence images. Scale bar, 5 microm. *b*, Normalized density of bioluminescence of individual cyanobacterial cells. Each colour corresponds to the progeny from one of the initial cells: red line, colony A; black line, colony B. *c*, Phase of individual oscillators as a function of their original colony and their evolution in time: red square, colony A; asterisk, colony B. An example of the exact location for three of the cells tracked and their phase evolution is shown, marked by the corresponding coloured lines: magenta, orange and purple. The change of the phase in time was quantified by a fit over a different period of time: the first 2 days (days 5–7), the entire time (days 5–10.5) and the last 2 days of the measurement (days 8.5–10.5). The fit function is  $\text{left fenced}(t)\text{right fence} = B + A \cos(2\pi t/T_0 + \phi)$ , with  $T_0 = 24.78$  h. The line segments in each graph, with corresponding colours, represent the resulting vector  $\text{Pres} = \sum \text{Pi}$ , where  $\text{Pi}$  is the unit vector whose orientation is the measured angle of the same colony cell *i*.

# SYNTHETIC TRANSCRIPTIONAL OSCILLATOR



(Elowitz, Leibler, Nature 2002)



# COUPLING OF GENES IN NETWORKS

