Noise reduction and information transfer in the cell

Glenn Vinnicombe (Dept. of Engineering, Cambridge) in collaboration with Johan Paulsson (Harvard Medical School) Ioannis Lestas (Dept. of Engineering, Cambridge)

Overview

- The cell is a noisy cell, in spite over being packed full of feedback loops.
- Why?





Fundamental limits on the suppression of molecular fluctuations

Ioannis Lestas¹, Glenn Vinnicombe¹ & Johan Paulsson²

REVIEWS

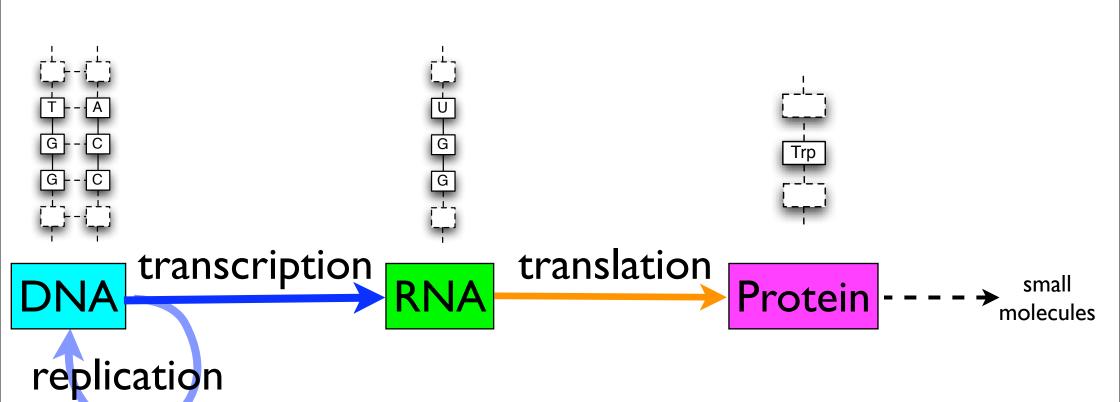
Functional roles for noise in genetic circuits

Avigdor Eldar¹† & Michael B. Elowitz¹

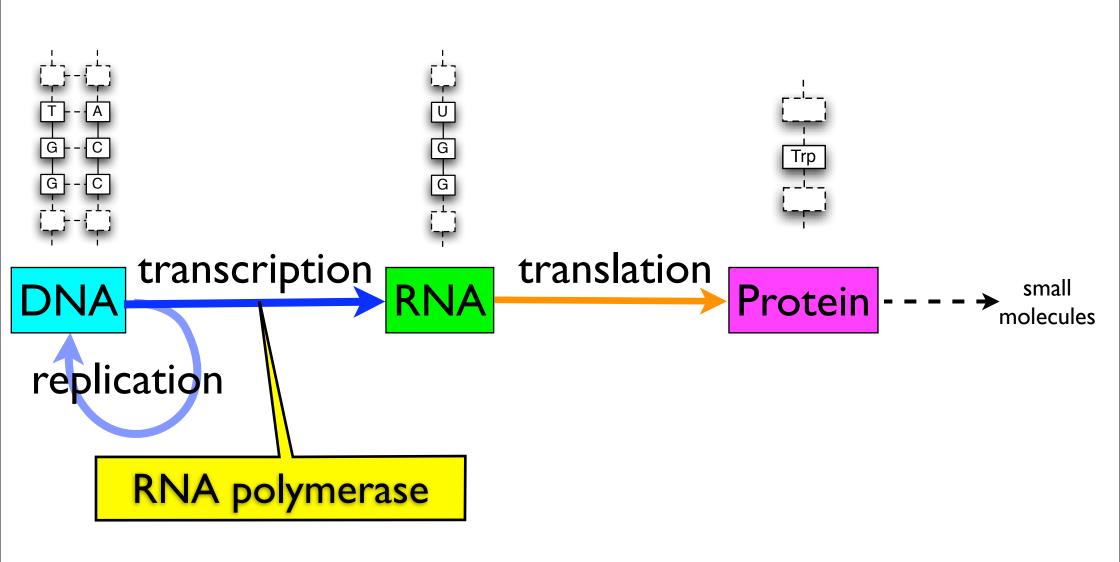
Overview

- The cell is a noisy cell, in spite over being packed full of feedback loops.
- Why?
- I shall present some fundamental limitations for biological systems, in terms of minimum achievable variances.
- These limits apply to the regulation of a single species within an arbitrarily complex network, and the suggest that the cost of reducing noise can be extremely high.

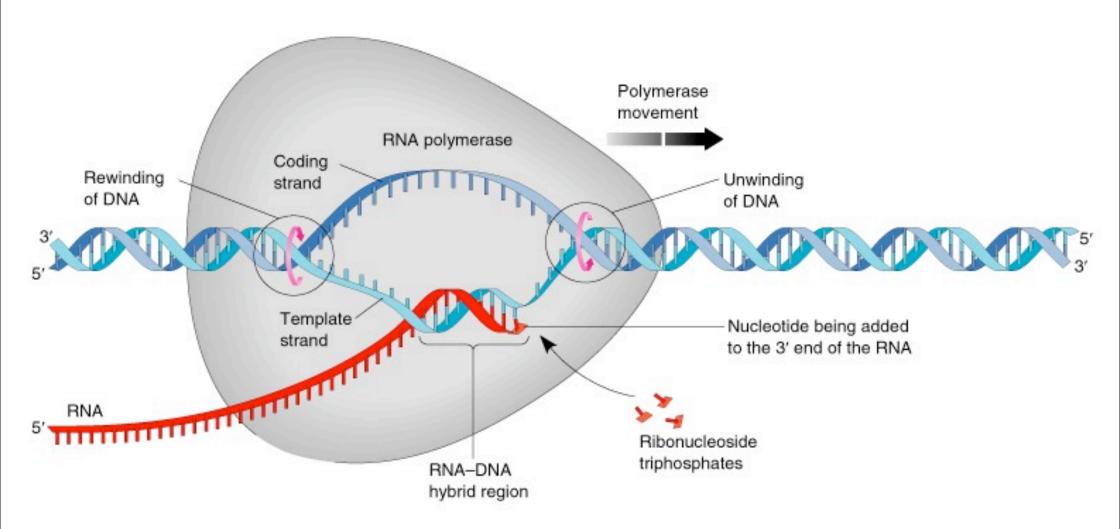
The Central Dogma



The Central Dogma



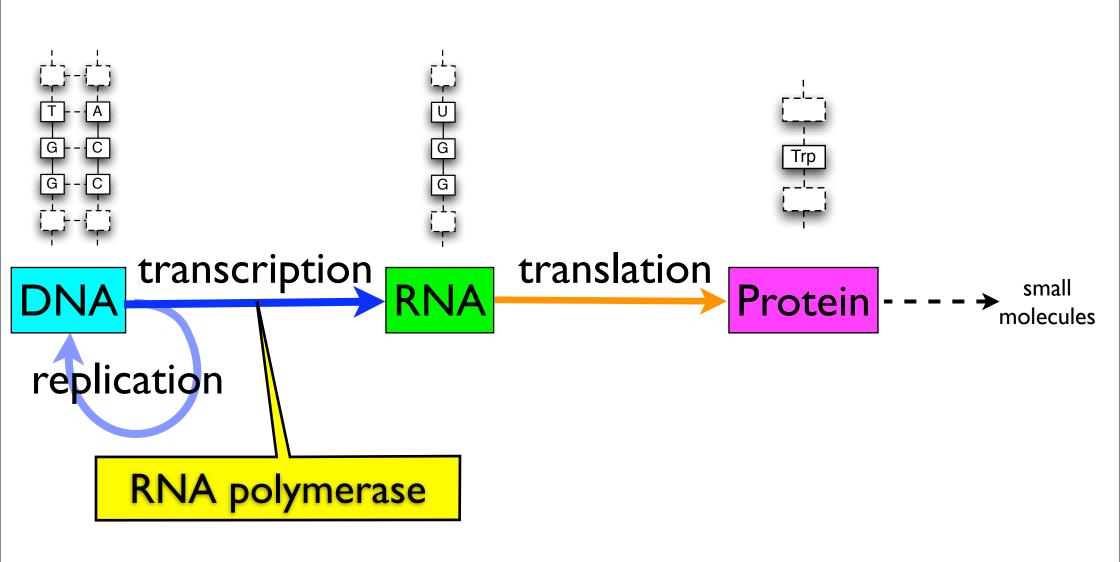
Transcription



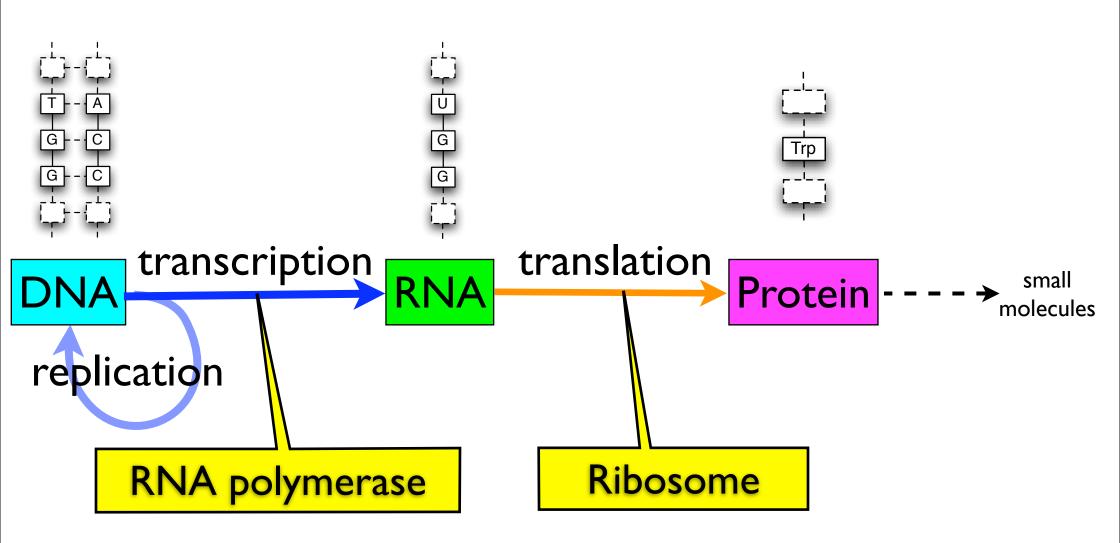
- RNA polymerase slides along the DNA, creating an open complex as it moves.
- The DNA strand known as the template strand is used to make a complementary copy of RNA as an RNA-DNA hybrid.
- The RNA is synthesized in a 5' to 3' direction using ribonucleoside triphosphates as precursors. Pyrophosphate is released (not shown).
- The complementarity rule is the same as the A-T and G-C rule except that U is substituted for T in the RNA.

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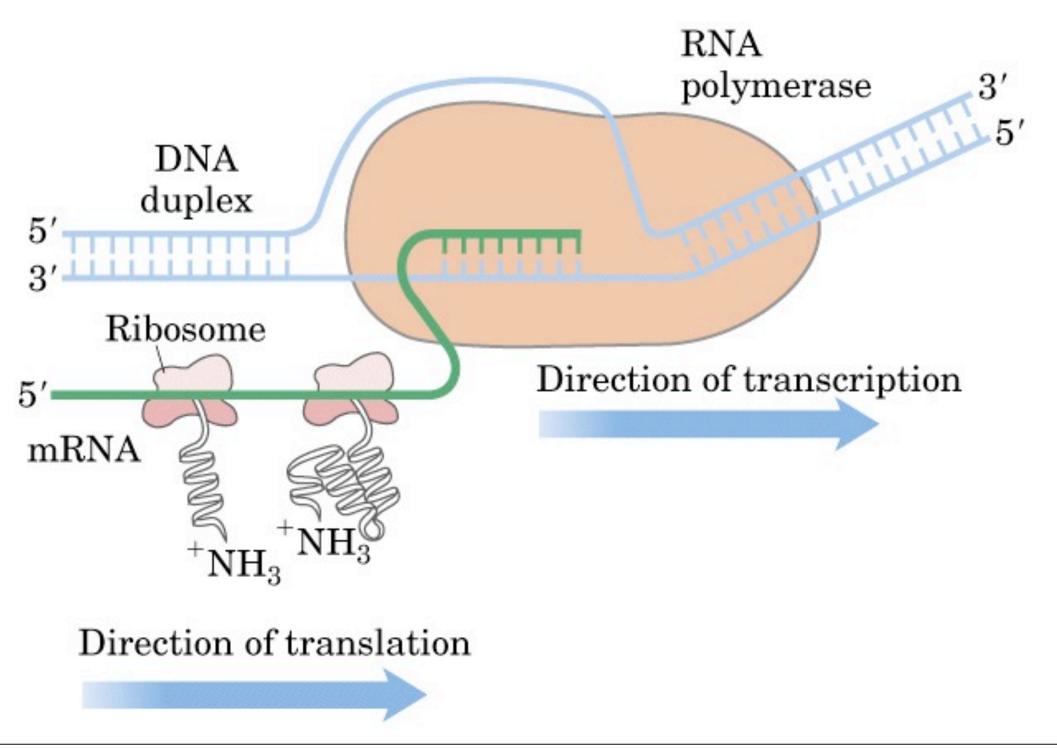
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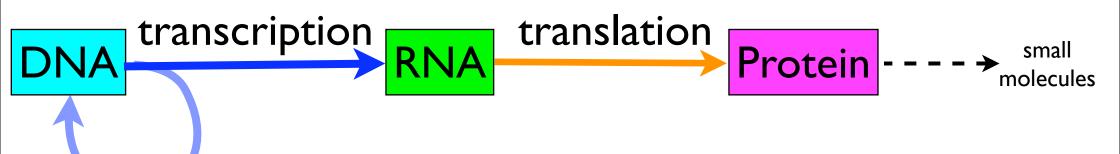


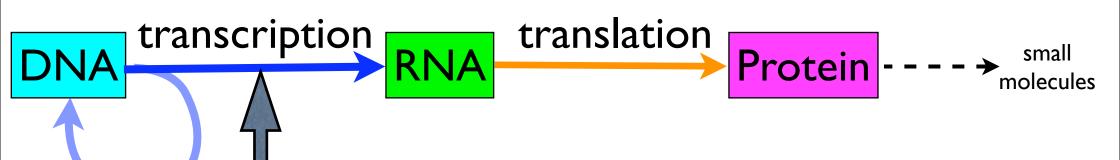
The Central Dogma



Transcription & Translation in Prokaryotes





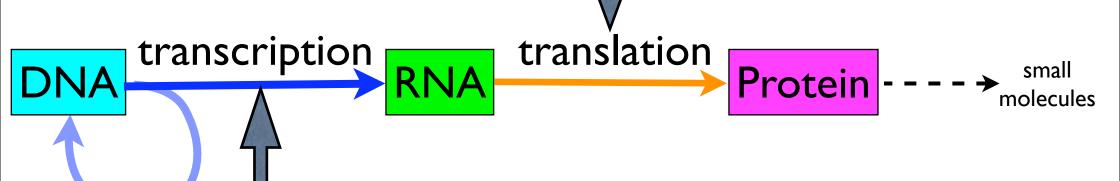


- Gene silencing
- Gene regulation by

DNA binding proteins:

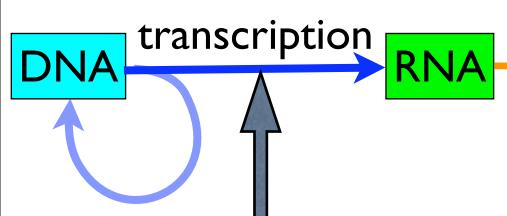
- Activators/repressors
- Sigma factors

- post-transcriptional control
 - antisense RNA / RNAi
 - temperature sensors
 - RNA binding small molecules
 - @ control of_splicing (in eukaryotes)

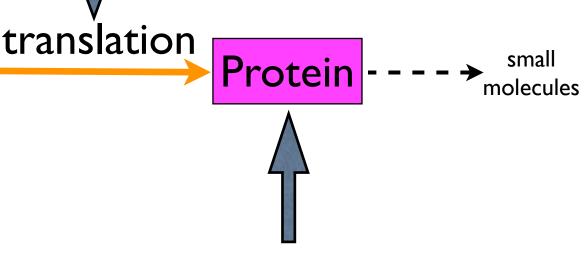


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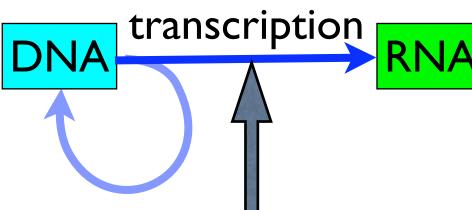


post-translational modification e.g.phosphorylation

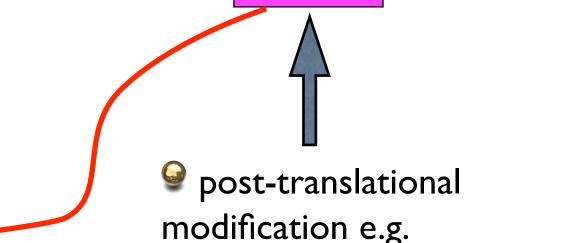
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phosphorylation

Protein

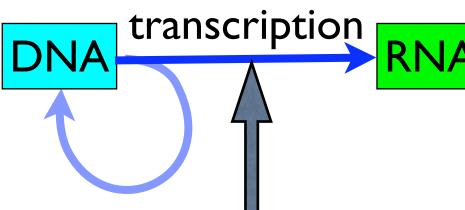
small

molecules

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Gene silencing

Gene regulation by DNA binding proteins:

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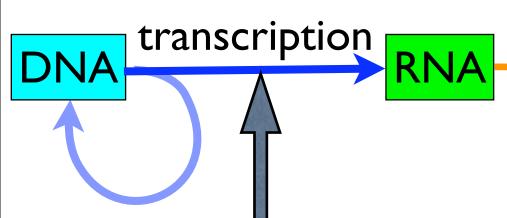
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Protein

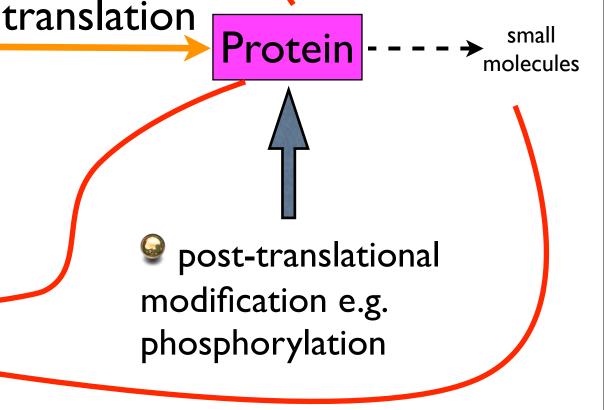
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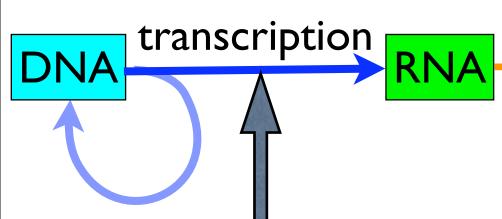
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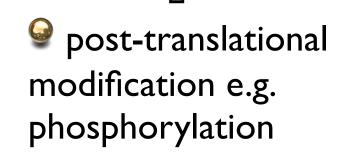
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Protein

smal

molecules

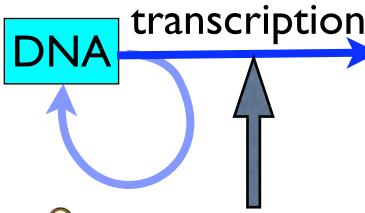
(and this is just part of the story!)

post-transcriptional control

antisense RNA / RNAi

translation

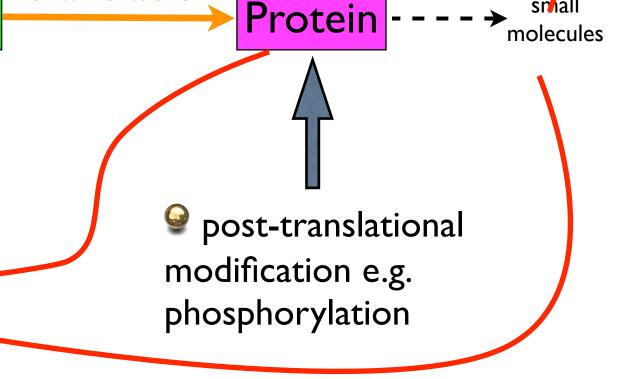
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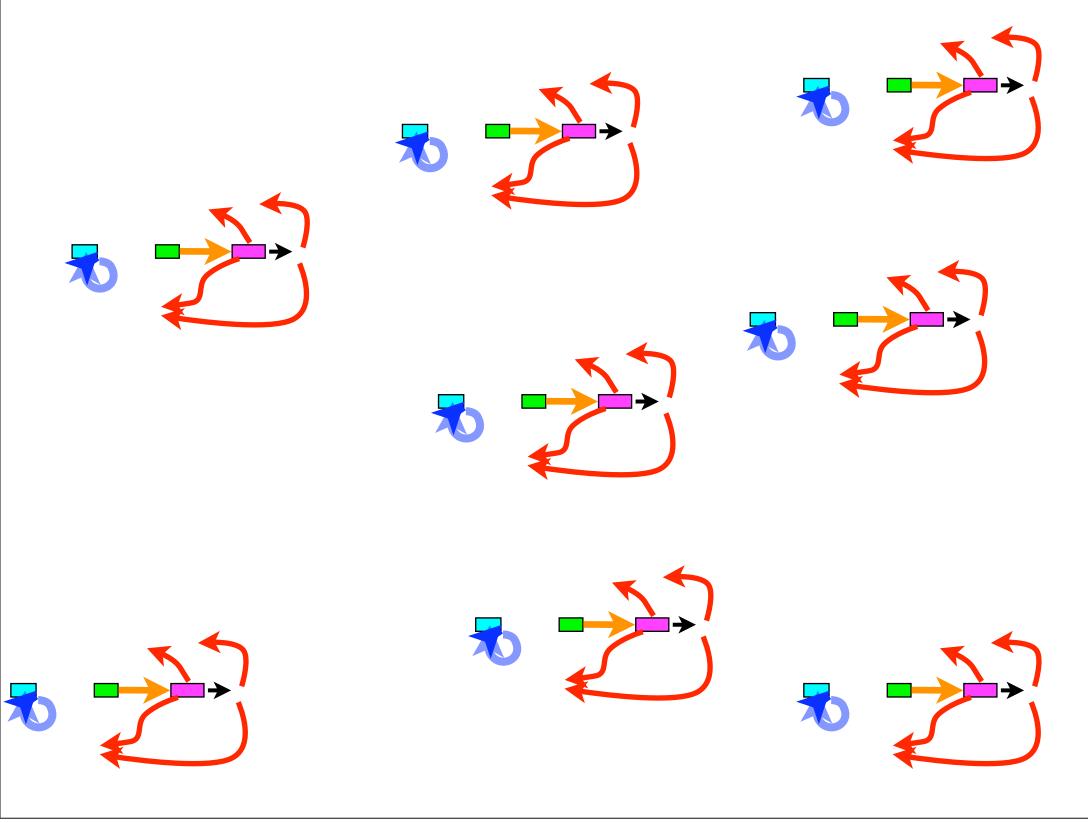


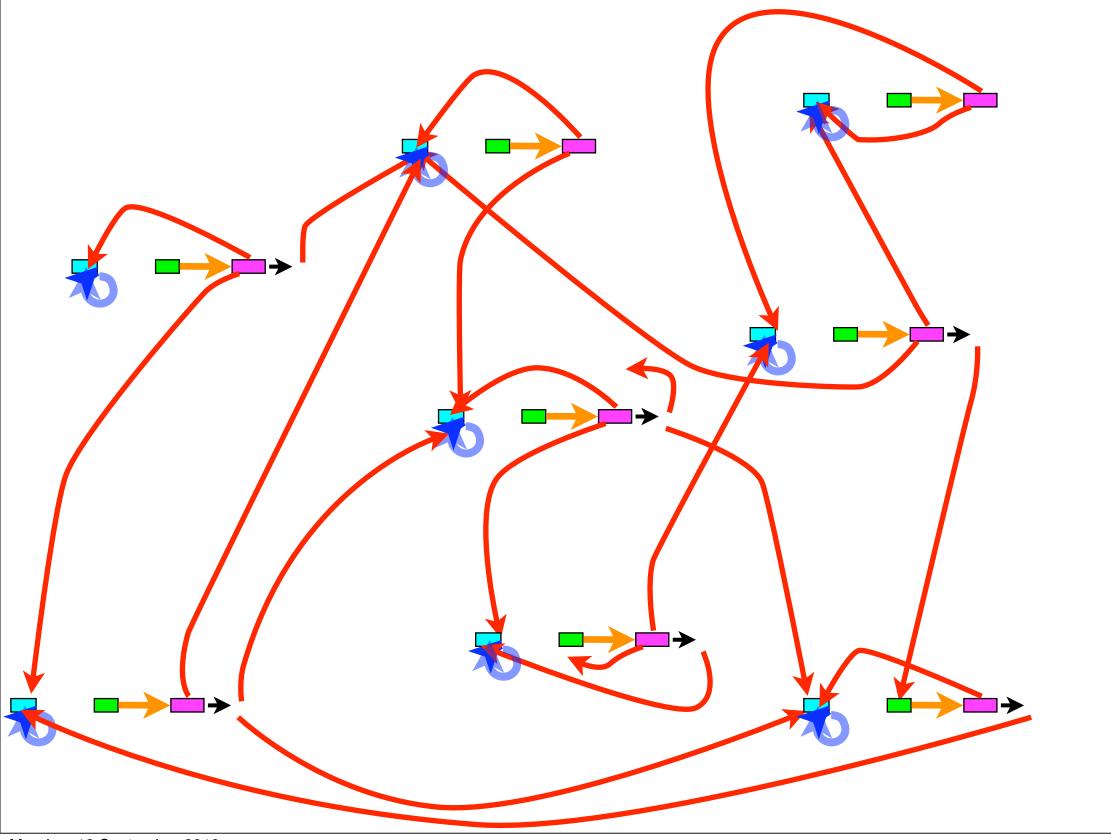
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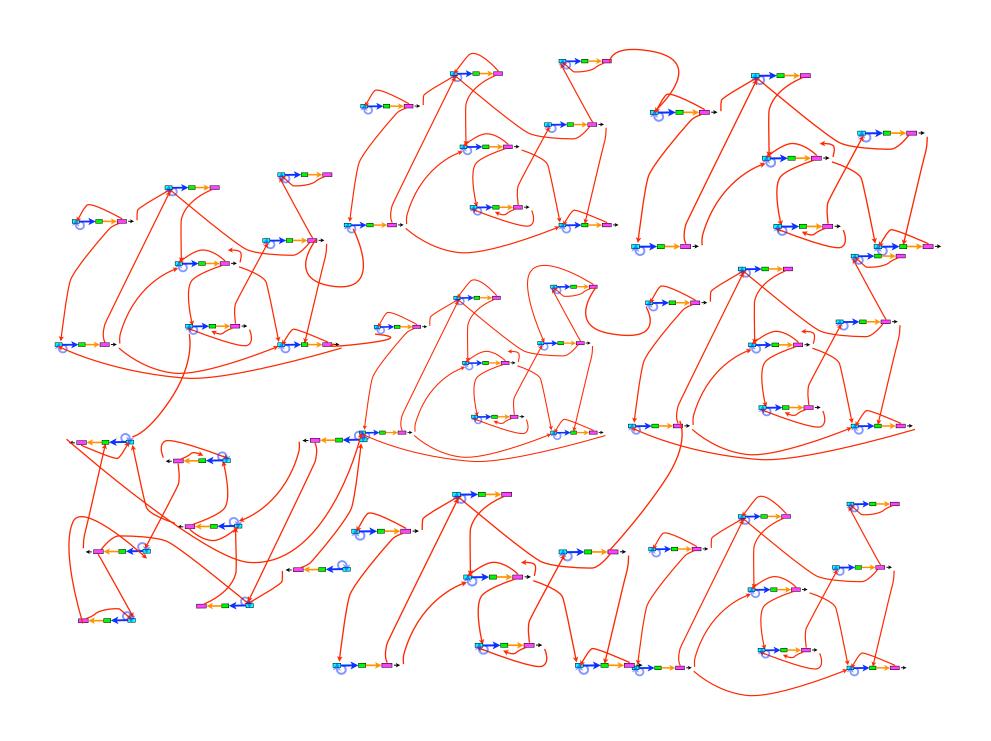
Gene regulation by DNA binding proteins:

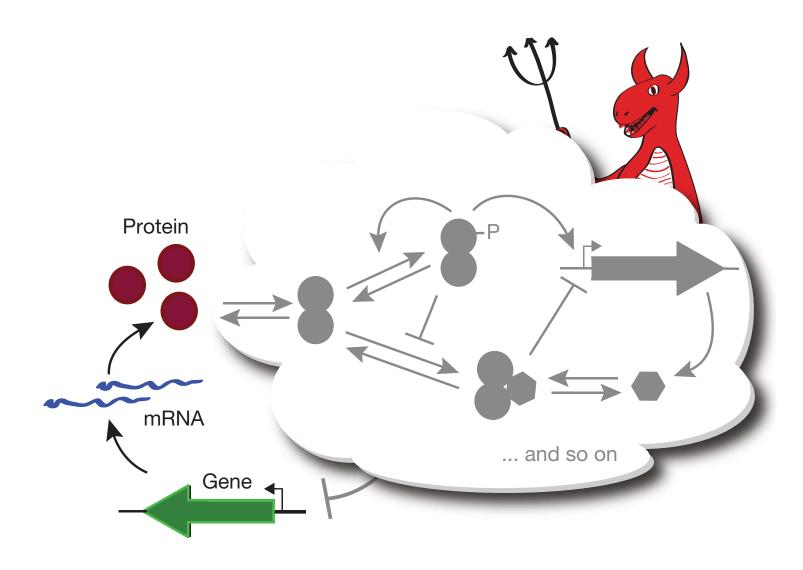
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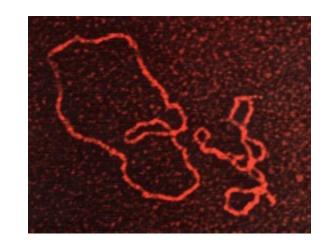


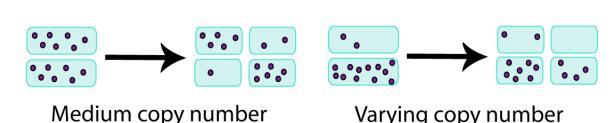


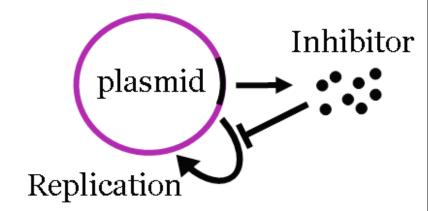


Minimizing variance: ColE1 replication control

- ⊕ Approx 16 plasmid copies per cell
- Partitioned randomly at cell division
- Under strong selection for small variance



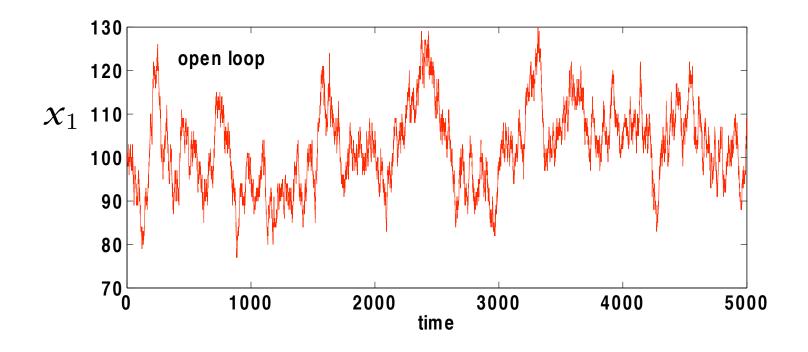




Consider a single species: e.g. mRNA of a constitutively expressed gene

$$\begin{array}{c} x_1 \xrightarrow{c} x_1 + 1 \\ x_1 \xrightarrow{x_1/\tau_1} x_1 - 1 \end{array}$$

$$\emptyset \quad \stackrel{k_1}{\underset{k_2}{\longleftrightarrow}} X_1$$



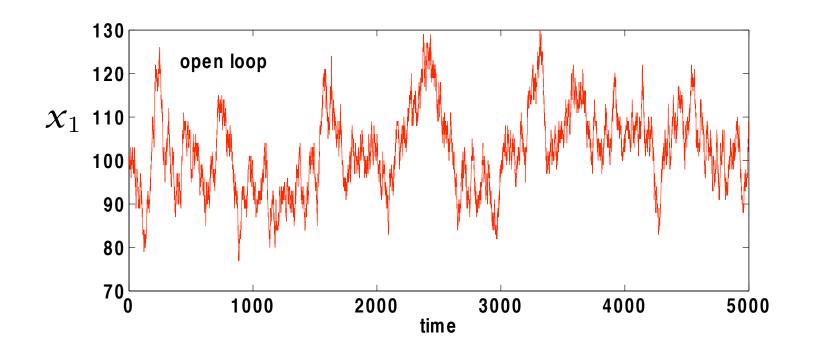
$$\sigma_1^2 = \langle x_1 \rangle$$

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$$\Pr(\mathbf{x}_1(t+dt) = N+1|\mathbf{x}_1(t) = N) = c dt$$



$$\sigma_1^2 = \langle x_1 \rangle$$

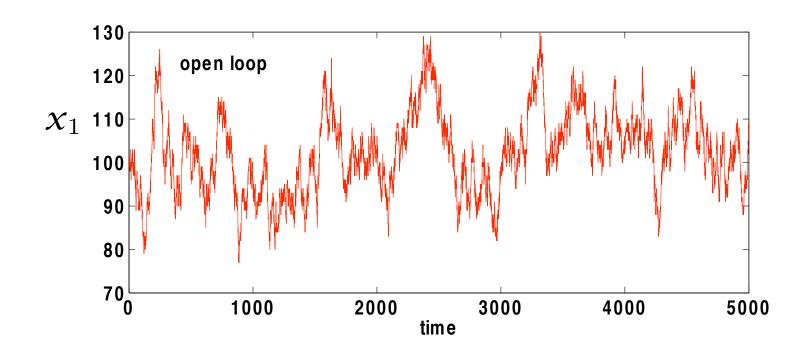
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$$\Pr(x_1(t + dt) = N + 1 | x_1(t) = N) = c dt$$

$$\Pr(x_1(t + dt) = N - 1 | x_1(t) = N) = N/\tau_1 dt$$



$$\sigma_1^2 = \langle x_1 \rangle$$

(with feedback)

$$x_1 \xrightarrow{u_t} x_1 + 1$$

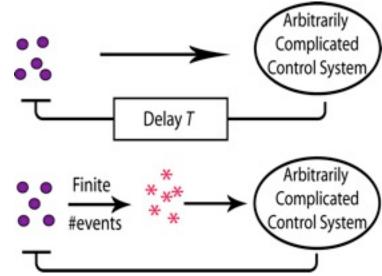
$$x_1 \xrightarrow{x_1/\tau_1} x_1 - 1$$

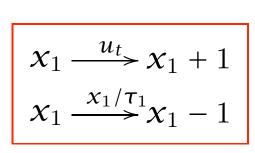
where
$$u_t = f(\{x_1(t') : t' < t\})$$

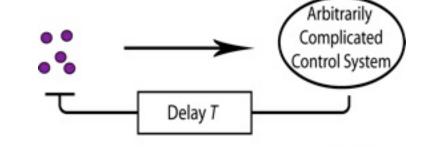
ullet Can make $rac{\sigma_1^2}{\langle \chi_1
angle}$ arbitrarily small by appropriate choice of f .

However, limitations are imposed by:

- Delays
- Feedback mechanisms/capacity



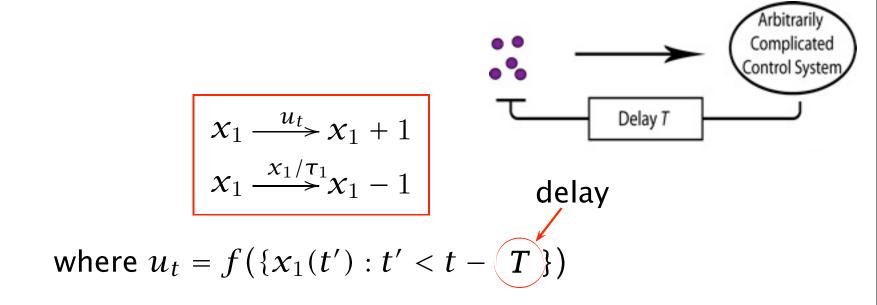




where
$$u_t = f(\{x_1(t') : t' < t - T\})$$

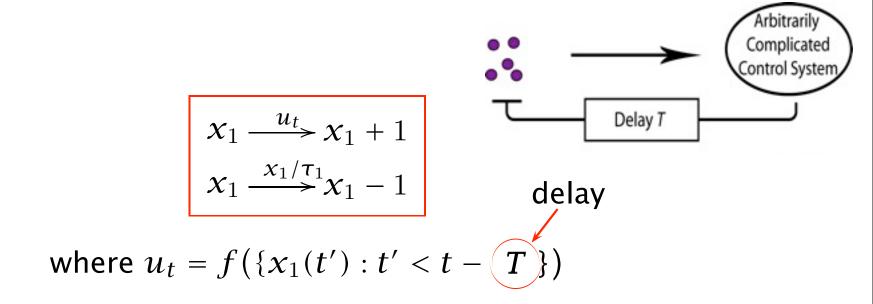
Theorem: If x_1 is a stationary process then

$$\frac{\sigma_1^2}{\langle x_1 \rangle} \ge (1 - e^{-2T/\tau_1})$$



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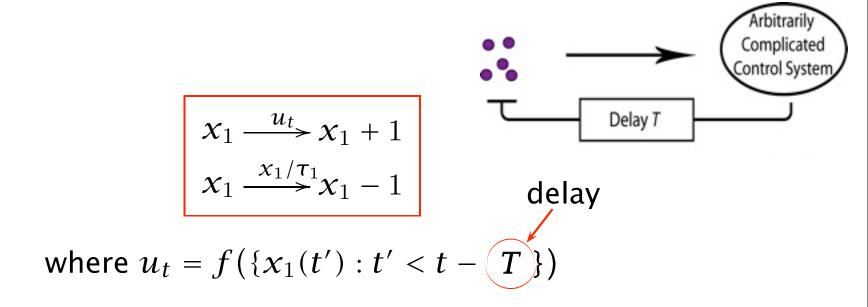
$$\frac{\sigma_1^2}{\langle x_1 \rangle} \ge (1 - e^{-2T/\tau_1})$$

Proof: Let
$$\mathcal{I}_t = \{x_1(t'), t' < t - T\}$$

$$\sigma_1^2 = E[(x_1 - E[x_1])^2] = E[E[x_1 - E[x_1])^2]|I_t]]$$

$$\geq E[E[(x_1 - E[x_1|I_t])^2|I_t]]$$

$$= E[E[x_1|\mathcal{I}_t] - x_1(t - T)e^{-2T/\tau_1}]$$



Theorem: If x_1 is a stationary process then

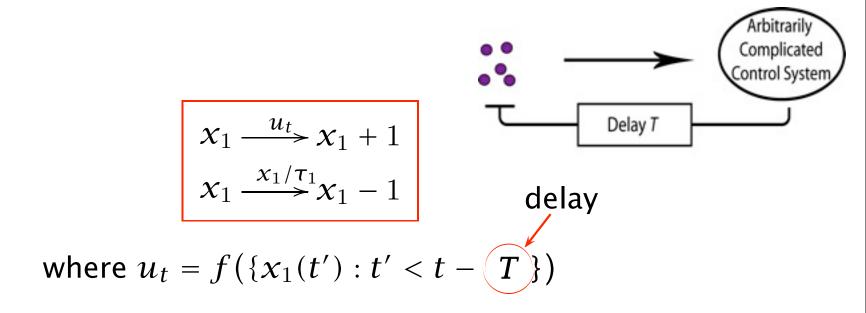
$$\frac{\sigma_1^2}{\langle x_1 \rangle} \ge (1 - e^{-2T/\tau_1})$$

$$\chi_1 \xrightarrow{u_t \chi_1} \chi_1 + 1$$

$$x_1 \xrightarrow{x_1/\tau_1} x_1 - 1$$

then

$$\frac{\sigma_1^2}{\langle \chi_1 \rangle} \ge 2T/\tau_1$$



Theorem: If x_1 is a stationary process then

$$\frac{\sigma_1^2}{\langle x_1 \rangle} \ge (1 - e^{-2T/\tau_1})$$
 replication

On the other hand, if

$$x_1 \xrightarrow{u(x_1)} x_1 + 1$$

$$x_1 \xrightarrow{x_1/\tau_1} x_1 - 1$$

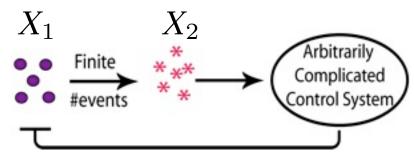
then

$$\frac{\sigma_1^2}{\langle \chi_1 \rangle} \ge 2T/\tau_1$$

Limitations due to mechanisms: molecular channels

System:

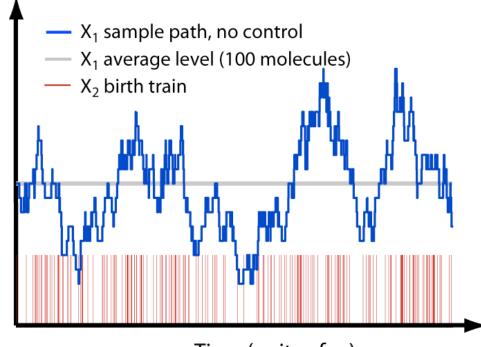
$$\begin{array}{c} x_1 \xrightarrow{u_t} x_1 + 1 \\ x_1 \xrightarrow{x_1/\tau_1} x_1 - 1 \end{array}$$



Sensor:

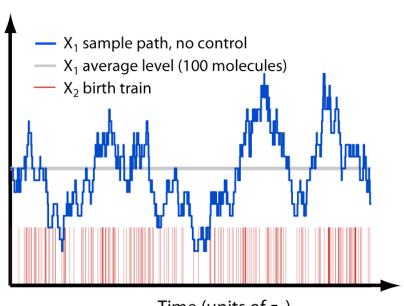
$$\begin{array}{c} x_2 \xrightarrow{\alpha x_1} x_2 + 1 \\ x_2 \xrightarrow{x_2/\tau_2} x_2 - 1 \end{array}$$

where $u_t = f(\{x_2(t') : t' < t\})$



Time (units of τ_1)

What is the capacity of a molecular channel?



Consider the channel:

Time (units of
$$\tau_1$$
)

$$\chi_2 \xrightarrow{z} \chi_2 + 1$$

$$x_2 \xrightarrow{x_2/\tau_2} x_2 - 1$$

• Capacity is related to that for a photon counting channel (but depends on what constraints are put on z)

(but depends on what constraints are put on
$$z$$
)

One answer is $C = \langle z \rangle \log \left(1 + \frac{\sigma_z^2}{\langle z \rangle^2}\right) \le \frac{\sigma_z^2}{\langle z \rangle}$ (nat/s)
$$= 1.443 \sigma_z^2/\langle z \rangle \text{ bit/s}$$

(where
$$C = \max_{z} I(x_2; z)$$
)

Feedback capacity and variance

Taking the diffusion approximation of the replication case:

$$x_1 \xrightarrow{u_t x_1} x_1 + 1$$

$$x_1 \xrightarrow{x_1/\tau_1} x_1 - 1$$

$$dx_1 = u_t \langle x_1 \rangle dt + \sqrt{2\langle x_1 \rangle / \tau_1} dw$$

gives (Gorbunov and Pinsker '74)

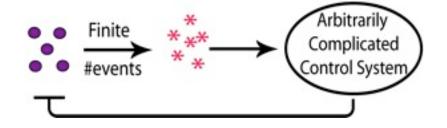
$$\frac{\sigma_1^2}{\langle x_1 \rangle} \ge \frac{1}{C\tau_1}$$
 (for $I(u; x_1) \le C$)

Putting this together with the bound on *C* gives:

$$\frac{\sigma_1^2}{\langle x_1 \rangle} \ge \sqrt{\frac{N_1}{N_2}}$$

where $N_2 = \langle x_2 \rangle \tau_1 / \tau_2 =$ no of molecules of X_2 made per lifetime of X_1 . $N_1 = \langle x_1 \rangle =$ no of molecules of X_1 made per lifetime of X_1 .

Summary: Limitations due to channel capacity



$$\begin{array}{c} x_1 \xrightarrow{u_t x_1} x_1 + 1 \\ x_1 \xrightarrow{x_1/\tau_1} x_1 - 1 \end{array}$$

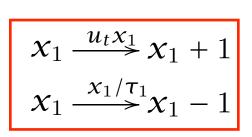
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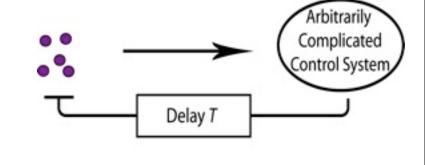
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where $N_2 = \langle x_2 \rangle \tau_1 / \tau_2 = \text{no of molecules of } X_2 \text{ made per lifetime of } X_1.$ $N_1 = \langle x_1 \rangle$ = no of molecules of X_1 made per lifetime of X_1 .

Summary: Limitations due to delay



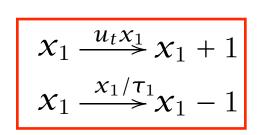


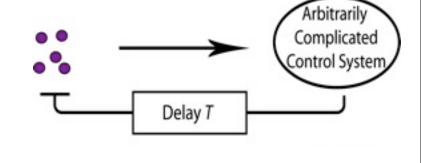
where
$$u_t = f(\{x_1(t') : t' < t - T\})$$

If x_1 is a stationary process then

$$\frac{\sigma_1^2}{\langle \mathbf{x}_1 \rangle} \ge 2 \frac{T}{\tau_1}$$

Summary: Limitations due to delay





where
$$u_t = f(\{x_1(t') : t' < t - T\})$$

If x_1 is a stationary process then

$$\frac{\sigma_1^2}{\langle x_1 \rangle} \ge 2 \frac{T}{\tau_1}$$

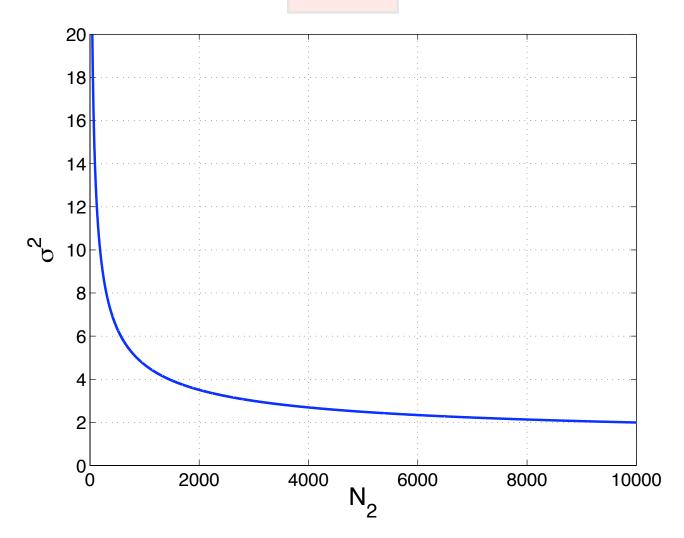
Can combine bounds:

$$\frac{\sigma_1^2}{\langle x_1 \rangle} \ge \frac{T}{\tau_1} + \sqrt{\frac{N_1}{N_2} + \left(\frac{T}{\tau_1}\right)^2}$$

Some numbers

For ColE1, assuming a mean of 16 copies immediately after cell division

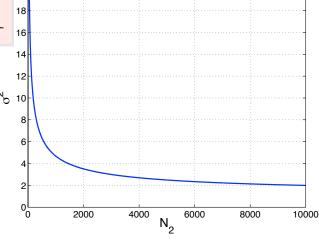
- Lower bound due to delays only (T = 44): $\sigma^2 \gtrsim 1$
- 10000 inhibitors/cell cycle: $\sigma^2 \gtrsim 2$



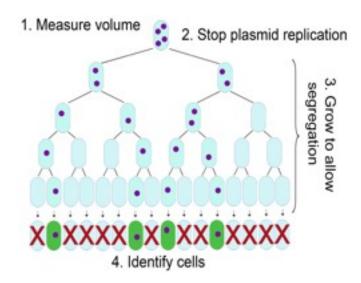
Some numbers

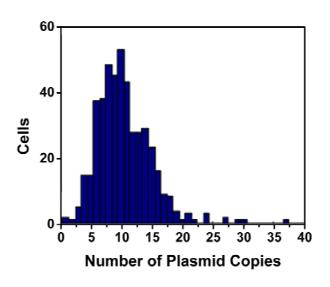
For ColE1, assuming a mean of 16 copies immediately after cell division

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• Early experimental results (Paulsson) suggest $\sigma^2 < 4$ (although for a different plasmid with the same copy number).





Extensions

Similar results hold for non-replication case (e.g. transcription/translation:

e.g.
$$\frac{x_1\stackrel{u_t}{\to}x_1+1}{\langle x_1\rangle}\geq \frac{2}{1+\sqrt{1+4N_2/N_1}},\quad 1-\exp(-2T/\tau_1)$$

and for nonlinear use of channel:

$$x_2 \stackrel{f(x_1)}{\to} x_2 + 1$$

(e.g. Hill functions
$$f(x_1) = v \frac{x_1^H}{K + x_1^H}$$
)

same bounds, but with $N_2 o \gamma N_{2
m max}$

Conclusions

- The ultimate bounds on feedback performance due to delays and finite numbers of synthesis events are sharp and appear biologically relevant.
- Biological questions are inspiring new theory here!

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and new theory is now also inspiring biological questions!