

# Modelos estocásticos en circuitos genéticos

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- Fluctuaciones aleatorias en expresión genética.
- En transcripción y traducción: Colisiones aleatorias entre moléculas que se encuentran en bajo número.
- Otros factores como la división celular, la variabilidad del ambiente.

$$\eta_X = \frac{\sigma_X}{\langle X \rangle}.$$

$$\nu_X = \frac{\sigma_X^2}{\langle X \rangle}.$$

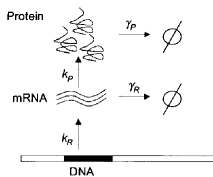
# Intrinsic noise in gene regulatory networks

Mukund Thattai and Alexander van Oudenaarden\*

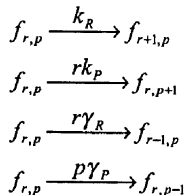
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[Thattai & van Oudenaarden, 2001].



[Thattai & van Oudenaarden, 2001].



[Thattai & van Oudenaarden, 2001].

$$\dot{r}(t) = k_R - \gamma_R r(t).$$

$$\dot{p}(t) = k_P r(t) - \gamma_P p(t).$$

$$\begin{aligned}
 \frac{df_{r,p}}{dt} = & k_R f_{r-1,p} - k_R f_{r,p} \\
 & + k_P r f_{r,p-1} - k_P r f_{r,p} + \gamma_R (r+1) f_{r+1,p} \\
 & - \gamma_R r f_{r,p} + \gamma_P (p+1) f_{r,p+1} - \gamma_P p f_{r,p}.
 \end{aligned}$$

## Promedio

$$\langle r \rangle = \frac{k_R}{\gamma_R}.$$

$$\langle p \rangle = \frac{k_R b}{\gamma_P}.$$

## Ruido

$$\nu_r = \frac{\sigma_r^2}{\langle r \rangle} = 1.$$

$$\nu_p = \frac{\sigma_p^2}{\langle p \rangle} = \frac{b}{1 + \eta} + 1 \approx b + 1.$$

$$b := \frac{k_P}{\gamma_R}, \quad \eta := \frac{\gamma_P}{\gamma_R}.$$

# Generalización - Ecs. deterministas

Las ecuaciones

$$\begin{aligned}\dot{r}(t) &= k_r - \gamma_r r(t), \\ \dot{p}(t) &= k_p r(t) - \gamma_p p(t),\end{aligned}$$

pueden ser escritas como

$$\dot{\mathbf{x}} = (A - \Gamma)\mathbf{x}.$$

Donde  $\mathbf{x}^T := (d, r, p)$  y

$$A := \begin{matrix} & \begin{matrix} (d) & (r) & (p) \end{matrix} \\ \begin{matrix} (d) \\ (r) \\ (p) \end{matrix} & \begin{pmatrix} 0 & 0 & 0 \\ k_R & 0 & 0 \\ 0 & k_P & 0 \end{pmatrix} \end{matrix}, \quad \Gamma := \begin{matrix} & \begin{matrix} (d) & (r) & (p) \end{matrix} \\ \begin{matrix} (d) \\ (r) \\ (p) \end{matrix} & \begin{pmatrix} 0 & 0 & 0 \\ 0 & \gamma_R & 0 \\ 0 & 0 & \gamma_P \end{pmatrix} \end{matrix}.$$

## Generalización - Ec. maestra

Se puede realizar en general. Si  $\mathbf{x}^T := (q_1, q_2, \dots, q_n)$ ,

$$f_{q_i} \xrightarrow{k_i^+(q_j)} f_{q_i+1}$$

$$f_{q_i} \xrightarrow{k_i^-(q_j)} f_{q_i-1}$$

$$k_i^+(q_j) = \sum_j A_{ij} q_j \quad k_i^-(q_j) = \sum_j \Gamma_{ij} q_j$$

[Thattai & van Oudenaarden, 2001].

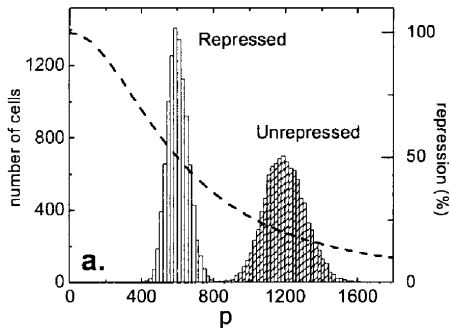
la ecuación maestra queda

$$\dot{f}_{q_i} = \sum_j [(A_{ij} q_j) (f_{q_{i-1}} - f_{q_i})] + \Gamma_{ii} q_{i+1} f_{q_{i+1}} - \Gamma_{ii} q_i f_{q_i}.$$

# Autorregulación - Modelo



[Thattai & van Oudenaarden, 2001].



[Thattai & van Oudenaarden, 2001].

- Ecuación de Hill.

$$k_R = \frac{k_R^{\max}}{1 + (p/K_d)^n}.$$

- Linearizar alrededor del promedio en estado estacionario.

$$k_R \approx k_0 - k_1 p.$$

$$A = \begin{pmatrix} 0 & 0 & 0 \\ k_0 & 0 & -k_1 \\ 0 & k_P & 0 \end{pmatrix}.$$

## Promedio

$$\langle p \rangle = \frac{1}{1 + b\phi} \cdot \frac{k_0 b}{\gamma_p}.$$

## Ruido

$$\nu_p = \frac{1 - \phi}{1 + b\phi} \cdot \frac{b}{1 + \eta} + 1.$$

$$b := \frac{k_P}{\gamma_R}, \quad \eta := \frac{\gamma_P}{\gamma_R}, \quad \phi := \frac{k_1}{\gamma_P}.$$

- Posibilidad de biestabilidad.
- Linearizar alrededor de cada punto de equilibrio.

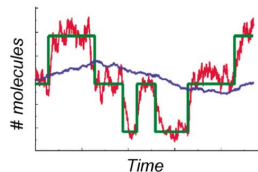
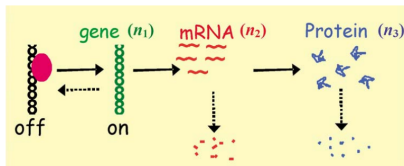


## Summing up the noise in gene networks

**Johan Paulsson**

*Department of Molecular Biology, Princeton University, Washington Road, Princeton, New Jersey 08544-1014, USA, and Department of Applied Mathematics and Theoretical Physics, Centre for Mathematical Sciences, Wilberforce Road, University of Cambridge, Cambridge CB3 0WA, UK*

[Paulsson, 2004].



[Paulsson, 2005].

$$\frac{d\sigma}{dt} = \mathbf{A}\sigma + \sigma\mathbf{A}^T + \mathbf{B}$$

Donde  $\sigma$  es la matriz de covarianzas.  $\mathbf{A}$  y  $\mathbf{B}$  dependen de las tasas.

# Promedio temporal en el ruido

$$\frac{\sigma_1^2}{\langle n_1 \rangle^2} = \frac{1}{n_1^{\max}} \frac{\lambda_1^-}{\lambda_1^+} = \frac{1 - P_{\text{on}}}{\langle n_1 \rangle}.$$

[Paulsson, 2005].

$$\frac{\sigma_2^2}{\langle n_2 \rangle^2} = \frac{1}{\langle n_2 \rangle} + \frac{1 - P_{\text{on}}}{\langle n_1 \rangle} \frac{\tau_1}{\tau_2 + \tau_1}.$$

[Paulsson, 2005].

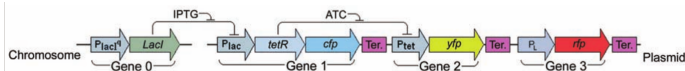
$$\frac{\overbrace{\sigma_3^2}^{\text{Total protein noise}}}{\langle n_3 \rangle^2} = \underbrace{\frac{1}{\langle n_3 \rangle}}_{\text{Poisson}} + \underbrace{\frac{1}{\langle n_2 \rangle}}_{\text{Poisson}} \underbrace{\frac{\tau_2}{\tau_3 + \tau_2}}_{\text{One-step time-averaging}} + \underbrace{\frac{1 - P_{\text{on}}}{\langle n_1 \rangle}}_{\text{Binomial}} \underbrace{\frac{\tau_2}{\tau_2 + \tau_3} \frac{\tau_1}{\tau_1 + \tau_3} \frac{\tau_1 + \tau_3 + \tau_1 \tau_3 / \tau_2}{\tau_1 + \tau_2}}_{\text{Two-step time-averaging}}.$$

[Paulsson, 2005].

# Noise Propagation in Gene Networks

Juan M. Pedraza and Alexander van Oudenaarden\*

[Pedraza & van Oudenaarden, 2005].



[Pedraza & van Oudenaarden, 2005].

# Ecuación de Langevin - Gen 0

Ecuación determinista con términos de ruido. Para el gen 0

$$\dot{p}_0 = k - \gamma p_0 + \mu_0 + \xi_0.$$

Los términos de ruido cumplen:

$$\langle \mu_0 \rangle = \langle \xi_0 \rangle = 0,$$

$$\langle \mu_0(t) \mu_0(t + \tau) \rangle = q_{0_{\text{int}}} \delta(\tau) = 2\gamma \tilde{b}_0 \bar{p}_0 \delta(\tau),$$

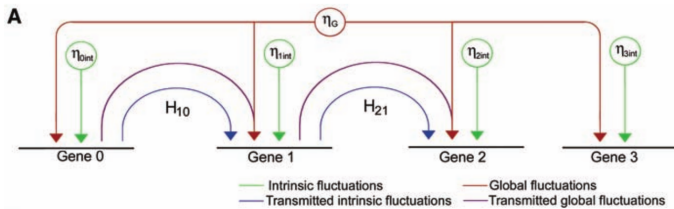
$$\langle \xi_0(t) \xi_0(t + \tau) \rangle = q_{0_G} \delta(\tau) = 2\gamma \eta_G^2 \bar{p}_0^2 \delta(\tau),$$

$$\langle \mu_0(t) \xi_0(t + \tau) \rangle = 0.$$

Luego de hacer el proceso:

$$\eta_0^2 = \eta_{0_{\text{int}}}^2 + \eta_{0_G}^2$$

# Distintas fuentes de ruido y su propagación



[Pedraza & van Oudenaarden, 2005].

Ahora para el gen 1

$$\dot{p}_1(t) = Nf_1(p_0) - \gamma p_1 + \mu_1 + \xi_1$$

Además de las anteriores autocorrelaciones, hay que incluir:

$$\langle \xi_0(t) \xi_1(t + \tau) \rangle = 2\gamma\eta_G^2 \bar{p}_0 \bar{p}_1 \delta(\tau),$$

$$\langle \mu_0(t) \mu_1(t + \tau) \rangle = 0.$$

Se obtiene al final

$$\eta_1^2 = \eta_{1\text{int}}^2 + \frac{1}{2} H_{10}^2 \eta_{0\text{int}}^2 + \eta_G^2 \left( 1 + \frac{1}{2} H_{10}^2 - H_{10} \right) + \frac{1}{2} \eta_N^2$$

Y similarmente para el gen 2

$$\eta_2^2 = \eta_{2\text{int}}^2 + \frac{1}{2}H_{21}^2\eta_{1\text{int}}^2 + \frac{3}{8}H_{21}^2H_{10}^2\eta_{0\text{int}}^2 + \eta_G^2 \left( 1 + \frac{1}{2}H_{21}^2 + \frac{3}{8}H_{21}^2H_{10}^2 - H_{21} - \frac{3}{4}H_{21}^2H_{10} + \frac{1}{2}H_{21}H_{10} \right) + \eta_N^2 \left( \frac{1}{2} + \frac{3}{8}H_{21}^2 - \frac{3}{4}H_{21} \right).$$

## Random partitioning of molecules at cell division

Dann Huh<sup>a,b</sup> and Johan Paulsson<sup>a,1</sup>

<sup>a</sup>Department of Systems Biology, Harvard University, Boston, MA 02115; and <sup>b</sup>Department of Chemistry and Chemical Biology, Harvard University, Cambridge, MA 02138

[Huh & Paulsson, 2011b].

Para un componente  $X$ , donde  $L$  y  $R$  copias se segregan a cada hija:

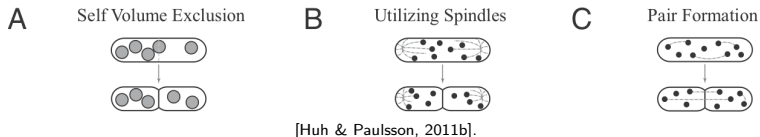
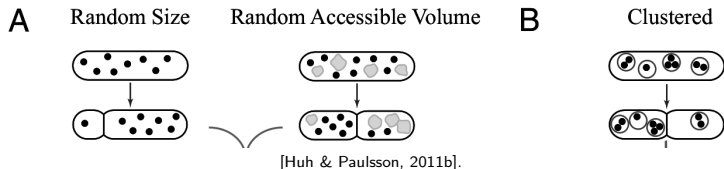
$$Q_X^2 = \frac{\langle (L - R)^2 \rangle}{\langle X \rangle^2}$$

Para segregación independiente:

$$Q_X = \frac{1}{\sqrt{X}}$$



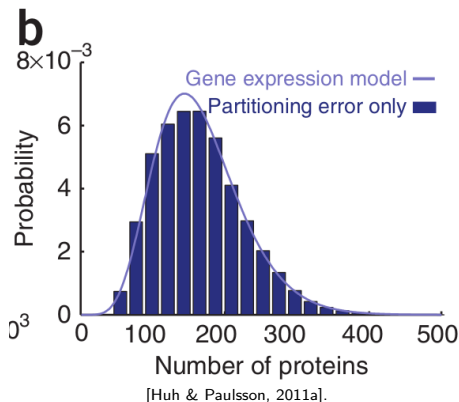
# Segregación ordenada y desordenada



Para los mecanismos considerados

$$Q_X^2 = \frac{A}{X}, \quad \text{donde} \quad \begin{cases} A = 1 & \text{para segregación independiente,} \\ A < 1 & \text{para segregación ordenada,} \\ A > 1 & \text{para segregación desordenada.} \end{cases}$$

# Consecuencias de errores de partición

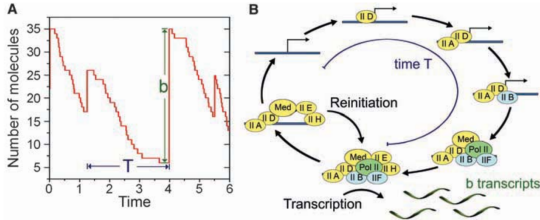


- Error por segregación desordenada vs. correcciones por ordenada.
- Hay que controlar cada componente por separado (vs. *feedback* negativo para expresión genética) e.g. segregación en clusters.

# Effects of Molecular Memory and Bursting on Fluctuations in Gene Expression

Juan M. Pedraza<sup>1</sup> and Johan Paulsson<sup>1,2\*</sup>


[Pedraza & Paulsson, 2008].




[Pedraza & Paulsson, 2008].


$$\frac{\sigma_p^2}{\langle p \rangle^2} = \frac{1}{\langle p \rangle} + \frac{1}{\langle r \rangle} \cdot \frac{\tau_r}{\tau_r + \tau_p} \cdot \frac{\langle b \rangle (\sigma_T^2 / \langle T \rangle^2 + \sigma_b^2 / \langle b \rangle^2) + 1}{2}$$

- Considerar las no-linealidades.
  - Solucionar exactamente la ecuación maestra.
  - Considerar la dinámica temporal del ruido.
  - Posibilidad de usar herramientas teóricas adicionales.
- 
- Contar moléculas individuales.
  - Seguir la dinámica temporal de los componentes celulares.

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