

Binary to graded response conversion in autoregulated genes: transcriptional leakage vs. noise



Anna Ochab-Marcinek
Institute of Physical Chemistry,
Polish Academy of Sciences, Warsaw, Poland
Micro and Macro Systems in Life Sciences
8 - 12 June 2015, Będlewo

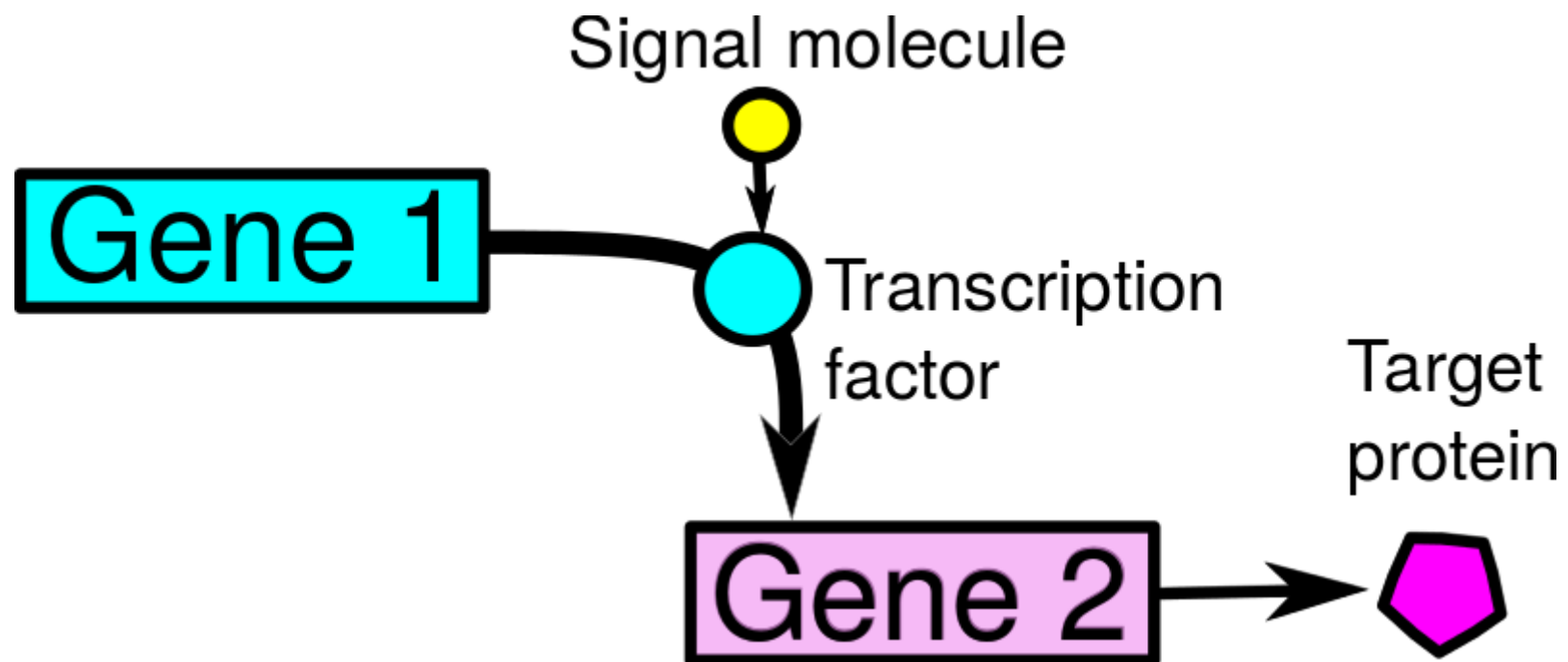


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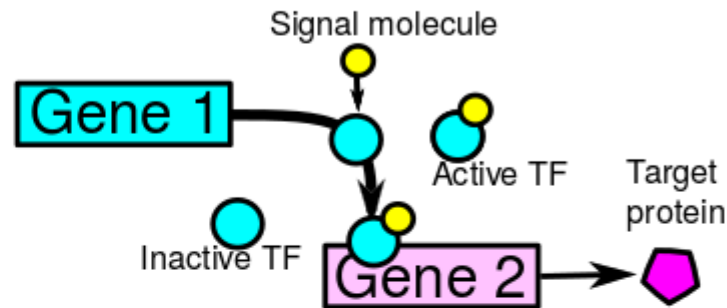


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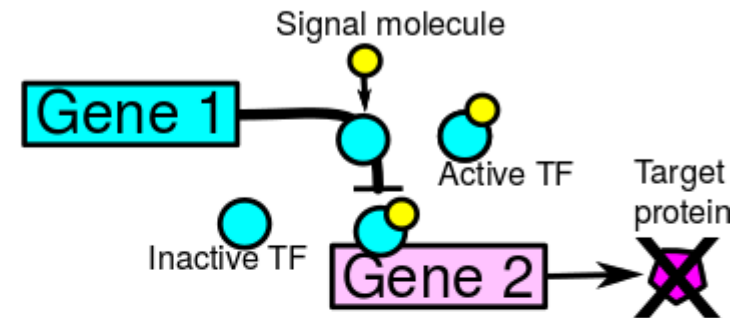


Positive

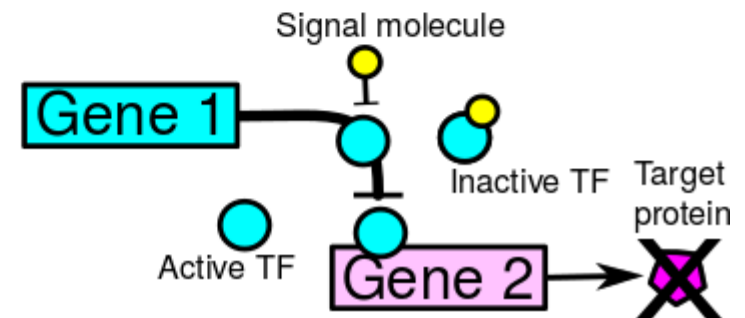
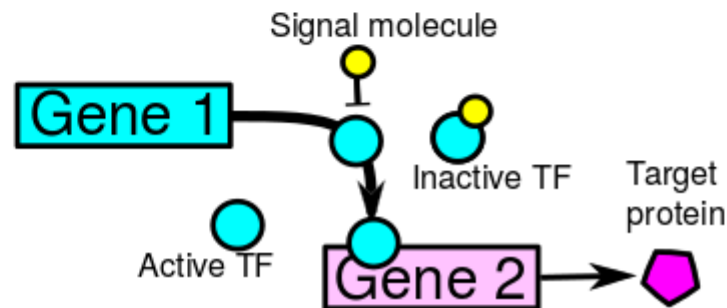
Activation

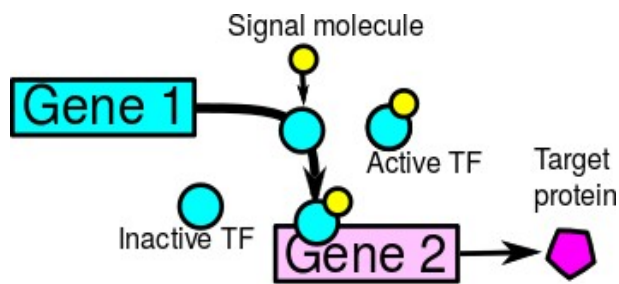


Repression



Negative





Binary / graded response

Inducer:



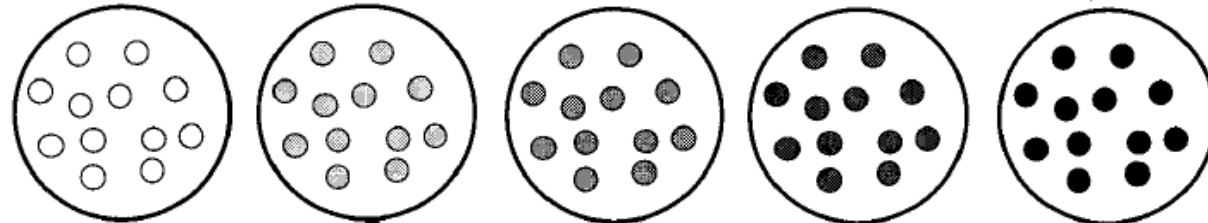
A. Bulk Assay



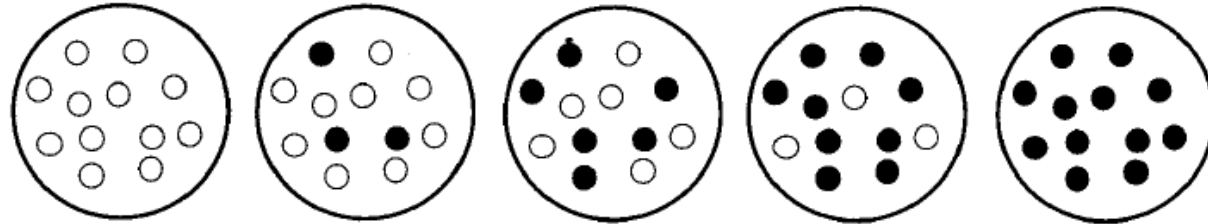
B. Single Cell Mechanisms

Units of activity

Graded Response

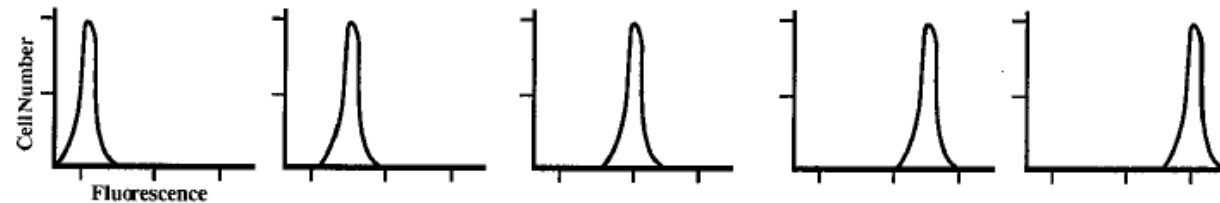


Threshold Response

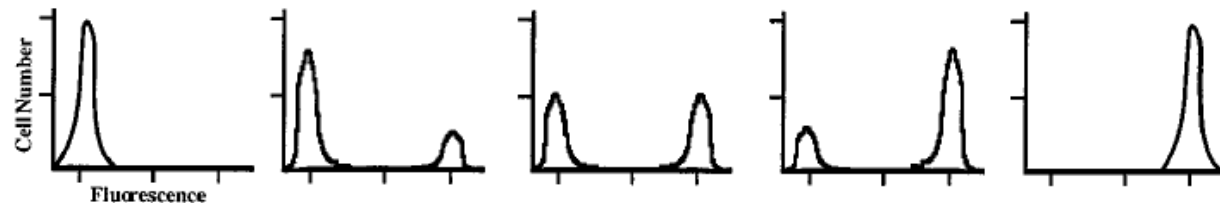


C. Single Cell Assay (FACS):

Graded Response

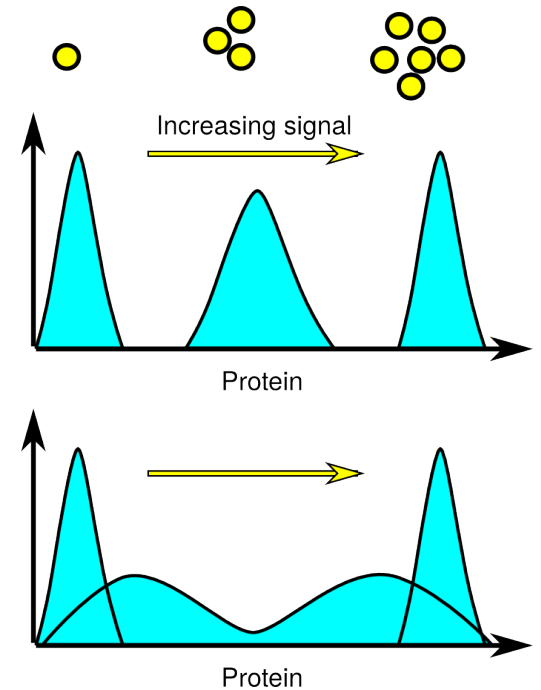


Threshold Response



Possible functions of binary/graded responses

- Graded: Precise
- Binary: Bet hedging

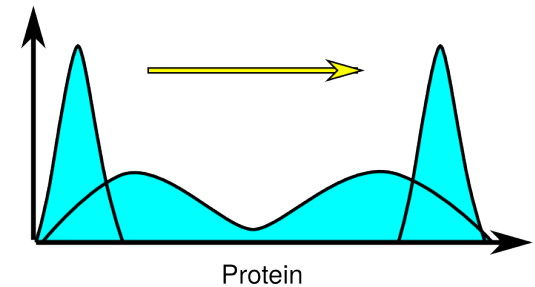
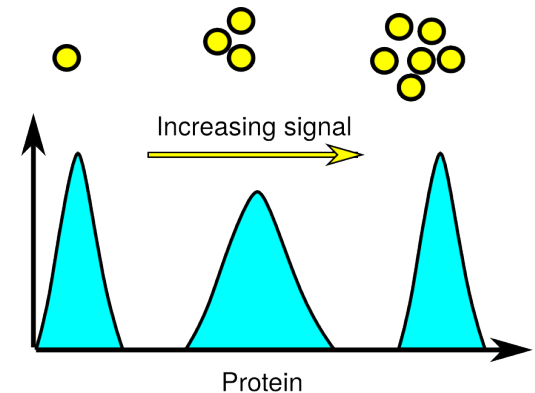
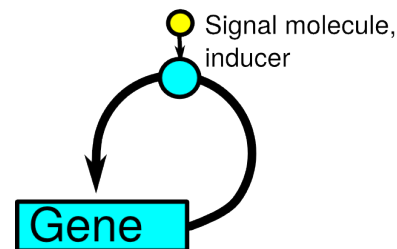
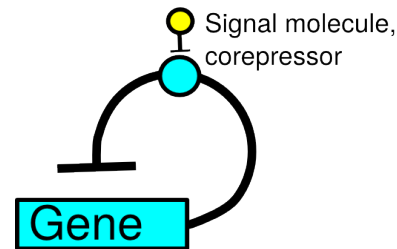


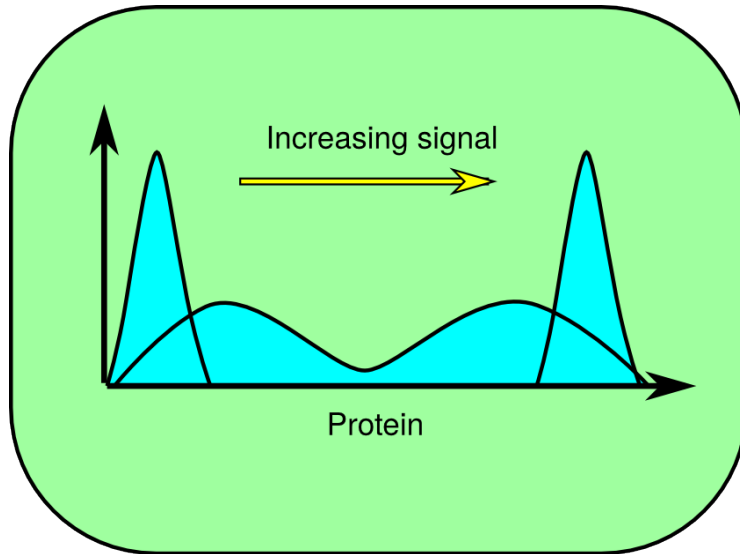
Self-regulation

- Common knowledge:

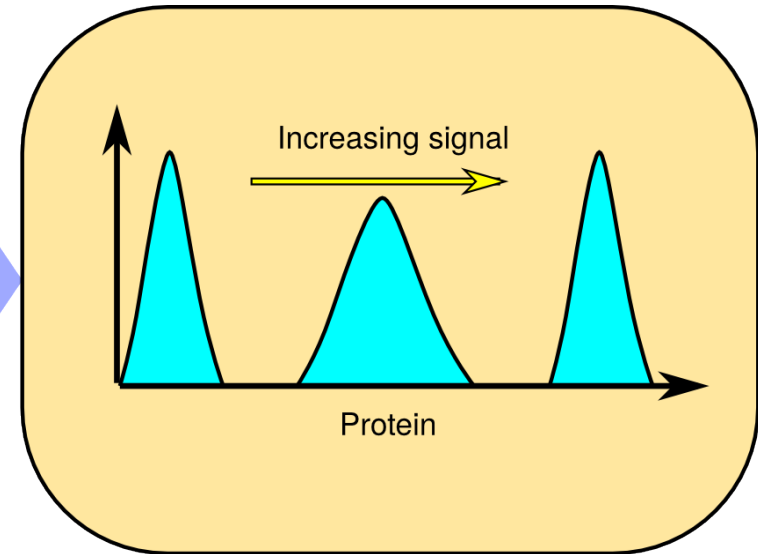
Negative
autoregulation →
unimodal
distributions →
graded response

Positive
autoregulation →
bimodal distributions
→ binary response?

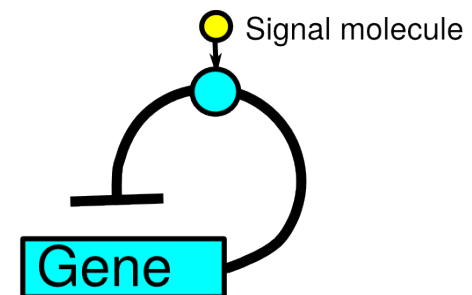
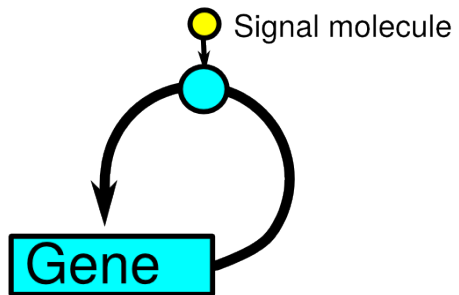


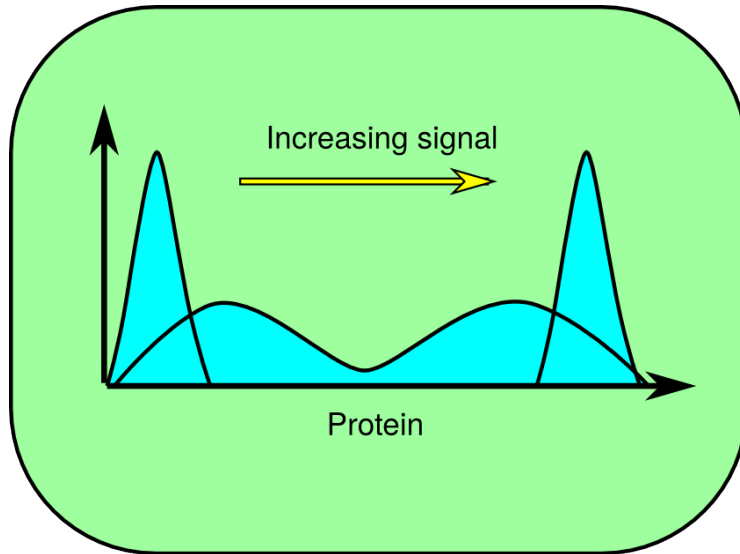


Environment 1: Binary response preferred

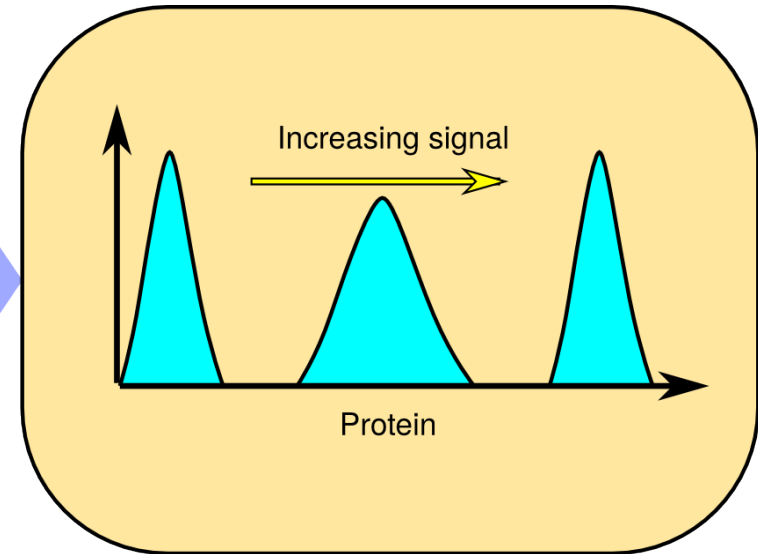


Environment 2: Graded response preferred

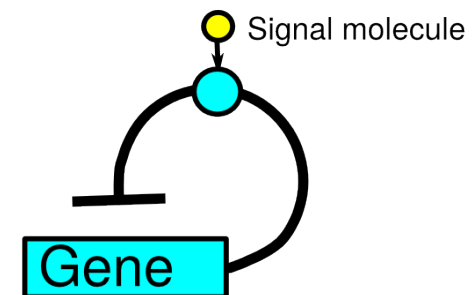
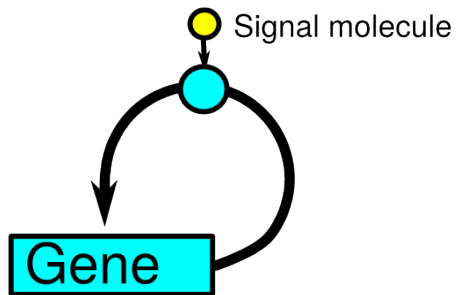




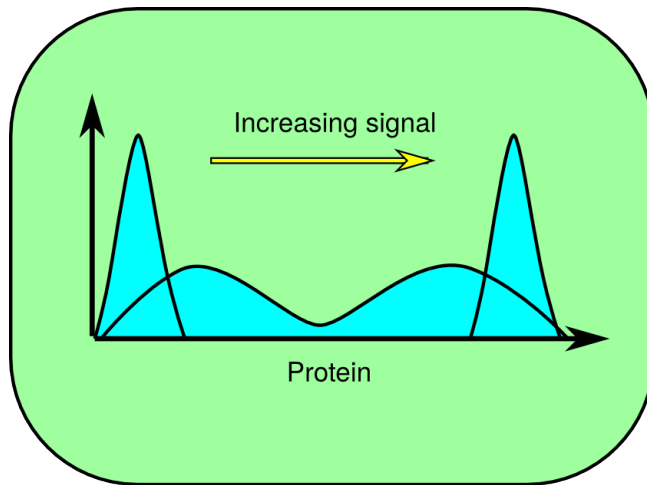
Environment 1: Binary response preferred



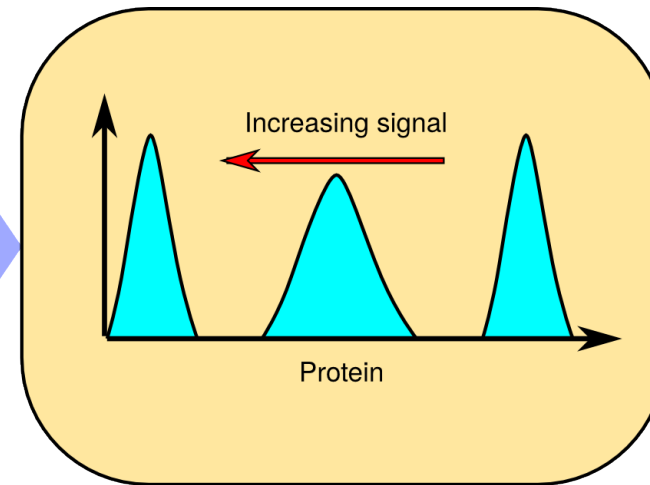
Environment 2: Graded response preferred



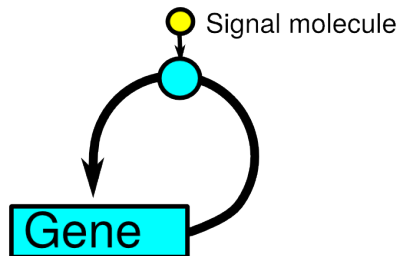
Not so easy!



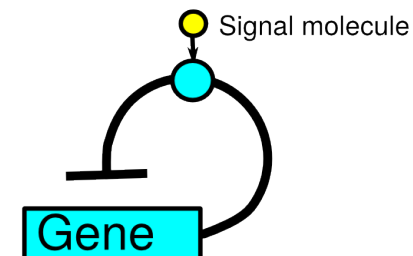
Environment 1: Binary response preferred



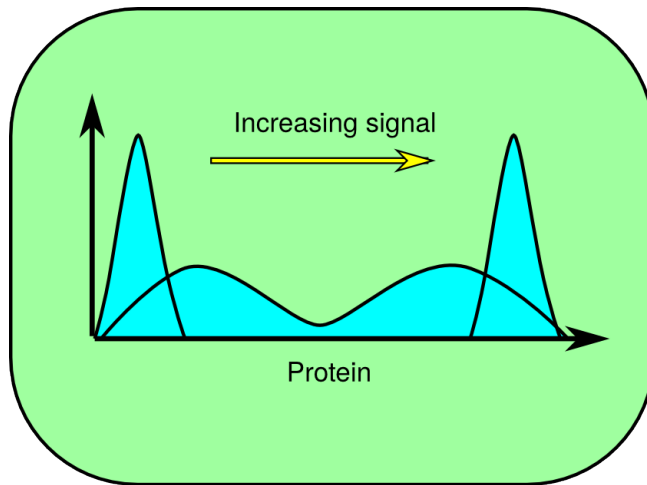
Environment 2: Graded response preferred



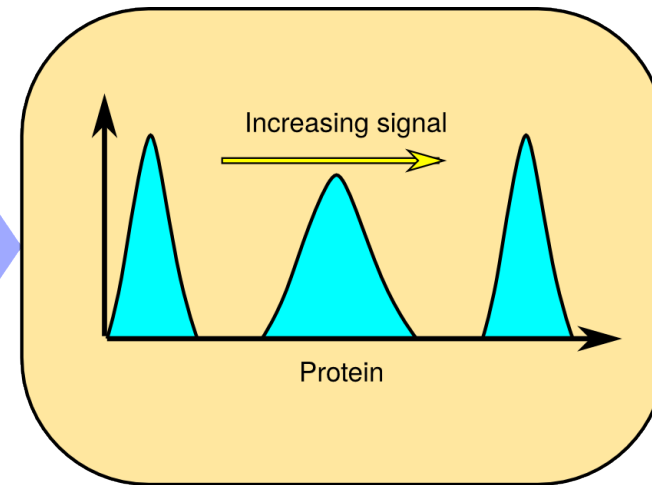
More effectors →
better transcription factor binding →
more activation



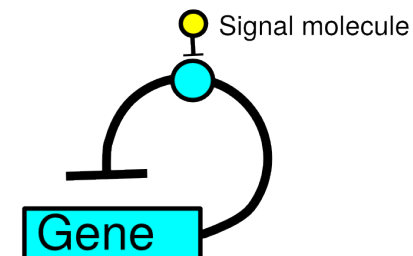
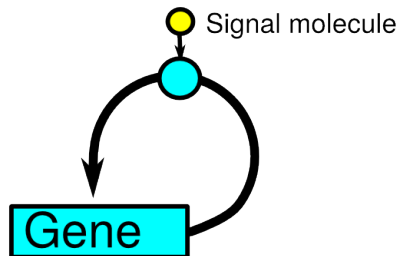
More effectors →
better transcription factor binding →
more repression



Environment 1: Binary response preferred

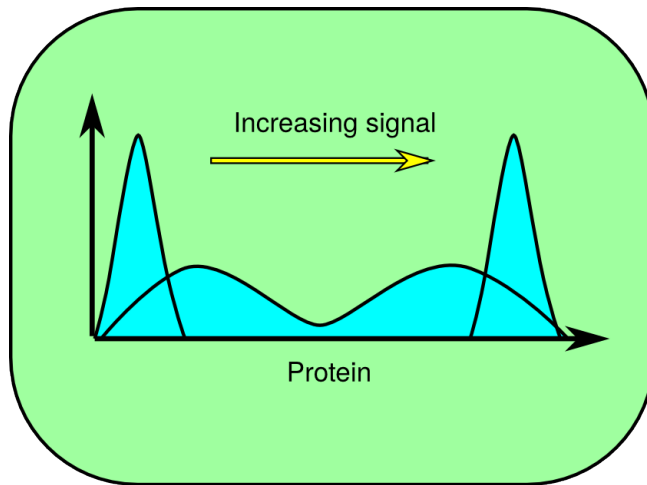


Environment 2: Graded response preferred

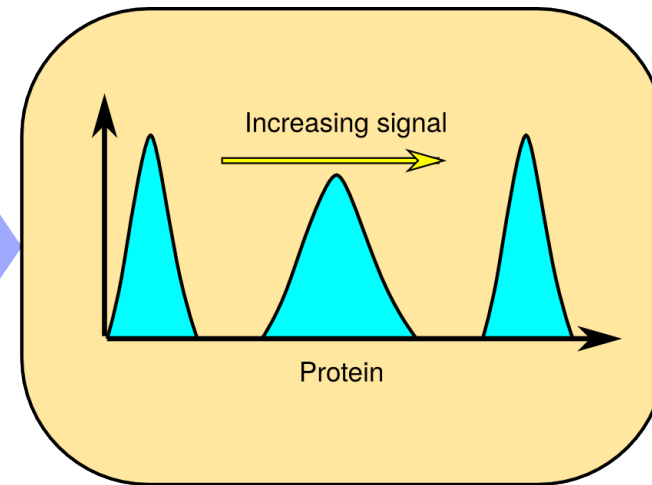


More effectors →
better transcription factor binding →
more activation

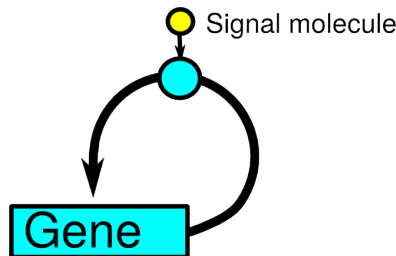
More effectors →
worse transcription factor binding →
less repression



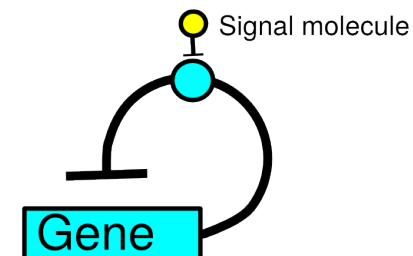
Environment 1: Binary response preferred



Environment 2: Graded response preferred



More effectors →
better transcription factor binding →
more activation

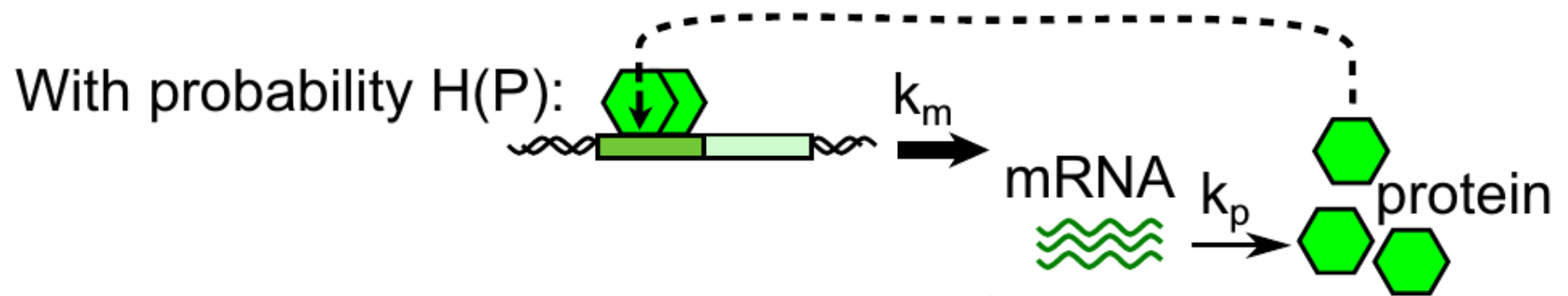


More effectors →
worse transcription factor binding →
less repression

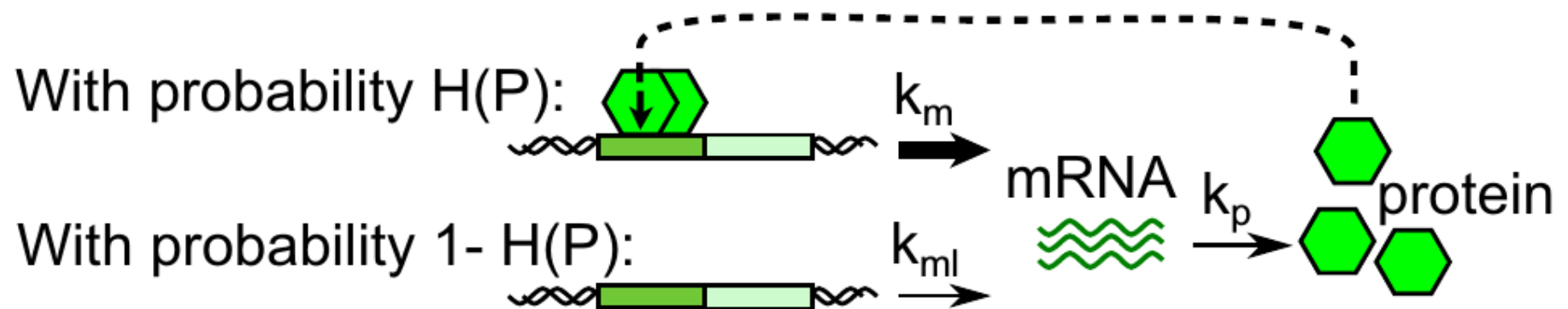
Multiple mutations needed:

- Transcription factor: Activator → repressor
- Effector: Inducer → corepressor

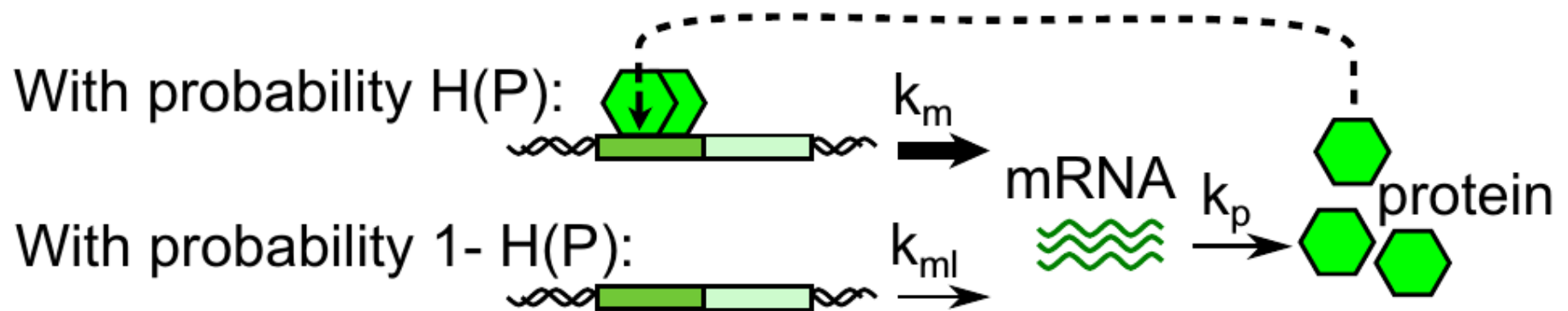
Transcriptional leakage (basal expression)



Transcriptional leakage (basal expression)



Transcriptional leakage (basal expression)



- No tight control over the promoter.
- Some level of transcription is maintained even when the promoter is in the *off* state.
- To date, the role of transcriptional leakage has been underappreciated.
- Most often described as unfavorable (for an experimenter).
- Is it favorable for cells?

Deterministic description of an autoregulated gene

- Rate equations:

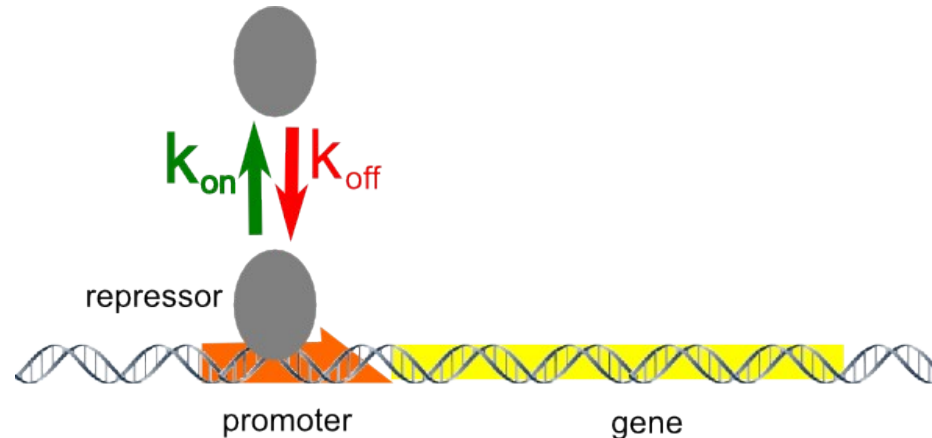
$$\frac{dM}{dt} = k_m h(\mathbf{P}) - k_{dm} M, \quad \frac{dP}{dt} = k_p M - k_{dp} P$$

- Transcription rate:
$$\begin{aligned} h(P) &= k_m H(P) + k_{ml}(1 - H(P)) = \\ &= H(P) \left(1 - \frac{k_{ml}}{k_m}\right) + \frac{k_{ml}}{k_m} = \\ &= H(P)(1 - \epsilon) + \epsilon \end{aligned}$$

- Transcription factor binding governed by Hill kinetics:

$$H(P) = \frac{1}{1 + cP^n}$$

Hill / Michaelis-Menten kinetics



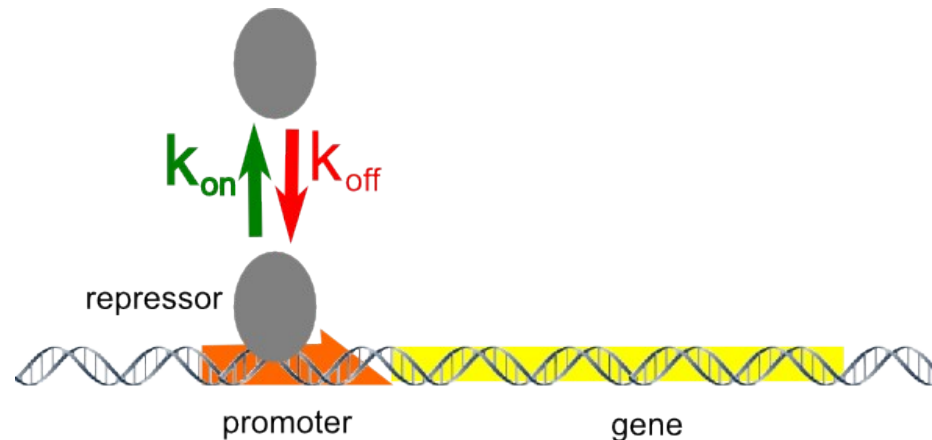
Repression:

Transcription when the operator is free

$$\frac{dM}{dt} = k_m O - k_{dm} M$$

O: probability that the operator is free

Hill / Michaelis-Menten kinetics



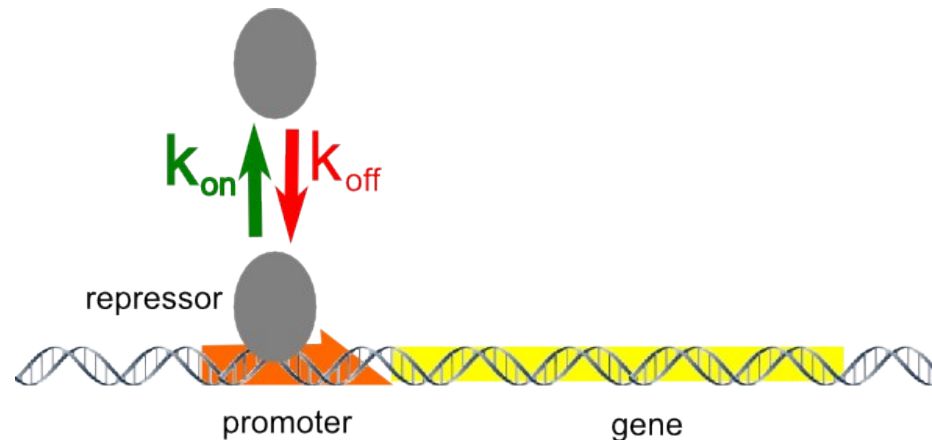
O : probability that the operator is free

O_R : probability that the operator is occupied

At steady state:

$$k_{on} \cdot R \cdot O = k_{off} \cdot O_R \quad \rightarrow \quad O_R = \frac{k_{on}}{k_{off}} R \cdot O$$

Hill / Michaelis-Menten kinetics



$$O + O_R = 1$$

$$O \left(1 + \frac{k_{on}}{k_{off}} R \right) = 1$$

$$O \equiv h(R) = \frac{1}{1 + \frac{k_{on}}{k_{off}} R}$$

Hill kinetics, n binding sites

- Detailed balance

$$k_{\text{on}}^1 R \cdot O = k_{\text{off}}^1 RO, \quad \dots, \quad k_{\text{on}}^n R \cdot R_{n-1}O = k_{\text{off}}^n R_n O$$

- Probabilities sum up to 1

$$O + R \cdot O \frac{k_{\text{on}}^1}{k_{\text{off}}^1} + \dots + R \cdot R_{n-1}O \frac{k_{\text{on}}^n}{k_{\text{off}}^n} = 1$$

- Full dose-response function

$$h(R) = \left(1 + \frac{k_{\text{on}}^1}{k_{\text{off}}^1} R + \dots + \frac{k_{\text{on}}^1 \cdot \dots \cdot k_{\text{on}}^n}{k_{\text{off}}^1 \cdot \dots \cdot k_{\text{off}}^n} R^n \right)^{-1}$$

- At strong cooperativity, Hill function:

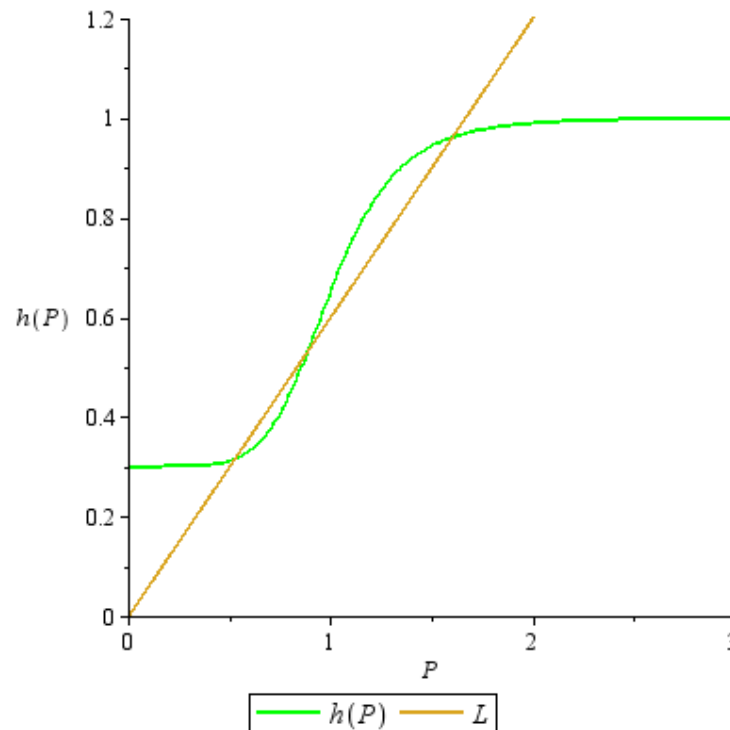
$$h(R) = \left(1 + \frac{k_{\text{on}}^1 \cdot \dots \cdot k_{\text{on}}^n}{k_{\text{off}}^1 \cdot \dots \cdot k_{\text{off}}^n} R^n \right)^{-1}$$

Deterministic description of an autoregulated gene

- Rate equations:

$$\frac{dM}{dt} = k_m h(\mathbf{P}) - k_{dm} M, \quad \frac{dP}{dt} = k_p M - k_{dp} P$$

- Steady states: $H(P)(1 - \epsilon) + \epsilon = \frac{1}{\alpha\beta} P$ $\alpha = k_m/k_{dp}$
 $\beta = k_p/k_{dm}$



Stochastic description

$$\frac{\partial p(P)}{\partial t} = \frac{\partial}{\partial P} [k_{dp} P p(P)] + k_m \int_0^P dP' w(P, P') p(P')$$

- Hybrid model (Friedman, PRL 2006)
- Deterministic degradation
- Production in stochastic bursts
- Exponential distribution of burst sizes

Stochastic description

- Steady state solution with leakage (Friedman, PRL 2006; Ochab-Marcinek, Tabaka, PRE 2015):

$$\begin{aligned} p(P) &= A P^{-1} e^{-P/\beta} e^{\alpha \int dP h(P)/P} \\ &= A P^{\alpha-1} e^{-P/\beta} H(P)^{\alpha(1-\epsilon)/n} \end{aligned}$$

- Maxima and minima given by an analogous geometric construction

$$H(P)(1 - \epsilon) + \epsilon = \frac{1}{\alpha\beta} P + \frac{1}{\alpha}$$

Stochastic description

- Steady state solution with leakage (Friedman, PRL 2006; Ochab-Marcinek, Tabaka, PRE 2015):

$$\begin{aligned} p(P) &= A P^{-1} e^{-P/\beta} e^{\alpha \int dP h(P)/P} \\ &= A P^{\alpha-1} e^{-P/\beta} H(P)^{\alpha(1-\epsilon)/n} \end{aligned}$$

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$$H(P)(1 - \epsilon) + \epsilon = \frac{1}{\alpha\beta}P + \left(\frac{1}{\alpha}\right)$$

Noise term

Stochastic description

- Steady state solution with leakage (Friedman, PRL 2006; Ochab-Marcinek, Tabaka, PRE 2015):

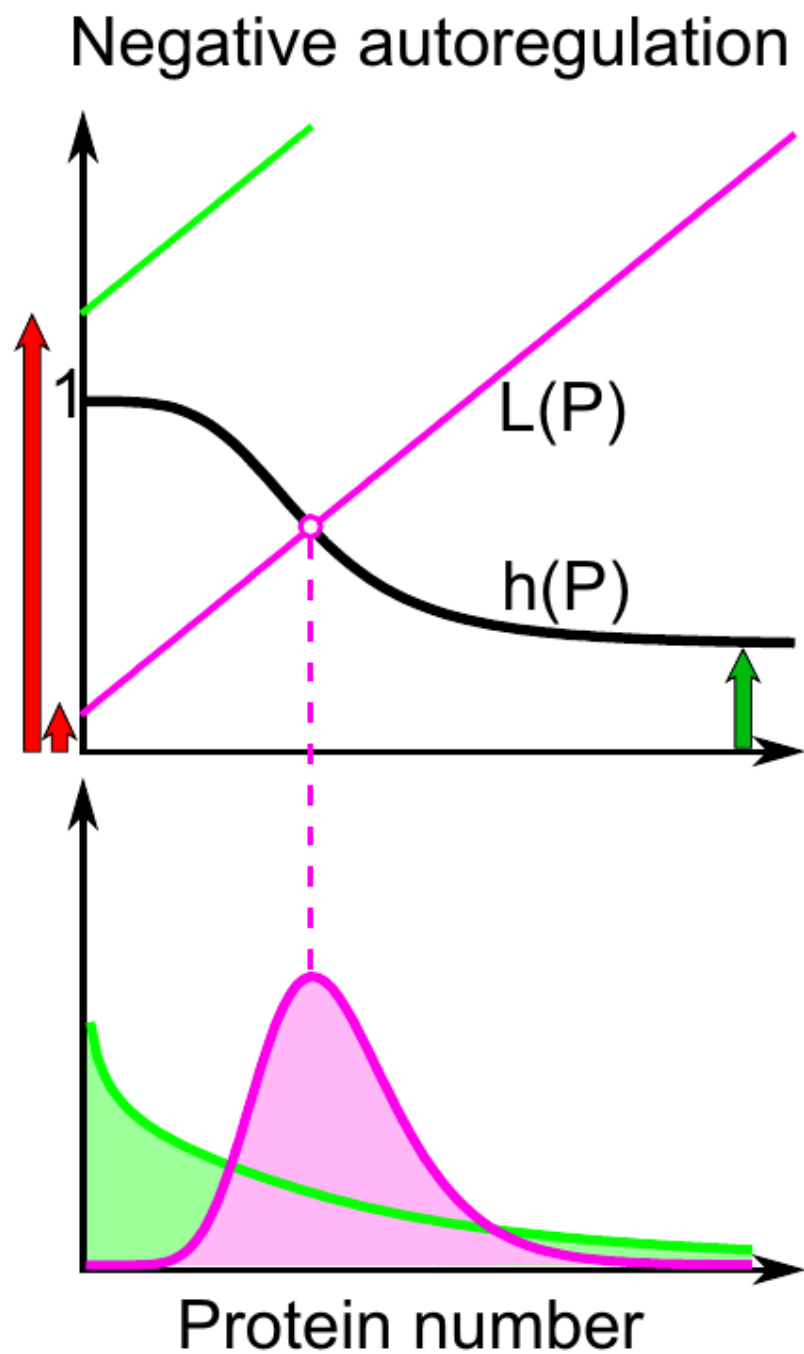
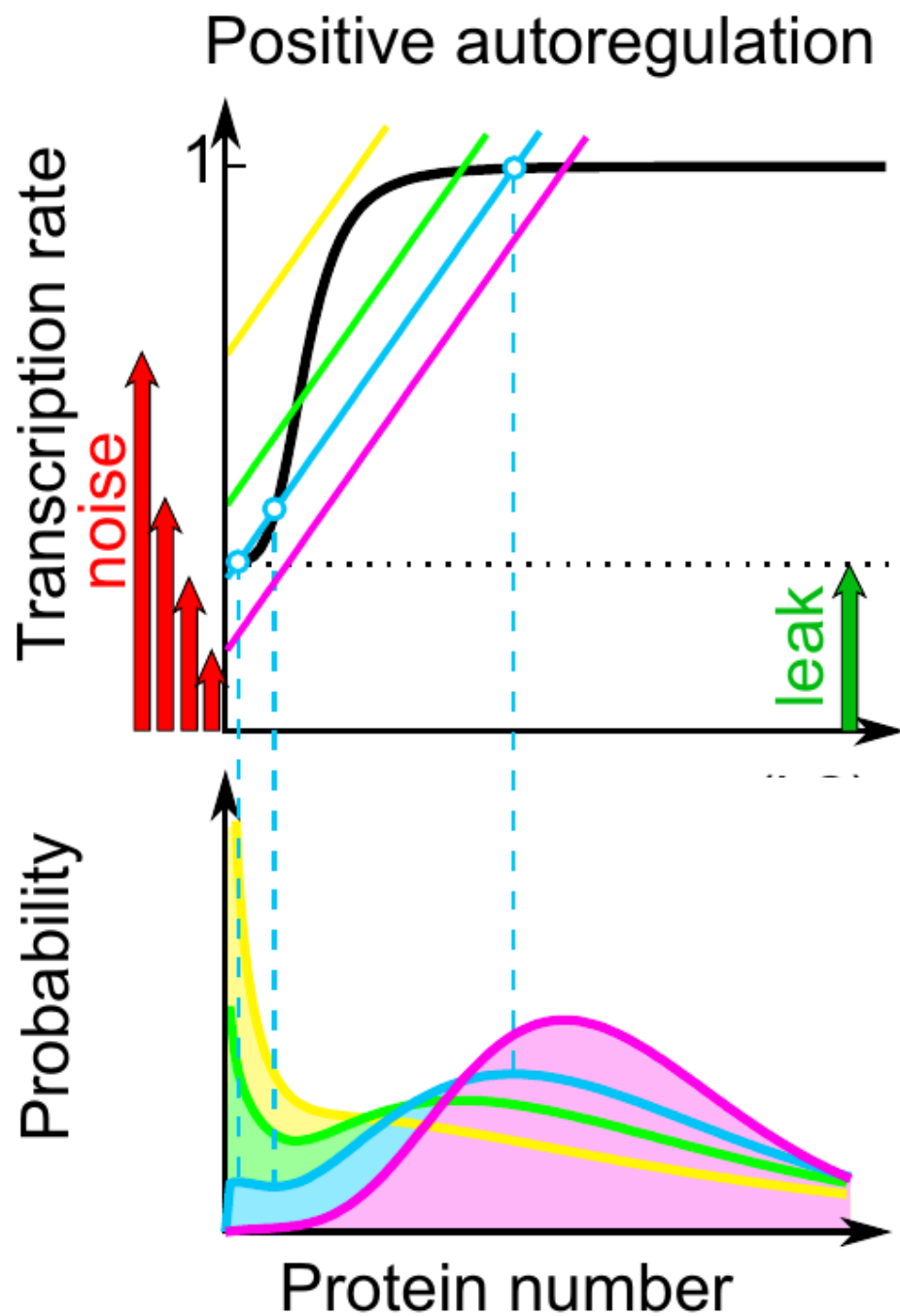
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- Maxima and minima given by an analogous geometric construction

$$H(P)(1 - \epsilon) + \epsilon = \frac{1}{\alpha\beta}P + \frac{1}{\alpha}$$

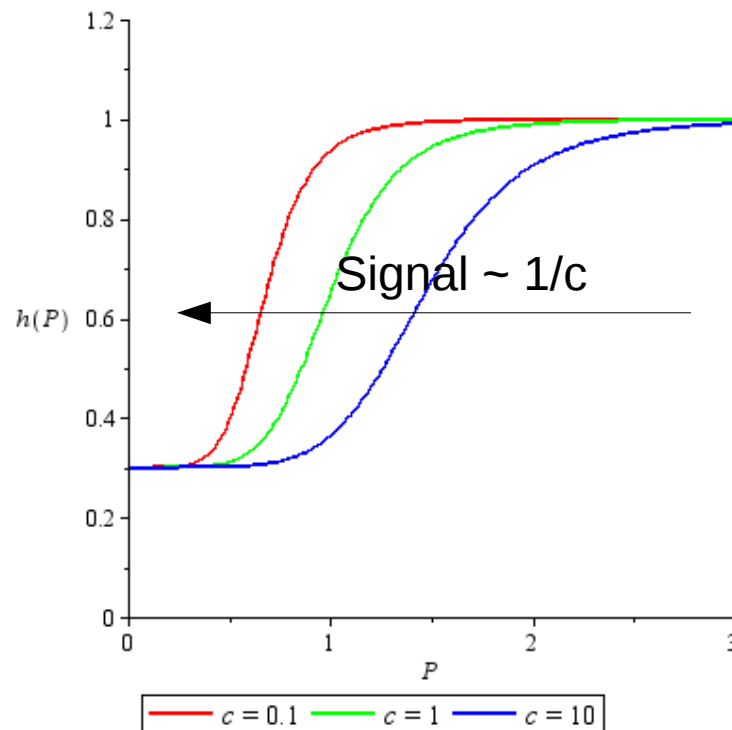
Noise term

$\alpha = k_m/k_{dp}$ Maximal frequency of protein bursts
(when gene is at its maximum expression)

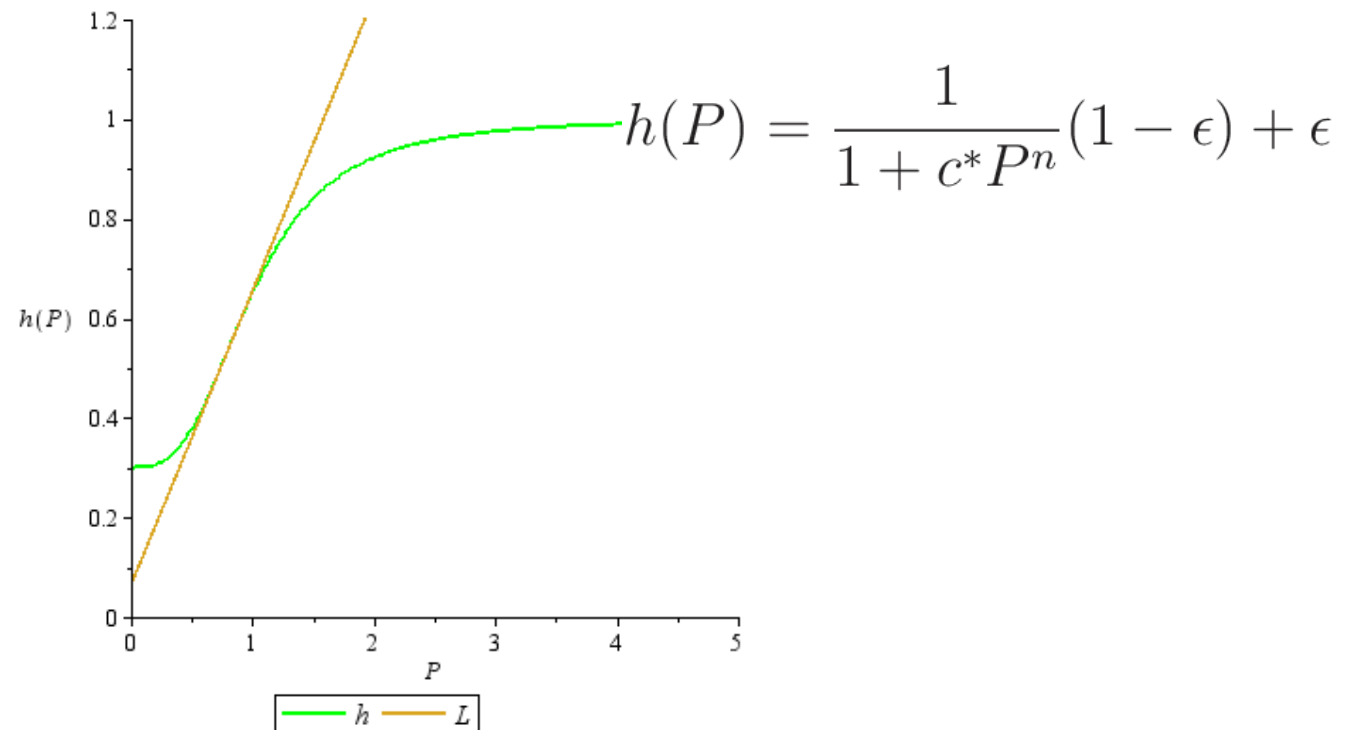


How signal changes the Hill function

- Slope increases as c decreases $H(P) = \frac{1}{1 + cP^n}$, $n < 0$

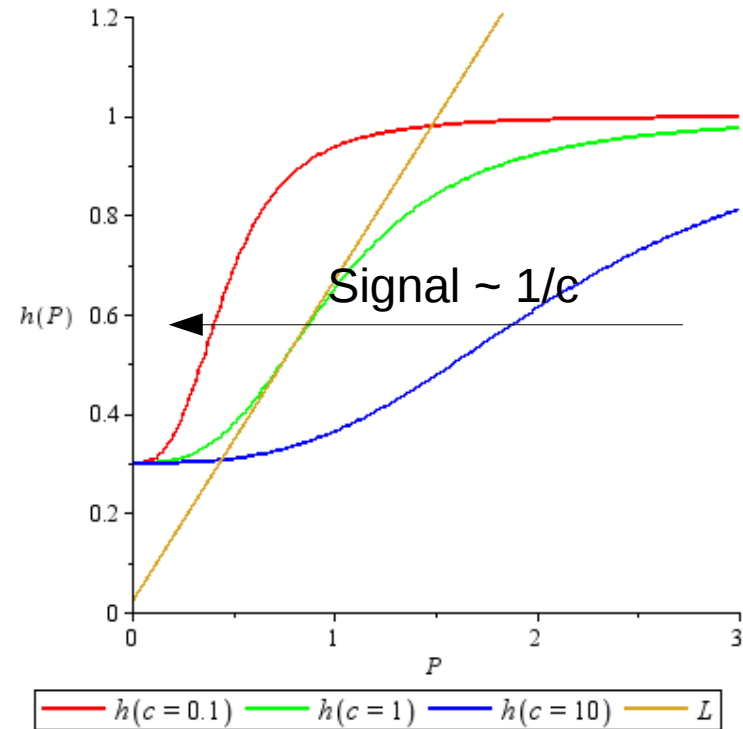
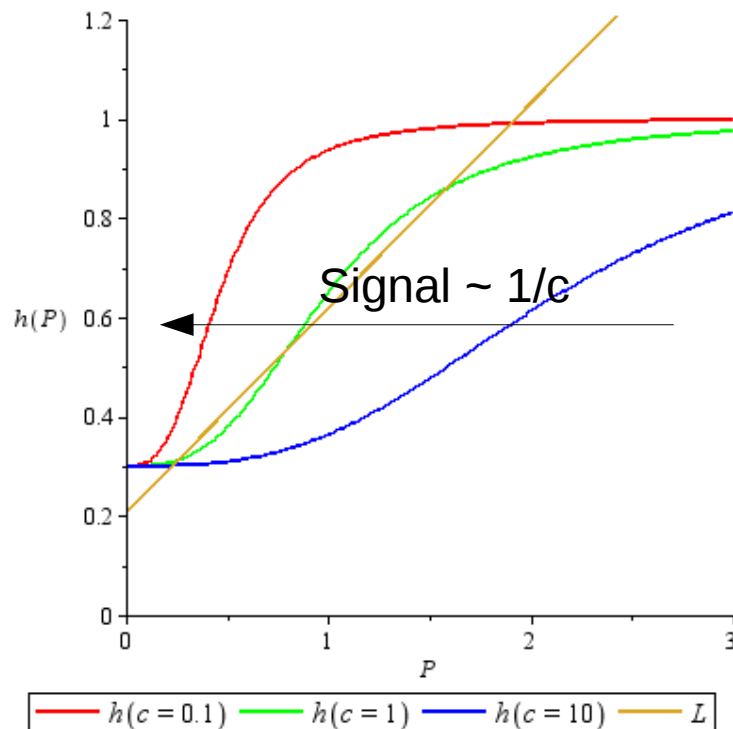


- We have certain α, β such that they define $L(P) = \frac{1}{\alpha\beta}P + \frac{1}{\alpha}$
- There exists $c=c^*$ such that $L(P)$ intersects $h(P)$ in its inflection point



Binary or graded response

- $L(P)$ intersects $h(P)$ in its inflection point
- $L(P)$ slope $<$ $h(P)$ slope in inflection point \rightarrow binary response
- $L(P)$ slope $>$ $h(P)$ slope in inflection point \rightarrow graded response



Condition for graded response

- At $c=c^*$, $L(P)$ intersects $h(P)$ in its inflection point P_p

$$h(P_p, c^*) = \frac{1}{\alpha\beta} P_p + \frac{1}{\alpha} \quad \leftarrow \text{intersection at } P_p$$

$$\frac{d}{dP_p} h(P_p, c^*) < \frac{1}{\alpha\beta} \quad \leftarrow L(P) \text{ slope} > h(P) \text{ slope in inflection point}$$

Nice properties of Hill function

$$H(P) = \frac{1}{1 + cP^n} \qquad h(P) = H(P)(1 - \epsilon) + \epsilon$$

- Inflection point: $P_p = \left(\frac{n-1}{c(n+1)} \right)^{1/n}$
- Value at inflection point: $H(P_p) = \frac{n+1}{2n}$
- Slope at inflection point: $H'(P_p) = -\frac{n^2-1}{4n P_p}$

Condition for graded response

$$h(P_p, c^*) = \frac{1}{\alpha\beta} P_p + \frac{1}{\alpha} \quad \leftarrow \text{intersection at } P_p$$

$$\frac{d}{dP_p} h(P_p, c^*) < \frac{1}{\alpha\beta} \quad \leftarrow L(P) \text{ slope} > h(P) \text{ slope in inflection point}$$

Dependence on β , c^* and P_p will disappear!

Condition for graded response

$$h(P_p, c^*) = \frac{1}{\alpha\beta} P_p + \frac{1}{\alpha} \quad \leftarrow \text{intersection at } P_p$$

$$\frac{d}{dP_p} h(P_p, c^*) < \frac{1}{\alpha\beta} \quad \leftarrow L(P) \text{ slope} > h(P) \text{ slope in inflection point}$$

$$\frac{1}{\alpha\beta} = \frac{1}{P_p} \left((1 - \epsilon) \overset{H(P_p)}{\boxed{\frac{n+1}{2n}}} + \epsilon - \frac{1}{\alpha} \right)$$

$$\overset{H'(P_p)}{(1 - \epsilon) \boxed{\frac{-(n^2 - 1)}{4n P_p}}} < \frac{1}{P_p} \left((1 - \epsilon) \frac{n+1}{2n} + \epsilon - \frac{1}{\alpha} \right)$$

Condition for graded response

$$h(P_p, c^*) = \frac{1}{\alpha\beta} P_p + \frac{1}{\alpha} \quad \leftarrow \text{intersection at } P_p$$

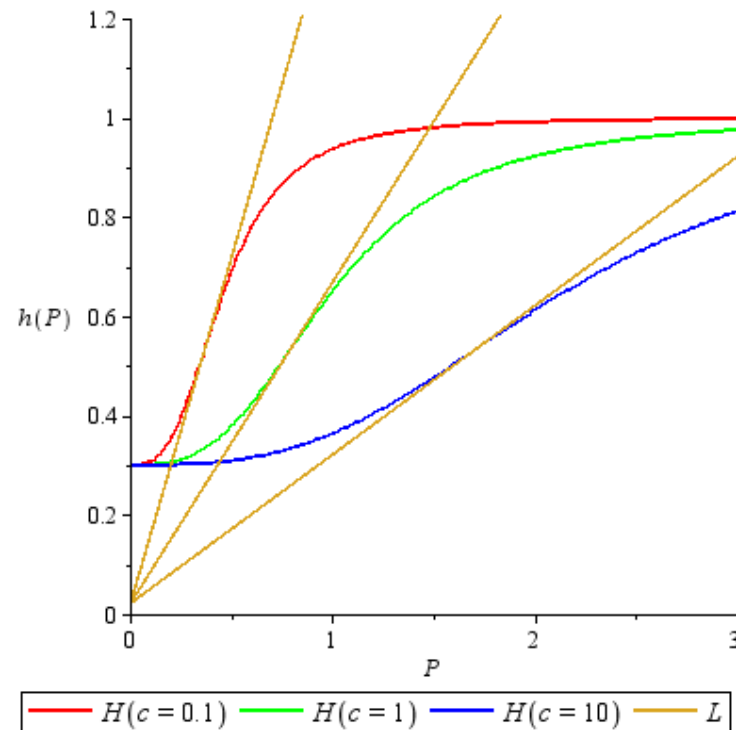
$$\frac{d}{dP_p} h(P_p, c^*) < \frac{1}{\alpha\beta} \quad \leftarrow L(P) \text{ slope} > h(P) \text{ slope in inflection point}$$

$$\frac{1}{\alpha\beta} = \frac{1}{P_p} \left((1 - \epsilon) \frac{n+1}{2n} + \epsilon - \frac{1}{\alpha} \right)$$

$$(1 - \epsilon) \frac{-(n^2 - 1)}{4n P_p} < \frac{1}{P_p} \left((1 - \epsilon) \frac{n+1}{2n} + \epsilon - \frac{1}{\alpha} \right)$$

One more nice property of Hill function

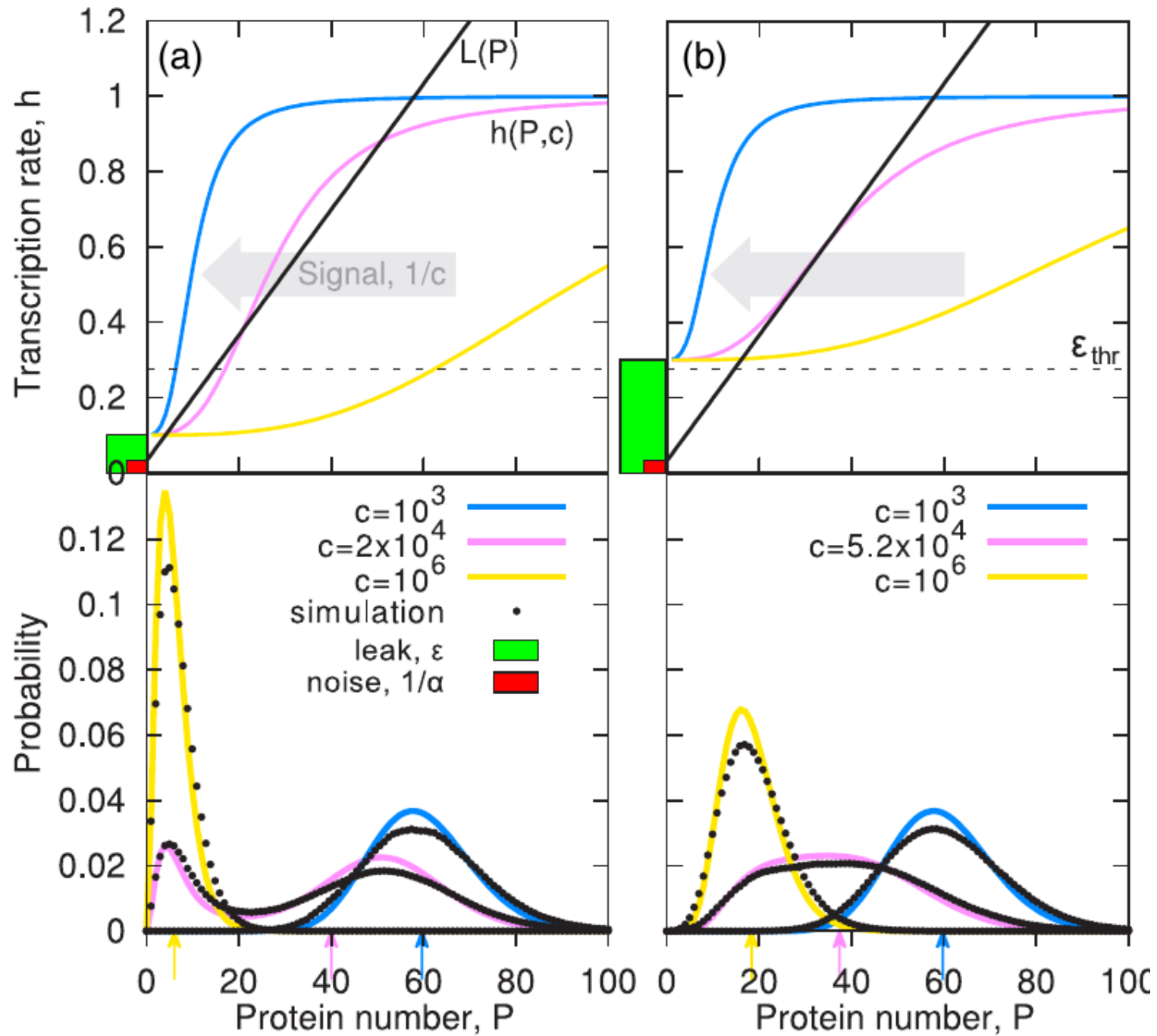
- Tangents to Hill function in its inflection point always meet at the same point



Condition for graded response

$$\epsilon > \frac{1}{\alpha} \frac{(-4n)}{(n-1)^2} + \frac{(n+1)^2}{(n-1)^2} \equiv \epsilon_{thr}$$

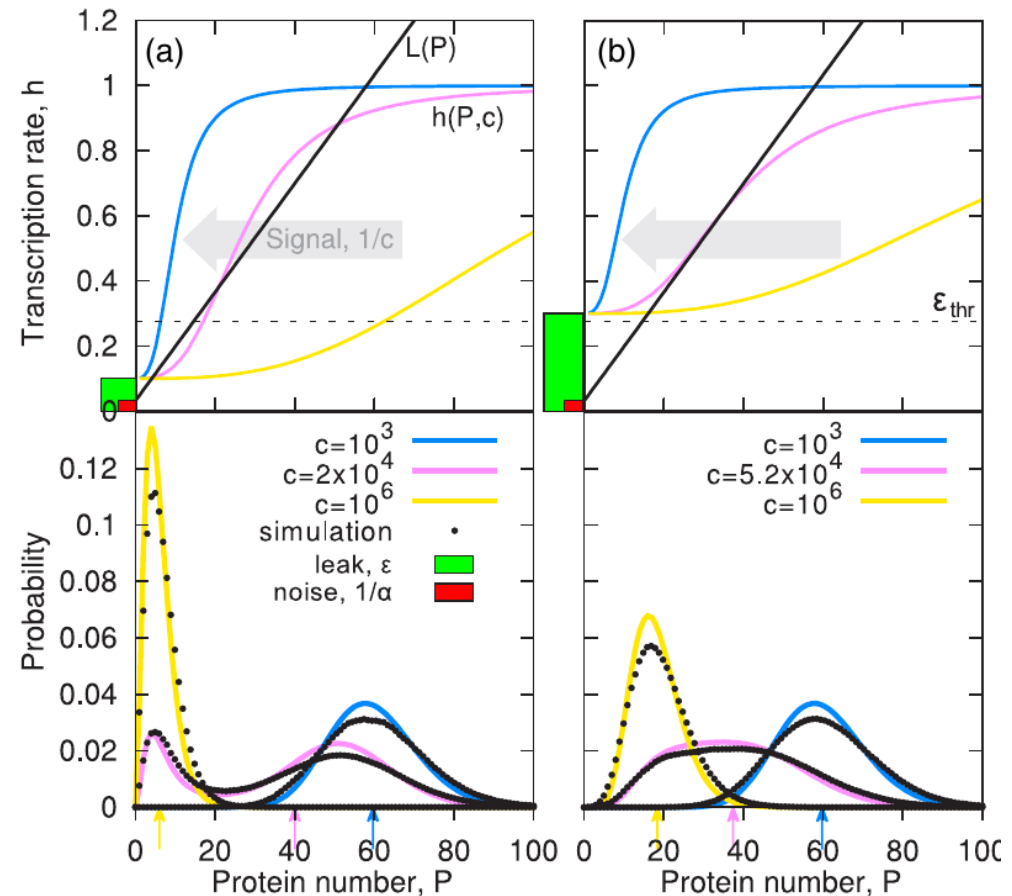
- If transcriptional leakage ϵ is greater than the threshold ϵ_{thr} , then the positively autoregulated gene will produce a graded response.
- For the leakage below that threshold, the response will be binary.



In a positively autoregulated gene, leakage acts against noise

$$\epsilon > \frac{1}{\alpha} \frac{(-4n)}{(n-1)^2} + \frac{(n+1)^2}{(n-1)^2} \equiv \epsilon_{thr}$$

- Increasing noise induces binary response
- Increasing leakage recovers graded response



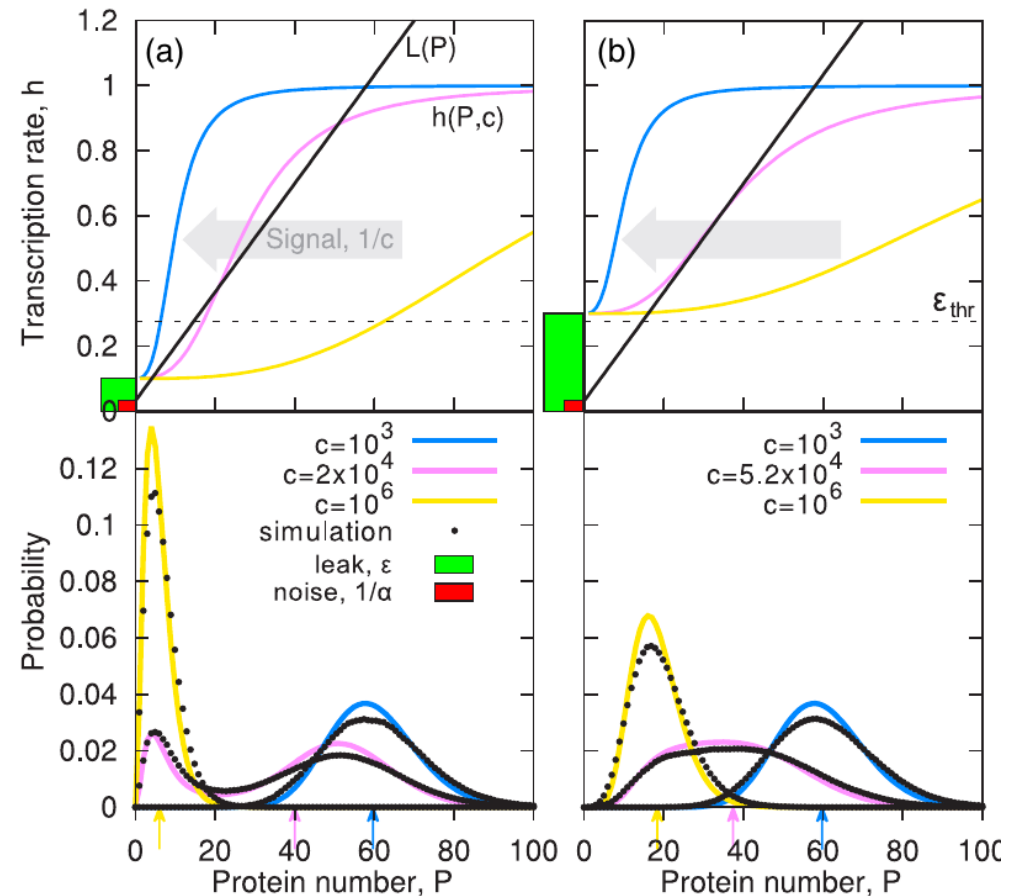
In a positively autoregulated gene, leakage acts against noise

$$\epsilon > \frac{1}{\alpha} \frac{(-4n)}{(n-1)^2} + \frac{(n+1)^2}{(n-1)^2} \equiv \epsilon_{thr}$$

- Low cooperativity: Low conversion threshold, low noise needed to obtain graded response
- High cooperativity: High conversion threshold, strong leakage needed to obtain graded response

Lowest possible threshold, for zero noise:

n	-2	-3	-4	-6
ϵ_{thr}	0.11	0.25	0.36	0.51



Summary

- Change in leaky transcription: Single mutations in the promoter (E.g. influencing RNA polymerase recruitment or binding of other TFs)
- Conversion from positive to negative autoregulation: Multiple mutations
(activator → repressor, inducer → corepressor)
- Existence of leaky transcription can be an evolutionary adaptation which facilitates conversion between binary and graded response to signal

Acknowledgements

- Marcin Tabaka, PhD, Jakub Jędrak, PhD, Institute of Physical Chemistry, Polish Academy of Sciences
- Polish Ministry of Science Iuventus Plus grant no. 0501/IP1/2013/72



Ministry of Science
and Higher Education

Republic of Poland