

Mechanistic  
links between  
cellular  
trade-offs,  
gene  
expression,  
and growth

Andrea Y.  
Weiße et al.,  
*PNAS* vol.  
112 no. 9

Description of  
the model

Varying the  
external  
medium

Relative  
transcription  
rates and  
energy levels

Gene dosage  
compensation

Adding a  
synthetic  
circuit

# Mechanistic links between cellular trade-offs, gene expression, and growth

Andrea Y. Weiße et al., *PNAS* vol. 112 no. 9

Théotime Grohens

# Outline of the presentation

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# A coarse-grained, ODE model

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- Describes intracellular levels of energy, nutrients, mRNAs and proteins
- Only 14 different variables, obeying simple differential equations obtained from chemical reactions
- Much simpler than whole-cell models, and thus simpler to reason about

# Goal of the model

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- Main goal: be able to study the trade-offs that cells have to make when growing
- Simplicity: allows us to tweak it easily and add extensions



# 3 cellular trade-offs

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- Finite energy levels: mRNA-ribosome complexes compete for energy to translate
- Finite ribosome levels: mRNAs compete for ribosomes to bind to
- Finite cell mass: proteins compete for proportion of cell mass

# Description

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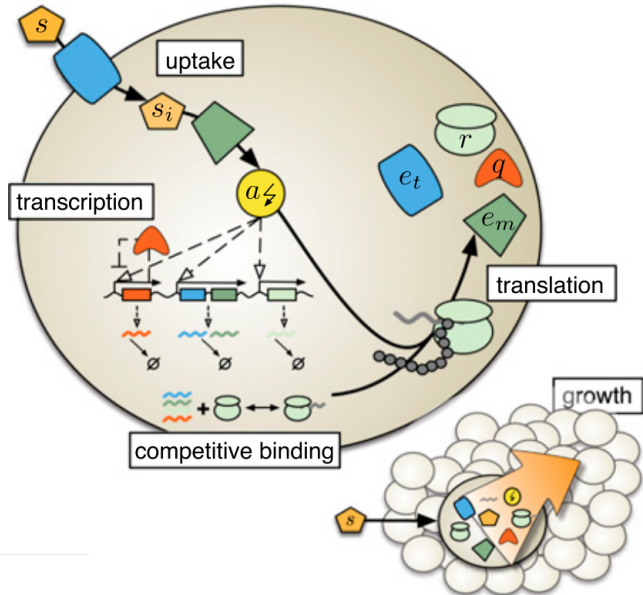
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# Differential equations

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$$\left\{ \begin{array}{l} \dot{s}_i = \nu_{imp}(e_t, s) - \nu_{cat}(e_m, s_i) - \lambda s_i \\ \dot{a} = n_s \nu_{cat}(e_m, s_i) - \sum_{x \in \{r, e_t, e_m, q\}} n_x \nu_x(c_x, a) - \lambda a \quad (1) \\ \dot{r} = \nu_r(c_r, a) - \lambda r + \sum (\nu_x(c_x, a) - k_b r m_x + k_u c_x) \\ \dot{e}_t = \nu_t(c_t, a) - \lambda e_t \\ \dot{e}_m = \nu_e(c_e, a) - \lambda e_m \\ \dot{q} = \nu_q(c_q, a) - \lambda q \\ \dot{m}_x = \omega_x(a) - (\lambda + d_m) m_x + \nu_x(c_x, a) - k_b r m_x + k_u c_x \quad (2) \\ \dot{c}_x = -\lambda c_x + k_b r m_x - k_u c_x - \nu_x(c_x, a) \end{array} \right.$$

# Differential equations

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$$\left\{ \begin{array}{ll} \nu_{imp}(e_t, s) &= e_t \frac{\nu_t s}{K_t + s} \\ \nu_{cat}(e_m, s_i) &= e_m \frac{\nu_m s_i}{K_m + s_i} \\ \nu_x(c_x, a) &= c_x \frac{\gamma(a)}{n_x} \quad (1) \\ \gamma(a) &= \gamma_{max} \frac{a}{K_\gamma + a} \\ \omega_x(a) &= w_x \frac{a}{\theta_x + a} \\ \omega_q(a) &= w_x \frac{a}{\theta_x + a} I(q) \\ I(q) &= \frac{1}{1 + (\frac{q}{K_q})^{h_q}} \\ R_t &= \sum_x c_x \\ M &= \sum_x n_x x + R_t \quad (3, \text{constant}) \\ \lambda &= \gamma(a) \frac{R_t}{M} \end{array} \right.$$

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# Nutrient efficiency and chloramphenicol

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- Varying nutrient efficiency changes the level of available energy in the cell, impacting the 1st tradeoff
- Chloramphenicol: antibiotic that inhibits translation, affects the 2nd tradeoff

# Experimental results

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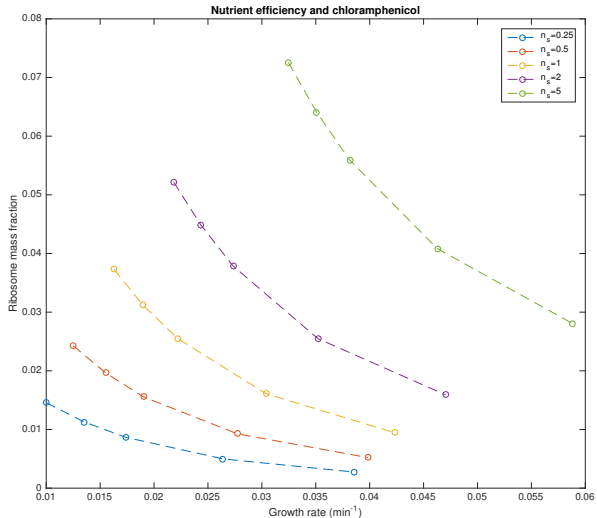
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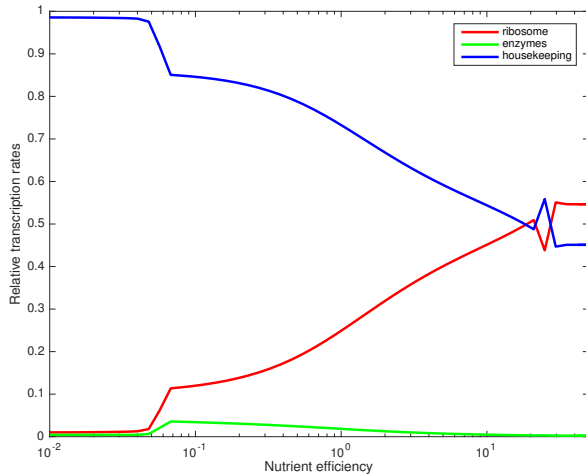


Figure: Evolution of transcription rates with nutrient efficiency.

# The cell chooses what to transcribe depending on the available energy level

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- At low energy: make more enzymes to increase energy levels
- At high energy: make more ribosomes to increase protein production

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# Gene dosage compensation

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- Delete one of two paralogous genes
- Observe the change in the expression rate
- Responsiveness:  $R(x) = \log\left(\frac{x^{\Delta y}}{\delta(x,y)x^{wt}}\right)$

# Experiments

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- Wild-type strain: with a gratuitous protein
- Protein deletion strain: halve the protein transcription
- Enzyme deletion strain: halve enzyme transcription

# Enzyme deletion strain

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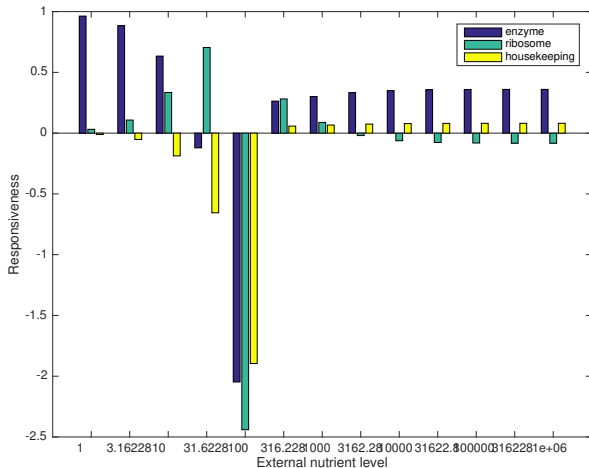


Figure: Responsiveness in the enzyme deletion strain.

# Protein deletion strain

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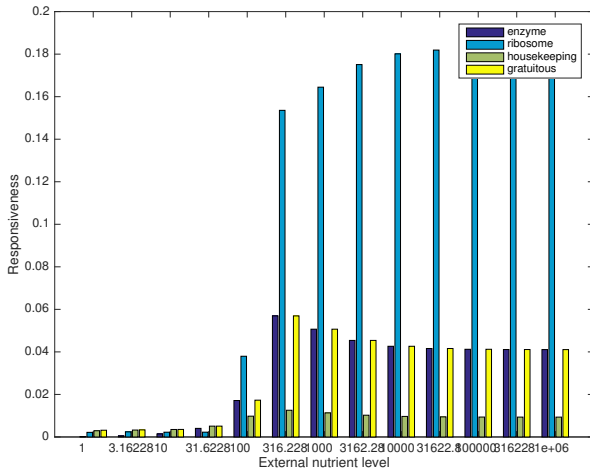


Figure: Responsiveness in the gratuitous protein deletion strain.

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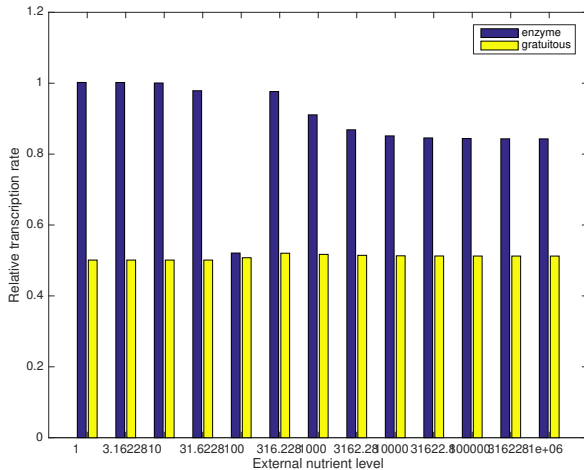


Figure: Relative transcription rates in the deletion strains.



# Responsiveness in the paper

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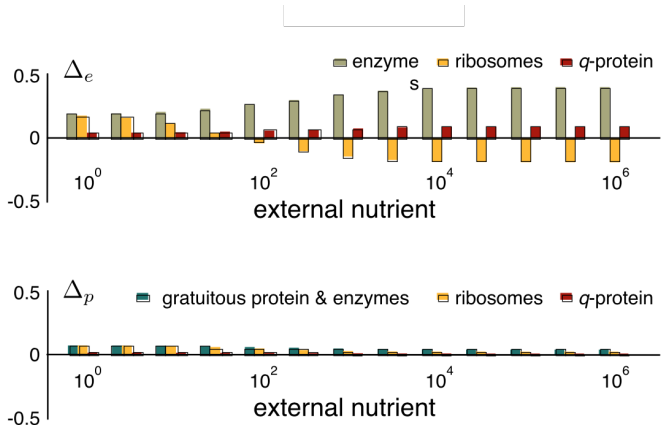
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**B**  
responsiveness

**C**  
responsiveness



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# The toggle switch

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- Two proteins: TetR and LacI
- Inhibit each other's transcription
- Don't interact with the metabolism apart from their use of cell resources

# Experiment

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- Vary the induction level of the external circuit
- Look at the relative and absolute translation (production) of the proteins involved
- Maximizing induction does not maximize output!

# Results

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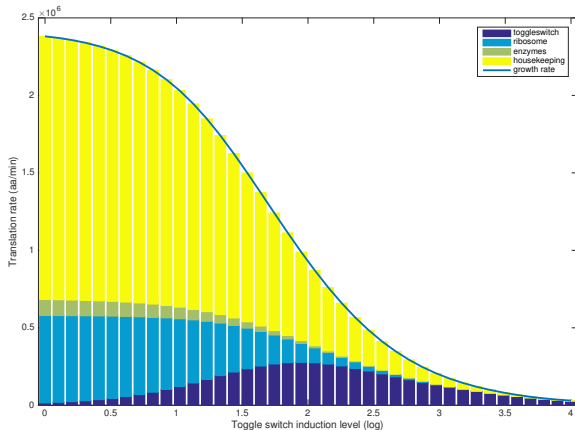


Figure: Protein transcription rates and cell growth rate (in  $\text{min}^{-1}$ ).

# Conclusion

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- Simple model: experiments are easier to make and to interpret
- The effects of the trade-offs are visible even with a very simple model
- The trade-offs interpretation does help understanding the experimental results