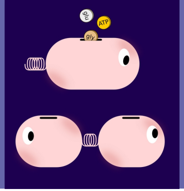
Economic Principles in Cell Biology

Vienna, July 23-26, 2025



Principles of cell growth

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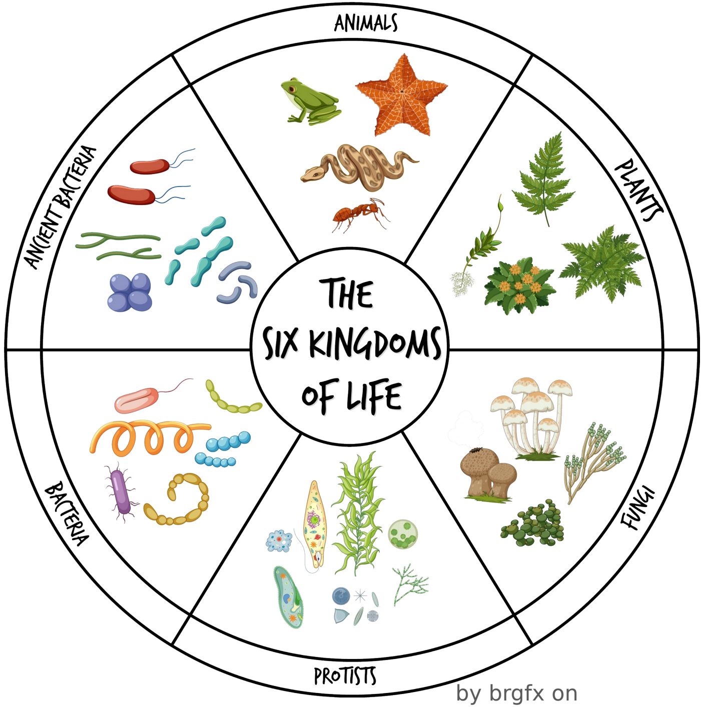
Département MathNum

Self-replication is a hallmark of life



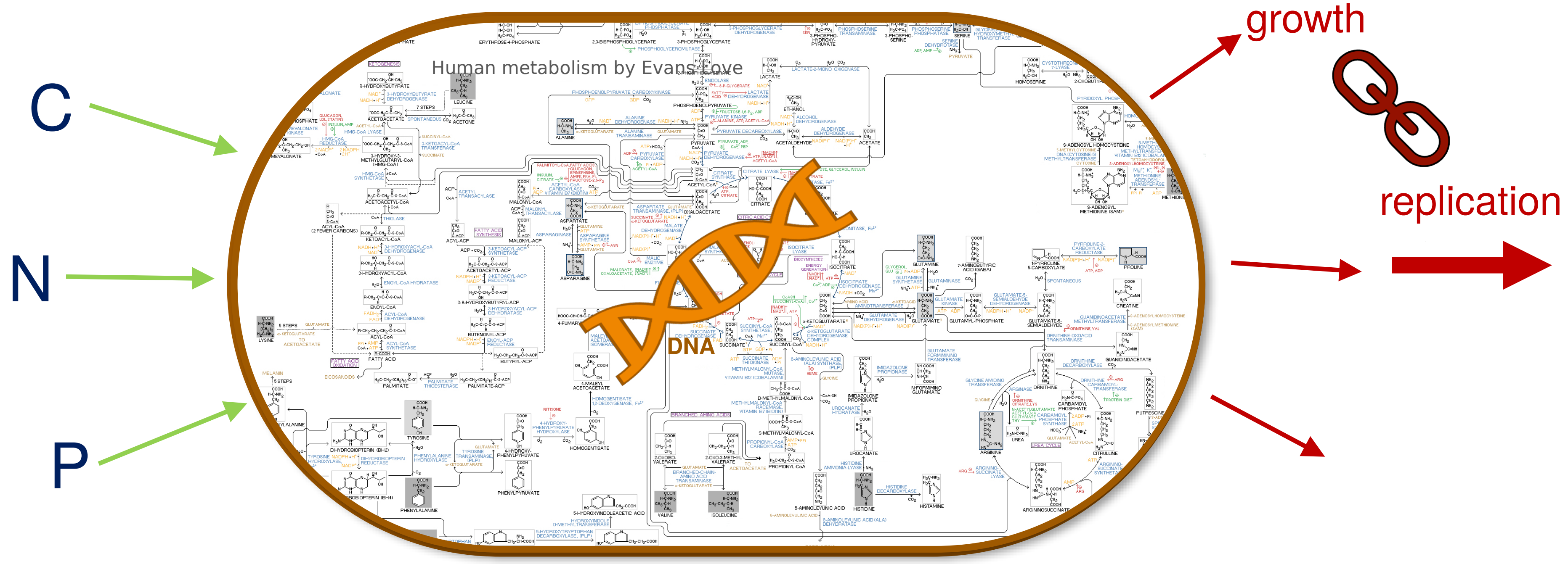
by brgfx on Freepik

Cells are building blocks of life

Cellular self-replication underpins reproduction of life

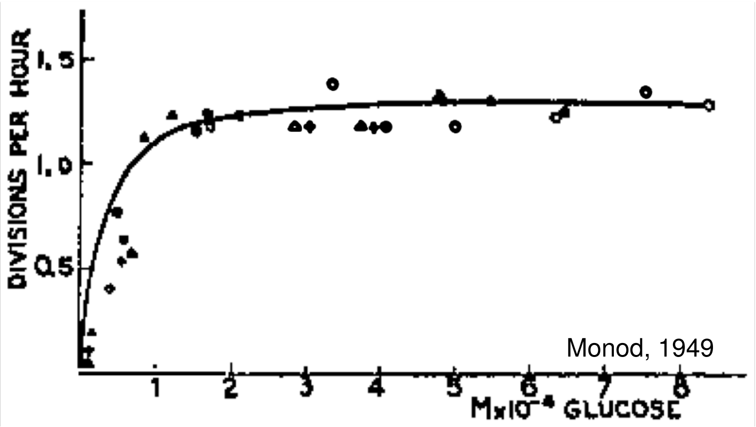
Self-replication is inherently coupled to growth

Cells absorb nutrients

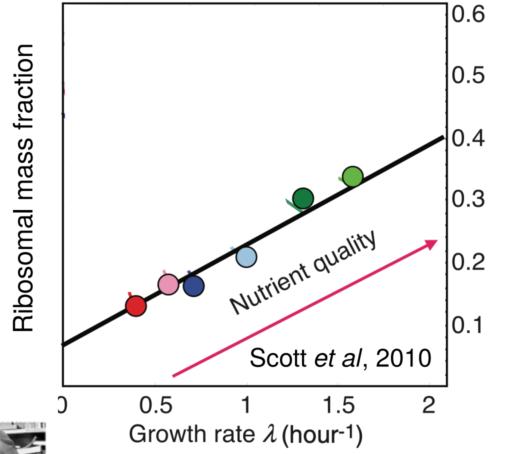


Growth laws govern the relation of growth with environmental & cellular features

Monod growth



Ribosomal growth laws



Monod — 1942, 1949

Schaechter — 1958

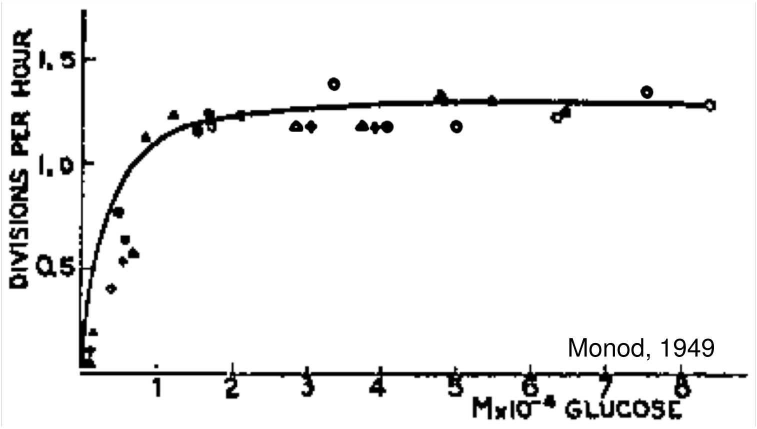
Maaløe and Kjeldgaard — 1966

Bremer and Dennis — 1996

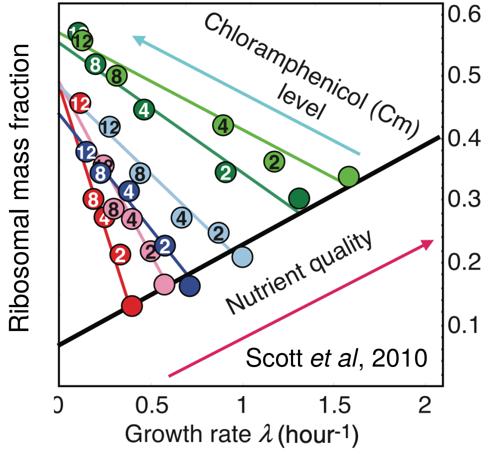
A brief history of bacterial growth physiology – Schaechter 2015

Growth laws govern the relation of growth with environmental & cellular features

Monod growth



Ribosomal growth laws

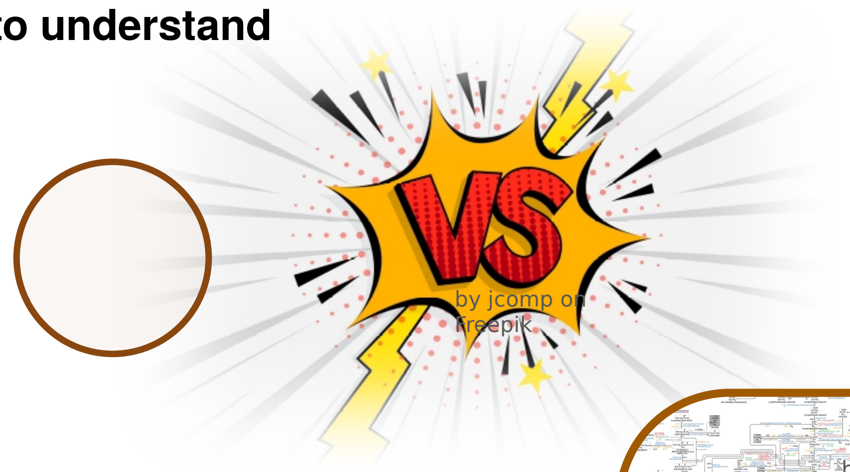


Other growth laws:

- cell size
- cell surface
- nutrient influx…

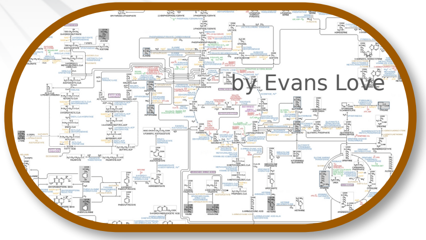
What model should we use?

Simple enough to understand



"All models are wrong, but some are useful."

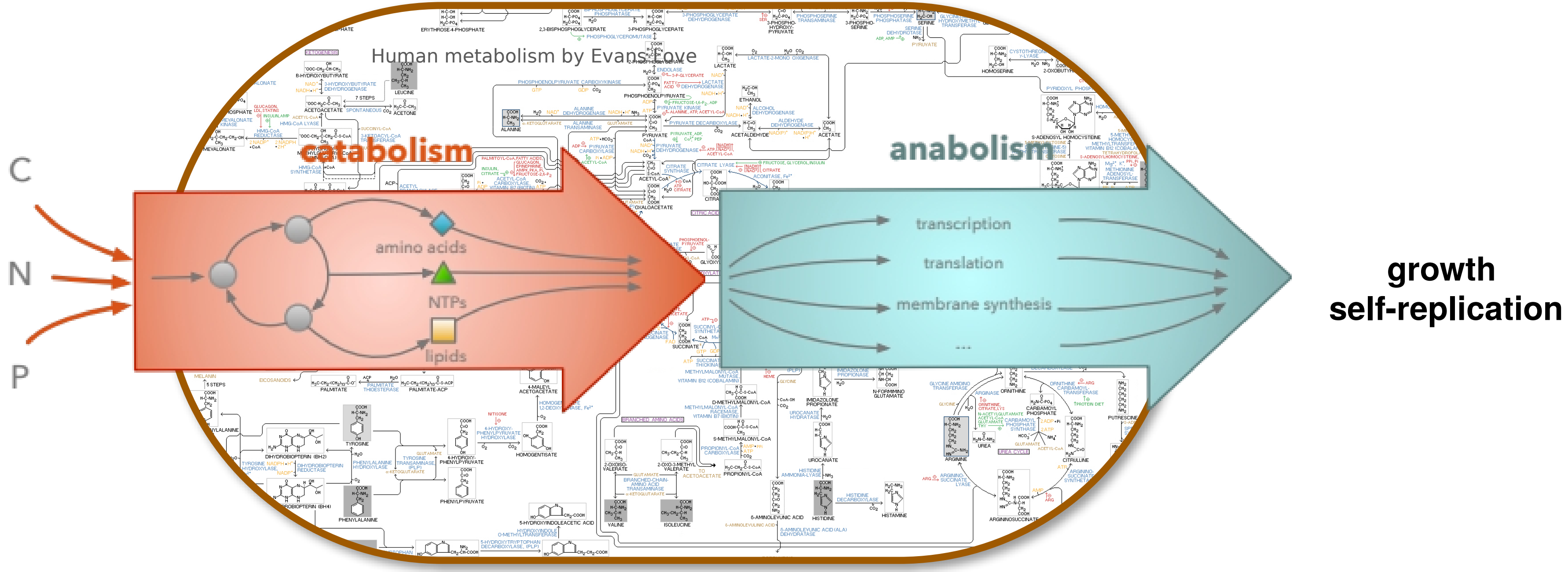
George E.P. Box



Complex enough to explain

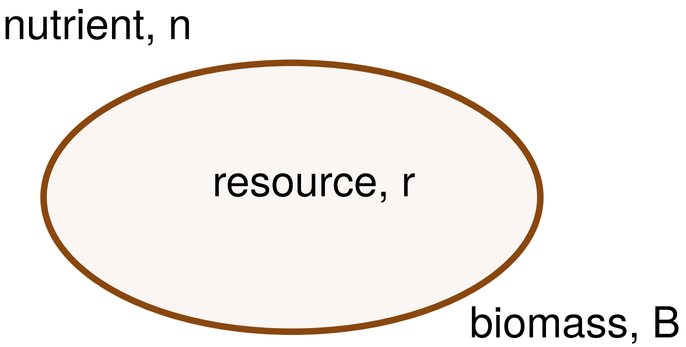
1. There is no one model.
2. What's the purpose of the model?

Many cell models share a common structure



Let’s start with a simple growth model

growth rate



Two reactions:

Assumptions:

- Proteome dominates biomass
- Cell has constant density

concentration of cell component y

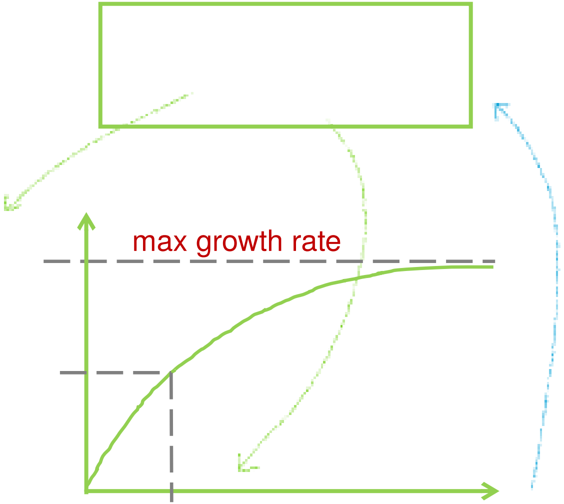
- Reaction rates are proportional to protein concentrations
- Steady-state assumption:

What determines the growth rate?

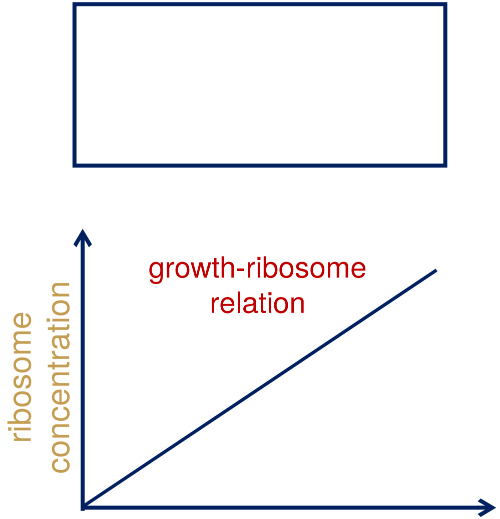
The simple model gives insight on growth laws

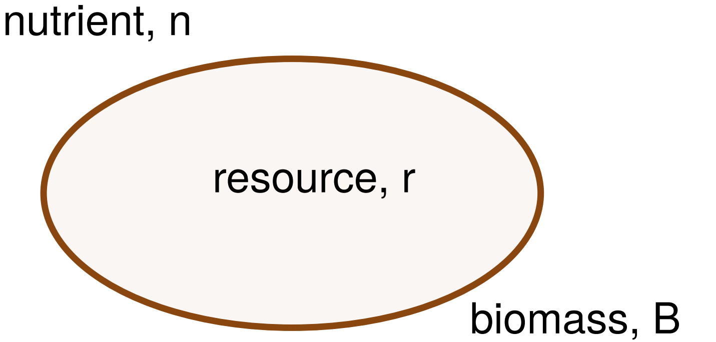
growth rate

at steady state:



but also:





What determines the growth rate?

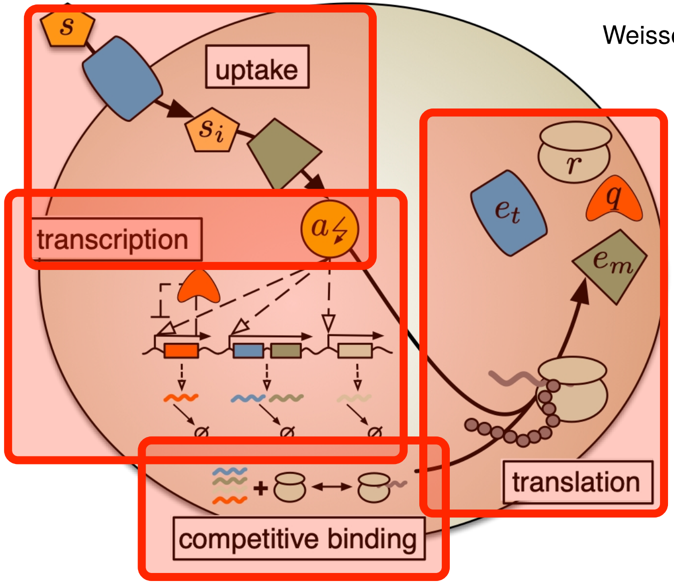
Further assume nutrient limiting

➡ → Monod growth

Basic mechanistic assumptions explain growth laws.

What can a more complex model teach us?

Weisse *et al*, PNAS 2015



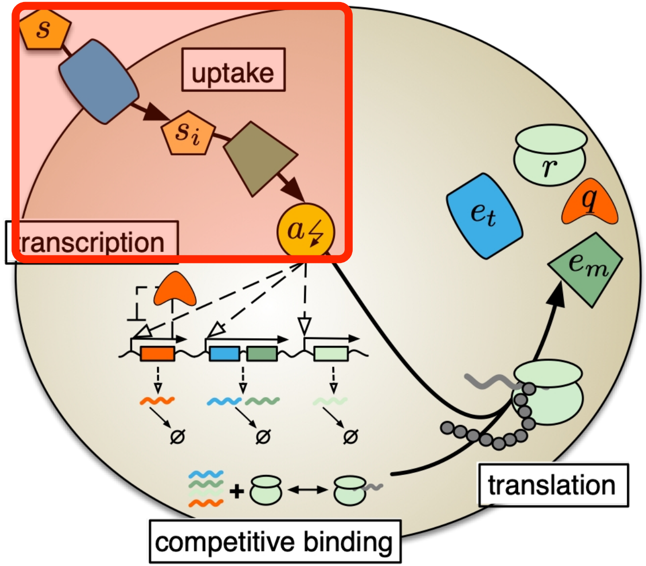
We focus on key mechanisms:

- nutrient uptake
- gene expression
- dilution

14 species

	dilution	transcription	dilution/degradation	ribosome binding	dilution	translation
ribosomes	$r \xrightarrow{\lambda} \varnothing$	$\varnothing \xrightarrow{\omega_r} m_r$	$m_r \xrightarrow{\lambda+d_m} \varnothing$	$r + m_r \overset{k_b, k_u}{\longleftrightarrow} c_r$	$c_r \xrightarrow{\lambda} \varnothing$	$n_r\, a + c_r \xrightarrow{\nu_r} r + m_r + r$
transporter enzyme	$e_t \xrightarrow{\lambda} \varnothing$	$\varnothing \xrightarrow{\omega_t} m_t$	$m_t \xrightarrow{\lambda+d_m} \varnothing$	$r + m_t \overset{k_b, k_u}{\longleftrightarrow} c_t$	$c_t \xrightarrow{\lambda} \varnothing$	$n_t\, a + c_t \xrightarrow{\nu_t} r + m_t + e_t$
metabolic enzyme	$e_m \xrightarrow{\lambda} \varnothing$	$\varnothing \xrightarrow{\omega_m} m_m$	$m_m \xrightarrow{\lambda+d_m} \varnothing$	$r + m_m \overset{k_b, k_u}{\longleftrightarrow} c_m$	$c_m \xrightarrow{\lambda} \varnothing$	$n_m\, a + c_m \xrightarrow{\nu_m} r + m_m + e_m$
growth-independent proteins	$q \xrightarrow{\lambda} \varnothing$	$\varnothing \xrightarrow{\omega_q} m_q$	$m_q \xrightarrow{\lambda+d_m} \varnothing$	$r + m_q \overset{k_b, k_u}{\longleftrightarrow} c_q$	$c_q \xrightarrow{\lambda} \varnothing$	$n_q\, a + c_q \xrightarrow{\nu_q} r + m_q + q$
internal nutrient	$s_i \xrightarrow{\lambda} \varnothing$	$s \xrightarrow{\nu_{\text{imp}}} s_i$	$s_i \xrightarrow{\nu_{\text{cat}}} n_s\, a$			
ATP	$a \xrightarrow{\lambda} \varnothing$	nutrient import	metabolism			

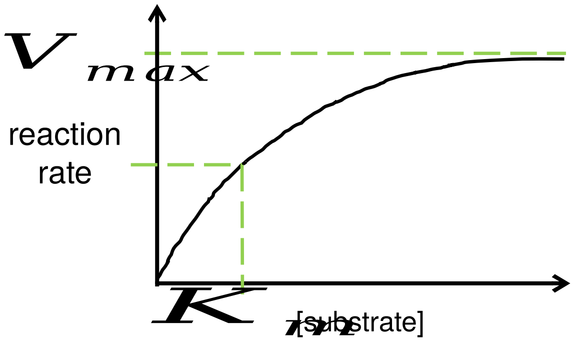
Enzymes catalyze nutrient uptake and metabolism.



Nutrient import & catabolism modelled as saturable enzymatic reactions:

$$s \xrightarrow{\nu_t} s_i \qquad \nu_t = v_t \frac{e_t \cdot s}{K_t + s}$$

$$s_i \xrightarrow{\nu_m} n_s\, a \qquad \nu_m = v_m \frac{e_m \cdot s_i}{K_m + s_i}$$



Translation is an ATP-consuming process.

Repeated binding and elongation with subsequent release occur with net rate:

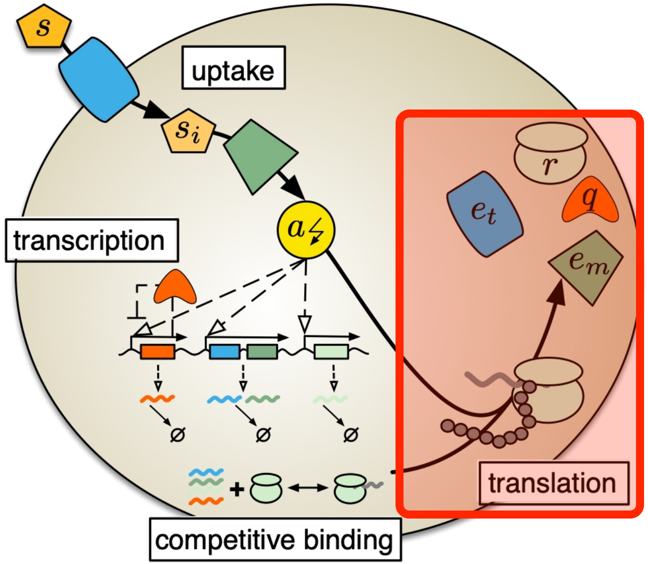
$$\nu_x = \quad \cdot \left(n_x \cdot \left(\frac{1}{K_p a} + \frac{1}{k_2} \right) + \frac{1}{k_p} \right)^{-1}$$

Assuming that release is fast, we can write this as:

$$\overset{k_p \gg 1}{\Rightarrow} \nu_x = \frac{\quad}{n_x} \cdot \underbrace{\frac{\gamma_{\max} \cdot a}{\frac{\gamma_{\max}}{K_p} + a}}_{=:\gamma(a)}$$

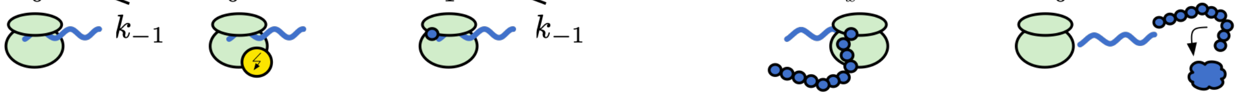
elongation rate

$$K_p := \frac{k_1 k_2}{k_{-1} + k_2}, \quad \gamma_{\max} := k_2$$



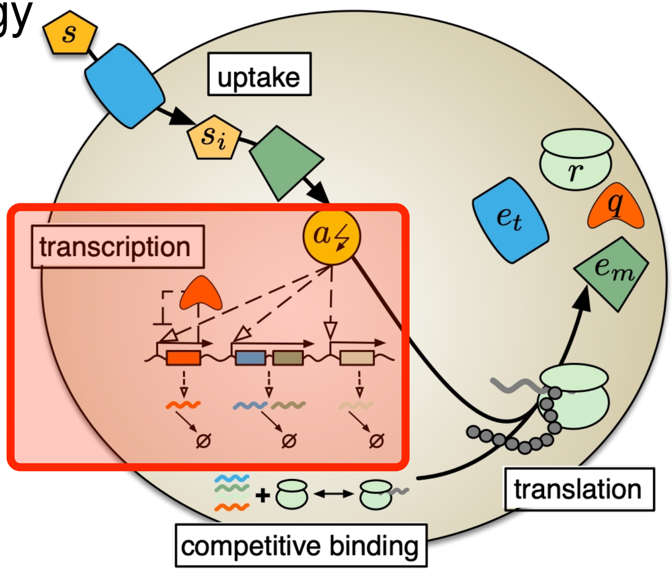
ATP consumption by translation ~2/3 of total consumption (Russel & Cook, 1995).
We assume a simplified mechanism where ATP directly binds the elongating complex:

$$R_0 M \underset{k_{-1}}{\overset{k_1 A}{\rightleftarrows}} R_0 M A \overset{k_2}{\longrightarrow} R_1 M \underset{k_{-1}}{\overset{k_1 A}{\rightleftarrows}} \cdots \overset{k_2}{\longrightarrow} R_{n_x} M \overset{k_p}{\longrightarrow} R_0 + M + P$$



Literature: Cleland, *Biochemistry*, 14(14):3220–3224, 1975.
Books on enzyme kinetics: Cornish-Bowden or Fersht.

Transcription has a low contribution to energy consumption.



We model transcription as an energy-dependent process but ignore its ATP-consumption:

$$\nu_{m,x} = \frac{c_x}{3n_x} \cdot \frac{\rho_{\max} a}{\theta_x + a}$$

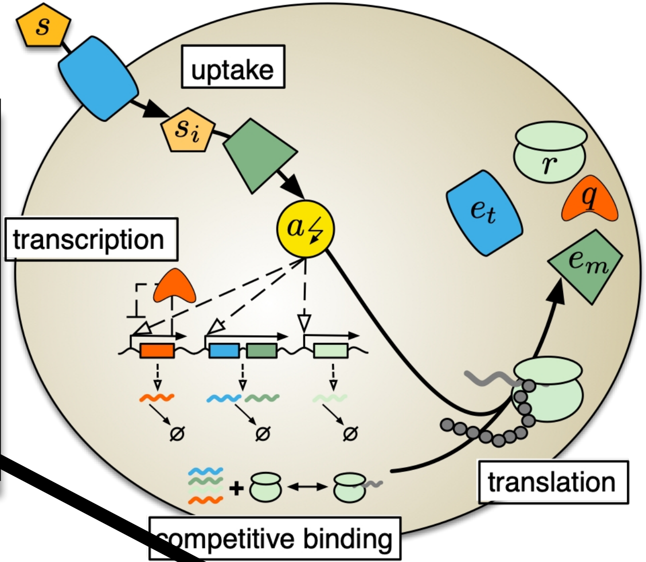
$$x \in \{e, \alpha, r, p\}$$

Translational activity determines growth.

From steady state follows

$$\lambda \propto \text{protein synthesis}$$

$$= \sum_x c_x \cdot \gamma(a)$$



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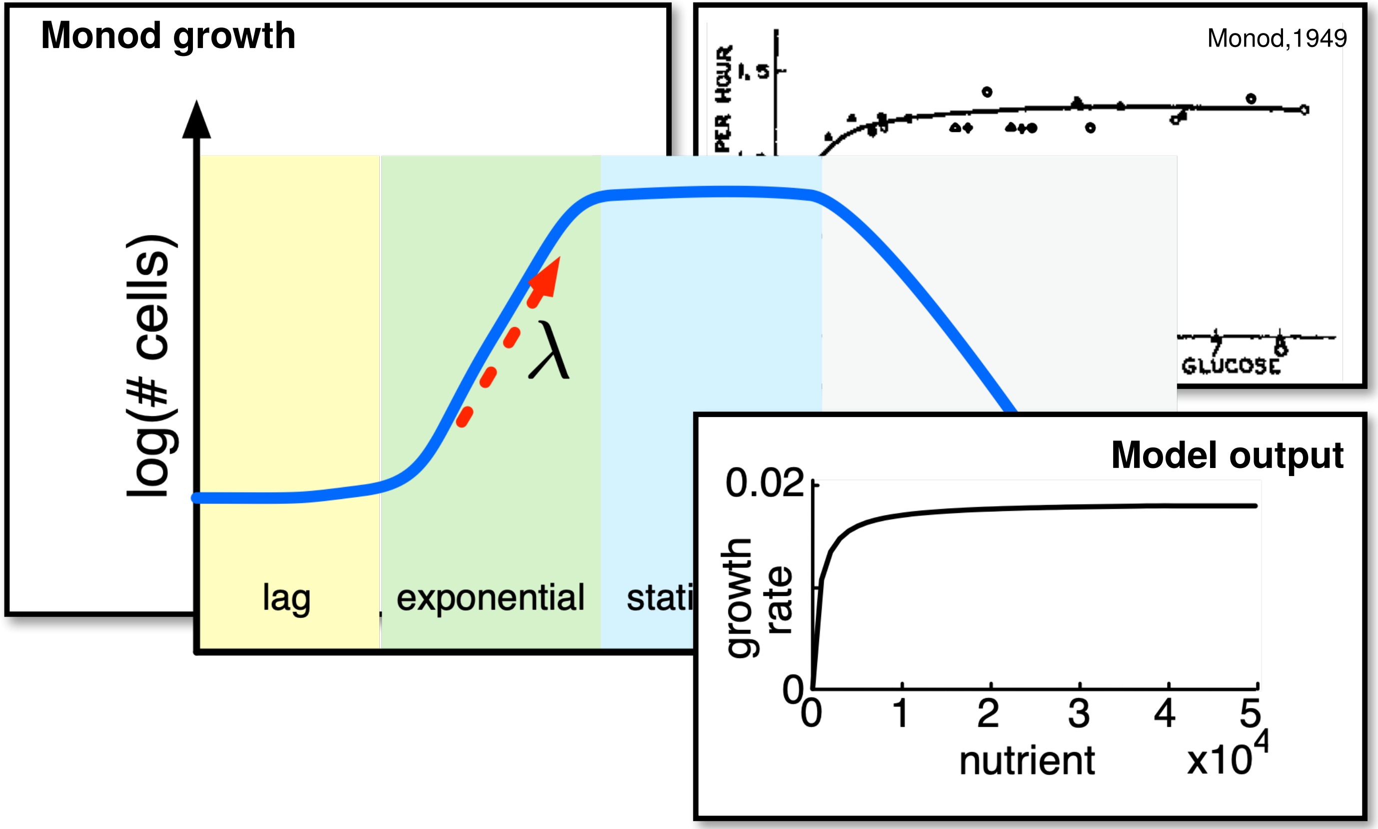
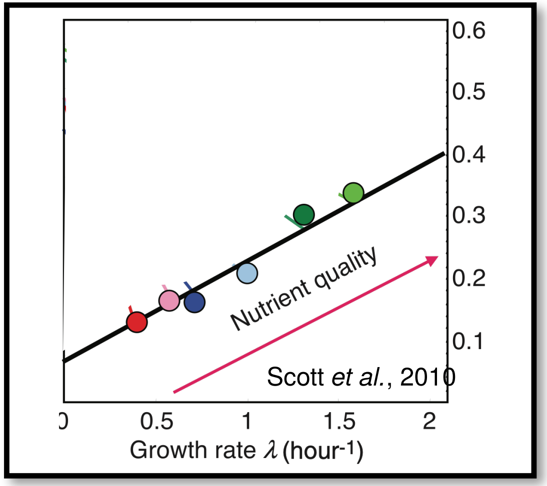
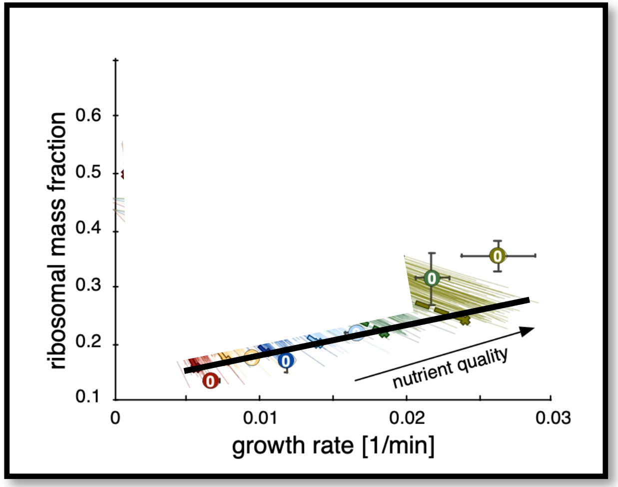
The model recovers Monod's growth law.

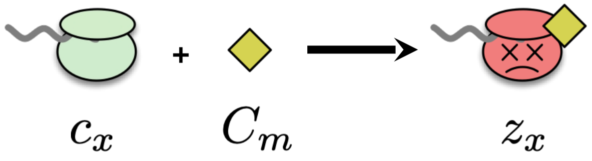


The model recovers the ribosomal growth laws.





Translational inhibition assuming chloramphenicol binds the mRNA-ribosome complexes, which then can't be translated anymore:



$$s_i \xrightarrow{\nu_{\mathrm{cat}}} n_s a$$

nutrient quality = energy yield

We can derive the empirical growth relations analytically.

1. When varying nutrient conditions

mass fractions
total & free ribosomes

$$\lambda = \frac{1}{\tau_\gamma}(\phi_R - \phi_r)$$

time to translate one ribosome

2. When inhibiting translation

housekeeping load

total ribosomes

$$\lambda \simeq \frac{1}{\tau_e}(1 - \phi_q - \phi_R) \cdot \frac{s}{K_t + s}$$

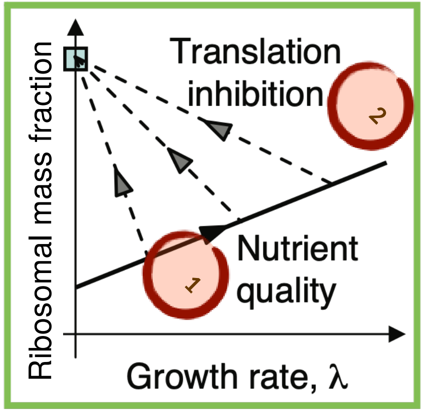
enzyme time

constant environment

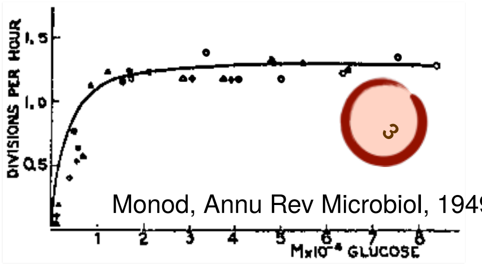
3. When changing amounts of external nutrient

$$\lambda \simeq \frac{(1-\phi_q)s}{K_t\tau_e + (\tau_e + \tau_\gamma)s}$$

import threshold



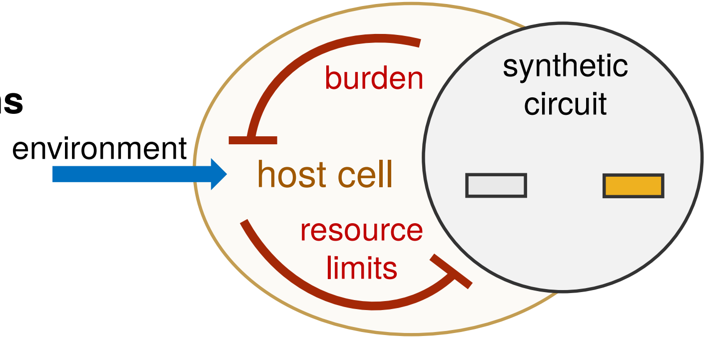
Scott & Hwa, Curr Opin Biotechnol, 2011



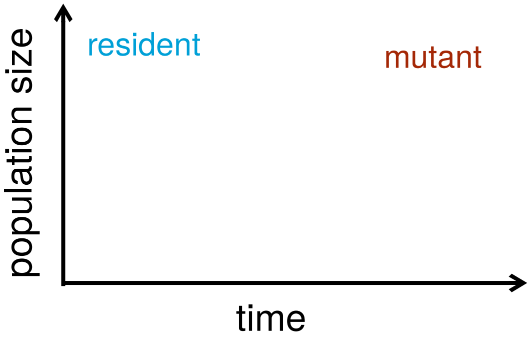
Monod, Annu Rev Microbiol, 1949

Other things we can investigate with such mechanistic model:

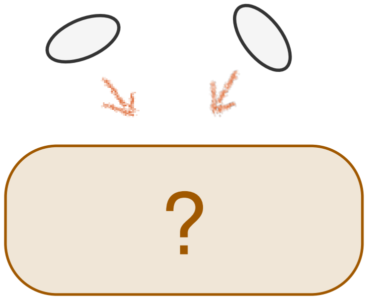
Host-circuit interactions



Evolutionary stability of cell mechanisms



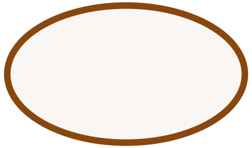
Antibiotic responses

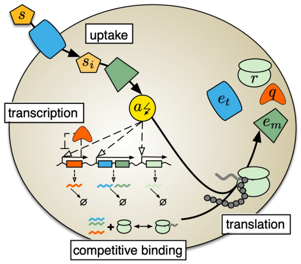


In summary

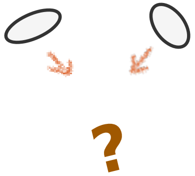
Cellular self-replication is inherently coupled with growth

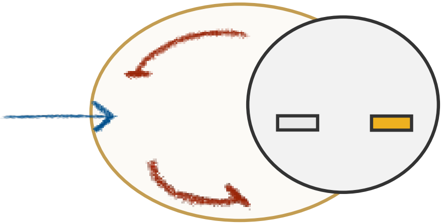
***Small* mechanistic models give insights on principles underpinning growth**





Complexity comes at cost but can give versatility





Further reading:

EPCP book chapter “Principles of growth”

Weiße *et al*, PNAS 2015

Economic principles?