

A unifying autocatalytic network-based framework for bacterial growth laws

Anjan Roy¹, Dotan Goberman¹, Rami Pugatch¹

¹Dept. of Industrial Engineering and Management

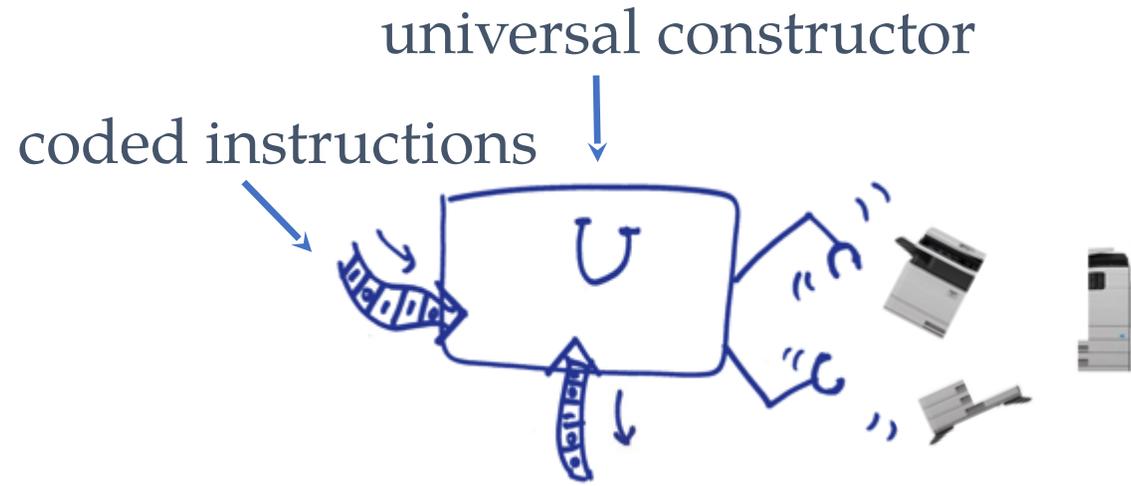
.Ben-Gurion University of the Negev, Israel

Take Home Message

Cell as an ecology of self-replicating molecular machines with the von Neuman's architecture. Universal constructor = transcription translation machinery.

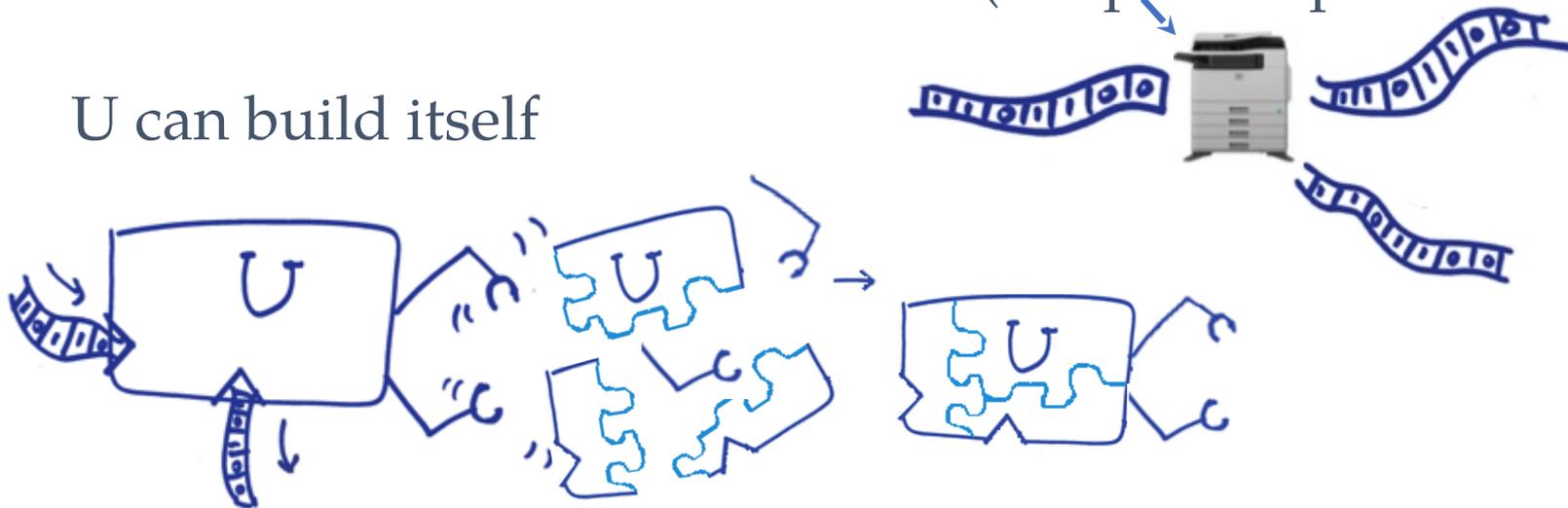
- Any essential element has two associated growth laws
- Going beyond the ribocentric view, we derive new growth laws e.g. RNA-Polymerase growth law
- Growth laws are a manifestation of the conservation of matter, i.e., somewhat uninteresting. The challenge - understand the controls and processing of information from external cues!

Nontrivial self-replication



R machine (template replicate instructions)

U can build itself

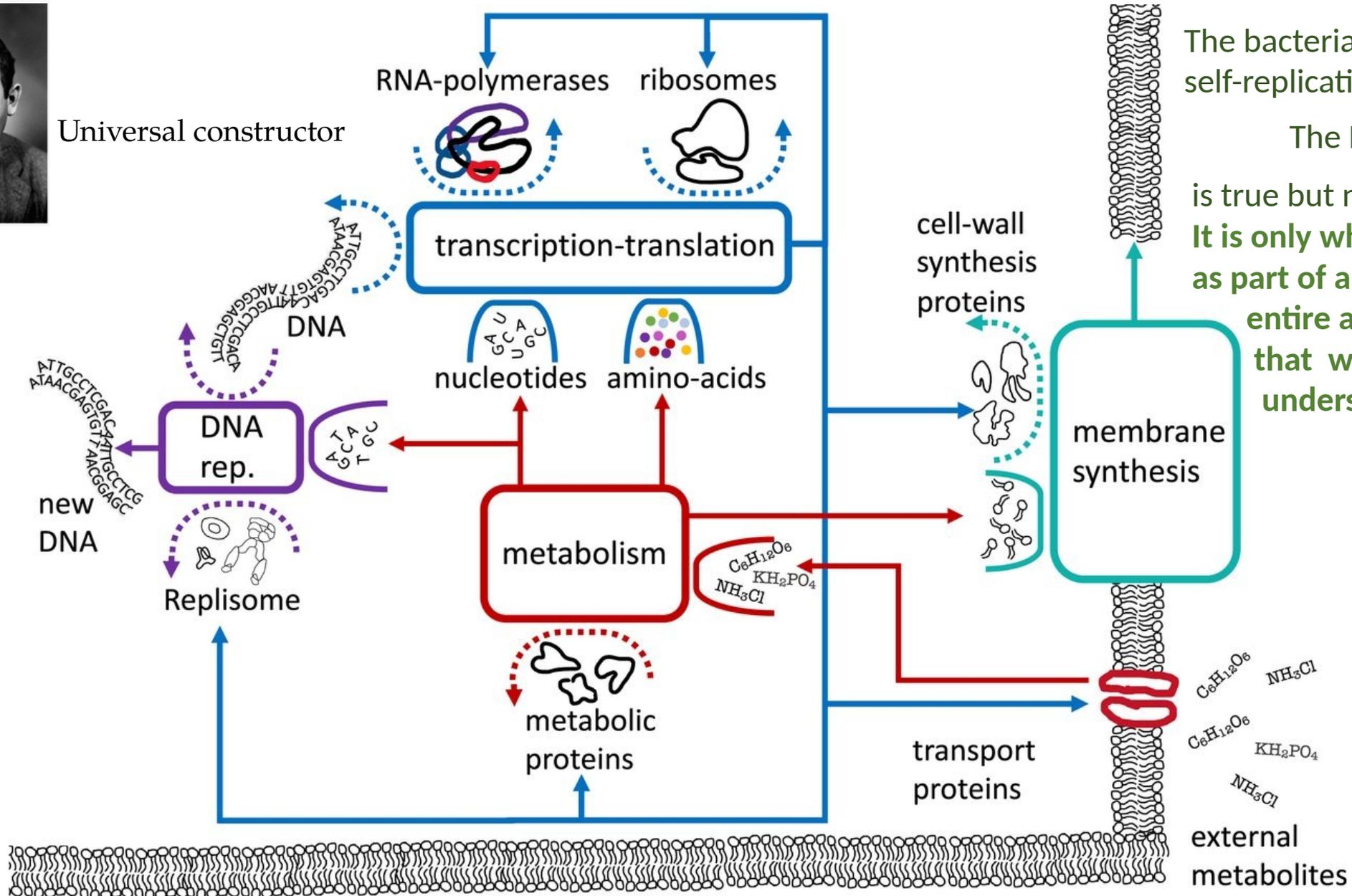


Universal constructor – the machine that makes machines

Schematic diagram of a bacterial autocatalytic network, showcasing different autocatalytic cycles coarsely grained.



Universal constructor



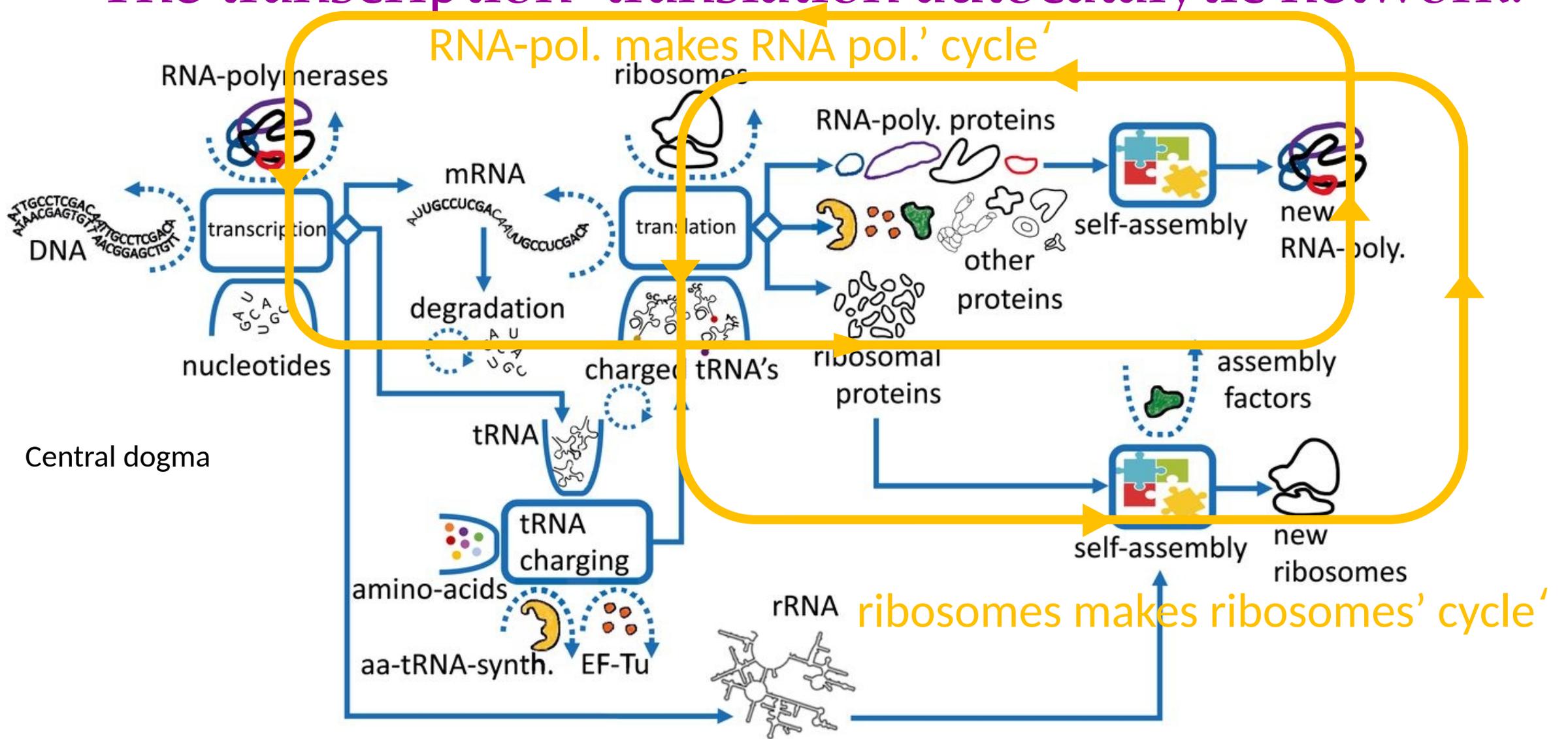
The bacterial cell as an ecology of self-replicating molecular machines

The Equation

is true but non-mechanistic

It is only when we view as part of an eigenvector of the entire autocatalytic network that we gain mechanistic understanding.

The transcription-translation autocatalytic network.



Our contribution

Using autocatalytic network with a specific structure that is common to all bacteria and using Leontief production function we derive

- Known growth laws
- New growth laws (in particular RNA-polymerase growth law)
- Employ RNAP growth law to explain reduction in growth rate at constant RNA/protein ratio as rifampicin concentration increases.

Autocatalysis 101 + a graphical language to code quantitative models

- Simple reactions consume substrates S_1, \dots, S_n , with a catalyst C and produce a product P

substrates reaction node de-novo synthesized
product



Wassily Leontief

catalyst

Autocatalysis 101 cont.

- Simple autocatalysis consume substrates S_1, \dots, S_n , employ a catalyst C and the product is more catalysts C. The newly created catalysts joins the existing ones and catalyze more copies. This can go on until one of the substrates is depleted.

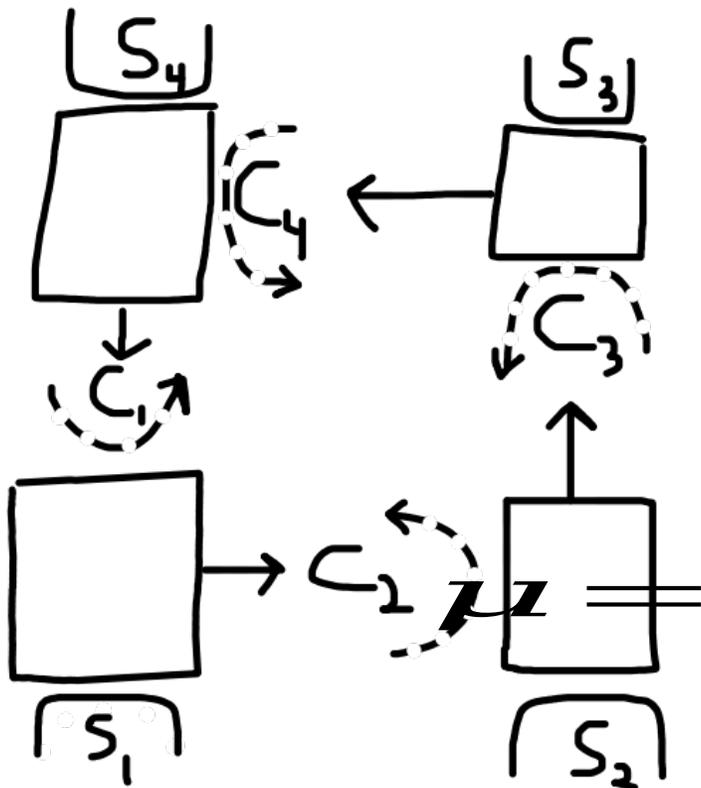
The product is another catalyst



Wassily Leontief

Autocatalytic networks

- networks which consume substrates and jointly autocatalyze all the catalysts in them. A famous (non biological) example is the Hinshelwood cycle (here of degree $n=4$):



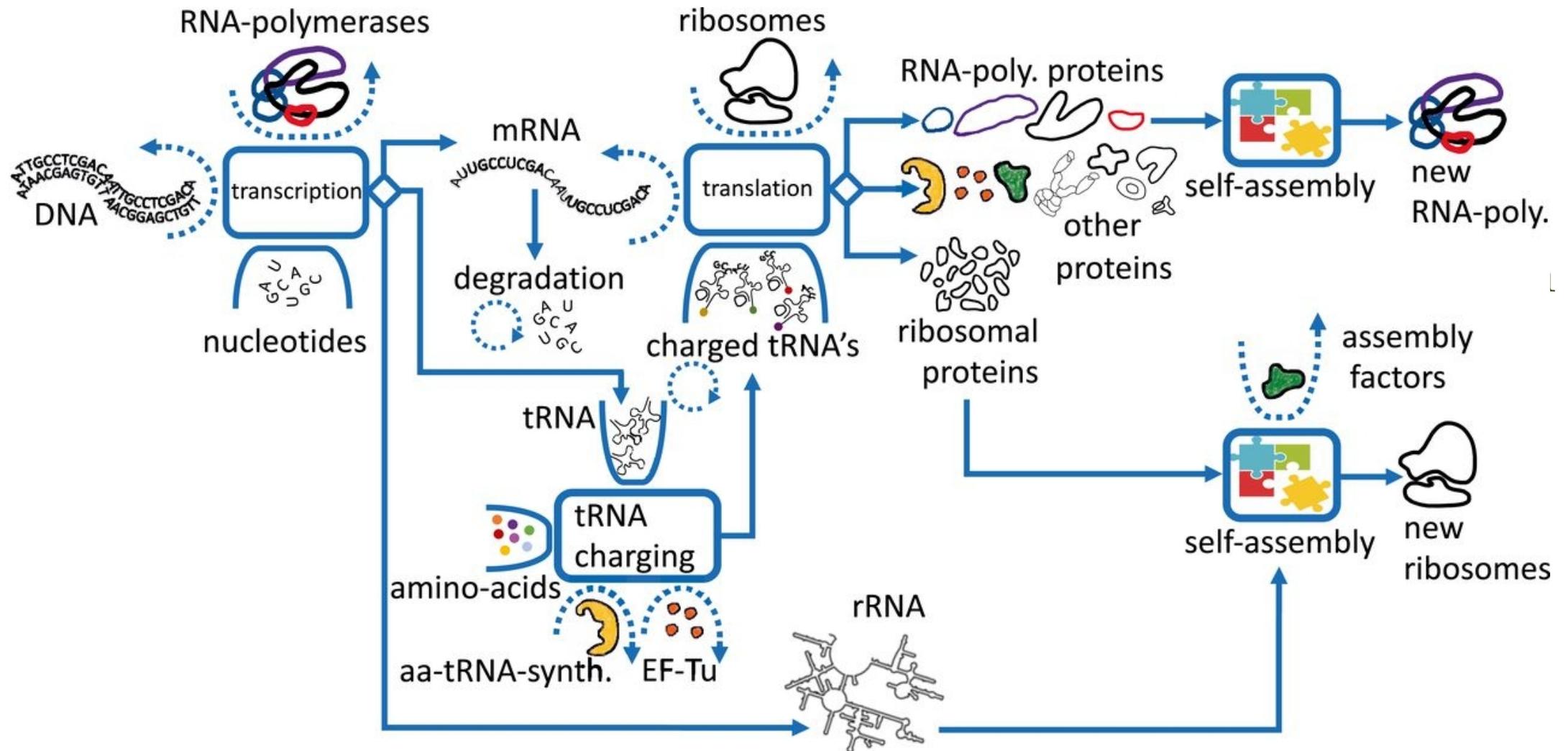
for example if all substrates are saturated it is easy to show that

$$\frac{1}{\sqrt[n]{\tau_1 \times \tau_2 \times \dots \times \tau_n}}$$



Cyril
Hinshelwood

The graphical depiction of autocatalytic network codes a quantitative model



Going beyond the ribo-centric view

- In an autocatalytic network, any element can be viewed as the center around which autocatalysis revolves \Rightarrow this leads to two growth laws per cycle.

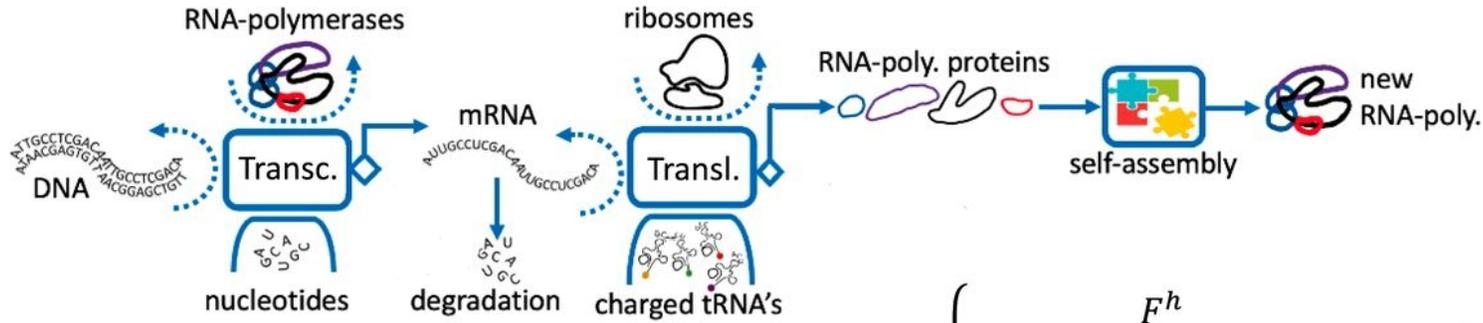
NOTE: cycle need not be limiting.

(i) a growth law involving all the time scales in the cycle (+allocation parameters).

(ii) a growth law involving relative abundance of a given catalyst, its synthesis rate and its allocation parameter (famous example: ribosome growth law).

The RNA polymerase growth law

A

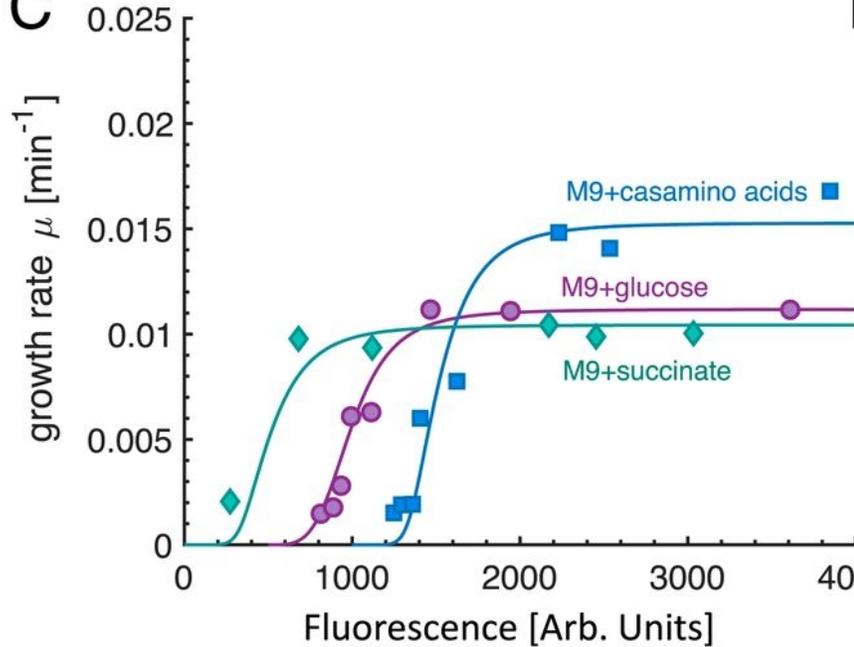


B

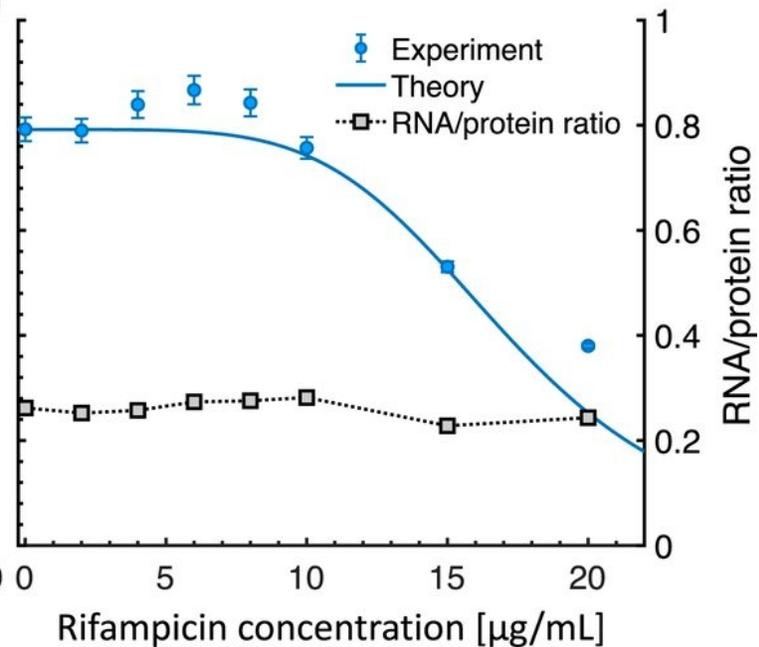
$$\hat{\tau}_{SA}\mu^2 + \mu = \frac{\hat{\phi}_b \alpha_{rpo} \tau_{lifetime}}{\tau_{transc.} \tau_{transl.}}$$

$$(\hat{\phi}_b, \hat{\tau}_{SA}) = \begin{cases} (\phi_b, \tau_{SA} \frac{F^h}{F^h + K^h}), & \text{inset (C)} \\ (\phi_b \frac{\kappa^H}{c^H + \kappa^H}, \tau_{SA}), & \text{inset (D)} \end{cases}$$

C

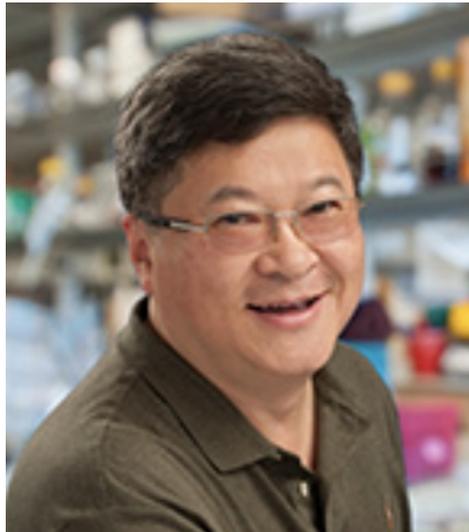
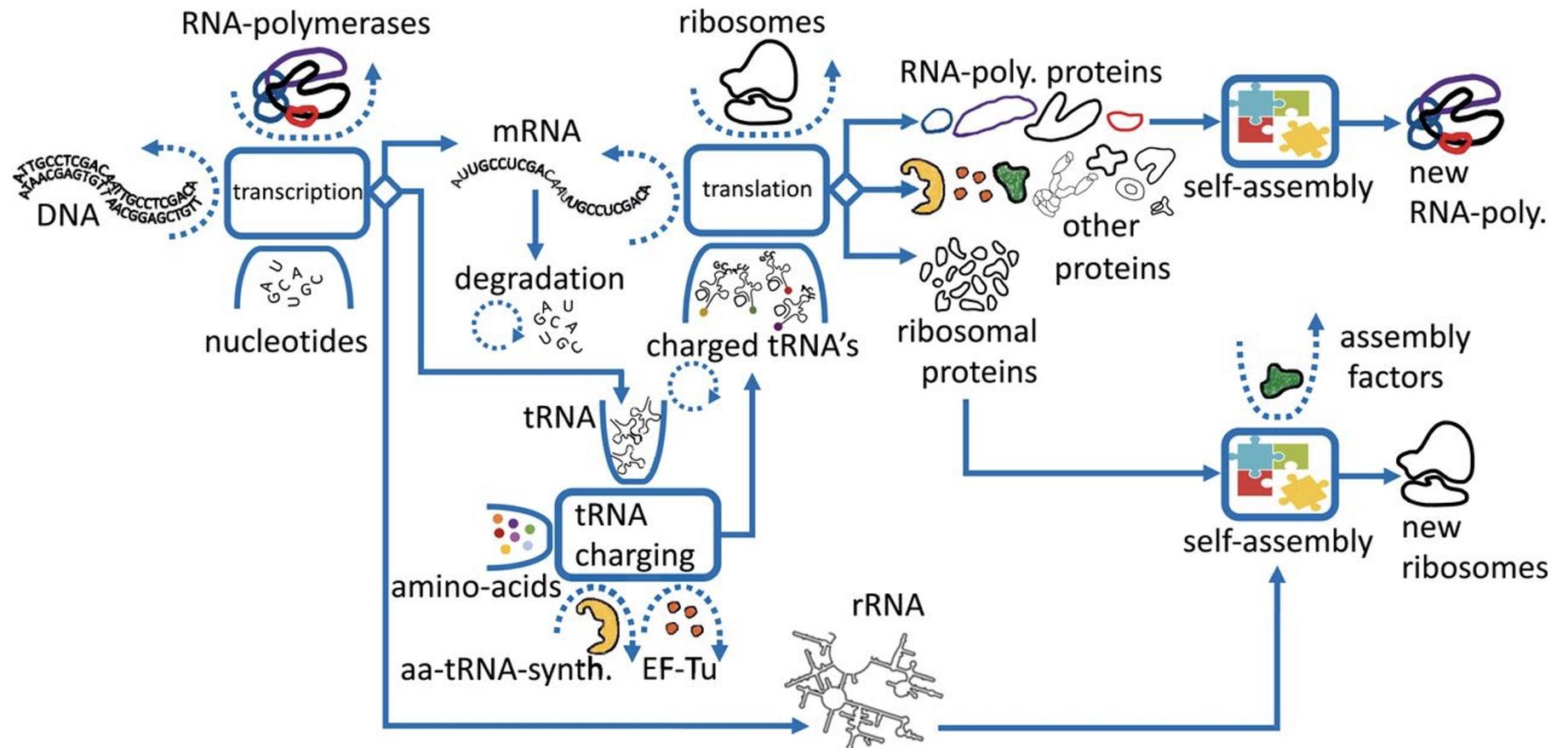


D



RNA/Protein = const.
yet growth rate goes
down

Bacterial growth laws



Growth rate dependence on temperature

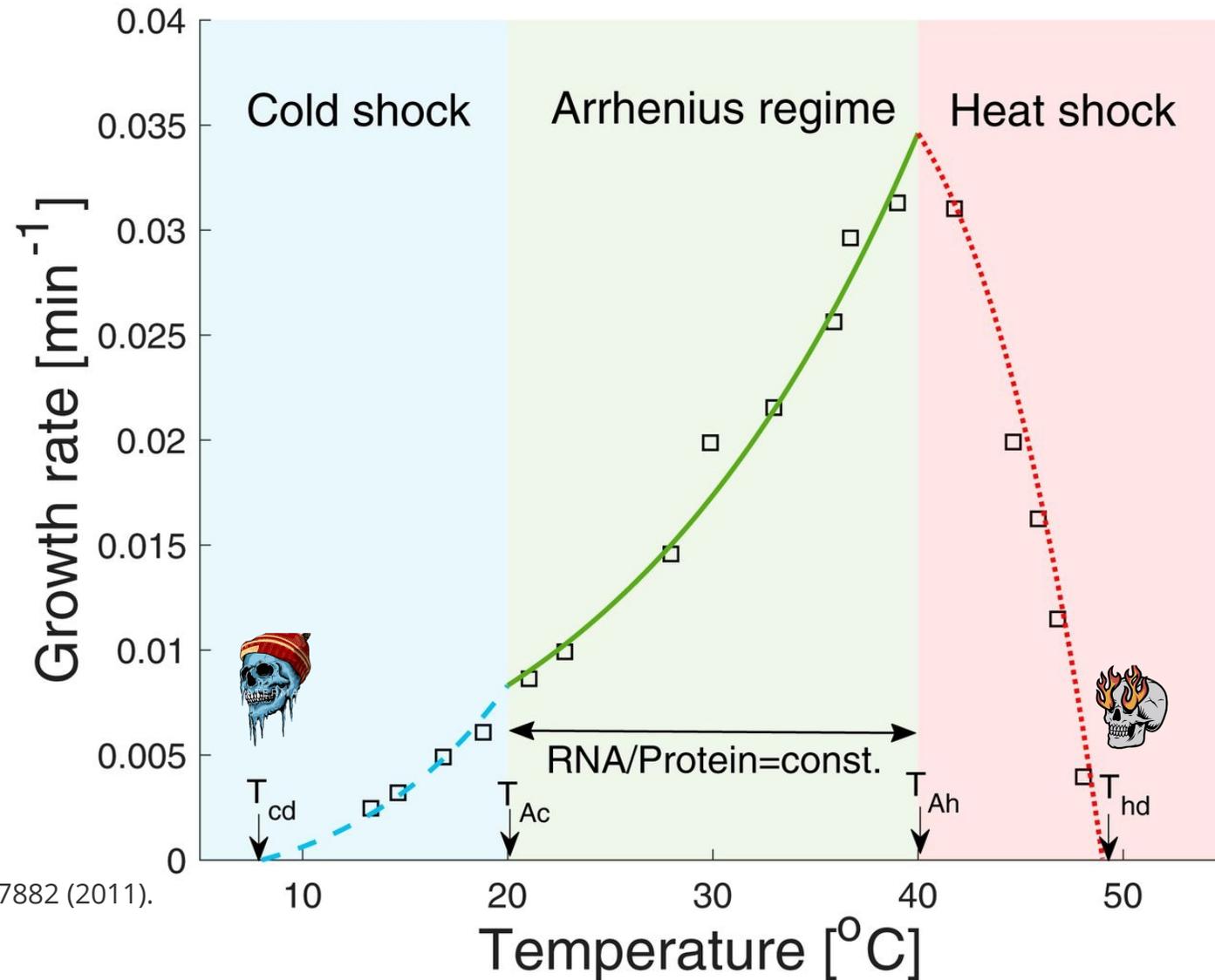
$$\mu(T) = \gamma_{\text{elong.}} e^{\frac{\Delta \tilde{G}}{k_B T}} \times$$

$$\begin{cases} \Delta \Phi \frac{(T - T_{Ac})}{(T_{Ac} - T_{cd})} + \Delta \Phi, T < T_{Ac} \\ \Delta \Phi, T \in [T_{Ac}, T_{Ah}] \\ \Delta \Phi \frac{(T - T_{Ah})}{(T_{Ah} - T_{hd})} + \Delta \Phi, T > T_{Ah} \end{cases}$$

$$\Delta G(T) = \Delta H + \Delta C_p (T - \hat{T}) - T \Delta S - T \Delta C_p \ln \left(\frac{T}{385} \right),$$

$$\Delta \tilde{G} = \Delta G - \Delta G(T = 37^\circ \text{C})$$

K. A. Dill, K. Ghosh, J. D. Schmit, Proc. Natl. Acad. Sci. U.S.A. **108**, 17876–17882 (2011).



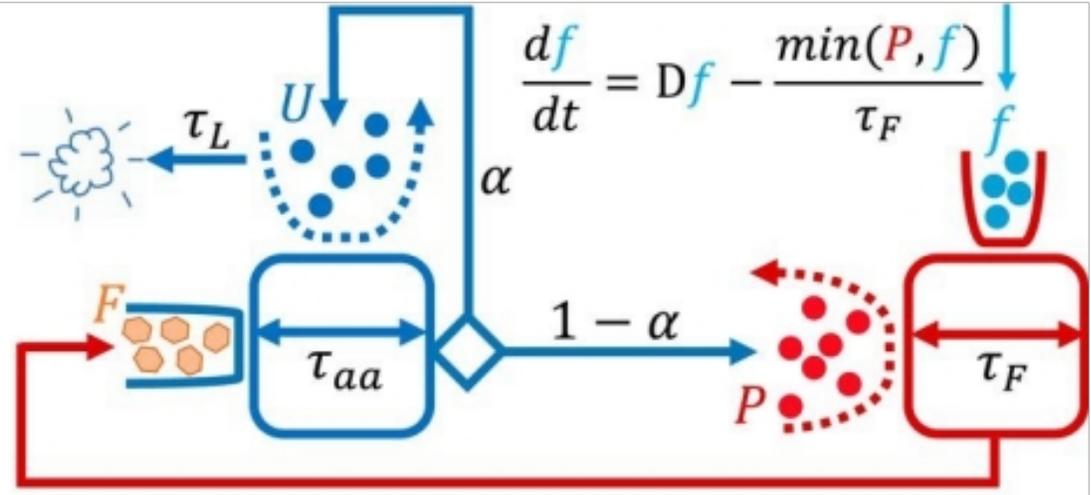
Two-step model buildup.

A

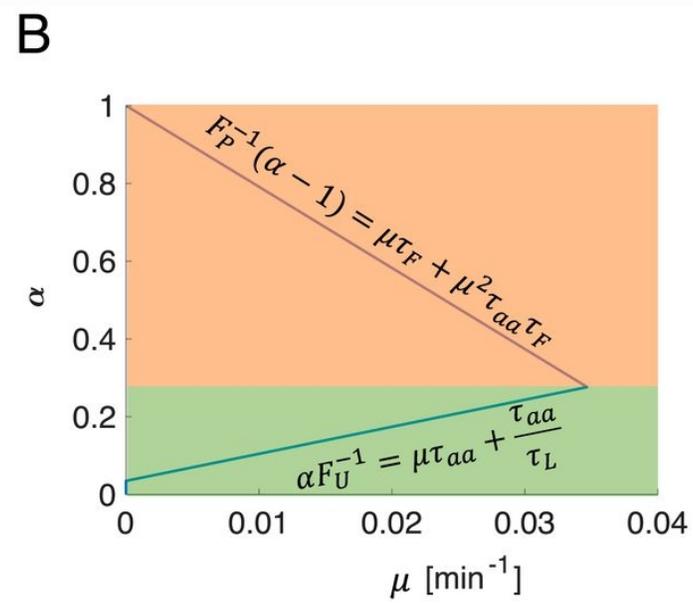
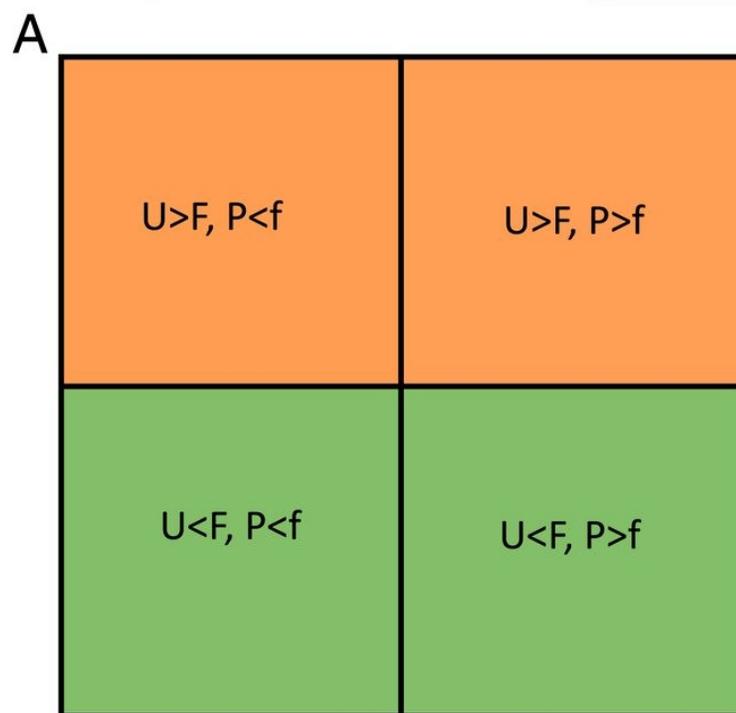
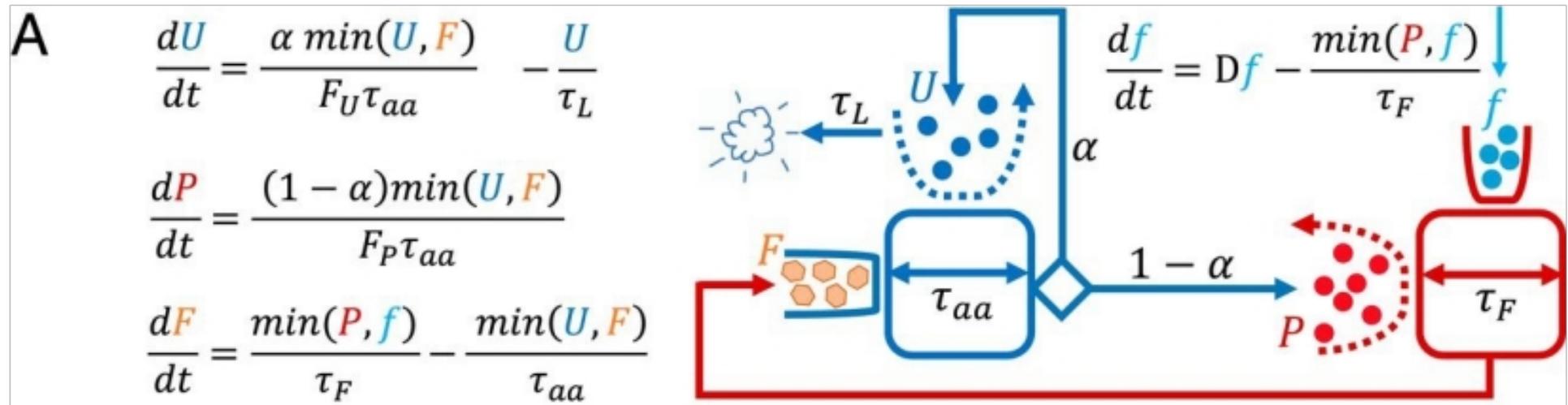
$$\frac{dU}{dt} = \frac{\alpha \min(U, F)}{F_U \tau_{aa}} - \frac{U}{\tau_L}$$

$$\frac{dP}{dt} = \frac{(1 - \alpha) \min(U, F)}{F_P \tau_{aa}}$$

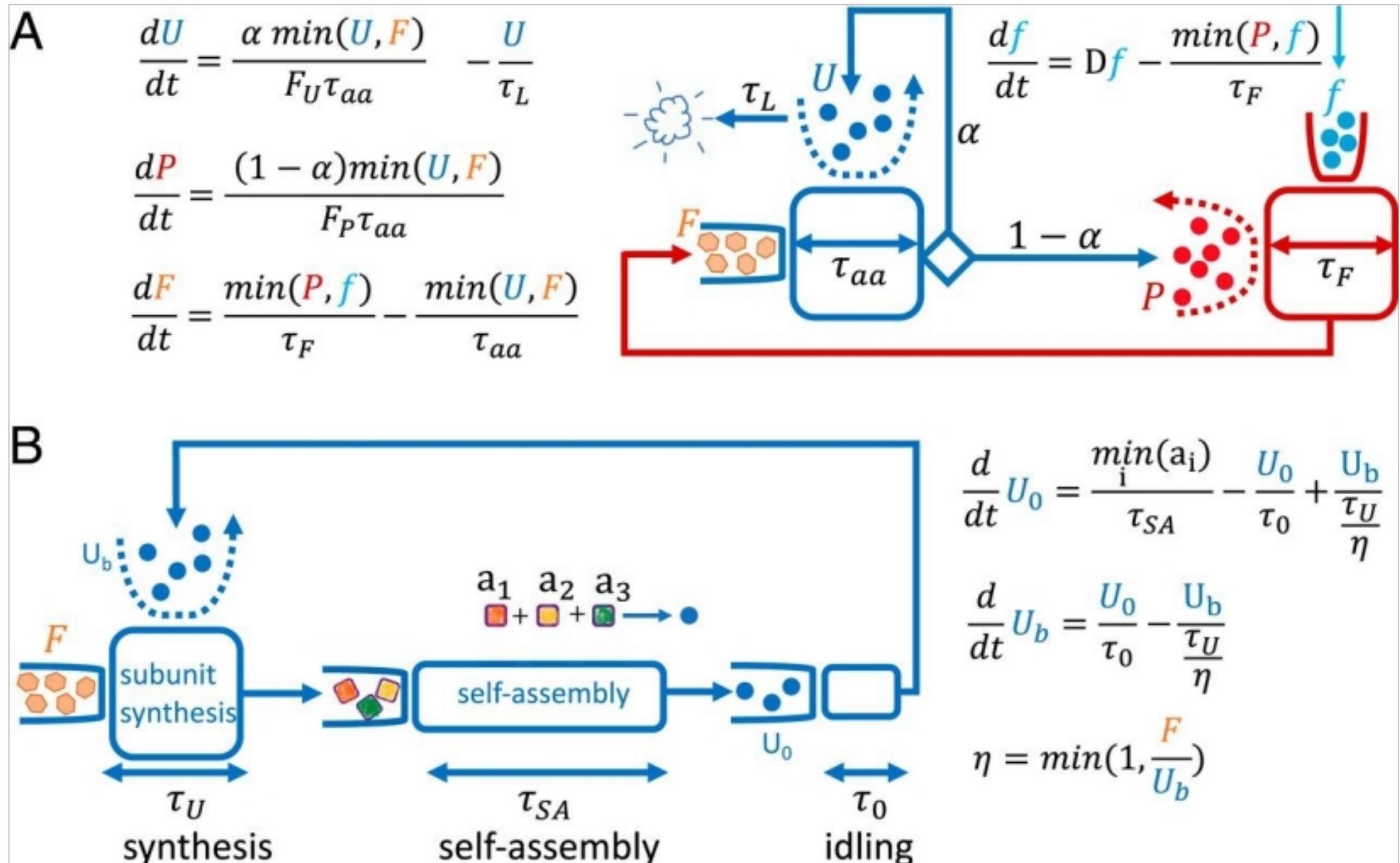
$$\frac{dF}{dt} = \frac{\min(P, f)}{\tau_F} - \frac{\min(U, F)}{\tau_{aa}}$$

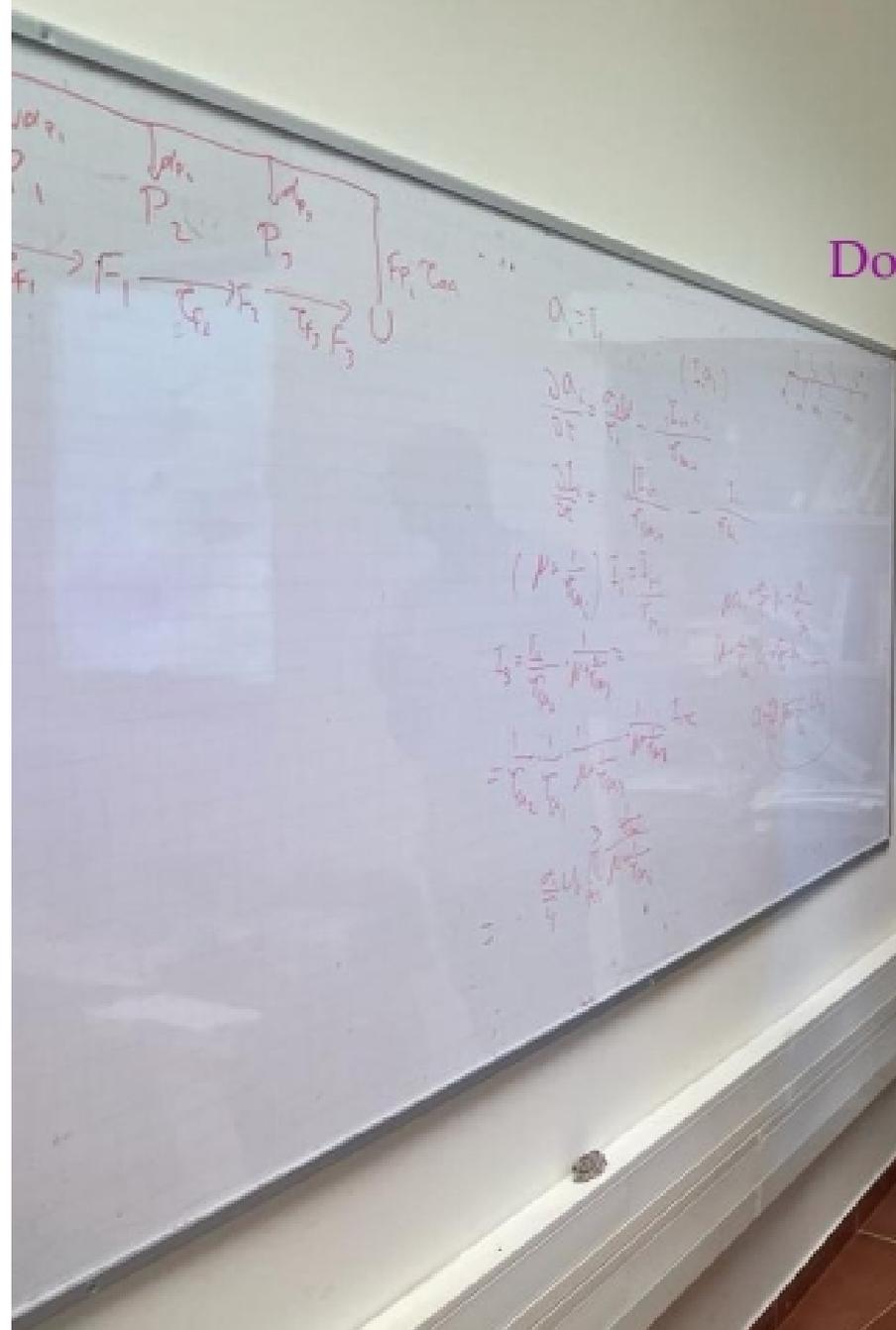


Two-step model buildup.



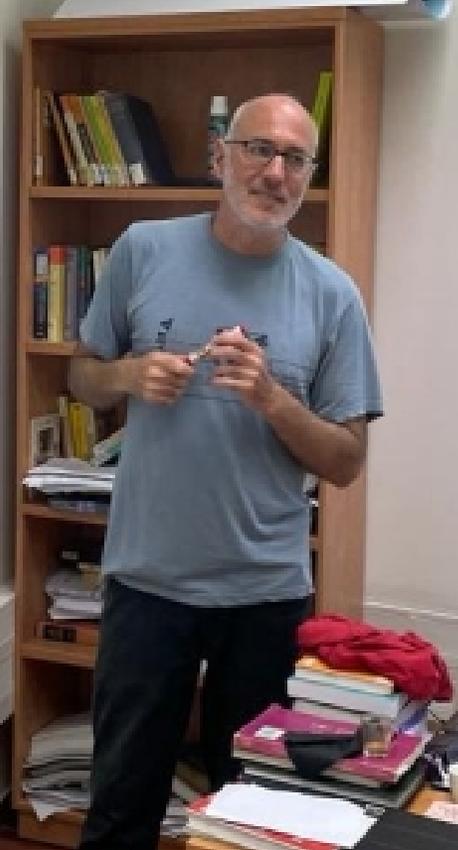
Two-step model buildup.





Dotan Goberman, M. Sc

Dr. Anjan Roy



What's next?

- Design rules for streamlining ribosome assembly
- Control in general and metabolic switchings
- Classification and analysis of all cost-benefit scenarios

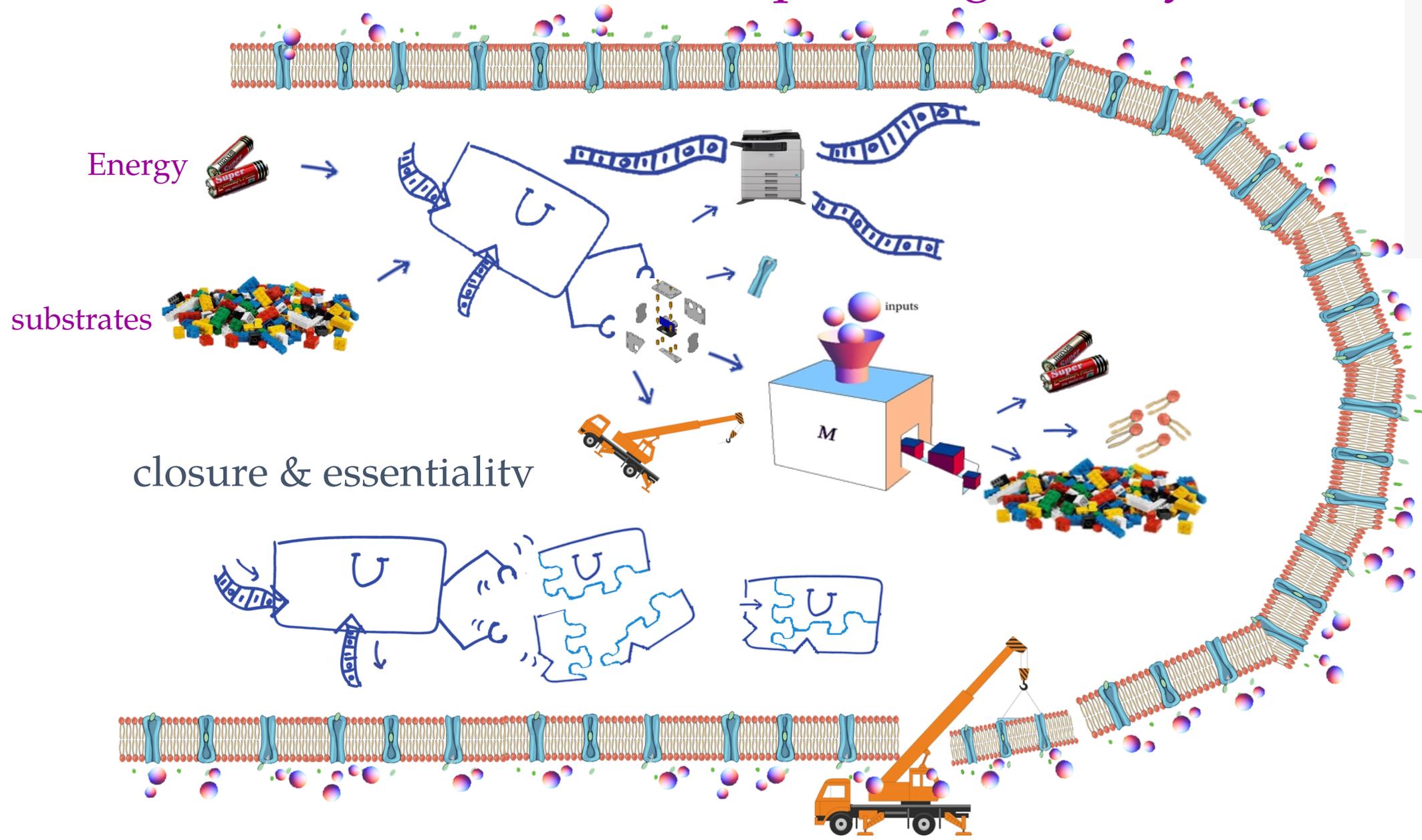
“All model are wrong,
some are useful.”

G. Box





The Non-trivial Self-replicating Factory



Energy

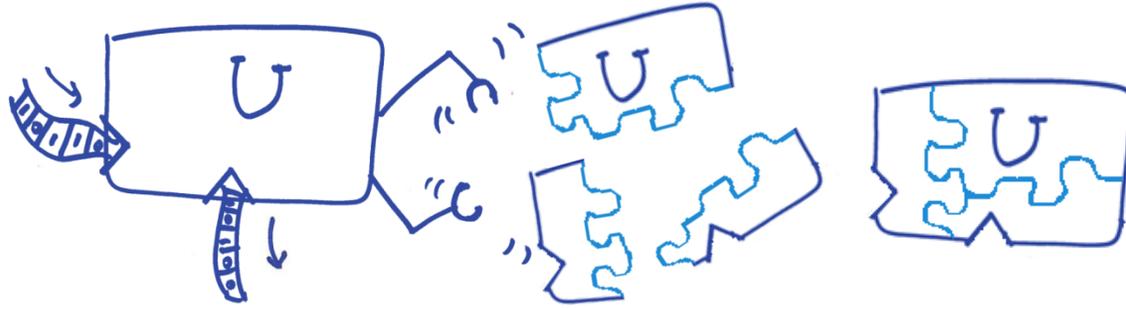
substrates

closure & essentiality

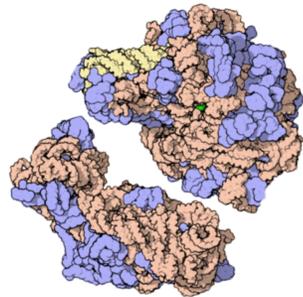
inputs

M

Who's the universal constructor in the cell?

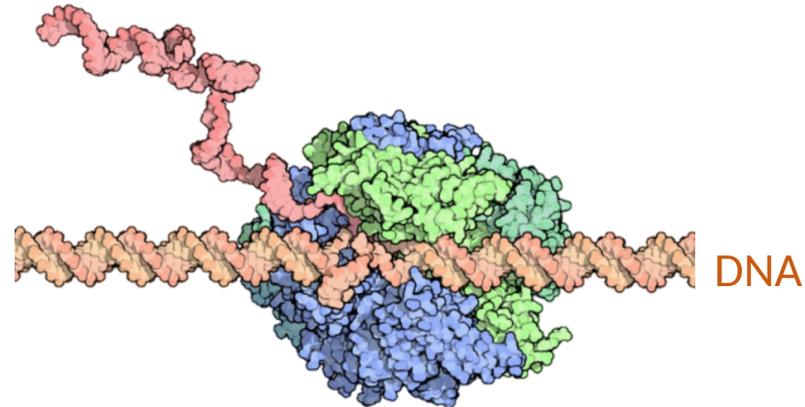


key players : RNA polymerase

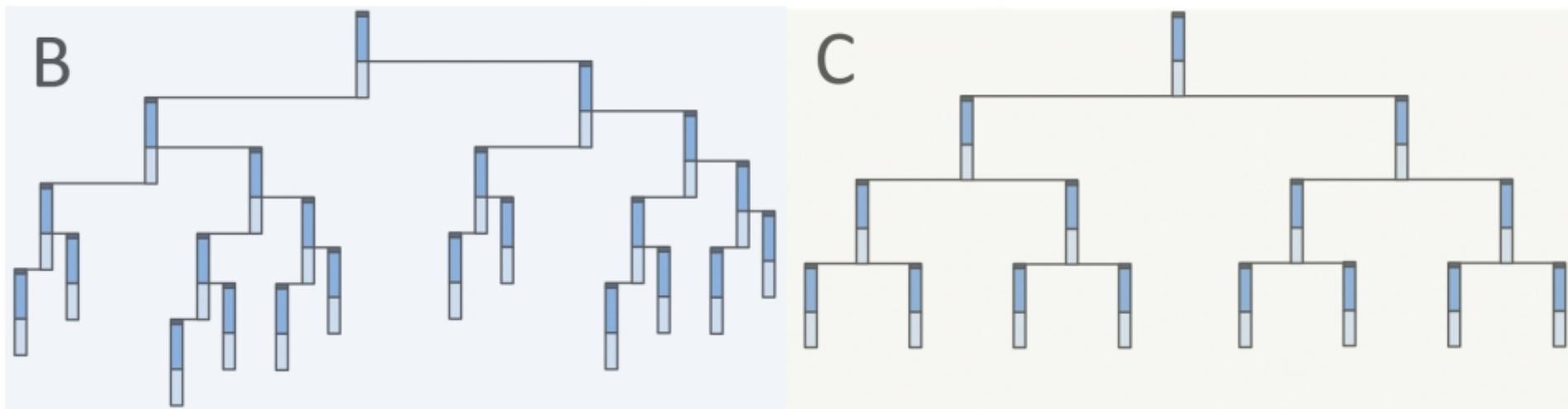
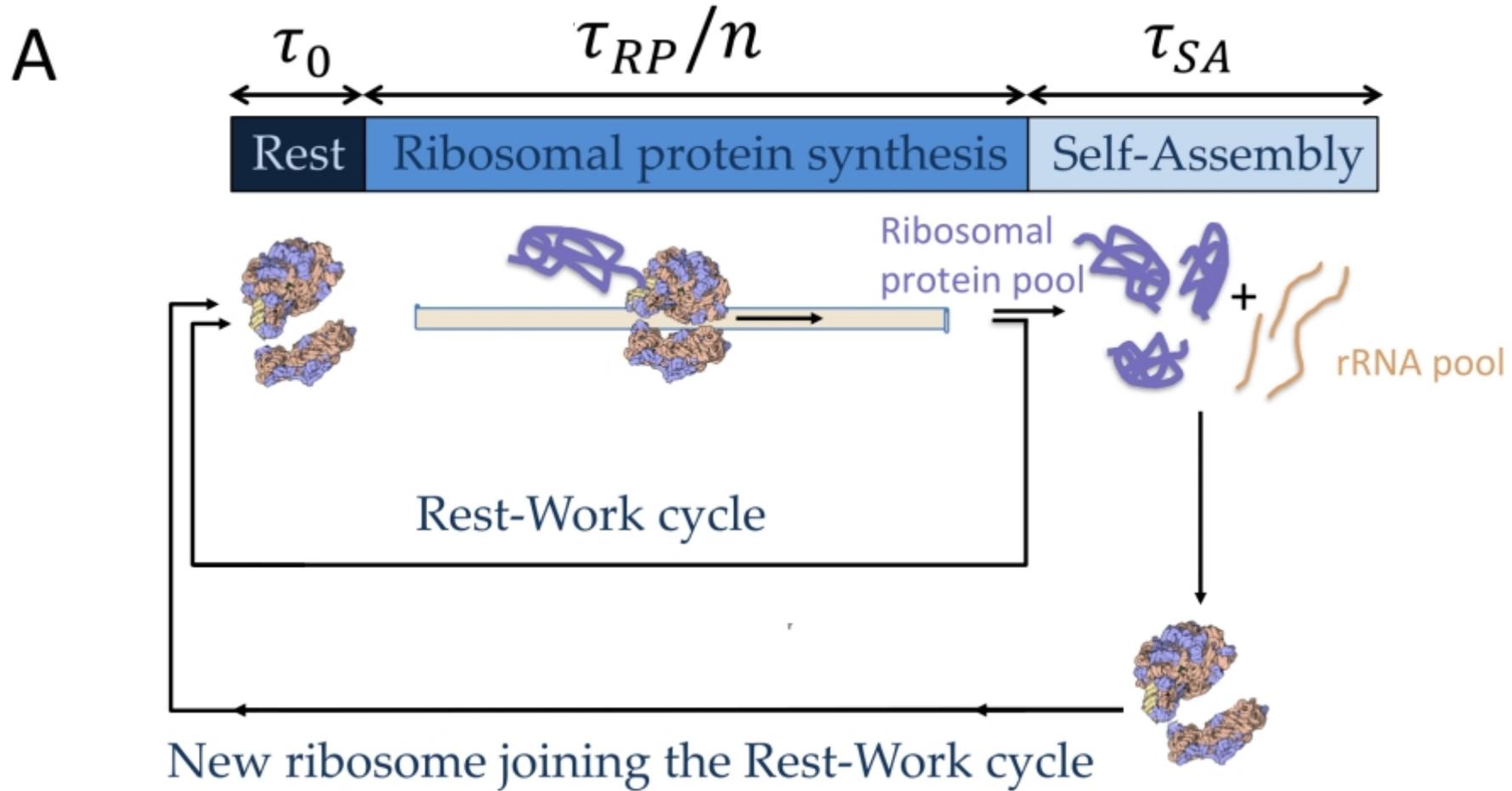


Ribosome

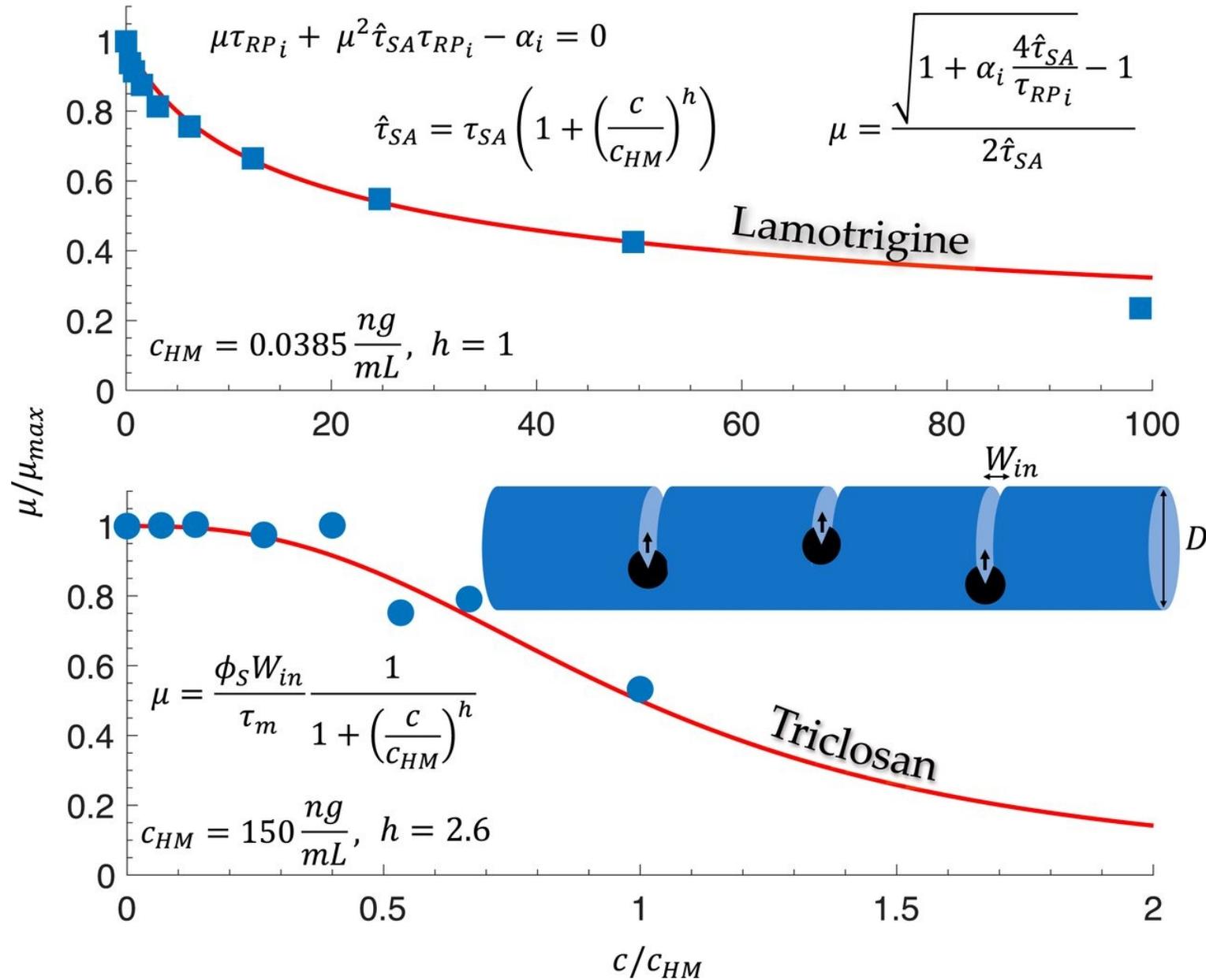
mRNA



DNA



Effect of two antibacterial agents—lamotrigine and triclosan—on E. coli



Q: What about noise?

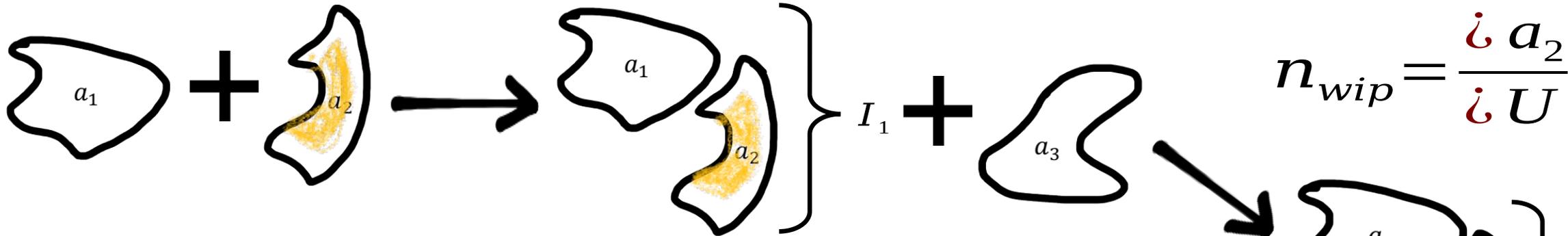
A: Surprisingly unimportant

*Approximate growth law:
Little's law for self-replicating factories*

$$\mu \approx \frac{(1 - \sqrt{1 - cv^2 n_{WIP}})}{\tau_{SA} \frac{cv^2}{2}} \approx \frac{n_{WIP}}{\tau_{SA}}$$

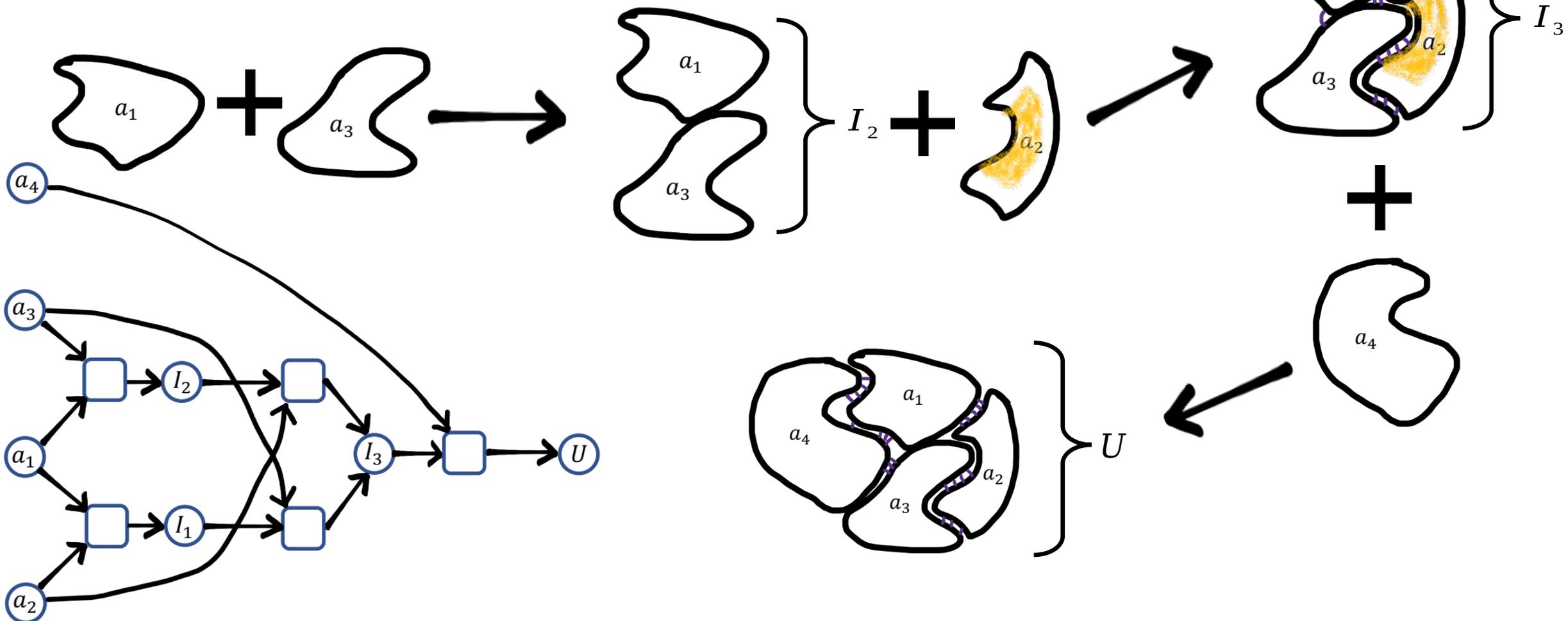
2nd order (cv = coefficient of variation)

1st order (n_{WIP} = relative work in process – percentage)



Parallel assembly with competing pathways (PACA)

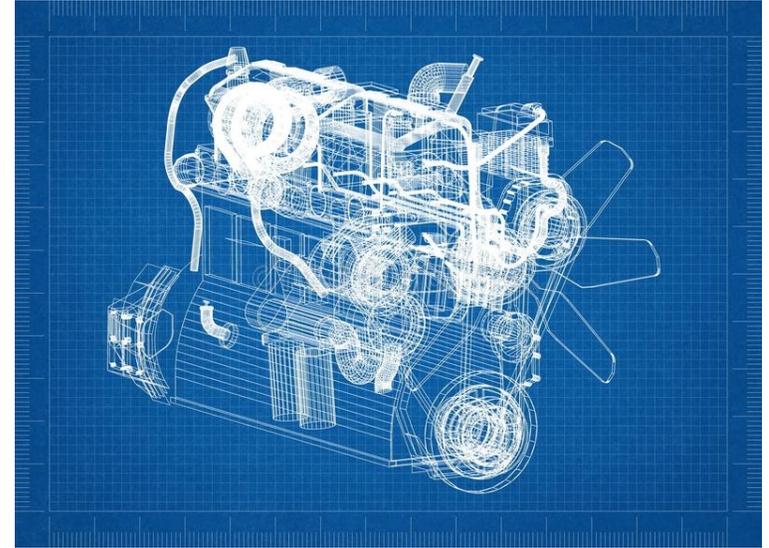
$$n_{wip} = \frac{i a_2}{i U}$$



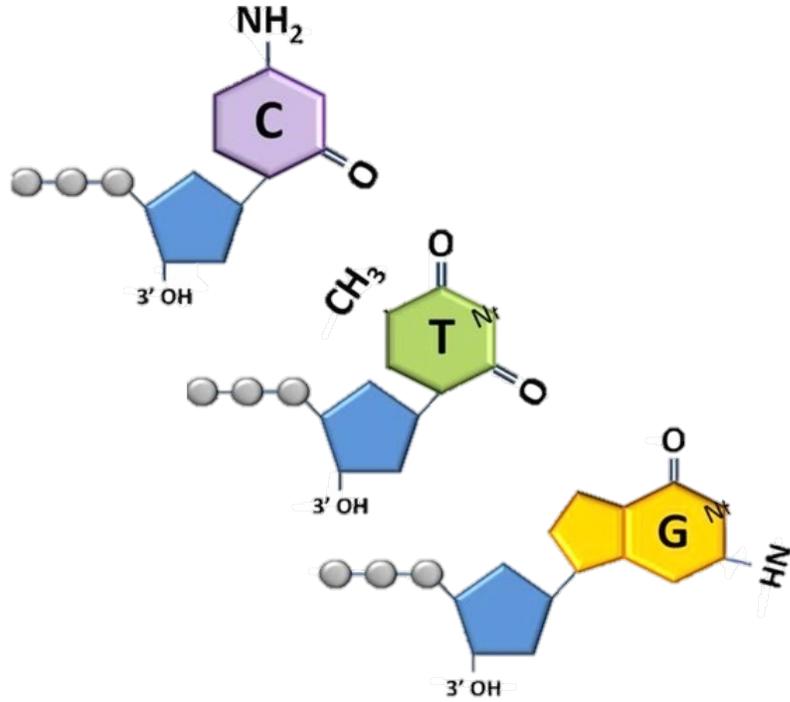
Coolant Leakage due to a hole in the radiator



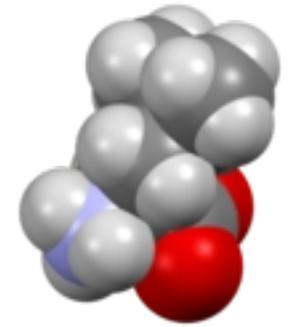
Inspecting engine blueprints will not reveal the cause unless malfunction is due to an inherent design flaw



The genetic code



CTG



Leucine

“Laplace transform of assembly time evaluated at $s =$ growth rate $= 1/(1+\text{relative WIP})$ ”

$$P_{SA}(\mu) = \frac{1}{1 + n_{WIP}}$$

Distribution	Laplace transform	Growth rate	Relative WIP
Deterministic	$e^{-\mu\tau_{SA}}$	$\mu = \frac{1}{\tau_{SA}} \ln(1 + n_{WIP})$	$n_{WIP} = e^{\mu\tau_{SA}} - 1$
Exponential	$\frac{1}{1 + \mu\tau_{SA}}$	$\mu = \frac{n_{WIP}}{\tau_{SA}}$	$n_{WIP} = \mu\tau_{SA}$
Erlang -k	$\frac{1}{\left(1 + \frac{\mu\tau_{SA}}{k}\right)^k}$	$\mu = \frac{k}{\tau_{SA}} \left(\sqrt[k]{1 + n_{WIP}} - 1\right)$	$n_{WIP} = \left(1 + \frac{\mu\tau_{SA}}{k}\right)^k - 1$
Mixture of two exponentials	$\frac{p\lambda_1}{\lambda_1 + \mu} + \frac{(1-p)\lambda_2}{\lambda_2 + \mu}$	Numerical	Numerical
Shifted exponential	$\frac{e^{-\mu\tau}}{1 + \frac{\mu}{\lambda}}$	$\mu = \frac{\mathcal{L}_w \lambda \left(\tau e^{\lambda\tau} (1 + n_{WIP})\right)}{\tau} - \lambda$	$n_{WIP} = e^{\mu\tau} \left(1 + \frac{\mu}{\lambda}\right) - 1$