

Part 2: Dynamical cell models

What is a cell model?

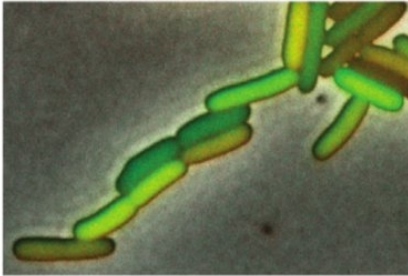
How would you design a mathematical model of a cell?

What do you recall about differential equations and linear algebra?

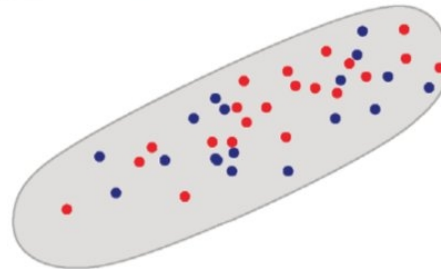
From pictures of cells to mathematical models

Simulation models are simple pictures of cells, in a mathematical form

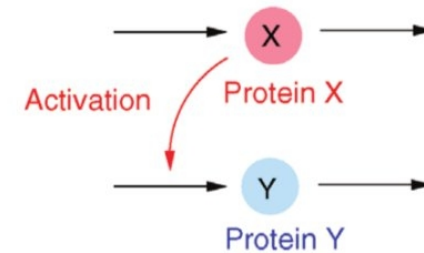
(a) Biological system



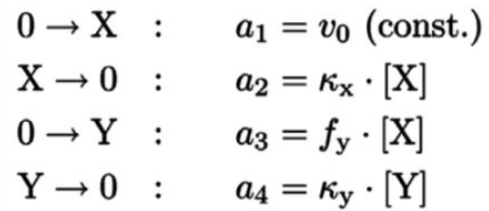
(b) Mental model



(c) Model scheme



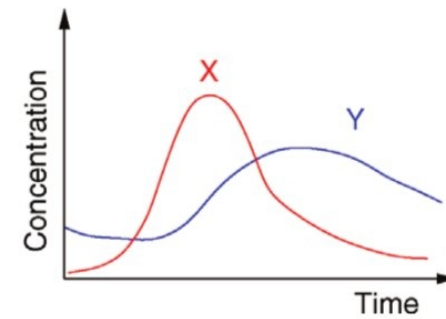
(d) Process model



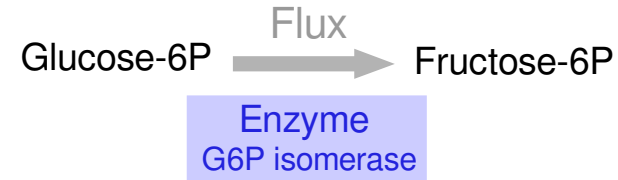
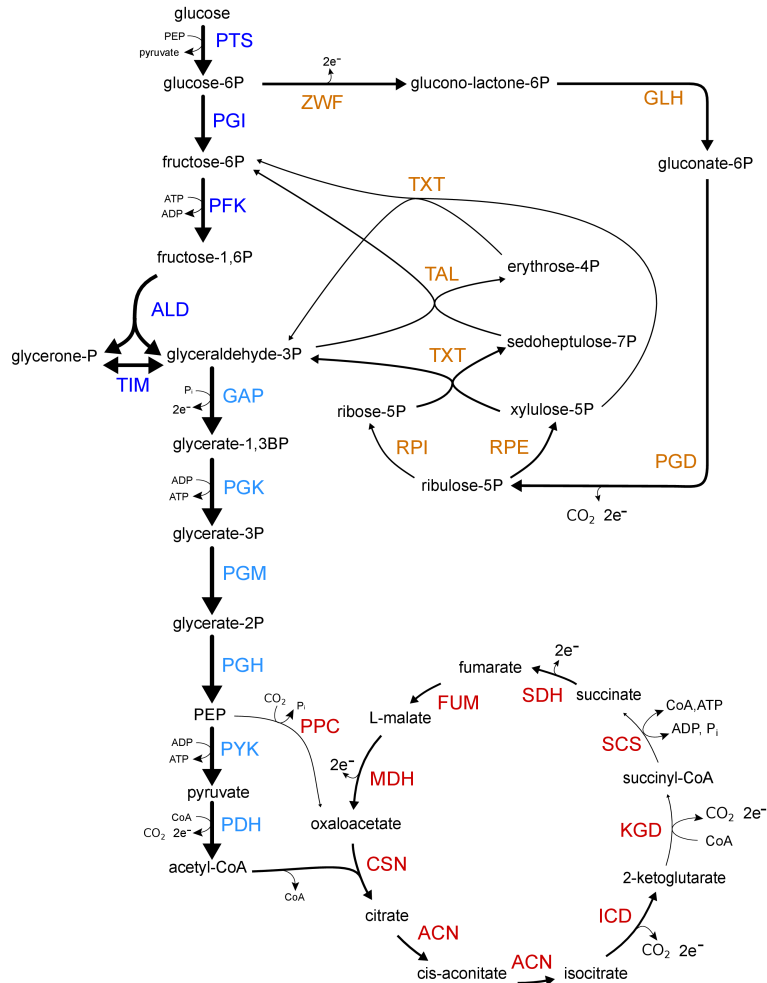
(e) Dynamical model

$$\begin{aligned}
 dx/dt &= v_0 - \kappa_x x \\
 dy/dt &= f_y x - \kappa_y y \\
 x(0) &= x_0 \\
 y(0) &= y_0
 \end{aligned}$$

(f) Quantitative results



Metabolic pathway models



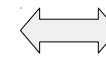
Rate law

$$v = [\text{enzyme}] \frac{k_{\text{cat}} [\text{G6P}]}{[\text{G6P}] + K_M}$$

Main model types

Kinetic models

- predict dynamics
- high data demand
- fully mechanistic

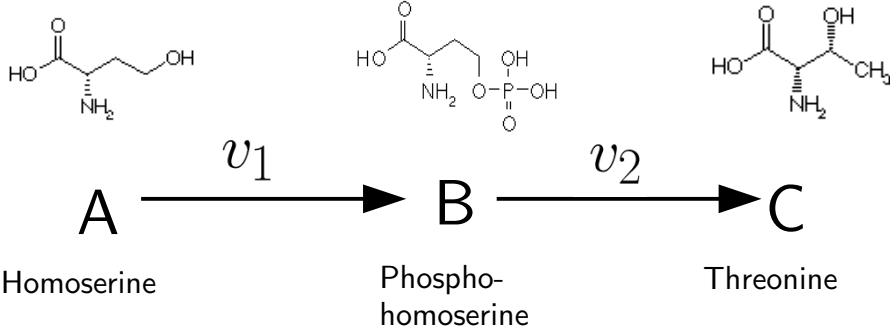


Constraint-based models

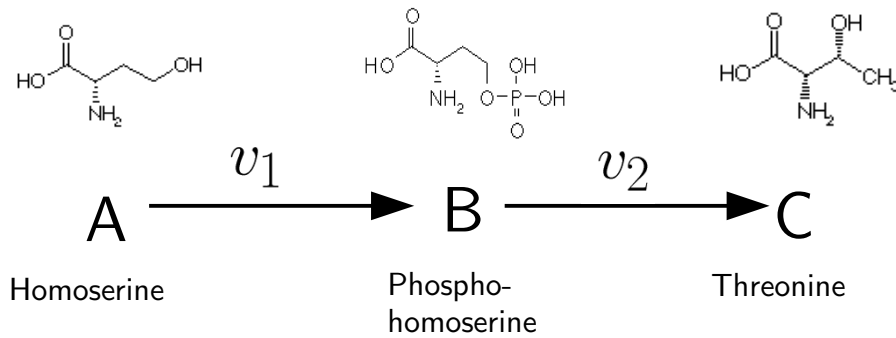
- predict stationary fluxes
- use network structure only
- use heuristic principles

Kinetic models of metabolic pathways

Kinetic models describe the dynamics of biochemical reactions



Kinetic models describe the dynamics of biochemical reactions



Kinetic rate law: “mass-action kinetics”

How often does the reaction occur per time?

$$v_1(a, b) = k_{1+} a - k_{1-} b$$

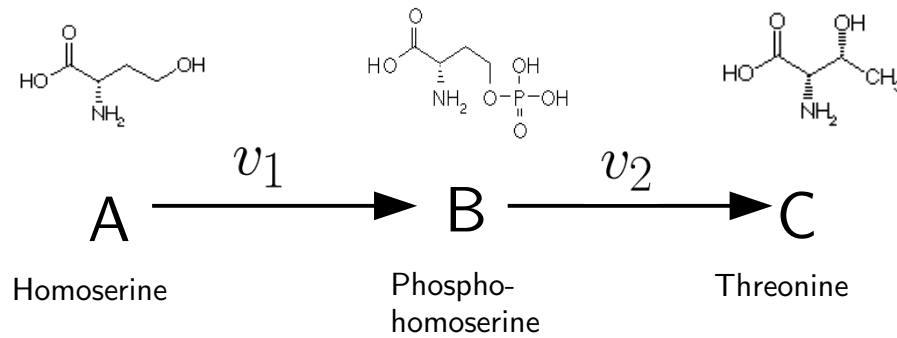
$$v_2(b, c) = k_{2+} b - k_{2-} c$$

↑
reaction rate

↑
kinetic
constant

↑
metabolite
concentration

Kinetic models describe the dynamics of biochemical reactions



Kinetic rate law: “mass-action kinetics”

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↑
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↑
kinetic constant

↑
metabolite concentration

System equations

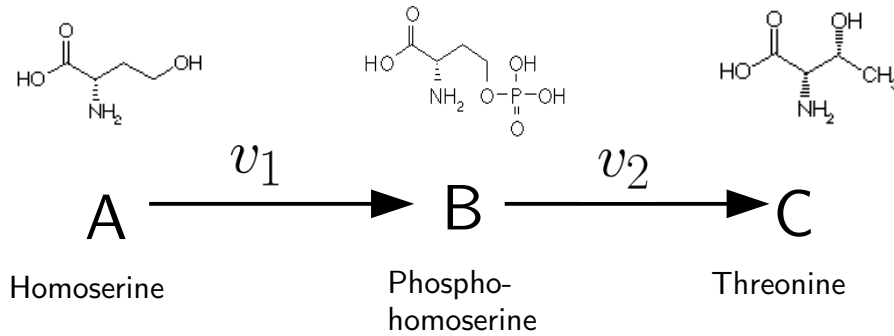
How do the concentrations change over time?

$$da/dt = -v_1$$

$$db/dt = v_1 - v_2$$

$$dc/dt = v_2$$

Kinetic models describe the dynamics of biochemical reactions



Kinetic rate law: "mass-action kinetics"

How often does the reaction occur per time?

$$v_1(a, b) = k_{1+} a - k_{1-} b$$

$$v_2(b, c) = k_{2+} b - k_{2-} c$$

↑
reaction rate

↑
kinetic constant

↑
metabolite concentration

concentration change

stoichiometric coefficient

kinetic rate law (reaction rate)

$$\frac{ds_i}{dt} = \sum_l n_{il} v_l(s, k)$$

metabolite concentrations

kinetic parameters, enzyme concentrations

System equations

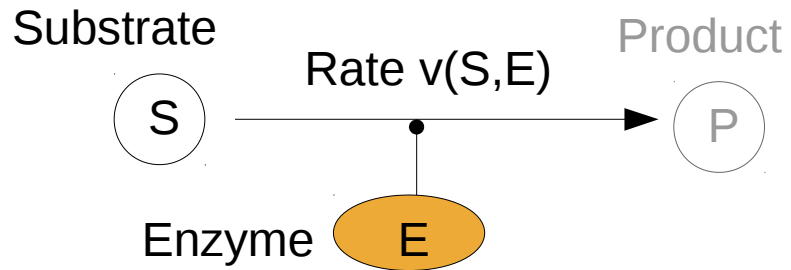
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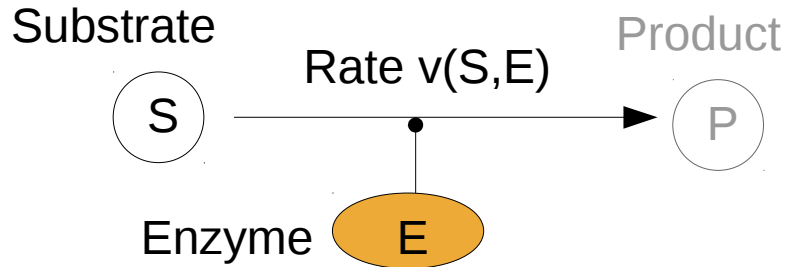
$$dc/dt = v_2$$

The irreversible Michaelis-Menten rate law

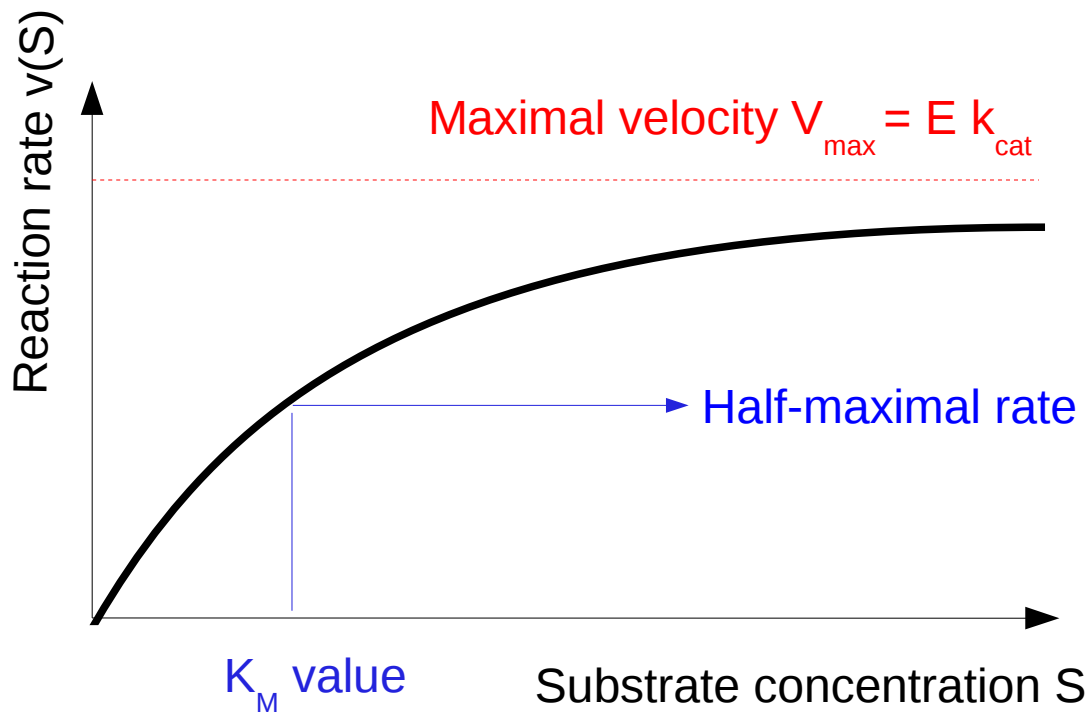


$$v(S, E) = \underbrace{E k_{\text{cat}}}_{V_{\text{max}}} \frac{S}{S + K_M}$$

The irreversible Michaelis-Menten rate law



$$v(S, E) = \underbrace{E k_{\text{cat}}}_{V_{\text{max}}} \frac{S}{S + K_M}$$



Variables:

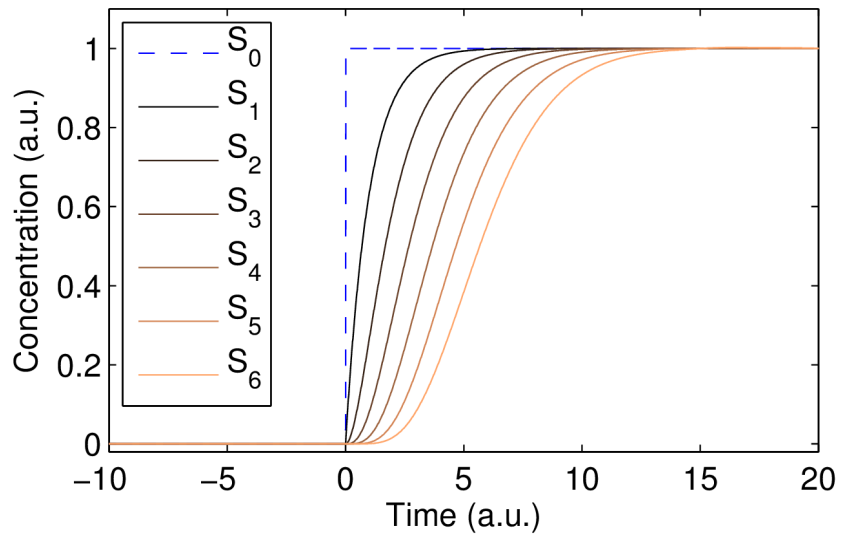
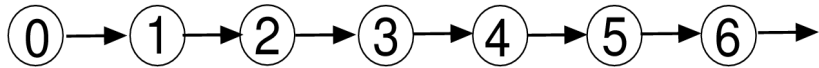
- Substrate concentration s
- Enzyme concentration E

Parameters:

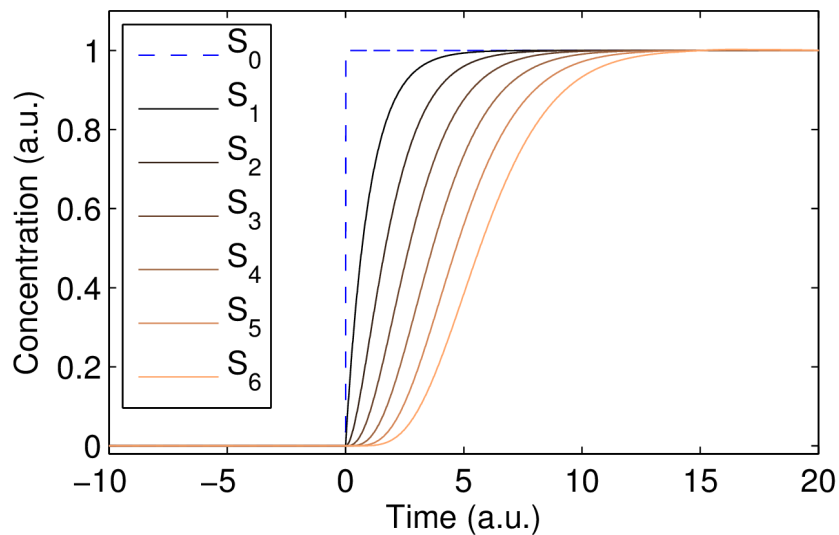
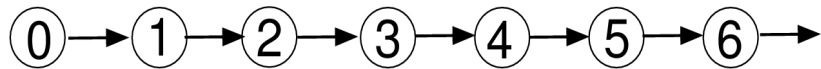
- K_M value (in mM): inverse binding affinity
- Catalytic constant k_{cat} (in 1/s)
Maximal number of conversions per time and enzyme molecule

Dynamic behaviour and steady state

Differential equations describe the change in a moment - numerical integration yields the overall behaviour in time



Differential equations describe the change in a moment - numerical integration yields the overall behaviour in time



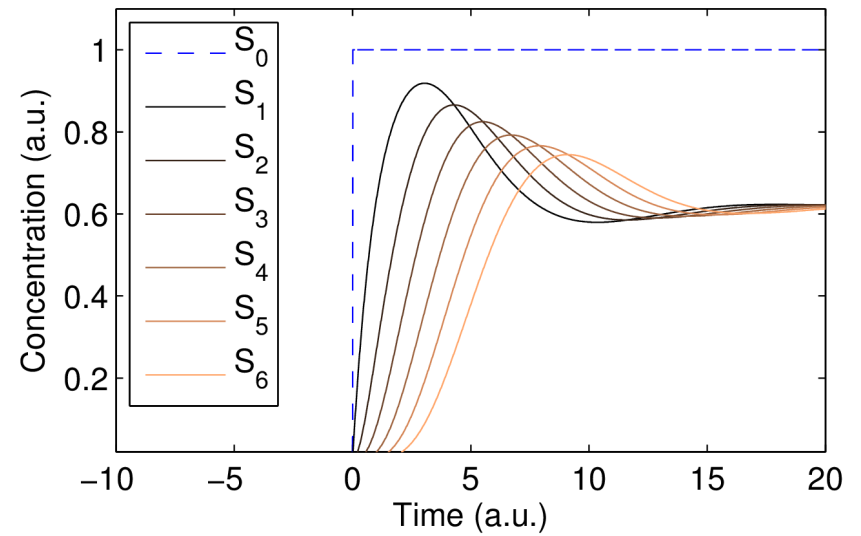
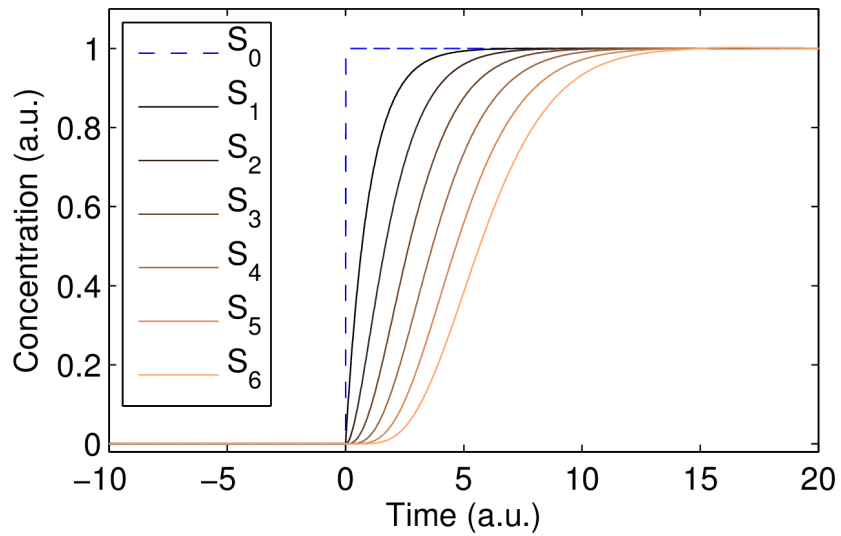
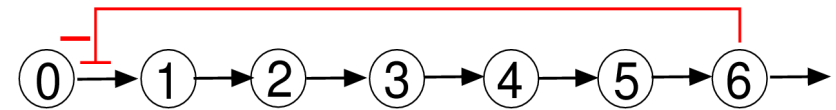
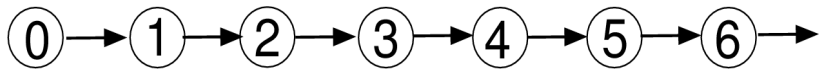
A simple way to solve differential equations numerically (“Euler method”)

- Consider fixed, small time step!
- Start with initial values $s(t=0)$
- Use the updating rule:

$$s(t + \Delta t) = s(t) + \frac{ds}{dt} \Delta t$$

- Repeat the last step many times

Dynamic behaviour depends on small details of a model



In steady states, all substance levels remain constant in time

Stationarity condition in kinetic models

$$\frac{dc}{dt} = Nv = 0$$

Condition on the flux vector
Kinetic rate laws do not play a role!

External metabolites (e.g. extracellular or buffered)

→ Treated as fixed parameters

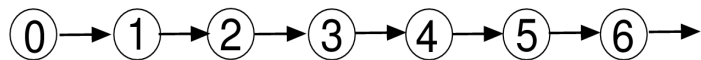
Intracellular metabolites (dynamic)

→ Concentration varies due to chemical reactions

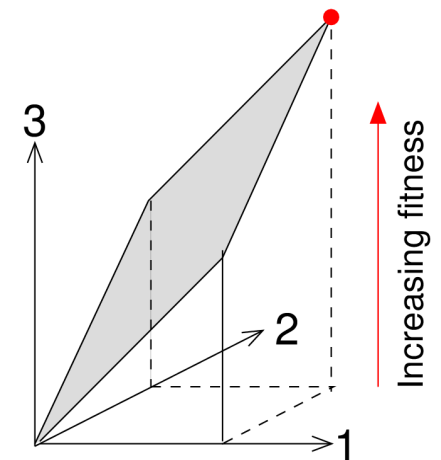
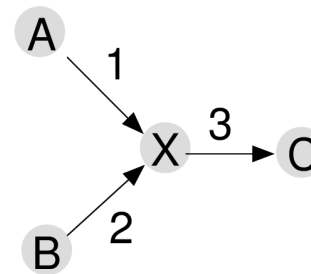
Stationary (=steady) state

A state in which all variables remain constant in time

Linear pathway

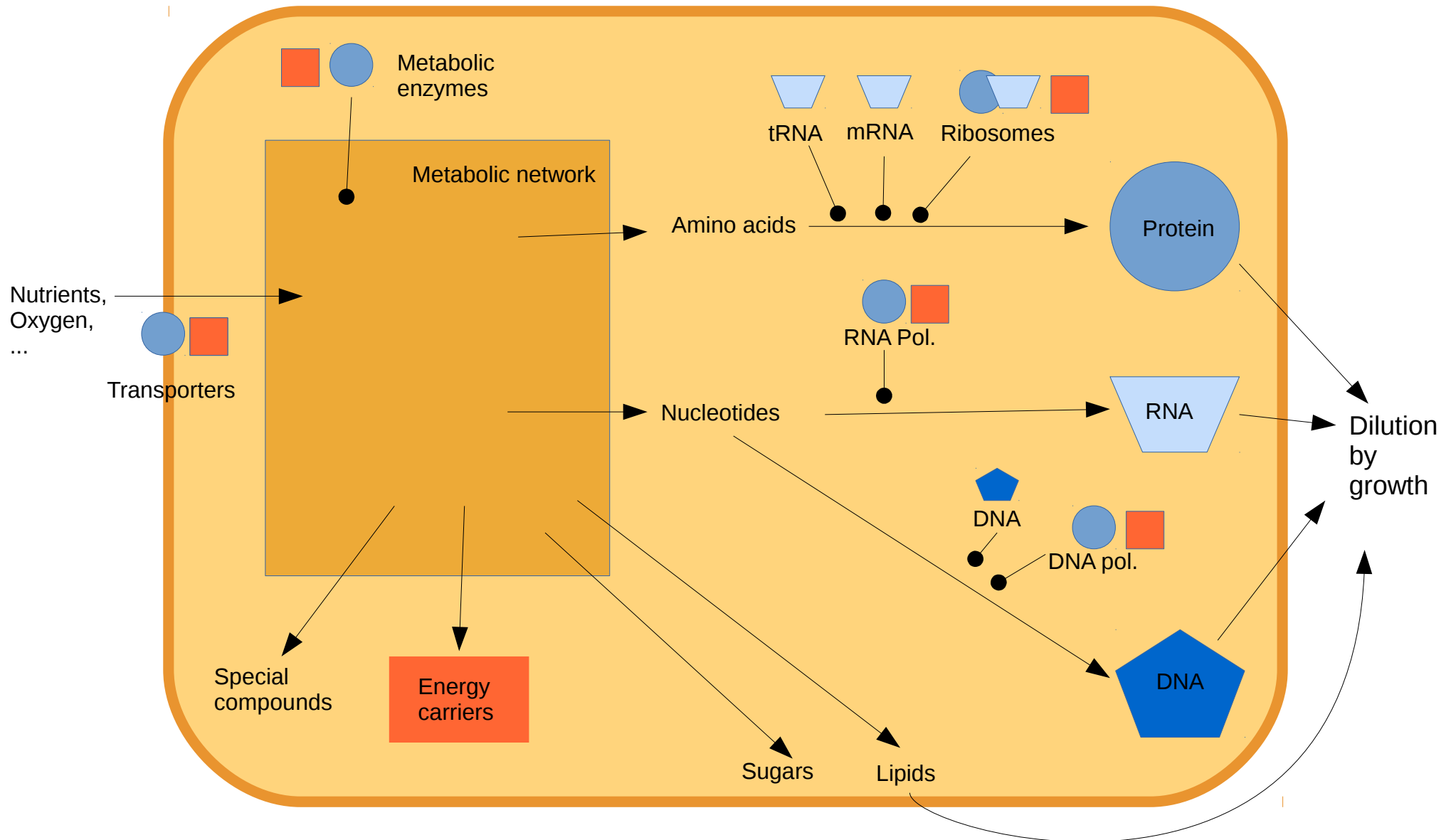


Branch point



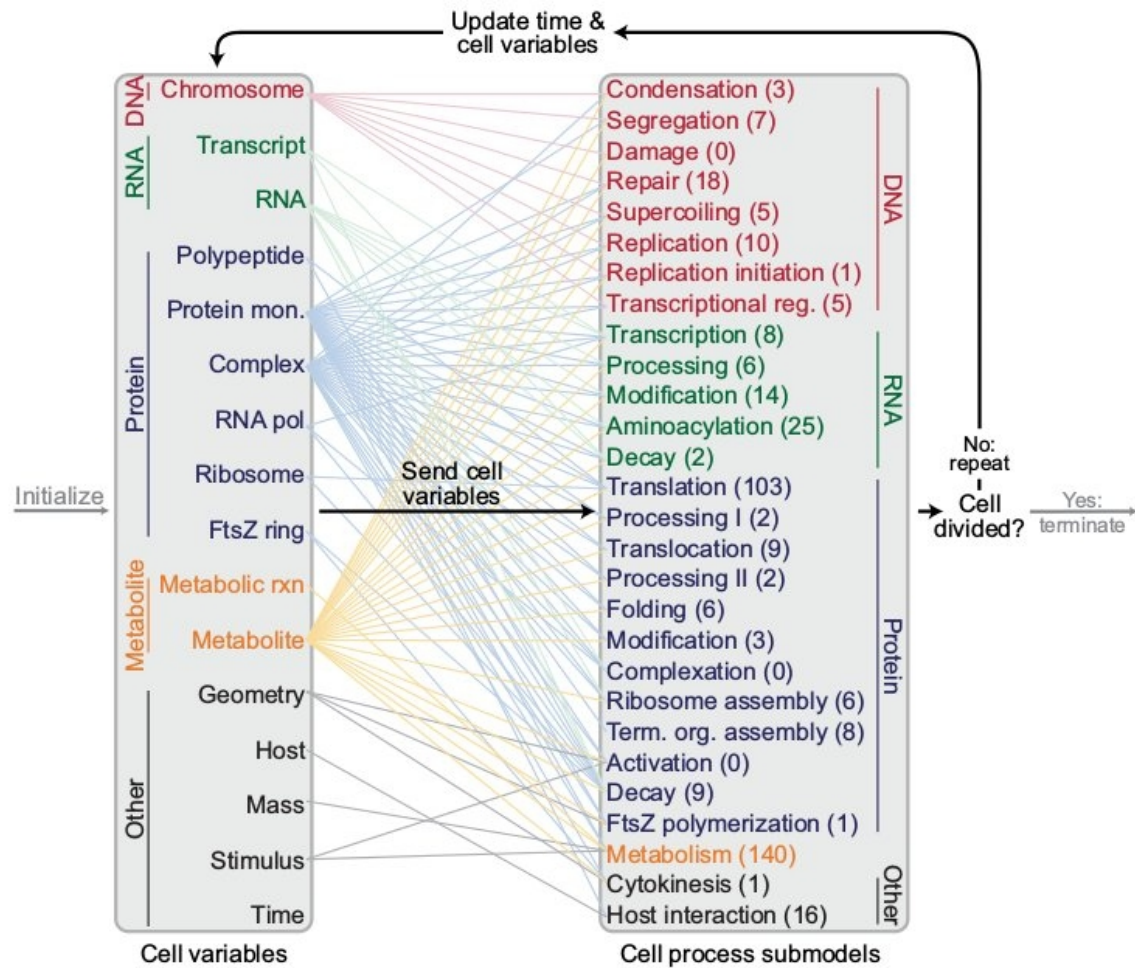
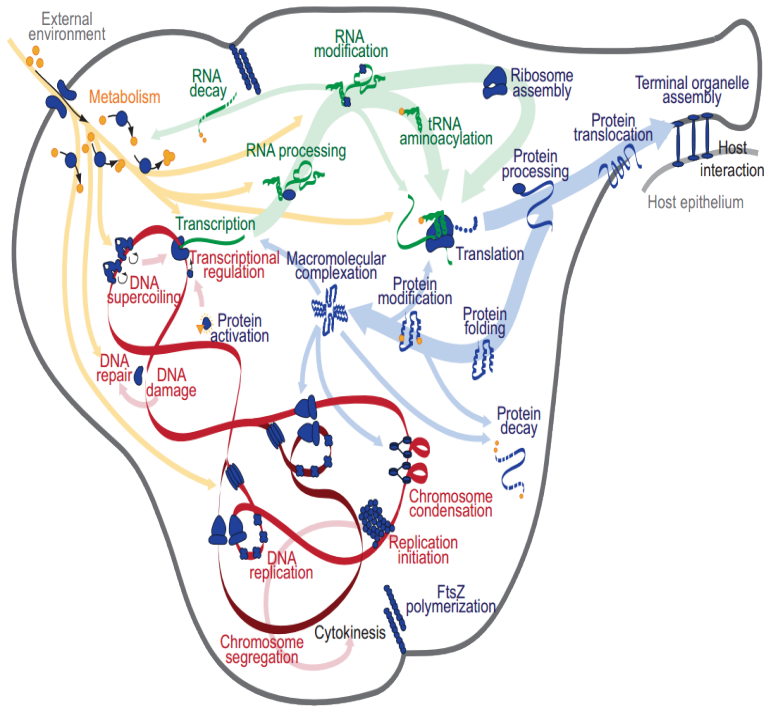
Modular whole-cell models

The cell as a self-replicating factory



A whole-cell model for *Mycoplasma pneumoniae*

Whole-cell model overview



How the modular whole-cell model is simulated

