

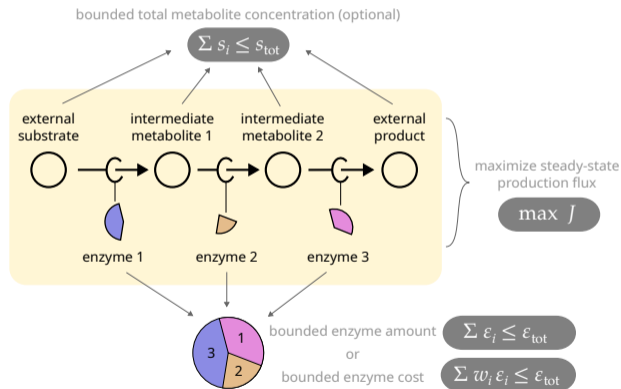
Optimal enzyme profiles in metabolic pathways: principles and simple solutions

Workshop SPT Chemical Reaction Networks

Elad Noor, Wolfram Liebermeister

June 10-14, 2024

The problem: allocate enzymes to maximize a metabolic pathway flux



Kinetic metabolic models and flux balance models

Kinetic metabolic models describe the metabolic reaction rates v_l depending on enzyme levels ε_l and metabolite concentrations c_i :

$$v_l = \varepsilon_l f_l(\mathbf{c})$$

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Metabolite dynamics (for “internal” metabolites i) depends on the rates v_l and on stoichiometric coefficients n_{il} :

$$\frac{dc_i}{dt} = \sum_l n_{il} v_l(\mathbf{c})$$

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Flux analysis models ignore dynamics and determine steady fluxes $J_l = v_l$ satisfying

$$0 = \sum_l n_{il} J_l$$

What is the enzyme cost of a metabolic flux distribution?

Given a stationary flux distribution J_l and remembering the rate laws

$$v_l = \varepsilon_l f_l(\mathbf{c}),$$

by solving for the enzyme levels ε_l we obtain the overall enzyme demand

$$\varepsilon_{\text{tot}}(\mathbf{J}) = \sum_l \varepsilon_l = \sum_l \frac{J_l}{f_l(\mathbf{c})}$$

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For fixed concentrations c_i , the enzyme efficiencies $k_l^{\text{app}} = f_l(\mathbf{c})$ are constant and

$$\varepsilon_{\text{tot}}(\mathbf{J}) = \sum_l \frac{J_l}{k_l^{\text{app}}}$$

The demand scales linearly with the fluxes (and hence, with the system's “output flux”)

With “trivial” kinetics: enzyme efficiencies are inversely additive

We assume a pathway with stationary flux J and constant efficiencies, $v_l = \varepsilon_l k_l^{\text{app}}$.
Setting $v_i = J$ and solving for ε_l , we obtain the enzyme demand

$$\varepsilon_{\text{tot}} = \sum_l \varepsilon_l = \sum_l \frac{1}{k_l^{\text{app}}} \cdot J$$

So we can write the pathway flux as

$$J = k_{\text{tot}}^{\text{app}} \varepsilon_{\text{tot}}$$

with the effective pathway efficiency

$$k_{\text{tot}}^{\text{app}} = \frac{1}{\sum_l \frac{1}{k_l^{\text{app}}}}$$

The inverse k^{app} are times, and additive like resistances in a series of resistors.

Reversible enzyme kinetics based on Haldane

For a reversible enzyme catalyzed reaction¹: $S \xrightleftharpoons{E} P$

$$v = \varepsilon \cdot \underbrace{\frac{k_+^{\text{cat}} s/K_S - k_-^{\text{cat}} p/K_P}{1 + s/K_S + p/K_P}}_{k^{\text{app}}}$$

¹ s , p , and ε are the concentrations of S , P , and E

Reversible enzyme kinetics based on Haldane

For a reversible enzyme catalyzed reaction¹: $S \xrightleftharpoons{E} P$

$$v = \varepsilon \cdot \underbrace{\frac{k_+^{\text{cat}} s/K_S - k_-^{\text{cat}} p/K_P}{1 + s/K_S + p/K_P}}_{k^{\text{app}}}$$

Haldane further showed that the equilibrium constant satisfies the following relationship:

$$K^{\text{eq}} = \frac{k_+^{\text{cat}} K_P}{k_-^{\text{cat}} K_S}$$

¹ s , p , and ε are the concentrations of S , P , and E

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The Haldane rate law can be rewritten (Noor et al. [2013]) as²:

$$v = \underbrace{\varepsilon \cdot k_+^{\text{cat}}}_{V_{\text{max}}} \cdot \underbrace{\left(1 - e^{\frac{\Delta_r G'}{RT}}\right)}_{\eta^{\text{for}}} \cdot \underbrace{\frac{\frac{s}{K_S}}{1 + \frac{p}{K_P} + \frac{s}{K_S}}}_{\eta^{\text{kin}}}$$

¹ s , p , and ε are the concentrations of S , P , and E

²where $\Delta_r G' \equiv \Delta_r G'^{\circ} + R T \ln(p/s)$ and $\Delta_r G'^{\circ} = -R T \ln(K^{\text{eq}})$

Enzyme Cost Minimization: minimize the enzyme demand of a given flux!

Given a pathway with fixed flux and with enzymatic reactions with Haldane rate laws, look for metabolite and enzyme levels that minimize the sum of all enzyme demands.

Enzyme Cost Minimization: minimize the enzyme demand of a given flux!

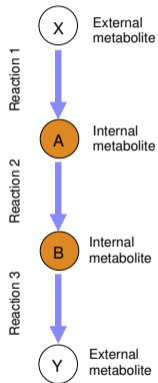
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Enzyme demand in one reaction

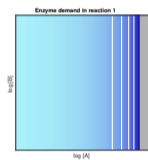
$$\varepsilon = J \cdot \frac{1}{k_+^{\text{cat}}} \cdot \underbrace{\left(1 - e^{-\frac{\Delta_r G'}{RT}}\right)^{-1}}_{1/\eta^{\text{for}}} \cdot \underbrace{\frac{1 + \frac{p}{K_P} + \frac{s}{K_S}}{\frac{s}{K_S}}}_{1/\eta^{\text{kin}}}$$

The pathway cost per flux ($\varepsilon_{\text{tot}}/J$) is the sum of demands for all reactions: a **convex** function of metabolite log-concentrations (Liebermeister and Noor [2015]).

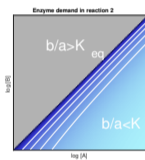
Example: the enzyme demand in a 3-step pathway



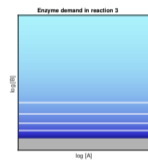
demand in reaction 1



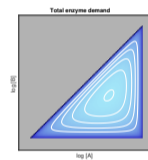
demand in reaction 2



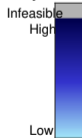
demand in reaction 3



total demand



Enzyme demand



Can we find analytical solutions to ECM?

Analytical solutions¹ are useful because they:

- 1 Ensure solution optimality
- 2 Help find hidden relationships
- 3 Inspire design principles
- 4 Suggest mechanisms

¹Noor and Liebermeister [2024]

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Problem

Kinetic models, where reactions have multi-substrate or Haldane rate laws, do not have known analytical solutions.

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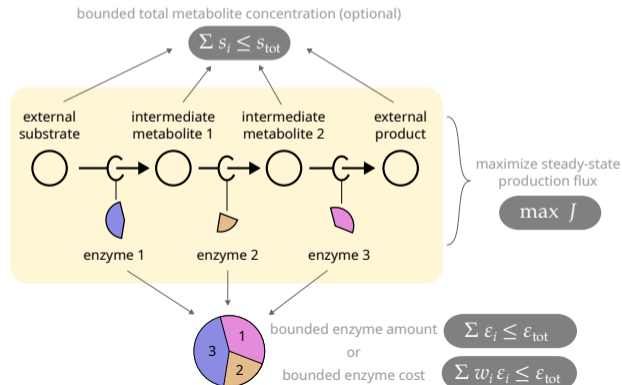
Kinetic models, where reactions have multi-substrate or Haldane rate laws, do not have known analytical solutions.

Solution: focus only on unbranched pathways with simplified kinetics.

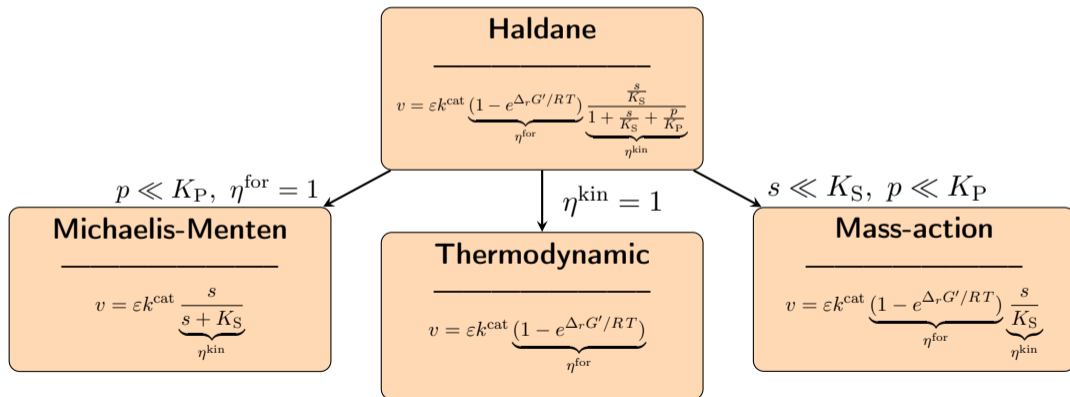
¹Noor and Liebermeister [2024]

We come back to our full optimality problem

Instead of Enzyme Cost Minimization (minimizing enzyme at given fluxes):
 Maximize the pathway flux with a bound on enzyme (and possible on metabolite) levels!



The factorized Haldane rate law and some simplifications



The “mass-action” approximation

Haldane:

$$v = \varepsilon \cdot \frac{k_+^{\text{cat}} s/K_S - k_-^{\text{cat}} p/K_P}{1 + s/K_S + p/K_P}$$

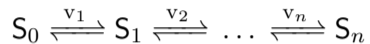
If we assume:

$$s \ll K_S, p \ll K_P$$

Therefore:

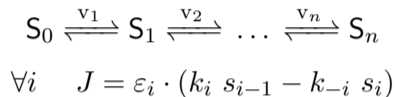
$$v = \varepsilon \cdot \left(\underbrace{\frac{k_+^{\text{cat}}}{K_S}}_{k_+} \cdot s - \underbrace{\frac{k_-^{\text{cat}}}{K_P}}_{k_-} \cdot p \right)$$

Unbranched pathway with “mass-action” kinetics



$$\forall i \quad J = \varepsilon_i \cdot (k_i s_{i-1} - k_{-i} s_i)$$

Unbranched pathway with “mass-action” kinetics

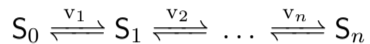
Optimized flux solution²

$$J^* = \varepsilon_{\text{tot}} \cdot \frac{s_0 - s_n / K^{\text{eq}}}{(\sum_i \sqrt{\gamma_i})^2}$$

where $\gamma_i \equiv \frac{\prod_{j=i+1}^n k_j}{\prod_{j=i}^n k_{-j}}$ and $K^{\text{eq}} \equiv \frac{\prod_{j=1}^n k_j}{\prod_{j=1}^n k_{-j}}$

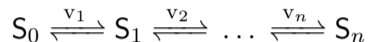
²Waley [1964], Burns [1971]

Unbranched pathway with “thermodynamic” kinetics



$$J = \varepsilon_i k_i^{\text{cat}} \left(1 - e^{\Delta_r G'_i / RT} \right)$$

Unbranched pathway with “thermodynamic” kinetics



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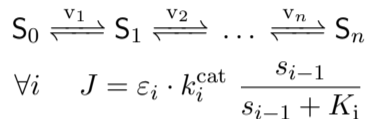
Optimized flux (approximated) solution³

$$J^* \approx \varepsilon_{\text{tot}} \cdot \frac{1}{a} \left(1 - \exp \left(\frac{a}{b} \frac{\Delta_r G'_{\text{tot}}}{RT} \right) \right)$$

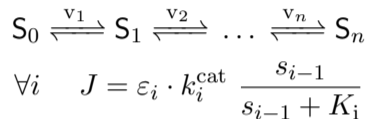
where $a \equiv \sum_j \frac{1}{k_j^{\text{cat}}}$, $b \equiv \sum_j \frac{1}{\sqrt{k_j^{\text{cat}}}}$, and $\Delta_r G'_{\text{tot}} \equiv \sum_j \Delta_r G'_j$

³Noor and Liebermeister [2024]

Unbranched pathway with Michaelis-Menten kinetics

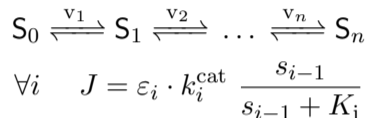


Unbranched pathway with Michaelis-Menten kinetics



Optimizing J would require infinite metabolite concentrations!
 Therefore we add a total metabolite constraint: $\sum_i s_i \leq s_{\text{tot}}$

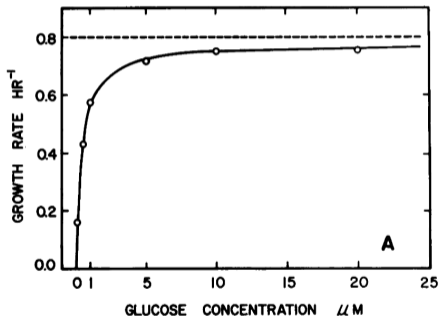
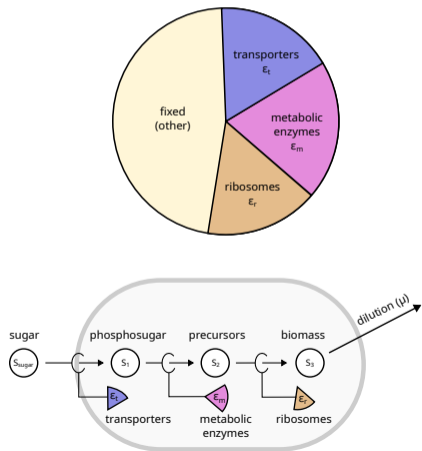
Unbranched pathway with Michaelis-Menten kinetics

Optimized flux solution⁴

$$J^* = \varepsilon_{\text{tot}} \cdot \frac{1}{\sum_j 1/k_j^{\text{cat}} + \left(\sum_j \sqrt{K_j/k_j^{\text{cat}}} \right)^2 / s_{\text{tot}}}$$

⁴Noor and Liebermeister [2024]

An application of simple pathway models: a model of a growing cell

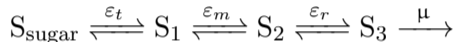


Monod curve for *E. coli* on glucose (Shehata and Marr [1971]).

An application of simple pathway models: a model of a growing cell

Assume:

- **Coarse-graining:** 3 enzymatic processes



- **Controlled parameter:** s_{sugar}

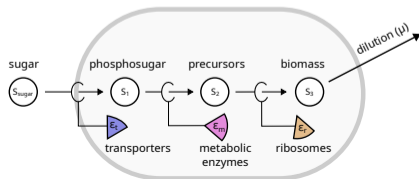
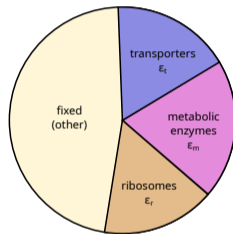
- **Constraint:** $\varepsilon_t + \varepsilon_m + \varepsilon_r = \varepsilon_{\text{tot}}$

- **Optimization:** maximize growth rate (μ)

- **Rate laws:** mass-action, thermodynamic, or Michaelis-Menten^a

- **Not included:** metabolite dilution by growth

^aExtra constraint: $s_{\text{tot}} \geq s_1 + s_2 + s_3$



Cell model example (1): mass-action kinetics

$$\mu = \varepsilon_{\text{tot}} \cdot \frac{s_0 - s_n / K^{\text{eq}}}{\left(\sum_i \sqrt{\gamma_i}\right)^2}$$

where

$$\gamma_t \equiv \frac{K_{M;t}}{k_t^{\text{cat}}} \cdot K_r^{\text{eq}} \cdot K_m^{\text{eq}} \cdot K_t^{\text{eq}}$$

$$\gamma_m \equiv \frac{K_{M;m}}{k_m^{\text{cat}}} \cdot K_r^{\text{eq}} \cdot K_m^{\text{eq}}$$

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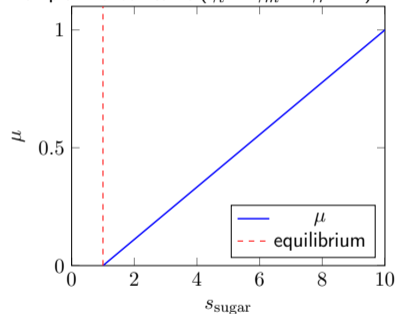
where

$$\gamma_t \equiv \frac{K_{M;t}}{k_t^{\text{cat}}} \cdot K_r^{\text{eq}} \cdot K_m^{\text{eq}} \cdot K_t^{\text{eq}}$$

$$\gamma_m \equiv \frac{K_{M;m}}{k_m^{\text{cat}}} \cdot K_r^{\text{eq}} \cdot K_m^{\text{eq}}$$

$$\gamma_r \equiv \frac{K_{M;r}}{k_r^{\text{cat}}} \cdot K_r^{\text{eq}}$$

Example "Monod" curve ($\gamma_t = \gamma_m = \gamma_r = 1$)



Cell model example (2): “thermodynamic” kinetics

$$\mu \approx \varepsilon_{\text{tot}} \cdot \frac{1}{a} \left(1 - e^{-\frac{a}{b} \cdot \ln\left(s_{\text{sugar}} \frac{K^{\text{eq}}}{s_3}\right)} \right)$$

where

$$a \equiv \frac{1}{k_t^{\text{cat}}} + \frac{1}{k_m^{\text{cat}}} + \frac{1}{k_r^{\text{cat}}}$$

$$b \equiv \frac{1}{\sqrt{k_t^{\text{cat}}}} + \frac{1}{\sqrt{k_m^{\text{cat}}}} + \frac{1}{\sqrt{k_r^{\text{cat}}}}$$

$$K^{\text{eq}} \equiv K_r^{\text{eq}} \cdot K_m^{\text{eq}} \cdot K_t^{\text{eq}}$$

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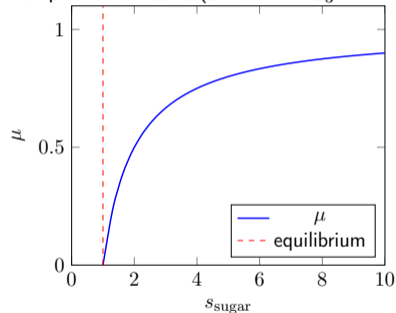
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$$K^{\text{eq}} \equiv K_r^{\text{eq}} \cdot K_m^{\text{eq}} \cdot K_t^{\text{eq}}$$

Example “Monod” curve ($a = b = 1 = s_3 = K^{\text{eq}} = 1$)

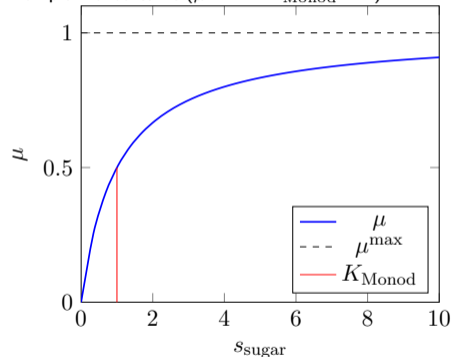


Cell model example (3): Michaelis-Menten kinetics

$$\mu = \mu^{\max} \cdot \frac{s_{\text{sugar}}}{s_{\text{sugar}} + K_{\text{Monod}}}$$

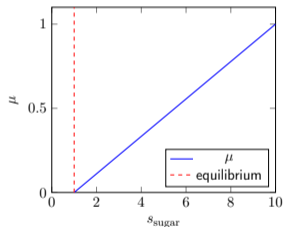
$$\mu^{\max} \equiv \frac{\varepsilon_{\text{tot}}}{\frac{1}{k_t^{\text{cat}}} + \frac{1}{k_m^{\text{cat}}} + \frac{1}{k_r^{\text{cat}}} + \left(\sqrt{\frac{K_{\text{M};m}}{k_m^{\text{cat}}} + \sqrt{\frac{K_{\text{M};r}}{k_r^{\text{cat}}}} \right)^2 \frac{1}{s_{\text{tot}}}}$$

$$K_{\text{Monod}} \equiv \frac{K_{\text{M};t}/k_t^{\text{cat}}}{\frac{1}{k_t^{\text{cat}}} + \frac{1}{k_m^{\text{cat}}} + \frac{1}{k_r^{\text{cat}}} + \left(\sqrt{\frac{K_{\text{M};m}}{k_m^{\text{cat}}} + \sqrt{\frac{K_{\text{M};r}}{k_r^{\text{cat}}}} \right)^2 \frac{1}{s_{\text{tot}}}}$$

Example Monod curve ($\mu^{\max} = K_{\text{Monod}} = 1$)

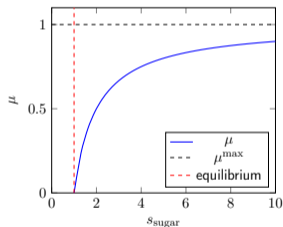
Summary of three cell models

Mass-action



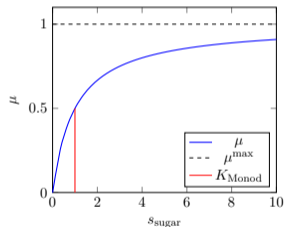
$$\mu = a \cdot s_{\text{sugar}} \cdot \left(1 - \frac{s_3}{s_{\text{sugar}} K^{\text{eq}}}\right)$$

Thermodynamic



$$\mu \approx \mu_{\text{max}} \cdot \left(1 - \left(\frac{s_3}{s_{\text{sugar}} K^{\text{eq}}}\right)^b\right)$$

Michaelis-Menten



$$\mu = \mu_{\text{max}} \cdot \frac{s_{\text{sugar}}}{s_{\text{sugar}} + K_{\text{Monod}}}$$

Take-home messages

- Enzyme Cost Minimization is a **convex** problem

Take-home messages


- Enzyme Cost Minimization is a **convex** problem
- For some special cases, we provide **analytical** solutions

Take-home messages

- Enzyme Cost Minimization is a **convex** problem
- For some special cases, we provide **analytical** solutions
- We can use these results to build **coarse-grained** cell models

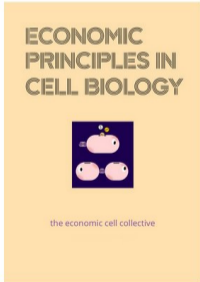
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Economic Principles in Cell Biology



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Economic Principles in Cell Biology


A free textbook

How can a cell maintain itself as a living being? Living cells, shaped by billions of years of evolution, have developed many ways to adapt to their environment, for example by regulation of gene expression. But the rules of physics and chemistry enforce certain boundaries on what cells can achieve and how they can allocate their own resources. Shaped by evolution, cells are able to "do certain things right", and our goal is to uncover some of the principles behind this.

In our free and open textbook, to which anyone can contribute, we give an overview of established approaches to cellular economics, from descriptions of simple metabolic systems to cell growth, variability, and dynamic behaviour.

For more information about our project, please see our [website for authors](#).

To **join us in writing this textbook**, please get in touch!



Activities around Economic Principles in Cell Biology

- Online seminar Economic principles in cell physiology
1st Thursday of each month

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- Summer school at Learning Planet Institute Paris
July 8-11, 2024 register for free online participation

For more information, see <https://principlescellphysiology.org>

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