

Economic Principles in Cell Biology

Vienna, July 23–26, 2025



Constraint-based modeling of microbial communities: from polyhedral geometry to ecology

S. Müller, M. Predl, D. Széliová, J. Zanghellini

Joint work: math/biochem

Stefan Müller

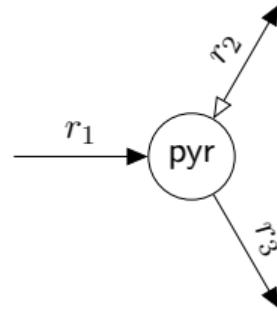
Faculty of Mathematics
University of Vienna

Michael Predl, Diana Széliová, Jürgen Zanghellini

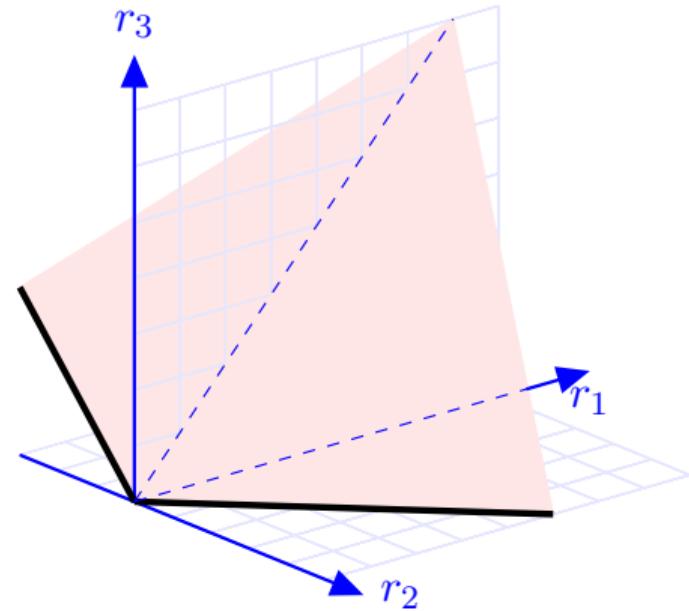
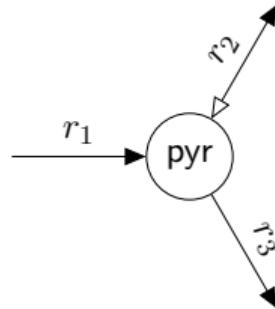
Biochemical Network Analysis
Department of Analytical Chemistry
University of Vienna

Preprint on bioRxiv by end of July ...

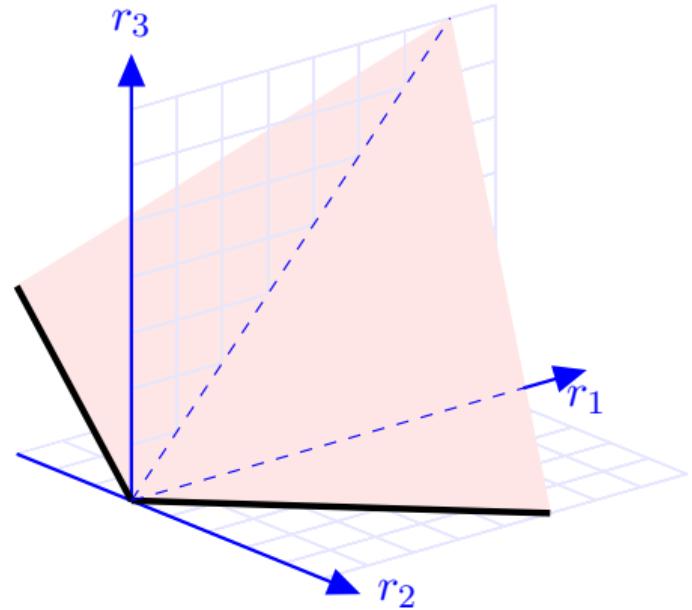
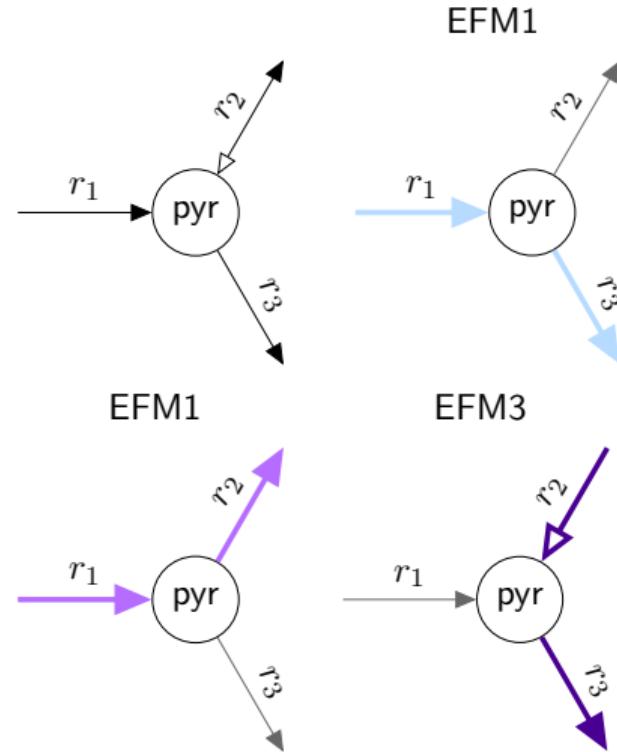
Reminder: What are elementary flux modes?



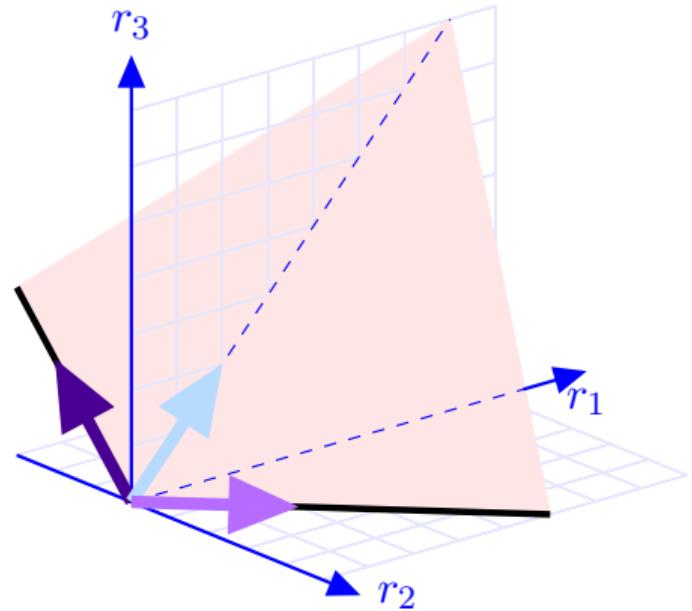
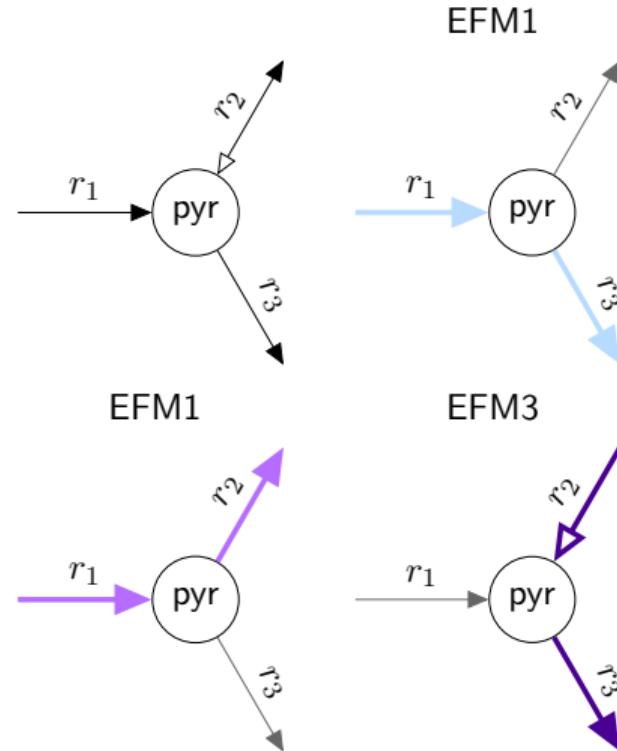
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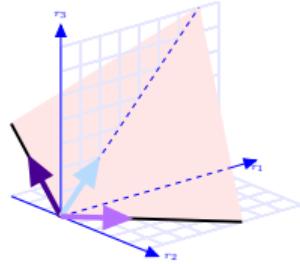
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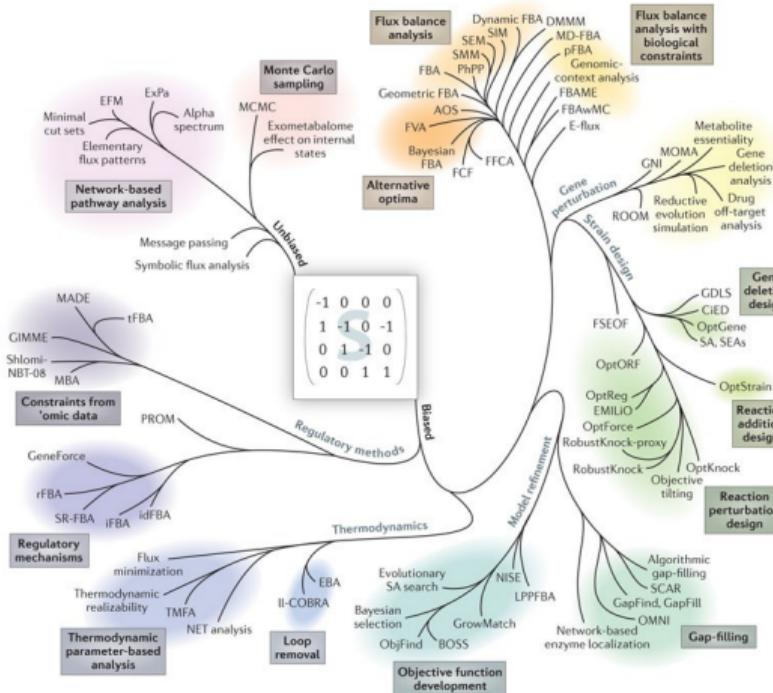
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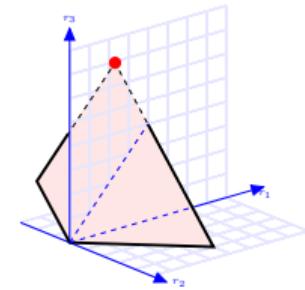
The forest of methods



- + principle importance
- + metabolic lego blocks
- + characterize full space
- computationally difficult
- constraints $\geq 0, = 0$
- yields only



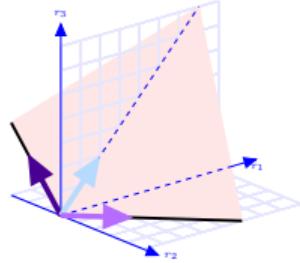
Nature Reviews | Microbiology



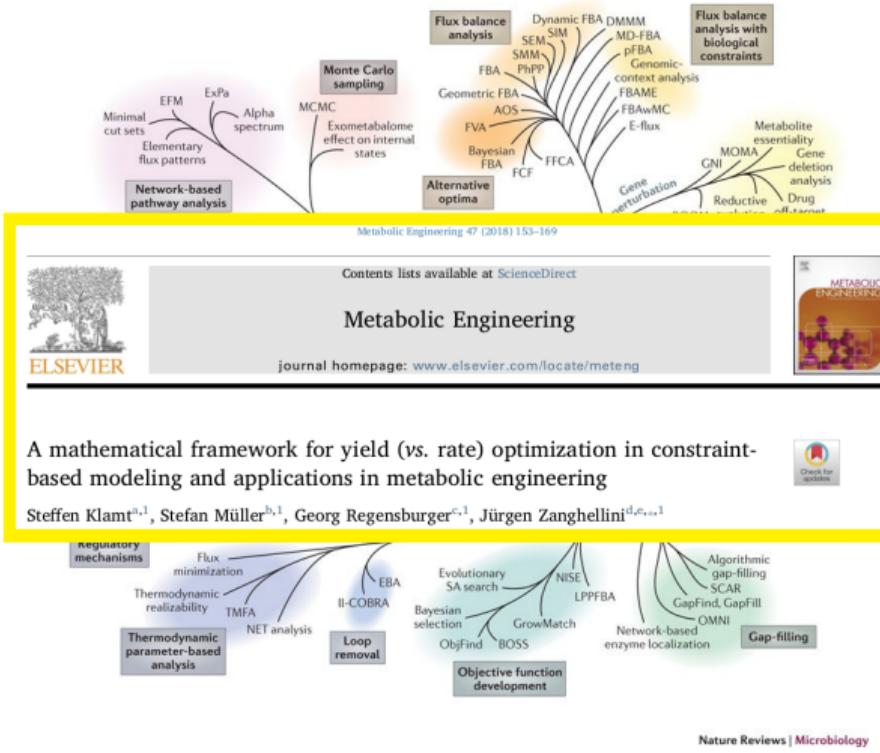
- + any linear constraints
- + computationally easy
- + flux rates & yields
- only one point
- optimally

doi:10.1038/nrmicro2737

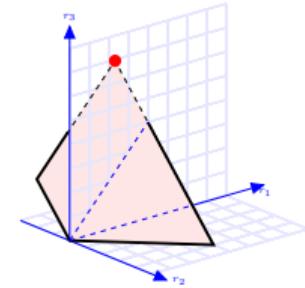
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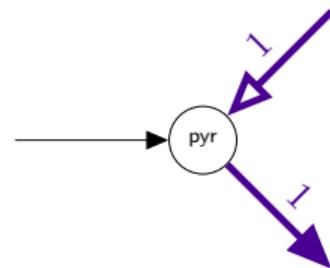
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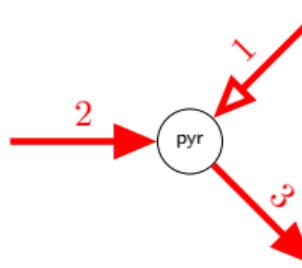
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Zoo of minimal pathways: Elementary flux vectors (EFVs)

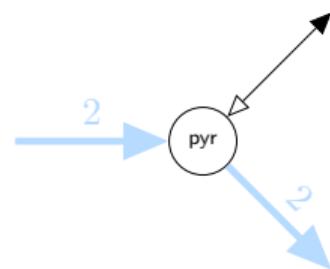
EFV1



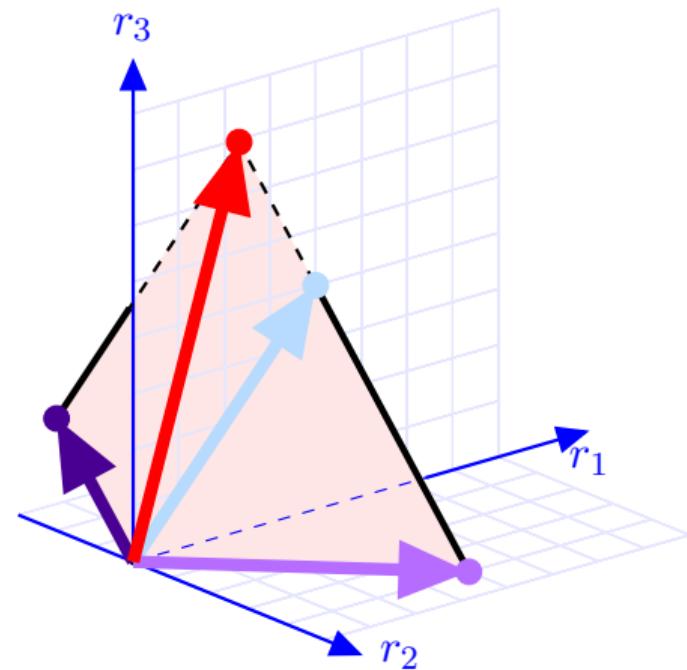
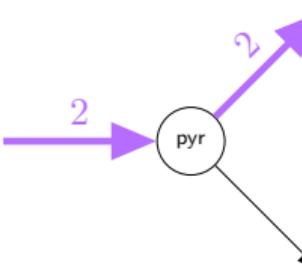
EFV2 = EFM1 + EFM2



EFV3



EFV4



- ▶ unique, but not support-minimal
- ▶ defined rates and yields
- ▶ respect capacity constraints
- ▶ any flux convex sums of pathways

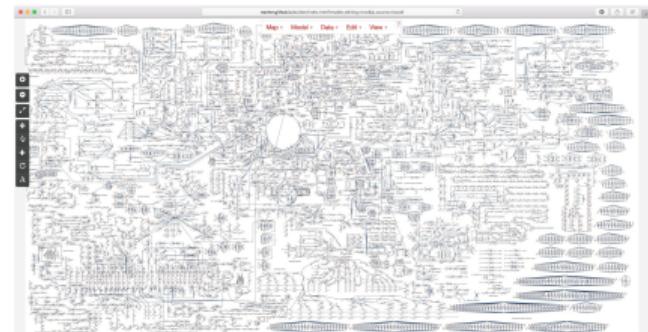
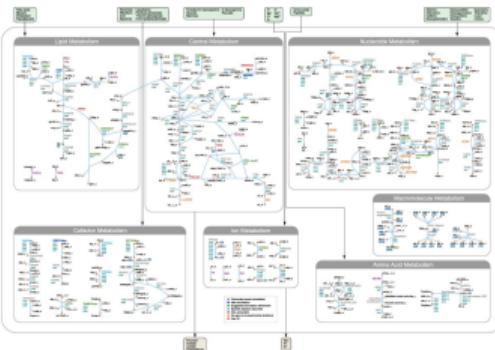
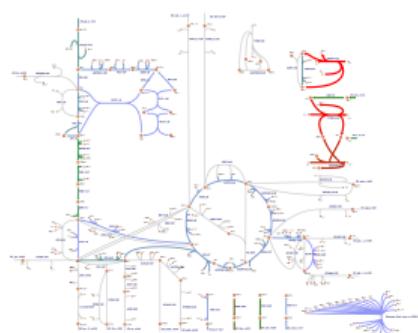
How many EFM_s does ... have?

- ▶ *E. coli*'s central carbon metabolism,
- ▶ a Minimal cell, JCVI-syn3A,
- ▶ a Human cell

doi:10.1186/s12918-018-0607-5

doi:10.7554/eLife.36842

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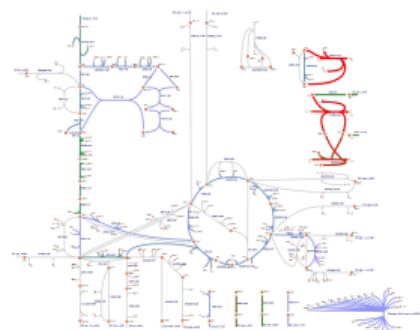
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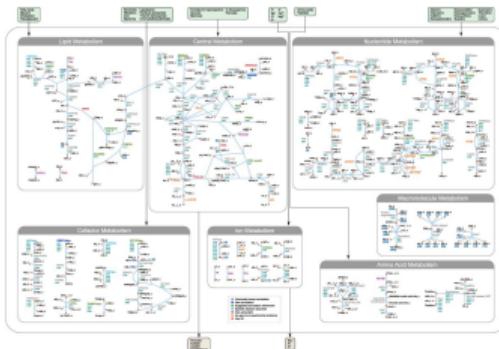
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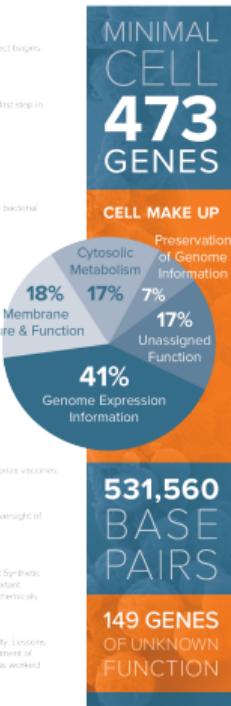
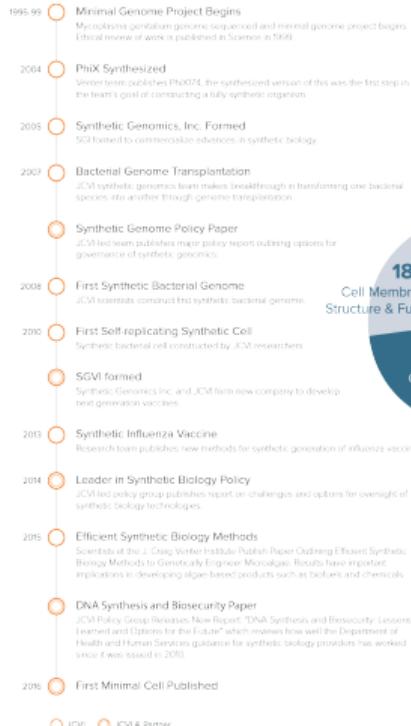


$\approx 10^{12}$ (one trillion)

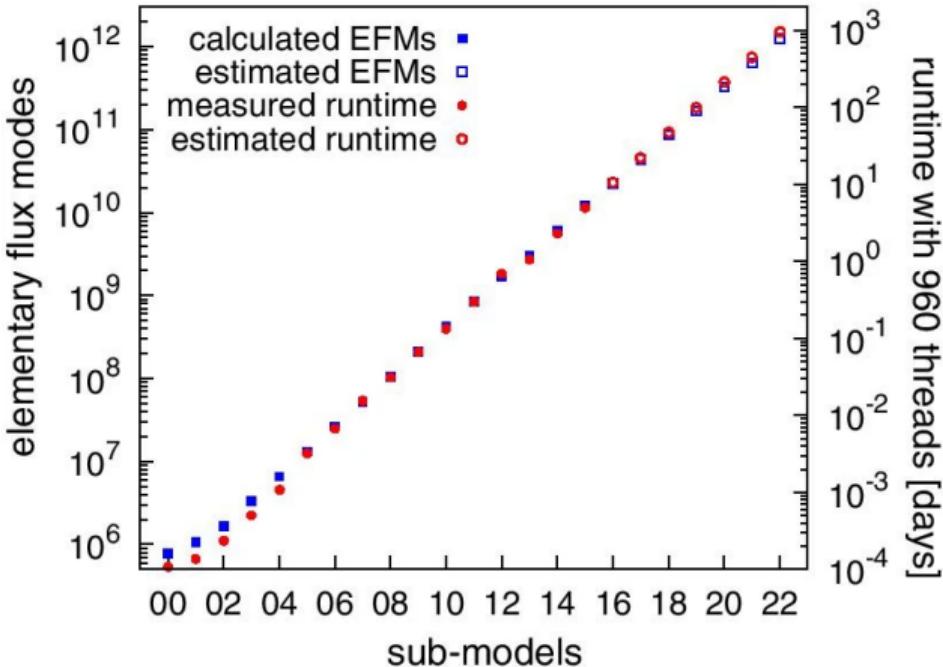


$> 10^{29}$

Functional space of a minimal cell



- ▶ > 1 trillion EFM_s, $\approx 1\% = 12,051,382,513$ computed
- ▶ 2.5 years w/ 1000 CPUs and 33×10^6 GB = 33PB storage for full set



Why do we do this? (Personal motivation)

- ▶ fundamental understanding of biological processes

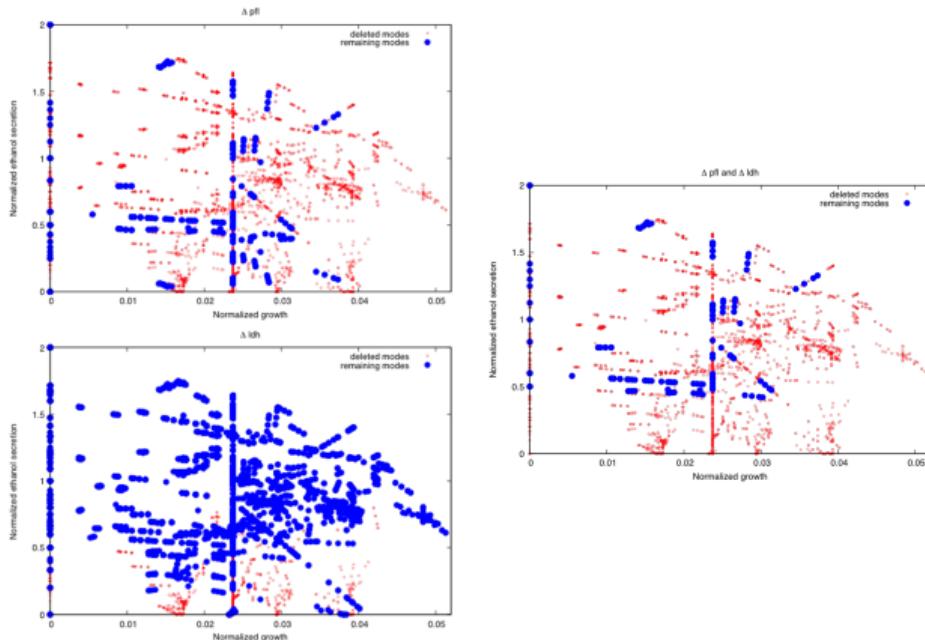
Theorem 1. The flux distribution that maximizes an objective flux over the total enzyme cost in a metabolic network without additional constraints is an Elementary Flux Mode.

Why do we do this? (Personal motivation)

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- ▶ metabolic engineering
- ▶ synthetic biology

Theorem 1. The flux distribution that maximizes an objective flux over the total enzyme cost in a metabolic network without additional constraints is an Elementary Flux Mode.



The Problem: Pilsbach, Upper Austria



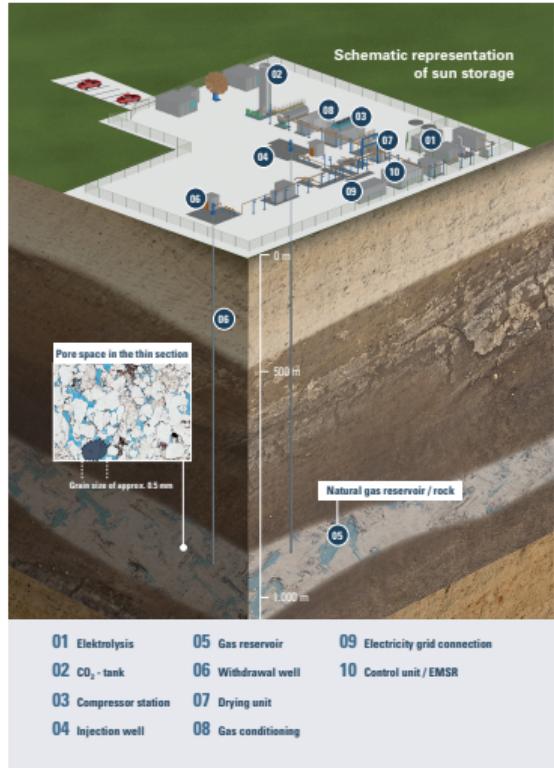
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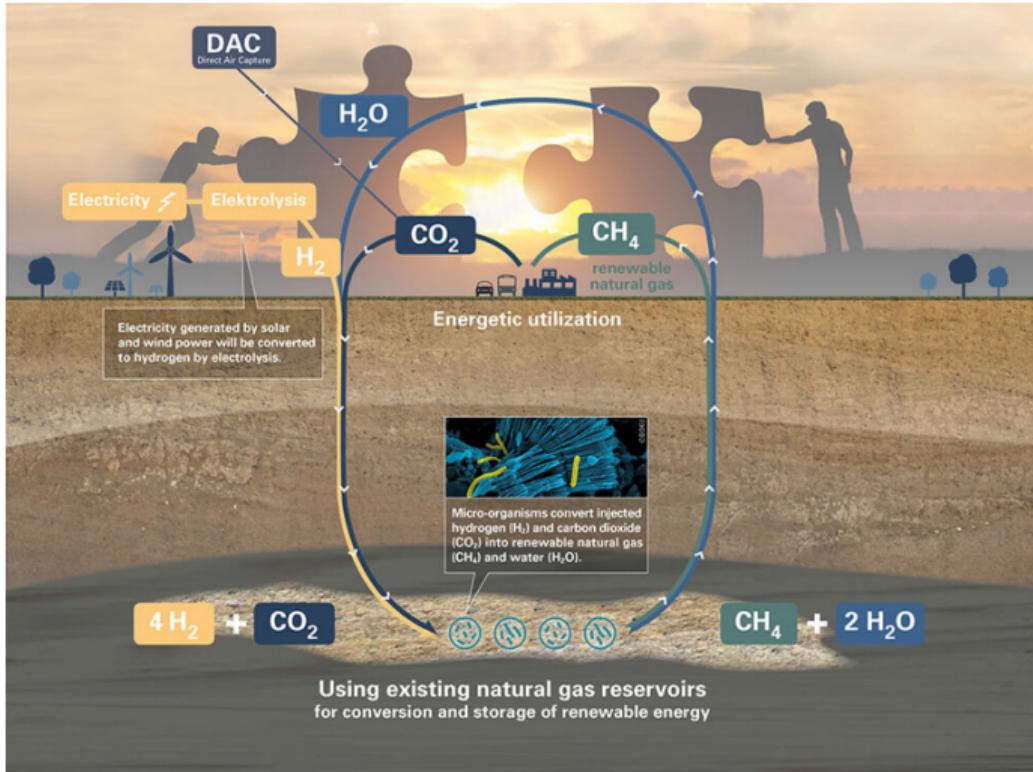
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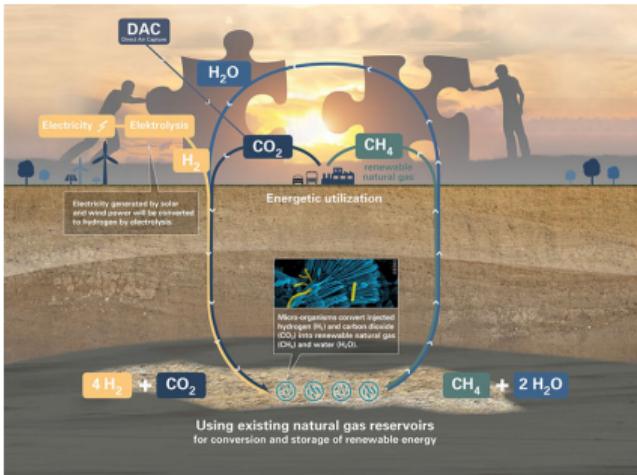
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Underground Sun Conversion

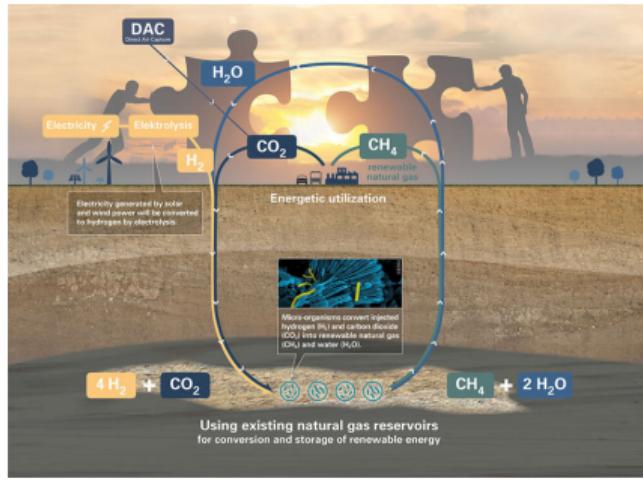


How can we maximize “biogas” production?

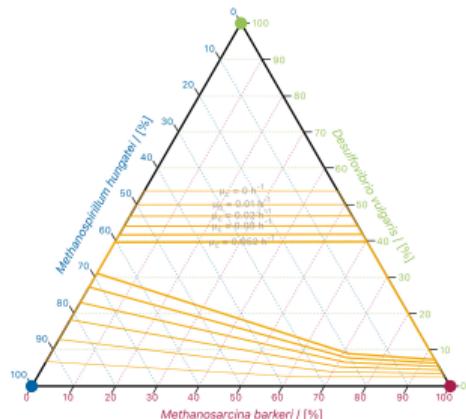


- ▶ What community compositions are feasible?
- ▶ What community composition is optimal?

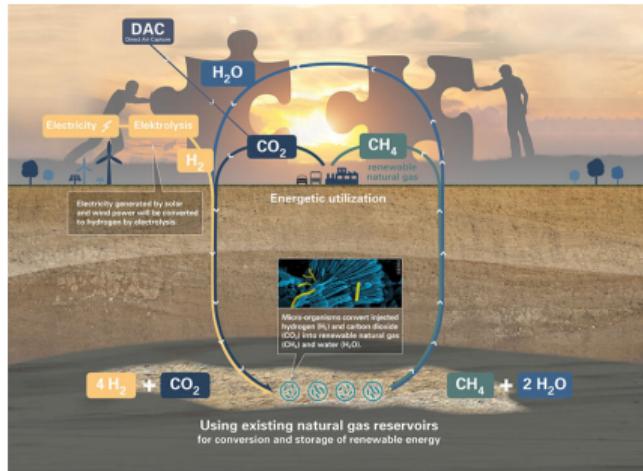
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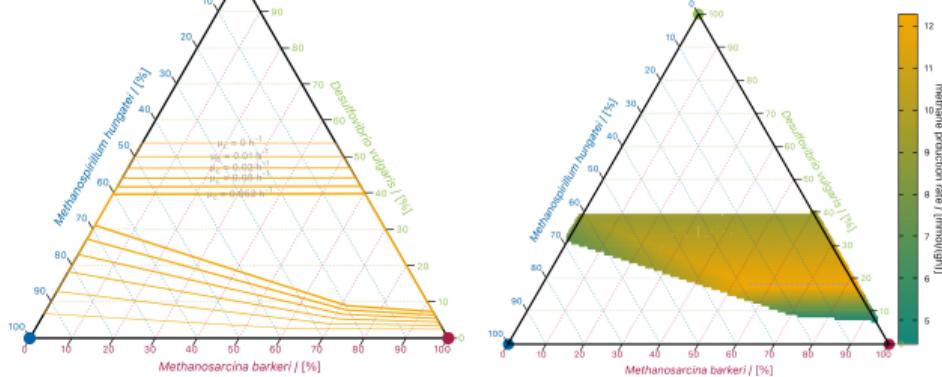
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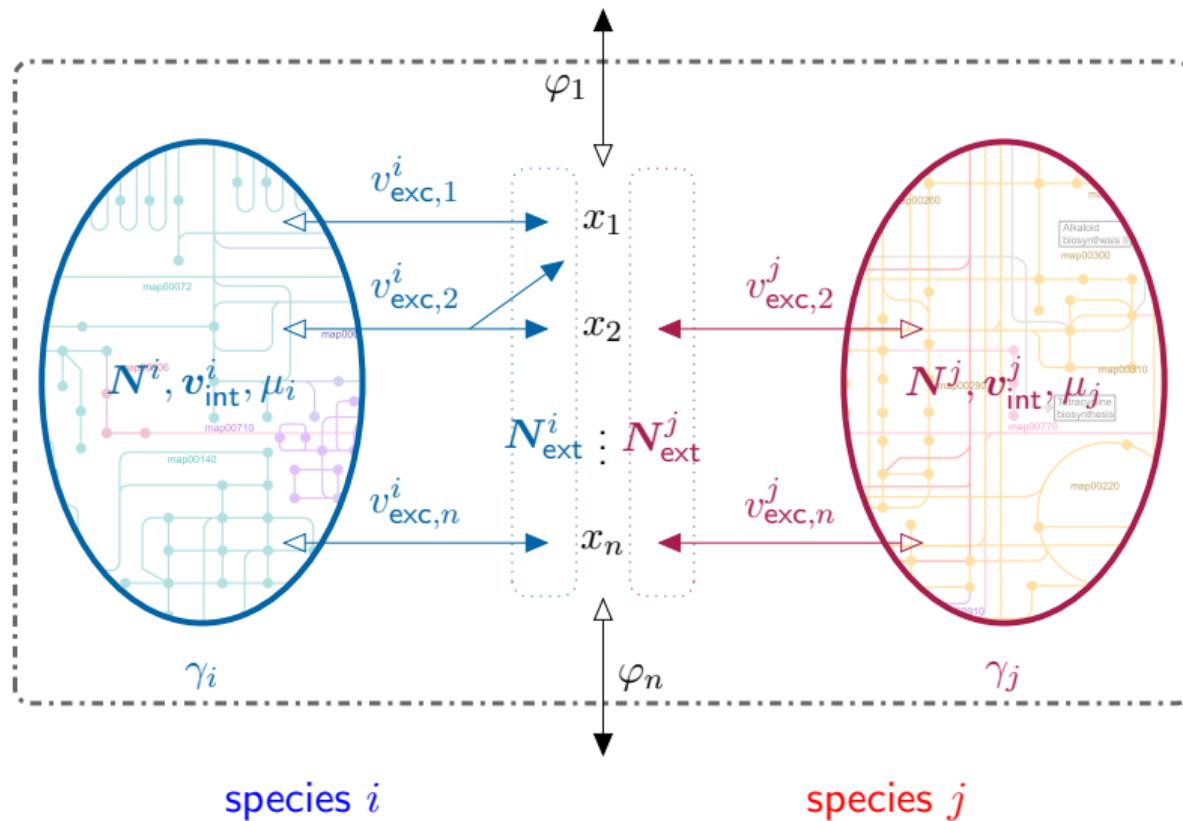
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Microbial community



Q&A

Given

- a set of microbial species (their metabolic models),
- a medium, and
- a growth rate:

What are all feasible community compositions and metabolic interactions?

What are the minimal communities?



Q&A

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- a set of microbial species (their metabolic models),
- a medium, and
- a growth rate:

What are all feasible community compositions and metabolic interactions?

What are the minimal communities?

We define:

community metabolic space (a polytope)
elementary compositions & exchange fluxes (ECXs)

Elementary vectors in metabolic pathway analysis

- ▶ Elementary flux modes (EFMs) flux cone
Elementary flux vectors (EFVs) flux polyhedron (FBA)
- ▶ Elementary conversion modes (ECMs) exchange fluxes
- ▶ Elementary growth modes (EGMs) next-generation models
resource balance analysis (RBA)
- ▶ ECXs microbial communities
ECs, EXs



Elementary vectors

Linear subspace S :

elementary vector (EV): $e \in S$ with **minimal support**

Theorem (Rockafellar 1969)

Every $f \in S$ is a finite, conformal sum of EVs:

$$f = \sum_e e \quad \text{with} \quad \text{sign}(e) \leq \text{sign}(f)$$

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Reaction directions, thermodynamics

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Generalization (Müller, Regensburger 2016)

*linear subspace $S \rightarrow$ general polyhedral cone (e.g. flux cone),
polyhedron (e.g. flux polyhedron)*

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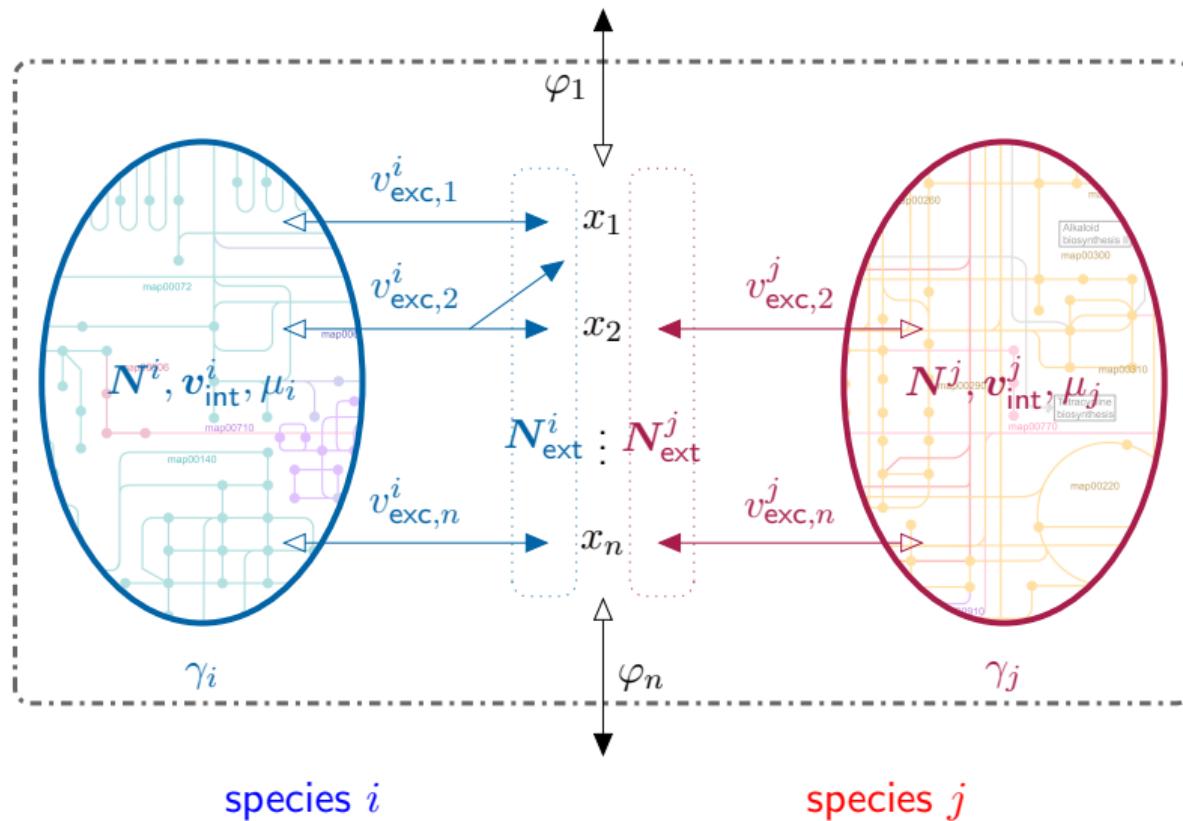
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Generalization (Müller, Regensburger 2016)

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polyhedron (e.g. flux polyhedron)*

elementary vector: **(convex-)conformally non-decomposable**

Microbial community



(Constraint-based) metabolic modeling of microbial communities

- ▶ Single species growth
- ▶ Exchange with medium
- ▶ From dynamics to steady state

Single species growth

Πάντα αὔξανεται (Panta auxanetai) ... 'Everything grows'

Single species growth

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Self-fabricating cell:

$$\frac{d}{dt} \begin{pmatrix} x \\ y \end{pmatrix} = \underbrace{\begin{pmatrix} N & S \\ 0 & I \end{pmatrix}}_{N_{\text{nxt-gen}}} \begin{pmatrix} v(x, y) \\ w(x, y) \end{pmatrix} - \mu \begin{pmatrix} x \\ y \end{pmatrix}$$

x ... metabolites, y ... macromolecules

Single species growth

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x ... metabolites, y ... macromolecules

CBM: RBA (resource balance analysis)

Single species growth

Dynamics of growth:

$$\frac{d}{dt} \begin{pmatrix} x \\ y \end{pmatrix} = \underbrace{\begin{pmatrix} N & -S \\ 0 & I \end{pmatrix}}_{N_{\text{nxt-gen}}} \begin{pmatrix} v(x, y) \\ w(x, y) \end{pmatrix} - \mu \begin{pmatrix} x \\ y \end{pmatrix}$$

CBM: FBA (flux balance analysis) and EFM analysis



Single species growth

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CBM: FBA (flux balance analysis) and EFM analysis

$$\frac{dy}{dt} = 0 \quad \rightarrow \quad w = \mu y \quad \rightarrow \quad S w = \mu \underbrace{S y}_{x_{\text{bound}}} \quad \rightarrow \quad \frac{dx}{dt} = N v(x) - \mu \underbrace{(x_{\text{bound}} + x)}_{x_{\text{total}}}$$



Single species growth

Dynamics of growth:

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$$\frac{dx}{dt} = 0 \quad \rightarrow \quad 0 = N v - \mu x_{\text{total}} \quad \rightarrow \quad 0 = \underbrace{\begin{pmatrix} N & -x_{\text{total}} \frac{\text{g}}{\text{mol}} \end{pmatrix}}_{N_{\text{bm}}} \begin{pmatrix} v \\ \mu \frac{\text{mol}}{\text{g}} \end{pmatrix}$$

Single species growth

$$0 = N_{\text{bm}} \left(\mu \frac{v}{\frac{\text{mol}}{\text{g}}} \right),$$
$$l \leq v \leq u$$

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$$\gamma_i = \frac{m_i}{m} \quad \text{with} \quad m = \sum_i m_i$$

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Individual species i :

$$0 = N_{\text{bm}}^i \left(\mu_i \frac{v^i}{\frac{\text{mol}}{\text{g}}} \right),$$

$$l^i \leq v^i \leq u^i,$$

$$\gamma_i \geq 0$$

Exchange with medium

Internal metabolites:

$$N = \text{Met} \begin{pmatrix} \text{Exc} & \text{Int} \\ N_{\text{exc}} & N_{\text{int}} \end{pmatrix}$$



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Metabolites in medium:

$$\begin{pmatrix} * \\ N \end{pmatrix} = \text{Med} \begin{pmatrix} \text{Exc} & \text{Int} \\ N_{\text{ext}} & 0 \\ N_{\text{exc}} & N_{\text{int}} \end{pmatrix} \text{Met}$$

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Dynamics in medium:

$$\frac{dX_{\text{Med}}}{dt} = m \sum_i \gamma_i N_{\text{ext}}^i v_{\text{exc}}^i - \Phi$$

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$$\frac{dX_{\text{Med}}}{dt} = 0 \rightarrow 0 = \sum_i \gamma_i N_{\text{ext}}^i v_{\text{exc}}^i - \Phi/m \rightarrow \Phi_j \geq 0: \sum_i \gamma_i N_{\text{ext}}^i v_{\text{exc}}^i \geq 0, \dots$$

Community model in μ , γ and v^i

$$0 = N_{\text{bm}}^i \left(\frac{v^i}{\mu \frac{\text{mol}}{\text{g}}} \right),$$

$$l^i \leq v^i \leq u^i,$$

$$\gamma_i \geq 0,$$

for $i = 1, \dots, \#\text{species}$, and

$$\sum_i \gamma_i (N_{\text{ext}}^i v_{\text{exc}}^i)_j \begin{cases} = 0, & \text{if } j \in \text{Med}_0, \\ \leq 0, & \text{if } j \in \text{Med}_{\text{in}}, \\ \geq 0, & \text{if } j \in \text{Med}_{\text{out}}, \end{cases}$$

$$\sum_i \gamma_i = 1.$$

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$$\sum_i \gamma_i = 1.$$

Introduce $\bar{v}^i = \gamma_i v^i$ (scaled fluxes)

Koch, ..., Klamt (2019), Plos Comp. Biol.

Community model in μ , γ and \bar{v}^i

$$0 = N_{\text{bm}}^i \left(\frac{\bar{v}^i}{\gamma_i \mu \frac{\text{mol}}{\text{g}}} \right),$$
$$\gamma_i l^i \leq \bar{v}^i \leq \gamma_i u^i,$$
$$\gamma_i \geq 0,$$

for $i = 1, \dots, \#\text{species}$, and

$$\sum_i (N_{\text{ext}}^i \bar{v}_{\text{exc}}^i)_j \begin{cases} = 0, & \text{if } j \in \text{Med}_0, \\ \leq 0, & \text{if } j \in \text{Med}_{\text{in}}, \\ \geq 0, & \text{if } j \in \text{Med}_{\text{out}}, \end{cases}$$
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$$\sum_i \gamma_i = 1.$$

Project fluxes to exchange fluxes ($\bar{v}^i \rightarrow \bar{v}_{\text{exc}}^i$)

Community model in μ , γ and \bar{v}_{exc}^i

$$A^i \bar{v}_{\text{exc}}^i + b^i(\mu) \gamma_i \geq 0,$$

$$\gamma_i l_{\text{exc}}^i \leq \bar{v}_{\text{exc}}^i \leq \gamma_i u_{\text{exc}}^i,$$

$$\gamma_i \geq 0,$$

for $i = 1, \dots, \#\text{species}$, and

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$$A^i \bar{v}_{\text{exc}}^i + b^i(\mu) \gamma_i \geq 0,$$

$$\gamma_i l_{\text{exc}}^i \leq \bar{v}_{\text{exc}}^i \leq \gamma_i u_{\text{exc}}^i,$$

$$\gamma_i \geq 0,$$

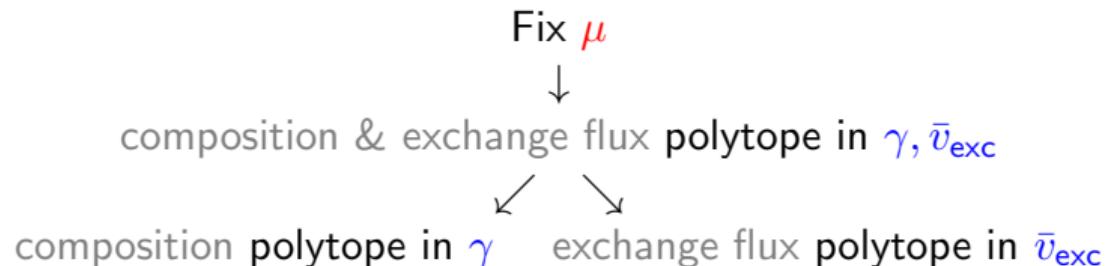
for $i = 1, \dots, \#\text{species}$, and

$$\sum_i (N_{\text{ext}}^i \bar{v}_{\text{exc}}^i)_j \begin{cases} = 0, & \text{if } j \in \text{Med}_0, \\ \leq 0, & \text{if } j \in \text{Med}_{\text{in}}, \\ \geq 0, & \text{if } j \in \text{Med}_{\text{out}}, \end{cases}$$

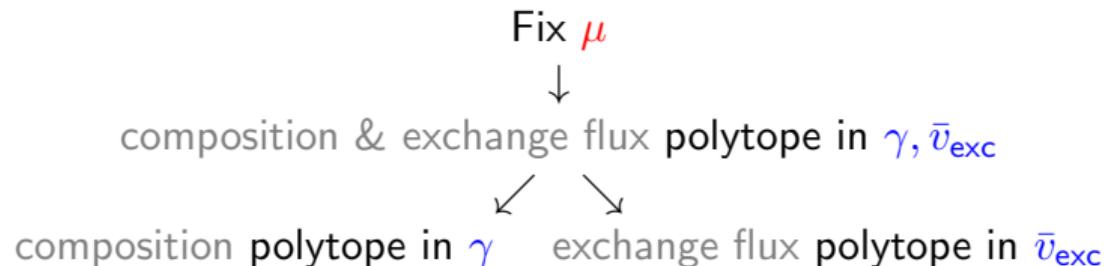
$$\sum_i \gamma_i = 1.$$

Fix μ (define polytope)

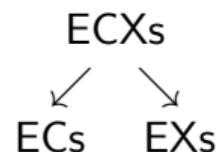
Community model \rightarrow community modes



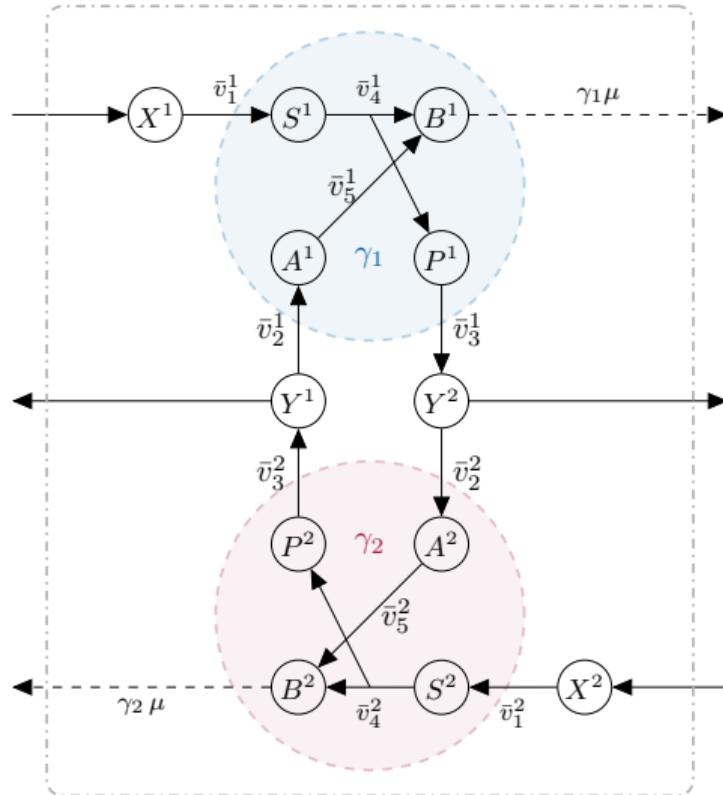
Community model \rightarrow community modes



Convex-conformally non-decomposable vectors:



Example



Example: elementary compositions & exchange fluxes

$\hat{\mu} \in [0, 1]$:

$$\gamma_1, \gamma_2; \quad \hat{v}_1^1, \hat{v}_2^1, \hat{v}_3^1; \quad \hat{v}_1^2, \hat{v}_2^2, \hat{v}_3^2$$

$$\text{ECX}_1 = (\quad 1, 0; \quad \hat{\mu}, 0, \hat{\mu}; \quad 0, 0, 0 \quad)^\top,$$

$$\text{ECX}_2 = (\quad 0, 1; \quad 0, 0, 0; \quad \hat{\mu}, 0, \hat{\mu} \quad)^\top,$$

$$\text{ECX}_3 = (\quad \frac{1}{2}, \frac{1}{2}; \quad \frac{\hat{\mu}}{2}, 0, \frac{\hat{\mu}}{2}; \quad 0, \frac{\hat{\mu}}{2}, 0 \quad)^\top,$$

$$\text{ECX}_4 = (\quad \frac{1}{2}, \frac{1}{2}; \quad 0, \frac{\hat{\mu}}{2}, 0; \quad \frac{\hat{\mu}}{2}, 0, \frac{\hat{\mu}}{2} \quad)^\top.$$

Example: elementary compositions & exchange fluxes

$\hat{\mu} \in [0, 1]$:

$$\gamma_1, \gamma_2; \quad \hat{v}_1^1, \hat{v}_2^1, \hat{v}_3^1; \quad \hat{v}_1^2, \hat{v}_2^2, \hat{v}_3^2$$

$$\text{ECX}_1 = (1, 0; \hat{\mu}, 0, \hat{\mu}; 0, 0, 0)^\top,$$

$$\text{ECX}_2 = (0, 1; 0, 0, 0; \hat{\mu}, 0, \hat{\mu})^\top,$$

$$\text{ECX}_3 = \left(\frac{1}{2}, \frac{1}{2}; \frac{\hat{\mu}}{2}, 0, \frac{\hat{\mu}}{2}; 0, \frac{\hat{\mu}}{2}, 0\right)^\top,$$

$$\text{ECX}_4 = \left(\frac{1}{2}, \frac{1}{2}; 0, \frac{\hat{\mu}}{2}, 0; \frac{\hat{\mu}}{2}, 0, \frac{\hat{\mu}}{2}\right)^\top.$$

$\hat{\mu} \in [1, 2]$:

$$\text{ECX}_5 = \left(\frac{1}{\hat{\mu}}, \frac{\hat{\mu}-1}{\hat{\mu}}; \frac{1}{\hat{\mu}}, \frac{\hat{\mu}-1}{\hat{\mu}}, \frac{1}{\hat{\mu}}; \frac{\hat{\mu}-1}{\hat{\mu}}, \frac{(\hat{\mu}-1)^2}{\hat{\mu}}, \frac{\hat{\mu}-1}{\hat{\mu}}\right)^\top,$$

$$\text{ECX}_6 = \left(\frac{\hat{\mu}-1}{\hat{\mu}}, \frac{1}{\hat{\mu}}; \frac{\hat{\mu}-1}{\hat{\mu}}, \frac{(\hat{\mu}-1)^2}{\hat{\mu}}, \frac{\hat{\mu}-1}{\hat{\mu}}; \frac{1}{\hat{\mu}}, \frac{\hat{\mu}-1}{\hat{\mu}}, \frac{1}{\hat{\mu}}\right)^\top,$$

$$\text{ECX}_7 = \left(\frac{1}{2}, \frac{1}{2}; \frac{1}{2}, \frac{\hat{\mu}-1}{2}, \frac{1}{2}; \frac{\hat{\mu}-1}{2}, \frac{1}{2}, \frac{\hat{\mu}-1}{2}\right)^\top,$$

$$\text{ECX}_8 = \left(\frac{1}{2}, \frac{1}{2}; \frac{\hat{\mu}-1}{2}, \frac{1}{2}, \frac{\hat{\mu}-1}{2}; \frac{1}{2}, \frac{\hat{\mu}-1}{2}, \frac{1}{2}\right)^\top.$$

Example: elementary compositions

$\hat{\mu} \in [0, 1]$:

$$\begin{aligned}\gamma_1, \gamma_2 \\ \text{EC}_1 = (1, 0)^\top, \\ \text{EC}_2 = (0, 1)^\top.\end{aligned}$$

$\hat{\mu} \in [1, 2]$:

$$\begin{aligned}\text{EC}_5 = \left(\frac{1}{\hat{\mu}}, \frac{\hat{\mu}-1}{\hat{\mu}}\right)^\top, \\ \text{EC}_6 = \left(\frac{\hat{\mu}-1}{\hat{\mu}}, \frac{1}{\hat{\mu}}\right)^\top.\end{aligned}$$

Example: elementary compositions

$\hat{\mu} \in [0, 1]$:

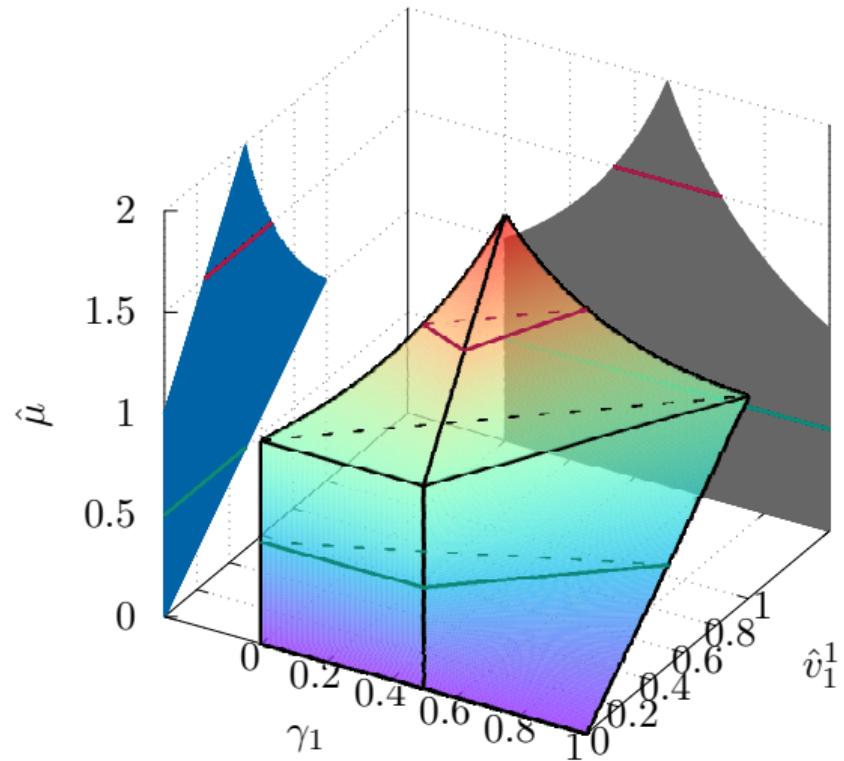
$$\begin{aligned}\gamma_1, \gamma_2 \\ \text{EC}_1 = (1, 0)^\top, \\ \text{EC}_2 = (0, 1)^\top.\end{aligned}$$

$\hat{\mu} \in [1, 2]$:

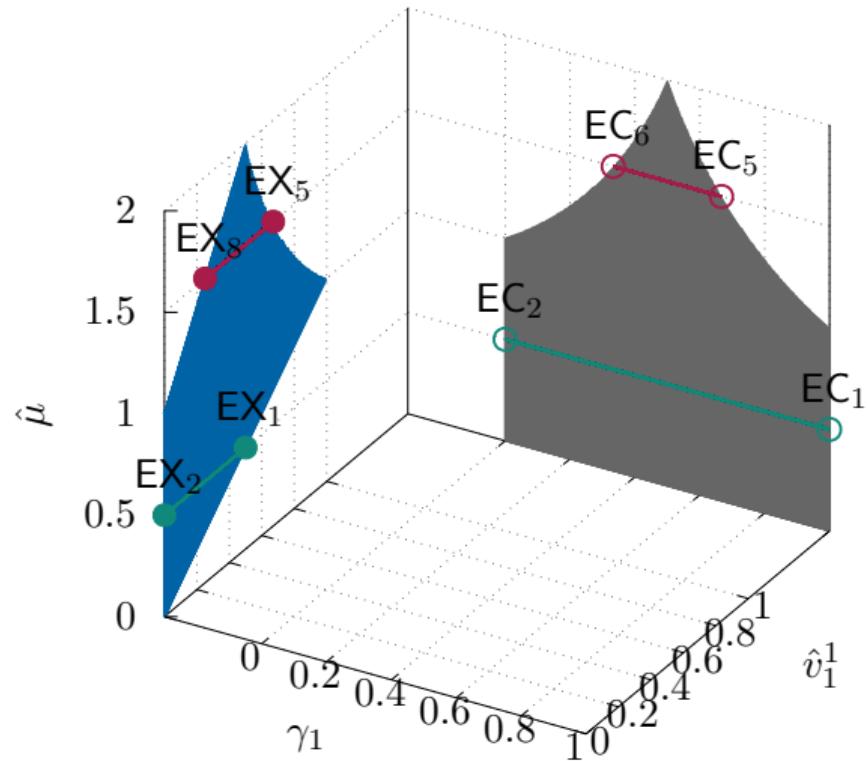
$$\begin{aligned}\text{EC}_5 = \left(\frac{1}{\hat{\mu}}, \frac{\hat{\mu}-1}{\hat{\mu}}\right)^\top, \\ \text{EC}_6 = \left(\frac{\hat{\mu}-1}{\hat{\mu}}, \frac{1}{\hat{\mu}}\right)^\top.\end{aligned}$$

analogously for elementary exchange fluxes (EXs)

Example: projection to $\mu, \gamma_1, \bar{v}_1^1$



Example: ECs and EXs

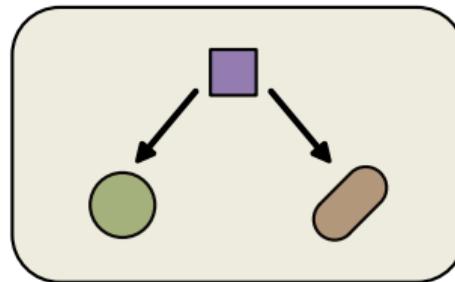


Ecological significance

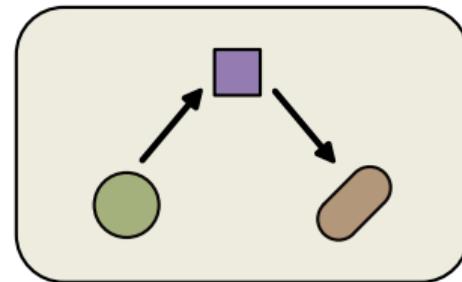
ECX	$\hat{\mu} \in [0, 1]$				$\hat{\mu} \in (1, 2]$			
	1	2	3	4	5	6	7	8
specialization	✓	✓						
commensalism			✓	✓				
mutualism					✓	✓	✓	✓
maximum uptake					✓	✓		
maximum yield			✓	✓			✓	✓
nonlinear in $\hat{\mu}$					✓	✓		

Interpretation of flux patterns: Topology

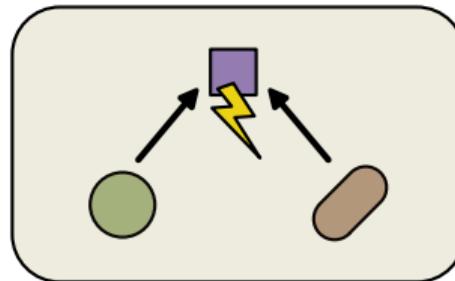
- ▶ Based on network structure
- ▶ Independent of growth or objective
- ▶ Applicable to any flux pattern
- ▶ Descriptive
- ▶ Biological implication not straight forward



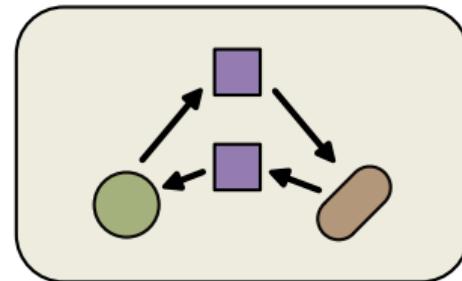
Nutrient competition



Unidirectional cross-feeding



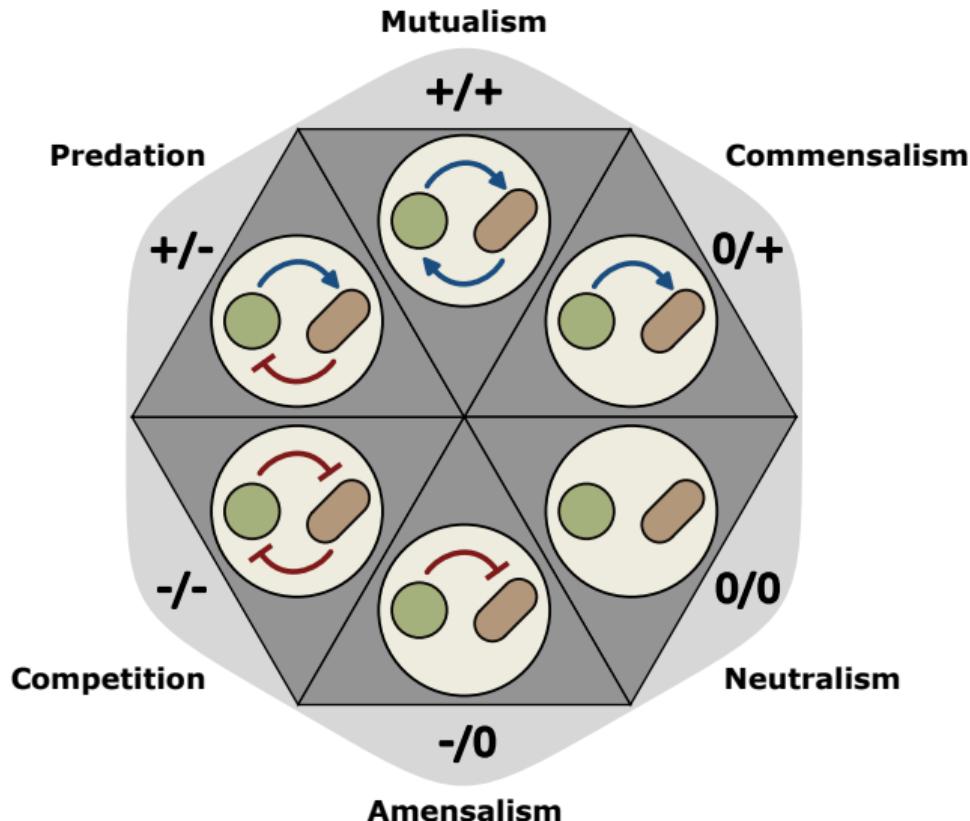
Product competition



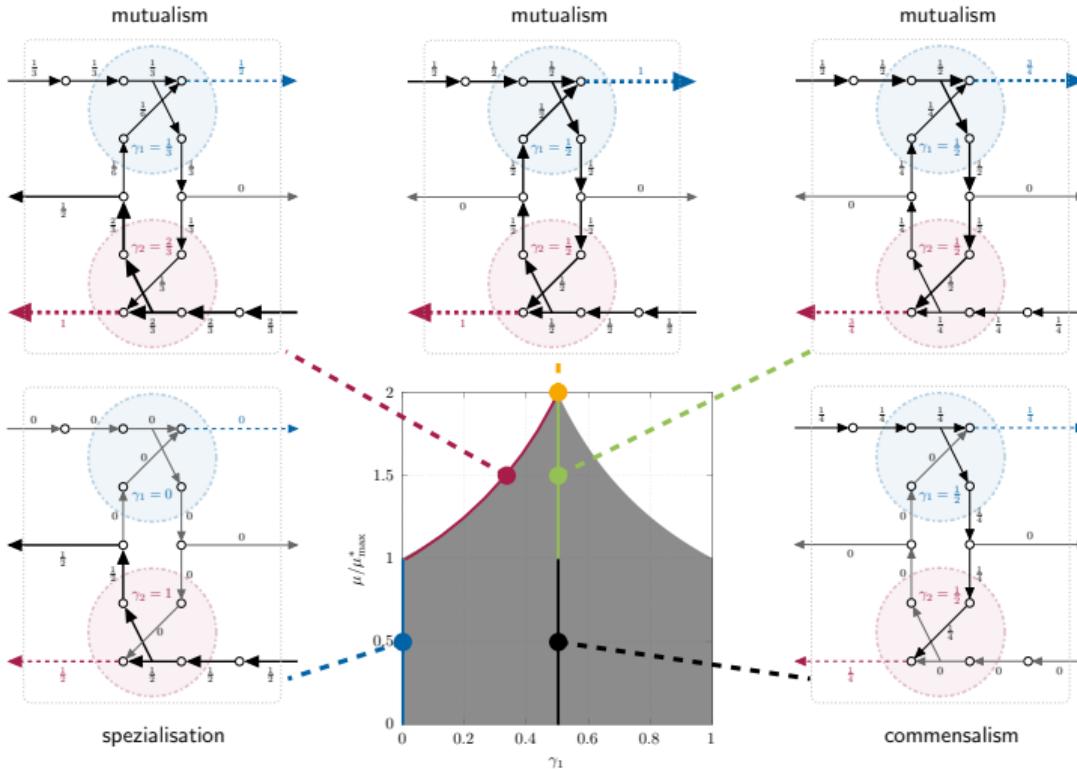
Bidirectional cross-feeding

Interpretation of flux patterns: Ecology

- ▶ Classical ecology framework
- ▶ Sign-based classification (+/-/0)
- ▶ Requires *ecological outcome*
- ▶ Requires comparison of states
- ▶ Direct translation to biological significance



Interpretation of flux patterns: Example

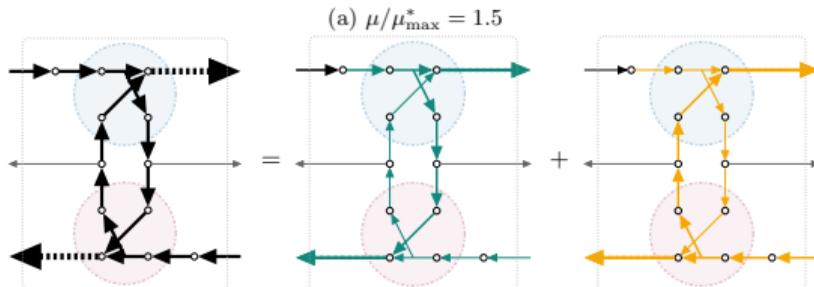


Isotypic vs. anisotypic mutualism

Isotypic Mutualism

When deconstructed into ECFMs, *at least one* ECFM is mutualistic.

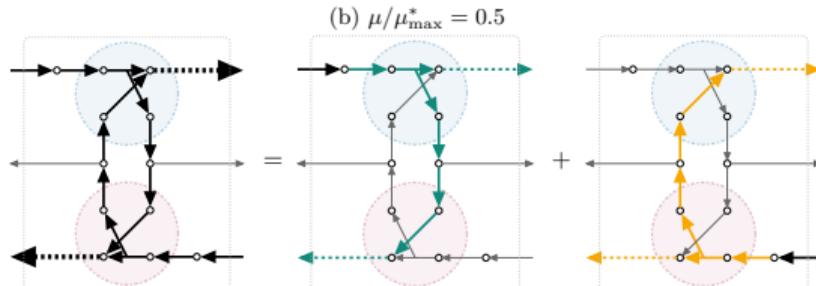
In example (a) all ECFM are mutualistic.



Anisotypic Mutualism

When deconstructed into ECFMs, *no* ECFM is mutualistic.

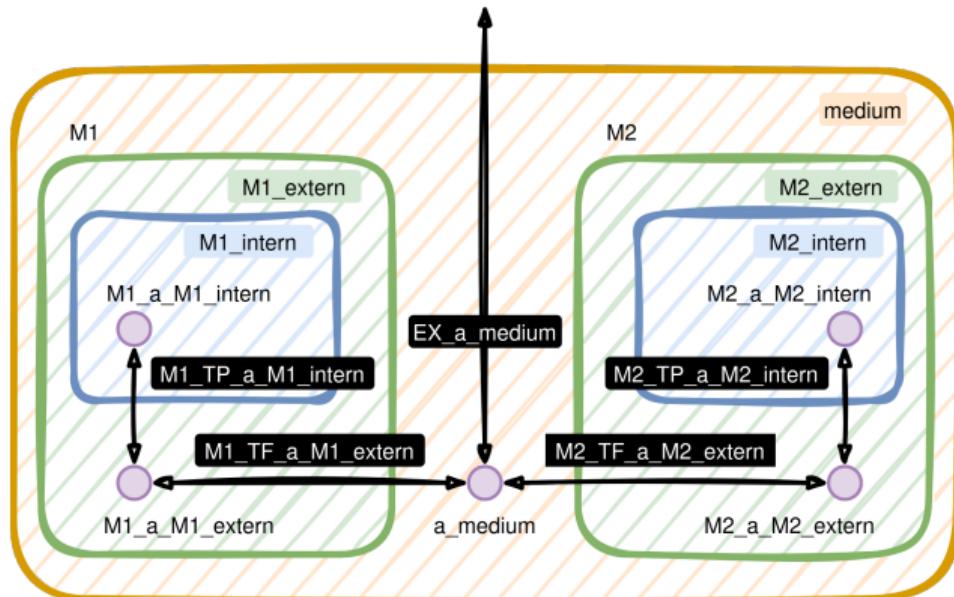
In example (b) all ECFM are commensalistic, and non is mutualistic.



Community model generation

Additional structure

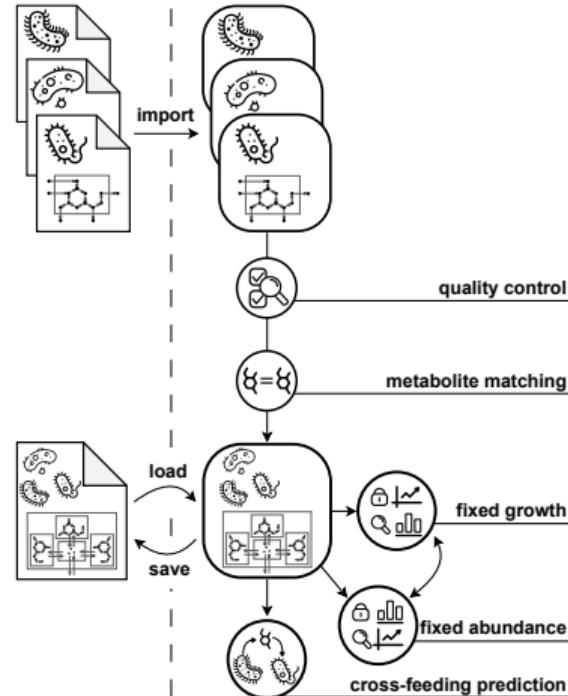
- ▶ Shared medium compartment
- ▶ Transfer reactions
- ▶ Community exchange reactions
- ▶ Community biomass reaction



Python package for community modeling (PyCoMo)

Model generation steps

- ▶ Match external metabolites
- ▶ Merge models
- ▶ Add shared medium compartment
- ▶ Manage exchange reactions
- ▶ Add community biomass function
- ▶ Scale member fluxes by mass fraction
- ▶ Check for mass and charge balance



Genome-scale example

A co-culture of two human gut microbes

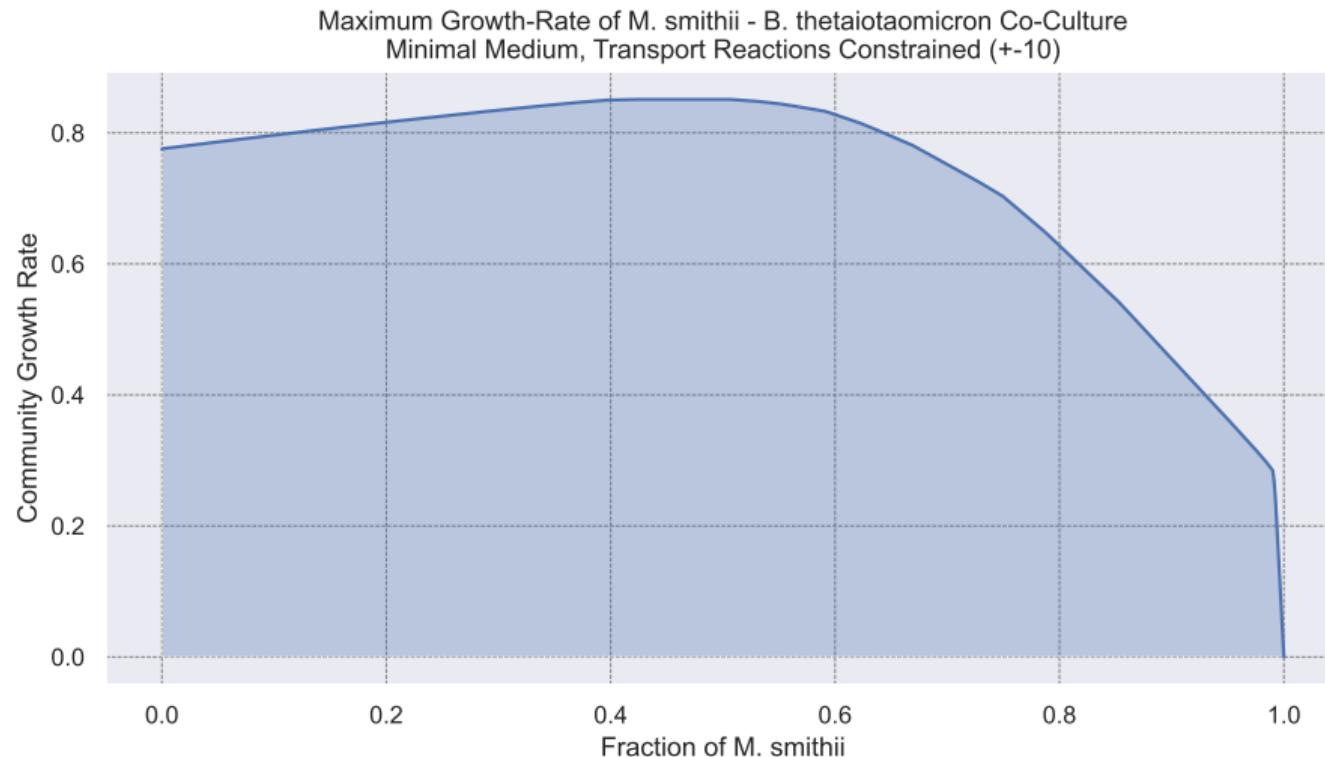
M. smithii: A methanogenic archaeon

B. thetaiotaomicron: A polysaccharide degrading bacterium

The community metabolic model is big!

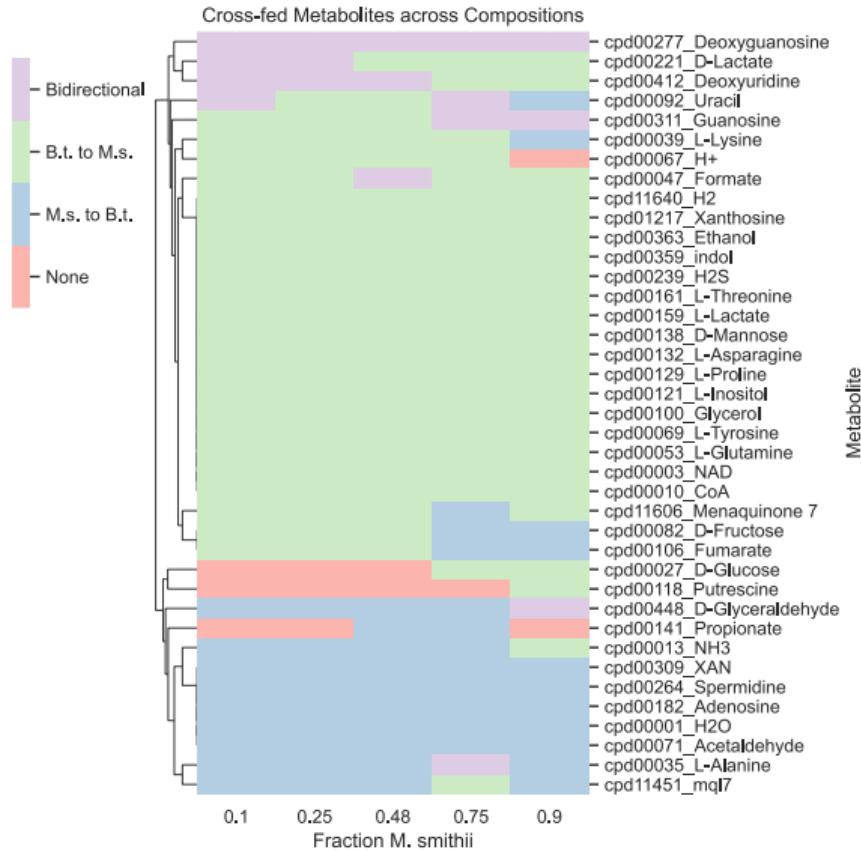
- ▶ # Reactions: 3860
- ▶ # Metabolites: 3355
- ▶ # Genes: 1141

Analysis options: growth rate



Analysis options: interactions

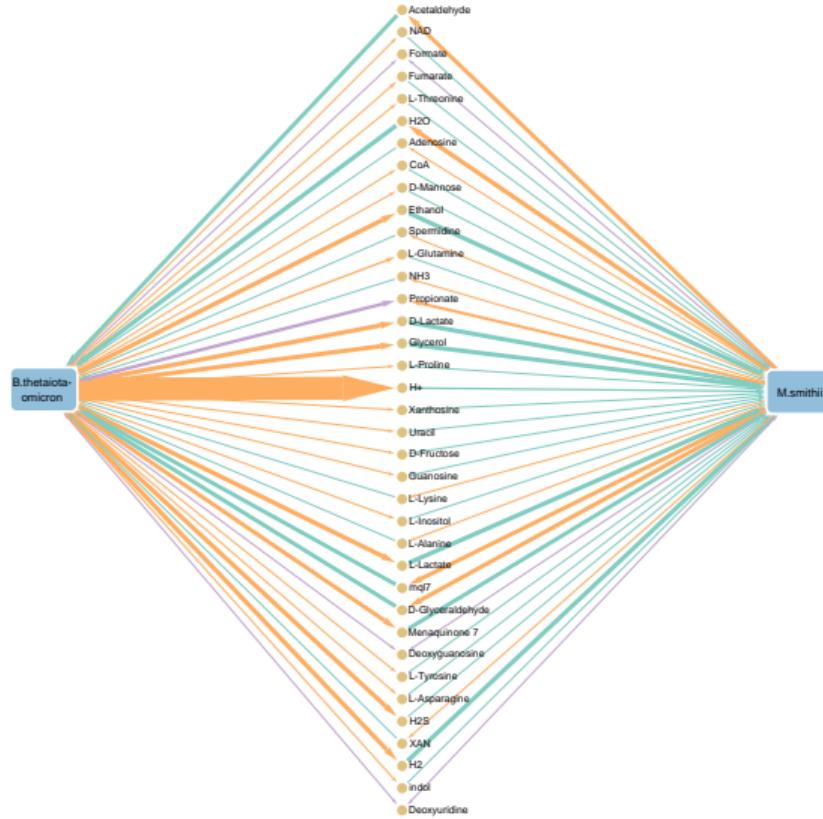
- ▶ FBA and FVA allow the detection of feasible cross-feeding
- ▶ Metabolic plasticity of the model: some cross-feeding interactions can occur in either direction
- ▶ Feasible cross-feeding patterns change across growth rate and composition



Analysis options: visualization

Visualization with ScyNet and Cytoscape

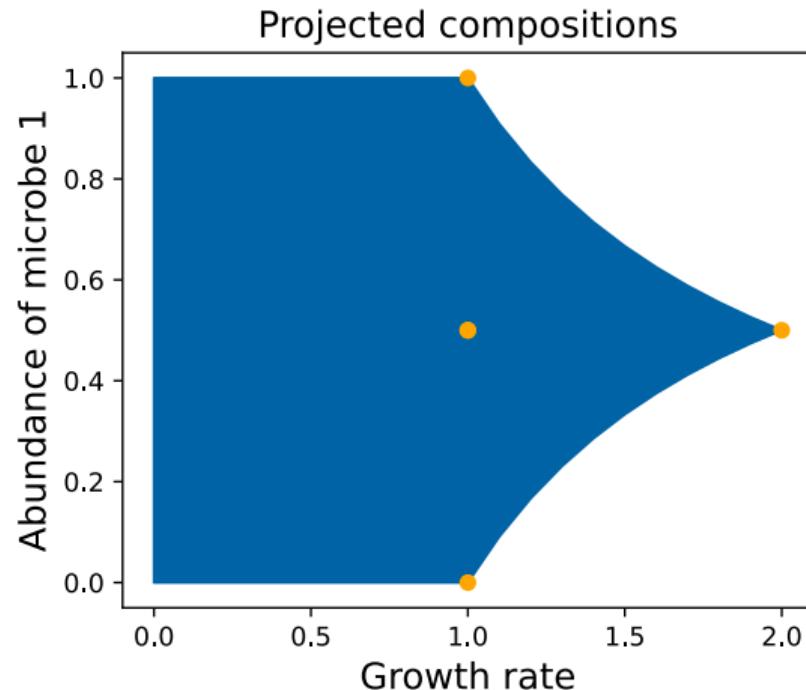
- ▶ Allows exploration of the model
- ▶ Reduced complexity by hiding internal reactions
- ▶ Reactions arrows can be contextualized with flux data



Analysis options: ECFMs

Computation of ECFMs with PyCoMo and efmtool

- ▶ PyCoMo community models can be used as input
- ▶ efmtool calculates ECFMs for fixed μ
- ▶ As of now, computation only feasible for smaller models (e.g. two *E. coli* core models)



Summary

