



# Constraint-based Modeling of Metabolic Networks

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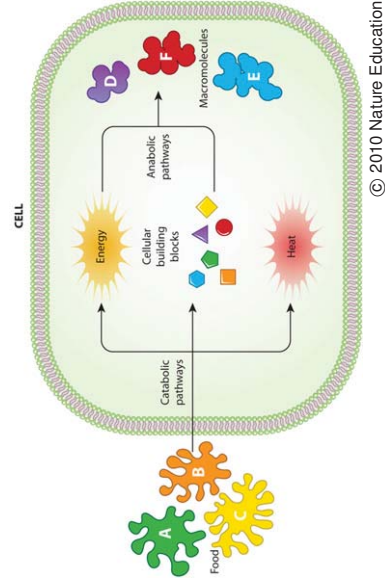
Research Center MATHEON  
*Mathematics for key technologies*

Network analysis, FU Berlin, SoSe 2017

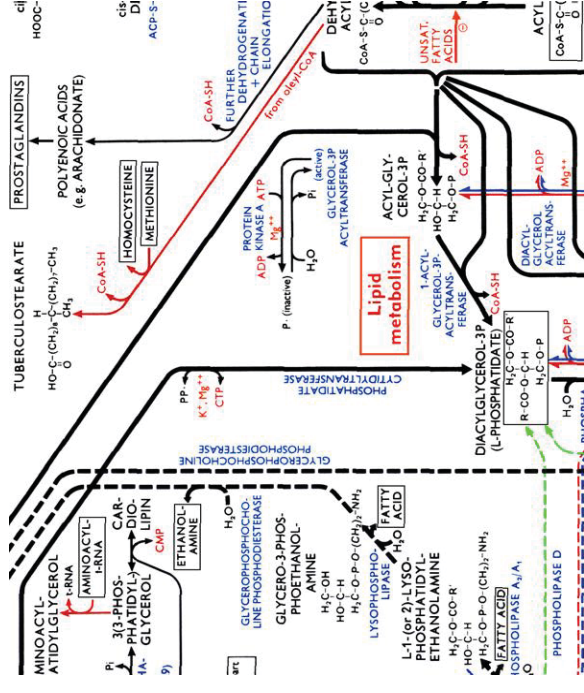


## Importance

- △ Biology
  - ▶ Cell metabolism
  - ▶ Catabolism, anabolism
- △ Medicine
  - ▶ Metabolic disorders
  - ▶ Cancer
- △ Biotechnology
  - ▶ Biofuel
  - ▶ Bioleaching



## Metabolic networks



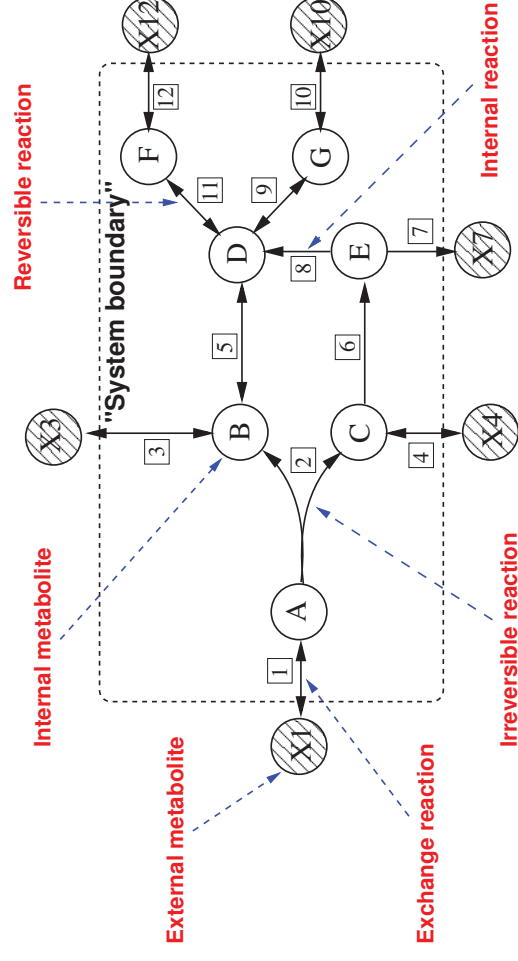
<http://web.expasy.org/pathways/>

A. Bockmayr, Network analysis, SoSe 17

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## Mathematical representation



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- ▷ Stoichiometric matrix
  - ▶ Rows  $\rightsquigarrow$  internal metabolites  $i = 1, \dots, m$
  - ▶ Columns  $\rightsquigarrow$  internal and exchange reactions  $j = 1, \dots, n$
  - ▶  $S_{ij}$ : stoichiometric coefficient of reactant  $i$  in reaction  $j$
- ▷ Set of irreversible reactions *lrr*
- ▷ Metabolic model  $\mathcal{M} = (S, lrr)$

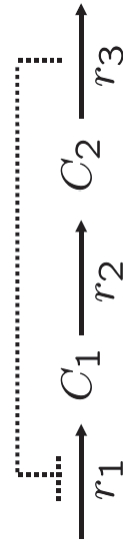
$$S \in \mathbb{R}^{m \times n}$$



- ▷ Metabolites  $i$  and reactions  $j$
- ▷  $C_i(t)$ : metabolite concentrations at time  $t$
- ▷  $v_j(t) = v_j(C(t), k)$ : reaction rates, depending on kinetic law and kinetic parameters  $k$
- ▷  $S_{ij}$ : stoichiometric coefficient

$$\frac{dC_i}{dt} = \sum_{j=1}^n S_{ij} v_j \quad \text{or} \quad \frac{dC}{dt} = S \cdot v(C, k)$$

- ▷ System of ordinary differential equations (ODEs)



$$\begin{pmatrix} dC_1/dt \\ dC_2/dt \end{pmatrix} = \begin{pmatrix} 1 & -1 & 0 \\ 0 & 1 & -1 \end{pmatrix} \cdot \begin{pmatrix} v_1(C, k) \\ v_2(C, k) \\ v_3(C, k) \end{pmatrix}$$

$$\begin{aligned} v_1(C, k) &= v_{m1} / (1 + (C_2/k_1)^p) \\ v_2(C, k) &= v_{m2} \cdot C_1 / (k_1 + C_1) \\ v_3(C, k) &= v_{m3} \cdot C_2 / (k_2 + C_2) \end{aligned}$$

Which kinetic laws?  
Which kinetic parameters?



- ▷ **Steady-state assumption**  
Assume metabolite concentrations  $C_i$  and reaction rates  $v_j$  are constant (over some time interval)  
 $\rightsquigarrow$  steady-state flux vector  $v \in \mathbb{R}^n$
- ▷ **Stoichiometric constraints** (mass balance):

$$\sum_{j=1}^n S_{ij} v_j = 0, \quad \text{for all } i = 1, \dots, m$$

- ▷ **Thermodynamic irreversibility constraints:**  
 $v_j \geq 0$ , if  $j$  is irreversible  
 $\rightsquigarrow$  system of linear equations and inequalities in  $\mathbb{R}^n$

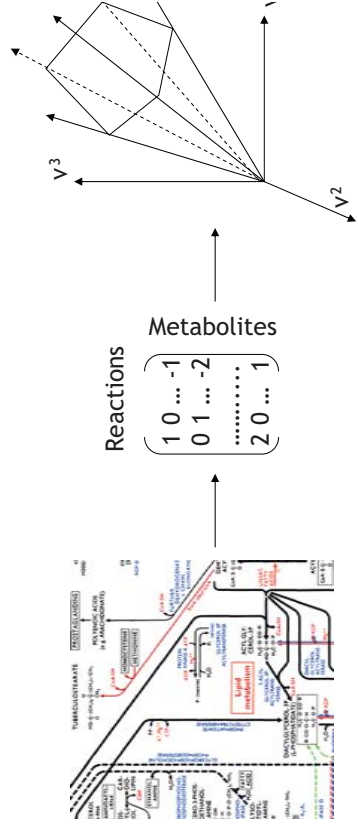


# Steady-state flux cone

Set of all possible steady-state flux distributions

$$C = \{v \in \mathbb{R}^n \mid Sv = 0, v_i \geq 0, i \in Irr\}$$

→ polyhedral cone



# Example

**a** Genome-scale metabolic reconstruction

**b** Mathematically represent metabolic reactions and constraints

**c** Mass balance defines a system of linear equations

**d** Define objective function ( $Z = c_1 v_1 + c_2 v_2 \dots$ )

**e** Calculate fluxes that maximize Z

**E. coli** metabolism  
Genome-scale reconstruction (iJO1366)  
1336 metabolites, 2251 reactions

Objective function: biomass  
Glucose and oxygen uptake reactions  
Aerobic and anaerobic growth  
Software: e.g. COBRA Toolbox 2.0

Orth/Thiele/Palsson 10



# 3. Flux balance analysis (FBA)

- Assume cellular behavior is determined by a certain biological objective.
- Determine a corresponding “best” flux distribution.
- Use mathematical optimization to predict phenotype.

Simplest case: **Linear programming (LP)**

$$\max\{c^T x \mid Ax \leq b, x \in \mathbb{R}^n\}$$

Flux balance problem (**FBA**)

$$\max\{c^T v \mid Sv = 0, l \leq v \leq u\} \quad (\text{FBA})$$



# 4. Flux variability analysis (FVA)

- Optimal solutions to FBA problems need not be unique.
- Enumerating all optimal solutions is computationally expensive.
- Alternative: **Flux variability analysis (FVA)**

$$Z_{opt} = \max\{z = c^T v \mid Sv = 0, l \leq v \leq u\} \quad (\text{FBA})$$

For all  $j = 1, \dots, n$ :

$$\max\{\pm v_j \mid Sv = 0, l \leq v \leq u, c^T v = Z_{opt}\} \quad (\text{FVA})$$