

Biomeg 261 Lecture 07 2017

- Parameter estimation cont'd
 - ↳ Challenges — large number of parameters
 - trade-offs!
 - Example: Metabolic models & estimation of these
 - Approach: Flux Balance Analysis (FBA)
 - constraints
 - linear alg.
 - optimisation
- (new)

Interesting paper (just published):

'How to deal with parameters for whole-cell modelling'

Babtie & Stumpf (2017)

Quotes: (Babbie & Stumpf 2017)

1. currently no suitable framework
to reliably estimate hundreds,
let alone thousands, of
reaction rate parameters

→ see paper/slides

Trade-offs involved.

Goals: Again, Systems Biology

want to tackle
increasingly larger
scale* / complex
systems

* (ie lots of parameters)

Example: Metabolic Models

Recall: Metabolism (cellular)

'all the chemical processes
keeping the cell alive'

→ lots!

Many 'pathways'

- series of enzyme-catalysed reactions
- each lead to breakdown (catabolism) or synthesis (anabolism) of specific metabolites (subst. formed as part of or necessary for metabolism)
- they interact too!

Examples

- see slides
- Key point: large systems
 - ↳ even 'simple' red blood cell model
 - ↳ ~100 ODEs!
 - ↳ each with many parameters
- Parameters often unknown (to be estimated)
 - ↳ systematic search infeasible
 - ↳ 'non-identifiable': no unique 'best' set } 'ill-posed'

Approaches

- ↳ { - search for smaller sets of important param.
 - ↳ complexity penalty
 - ↳ see eg Babtie & Stumpf
- Today { - Try something else!

Babtie & Stumpf (2017)

'Perhaps the best established
[large-scale cell models] are
metabolic models... based around
flux balance analysis (FBA)...'

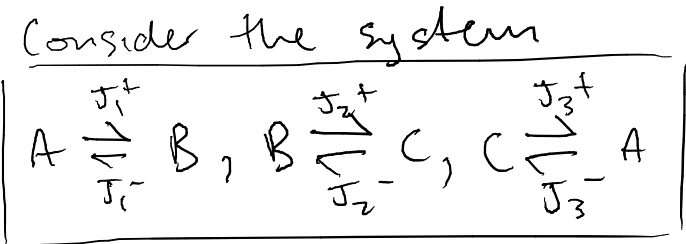
→ makes whole genome-scale
models feasible
→ comes at a cost (trade-offs!)

↳ only considers overall eg
mass balances of reactions
(stoichiometry) - no constitutive
eqns.

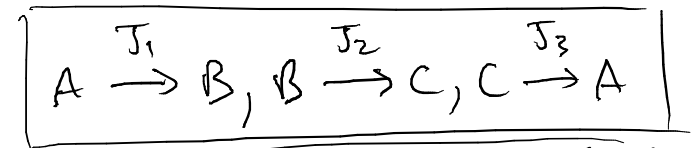
(Can also include some overall
energetic/thermodynamic
into too)

↳ primarily steady-state-based

Simple motivating example



In terms of net fluxes,
ie $|J_i = J_i^+ - J_i^-|$, we can write



where $\left[\xrightarrow{J_i} \right]$ represents $\xrightleftharpoons[J_i^-]{J_i^+}$ etc.

Conservation of mass is then

$$\left[\begin{array}{l} \frac{d[A]}{dt} = -J_1 + J_3 \\ \frac{d[B]}{dt} = +J_1 - J_2 \\ \frac{d[C]}{dt} = +J_2 - J_3 \end{array} \right]$$

Now, write this using matrices/vectors

define:

$$\bar{C} = \begin{bmatrix} [A] \\ [B] \\ [C] \end{bmatrix}, \quad \frac{d\bar{C}}{dt} = \begin{bmatrix} \frac{d[A]}{dt} \\ \frac{d[B]}{dt} \\ \frac{d[C]}{dt} \end{bmatrix}$$

concentrations vector

$$\bar{J} = \begin{bmatrix} J_1 \\ J_2 \\ J_3 \end{bmatrix}$$

net flux vector

(overbar: vector
underbar: matrix)

⇒ gives

$$\frac{d\bar{C}}{dt} = \begin{bmatrix} -1 & 0 & +1 \\ +1 & -1 & 0 \\ 0 & +1 & -1 \end{bmatrix} \bar{J}$$

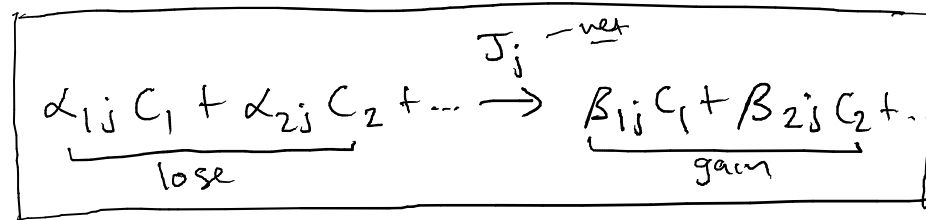
note:
(also use ν instead of J sometimes)

defines matrix \underline{S} :

$$\Rightarrow \underline{\frac{d\bar{C}}{dt}} = \underline{S} \bar{J}$$

Stoichiometric matrix \underline{S}

Given M species & N reactions,
each of the form



⇒ define the Stoichiometric Matrix

$$\underline{S} = \begin{matrix} & \begin{matrix} J_1 & \dots & J_N \end{matrix} \\ \begin{matrix} C_1 \\ C_2 \\ \vdots \\ C_M \end{matrix} & \begin{bmatrix} B_{11}-\alpha_{11} & \dots & B_{1N}-\alpha_{1N} \\ \vdots & \ddots & \vdots \\ B_{M1}-\alpha_{M1} & \dots & B_{MN}-\alpha_{MN} \end{bmatrix} \end{matrix}$$

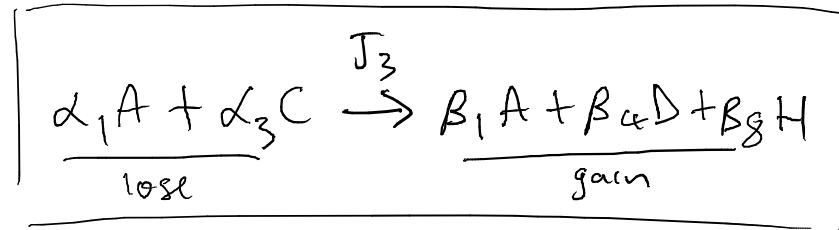
J_j just to help fill in matrix

C_s just to help fill in matrix

Note: $+B, -\alpha$

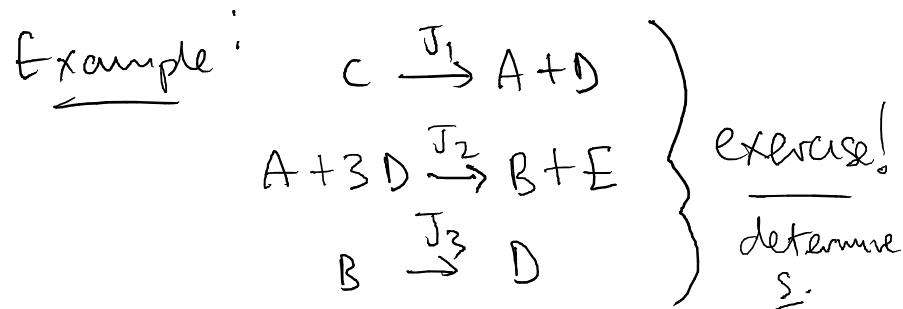
⇒ Sign determined by choice of sign for net flux.

Example: 3rd reaction in some system is



$$\underline{S} = \begin{matrix} A \\ B \\ C \\ D \\ \vdots \\ H \end{matrix} \begin{bmatrix} J_3 \\ \beta_1 - \alpha_1 \\ 0 \\ -\alpha_3 \\ \beta_4 \\ \vdots \\ \beta_8 \end{bmatrix}$$

\uparrow
 3rd reaction.



Mathematical Framework Pt.

Note: we are working in terms of
pure fluxes & conservation
of mass

→ No constitutive eq^s

→ No rate parameters

Problem: 'closure'

→ can't connect J
back to concentrations

ie No ODEs of form $\left| \frac{dc}{dt} = f(c) \right|$

↑
 don't know
 functional
 form.

'Solution': just consider steady states
 & treat fluxes as the
unknowns to be det.

Steady state flux balance analysis (FBA)

- Makes some sense when thinking about overall metabolism in particular (hence popular in this area)
- only need stoichiometry (mass balance)
- often available eg metabolic network maps

⇒ New goal

Solve

$$\underline{S} \bar{J} = \bar{O}$$

for fluxes \bar{J} ← now unknowns of interest
(not [↑] rate constants)

No free lunch: difficulties

- usually more reactions than metabolites (concentrations)
- remember, the reaction fluxes are the unknowns
- often don't know all metabolites involved

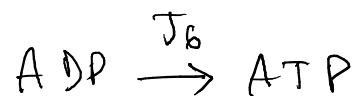
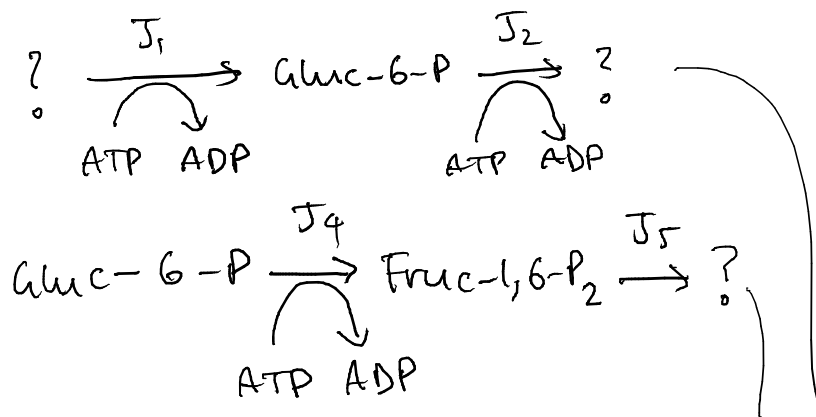
$$\begin{matrix} c_1 \\ \vdots \\ c_M \end{matrix} \left[\begin{array}{c} J_1 \quad J_2 \quad \dots \quad J_N \\ \xleftarrow{\text{under}} \xrightarrow{\hspace{1cm}} \end{array} \right] \quad \underline{N > M}$$

More columns (unknowns J) than rows (equations)

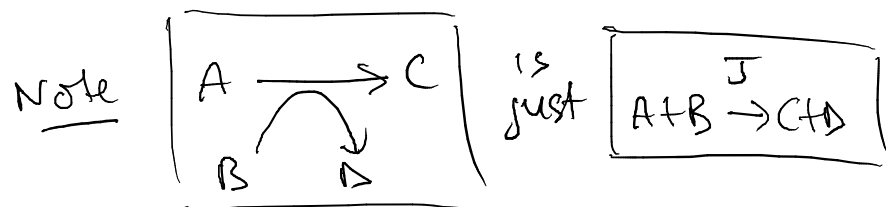
⇒ typically underdetermined ie multiple solutions for J

(Makes sense: conservation: possible
constitutive: actual)

Example: Glycolysis (partial)



allow
'unknown'
metabolites
→ no rows
but reaction
cols is
included.



also often see $A \xrightarrow{\sim} C$ ie \sim instead of J .

$$\underline{S} = \begin{pmatrix} 1 & -1 & -1 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 1 & -1 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 1 & -1 & 0 & 0 & 0 \\ -1 & -1 & 0 & -1 & 0 & 1 & -1 & -1 \\ 1 & 1 & 0 & 1 & 0 & -1 & 1 & 2 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 1 \end{pmatrix} \begin{array}{l} \leftarrow \text{Gluc-6P} \\ \leftarrow \text{Fruc-6P} \\ \leftarrow \text{Fruc-1,6-P}_2 \\ \leftarrow \text{ATP} \\ \leftarrow \text{ADP} \\ \leftarrow \text{AMP} \end{array}$$

6 rows, 8 cols
Unknowns: (J)

$$\underline{\text{Unknowns}} > \underline{\text{eqns!}}$$

$$\underline{S} \underline{J} = \underline{0}$$

2 sol^{ns}: $\underline{J} = \begin{pmatrix} 1 \\ 1 \\ 0 \\ 0 \\ 0 \\ 2 \\ 0 \\ 0 \end{pmatrix}$ or $\underline{J} = \begin{pmatrix} 0 \\ -1 \\ 1 \\ 1 \\ 1 \\ 0 \\ 0 \\ 0 \end{pmatrix}$
(at least)

"Non trivial null space"

↳ set of solutions x
to $\underline{A}x = 0$

→ next time!

non-unique solⁿ