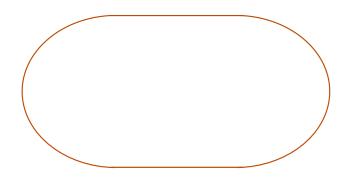
Null Space, Subsets, Elementary Modes and Conserved Cycles Nepal 2018

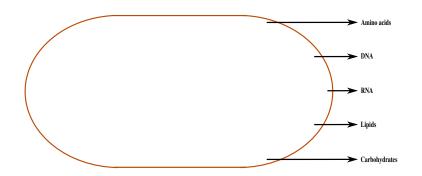
Mark Poolman

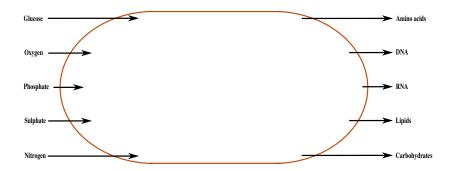
June 29, 2018

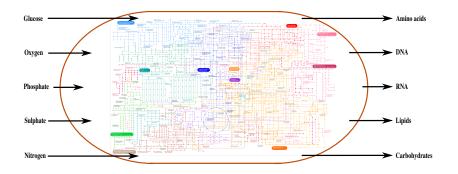
Friday L3



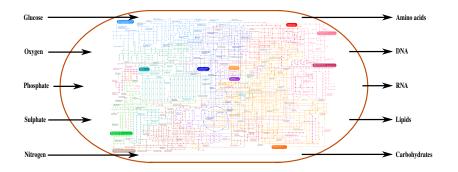








How to connect input(s) to output(s) ??



How to connect input(s) to output(s) ??

Motivation

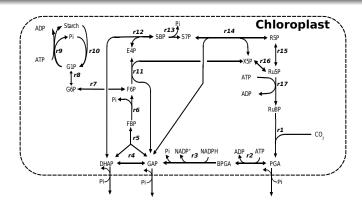
What do we want to know - can we:

• Predict network behaviour (assign fluxes to reactions)?

Predict the effect of network modification?

 Predict the modification needed to achieve a specific effect?

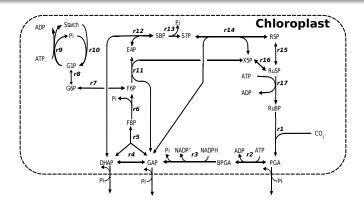
Example - The Calvin Cycle



Questions

- Which reactions are essential?
- What does knowledge of flux in one reaction tell us about flux in another?
- What does knowledge of one metabolite concentration tell us about the concentration of another?

Example - The Calvin Cycle



Questions:

- Which reactions are essential?
- What does knowledge of flux in one reaction tell us about flux in another?
- What does knowledge of one metabolite concentration tell us about the concentration of another?

Definition of a metabolic model

- A set of External metabolites inputs and outputs.
- A set of *Internal* metabolites no net production or consumption.
- A set of reactions that inter-convert them defined by:
 - Stoichiometry.
 - Directionality.
 - Reversibility.



Fundamental assumptions

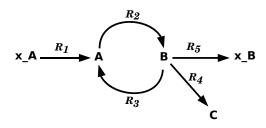
- Reactions interconvert substrates and products whilst conserving mass.
- Transporters are a special case of reaction (interconvert internal with external metabolites)
- Rate of change concentration is sum of reaction rates.
- This is assumed to tend to zero in the long term (steady state)



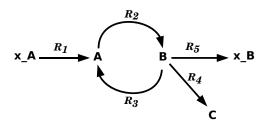
Note

Reactions are not enzymes.

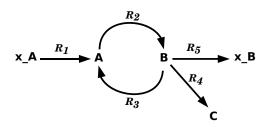
Enzymes are not genes.



$$\begin{array}{rcl} \frac{dA}{df} & = & R_1 + R_3 - R_2 \\ \frac{dB}{df} & = & R_2 - R_3 - R_4 - R_5 \\ \frac{dC}{df} & = & R_4 \end{array}$$



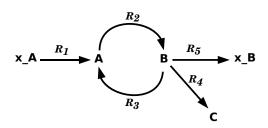
$$\begin{array}{rcl} \frac{dA}{df} & = & R_1 + R_3 - R_2 \\ \frac{dB}{df} & = & R_2 - R_3 - R_4 - R_5 \\ \frac{dC}{dt} & = & R_4 \end{array}$$



$$\begin{bmatrix} \frac{dA}{dt} \\ \frac{dB}{dt} \\ \frac{dC}{dt} \end{bmatrix} = \begin{bmatrix} 1 & -1 & 1 & 0 & 0 \\ 0 & 1 & -1 & -1 & -1 \\ 0 & 0 & 0 & 1 & 0 \end{bmatrix} \begin{bmatrix} R_1 \\ R_2 \\ R_3 \\ R_4 \\ R_5 \end{bmatrix} = \begin{bmatrix} 0 \\ 0 \\ 0 \end{bmatrix}$$

$$Nv = 0$$

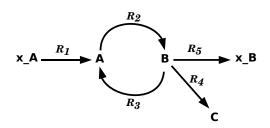




$$\begin{bmatrix} \frac{dA}{glt} \\ \frac{dB}{gt} \\ \frac{dC}{dt} \end{bmatrix} = \begin{bmatrix} 1 & -1 & 1 & 0 & 0 \\ 0 & 1 & -1 & -1 & -1 \\ 0 & 0 & 0 & 1 & 0 \end{bmatrix} \begin{bmatrix} R_1 \\ R_2 \\ R_3 \\ R_4 \\ R_5 \end{bmatrix} = \begin{bmatrix} 0 \\ 0 \\ 0 \end{bmatrix}$$

$$Nv = 0$$

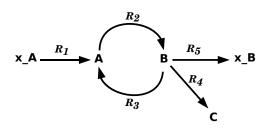




$$\begin{bmatrix} \frac{dA}{gt} \\ \frac{dB}{gt} \\ \frac{dC}{dt} \end{bmatrix} = \begin{bmatrix} 1 & -1 & 1 & 0 & 0 \\ 0 & 1 & -1 & -1 & -1 \\ 0 & 0 & 0 & 1 & 0 \end{bmatrix} \begin{bmatrix} R_1 \\ R_2 \\ R_3 \\ R_4 \\ R_5 \end{bmatrix} = \begin{bmatrix} 0 \\ 0 \\ 0 \end{bmatrix}$$

$$Nv = 0$$

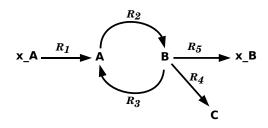




$$\begin{bmatrix} \frac{dA}{gf_1} \\ \frac{dB}{gf_2} \\ \frac{dC}{dt} \end{bmatrix} = \begin{bmatrix} 1 & -1 & 1 & 0 & 0 \\ 0 & 1 & -1 & -1 & -1 \\ 0 & 0 & 0 & 1 & 0 \end{bmatrix} \begin{bmatrix} R_1 \\ R_2 \\ R_3 \\ R_4 \\ R_5 \end{bmatrix} = \begin{bmatrix} 0 \\ 0 \\ 0 \end{bmatrix}$$

$$Nv = 0$$

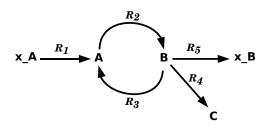




$$Nv = 0$$

So What ?!

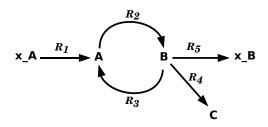
v is not unique



$$Nv = 0$$

So What ?!

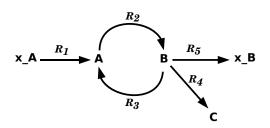
v is not unique



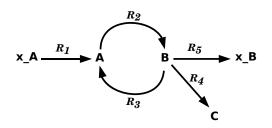
$$Nv = 0$$

So What ?!

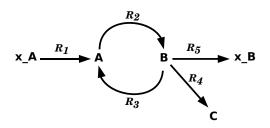
v is not unique



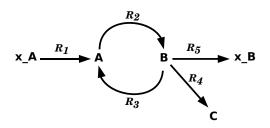
$$\mathbf{K} = \begin{bmatrix} 1 & 0 \\ 1 & 1 \\ 0 & 1 \\ 0 & 0 \\ 1 & 0 \end{bmatrix} \begin{bmatrix} w_1 \\ w_2 \end{bmatrix} = \begin{bmatrix} R_1 \\ R_2 \\ R_3 \\ R_4 \\ R_5 \end{bmatrix} = \begin{bmatrix} 1w_1 + 0w_2 \\ 1w_1 + 1w_2 \\ 0w_1 + 1w_2 \\ 0w_1 + 0w_2 \\ 1w_1 + 0w_2 \end{bmatrix} \leftarrow \text{subset}$$



$$\mathbf{K} = \begin{bmatrix} 1 & 0 \\ 1 & 1 \\ 0 & 1 \\ 0 & 0 \\ 1 & 0 \end{bmatrix} \begin{bmatrix} w_1 \\ w_2 \end{bmatrix} = \begin{bmatrix} R_1 \\ R_2 \\ R_3 \\ R_4 \\ R_5 \end{bmatrix} = \begin{bmatrix} 1w_1 + 0w_2 \\ 1w_1 + 1w_2 \\ 0w_1 + 1w_2 \\ 0w_1 + 0w_2 \\ 1w_1 + 0w_2 \end{bmatrix} \longleftrightarrow \text{subset}$$



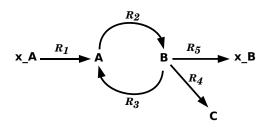
$$\mathbf{K} = \begin{bmatrix} 1 & 0 \\ 1 & 1 \\ 0 & 1 \\ 0 & 0 \\ 1 & 0 \end{bmatrix} \begin{bmatrix} w_1 \\ w_2 \end{bmatrix} = \begin{bmatrix} R_1 \\ R_2 \\ R_3 \\ R_4 \\ R_5 \end{bmatrix} = \begin{bmatrix} 1w_1 + 0w_2 \\ 1w_1 + 1w_2 \\ 0w_1 + 1w_2 \\ 0w_1 + 0w_2 \\ 1w_1 + 0w_2 \end{bmatrix} \longleftrightarrow \text{subset}$$



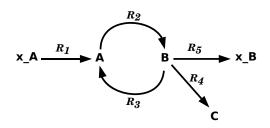
$$\mathbf{K} = \begin{bmatrix} 1 & 0 \\ 1 & 1 \\ 0 & 1 \\ 0 & 0 \\ 1 & 0 \end{bmatrix} \begin{bmatrix} w_1 \\ w_2 \end{bmatrix} = \begin{bmatrix} R_1 \\ R_2 \\ R_3 \\ R_4 \\ R_5 \end{bmatrix} = \begin{bmatrix} 1w_1 + 0w_2 \\ 1w_1 + 1w_2 \\ 0w_1 + 1w_2 \\ 0w_1 + 0w_2 \\ 1w_1 + 0w_2 \end{bmatrix} \longleftrightarrow \text{dead}$$

$$\longleftrightarrow \text{dead}$$

$$\longleftrightarrow \text{subset}$$



$$\mathbf{K} = \begin{bmatrix} 1 & 0 \\ 1 & 1 \\ 0 & 1 \\ 0 & 0 \\ 1 & 0 \end{bmatrix} \begin{bmatrix} w_1 \\ w_2 \end{bmatrix} = \begin{bmatrix} R_1 \\ R_2 \\ R_3 \\ R_4 \\ R_5 \end{bmatrix} = \begin{bmatrix} 1w_1 + 0w_2 \\ 1w_1 + 1w_2 \\ 0w_1 + 1w_2 \\ 0w_1 + 0w_2 \\ 1w_1 + 0w_2 \end{bmatrix} \leftarrow \text{subset}$$



$$\mathbf{K} = \begin{bmatrix} 1 & 0 \\ 1 & 1 \\ 0 & 1 \\ 0 & 0 \\ 1 & 0 \end{bmatrix} \begin{bmatrix} w_1 \\ w_2 \end{bmatrix} = \begin{bmatrix} R_1 \\ R_2 \\ R_3 \\ R_4 \\ R_5 \end{bmatrix} = \begin{bmatrix} 1w_1 + 0w_2 \\ 1w_1 + 1w_2 \\ 0w_1 + 1w_2 \\ 0w_1 + 0w_2 \\ 1w_1 + 0w_2 \end{bmatrix} \leftarrow \text{subset}$$

More about subsets

- All reactions in a subset must carry flux in a fixed ratio.
- 2 Subsets have a single net stoichiometry.
- If any single reaction is removed from a subset, the remaining reactions will be dead.
- If one or more reactions in a subset are irreversible, the whole subset is irreversible.

See: Pfieffer et al (1999) 15, 251-257.

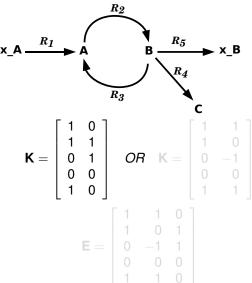


Significance of the kernel

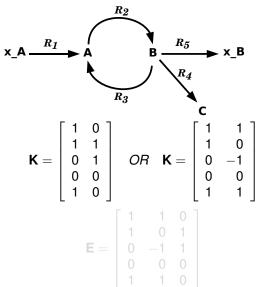
- The kernel captures steady-state invariants of a network that are independent of environment, metabolite levels etc.
- Any and all steady state flux distributions can be represented as a linear combination of columns of the null space.
- A dead reaction will always be dead regardless of kinetic parameters.
- Reactions in subsets carry steady-state flux in fixed ratio regardless of kinetic parameters.
- Unexpected behaviour in other results can often be explained by consideration of the kernel.



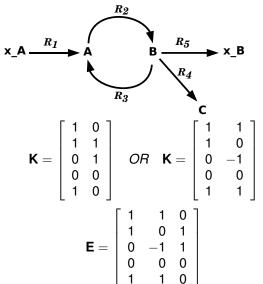
Kernels are not unique



Kernels are not unique



Kernels are not unique



Elementary modes (1)

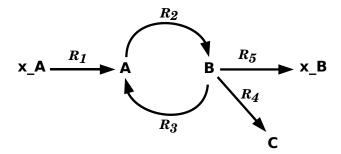
Definition:

A set of reactions in a system that:

- Balance all internal metabolites.
- Respect reversibility.
- Cannot be decomposed. (ie a minimal set of reactions)
- Are associated with a single net stoichiometry involving only external metabolites (or none).

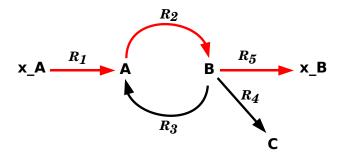
Elementary modes (2)

Non Elementary modes



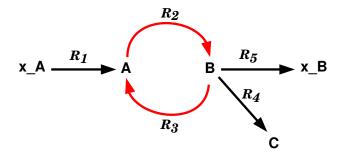
Elementary modes (2)

Non Elementary modes



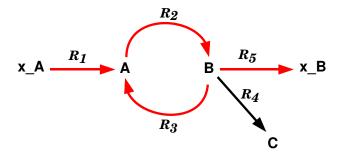
Elementary modes (2)

Non Elementary modes



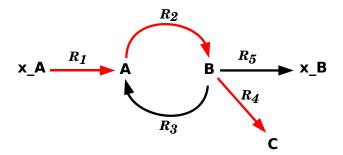
Elementary modes (2)

Non Elementary modes



Elementary modes (2)

Non Elementary modes



Elementary modes - Summary

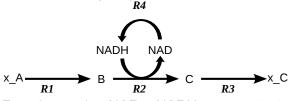
- Elementary modes represent independent paths in a system.
- They provide an objective definition of pathways.
- The set of reactions in an EM is unique.
- Every EM is associated with a net stoichiometry which may or may not be unique.
- The net metabolic behaviour of a system can always be expressed as a linear combination of its EMs.



So far we have considered relationships between steady-state reaction fluxes.

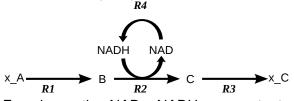
Can we say anything about metabolite concentrations?

Consider a simple cycle:



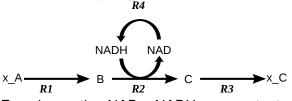
From inspection NAD + NADH are constant.

Consider a simple cycle:



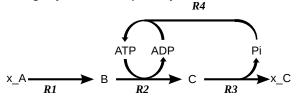
From inspection NAD + NADH are constant.

Consider a simple cycle:



From inspection NAD + NADH are constant.

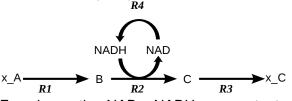
A slightly more complex cycle:



From inspection ADP + ATP and ATP + Pi are constant (?).

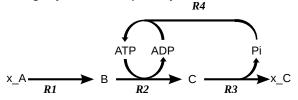


Consider a simple cycle:



From inspection NAD + NADH are constant.

A slightly more complex cycle:



From inspection ADP + ATP and ATP + Pi are constant (?).

These relationships are called

Moiety Conservation relationships.

They can be determined by analysis of the stoichiometry matrix.

$$dNAD/dt = -dNADH/dt$$

Integrating:

$$NAD = -NADH + k$$

$$NAD + NADH = k$$



$$dNAD/dt = -dNADH/dt$$

Integrating:

$$NAD = -NADH + k$$

$$NAD + NADH = k$$



$$dNAD/dt = -dNADH/dt$$

Integrating:

$$NAD = -NADH + k$$

$$NAD + NADH = k$$



$$dNAD/dt = -dNADH/dt$$

Integrating:

$$NAD = -NADH + k$$

$$NAD + NADH = k$$



$$dNAD/dt = -dNADH/dt$$

Integrating:

$$NAD = -NADH + k$$

$$NAD + NADH = k$$



$$dNAD/dt = -dNADH/dt$$

Integrating:

$$NAD = -NADH + k$$

$$NAD + NADH = k$$



$$dNAD/dt = -dNADH/dt$$

Integrating:

$$NAD = -NADH + k$$

$$NAD + NADH = k$$



$$dNAD/dt = -dNADH/dt$$

Integrating:

$$NAD = -NADH + k$$

$$NAD + NADH = k$$



$$dNAD/dt = -dNADH/dt$$

Integrating:

$$NAD = -NADH + k$$

$$NAD + NADH = k$$



Such relationships can be identified from the *left* null space $\mathbf{K}_{\mathbf{l}}$ which has the property:

$$\boldsymbol{K_IN}=\boldsymbol{0}$$

the dimension of which is equal to the number of conservation relationships in the system:

for the first example

$$\mathbf{K_I} = \begin{pmatrix} \mathbf{B} & \mathbf{C} & \mathsf{NAD} & \mathsf{NADH} \\ \mathbf{0} & \mathbf{0} & \mathbf{1} & \mathbf{1} \end{pmatrix}$$
 (one conservation relationship)



Such relationships can be identified from the *left* null space $\mathbf{K}_{\mathbf{l}}$ which has the property:

$$K_IN=0$$

the dimension of which is equal to the number of conservation relationships in the system: for the first example

$$\mathbf{K_I} = \begin{array}{cccc} \mathbf{B} & \mathbf{C} & \mathsf{NAD} & \mathsf{NADH} \\ \mathbf{0} & \mathbf{0} & \mathbf{1} & \mathbf{1} \end{array}$$
 (one conservation relationship)



Such relationships can be identified from the *left* null space $\mathbf{K}_{\mathbf{l}}$ which has the property:

$$K_IN=0$$

the dimension of which is equal to the number of conservation relationships in the system: for the first example

$$\mathbf{K_I} = \begin{array}{cccc} B & C & NAD & NADH \\ 0 & 0 & 1 & 1 \end{array}$$
 (one conservation relationship)



Such relationships can be identified from the *left* null space $\mathbf{K_l}$ which has the property:

$$\boldsymbol{K_IN}=\boldsymbol{0}$$

the dimension of which is equal to the number of conservation relationships in the system: for the first example

$$\mathbf{K_I} = \begin{array}{cccc} B & C & NAD & NADH \\ 0 & 0 & 1 & 1 \end{array}$$
 (one conservation relationship)

$$\begin{matrix} \textbf{K}_I = & B & C & ADP & ATP & Pi \\ 0 & 0 & 1 & 1 & 0 \\ 0 & 1 & 0 & 1 & 1 \end{matrix}$$
 two conservation relationships



Such relationships can be identified from the *left* null space $\mathbf{K_l}$ which has the property:

$$\boldsymbol{K_IN}=\boldsymbol{0}$$

the dimension of which is equal to the number of conservation relationships in the system: for the first example

$$\mathbf{K_I} = \begin{array}{cccc} B & C & NAD & NADH \\ 0 & 0 & 1 & 1 \end{array}$$
 (one conservation relationship)



Notes:

- K_I is not always unique there may not be a single way to represent the conservation relationships in a system.
- Negative elements in K_I do not imply negative concentrations.
- It is not possible to guarantee that an all positive $\mathbf{K}_{\mathbf{I}}$ can be found.

Significance of **K**_I

- Very important consideration in design of kinetic modelling software.
- Introduces "hidden" parameters in kinetic models.
- Changing concentrations in a model can lead to unexpected results.
- Need to identify the dependent metabolite in each relationship.
- The left null-space has received relatively scant attention and represents a potentially fruitful area for further theoretical research.

Conclusions

From consideration of the stoichiometry matrix, along with assumptions about reaction reversibility, we can:

Identify independent routes through metabolic networks.

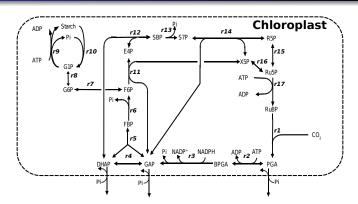
Identify sets of reactions that carry flux in fixed ratios.

 Identify groups of metabolites with interdependent concentration values.

So Now ...

We have the *theoretical* tools to answer the questions posed earlier.

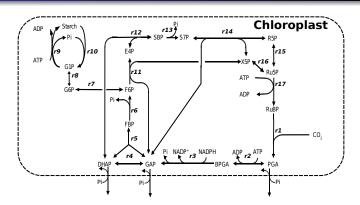
Example - The Calvin Cycle (Practical 4)



Questions:

- What are the routes from starch to triose phosphate. Will they work in the dark?
- Which reactions will show correlated flux.
- Why do plants need the triose-phosphate phosphate anti-porter?

Example - The Calvin Cycle (Practical 4)



Questions:

- What are the routes from starch to triose phosphate. Will they work in the dark?
- Which reactions will show correlated flux.
- Why do plants need the triose-phosphate phosphate anti-porter?