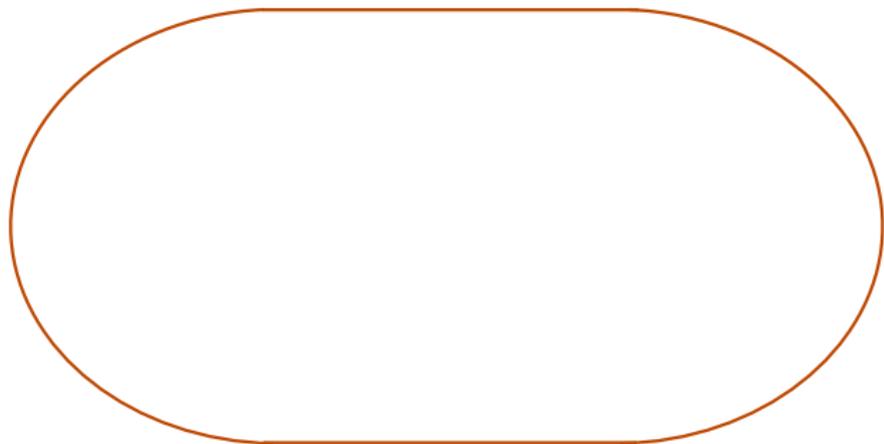


Null Space, Subsets, Elementary Modes and Conserved Cycles Nottingham 2022

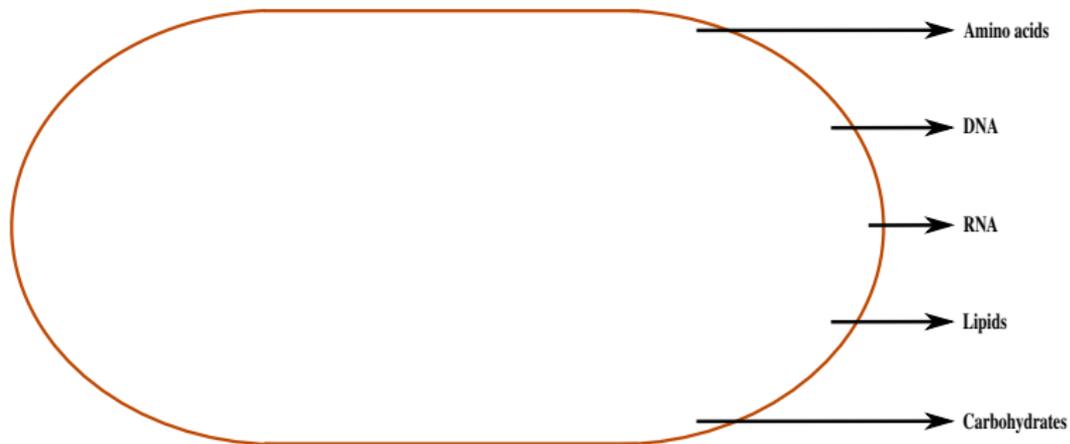
Mark Poolman

May 18, 2023

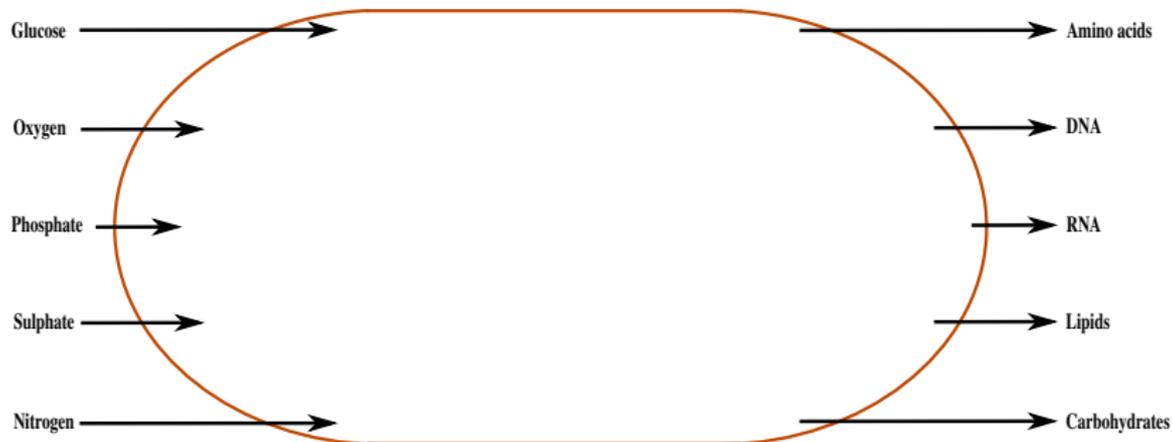
Recap - The Problem



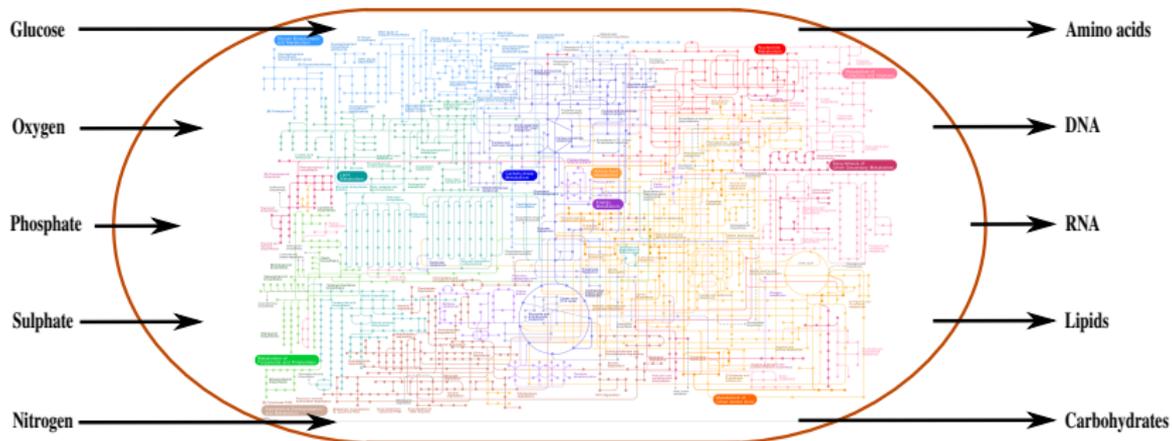
Recap - The Problem



Recap - The Problem

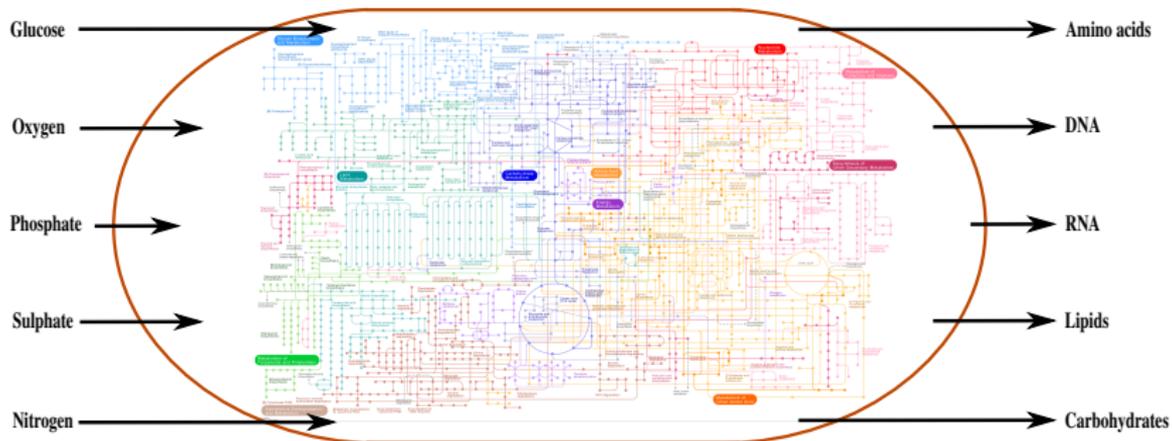


Recap - The Problem



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

Recap - The Problem

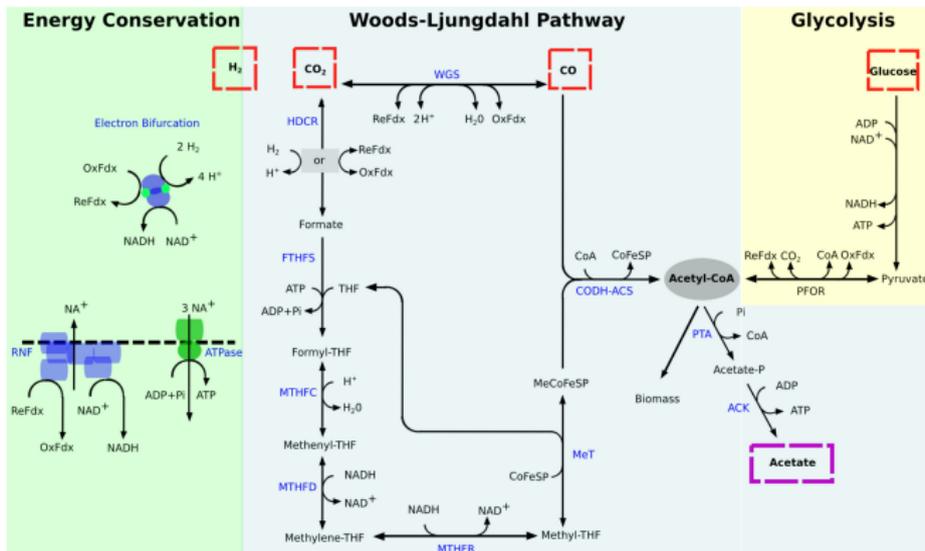


How to connect input(s) to output(s) ??

What do we want to know - can we:

- **Determine** network behaviour (assign fluxes to reactions)?
- **Predict** the effect of network modification?
- **Identify** the modification needed to achieve a specific effect?

Example - The Woods-Ljungdahl Pathway

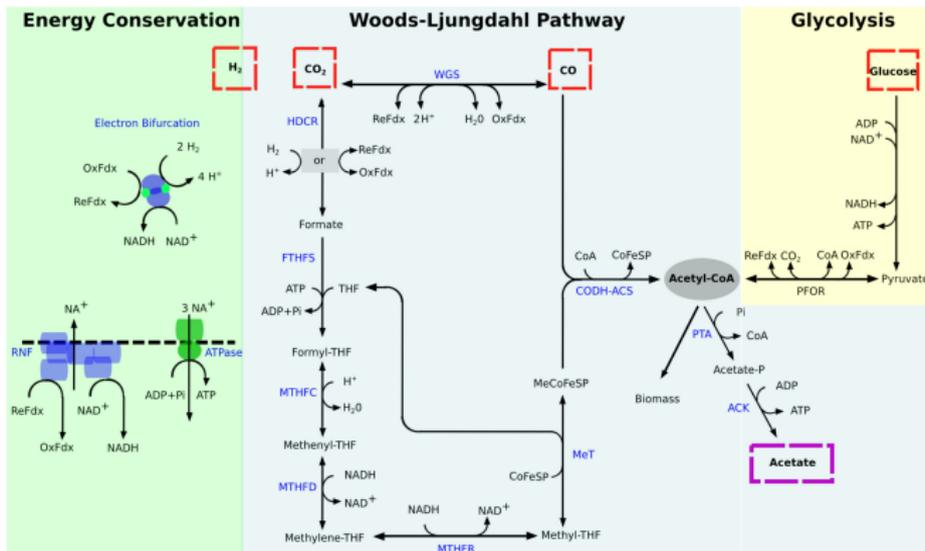


TO DECIDE: We need a suitable, realistic, small model to illustrate and to then use as a basis for the following practical. Do we stick with WLP (a bit exotic) or use something else?

Questions:

- Which reactions are essential?

Example - The Woods-Ljungdahl Pathway



TO DECIDE: We need a suitable, realistic, small model to illustrate and to then use as a basis for the following practical. Do we stick with WLP (a bit exotic) or use something else?

Questions:

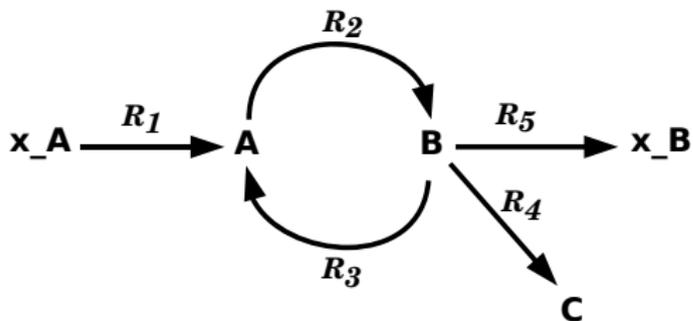
- Which reactions are essential?

!! Remove before use !!

The first few slides here replicate the L1 material for pedagogic correctness.

Remove/edit as you think best

Modelling networks of reactions

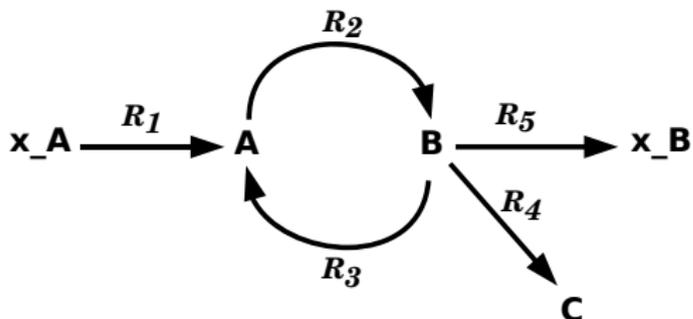


$$Nv = 0$$

So What ?!

v is not unique

Modelling networks of reactions

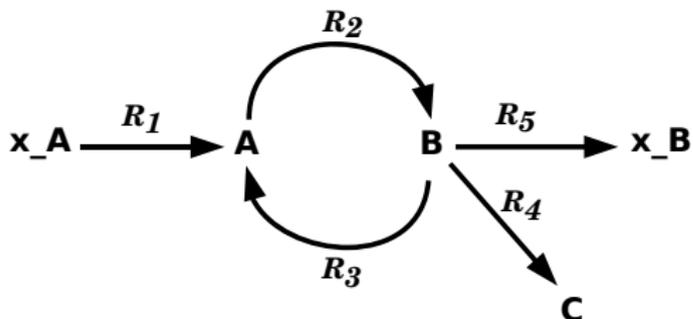


$$Nv = 0$$

So What ?!

v is not unique

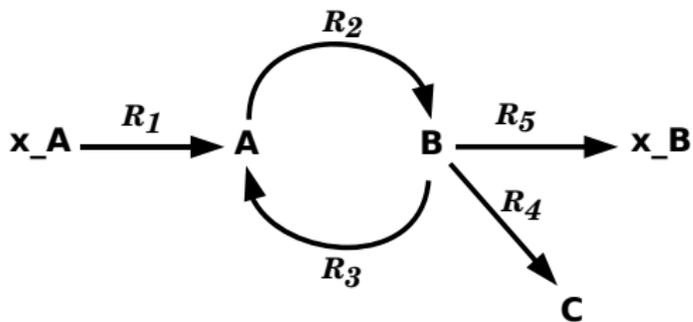
Modelling networks of reactions



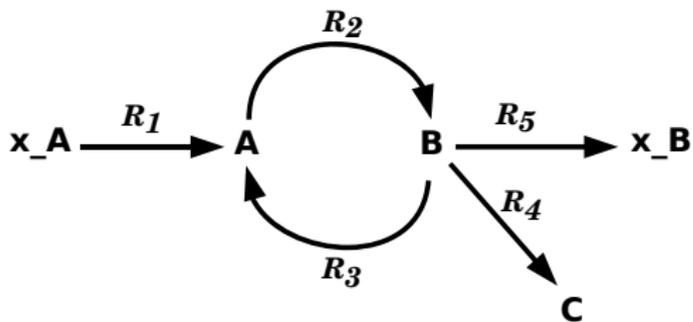
$$Nv = 0$$

So What ?!

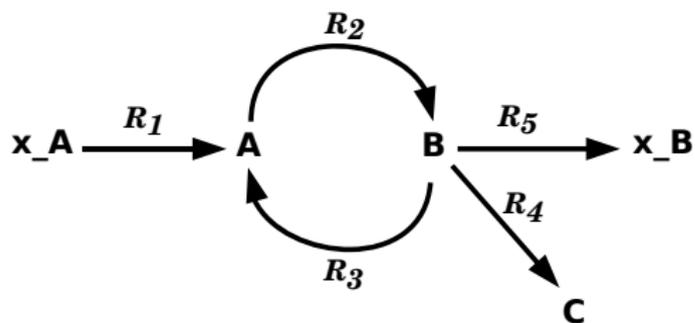
v is not unique



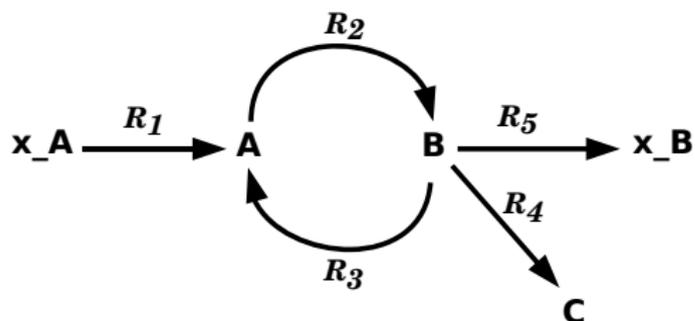
$$\mathbf{K} = \begin{bmatrix} 1 & 0 \\ 1 & 1 \\ 0 & 1 \\ 0 & 0 \\ 1 & 0 \end{bmatrix} \begin{bmatrix} w_1 \\ w_2 \end{bmatrix} = \begin{bmatrix} R_1 \\ R_2 \\ R_3 \\ R_4 \\ R_5 \end{bmatrix} = \begin{bmatrix} 1w_1 + 0w_2 \\ 1w_1 + 1w_2 \\ 0w_1 + 1w_2 \\ 0w_1 + 0w_2 \\ 1w_1 + 0w_2 \end{bmatrix} \begin{matrix}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



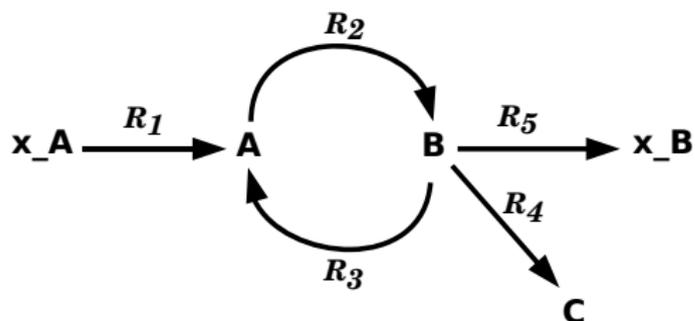
$$\mathbf{K} = \begin{bmatrix} 1 & 0 \\ 1 & 1 \\ 0 & 1 \\ 0 & 0 \\ 1 & 0 \end{bmatrix} \begin{bmatrix} w_1 \\ w_2 \end{bmatrix} = \begin{bmatrix} R_1 \\ R_2 \\ R_3 \\ R_4 \\ R_5 \end{bmatrix} = \begin{bmatrix} 1w_1 + 0w_2 \\ 1w_1 + 1w_2 \\ 0w_1 + 1w_2 \\ 0w_1 + 0w_2 \\ 1w_1 + 0w_2 \end{bmatrix} \begin{matrix}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



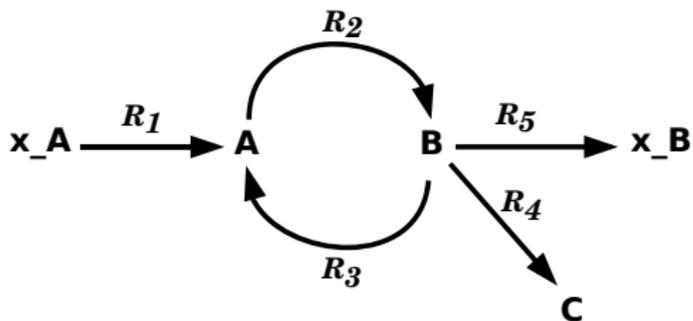
$$\mathbf{K} = \begin{bmatrix} 1 & 0 \\ 1 & 1 \\ 0 & 1 \\ 0 & 0 \\ 1 & 0 \end{bmatrix} \begin{bmatrix} w_1 \\ w_2 \end{bmatrix} = \begin{bmatrix} R_1 \\ R_2 \\ R_3 \\ R_4 \\ R_5 \end{bmatrix} = \begin{bmatrix} 1w_1 + 0w_2 \\ 1w_1 + 1w_2 \\ 0w_1 + 1w_2 \\ 0w_1 + 0w_2 \\ 1w_1 + 0w_2 \end{bmatrix} \begin{matrix}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



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



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

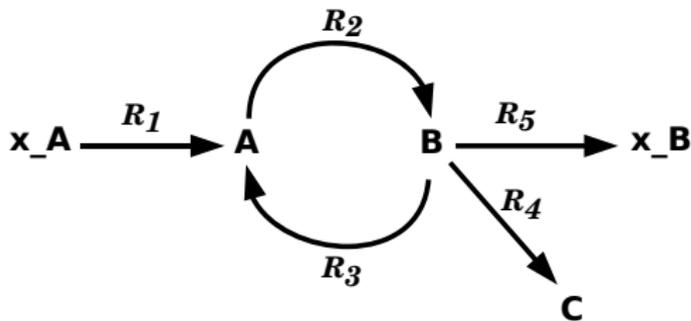


$$\mathbf{K} = \begin{bmatrix} 1 & 0 \\ 1 & 1 \\ 0 & 1 \\ 0 & 0 \\ 1 & 0 \end{bmatrix} \begin{bmatrix} w_1 \\ w_2 \end{bmatrix} = \begin{bmatrix} R_1 \\ R_2 \\ R_3 \\ R_4 \\ R_5 \end{bmatrix} = \begin{bmatrix} 1w_1 + 0w_2 \\ 1w_1 + 1w_2 \\ 0w_1 + 1w_2 \\ 0w_1 + 0w_2 \\ 1w_1 + 0w_2 \end{bmatrix} \begin{matrix}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

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



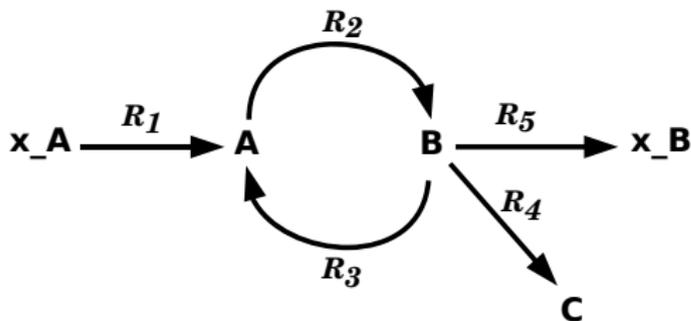
$$K = \begin{bmatrix} 1 & 0 \\ 1 & 1 \\ 0 & 1 \\ 0 & 0 \\ 1 & 0 \end{bmatrix}$$

OR

$$K = \begin{bmatrix} 1 & 1 \\ 1 & 0 \\ 0 & -1 \\ 0 & 0 \\ 1 & 1 \end{bmatrix}$$

$$E = \begin{bmatrix} 1 & 1 & 0 \\ 1 & 0 & 1 \\ 0 & -1 & 1 \\ 0 & 0 & 0 \\ 1 & 1 & 0 \end{bmatrix}$$

Kernels are not unique



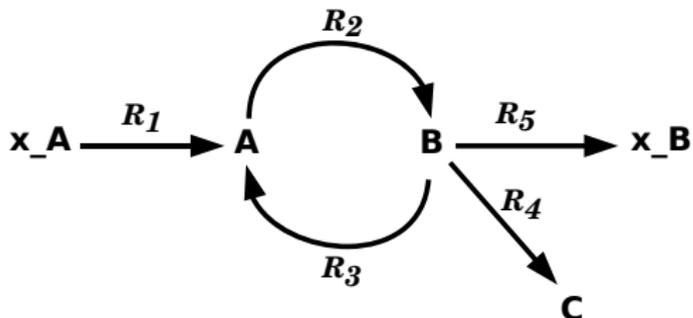
$$K = \begin{bmatrix} 1 & 0 \\ 1 & 1 \\ 0 & 1 \\ 0 & 0 \\ 1 & 0 \end{bmatrix}$$

OR

$$K = \begin{bmatrix} 1 & 1 \\ 1 & 0 \\ 0 & -1 \\ 0 & 0 \\ 1 & 1 \end{bmatrix}$$

$$E = \begin{bmatrix} 1 & 1 & 0 \\ 1 & 0 & 1 \\ 0 & -1 & 1 \\ 0 & 0 & 0 \\ 1 & 1 & 0 \end{bmatrix}$$

Kernels are not unique



$$\mathbf{K} = \begin{bmatrix} 1 & 0 \\ 1 & 1 \\ 0 & 1 \\ 0 & 0 \\ 1 & 0 \end{bmatrix}$$

OR

$$\mathbf{K} = \begin{bmatrix} 1 & 1 \\ 1 & 0 \\ 0 & -1 \\ 0 & 0 \\ 1 & 1 \end{bmatrix}$$

$$\mathbf{E} = \begin{bmatrix} 1 & 1 & 0 \\ 1 & 0 & 1 \\ 0 & -1 & 1 \\ 0 & 0 & 0 \\ 1 & 1 & 0 \end{bmatrix}$$

Elementary modes (1)

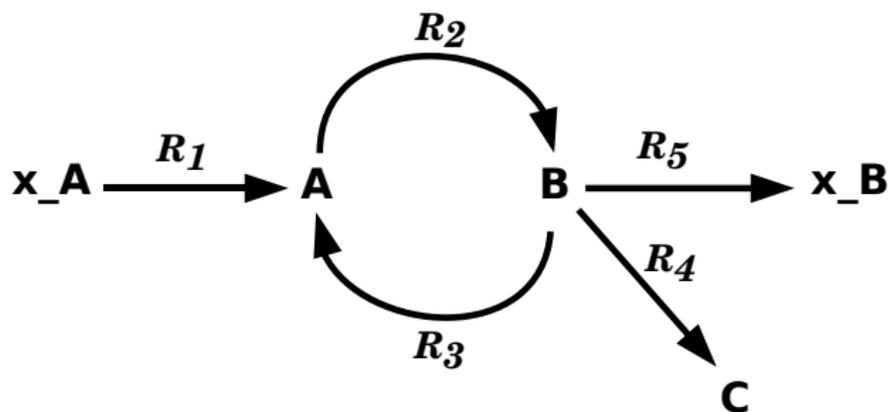
Definition:

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).

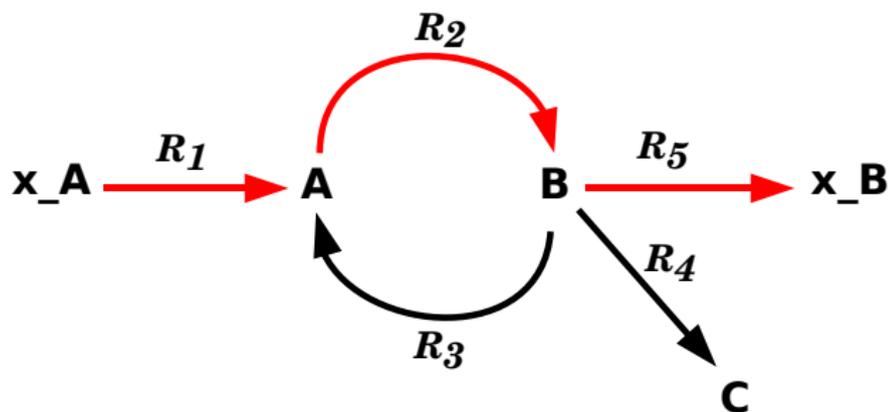
Elementary modes (2)

Non Elementary modes



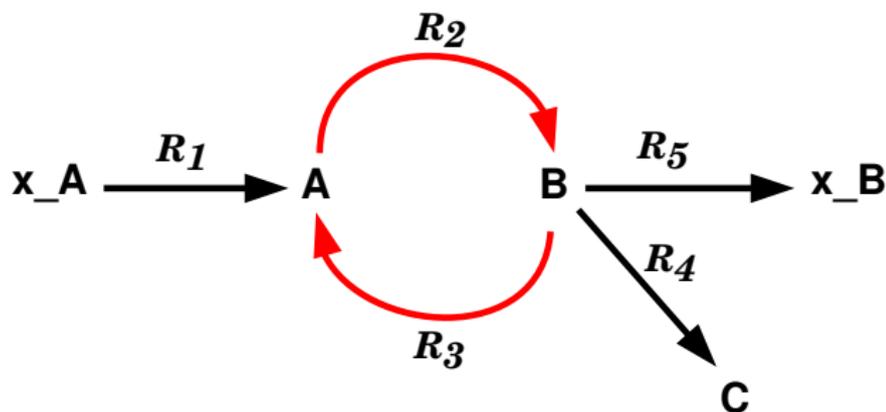
Elementary modes (2)

Non Elementary modes



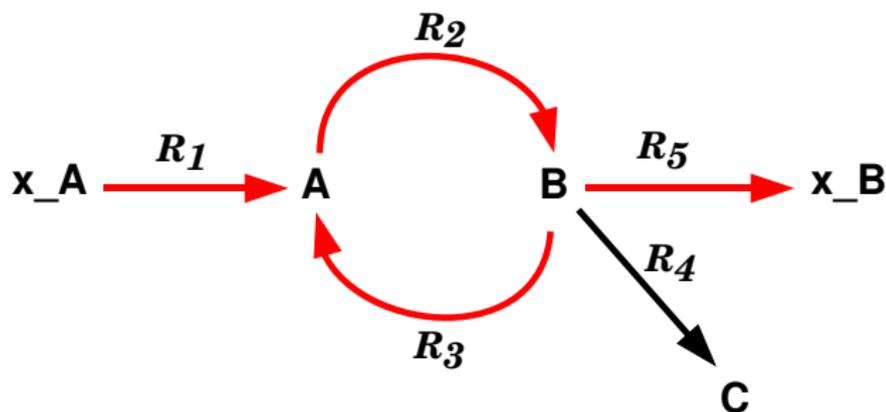
Elementary modes (2)

Non Elementary modes



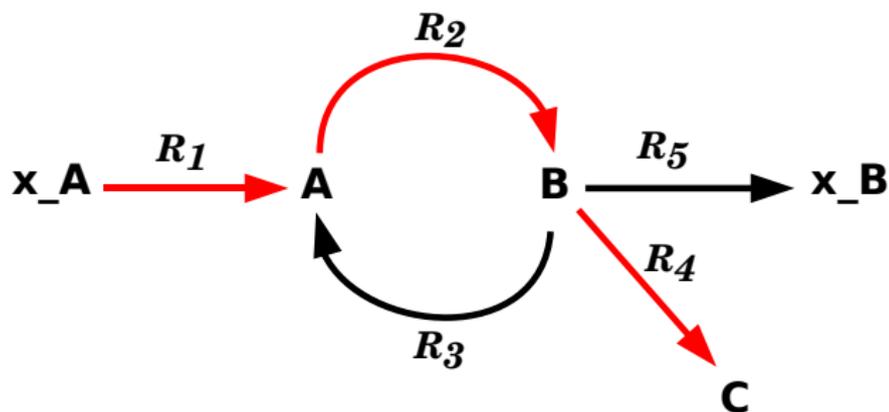
Elementary modes (2)

Non Elementary modes



Elementary modes (2)

Non Elementary modes



Elementary modes - Summary

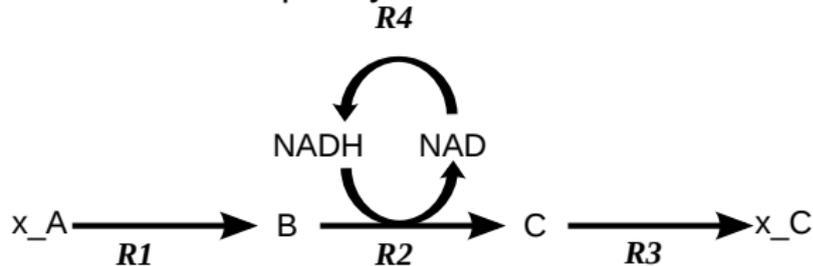
- Elementary modes represent independent paths in a system.
- They provide an *objective* definition of pathways.
- The set of reactions in an EM is unique.
- Every EM is associated with a net stoichiometry which may or may not be unique.
- The net metabolic behaviour of a system can always be expressed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

Conserved cycles

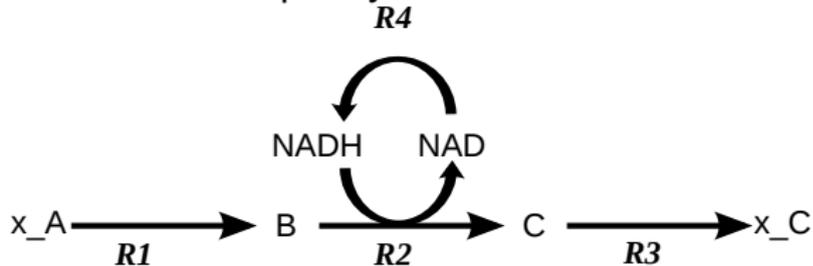
Consider a simple cycle:



From inspection $NAD + NADH$ are constant.

Conserved cycles

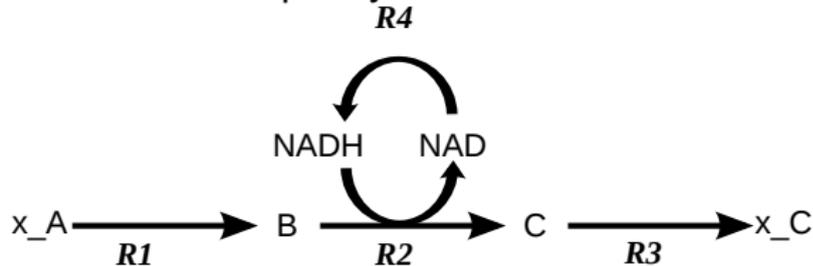
Consider a simple cycle:



From inspection $NAD + NADH$ are constant.

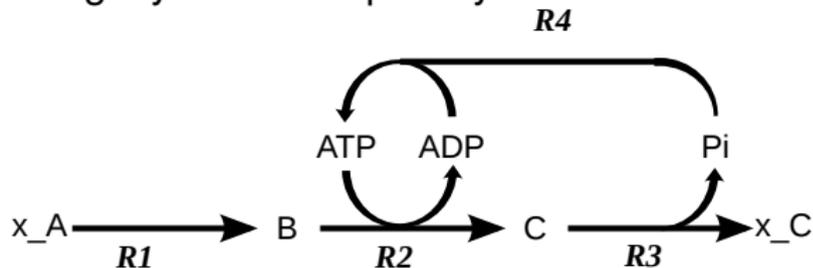
Conserved cycles

Consider a simple cycle:



From inspection $NAD + NADH$ are constant.

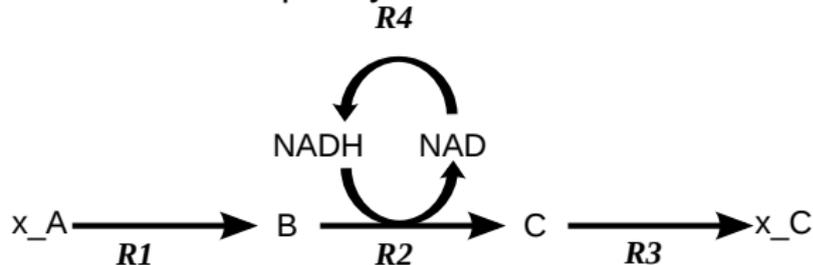
A slightly more complex cycle:



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

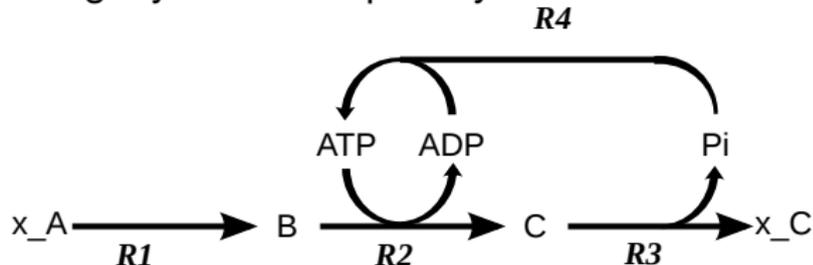
Conserved cycles

Consider a simple cycle:



From inspection $NAD + NADH$ are constant.

A slightly more complex cycle:



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

These relationships are called

Moiety Conservation relationships.

They can be determined by analysis of the stoichiometry matrix.

Conserved cycles

		R1	R2	R3	R4	
N =	B	1	-1	0	0	$dB/dt = R1 - R2$
	C	0	1	-1	0	$dC/dt = R2 - R3$
	NAD	0	1	0	-1	$dNAD/dt = R2 - R4$
	NADH	0	-1	0	1	$dNADH/dt = R4 - R2$

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

Integrating:

$$NAD = -NADH + k$$

$$NAD + NADH = k$$

k is the conserved total.

Conserved cycles

		R1	R2	R3	R4	
N =	B	1	-1	0	0	$dB/dt = R1 - R2$
	C	0	1	-1	0	$dC/dt = R2 - R3$
	NAD	0	1	0	-1	$dNAD/dt = R2 - R4$
	NADH	0	-1	0	1	$dNADH/dt = R4 - R2$

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

Integrating:

$$NAD = -NADH + k$$

$$NAD + NADH = k$$

k is the conserved total.

Conserved cycles

		R1	R2	R3	R4	
N =	B	1	-1	0	0	$dB/dt = R1 - R2$
	C	0	1	-1	0	$dC/dt = R2 - R3$
	NAD	0	1	0	-1	$dNAD/dt = R2 - R4$
	NADH	0	-1	0	1	$dNADH/dt = R4 - R2$

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

Integrating:

$$NAD = -NADH + k$$

$$NAD + NADH = k$$

k is the conserved total.

Conserved cycles

		R1	R2	R3	R4	
N =	B	1	-1	0	0	$dB/dt = R1 - R2$
	C	0	1	-1	0	$dC/dt = R2 - R3$
	NAD	0	1	0	-1	$dNAD/dt = R2 - R4$
	NADH	0	-1	0	1	$dNADH/dt = R4 - R2$

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

Integrating:

$$NAD = -NADH + k$$

$$NAD + NADH = k$$

k is the conserved total.

Conserved cycles

		R1	R2	R3	R4	
N =	B	1	-1	0	0	$dB/dt = R1 - R2$
	C	0	1	-1	0	$dC/dt = R2 - R3$
	NAD	0	1	0	-1	$dNAD/dt = R2 - R4$
	NADH	0	-1	0	1	$dNADH/dt = R4 - R2$

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

Integrating:

$$NAD = -NADH + k$$

$$NAD + NADH = k$$

k is the conserved total.

Conserved cycles

		R1	R2	R3	R4	
N =	B	1	-1	0	0	$dB/dt = R1 - R2$
	C	0	1	-1	0	$dC/dt = R2 - R3$
	NAD	0	1	0	-1	$dNAD/dt = R2 - R4$
	NADH	0	-1	0	1	$dNADH/dt = R4 - R2$

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

Integrating:

$$NAD = -NADH + k$$

$$NAD + NADH = k$$

k is the conserved total.

Conserved cycles

		R1	R2	R3	R4	
N =	B	1	-1	0	0	$dB/dt = R1 - R2$
	C	0	1	-1	0	$dC/dt = R2 - R3$
	NAD	0	1	0	-1	$dNAD/dt = R2 - R4$
	NADH	0	-1	0	1	$dNADH/dt = R4 - R2$

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

Integrating:

$$NAD = -NADH + k$$

$$NAD + NADH = k$$

k is the conserved total.

Conserved cycles

		R1	R2	R3	R4	
N =	B	1	-1	0	0	$dB/dt = R1 - R2$
	C	0	1	-1	0	$dC/dt = R2 - R3$
	NAD	0	1	0	-1	$dNAD/dt = R2 - R4$
	NADH	0	-1	0	1	$dNADH/dt = R4 - R2$

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

Integrating:

$$NAD = -NADH + k$$

$$NAD + NADH = k$$

k is the conserved total.

Conserved cycles

		R1	R2	R3	R4	
N =	B	1	-1	0	0	$dB/dt = R1 - R2$
	C	0	1	-1	0	$dC/dt = R2 - R3$
	NAD	0	1	0	-1	$dNAD/dt = R2 - R4$
	NADH	0	-1	0	1	$dNADH/dt = R4 - R2$

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

Integrating:

$$NAD = -NADH + k$$

$$NAD + NADH = k$$

k is the conserved total.

Structural analysis - The left Null-space

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

$$\mathbf{K}_l \mathbf{N} = \mathbf{0}$$

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

for the first example

$$\mathbf{K}_l = \begin{array}{c} \text{B} \quad \text{C} \quad \text{NAD} \quad \text{NADH} \\ 0 \quad 0 \quad 1 \quad 1 \end{array} \quad (\text{one conservation relationship})$$

and for the second example

$$\mathbf{K}_l = \begin{array}{c} \text{B} \quad \text{C} \quad \text{ADP} \quad \text{ATP} \quad \text{Pi} \\ 0 \quad 0 \quad 1 \quad 1 \quad 0 \\ 0 \quad 1 \quad 0 \quad 1 \quad 1 \end{array} \quad (\text{two conservation relationships})$$

Structural analysis - The left Null-space

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

$$\mathbf{K}_l \mathbf{N} = \mathbf{0}$$

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

$$\mathbf{K}_l = \begin{array}{c} \text{B} \quad \text{C} \quad \text{NAD} \quad \text{NADH} \\ 0 \quad 0 \quad 1 \quad 1 \end{array} \quad (\text{one conservation relationship})$$

and for the second example

$$\mathbf{K}_l = \begin{array}{c} \text{B} \quad \text{C} \quad \text{ADP} \quad \text{ATP} \quad \text{P}_i \\ 0 \quad 0 \quad 1 \quad 1 \quad 0 \\ 0 \quad 1 \quad 0 \quad 1 \quad 1 \end{array} \quad (\text{two conservation relationships})$$

Structural analysis - The left Null-space

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

$$\mathbf{K}_l \mathbf{N} = \mathbf{0}$$

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

$$\mathbf{K}_l = \begin{array}{ccccc} & \text{B} & \text{C} & \text{NAD} & \text{NADH} \\ & 0 & 0 & 1 & 1 \end{array} \quad (\text{one conservation relationship})$$

and for the second example

$$\mathbf{K}_l = \begin{array}{ccccc} & \text{B} & \text{C} & \text{ADP} & \text{ATP} & \text{Pi} \\ & 0 & 0 & 1 & 1 & 0 \\ & 0 & 1 & 0 & 1 & 1 \end{array} \quad (\text{two conservation relationships})$$

Structural analysis - The left Null-space

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

$$\mathbf{K}_l \mathbf{N} = \mathbf{0}$$

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

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

and for the second example

$$\mathbf{K}_l = \begin{array}{ccccc} & \text{B} & \text{C} & \text{ADP} & \text{ATP} & \text{Pi} \\ & 0 & 0 & 1 & 1 & 0 \\ & 0 & 1 & 0 & 1 & 1 \end{array} \quad \text{two conservation relationships}$$

Structural analysis - The left Null-space

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

$$\mathbf{K}_l \mathbf{N} = \mathbf{0}$$

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

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

and for the second example

$$\mathbf{K}_l = \begin{array}{ccccc} & \text{B} & \text{C} & \text{ADP} & \text{ATP} & \text{P}_i \\ & 0 & 0 & 1 & 1 & 0 \\ & 0 & 1 & 0 & 1 & 1 \end{array} \quad \text{two conservation relationships}$$

Structural analysis - The left Null-space

Notes:

- \mathbf{K}_1 is not always unique - there may not be a single way to represent the conservation relationships in a system.
- Negative elements in \mathbf{K}_1 do not imply negative concentrations.
- It is not possible to guarantee that an all positive \mathbf{K}_1 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.

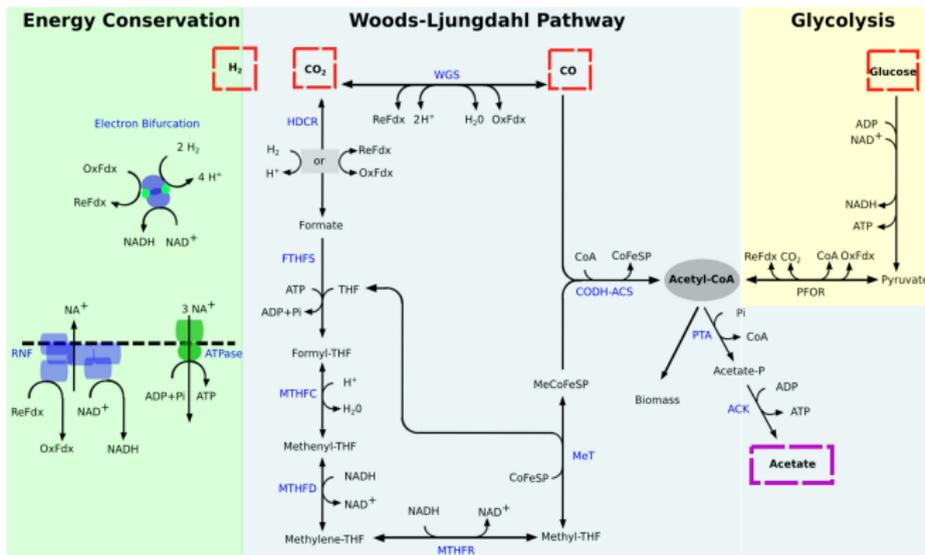
Conclusions

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.

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

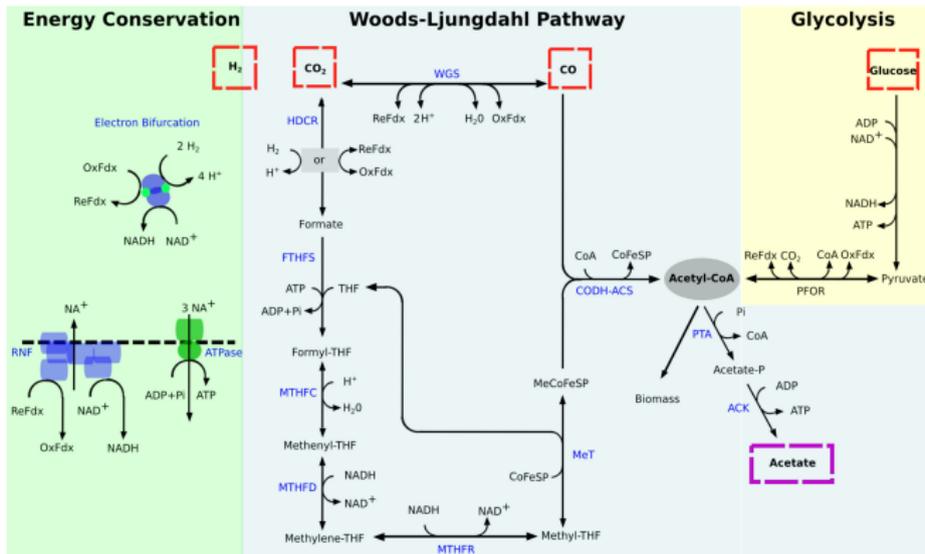
Example - WLP (Practical 4)



Questions:

- What combinations of inputs can be used to generate ATP?
- How many independent routes (aka *Elementary Modes*) are their?
- Which has the optimal yield (ATP/Ac)?

Example - WLP (Practical 4)



Questions:

- What combinations of inputs can be used to generate ATP?
- How many independent routes (aka *Elementary Modes*) are their?
- Which has the optimal yield (ATP/Ac)?