

Biotechnological Applications of Elementary Modes Analysis

Delhi Workshop 1; Structural Modelling of Metabolism; Day 2

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● Outline

Predicting new pathways

Designing metabolic
engineering strategies

Functional analysis of changing
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Summary

- Predicting new pathways
- Designing metabolic engineering strategies
- Functional analysis of changing metabolic flux patterns

● Outline

Predicting new pathways

- Analysis of Central Carbon Metabolism
- Finding a New Pathway
- The Experimental Confirmation
- Gene ontologies and annotation - 2

Designing metabolic engineering strategies

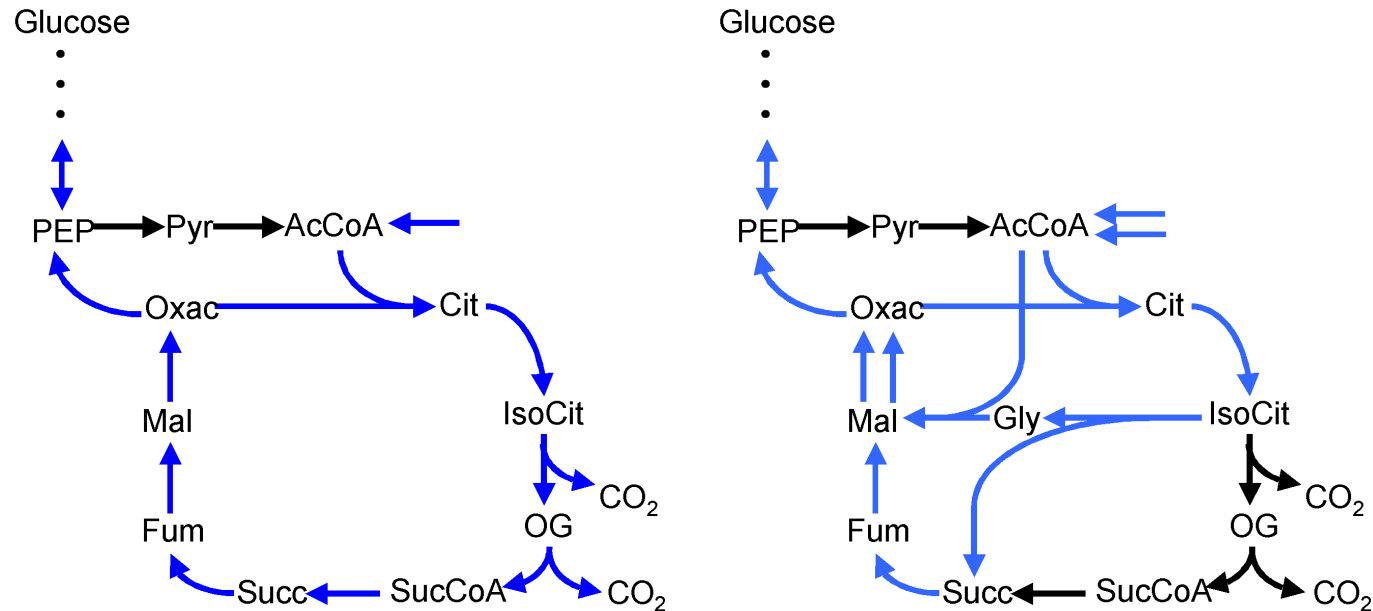
Functional analysis of changing metabolic flux patterns

Summary

Predicting new pathways

Analysis of Central Carbon Metabolism

In Schuster, Dandekar & Fell, *TIBS* (1999), we were analysing gluconeogenesis and the glyoxylate cycle:



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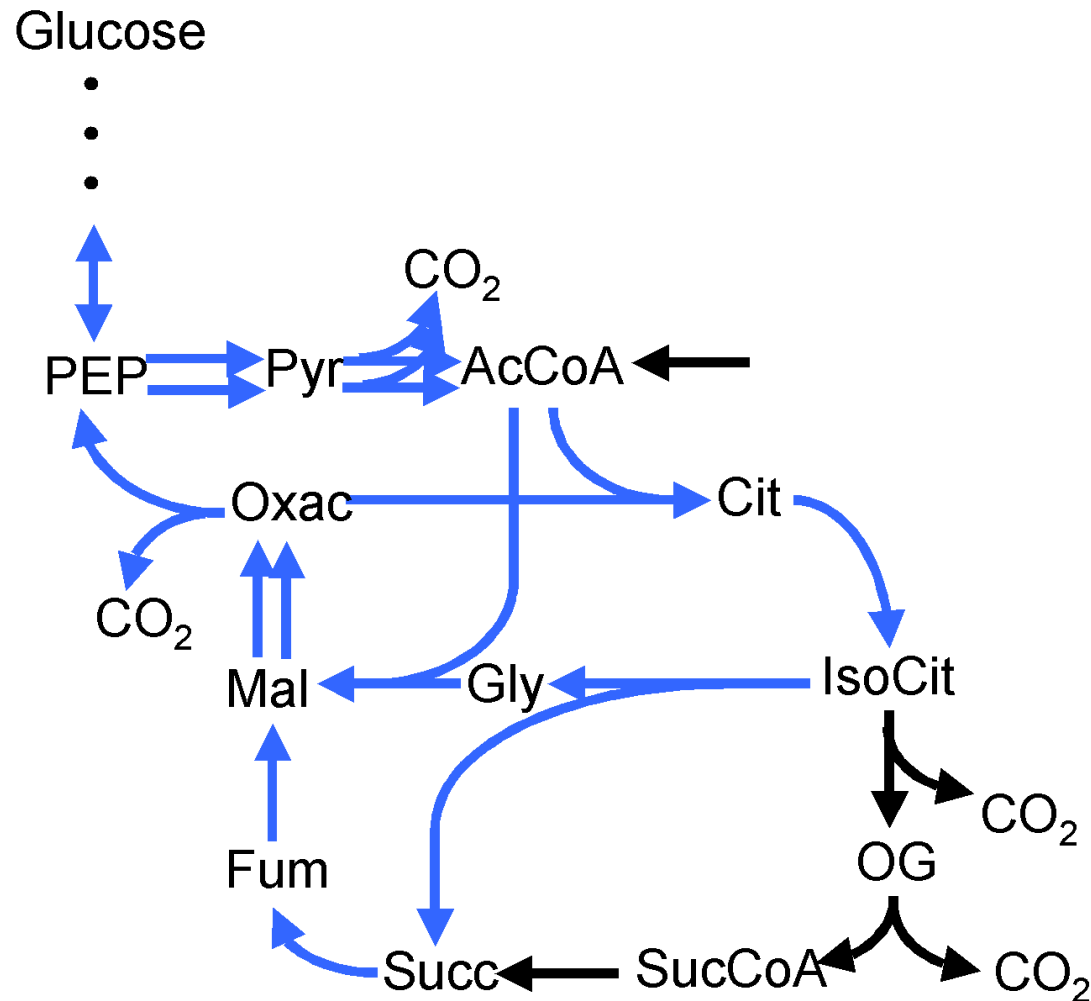
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Finding a New Pathway

In Schuster, Dandekar & Fell, *TIBS* (1999), we described the following:



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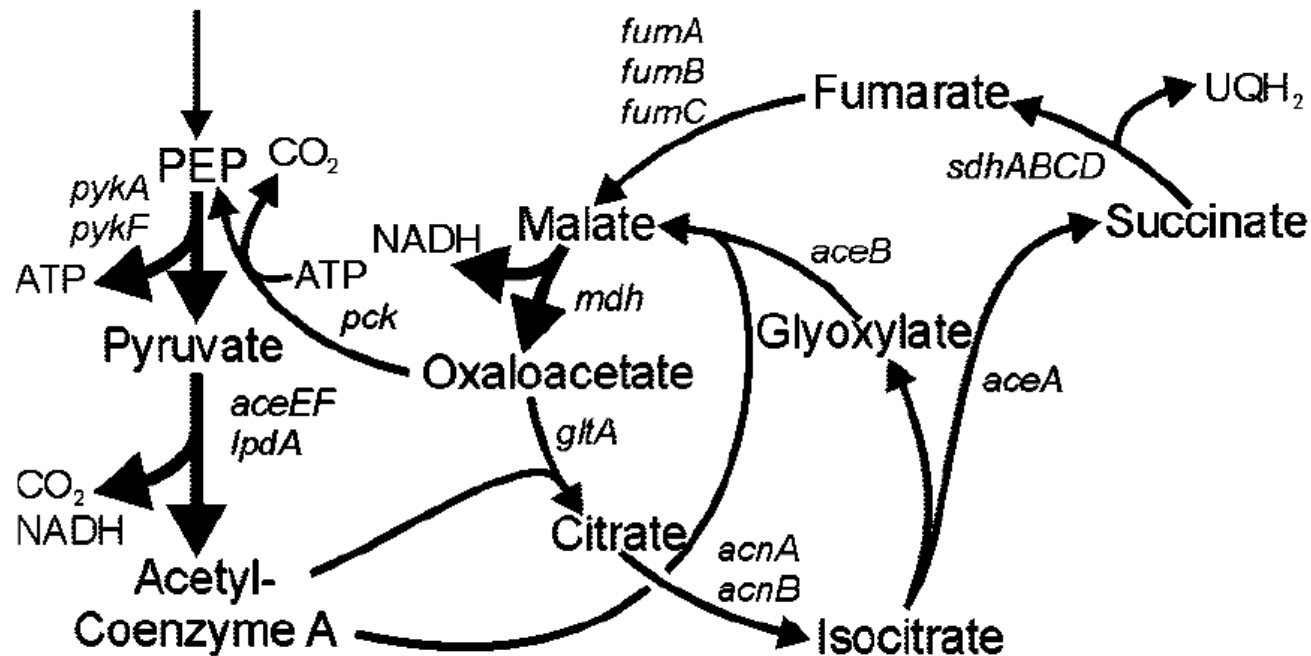
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In *J Biol Chem* in 2003, Fischer and Sauer observed this pathway in *E coli* cells growing at low glucose levels:



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How relevant are they? e.g. the Gene Ontology Consortium:

glyoxylate cycle

* Accession: GO:0006097

* Aspect: process

* Synonyms: glyoxylate bypass

* Definition:

o A modification of the TCA cycle occurring in some plants and microorganisms, in which isocitrate is cleaved to glyoxylate and succinate. Glyoxylate can then react with acetyl-CoA to form malate.

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- Polyhydroxybutyrate synthesis
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- Optimal yields of PHB
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- Ethanol from Plant Waste
- A Demonstration Solution
- The Model
- The Analysis

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Polyhydroxybutyrate synthesis in yeast

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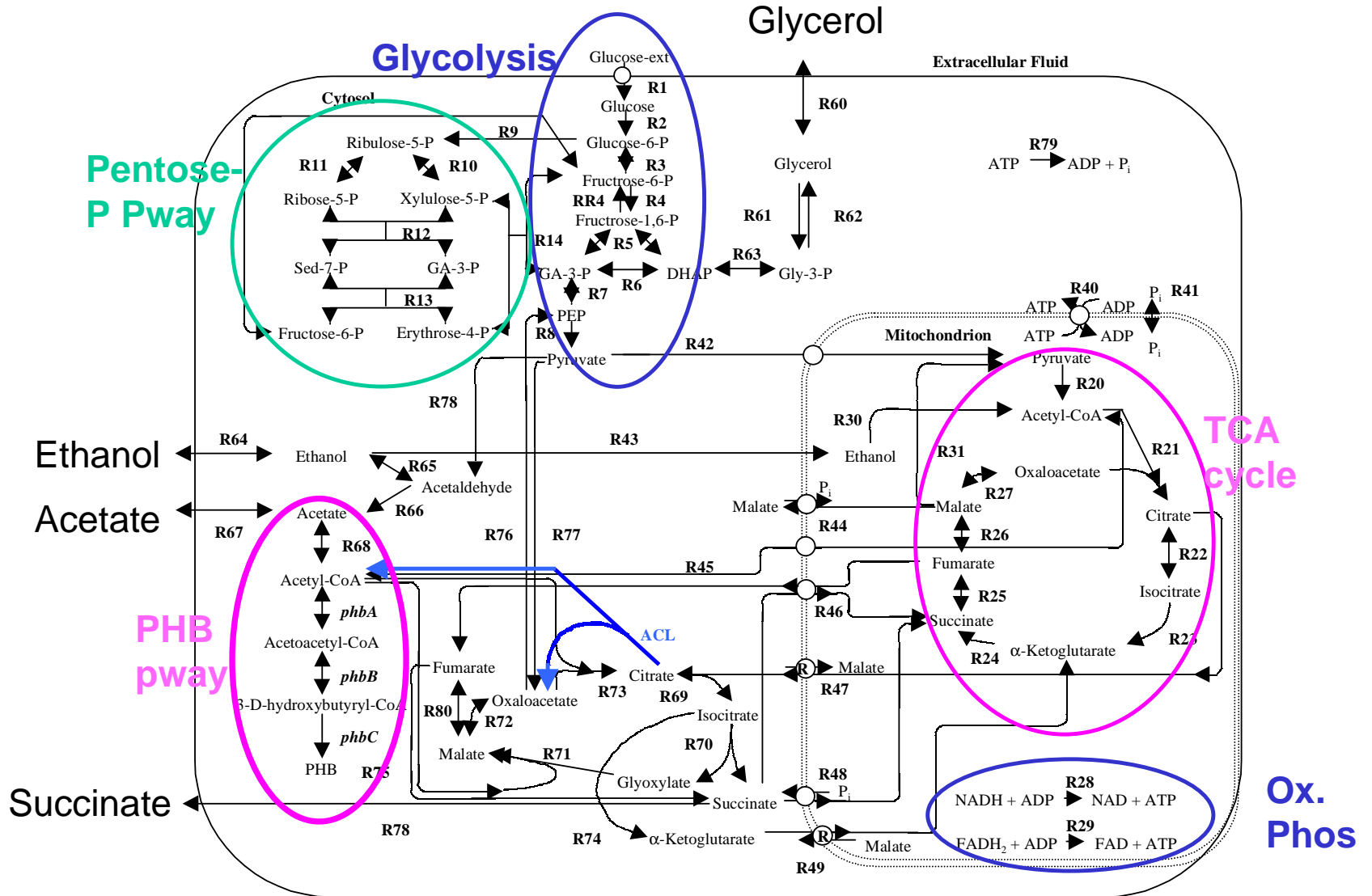
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Wild-type yeast + PHB pathway

1. $2 \text{ Acetate} + \text{EtOH} \rightarrow \text{PHB} + 2 \text{ CO}_2$ 0.67
2. $65 \text{ Ac.} + 31 \text{ EtOH} \rightarrow 30 \text{ PHB} + 72 \text{ CO}_2$ 0.63

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Wild-type yeast + ATP–citrate lyase + PHB pathway

3. $12 \text{ EtOH} \rightarrow 5 \text{ PHB} + 4 \text{ CO}_2$ 0.83
4. $77 \text{ EtOH} + 31 \text{ Glycerol} \rightarrow$
 $48 \text{ PHB} + 4 \text{ Ac.} + 47 \text{ CO}_2$ 0.78

(Number following each mode is the fractional carbon conversion.)

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Summary

Some of the issues:

- Plant wastes (e.g. straw) contain cellulose and hemicellulose which can be hydrolysed to glucose and pentose sugars.
- Yeasts convert glucose to ethanol, but don't readily use the pentoses.
- *Escherichia coli* can use pentoses as well as glucose, but ethanol is not its preferred product.
- E. coli is easy to engineer, but can it be modified to make ethanol from pentoses in such a way that it cannot mutate back to its original state?

A Demonstration Solution

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Summary

- Friedrich Sreenc's group (Trinh et al, Appl. Env. Microbiol, 74, 3634-3643, 2008) built a medium-sized structural model of E coli central carbon metabolism.
- They computed the elementary modes leading from glucose and pentoses to products including ethanol and biomass.
- They searched for reactions that were *needed* for modes leading to other products but which were *not needed* for *some* of the routes to biomass and ethanol.
- They found a set of *eight* reactions that between them disabled all the modes except those leading to either ethanol alone or biomass and ethanol.
- They made a the deletion mutants and obtained close to the theoretically-predicted yields of ethanol.

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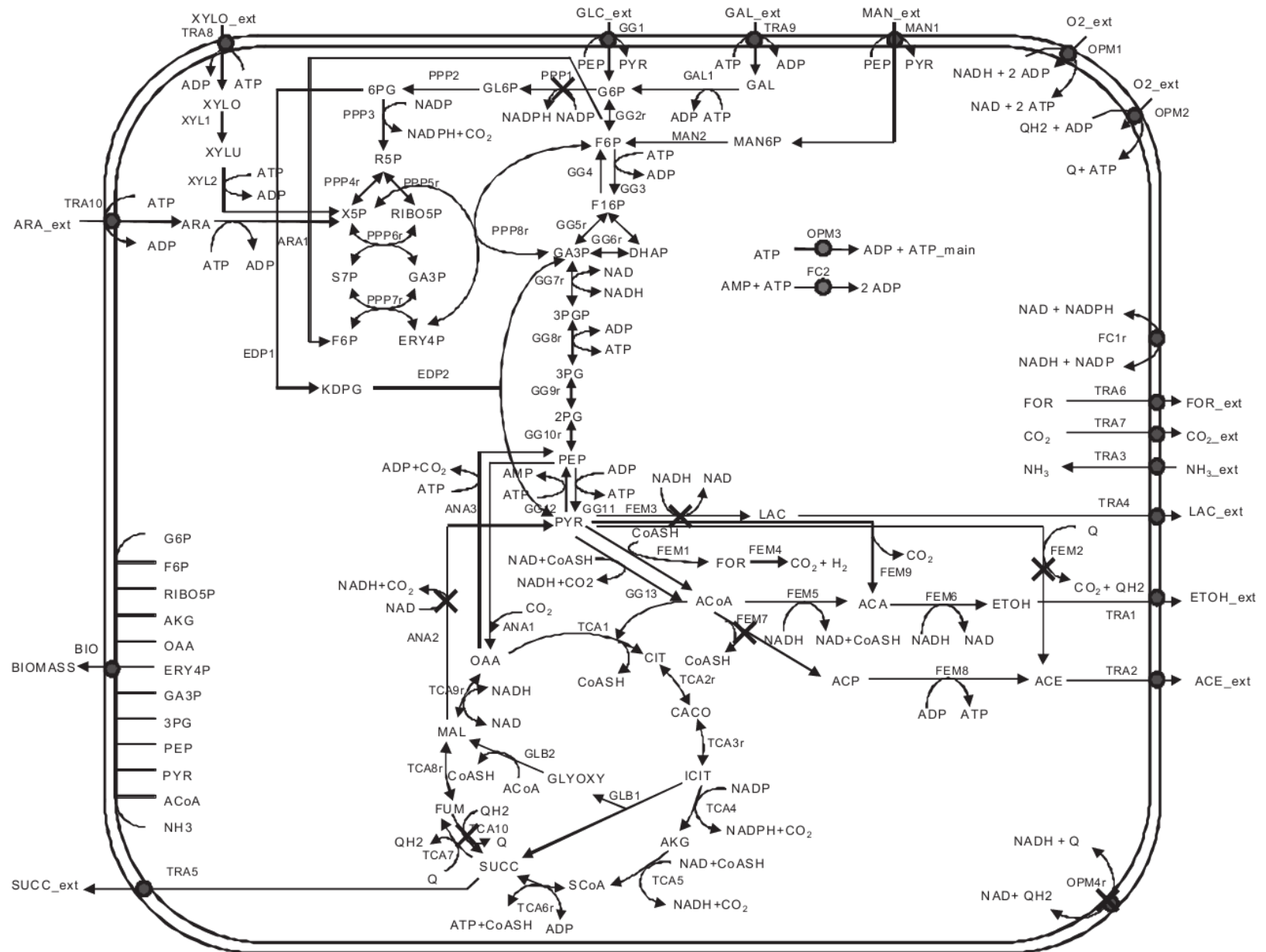
● A Demonstration Solution

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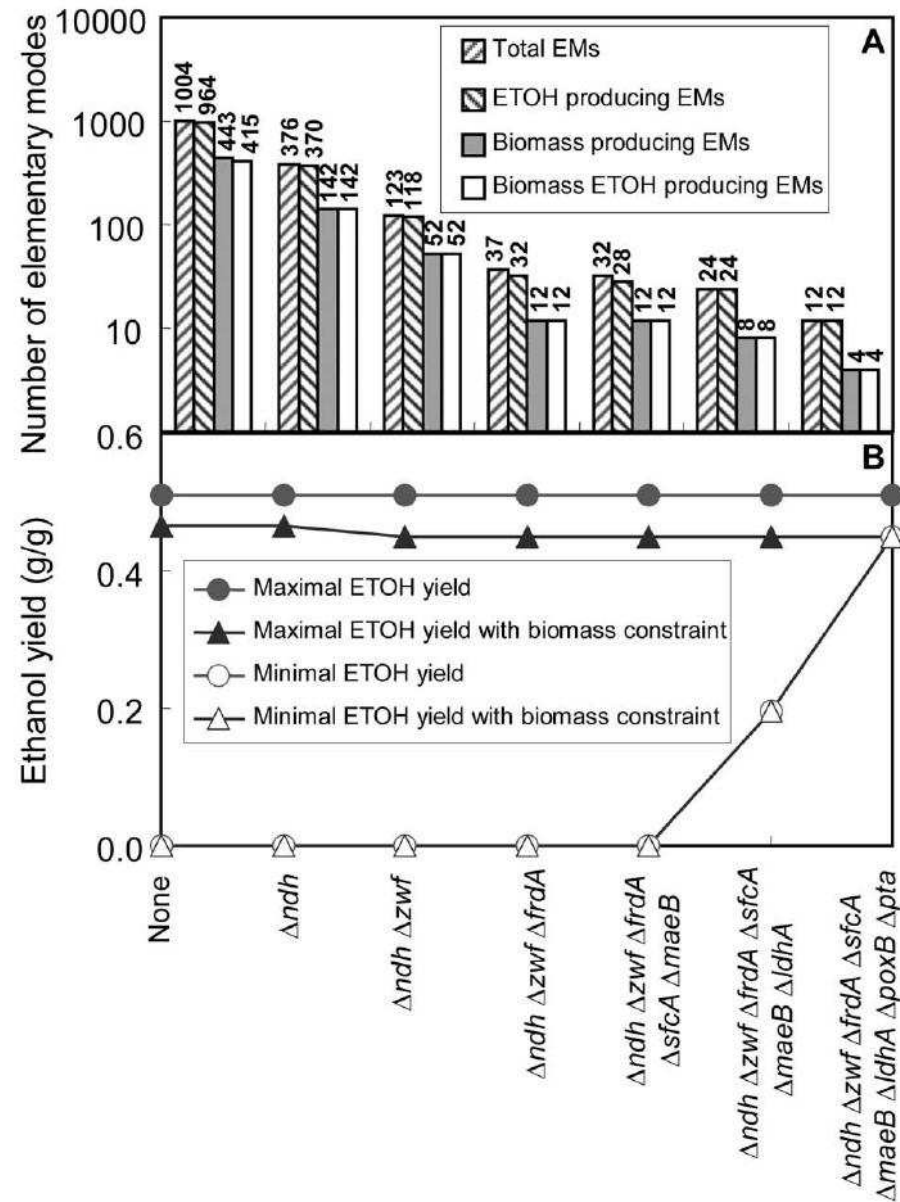
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Summary

The steady state requirement is:

$$\mathbf{N} \cdot \mathbf{v} = \mathbf{0}$$

But each elementary mode vector \mathbf{e}_i in a matrix of elementary mode vectors \mathbf{E} is also a steady state solution, i.e.:

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So the actual velocities, \mathbf{v} are a weighted combination of the elementary modes:

$$\mathbf{v} = \mathbf{E} \cdot \mathbf{w}$$

where \mathbf{w} is a vector of weighting factors.

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Although there is not a unique solution for \mathbf{w} because \mathbf{E} is generally non-invertible and the system under-determined:

$$\hat{\mathbf{w}} = \mathbf{E}^\# \mathbf{v}$$

where $\mathbf{E}^\#$ is the generalised Penrose inverse of \mathbf{E} . Even if we have not measured all the fluxes in \mathbf{v} , we can partition observed \mathbf{v}_o and non-observed \mathbf{v}_x fluxes:

$$\mathbf{v} = [\mathbf{v}_o, \mathbf{v}_x]^T, \text{ and } \mathbf{E} = \begin{bmatrix} \mathbf{E}_o \\ \mathbf{E}_x \end{bmatrix}.$$

Then:

$$\hat{\mathbf{w}} = \mathbf{E}_o^\# \mathbf{v}_o$$

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Why select $\hat{\mathbf{w}}$ from the many feasible values of \mathbf{w} ?

- It is the minimum norm solution. i.e. it minimizes

$$\sqrt{\sum \hat{w}_i^2}$$

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Why select \hat{w} from the many feasible values of w ?

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- This ensures that zero flux is assigned to cycles with no overall stoichiometry.

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- It is the minimum norm solution. i.e. it minimizes

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- This ensures that zero flux is assigned to cycles with no overall stoichiometry.
- It assigns flux as evenly as possible over available modes (the 'democratic' option).
- When v_o changes smoothly, so does \hat{w} . (Not the case for other extreme solutions, e.g. the 'autocratic' optionx.)

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Flux analysis of lactic acid metabolism

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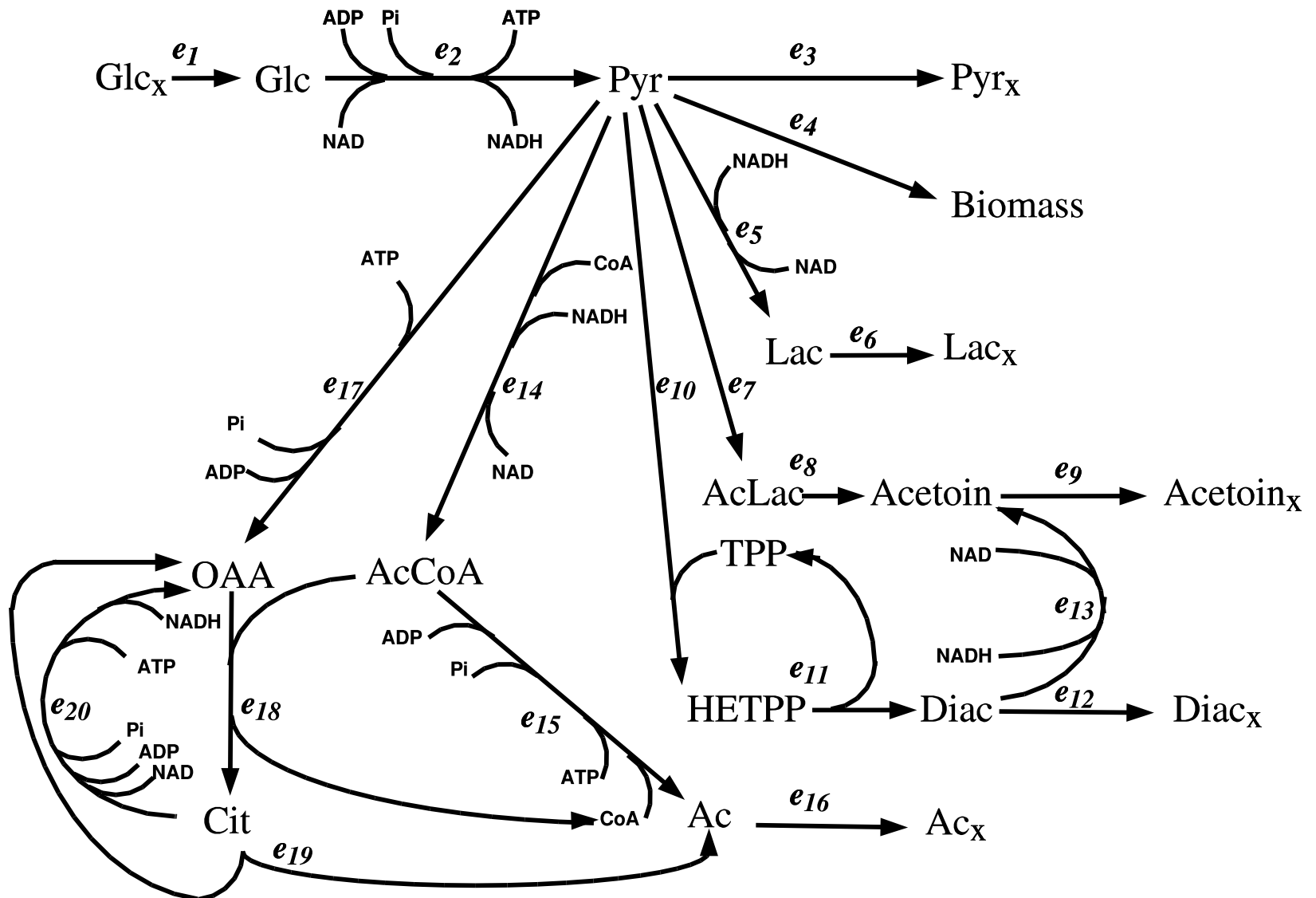
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- This reduced scheme has 191 modes.

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Summary

- This reduced scheme has 191 modes.
- Only 83 modes consumed nutrients and metabolites observed to be used in the experiments.

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- This reduced scheme has 191 modes.
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- Flux was assigned to these 83 at different time points through a 48 h fermentation.

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Summary

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- Only 83 modes consumed nutrients and metabolites observed to be used in the experiments.
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- Modes with equivalent overall stoichiometries were grouped and their assigned flux summed to a single figure, giving 23 assigned fluxes.

Elementary modes analysis

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- Modes with equivalent overall stoichiometries were grouped and their assigned flux summed to a single figure, giving 23 assigned fluxes.
- The time-dependence of these fluxes defined 4 groups.

Mode assignment

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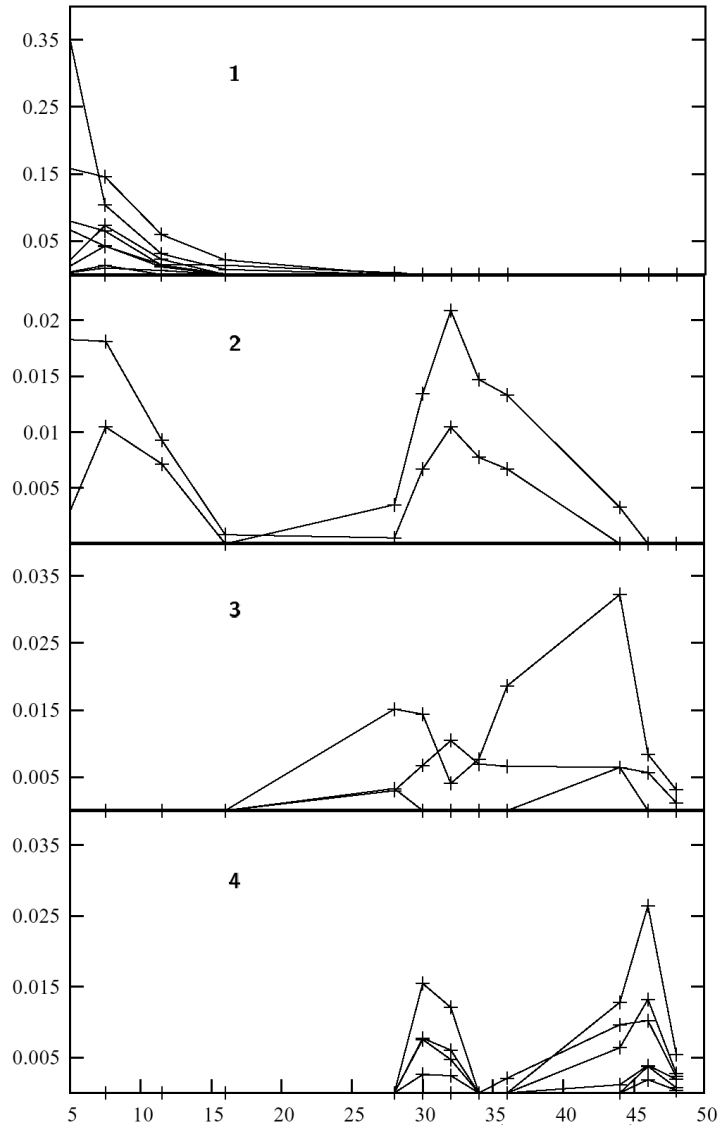
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Stoichiometry	Peak flux $\text{mol.hr}^{-1} \cdot (\text{Mol. Org.})^{-1}$
Group 1	
Glc \rightarrow 2 Lac	0.45
1/2 + Glc \rightarrow 2 Biomass	0.16
1/2 + Glc \rightarrow 2 + Acetoin	0.086
+ Glc \rightarrow 2 Ac + 2	0.077
1/2 + Glc \rightarrow 2 Pyr	0.073
Pyr \rightarrow 5/6 Lac + 1/2	0.042
3/4 + Glc \rightarrow Diac + 2	0.014
3/4 + Glc \rightarrow Cit	0.01
3 + Glc \rightarrow 6	0.01
Glc + 6 Pyr \rightarrow 4 Lac + 2 Cit	0.0003

Mode assignment

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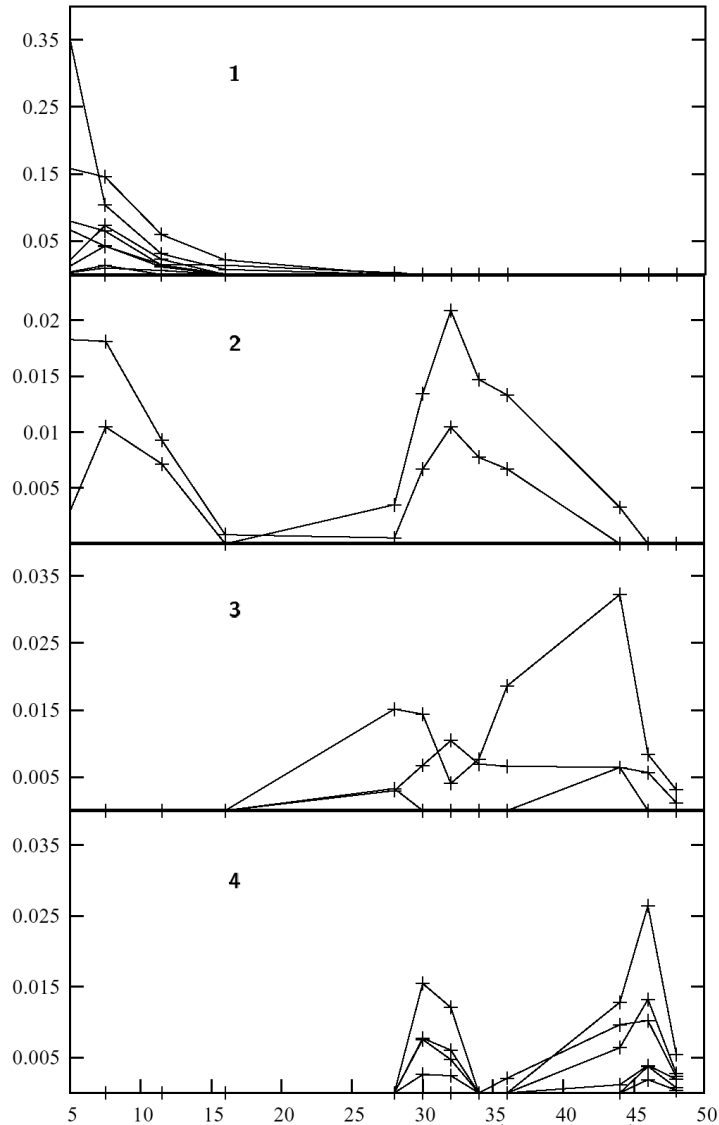
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Stoichiometry	Peak flux $\text{mol.hr}^{-1} \cdot (\text{Mol. Org.})^{-1}$
Group 2	
Lac 1/4 + \rightarrow Biomass	0.021
Pyr \rightarrow Biomass	0.018

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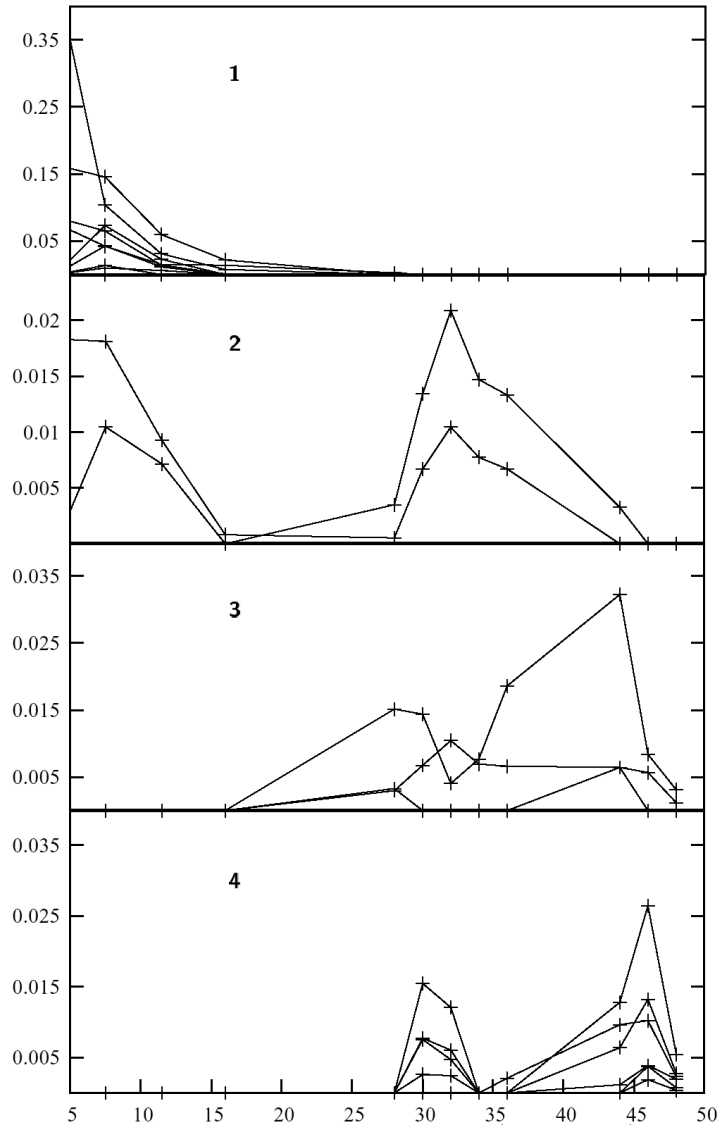
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Stoichiometry	Peak flux $\text{mol.hr}^{-1} \cdot (\text{Mol. Org.})^{-1}$
Group 3	
Lac 1/2 + \rightarrow Ac +	0.032
Lac 1/4 \rightarrow Pyr	0.01
1/4 + Pyr \rightarrow Ac +	0.006

Mode assignment

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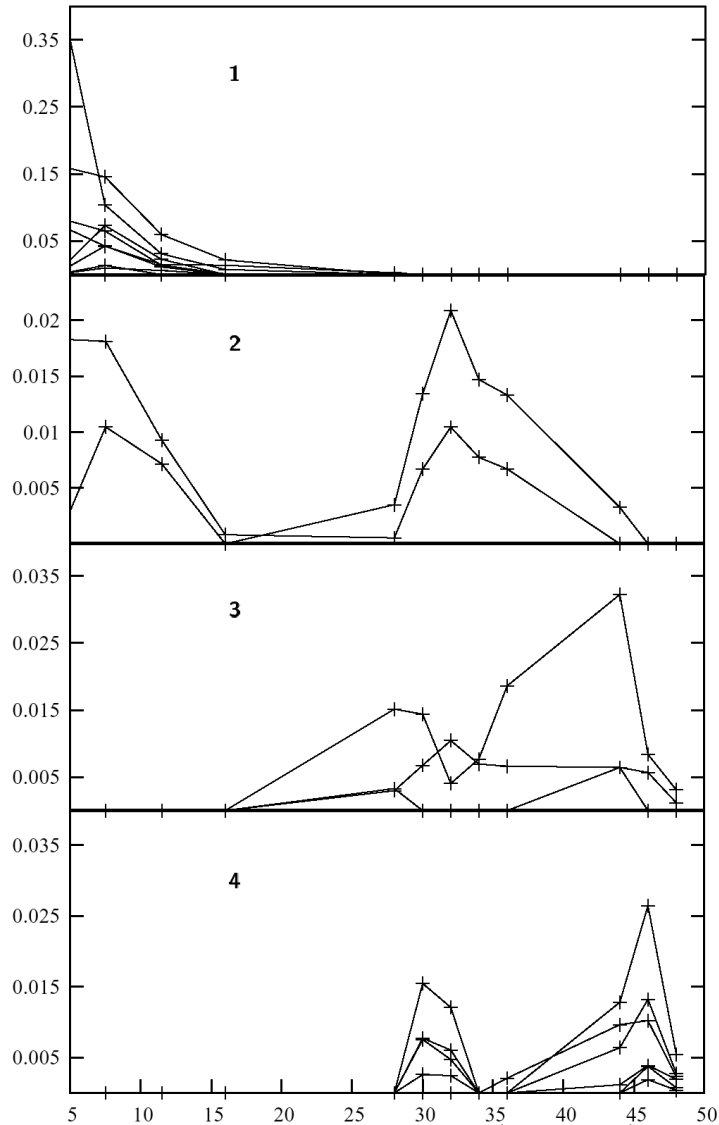
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Stoichiometry	Peak flux $\text{mol.hr}^{-1} \cdot (\text{Mol. Org.})^{-1}$
Group 4	
Lac + 3/2 \rightarrow 3	0.026
Lac + 3/4 \rightarrow 1/3 Cit +	0.013
Lac + 5/12 \rightarrow 1/3 Cit + 1/3 Ac + 1/3	0.010
Lac + 1/4 \rightarrow 1/2 Acetoin	0.0039
5/4 + Pyr \rightarrow 3	0.0038
1/2 + Pyr \rightarrow 1/3 Cit +	0.0019

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- Elementary modes analysis helps to highlight modes of operation of small to medium scale metabolic networks
- Unlike FBA, it provides all routes in one computation.
- It has correctly predicted previously unrecognised pathways.
- It can be used to analyse and design biotechnological processes.

Acknowledgements — My Group

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Hassan Hartman

ScrumPy is available from
<http://mudshark.brookes.ac.uk/Software>

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