2. Introduction to Metabolic Modelling

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November 29, 2024

Preamble

- Complicated or Complex?
- Modelling and Simulation
- Simulated Life
- Virtual Biochemistry
- Why Model

Metabolism?

Industrial

Biotechnology and Synthetic Biology

- Design Issues in Synthetic Metabolism
- Aims of Modelling

Model Formulation

A little mathematics



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- However, if studying a system composed of interacting and possibly differing parts, it soon becomes increasingly difficult to find a simple, reliable description as the number of interactions rises, i.e. becomes more complicated.

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- This is even more so if the system is also complex, that is, it has
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- At this point we often turn to modelling and simulation.

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 Modelling is the process of making a tractable representation of a system that can be reasoned over or is computable.

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- Modelling is the process of making a tractable representation of a system that can be reasoned over or is computable.
- Simplification is intrinsic to modelling; the aim is to reduce the complicatedness of the representation without also losing any of the complexity of the system behaviour.
- i.e. Simplify enough, but not too much.

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- i.e. Simplify enough, but not too much.
- Simulation is an implementation of the model to produce an imitation of the system's behaviour.

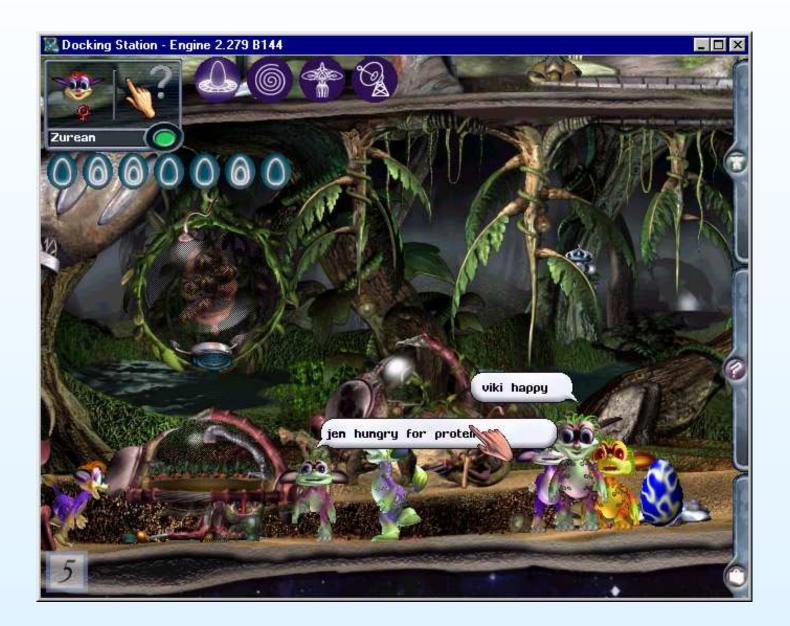
Simulated Life

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Virtual Biochemistry

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Summary



A major naturnal instructive fundati by the German Federal Finistry for Education and Research

Virtual Liver Network

The Virtual Liver will be a dynamic model that represents, rather than fully replicates, human liver physiology morphology and function, integrating quantitive data from all levels of organisation.



Contact | familiary-Login | familiary-source | Declarity

SiC!: The Silicon Cells

A silicon cell is a precise replica of (part of) a living cell. It is based on experimentally determined rate law parameter values, i.e. only on data, not on fitted values or assumptions. It merely calculates the system biology implications of molecular properties that are already known. Silicon cell is not a package of software for simulations. The international silicon

program thereby differs (i cell biology that can be us models for the purpose of down-loading to one's ow (http://www.genomatica.c calculates kinetics, rather

Feature Article

The Virtual Human: Towards a Global Systems Biology of Mu Distributed Biochemical Network Models

Douglas B. Kell

School of Chemistry and The Manchester Centre for Integrative Systems Biology, The Manchester Inter Biocentre, The University of Manchester, Manchester, UK

It came first!

- Metabolism is essential: it is a fundamental process of all living organisms, encompassing all the chemical conversions that convert nutrients into new cellular materials and provide energy for other processes such as movement.
- Metabolism can be useful: bread, alcoholic drinks, cheese, yoghurt, monosodium glutamate, biofuels.
- Metabolism can go wrong: single gene metabolic diseases;
 obesity, diabetes, heart disease, even cancer, are multi-factorial diseases with a metabolic component.
- We understand how the genes encode metabolism. But how do we exploit that understanding to predict metabolic responses?
- Biotechnological applications: for designing metabolic engineering and synthetic biology strategies.
- Another: design of effective drug therapies.
- Other cell processes yield to similar approaches: signal transduction; cell cycle; apoptosis.

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Industrial Biotechnology and Synthetic Biology

Targets for biological production of "platform chemicals" (green chemistry):

Chemical	Derivatives	Chemical	Derivatives
Succinate	1,4 butanediol	Isoprene	Synthetic rubber
3-OH propionate	Acrylate	Farnesene	
Itaconic acid	Methylmethacrylate	Glycerol	Propylene glycol
Ethanol	ethylene, biofuel	Sorbitol	
Lactate	Polylactic acid	Xylitol	
Biohydrocarbons	Biofuel	Furfural	

Choi et al, Metabolic Engineering, 28, 223–239 (2015)

Raw materials include: lignocellulosic biomass, starch, syngas and flue gases $(CO_2/CO/H_2 \text{ mixtures})$, methane, CO_2 and light in algae.

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A little mathematics

- Can matter flow from inputs to the desired product?
- What is the maximum conversion efficiency obtainable?
- Can the host cell cope with the energy and redox demands of production?
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Summary

Not primarily prediction.

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- As models are simplifications, they have to be designed for the specific aims.

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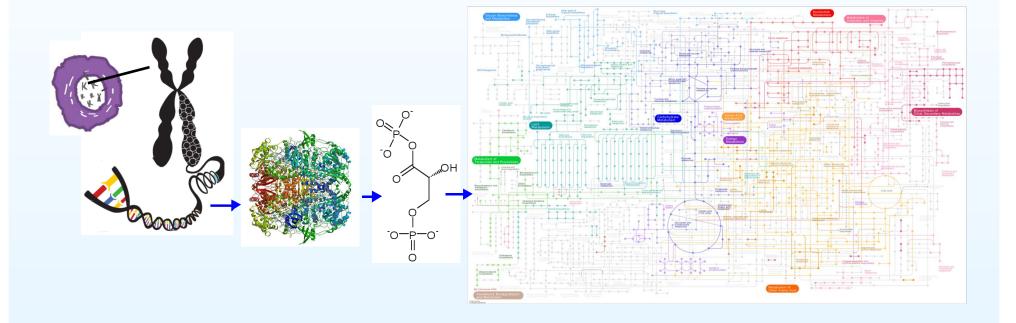
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- Michaelis–Menten
- **Enzyme Kinetics**
- The Reversible M–M Eqn.
- Steady State
- External and Internal
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- Summary of Types of Metabolic Model

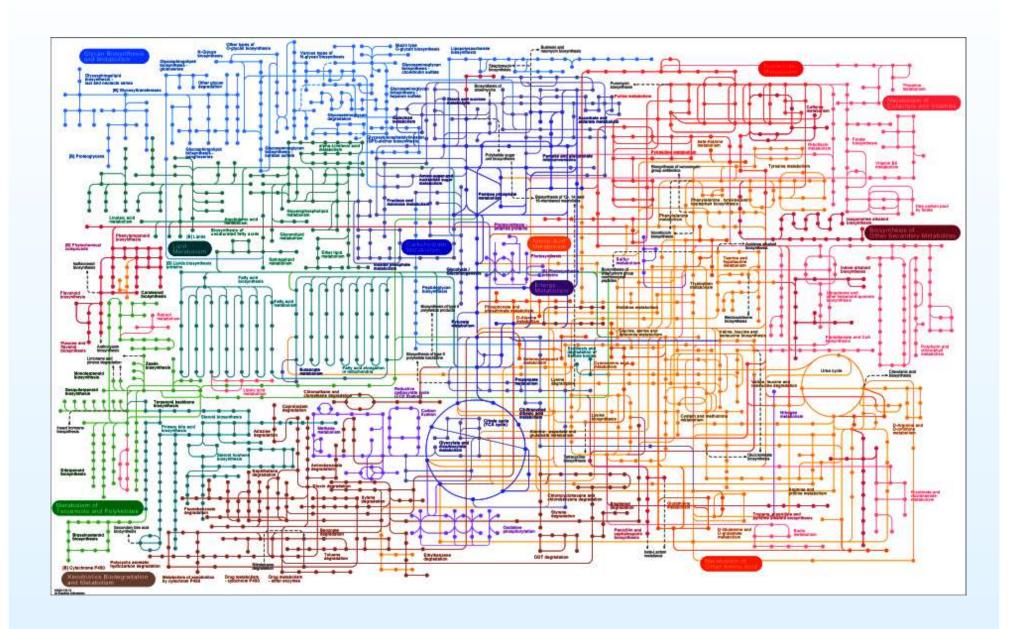
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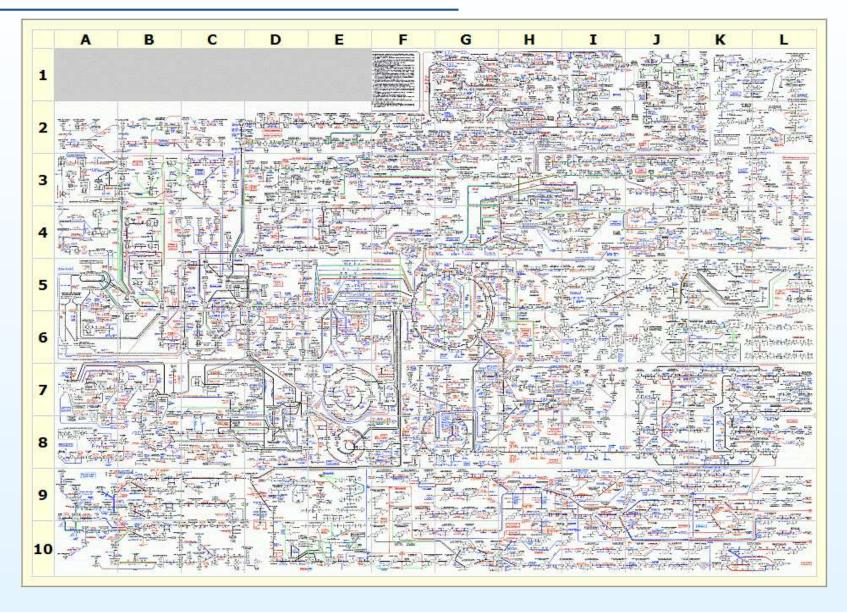
Genotype to Metabolic Phenotype



The Metabolic Network



The Metabolic Network — More Detail



From Expasy Biochemical Pathways: http://www.expasy.ch/cgi-bin/search-biochem-index

The Metabolic Network — Zoom in

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Model Formulation

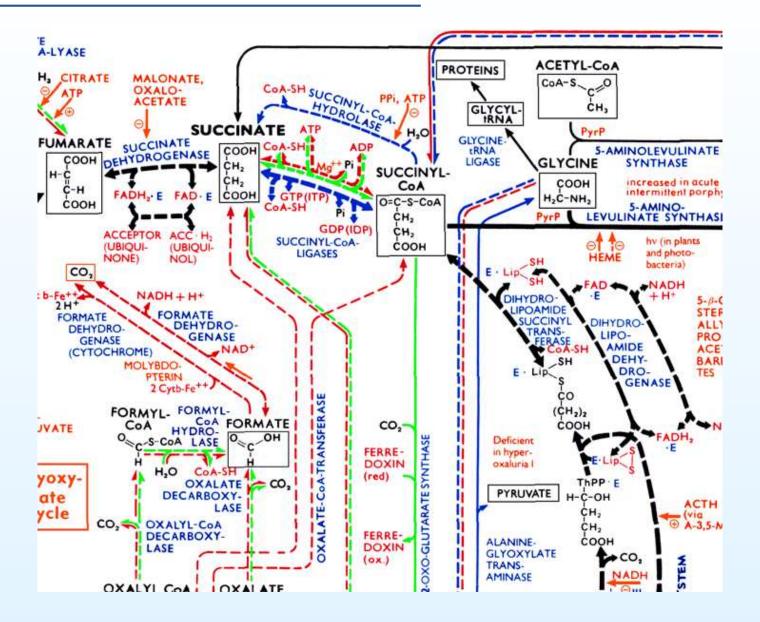
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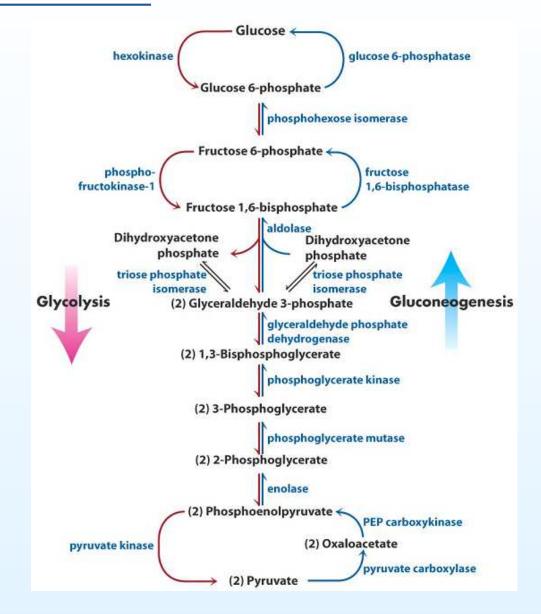
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From Nelson & Cox, Lehninbger's Biochemistry, 4th ed.

Michaelis-Menten Enzyme Kinetics

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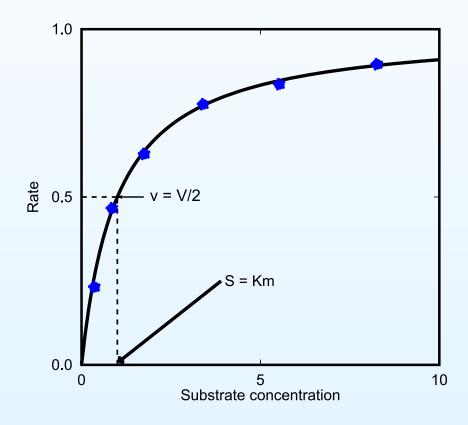
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Summary





The $K_{
m m}$ and V have arbitarily been set to 1, where V is the *limiting rate* (or maximum velocity, $V_{
m m}$) and $K_{
m m}$ is the

Michaelis constant.

The Reversible M–M Eqn.

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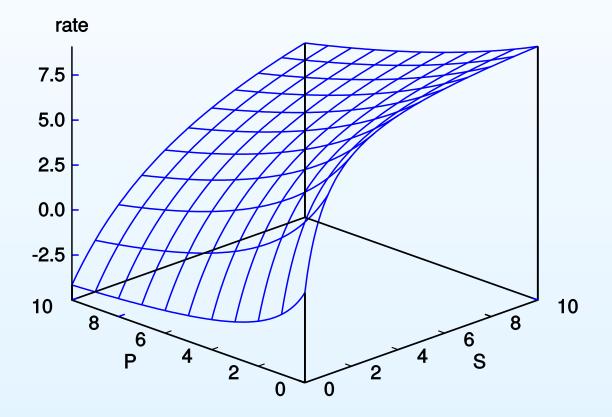
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 Summary of Types of Metabolic Model

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Summary

$$v_{net} = \frac{(V_f/K_{m,S})(S - P/K_{eq})}{1 + S/K_{m,S} + P/K_{m,P}}$$
 or $v = f(S, P)$



Simultaneous dependence of enzyme rate on both substrate and product. The parameters have been set to: $K_{
m m,S}$ =1;

$$V_{
m m,f}$$
 = 10; $K_{
m m,P}=2$, and $K_{
m eq}=4$.

Steady State

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Summary

In a metabolic network there is a flow of matter from the *source* to the *sink*. At steady state, the concentrations of the intermediates remain constant because their rates of formation exactly equal their rates of degradation. The flow through the pathway also remains constant.

If there are very slow changes in the concentrations of metabolites, or the pathway flux, because of slow changes in the source or sink, the pathway may be regarded as being in *quasi steady state* provided the time scale of the changes is very much longer than the time taken by the pathway to approach steady state.

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The source and sink are instances of **external** metabolites in a model: those whose effective concentration is not appreciably modified by metabolic system.

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- The source and sink are instances of external metabolites in a model: those whose effective concentration is not appreciably modified by metabolic system.
- Though extracellular metabolites may be external on account of the extracellular space being larger than the intracellular, some external metabolites can be intracellular.

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- Examples include lipid droplets and starch granules that are only slowly depleted.

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- **Internal** metabolites are those whose concentrations respond to the balance of formation and consumption and therefore are the variables of a metabolic model.

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- **Internal** metabolites are those whose concentrations respond to the balance of formation and consumption and therefore are the variables of a metabolic model.
- Most intracellular metabolites of a model will count as internal, but it is not impossible for an extracellular metabolite to be internal to the model.

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Model Formulation

- Genotype to Metabolic Phenotype
- The Metabolic
 Network
- The Metabolic

Network — More Detail

- The Metabolic
 Network Zoom in
- A Metabolic 'Pathway'
- Michaelis-Menten
 Enzyme Kinetics
- The Reversible M–M Eqn.
- Steady State
- External and Internal Metabolites
- Summary of Types of Metabolic Model

A little mathematics

Summary

 Structural — needs reaction list; gives existence and number of routes; optimal stoichiometries; network flux values.

 Dynamic or Kinetic — needs full kinetic description of each enzyme/step; predicts time—courses, steady—states, sensitivity analysis or control distribution . . . Can be deterministic or stochastic.

Sensitivity analysis / Control analysis / S—systems — needs
effective kinetics near steady—state; predicts control distribution,
response of steady state to perturbations.

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- Structural Analysis Methods
- MethodsAren't Graph

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Reaction Network to Mathematical Object

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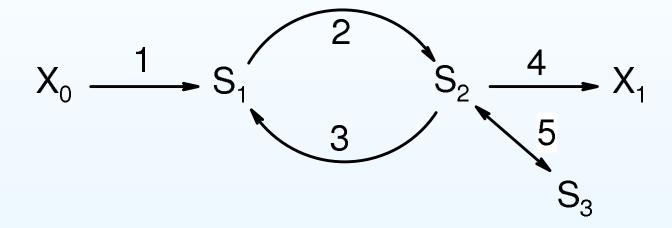
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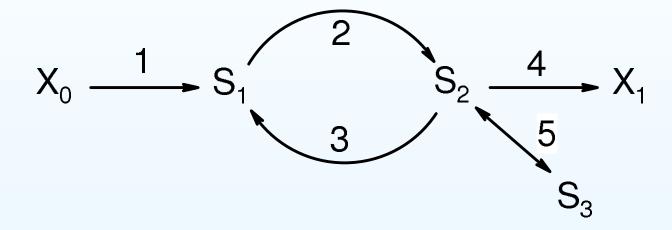
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Consider a simple metabolic network, e.g.:



r1:
$$X_0 \rightarrow S_1 \sim$$

r2:
$$S_1 -> S_2 \sim$$

r3:
$$S_2 -> S_1 \sim$$

r4:
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r5: S
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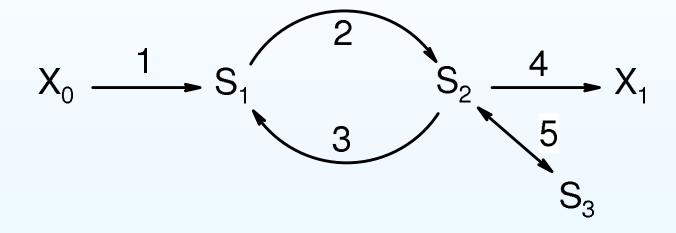
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Kinetics of the Metabolites

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Summary

$X_0 \xrightarrow{1} S_1 \xrightarrow{2} S_2 \xrightarrow{4} X_1$ $S_3 \xrightarrow{5} S_3$

By inspection of the diagram:

$$\frac{dS_1}{dt} = v_1 - v_2 + v_3$$

$$\frac{dS_2}{dt} = v_2 - v_3 - v_4 - v_5$$

$$\frac{dS_3}{dt} = v_5$$

How can we generalize this?

Separation of Structure and Kinetics

The rate at which the substrate concentrations are changing is given by N.v, where N is the stoichiometry matrix, and v is a vector of enzyme kinetic functions. So for our substrate cycle network:

$$\begin{bmatrix} \frac{dS_1}{dt} \\ \frac{dS_2}{dt} \\ \frac{dS_3}{dt} \end{bmatrix} = \begin{bmatrix} 1 & -1 & 1 & 0 & 0 \\ 0 & 1 & -1 & -1 & -1 \\ 0 & 0 & 0 & 0 & 1 \end{bmatrix} \cdot \begin{bmatrix} v_1 \\ v_2 \\ v_3 \\ v_4 \\ v_5 \end{bmatrix}$$

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where each v_i is the rate function for enzyme i, depending on the variable metabolites and the parameters $V_{m,i}$, $K_{m,i}$ etc, as $f_i(\mathbf{S})$.

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Integrating this set of non-linear differential equations gives a **dynamic model** of our network.

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Integrating this set of non-linear differential equations gives a **dynamic model** of our network.

The steady state is a set of non–linear simultaneous equations that can be solved for the steady state values of S.

Steady State Structural Modelling

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Any metabolic network at steady state satisfies the relationship $\mathbf{N}.\mathbf{v}=\mathbf{0}$, where \mathbf{N} is the stoichiometry matrix, exemplified by our model network:

$$\begin{bmatrix} S_1 & \begin{bmatrix} 1 & -1 & 1 & 0 & 0 \\ 0 & 1 & -1 & -1 & -1 \\ 0 & 0 & 0 & 0 & 1 \end{bmatrix} \cdot \begin{bmatrix} v_1 \\ v_2 \\ v_3 \\ v_4 \end{bmatrix} = \begin{bmatrix} 0 \\ 0 \\ 0 \end{bmatrix}$$

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Structural modelling involves exploring the solutions of this equation, regarding the v_i as the unknown variables.

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Any metabolic network at steady state satisfies the relationship $\mathbf{N}.\mathbf{v}=\mathbf{0}$, where \mathbf{N} is the stoichiometry matrix, exemplified by our model network:

Structural modelling involves exploring the solutions of this equation, regarding the v_i as the unknown variables.

The equation is linear, but under–determined. Though solutions are not unique, they distinguish between **feasible** and **non–feasible** states of the network.

Advantages of Structural Analysis

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- Knowledge is more complete for network structure than for enzyme kinetics.
- Structural analysis involves simple linear equations; dynamic analysis involves non–linear enzyme kinetic functions.
- The network structure places limitations that constrain the network dynamics, irrespective of the kinetics, e.g.:
 - Whether viable routes exist from nutrients to stated metabolic products;
 - Whether some routes remain after deletion (knock-out mutation) of the steps catalysed by a particular enzyme;
 - What the maximum obtainable conversion yield is for formation of any metabolite from a given set of sources, and
- Structural models underlie kinetic models, and other techniques such as Metabolic Flux Analysis and Metabolic Control Analysis.

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- Computer construction of transformation routes Serriotsis & Bailey; Mavrovouniotis et al
- Graph analysis techniques various
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- Convex basis / Extreme pathways Palsson et al
- Reaction (enzyme) subsets
- Linear programming single optimal route *Small & Fell, Palsson et al.* Became Flux Balance Analysis and gave rise to genome—scale metabolic modelling.

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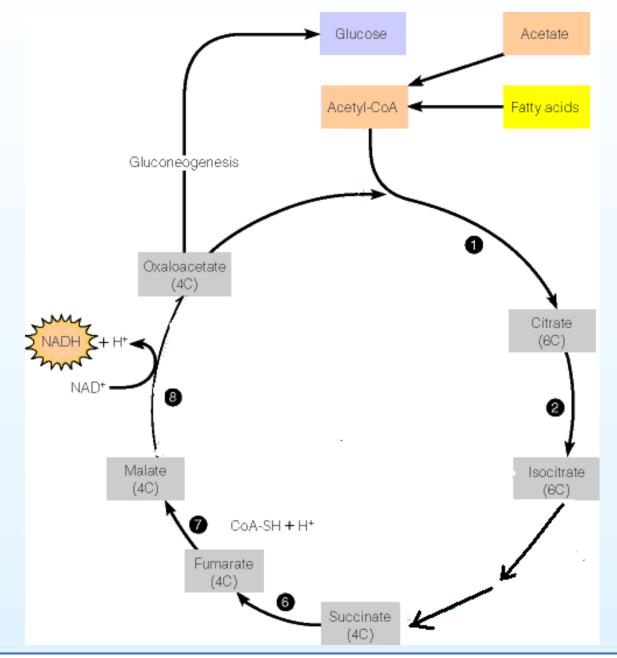
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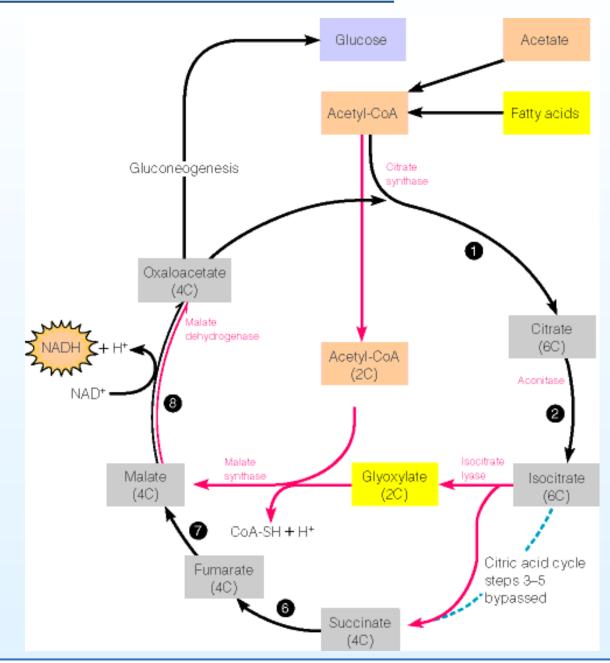
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- Structural modelling investigates the implications of these network constraints.