
Metabolic Engineering of New Routes to Biofuels

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Tuesday 20th May 2008

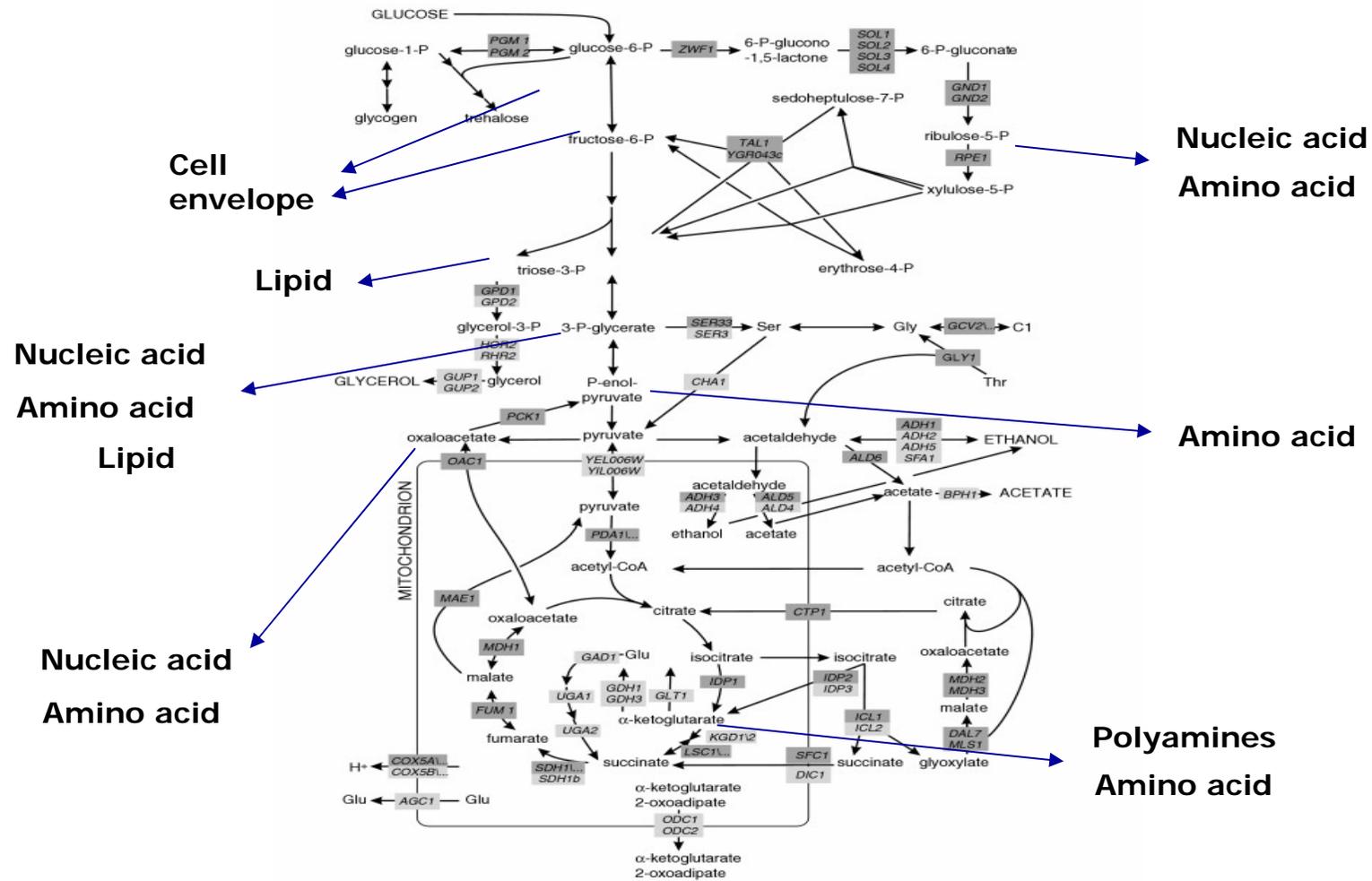


SCI Biofuels: Technology meets
Strategy Meeting

Overview

- Metabolism, enzymes, genes
- Bioethanol production in yeast
- Metabolic engineering successes and failures
- Computational systems biology approaches
- Utilisation of xylose as feedstock for yeast fermentation
- Production of butanol in E. Coli
- Future directions for research

Metabolic pathways for energy & biosynthesis



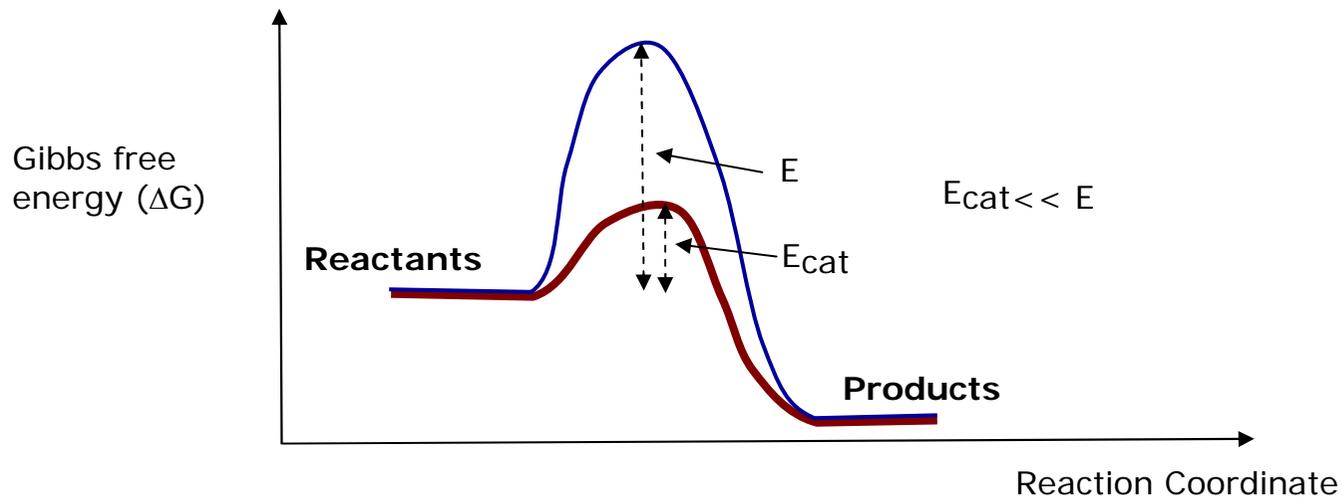
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SCI Biofuels: Technology meets Strategy Meeting

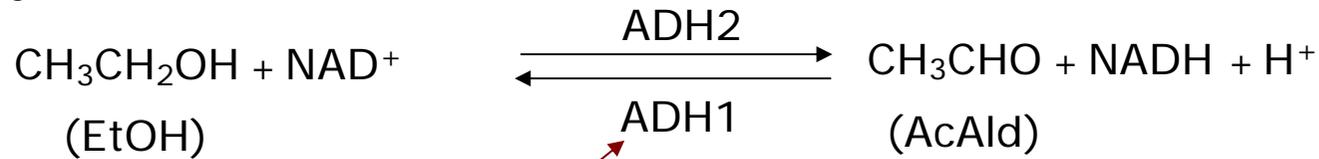
Enzymes

- Enzymes are proteins that catalyse biochemical reactions
- Specific enzymes for specific reactions: alcohol dehydrogenase
- Enzymes reduce the activation energy of the reaction enabling it to run faster



Enzyme Kinetics

- Example: Fermentation by yeast

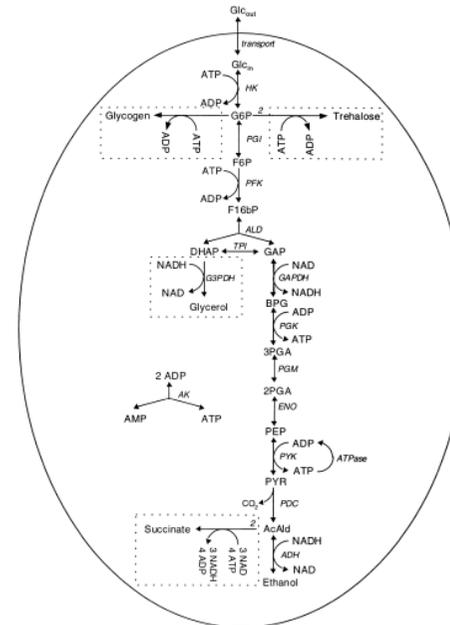


Alcohol dehydrogenase

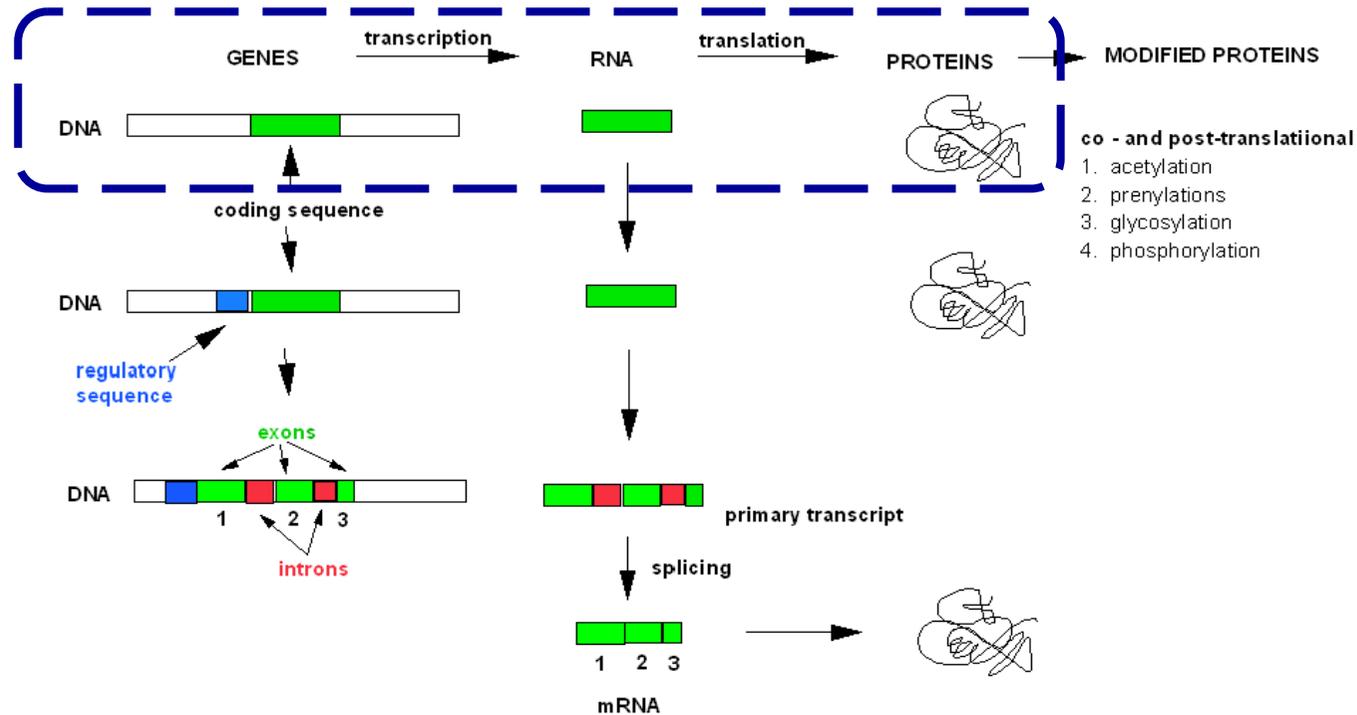
Byproduct of glycolysis

$$v = \frac{k_2 k_3 [E]_0 [S]}{k_2 \left(1 + \frac{[S]}{K_p} + \frac{[S]}{K_p K_{LL}} + \frac{[S]^2}{K_p^2 K_{LL}} \right) + k_3 \left(1 + K_L + \frac{[S]}{K_p} \right)}$$

$$[S] \rightleftharpoons \frac{k_2 K_p K_L}{1 + \theta \frac{[S]}{K_p}} \frac{k_3 K_p K_L}{1 + \theta \frac{[S]}{K_p}} \left(1 + \frac{[S]}{K_p} + \frac{[S]}{K_p K_{LL}} + \frac{[S]^2}{K_p^2 K_{LL}} \right) + k_3 \left(1 + K_L + \frac{[S]}{K_p} \right)$$



DNA, RNA and Proteins



How many genes?: Human = 40,000; yeast = 6,000

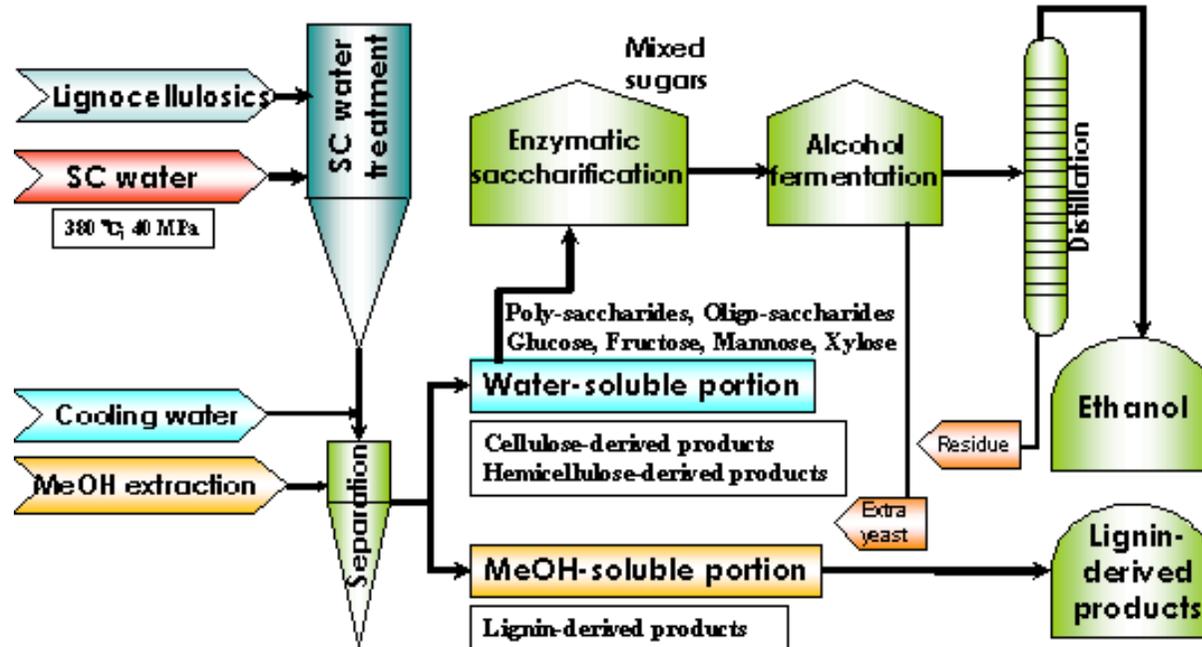
About yeast...

- *Saccharomyces cerevisiae*
- Bakers yeast, brewers yeast, budding yeast
- Single celled microorganism (fungi)
- One of the simplest eukaryotes
- Long history and well understood
- Tolerant to high ethanol concentration
- Works at low pH which avoids contamination



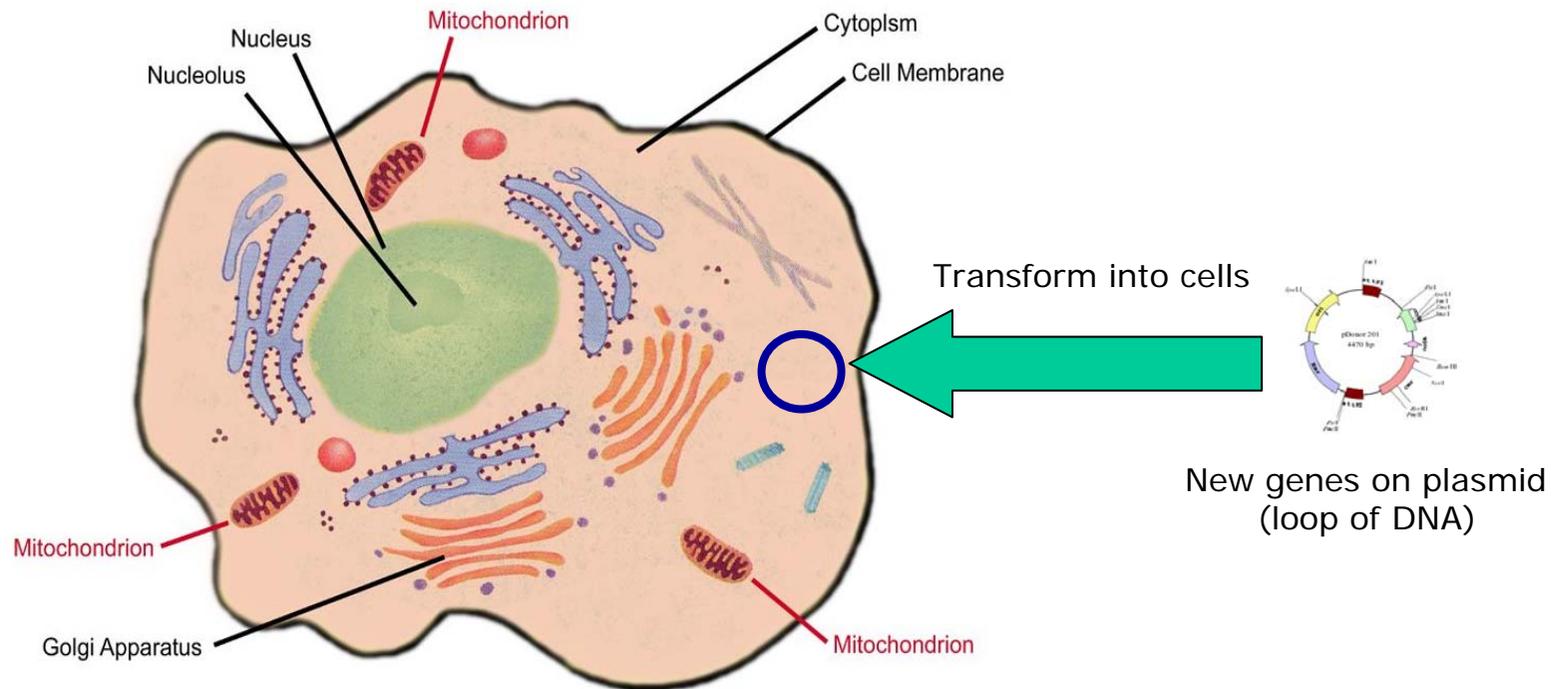
Bioethanol production in yeast

- 22% of all UK greenhouse gas from road transport
- 5-10%: max ethanol in petrol for vehicles to run unmodified



Metabolic Engineering

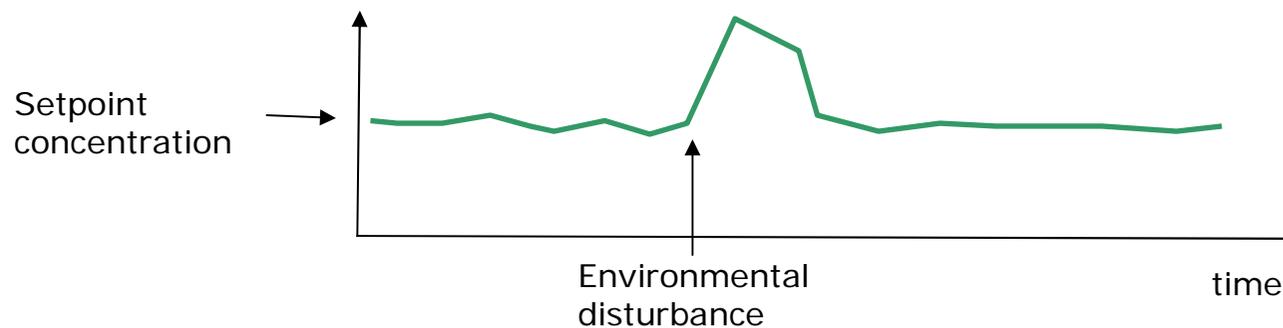
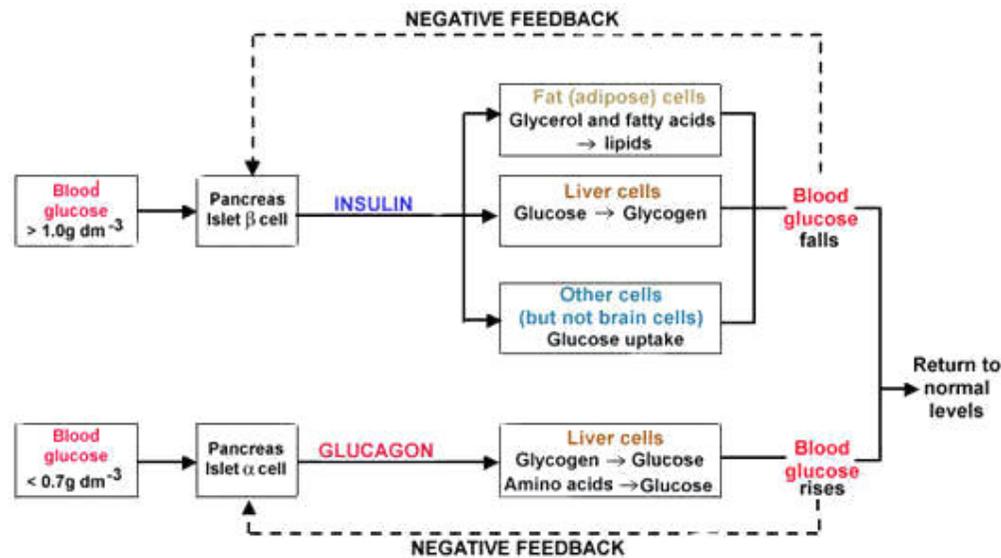
"Metabolic engineering is the improvement of industrial organisms using modern genetic tools" (James Bailey, ETH)



Metabolic Engineering Failures

- Simplistic approaches to find 'rate limiting' enzymes have usually failed
 - e.g. overexpression of hexokinase, phosphofructokinase and pyruvate kinase failed to increase the ethanol production rate of yeast
- Reason: cells have evolved to be robust
 - Intrinsic robustness of networks and enzymes
 - Natural redundancy in the metabolic networks
 - Sophisticated control systems for maintaining status quo
 - Regulation of gene expression

Cellular control systems for homeostasis

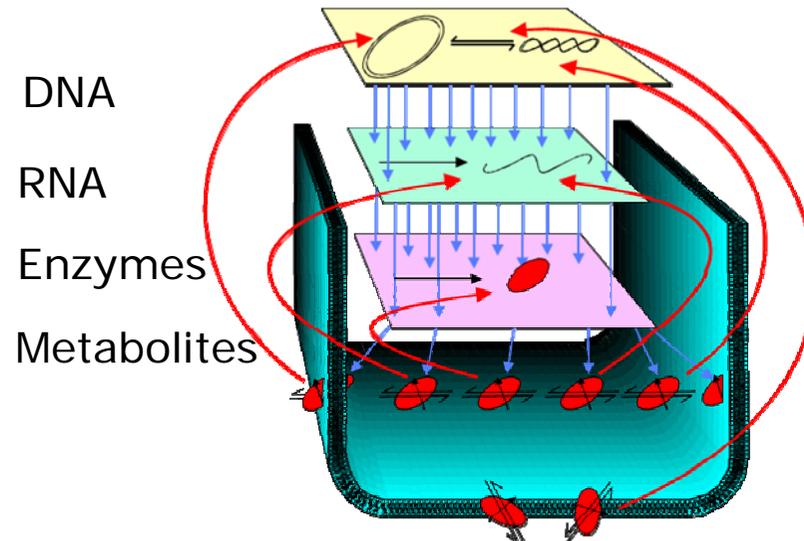


Regulation of genes by signalling pathways

- Glucose repression
 - Triggered by: high levels of glucose
 - Effect: switch off expression of enzymes for other sugars
- AMP kinase signalling
 - Triggered by: low energy levels (ATP:AMP ratio)
 - Effect: increase expression of energy producing enzymes

Computational Metabolic Engineering

- Detailed computational modelling of the cell
- Including all the complex interactions at the 'system' level
 - genes, RNA, proteins, metabolites



- Simultaneous and subtle changes in multiple genes required

Metabolic Control Analysis (MCA)

- MCA can be applied to both metabolic and signalling pathways
- MCA = sensitivity analysis
 - how does a small change in parameter X effect model output Y?
- e.g. Flux control coefficients C_e^J for metabolic networks
 - C_e^J = % change in flux J due to a 1% change in level of enzyme e
 - If 1% increase in enzyme gives 5% increase in flux then $C_e^J = 5$
 - If 1% increase in enzyme gives 0.4% increase in flux then $C_e^J = 0.4$

Differential Equations for Metabolic Networks

- Chemical equations governing interactions & transformations...



(Association, Dissociation, Catalysis)

- ...are converted into ordinary differential equations (ODEs):

$$\frac{dS}{dt} = -\frac{V_{max}S}{K_m + S}$$

Rate of change of
concentration with time

Stoichiometric Matrix

- Back to simple example

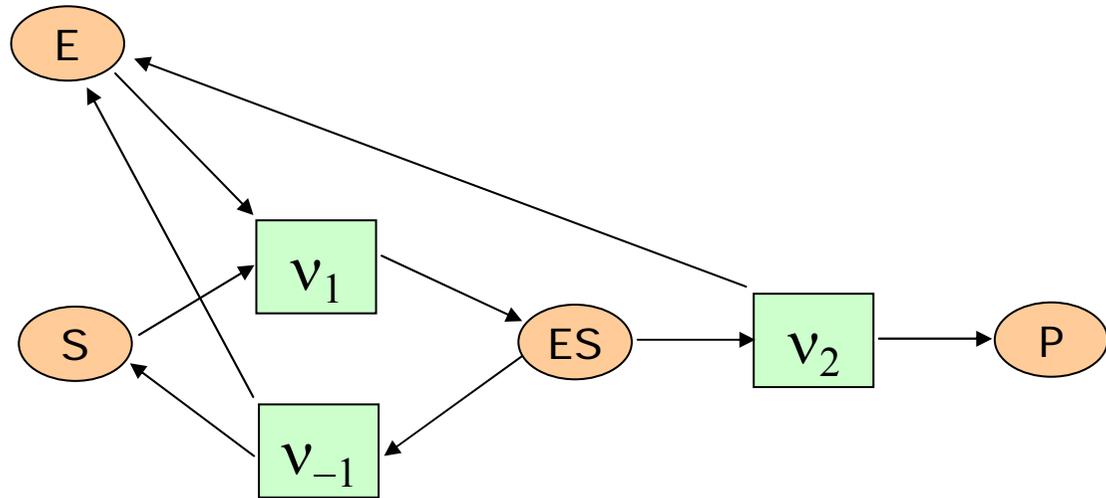


$$\frac{d[S]}{dt} = -v_1 + v_{-1}$$

$$\frac{d[E]}{dt} = -v_1 + v_{-1} + v_2$$

$$\frac{d[ES]}{dt} = v_1 - v_{-1} - v_2$$

$$\frac{d[P]}{dt} = v_2$$



$$\begin{matrix} \dot{S} \\ \dot{E} \\ \dot{ES} \\ \dot{P} \end{matrix} = \begin{bmatrix} -1 & +1 & 0 \\ -1 & +1 & +1 \\ +1 & -1 & -1 \\ 0 & 0 & +1 \end{bmatrix} \begin{bmatrix} v_1 \\ v_{-1} \\ v_2 \end{bmatrix}$$

vector of reaction rates

Stoichiometric matrix

General systems of Differential Equations

- Previous example:

vector of time derivative of species concentrations (system variables)

$$\begin{bmatrix} \dot{S} \\ \dot{E} \\ \dot{ES} \\ \dot{P} \end{bmatrix} = \begin{bmatrix} -1 & +1 & 0 \\ -1 & +1 & +1 \\ +1 & -1 & -1 \\ 0 & 0 & +1 \end{bmatrix} \begin{bmatrix} v_1 \\ v_{-1} \\ v_2 \end{bmatrix}$$

vector of reaction rates

Stoichiometric matrix

- Generally: $\Rightarrow \dot{X} = Nv$

Each reaction rate is a function of the species concentrations and some parameters

$$v_i = v_i \left(\overbrace{X_1, X_2, \dots, X_n}^{\text{variables}}, \overbrace{k_1, k_2, \dots, k_m}^{\text{parameters}} \right)$$

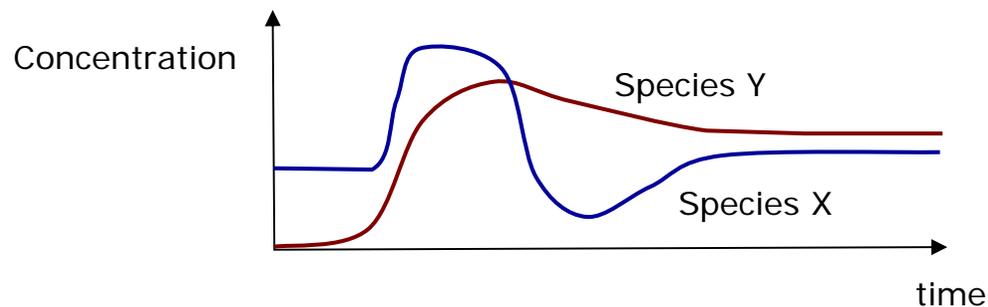
e.g. Michaelis-Menten $v = \frac{V_{max}[S]}{K_m + [S]}$

Data required to solve a dynamic (ODE) Model

- ✓ Stoichiometry linking the species and reactions (network structure)
- ✓ Functional form of the reaction rate equations
- ✓ The values of the rate constants in these equations
- ✓ The initial values of all species concentrations
- ✓ The time horizon

Solving (i.e. Integrating) ODE Models

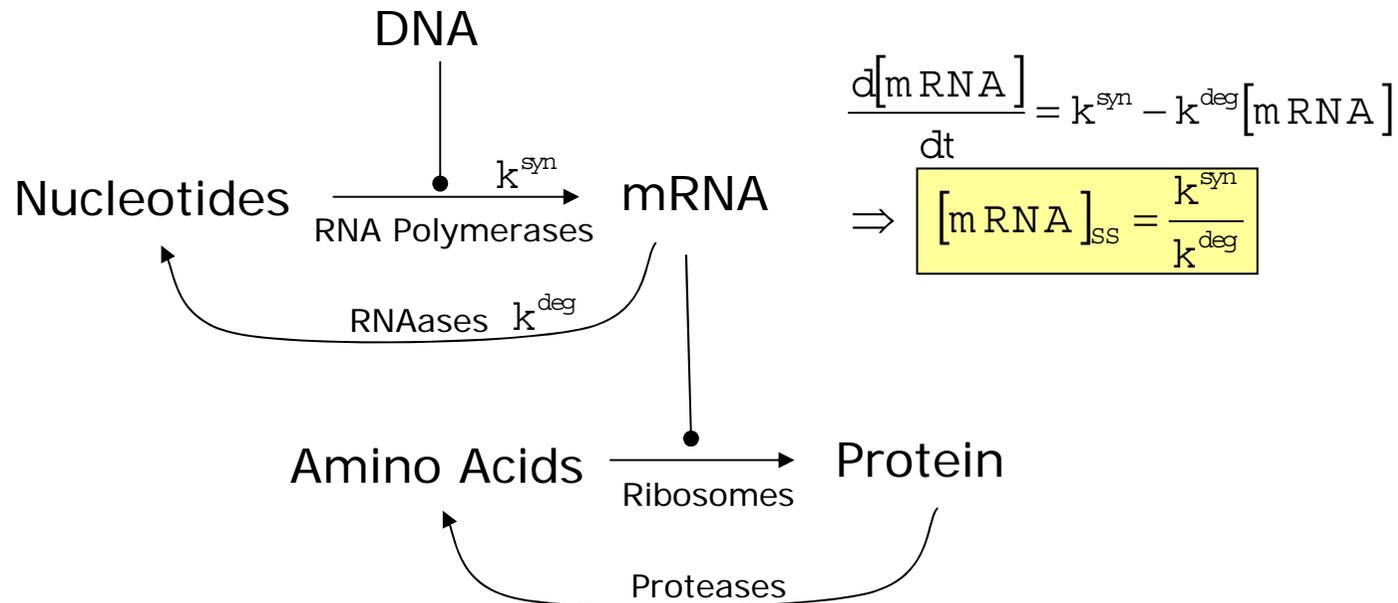
- Use an ODE solver (Matlab, Mathematica, Silicon Cell, etc.)
- Solver output is the concentration profiles over time



- Compare model output to measured concentration profiles
- If all profiles become flat then the system reaches 'steady state'

Steady States

- At steady state all the fluxes are in balance
- Total production of each species = total consumption
- Example: Synthesis and degradation of mRNA and proteins



Flux Balance Analysis

- Key idea: look for steady state flux patterns that optimise a given objective function
 - biomass production
 - product yield in metabolically engineered cells
- Use stoichiometric matrix only – flux patterns must satisfy
$$\dot{X} = Nv = 0$$
- Ignore kinetics – just have max/min bounds on fluxes
- Find balancing fluxes that maximise flux of product or biomass

Engineering xylose metabolism into yeast

- Xylose is a pentose ('difficult') sugar
- Second most abundant abundant carbohydrate in nature
- Major component of hemicellulose which is ~ 20% plant biomass
- Not a natural substrate for *Saccharomyces cerevisiae*...
- ...but there are other native xylose metabolising yeasts
 - e.g. *Pichia Stipitis*

Primary metabolic engineering strategy

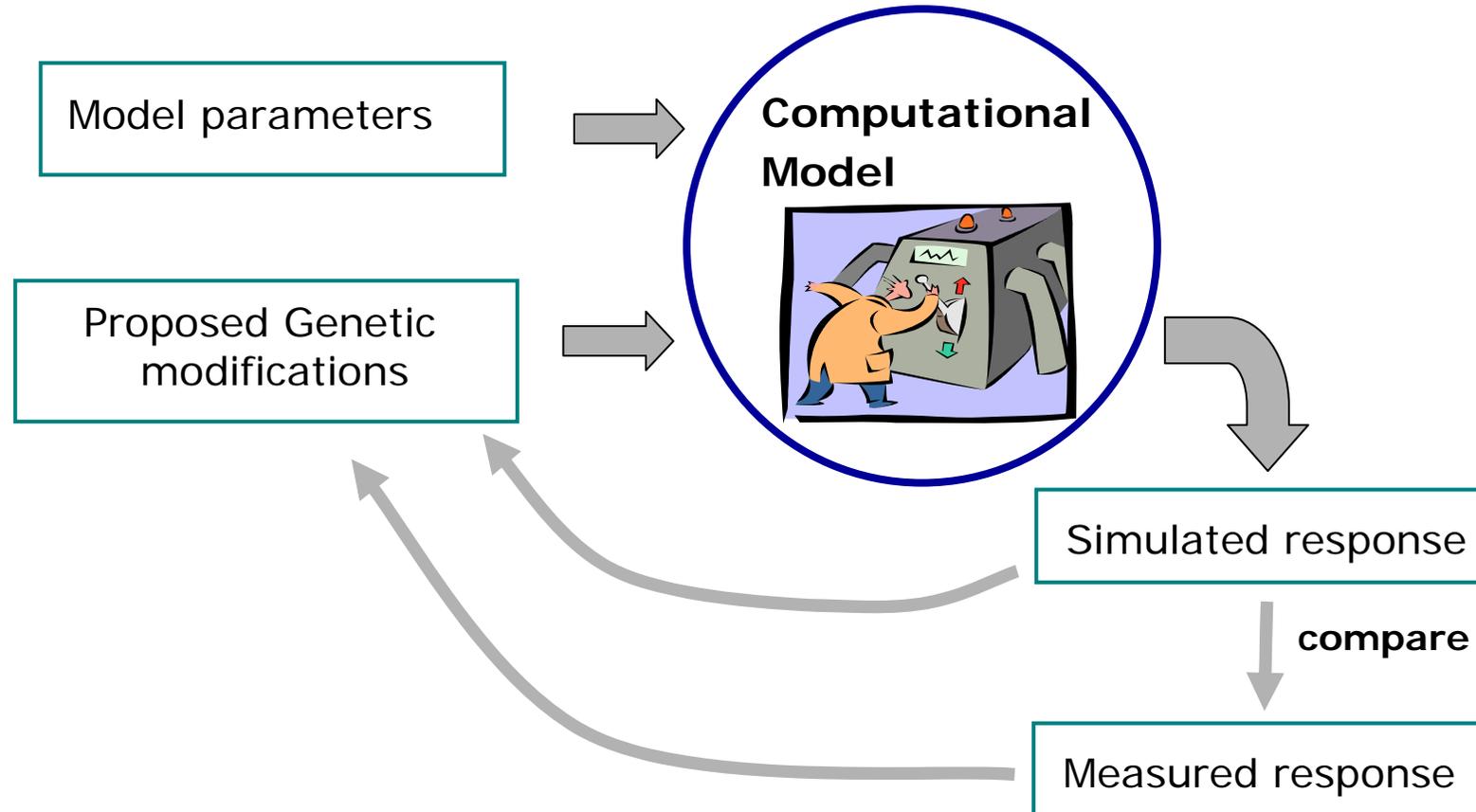
- Introduce the following genes (enzymes) from *Pichia stipitis*:
 - D-xylose reductase (XYL1)
 - xylitol dehydrogenase (XYL2)
 - D-xylulokinase (XYL3)
- Growth of this engineered yeast strain is very slow because...
- ...Reductive step and oxidative step both require co-factors:
 - NADPH and NAD⁺
 - producing NADP⁺ and NADH respectively

 Excess accumulation of NADH under oxygen limitation

Model based approaches to fix NADH problem

- Modify balance between glutamate dehydrogenase isoenzymes
 - Delete NADP⁺ dependent GDH1 – glutamate dehydrogenase
 - Overexpress NAD⁺ dependent GDH2
 - Improves ethanol production
- Genome-scale model found 56 out of 3,500 reactions that improved ethanol yield
 - e.g. introduction of a new glyceraldehyde 3-phosphate bypassing enzyme
- Evolutionary adaptation under continuous anaerobic conditions

Iterative Metabolic Engineering



Drawbacks of ethanol as transportation fuel

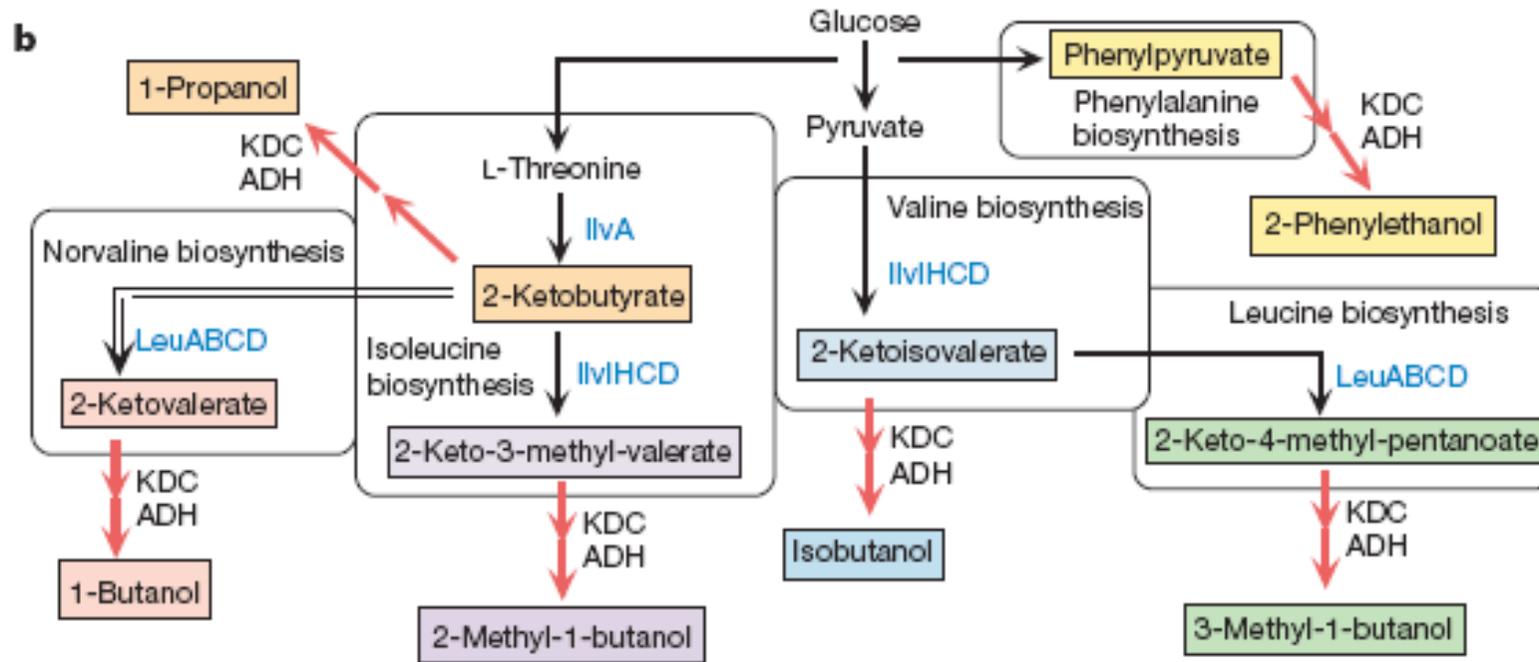
- Few vehicles can run unmodified on >10% EtOH fuel blends
- Lower energy content than gasoline
- Corrosive to metals in engines and pipelines
- Readily absorbs water
- Expensive to purify from fermentation broths

What are the alternatives?...

Butanol as a transportation fuel

- Butanol (4-carbons) is more like petrol (4-12 carbons)
- Higher energy density than ethanol (88% vs. 66%)
- Less corrosive and less water soluble than ethanol
- 85% Butanol/gasoline blends used in unmodified engines
- Can transport in the same pipelines as petrol
- Easier to integrate into the existing transportation infrastructure

Engineering production of butanol in E. Coli



Improving Butanol Yields

Genetic modification	Isobutanol production (mM)
Introduce 2-keto acid decarboxylase (KDC) from <i>lactococcus lactis</i>	-
Introduce alcohol dehydrogenase (ADH) from <i>saccharomyces cerevisiae</i>	4
Overexpression of <i>ilvHCD</i> genes to enhance 2-ketoisovalerate biosynthesis	23
Deletion of <i>adhE</i> , <i>ldhA</i> , <i>frdAB</i> , <i>fnr</i> , <i>pta</i> genes that contribute to by-product formation	30
Replace <i>ilvHCD</i> with <i>alsS</i> gene from <i>Bacillus subtilis</i> which has higher affinity for pyruvate	50
Deletion of <i>pflB</i> to decrease competition for pyruvate	300

300 mM = 22 g per litre butanol

Yield = 0.35 g butanol per g glucose = **86% of theoretical maximum**

Other directions for research

- Genetically engineered plants with less 'biomass recalcitrance'
- Engineered multi-enzyme systems - In vitro metabolic pathways
- 'Global transcription machinery engineering': gTME
 - Introduce mutations into yeast transcription factors
 - Select for improved ethanol & glucose tolerance
- Longer chain alcohols & alkanes from fatty acid synthesis routes

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