



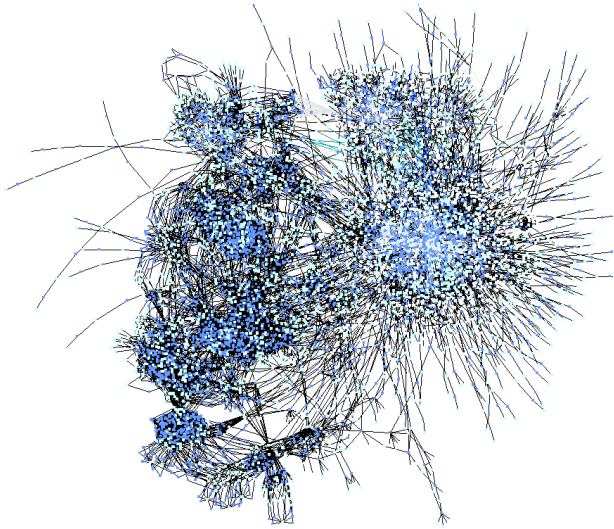
Metabolic modelling in industrial biotechnology

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Guest lecture

Modelling and Analysis in Bioinformatics

24.11.2015

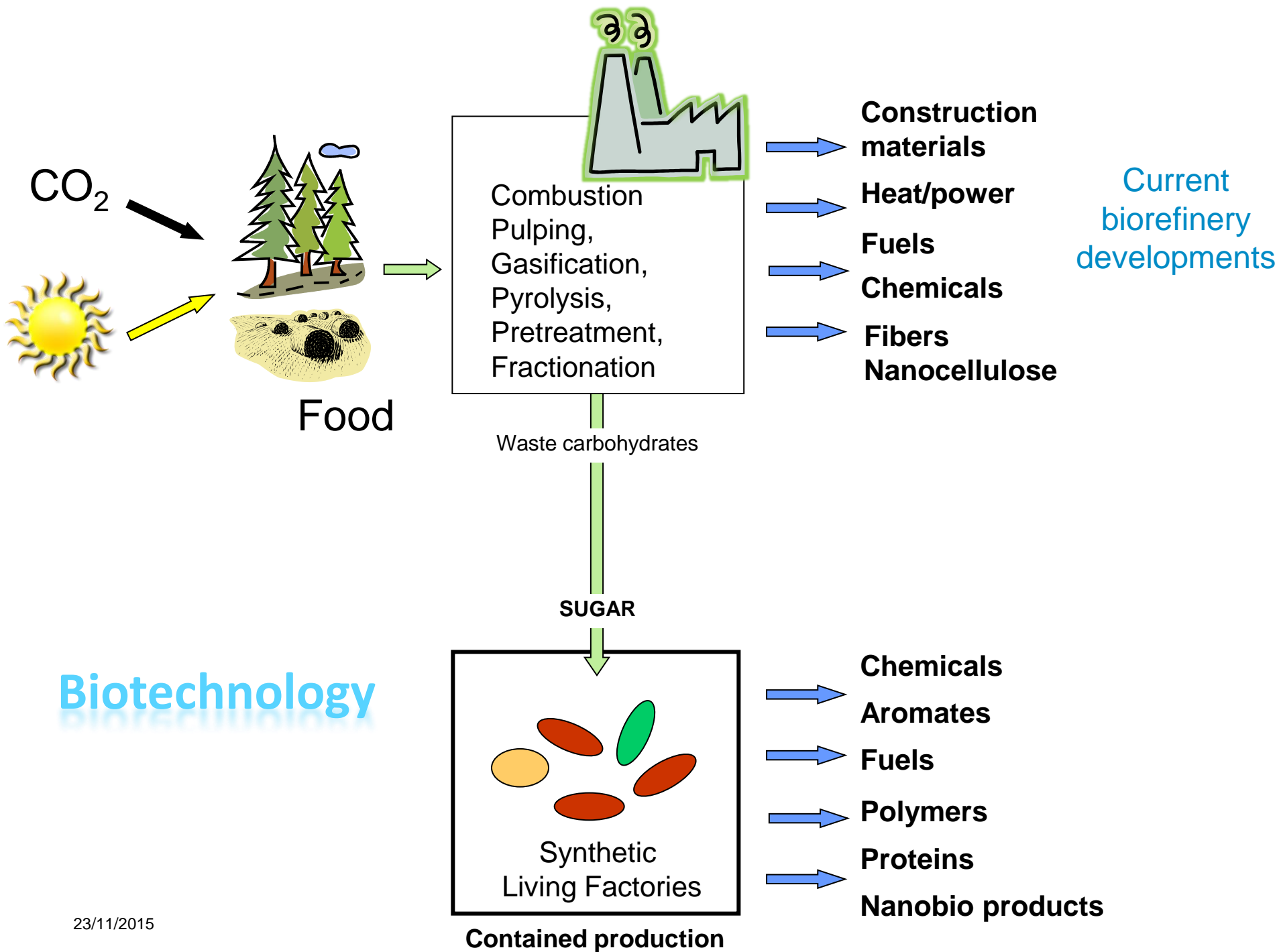


Outline

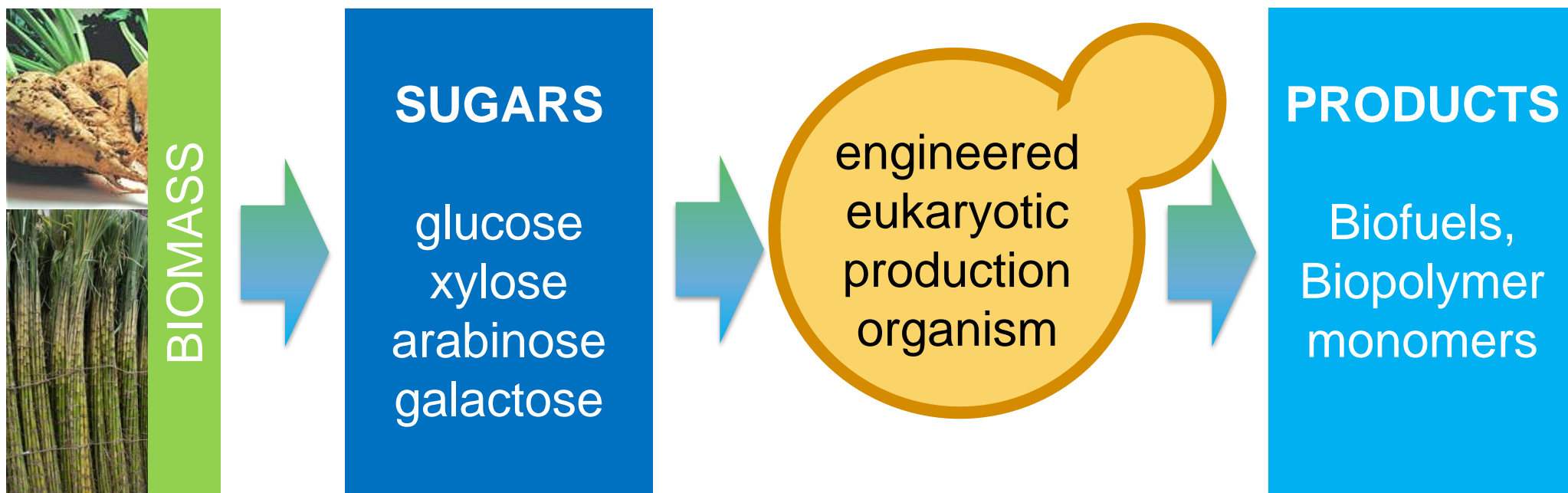
- Why metabolic modelling?
 - Needed in **industrial biotechnology**
 - Where production organisms are modified by **metabolic engineering**
- How metabolic modelling?
 - The metabolism of organisms can be simulated using metabolic models = **metabolic network**
 - **Constrain based methods** are used for simulation



Industrial Biotechnology and Metabolic engineering



Sustainable biotechnological solutions for production of fuels and chemicals from plant biomass



Metabolic engineering

- The goal of an metabolic engineering project is to produce maximal amount of a product (such as bioethanol or a bioplastic precursor) in a microbial host (such as bacterium, yeast cell, plant cell)
- The metabolism of the production host is modified by adding and/or deleting genes from the genome of the organism (genetic engineering)

Improved host for bioplastic production

Customer: Cargill / NatureWorks LLC

Challenge: To create a new production host for lactic acid production better suited for industrial production conditions

Solution: VTT engineered a yeast strain for more efficient conversion of plant materials to lactic acid. NatureWorks LLC, subsidiary of Cargill, is currently a leading producer of **plant based bioplastics**.

Key benefit:

- Contributed to lowering production costs

"Collaboration with VTT enabled Cargill to explore a larger technology space. VTT's strong expertise in working with non-conventional microbes was very beneficial in the Cargill project."

- Pirkko Suominen, AVP, Director Biotechnology Development Center



Production levels up to 92 g/l of lactic acid*

More efficient biomass-to-ethanol production

Customer: Mascoma Corporation

Challenge: Develop a novel production host for more cost-efficient lignocellulosic **ethanol production**

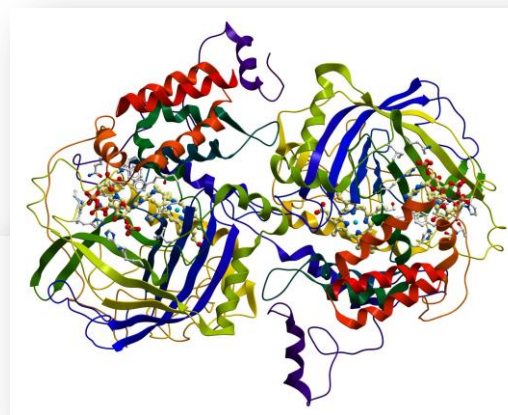
Solution: VTT engineered a yeast strain capable of **consolidated bioprocessing (CBP)**. This significantly reduced the need for external enzymes, improving the economics of ethanol production.

Key benefit:

- A more cost-efficient ethanol production method

"VTT's deep technical knowledge and great people helped us to deliver on our project. Working with them was truly a great experience!"

- John McBride, Sr. Director R&D, Mascoma Corp.



50 %

**reduction in
the amount
of external
enzymes**

Sustainable cosmetics from cloudberry cells

Customer: Lumene

Challenge: Enable the sustainable **production of bioactive compounds from a natural source**

Solution: The VTT Plant biotechnology team established a single cell culture from a rare cloudberry plant enabling the sustainable production of bioactive compounds in controlled bioreactor environment

Key benefits:

- Leveraging the bioactivities of Cloudberry stem cell culture enabled the creation of a new line of cosmetics

“Achieving international growth in the cosmetics industry requires not only solid innovative product development, but also good, world class partners. VTT is a natural and preferred partner for us, because they have innovative expertise and dedication to succeed in the utilization of Arctic berries with the latest technology.”

- Tiina Isohanni, VP Innovations and Development, Lumene



new line
of cosmetics
from
cloudberry
stem cells

Improved biomass-to-sugar enzymes

Customer: AB Enzymes, Roal Ltd.

Challenge: Develop efficient, thermo-stable enzymes / **enzyme mixtures for the production of sugars from biomass**

Solution: VTT evaluated candidate enzymes, developed optimised enzyme mixtures for a range of feedstocks, and improved the properties of mixture components via protein engineering.

Key benefits:

- Significantly reduced the enzyme dosage necessary for total biomass hydrolysis
- Positive results opened up new market opportunities in biorefinery applications

“With the help of VTT’s expertise and competence, we have reached significant improvements in enzyme / enzyme mixture performance.”



**Significantly
reduced
enzyme
dosage**

Novel bacterial strain for ethanol production

Customer: Deinove

Challenge: Unlock the potential of unique bacterial strains for ethanol production

Solution: VTT studied the production physiology of *Deinococcus* bacteria, analysing and characterising the hydrolytic enzymes they produced.

Key benefits:

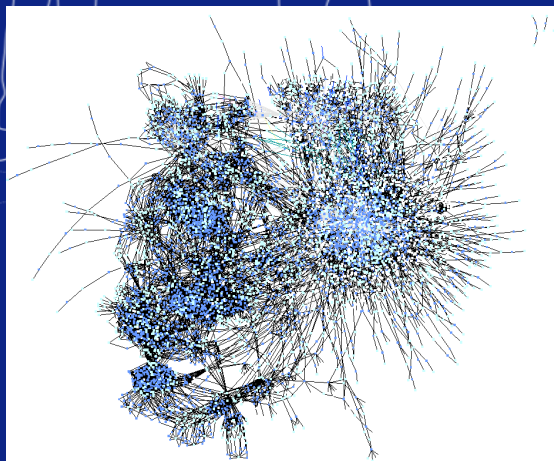
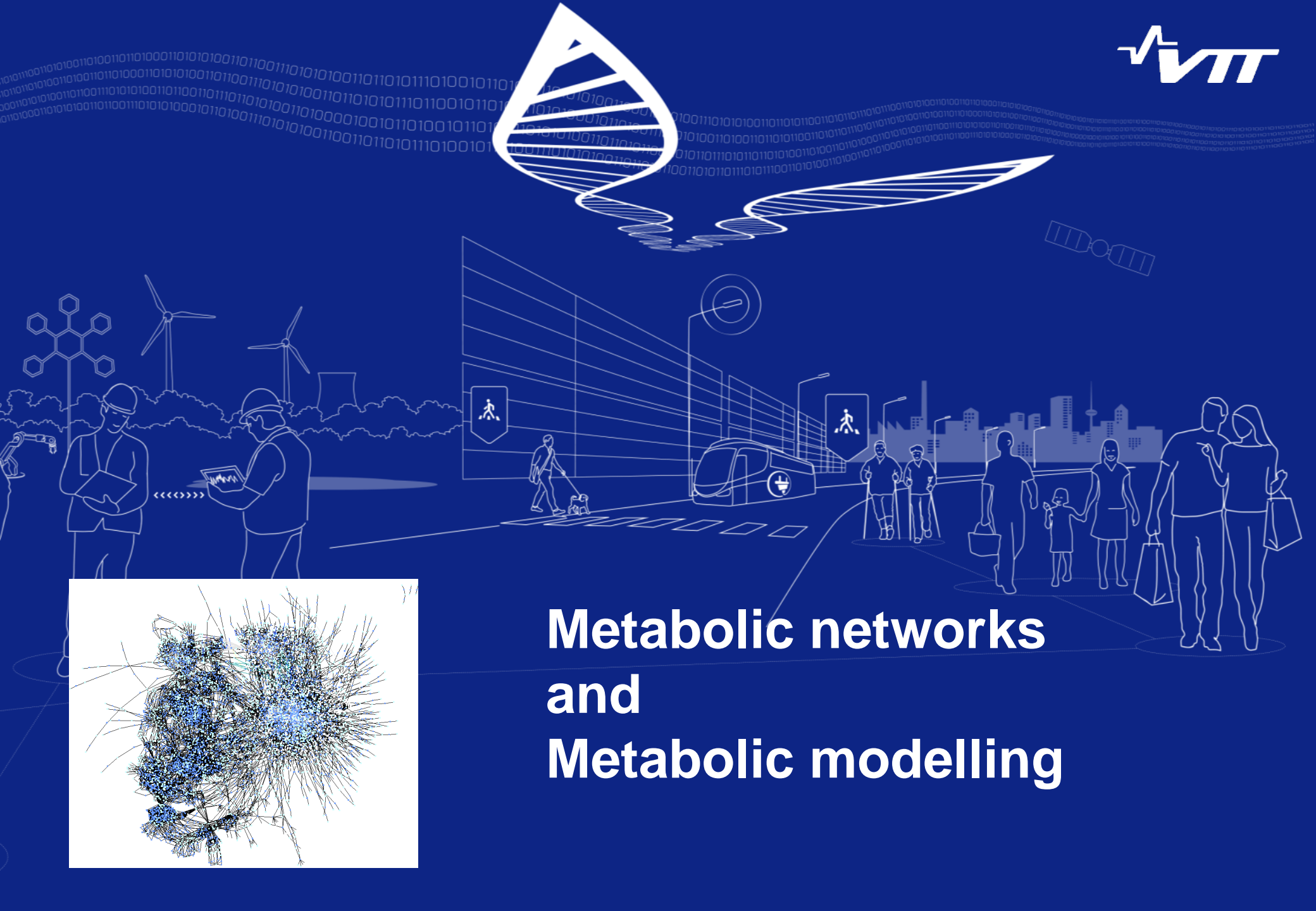
- Set the groundwork for commercialisation of the lignocellulosic ethanol production process

“Working with VTT is a great experience, their flexibility and multi-technology competencies are unmeasurable assets that help us speed up our R&D.”

- Jean-Paul Leonetti, VP, R&D Director, Deinove



60 fold
improvement
in ethanol
production



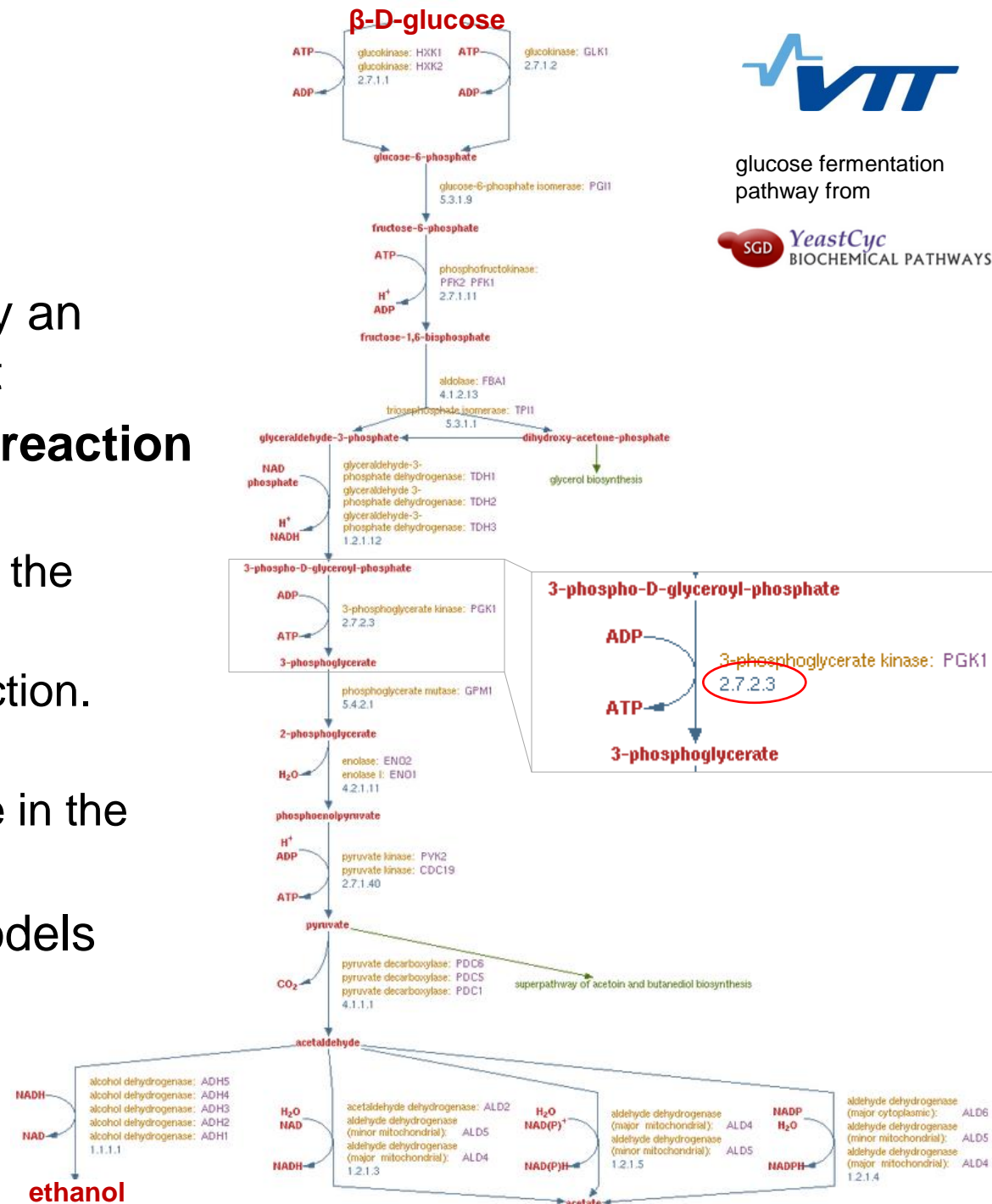
Metabolic networks and Metabolic modelling

Metabolic network

- Is a collection of reactions representing the biochemistry an organism could/can carry-out
- Key elements of a metabolic **reaction** are
 - Metabolites** participating in the reaction
 - Enzyme** catalysing the reaction. Identified by an EC number
 - Gene(s)** coding the enzyme in the organism in question
- Whole genome metabolic models have thousands of reactions

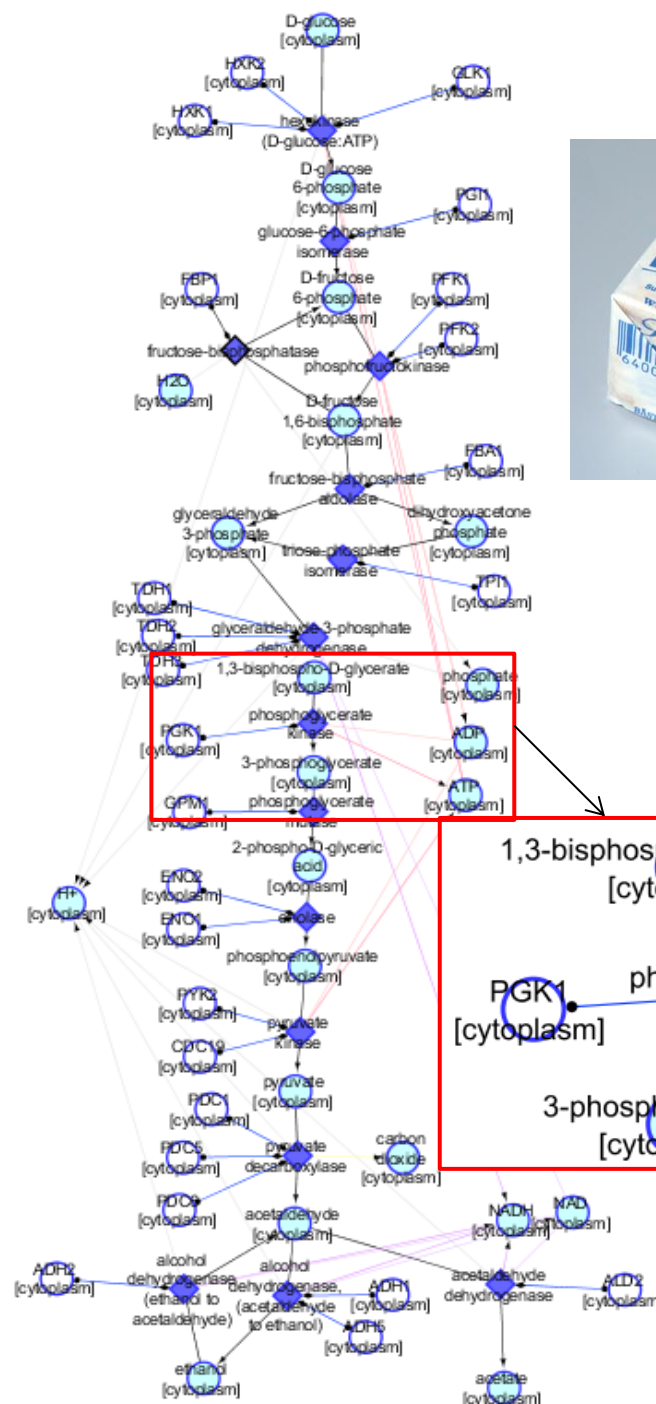
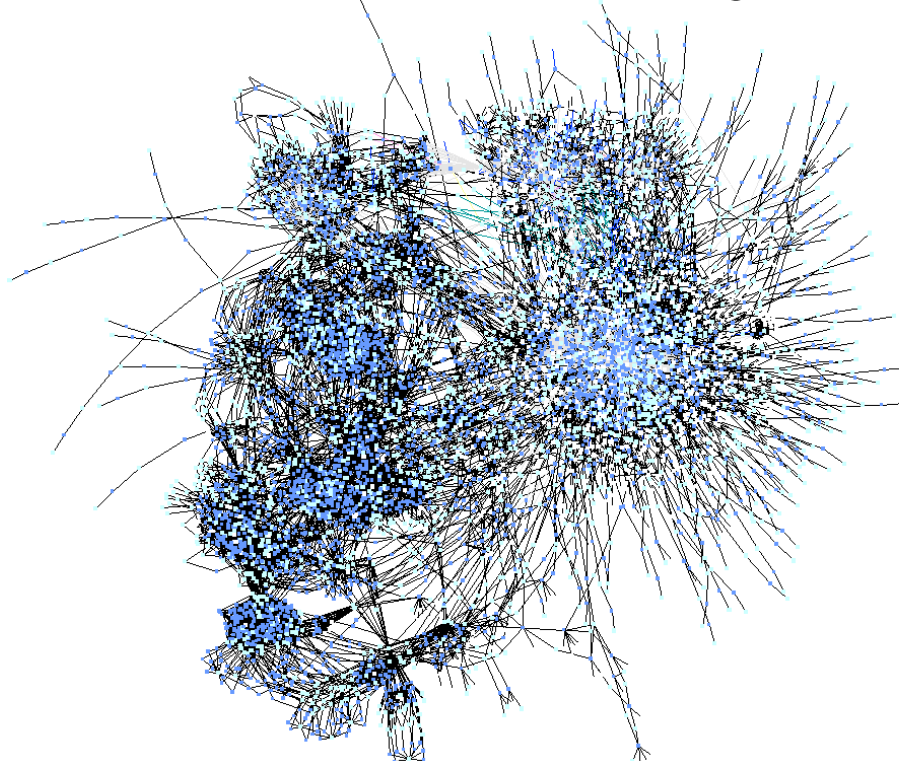


glucose fermentation pathway from



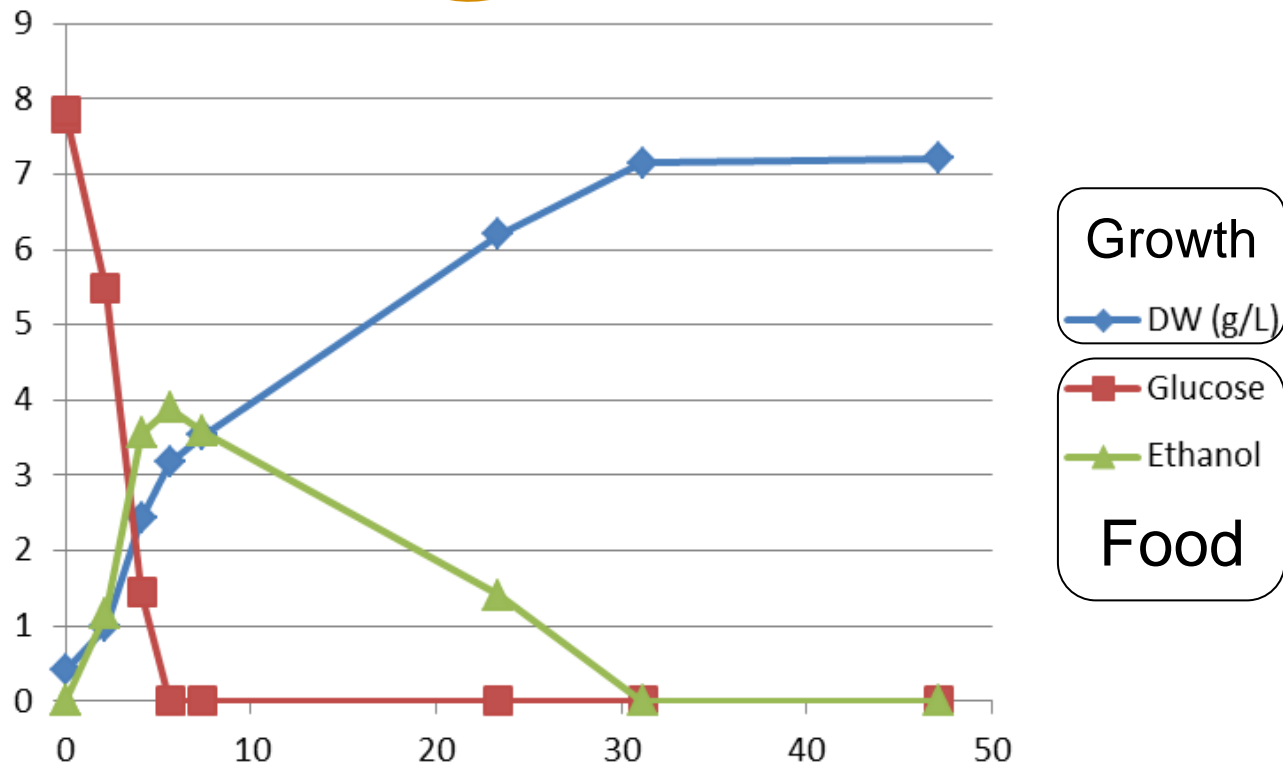
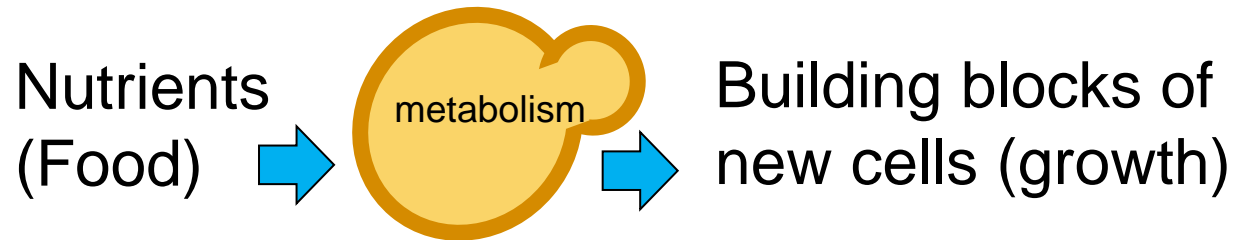
Example of a whole genome metabolic model: Baker's yeast *S. cerevisiae*

- *S. cerevisiae* model v7.5 has
 - 3494 reactions
 - 2221 metabolites
 - 909 genes
- In this network representation nodes are either reactions, metabolites or genes



Metabolic modelling is used to model cell behaviour

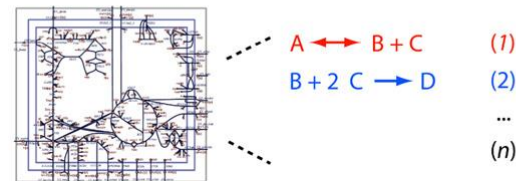
- Metabolic modelling estimates the flow of metabolites through the metabolic network. Modelling is used to predict the growth rate of an organism or the rate of production of a biotechnologically important metabolite.



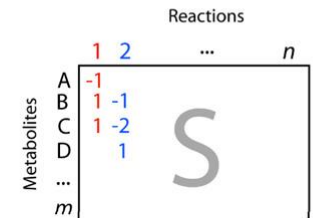
Flux balance analysis (FBA)

- Flux balance analysis is a technique used to solve what are the **fluxes** inside the cell
- The flux distribution explains which metabolic reactions are active and how much active
- Analysis the flux distribution allows understanding of cell behaviour

a Curate metabolic reactions



b Formulate **S** matrix



c Apply mass balance constraints

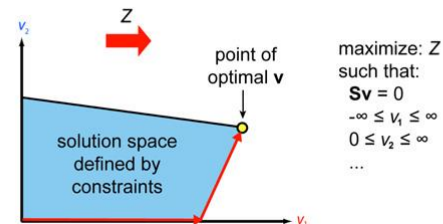
$$\begin{matrix} S & (m \times n) \\ \begin{bmatrix} -1 & & & \\ 1 & -1 & & \\ 1 & -2 & & \\ & & & 1 \\ & & & & \dots \\ & & & & & 1 \end{bmatrix} & * & \begin{matrix} v & (n \times 1) \\ \begin{bmatrix} v_1 \\ v_2 \\ \vdots \\ v_n \end{bmatrix} \end{matrix} & = & 0 & \rightarrow & \begin{matrix} m \text{ mass balance} \\ \text{equations} \\ -v_1 + \dots = 0 \\ v_1 - v_2 + \dots = 0 \\ v_1 - 2v_2 + \dots = 0 \\ v_2 + \dots = 0 \\ \dots \end{matrix} \end{matrix}$$

d Define objective function **Z**

$$Z = \begin{matrix} c^T & (1 \times n) \\ \begin{bmatrix} 1 & 0 & \dots & 0 \end{bmatrix} \end{matrix} * \begin{matrix} v & (n \times 1) \\ \begin{bmatrix} v_1 \\ v_2 \\ \vdots \\ v_n \end{bmatrix} \end{matrix}$$

sets reaction 1 as the objective

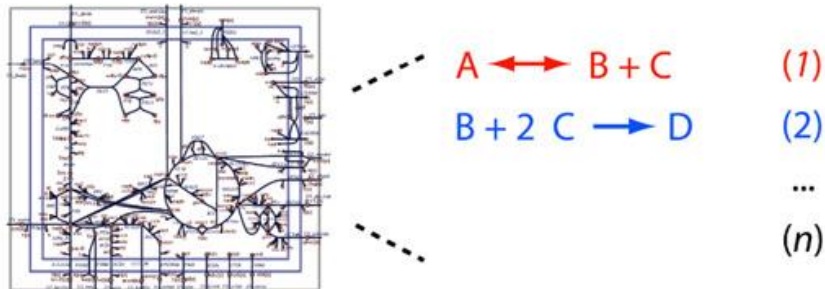
e Optimize **Z** using linear programming



Formulation of a FBA problem

- Representation of the metabolic network as stoichiometric matrix **S**
- Stoichiometric coefficients of each reaction (one column of the **S** matrix) are the constraints on the flow of metabolites through the network.

a Curate metabolic reactions



b Formulate **S** matrix

		Reactions			
		1	2	...	n
Metabolites	A	-1			
	B	1	-1		
	C	1	-2		
	D		1		
	...				
m					

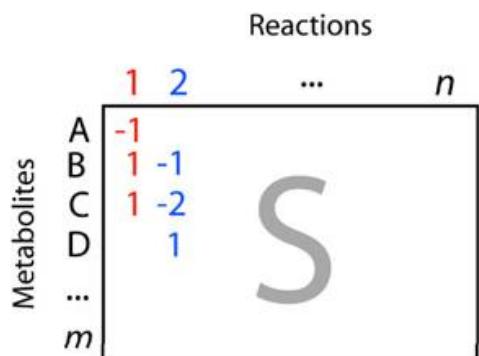
S

<http://www.ncbi.nlm.nih.gov/pmc/articles/PMC3108565/>

Formulation of a FBA problem

- Flux vector \mathbf{v} (length n) represents the flux through each of the reactions in the network.
- The concentrations of all metabolites are represented by the vector \mathbf{x} , with length m .
- Typically in FBA a steady state is assumed. This means that the fluxes will remain constant and metabolite concentrations do not change. Using this assumption we define $\mathbf{S} \mathbf{v} = d\mathbf{x}/dt = \mathbf{0}$

b Formulate \mathbf{S} matrix

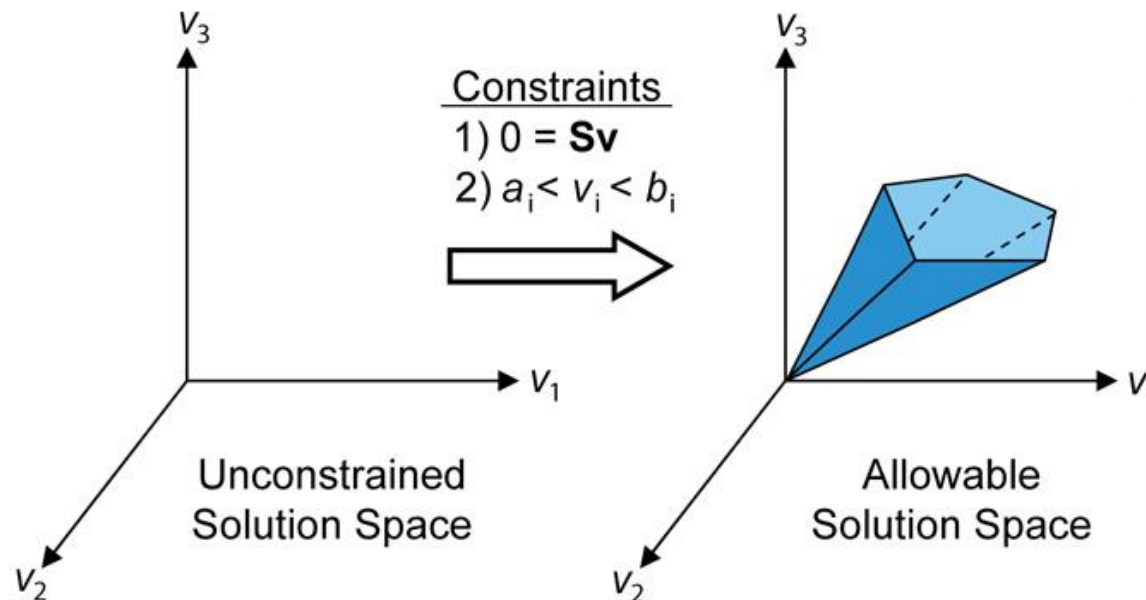


c Apply mass balance constraints

$$\begin{matrix} \mathbf{S} (m \times n) \\ \begin{matrix} -1 & & & \\ 1 & -1 & & \\ 1 & -2 & & \\ & & & 1 \end{matrix} \end{matrix} * \begin{matrix} \mathbf{v} (n \times 1) \\ \begin{matrix} v_1 \\ v_2 \\ \dots \\ v_n \end{matrix} \end{matrix} = \mathbf{0} \rightarrow \begin{matrix} m \text{ mass balance} \\ \text{equations} \\ -v_1 + \dots = 0 \\ v_1 - v_2 + \dots = 0 \\ v_1 - 2v_2 + \dots = 0 \\ v_2 + \dots = 0 \\ \dots \end{matrix}$$

Formulation of a FBA problem

- In any realistic large-scale metabolic model, there are more reactions than there are compounds ($n > m$). In other words, there are more unknown variables than equations, so there is no unique solution to the system of equations, $\mathbf{S} \mathbf{v} = \mathbf{0}$



Formulation of a FBA problem

- The $\mathbf{S} \mathbf{v} = \mathbf{0}$ constraints define a range of solutions, but it is still possible to identify and analyze single points within the solution space.
 - which point corresponds to the maximum growth rate?
 - or to maximum ATP (=energy) production of an organism?
- FBA seeks to maximize or minimize an objective function $Z = \mathbf{c}^T \mathbf{v}$

c Apply mass balance constraints

$$\begin{array}{|c|} \hline \mathbf{S} \ (m \times n) \\ \hline \begin{array}{cc} -1 & \\ 1 & -1 \\ 1 & -2 \\ & 1 \end{array} \\ \hline \end{array}
 \quad * \quad
 \begin{array}{|c|} \hline \mathbf{v} \ (n \times 1) \\ \hline \begin{array}{c} v_1 \\ v_2 \\ \dots \\ v_n \end{array} \\ \hline \end{array}
 = \mathbf{0} \rightarrow
 \begin{array}{l} m \text{ mass balance} \\ \text{equations} \\ -v_1 + \dots = 0 \\ v_1 - v_2 + \dots = 0 \\ v_1 - 2v_2 + \dots = 0 \\ v_2 + \dots = 0 \\ \dots \end{array}$$

d Define objective function Z

$$Z = \begin{array}{|c|} \hline \mathbf{c}^T \ (1 \times n) \\ \hline \begin{array}{cccc} 1 & 0 & \dots & 0 \end{array} \\ \hline \end{array}
 * \begin{array}{|c|} \hline \mathbf{v} \ (n \times 1) \\ \hline \begin{array}{c} v_1 \\ v_2 \\ \dots \\ v_n \end{array} \\ \hline \end{array}$$

sets reaction 1 as the objective

Formulation of a FBA problem

- Solve the problem

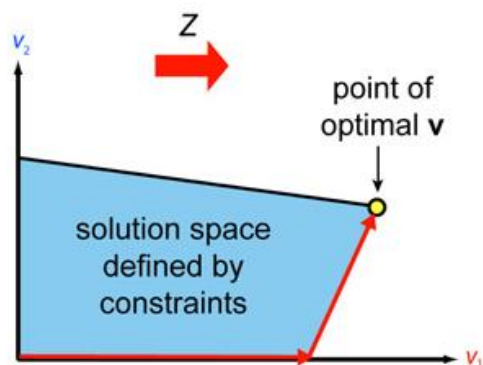
$$\max Z = \mathbf{c}^T \mathbf{v}$$

$$\mathbf{S} \mathbf{v} = \mathbf{0}$$

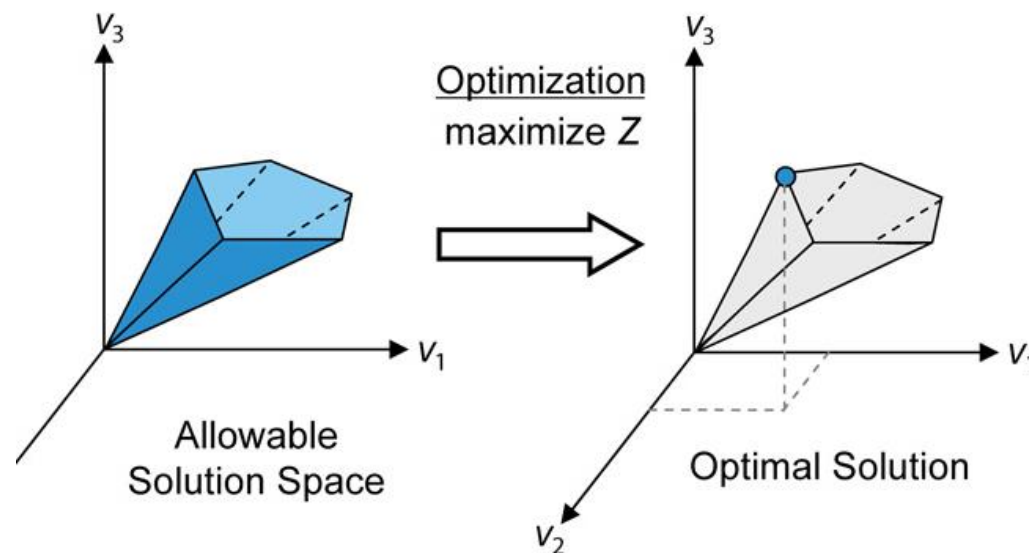
$$a_i < v_i < b_i$$

- In FBA this set of linear equations are solved using linear programming

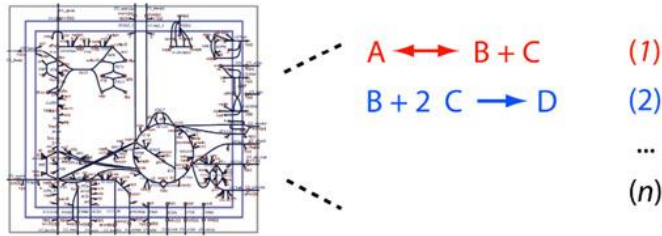
e Optimize Z using linear programming



maximize: Z
such that:
 $\mathbf{S} \mathbf{v} = \mathbf{0}$
 $-\infty \leq v_1 \leq \infty$
 $0 \leq v_2 \leq \infty$
...



a Curate metabolic reactions



b Formulate **S** matrix

		Reactions			
		1	2	...	n
Metabolites	A	-1			
	B	1	-1		
	C	1	-2		
	D		1		
	...				
		S			
		m			

c Apply mass balance constraints

S (m × n)	
-1	
1	-1
1	-2
	1

$$* \begin{matrix} v_1 \\ v_2 \\ \dots \\ v_n \end{matrix} = 0 \rightarrow$$

m mass balance equations

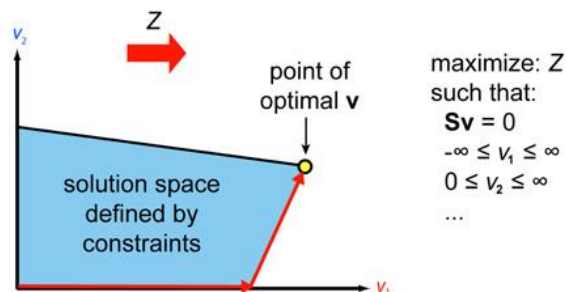
$$\begin{aligned}
 -v_1 + \dots &= 0 \\
 v_1 - v_2 + \dots &= 0 \\
 v_1 - 2v_2 + \dots &= 0 \\
 v_2 + \dots &= 0 \\
 \dots &
 \end{aligned}$$

d Define objective function **Z**

$$Z = \begin{matrix} c^T (1 \times n) \\ \hline 1 & 0 & \dots & 0 \end{matrix} * \begin{matrix} v (n \times 1) \\ \hline v_1 \\ v_2 \\ \dots \\ v_n \end{matrix}$$

sets reaction 1 as the objective

e Optimize **Z** using linear programming



Orth, J. D., Thiele, I., & Palsson, B. Ø. (2010). What is flux balance analysis? *Nat Biotechnol*, 28(3), 245–248. doi:10.1038/nbt.1614. <http://www.ncbi.nlm.nih.gov/pmc/articles/PMC3108565/>

FBA allows simulation

- Using the FBA framework different scenarios can be tested *in silico* before tedious laboratory experiments
 - Effect of different growth conditions
 - Effect of genetic modifications, i.e. deletion of gene(s)
- Analysis of the flux distributions allows understanding of
 - Which pathways are activated for production of the given target metabolite?
 - How is the cell generating energy (ATP) in the given conditions?
 - Are there problems in cofactor balancing, should more oxygen be given?

Additional analyses

- Alternate optimal solutions can be identified through flux variability analysis (FVA).
 - FBA is used to maximize and minimize every reaction in a network at a time
- FBA derived constraint based methods can be used to propose optimal genetic engineering strategies in metabolic engineering project
 - gene deletion(s)
 - OptKnock [Burgard, et al. 2003]
 - OptGene [Patil et al. 2005]
 - gene additions / deletions
 - OptStrain [Pharkya, et al. 2004]
 - gene overexpressions / known down
 - OptForce [Ranganathan, 2010]

Reading

- Orth, J. D., Thiele, I., & Palsson, B. Ø. (2010). What is flux balance analysis? *Nat Biotechnol*, 28(3), 245–248. doi:10.1038/nbt.1614.What
 - <http://www.ncbi.nlm.nih.gov/pmc/articles/PMC3108565/>

- If you are interested in metabolic engineering:
 - Nielsen, J., & Jewett, M. C. (2008). Impact of systems biology on metabolic engineering of *Saccharomyces cerevisiae*. *FEMS Yeast Research*, 8(1), 122–31. doi:10.1111/j.1567-1364.2007.00302.x

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- Burgard, A. P., Pharkya, P., & Maranas, C. D. (2003). **OptKnock**: A Bilevel Programming Framework for Identifying Gene Knockout Strategies for Microbial Strain Optimization. *Biotechnology and Bioengineering*, 84, 647–657. doi:10.1002/bit.10803
- Patil, K. R., Rocha, I., Förster, J., & Nielsen, J. (2005). Evolutionary programming as a platform for in silico metabolic engineering. *BMC Bioinformatics*, 6, 308. doi:10.1186/1471-2105-6-308 (**OptGene**)
- Pharkya, P., Burgard, A. P., & Maranas, C. D. (2004). **OptStrain**: A computational framework for redesign of microbial production systems. *Genome Research*, 14(814), 2367–2376. doi:10.1101/gr.2872004
- Ranganathan, S., Suthers, P. F., & Maranas, C. D. (2010). **OptForce**: An optimization procedure for identifying all genetic manipulations leading to targeted overproductions. *PLoS Computational Biology*, 6(4). doi:10.1371/journal.pcbi.1000744
- Rocha, I., Maia, P., Evangelista, P., Vilaça, P., Soares, S., Pinto, J. P., ... Rocha, M. (2010). **OptFlux**: an open-source software platform for in silico metabolic engineering. *BMC Systems Biology*. doi:10.1186/1752-0509-4-45



TECHNOLOGY «FOR BUSINESS»

