

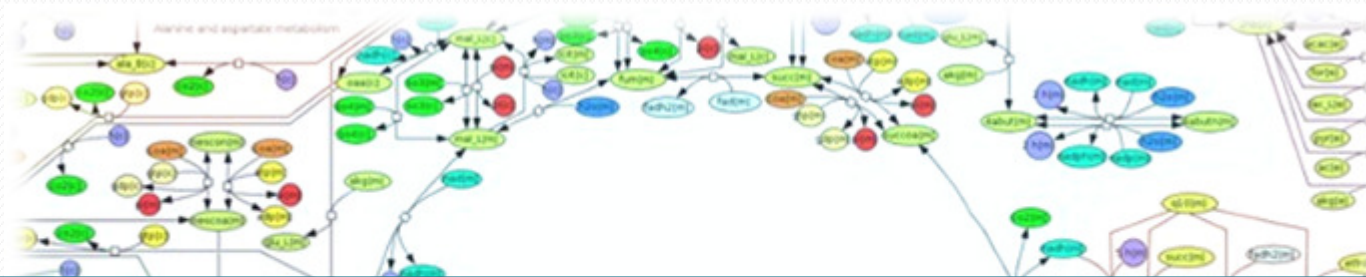
About OMICS Group

OMICS Group is an amalgamation of Open Access publications and worldwide international science conferences and events. Established in the year 2007 with the sole aim of making the information on Sciences and technology 'Open Access', OMICS Group publishes 500 online open access scholarly journals in all aspects of Science, Engineering, Management and Technology journals. OMICS Group has been instrumental in taking the knowledge on Science & technology to the doorsteps of ordinary men and women. Research Scholars, Students, Libraries, Educational Institutions, Research centers and the industry are main stakeholders that benefitted greatly from this knowledge dissemination. OMICS Group also organizes 500 International conferences annually across the globe, where knowledge transfer takes place through debates, round table discussions, poster presentations, workshops, symposia and exhibitions.

About OMICS International Conferences

OMICS International is a pioneer and leading science event organizer, which publishes around 500 open access journals and conducts over 500 Medical, Clinical, Engineering, Life Sciences, Pharma scientific conferences all over the globe annually with the support of more than 1000 scientific associations and 30,000 editorial board members and 3.5 million followers to its credit.

OMICS Group has organized 500 conferences, workshops and national symposiums across the major cities including San Francisco, Las Vegas, San Antonio, Omaha, Orlando, Raleigh, Santa Clara, Chicago, Philadelphia, Baltimore, United Kingdom, Valencia, Dubai, Beijing, Hyderabad, Bengaluru and Mumbai.



Systems Biology of nanocellulose synthesis: new approach to build a core metabolic model based on computational analysis



Samara Silva de Souza

2015







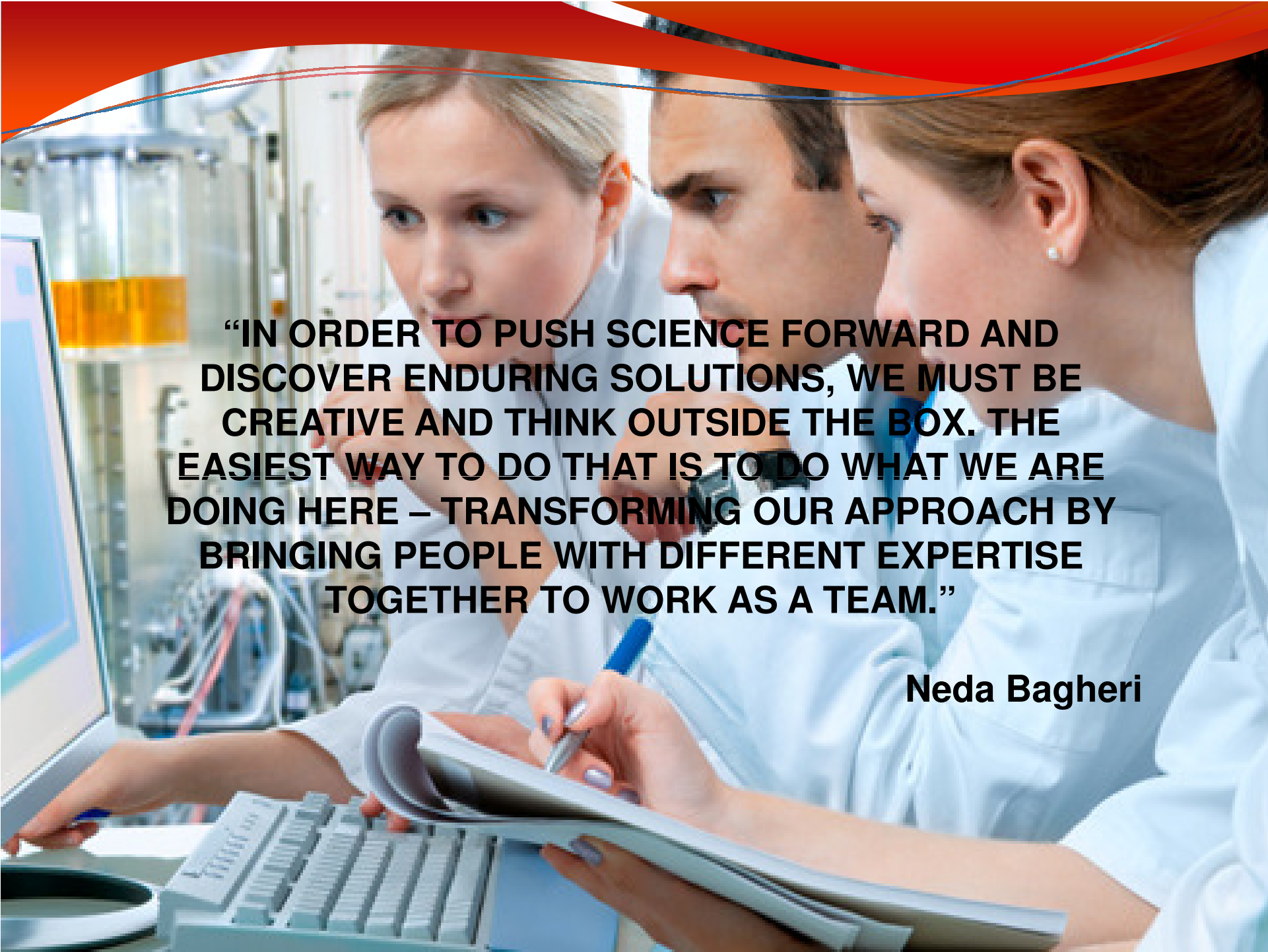
UNIVERSIDADE FEDERAL
DE SANTA CATARINA



iteLab

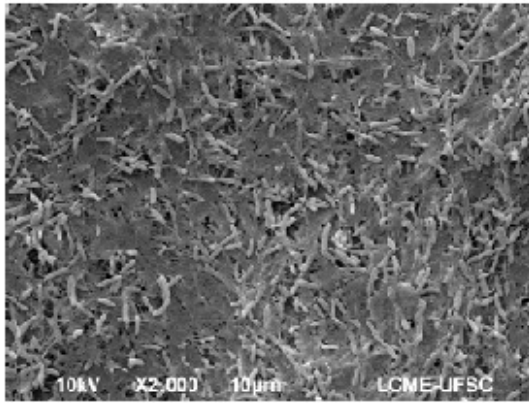
INTEGRATED TECHNOLOGIES
LABORATORY



A photograph of three scientists in white lab coats working in a laboratory. They are gathered around a computer monitor, looking intently at the screen. One scientist is pointing at the screen, another is holding a pen over a notebook, and a third is looking on. The background shows laboratory equipment, including a beaker with orange liquid. A red curved graphic element is at the top of the image.

“IN ORDER TO PUSH SCIENCE FORWARD AND DISCOVER ENDURING SOLUTIONS, WE MUST BE CREATIVE AND THINK OUTSIDE THE BOX. THE EASIEST WAY TO DO THAT IS TO DO WHAT WE ARE DOING HERE – TRANSFORMING OUR APPROACH BY BRINGING PEOPLE WITH DIFFERENT EXPERTISE TOGETHER TO WORK AS A TEAM.”

Neda Bagheri



Gluconacetobacter hansenii
ATCC 23769



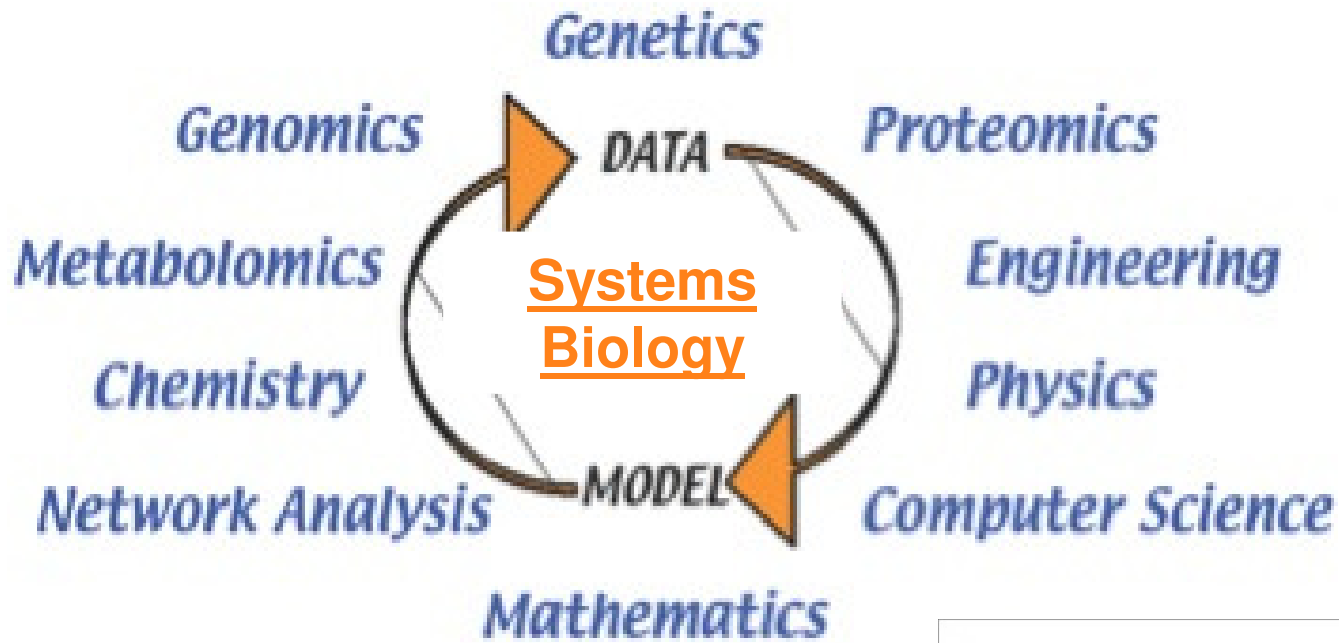
Komagataeibacter hansenii
ATCC 23769



NANOCELLULOSE

**TISSUE
ENGINEERING**





Ph: Daniel Hambury

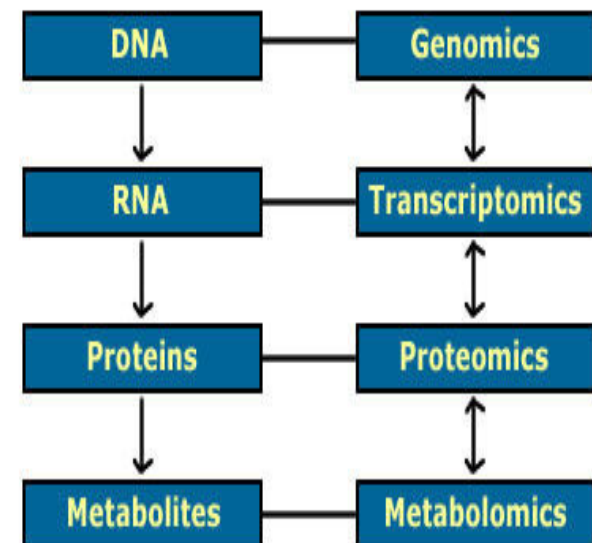
Systems Biology will usher in the next big technological wave, driving innovation and economic activity just as we saw at the dawn of the information age.

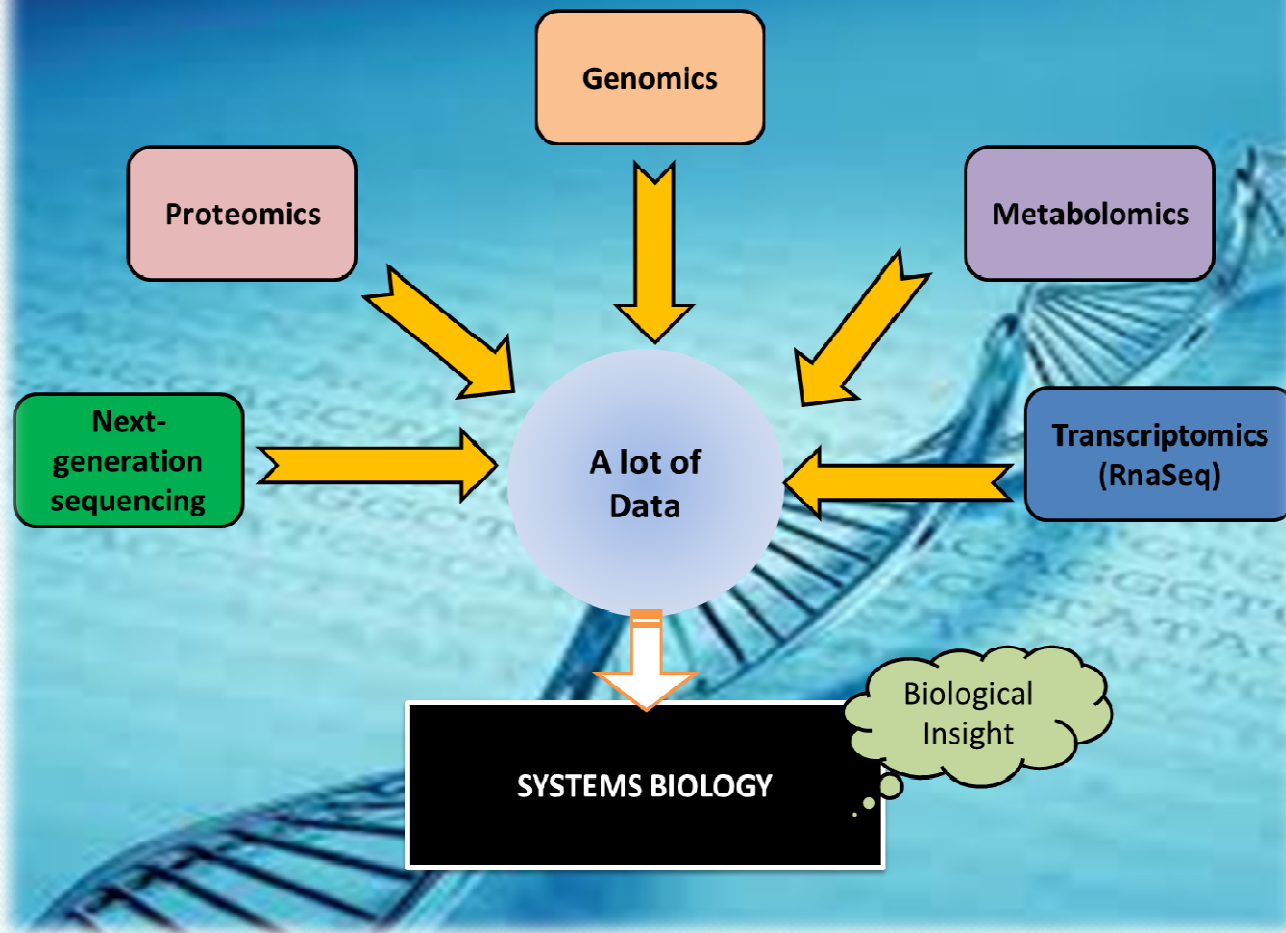
Metabolic ENGINEERING



- Metabolic Engineering: science which combining systematic analysis of metabolic pathways with other molecular biological techniques to improve cell properties (*Stephanopoulos, 1998*).
- One of the most important contribution is the emphasis of Metabolic Flux.

Study of the interactions between the components of biological systems, and how these interactions give rise to the function and behavior of that system.





Omic sciences and generation of amounts of biological data - The integration of different areas of knowledge allowed advances in studies related to genomics, transcriptomics, metabolomics and proteomics.



- ✓ The extensive data available now opens the way to use existing computational approaches and to develop new ones to extract new biological insights about a fundamental physiological process.
- ✓ Computational methods can then be used to model biological processes based on integrated data.

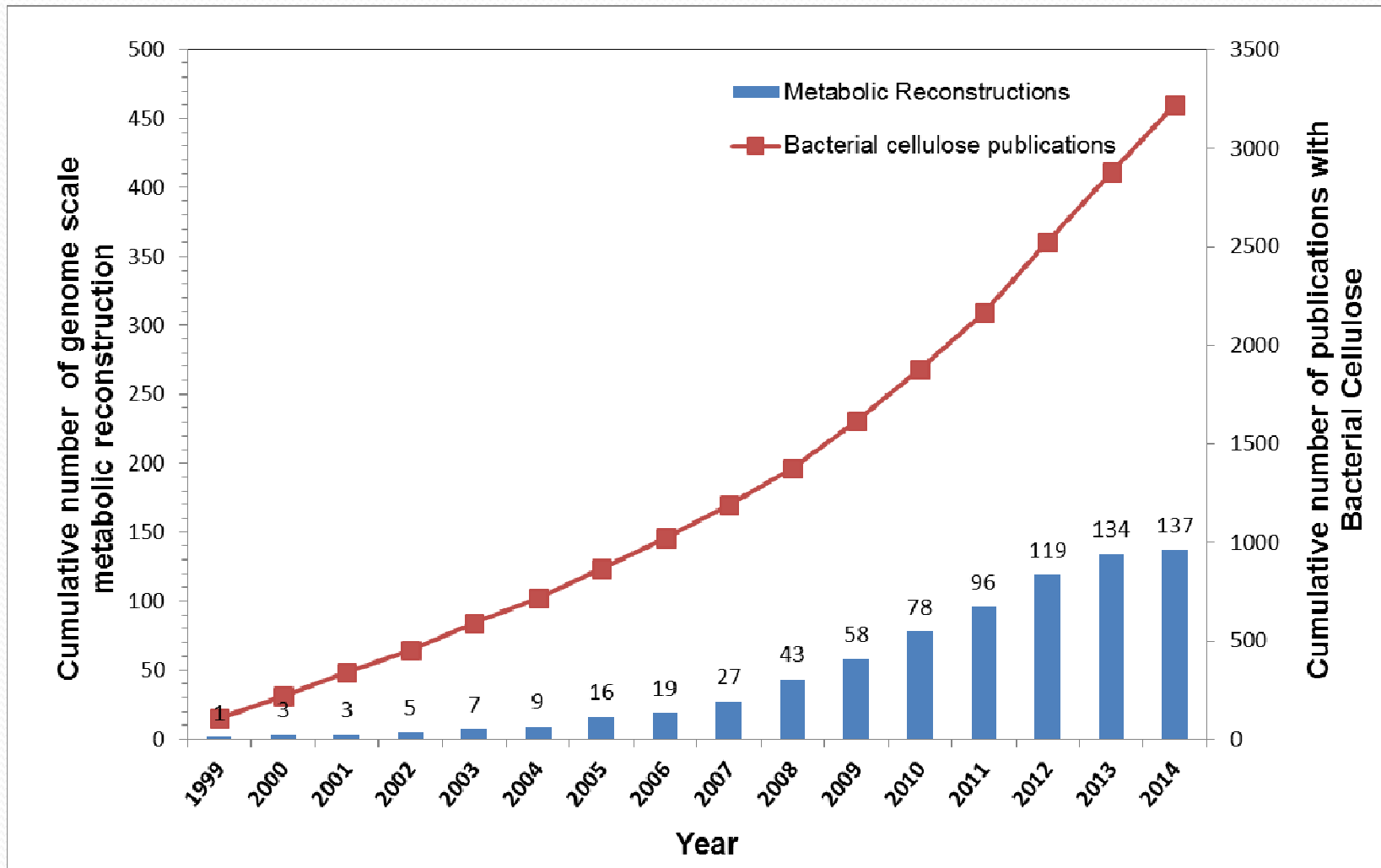
MOTIVATIONS

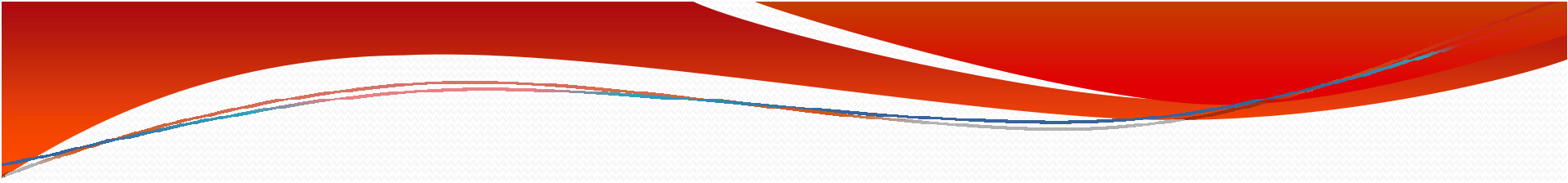
The bacterium *G. hansenii* produces a microstructure nanocellulose with high purity, a biomaterial of great interest for applications in tissue engineering and regenerative medicine.

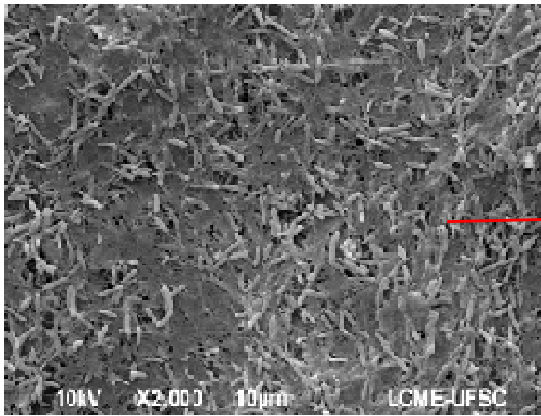
We need professionals who know how to manipulate and analyze the extensive amount of data generated by sequencing technologies

Systems biology and omics techniques: Approaches in expansion that will open new opportunities of knowledge leading to new discoveries in several areas.

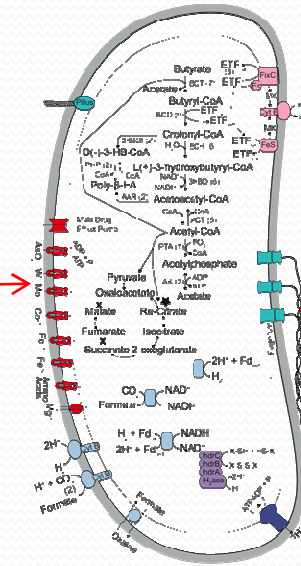
There are constantly new findings in computational tools and in omics techniques, promising major contributions to an understanding of overall cellular processes.



- 
- ✓ The core metabolic model developed can provide strategies for developing these biomaterials through a better understanding of *G. hansenii* metabolic pathways.
 - ✓ We presented from an initial draft of genome-scale metabolic reconstruction and network analysis of *G. hansenii*, a core metabolism model that capture its capabilities and nanocellulose biosynthesis functions. The constraint-based reconstruction and flux analysis approach was used to analyze the core model and simulate different conditions to evaluate its consistency and representativity for cellulose biosynthesis.



Bactéria
Gluconacetobacter hansenii
 ATCC 23769



reaction

metabolite

$$S = \begin{pmatrix} -1 & 0 & -1 & 0 & -1 & 0 & 0 & 0 \\ 1 & -1 & 0 & 0 & 0 & -1 & 0 & 0 \\ 0 & 1 & 1 & -1 & 0 & 0 & -1 & 0 \\ 0 & 0 & 0 & 1 & 0 & 0 & 0 & -1 \\ 0 & 0 & 0 & 0 & -1 & 0 & 0 & 0 \\ 1 & 0 & 0 & 0 & 1 & 0 & 0 & 0 \end{pmatrix}$$

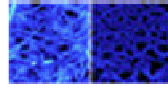


Generation of a mathematical model to investigate its metabolic behavior based on computational analysis.



A major objective is the determination of metabolic bottlenecks in cellulose biosynthesis, follow the step-strategy:

- (i) the establishment of the core model and manual curation,
- (ii) the application of the model for metabolic flux analysis (MFA) only to evaluate the flux distribution.
- (iii) the application of the model for flux balance analysis (FBA) by adding objective functions.



Sequenced genome annotated of *G. hansenii*

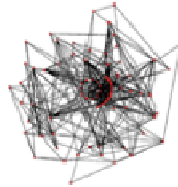
STEP 1

Automatic reconstruction (*Draft*)
Pathway tools / Model SEED

Pathway Tools



Genome-scale metabolic
network *draft*



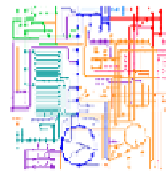
Manual
Curation



EXPASY
Bioinformatics Resource Portal

STEP 2

Core metabolic network



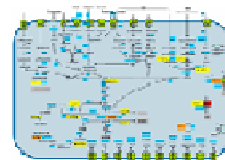
STEP 3

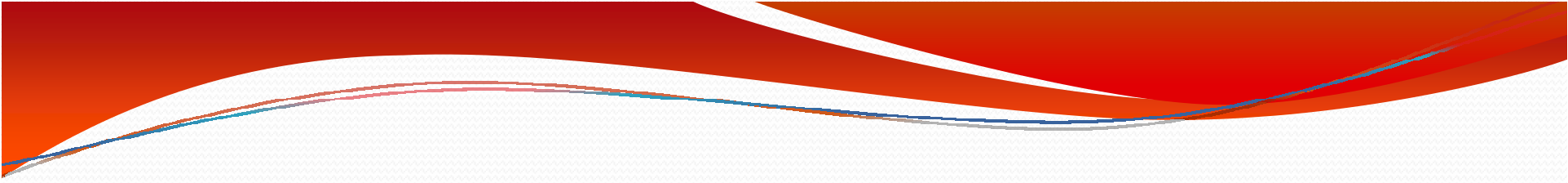
Conversion of reconstruction to a
computational model

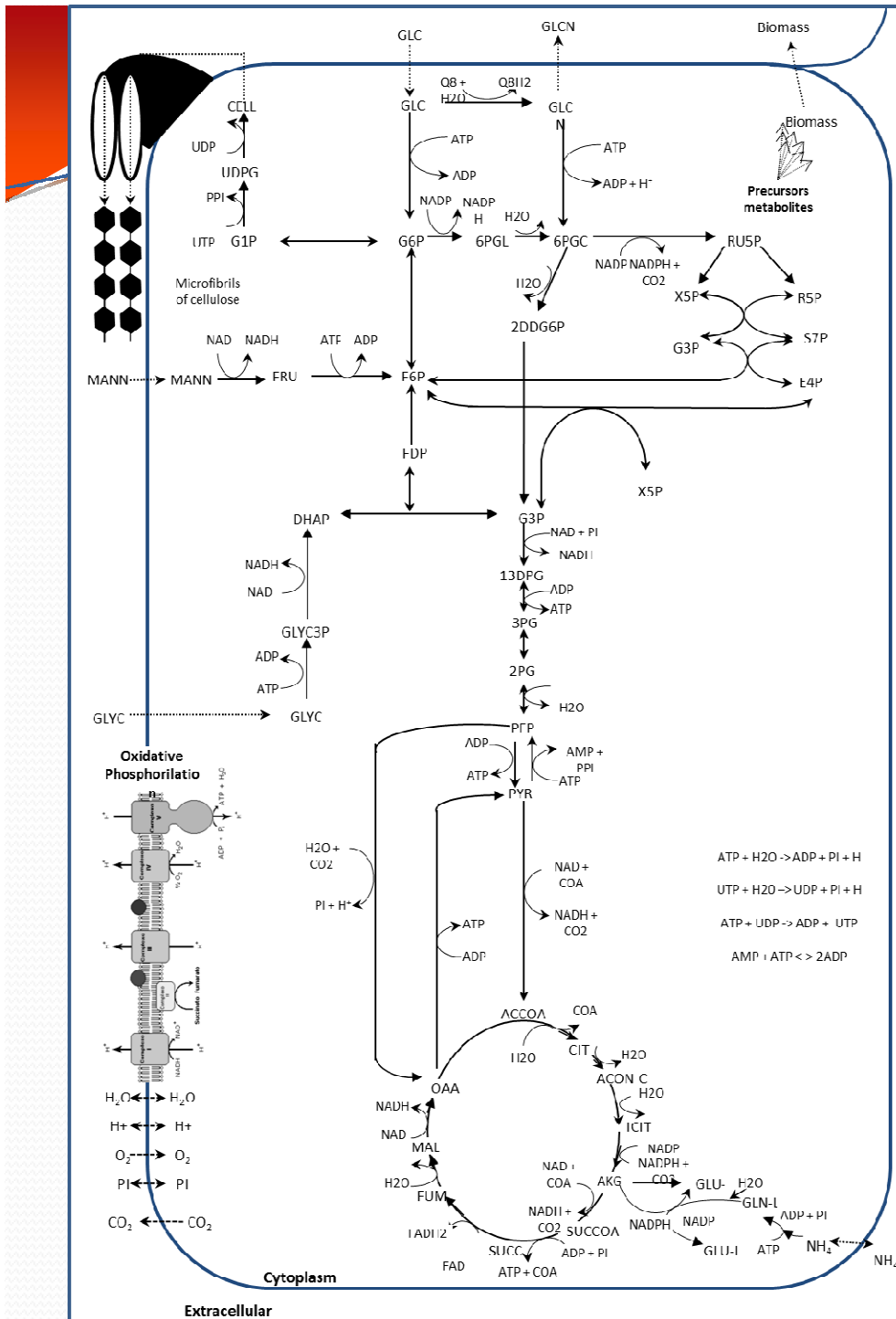


STEP 4

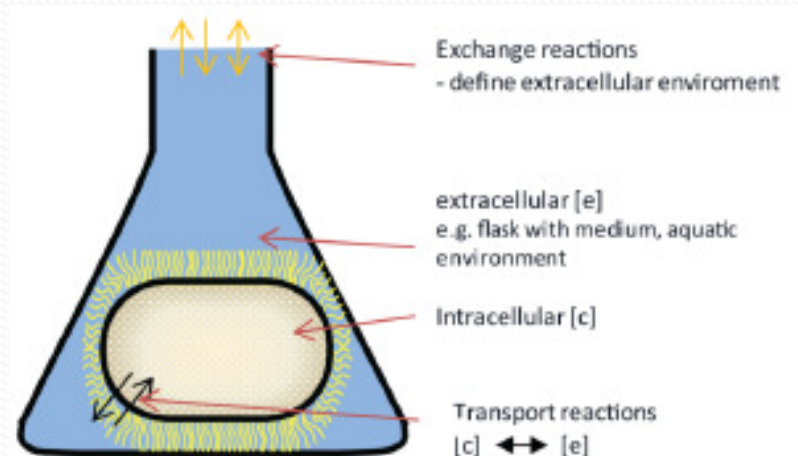
Analysis of the
network

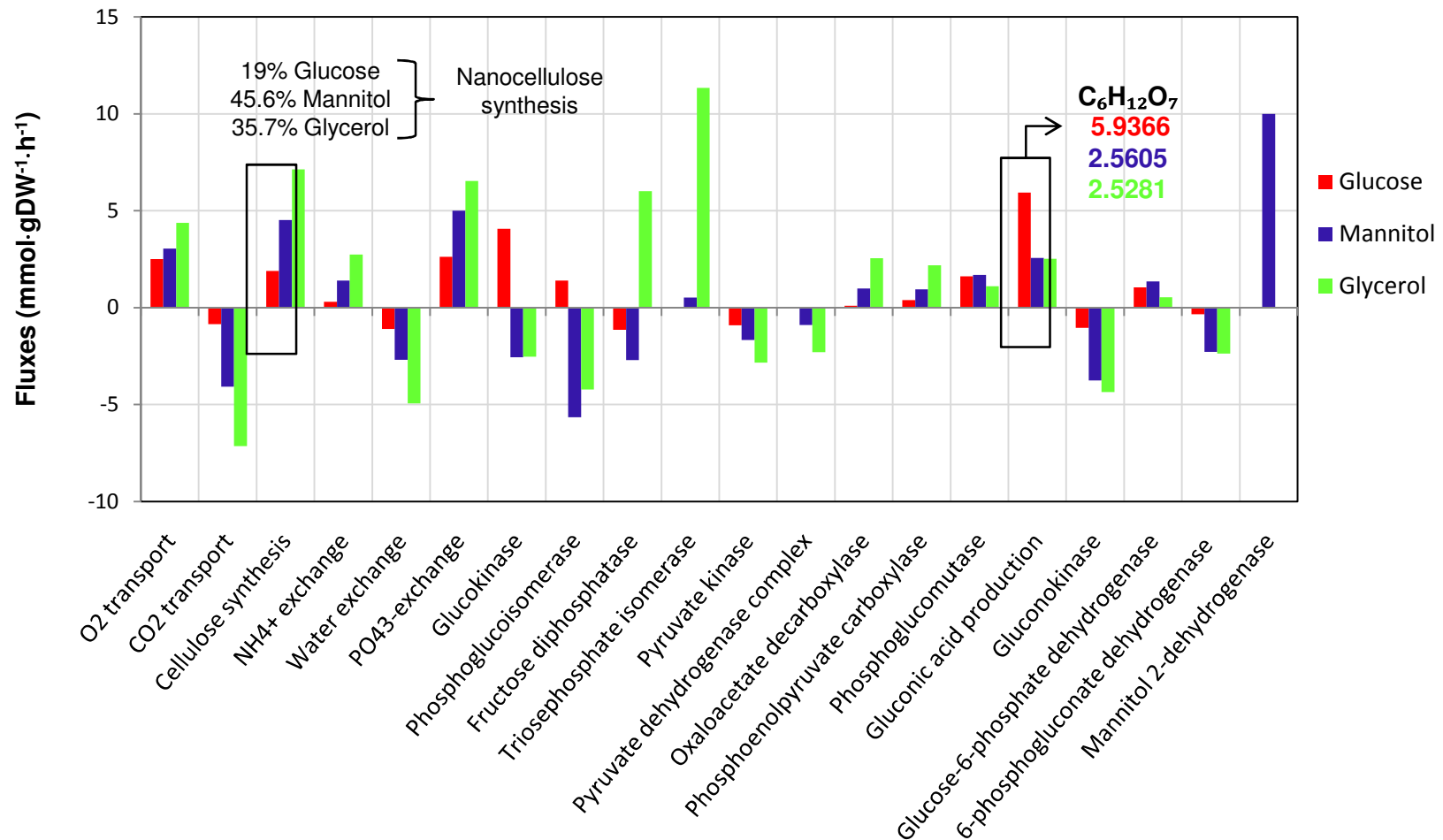


- 
- ✓ An initial metabolic reconstruction for *G. hansenii* was performed in accordance with a previously described protocol*, but adapting some steps in order to construct a representative core model.
 - ✓ This protocol is properly structured for large-scale metabolic networks and well-studied organisms when several experimental evidences are available. However, for organisms with few reported information on their metabolic capabilities, such as *G. hansenii*, some adaptations in the protocol were necessary for the construction of a simplified and representative model.



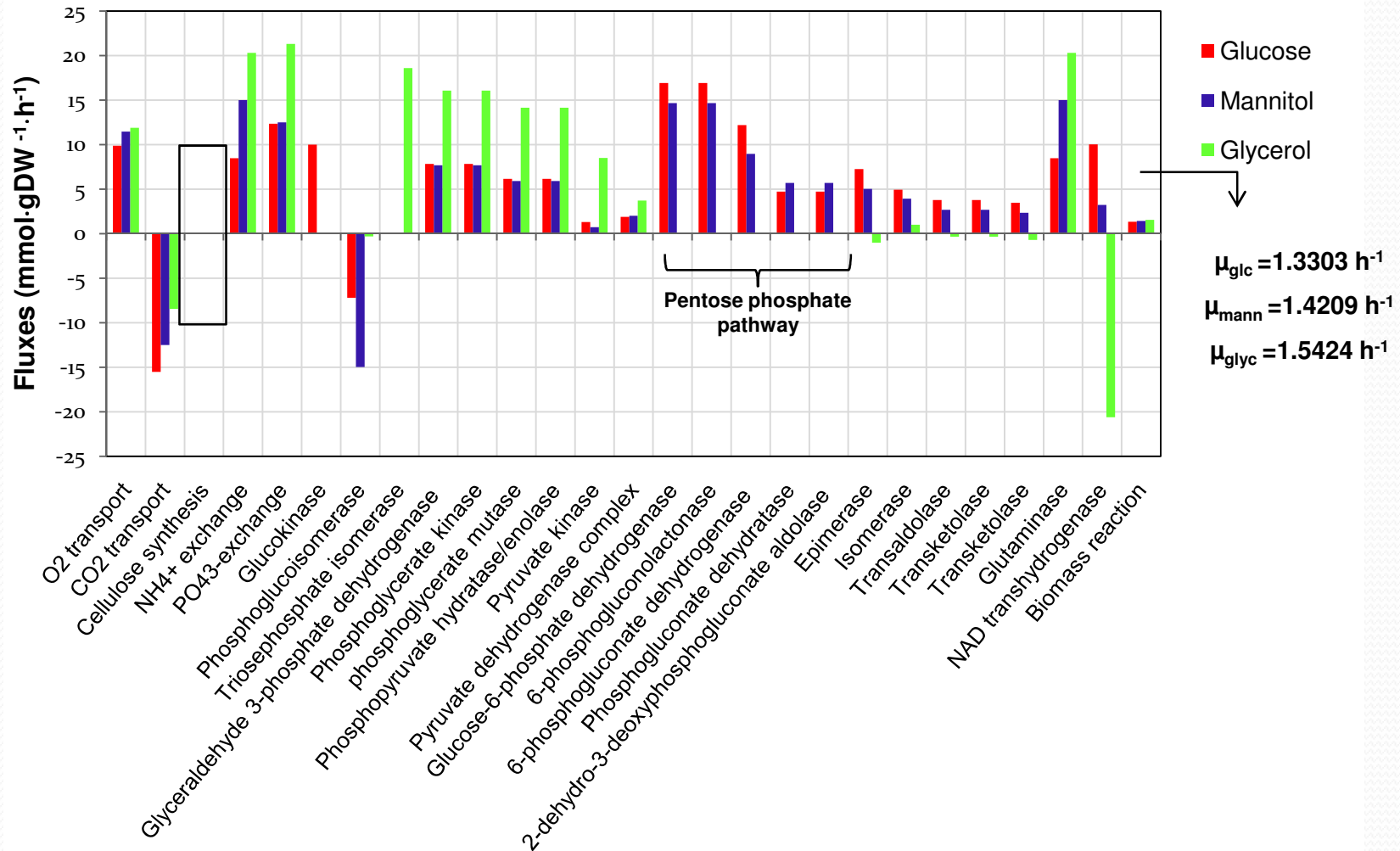
- ✓ Glycolysis and gluconeogenesis
- ✓ tricarboxylic acid cycle (TCA cycle)
- ✓ pentose phosphate pathway (PPP); nitrogen metabolism,
- ✓ ATP maintenance,
- ✓ electron transport chain
- ✓ oxidative phosphorylation
- ✓ cellulose biosynthesis
- ✓ biomass production
- ✓ exchange reactions



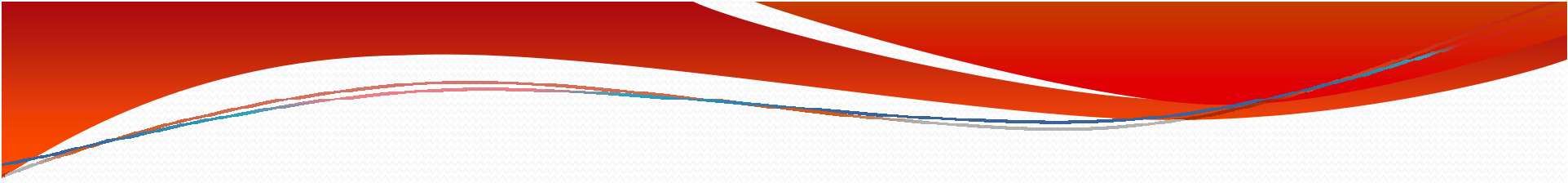


Metabolic Flux Analysis (MFA). Combines a set of measured flows (uptake rates of the substrates) to calculate the flux distribution of all reactions during *in silico* calculations.

Metabolic fluxes resulted from Flux Balance Analysis (FBA) to maximize cell growth during *in silico* calculations.

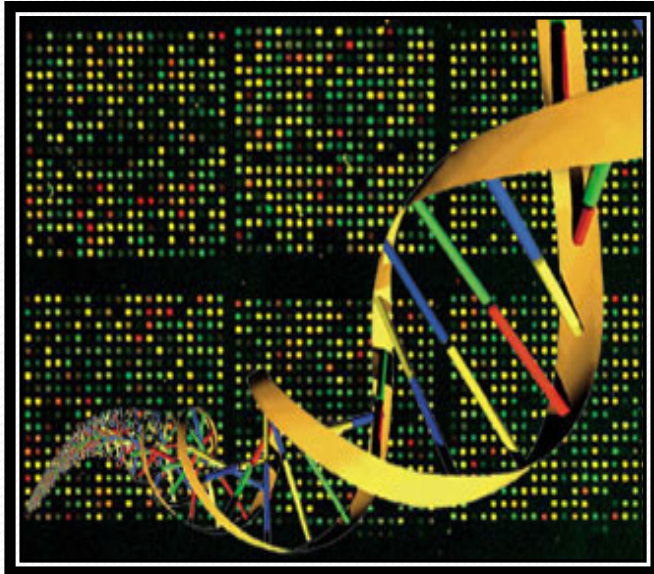


* The flux distribution in these conditions describes that using glycerol as a carbon source, the pentose phosphate pathway was not favored theoretically. The fraction of carbon directed to the pentose phosphate pathway was growth-rate dependent.

- 
- A description of minimal medium was essential to produce a metabolic model consistent with reality;
 - The determination of objective functions that were considered relevant was essential to analyze the metabolic network;
 - MFA analysis provided information about the contribution of each reaction to the metabolic processes and evaluated what had been evidenced experimentally in the literature.
 - By FBA analysis and simulations in different conditions showed that the *core* model was able to predict the phenotype cells will show in these conditions.
 - The core metabolic network was representative and consistent in all limits and defined boundary conditions.

FUTURE PROSPECTS

TRANSCRIPTOMICS

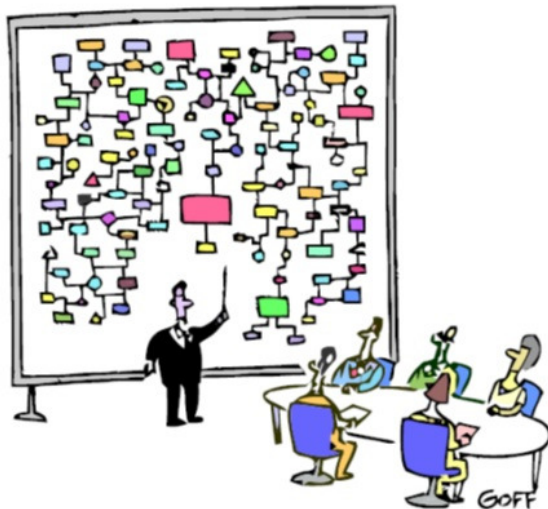


Integrated transcriptomics and metabolomics analysis is a powerful tool to build the relationship between information elements (genes/transcripts) and functional elements (metabolites) in cells.

“May I end up by suggesting the following modeling strategy: always start by trying the simplest model and then only add complexity to the extent needed. This is the \$10 approach, or as Einstein said, “Keep things as simple as possible, but not simpler”.”

Octave Levenspiel

Modeling Chemical Engineering, 2002



"And that's why we need a computer."

THANK YOU!!!



**3rd International Conference On
Integrative Biology**

August 04-06, 2015 Valencia, Spain

✉ samara@intelab.ufsc.br

Let Us Meet Again

We welcome you all to our future conferences
of OMICS International

Please Visit:

<http://integrativebiology.conferenceseries.com>

∟

<http://conferenceseries.com/>

<http://www.conferenceseries.com/genetics-and-molecular-biology-conferences.php>