Improving *in silico* predictions in Metabolic Engineering problems

Isabel Rocha

IBB - Institute for Biotechnology and Bioengineering, Centre of Biological Engineering, University of Minho, Campus de Gualtar, 4710-057 Braga – PORTUGAL

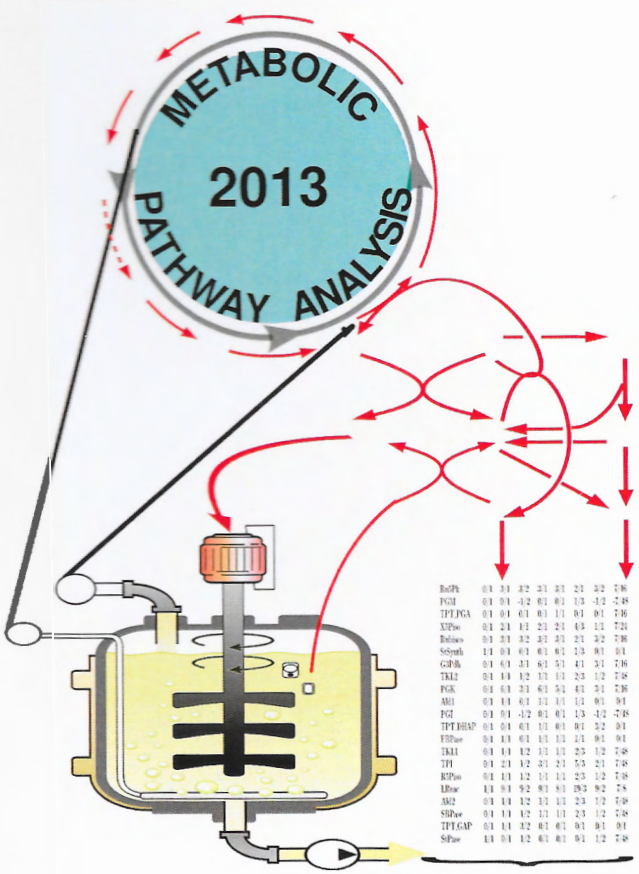
The field of Metabolic Engineering (ME) has gained a major importance, since it allows the design of improved microorganisms for industrial applications, starting with wild-type strains that usually have low production capabilities in terms of the target compounds. The ultimate aim of ME is to identify genetic manipulations *in silico* leading to improved microbial strains, that can be implemented using novel molecular biology techniques. This task, however, is a complex one, requiring the existence of reliable metabolic models for strain simulation and robust optimization algorithms for target identification.

Strain simulation is usually performed by using Linear or Quadratic Programing methods that assume a steady state over the intracellular metabolites. However, most of the available genome-scale models do not allow to make good predictions on flux distributions, ultimately leading to ineffective ME strategies.

Another important aspect associated with model predictions is the influence of the biomass equation added to the model. Since most simulation tools require directly or indirectly the computation of maximal biomass formation, this composition has a great impact in the predictive power of these models. Moreover, biomass composition is intrinsically related with essentiality predictions.

In this talk, a detailed analysis will be presented on the present prediction power of genome-scale metabolic models and simulation tools and on the impact of having accurate experimental measurements for model validation. Moreover, improved simulation and optimization tools based on different optimization formulations and on the concept of control effective fluxes will be introduced that allow to perform metabolic engineering tasks in a more reliable fashion.

Relevant Literature:
Gonçalves, E. et al. J Comp Biol, 19, 102, 2012.
Machado, D et al. Bioinformatics 28, i515, 2012.
Rocha I. et al. BMC Systems Biology, 4(45), 1-12, 2010.
Soons, Z. et al. PLoS One, 8(4), e61648, 2013.3



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