98. Next generation of the Yeast Genome-Scale Model: Reformulation and Improvement for Future Data Integration

Antonio Marras[1,*], Amir Feizi[1], Jens Nielsen[1], **Greg Stephanopoulos**[2]

[1]Chalmers University of Technology, Gothenburg, Sweden, [2]MIT, Cambridge, MA
*marrasa@chalmers.se

Project goals: The main goal of this project is to extend the current yeast genome scale models towards the next generation in order to capture current knowledge and use them as a scaffold for future data integration and modeling.

Genome-Scale Modeling and Flux balance analysis (FBA) are powerful tools to investigate the metabolic behavior of microbial cells. The recent development in high-throughput technologies produced a huge amount of data to be integrated and interpreted in their biological context. Integration of such high-throughput data with Genome-Scale models has valuable benefits for the understanding of the cell behavior. Nevertheless, this integration process with genome-scale models have been challenging in the area of research also due to a lack of a detailed description of the functions which have to be integrated.

Accordingly, we aim to reformulate and improve the current genome-scale yeast reconstruction approach to include more biological knowledge such as enzyme complex information which the previous approaches were lacking. For this aim, we use the knowledge available from structural proteomics and molecular level biochemistry in order to extend and accurate the gene-protein-reaction (GPR) relationships. Furthermore, the translation machineries and secretory machinery models will be reconstructed and integrated to the reformulated metabolic model. This provides the possibility to connect and investigate the metabolic demands of important cell processes in the cell.

The reformulation of the genome-scale models to include more molecular level mechanistic details will broad our ability to integrate various -*omics* data in order to get more systemic level understanding while it also increase the predictability property of the models.

References
Lerman, J. A., Hyduke, D. R., Latif, H., Portnoy, V. A., Lewis, N. E., Orth, J. D., Schrimpe-Rutledge, A. C., Smith, R. D., Adkins, J. N., Zengler, K., et al. (2012) In silico method for modelling metabolism and gene product expression at genome scale. Nat Commun, 3, 929.