

# Mathematical modelling of metabolism on a genome-scale: A pathway from DNA to FBA

Necessary preparation for working from your own laptop:

please install the appropriate thinlinc client from here:

<https://www.cendio.com/thinlinc/download>

This will allow you to connect to our educational server, thinlinc.oru.se. Logins and password will be supplied during the tutorial!

## **Background and Motivation**

Rapid advancement of cutting-edge technologies urges development of integrative methods and computational models. These approaches when applied at the systems level could mechanistically relate entities like gene, proteins and metabolites that might unveil the biological markers and related processes at the systems level. Genome-scale metabolic modeling (GSMM) is a constraint-based mathematical modeling approach evolving over the past 30 years. GSMM integrates biochemical, genetic and genomic informations within a computational framework. Thus, can help to understand metabolic genotype-phenotype relationship of an organism. Today, GSMM have been used to study cell, tissue and organ specific metabolism in the context of various diseases such as cancer, non-alcoholic fatty liver disease (NAFLD), and diabetes. Recently, it has been used to study the metabolic role of gut microbiota and its association with host. Furthermore, GSMM as an integrative tool has been used to model diet-tissue and multi-tissue interactions in humans.

In this workshop, we will highlight several aspects of GSMM applied to microbes, lower eukaryotes and human. We will get accustom with the structure of genome-scale models, flux balance analysis (FBA), web-based tools and standalone resources for automatic/manual model reconstruction. We will also perform hands-on tutorials analyzing multi-omics datasets in context of GSMM. A brief outline of the workshop is stated below: -

## **Workshop content (preliminary)**

- Introduction to Genome-Scale Metabolic Modelling (GSMM)
- Tools and resources for model reconstruction and analysis
  - COBRA (Matlab) (Intro)
  - RAVEN (Matlab) (**Tutorial**) (Argen et al., 2013) (<https://github.com/SysBioChalmers/RAVEN>)
  - ModelSEED & Kbase (web-based) (Intro)
  - Miscellaneous (Intro)
- Quality control (QC) checks in GSMM. (**Tutorial**)

- GSMM of microbes and lower eukaryotes: Modelling in Yeast (**Tutorial**)
- GSMM applied to Human (Recon2 & HMR2: intro)
- Integration of multi-omics data into the genome-scale framework (**Tutorial**)
- Contribution to GSMM/GEM community and resources involved.

### **Software to be installed in the local machines**

- Window OS (preferably)
- MAC OS (*not easy with MAC have to include many patches*)
- MATLAB (**mandatory**)
- COBRA + GLPK solver (*linear programming, **mandatory**, set in the path of Matlab*)  
<https://github.com/opencobra/cobratoolbox>
- RAVEN + MOSEK solver (*linear/quadratic programming, **mandatory**, set in the path of Matlab*) <https://github.com/SysBioChalmers/RAVEN>
- SBML toolbox (*set in the path of Matlab*) <http://sbml.org/Software/libSBML> (*For Matlab binding*)
- Microsoft excel (**mandatory**)