Metabolic modeling applied to metabolic engineering and systems medicine

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Genome-scale metabolic models (GEMs) are comprehensive description of cellular metabolism. We have over the last years reconstructed GEMs for a number of industrially important fungi, including the yeast Saccharomyces cerevisiae, and used these models for integrative analysis of omics data and for identification of novel metabolic engineering targets. Hereby we have developed advanced cell factories for the production of fuels and chemicals. Recently we have also embarked on building a Human Metabolic Atlas, a novel web-based database and modelling tool that can be used by medical and pharmaceutical researchers to analyse clinical data with the objectives of identifying biomarkers associated with disease development and improving health care. The central technology in the Human Metabolic Atlas is GEMs, which are tissue-specific. These models allow for context-dependent analysis of clinical data, providing much more information than traditional statistical correlation analysis, and hence advance the identification of biomarkers from high-throughput experimental data that can be used for early diagnosis of metabolic related diseases. In this presentations our technologies behind reconstruction, simulation and analysis of GEMs will be presented and results from studies in metabolic engineering and systems medicine will be presented. In connection with the latter it will also be discussed how we can advance towards modeling of the gut microbiome, which has recently demonstrated to be an active metabolic organ in the human body.