DISTINGUISHED LECTURE in BIOLOGICAL ENGINEERING

“Metabolism and its Role in Production of Advanced Biofuels, Obesity and Cancer”

Thursday – June 26, 2014 – 11:00 a.m.
EPFL – room MX F1

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Abstract

Metabolism is the core of functioning of any cell as it ensures provision of Gibbs free energy as well as precursors for synthesis of cellular constituents like proteins, lipids and DNA. Metabolism involves a large number of biochemical conversion processes. Thus, even Baker’s yeast that serves as the simplest model for studying human cells, contains more than 900 enzymes that catalyze more than 1,500 biochemical reactions. In human cells these numbers are much larger with more than 3,000 enzymes and more than 5,000 biochemical reactions. Even though the large number of reactions is organized into metabolic pathways, there is a high degree of connectivity between the reactions, and hence it is quite complicated to study these reactions individually. It is therefore necessary to take a systemic approach for analysis of metabolism, often referred to as systems biology. We are working on generating so-called genome-scale metabolic models (GEMs) that are comprehensive description of cellular metabolism. We have over the last years reconstructed GEMs for a number of industrially important fungi, including the Baker’s yeast Saccharomyces cerevisiae, and used these models for analysis of large data sets and for identification of novel targets where we can engineer the metabolism, often referred to as metabolic engineering. 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 presentation our technologies behind reconstruction, simulation and analysis of GEMs will be presented, as well as results from studies in metabolic engineering and systems medicine. 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.

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