DEBUGGING SYNTHETIC BIOLOGY BY METABOLOMICS AND SYSTEMS MODELING

Rainer Breitling

Faculty of Life Sciences, Manchester Institute of Biotechnology, University of Manchester, Manchester, M1 7DN, UK
rainer.breitling@manchester.ac.uk

Key words: metabolomics, systems biology, synthetic biology

The comprehensive engineering of microbial systems by synthetic biology requires powerful computational and postgenomic tools, both for the design phase and for the debugging of the engineered organisms. Metabolomics is a particularly suitable technology for the debugging work, providing an unbiased global profile of the metabolic state and functioning of an organism. In combination with the computational modeling of metabolism it can identify metabolic bottlenecks and unwanted side reactions and guide an iterative cycle of improved designs.

One of the major challenges in applying metabolomics and computational modeling to the favorite hosts of synthetic biology is often the incomplete knowledge of their metabolism, in particular the lack of enzyme kinetic information. Even where some information is available, it tends to be incomplete and noisy, especially when it is obtained by postgenomic methods like metabolomics.

In this talk I will present metabolomics results that illustrate the challenge of incomplete and uncertain knowledge and outline a general strategy for computational modeling in the face of incomplete data and uncertainty, which will enable the use of metabolomic systems biology in a wider range of synthetic biology applications than ever before.