The RAVEN toolbox and its use for generating a genome-scale metabolic model for Penicillium chrysogenum.

We present the RAVEN (Reconstruction, Analysis and Visualization of Metabolic Networks) Toolbox: a software suite that allows for semi-automated reconstruction of genome-scale models. It makes use of published models and/or the KEGG database, coupled with extensive gap-filling and quality control features. The software suite also contains methods for visualizing simulation results and omics data, as well as a range of methods for performing simulations and analyzing the results. The software is a useful tool for system-wide data analysis in a metabolic context and for streamlined reconstruction of metabolic networks based on protein homology. The RAVEN Toolbox workflow was applied in order to reconstruct a genome-scale metabolic model for the important microbial cell factory Penicillium chrysogenum Wisconsin54-1255. The model was validated in a bibliomic study of in total 440 references, and it comprises 1471 unique biochemical reactions and 1006 ORFs. It was then used to study the roles of ATP and NADPH in the biosynthesis of penicillin, and to identify potential metabolic engineering targets for maximization of penicillin production.