

Abstract

The overall goal of systems biology is the simultaneous study of all processes and dynamic interactions at molecular level in order to draw conclusions which may not be apparent when only individual components are considered. Genome-scale modeling is a promising approach to systematically analyze complex cellular systems. Metabolic models have proven to be valuable for increasing the product yield, predicting the effect of gene deletions, improving gene annotation, and identifying regulatory mechanisms. As models are constructed based on annotated genomes, current advancements in next generation sequencing technologies will foster the development of new models.

Therefore, a bioinformatics platform for the management, storage, and development of metabolic models has been established. The web based *Metabolic Model System* (MEMOSys) supports the development of new models by providing a built in version control system which offers access to the complete reconstruction history. Moreover, the integrated web board, the fine-grained authorization system, and the definition of user roles allow collaborations across departments and universities. Research on existing models is facilitated by a powerful search system, references to external databases, and a feature-rich comparison mechanism. MEMOSys provides customizable data exchange mechanisms using the SBML format to enable analysis in external tools. The web application is based on the Java EE framework and offers an intuitive user interface. It currently contains several well annotated and publicly available models.

In summary, the implemented bioinformatics platform provides researchers a novel application facilitating the management and development of metabolic models.

Keywords: Metabolic models, database, SBML, Java EE