A Database-supported Modular Modelling Platform for Systems and Synthetic Biology

Wolfgang Marwan

Lehrstuhl für Regulationsbiologie and Magdeburg Centre for Systems Biology, Otto-von-Guericke Universität, Universitätsplatz 2, 39106 Magdeburg, Germany
`wolfgang.marwan@ovgu.de`

Abstract. Petri nets are employed as a multifunctional integrative framework for biomodel engineering. We describe the general concept of a modular modelling approach that consideres the functional coupling of components of genome, transcriptome, and proteome with complex cellular phenotypes. For this purpose, the effects of genes and their mutated alleles on downstream components are modeled by composable, metadata-containing Petri net models organized in a database with version control, accessible through a web interface. Gene modules are coupled to protein modules through mRNA modules by specific interfaces designed for the automatic, database-assisted composition. Automatically assembled executable models may then consider cell type-specific gene expression patterns and take the resulting protein concentrations into account. With a sufficient number of protein modules in the database, the composed Petri nets can predict complex effects of gene mutations or uncover complex genotype/phenotype relationships. In this context, forward and reverse engineered modules are fully compatible.