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

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Extended Abstract

Background. Facilitating the handling of the increasing number of kinetic models is a challenging task in biomodel engineering. Usually advanced mathematical skills are required to generate, curate, update or to just perform simulations with a kinetic model. This makes modelling less popular in the life sciences. In addition, an on-going trend in biomodel engineering is the representation of biological systems in the form of monolithic models, which are inherently complex due to the numerous interwoven components. This makes them hardly accessible to others, especially for curation and updating. Moreover, monolithic models usually cannot be linked without extensive restructuring. Therefore, biomodel engineering would benefit from a universal and unifying modelling platform facilitating the use of models and making them more appealing even for wet lab life scientists.

Results. We developed a modular modelling concept, where modules focus on the reactions of each individual protein with its specific interaction partners as described by a Petri net [1–4]. These Petri net modules are graphically displayed, can be executed individually and may be coupled with via specific connection interfaces. Our concept is supported by a prototype database with a publically accessible web-interface [1]. In addition to the network structure of each module, the database contains metadata for documentation purposes. Therefore, each module corresponds to a wiki-like minireview. The database can manage multiple versions of each module. The organization of molecule-oriented modules in a database facilitates the automatic composition into coherent models containing an arbitrary number of molecular species chosen ad hoc by the user. Petri nets composed from modules can be executed as ODEs, stochastic, hybrid, or merely qualitative models and exported in SMBL format.

Conclusion. The modular modelling concept and its extension by a supportive database, facilitates the curation, documentation, version control, and update of individual modules and the subsequent automatic composition of complex models, without requiring mathematical skills [1–4]. Modules can be recombined according to user-defined scenarios, e.g., considering the gene expression patterns in given cell types, under certain physiological conditions, or states of disease. As synthetic biology application we propose we propose the fully automated generation of synthetic or synthetically rewired network models by composition of metadata-guided automatically modified modules representing altered protein binding sites.

References

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