

Poster Abstract

Identification of Components and Modular Verification of Biochemical Pathways

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Biochemical pathways are abstract descriptions of the interactions among the molecular species involved in a cellular process. Different molecular species mentioned in a pathway often represent different states of the same biological entity, such as the unbound and bound states of a certain molecule. Hence, a pathway can be seen as a network of interactions between entities changing state synchronously by means of reactions. We consider such biological entities as *pathway components*.

We defined in [1] a semi-automatic algorithm based on the mass-conservation principle that allows the components of a pathway to be inferred from their interactions, namely from the chemical reactions constituting the pathway itself. The identification of molecular components allows formal descriptions of the pathway by means of automata or process algebra to be automatically generated. This enables the application of formal methods (such as model checking and bisimulation) to analyse and compare behaviours of pathways. Moreover, once the molecular components are identified, it is rather easy to perform syntactic transformations (projections) aimed at simplifying the visualization of the pathway by focusing on a subset of its components. Reduced models obtained through projection can also be used to perform formal verification of properties in an abstract or modular way.

The component identification algorithm has been tested extensively on all of the curated SBML models available of the BioModels database [2]. Moreover, component identification and modular verification based on projection has been applied to a model of the EGF signalling pathway [1, 3].

References

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