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# Faithful handling of concentration- and time-scale separation in logical models of chemical reaction networks

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## Résumé

The construction and analysis of various modelling frameworks plays a pivotal role in inferring or predicting the behavior of biological systems. Among the variety of modelling frameworks, logical modelling has been successful at recapitulating biological behaviors in several contexts (e.g., metabolic networks, gene regulatory networks). Despite its success, a limitation of logical models underlies the model construction process which heavily relies on the implicit assumptions integrated by the user. Thus, the modelling framework is prone to biological artifacts which could lead to dubious conclusions. Moreover, present are limited tools that can rigorously identify, verify and expose biological artifacts. Accordingly, we propose the abstract interpretation framework as a tool to reason on formal relationships among several description of a same system at different level of granularities, hence explicating the underlying assumptions. Thus, an objective is to utilize formal methods to guide the automatic construction of qualitative models; and, to further refine the modelling process by rigorously testing sets of user-oriented assumptions to the mathematical structure arising from logical models. A case study for concentration- and time-scale separation in chemical reaction networks will be presented as a proof-of-principle to the capabilities of abstract interpretation techniques in biology.

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