Concurrent biological pathways from rule-based models

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Résumé

Rule-based modelling allows the construction of large models of molecular interactions by alleviating combinatorial complexity. As such models grow in size, they become increasingly difficult to understand. Namely, knowing which events lead to an observable of interest during the execution of a model can be non-trivial.
Causality analysis can be performed with the Kappa software suite [1] to provide compressed stories [2] that explain the occurrence of an observable of interest. Such stories are given in the form of configuration graphs [3] which unambiguously display concurrency. Although extremely informative, configuration graphs are very different from how biologists typically represent molecular systems. Biological pathways rather conflate all the possible paths to an observable of interest into a single graph at the expense of concurrency information.

In this work, a method is proposed to produce concurrent biological pathways. Using intermediary nodes to group concurrent edges together, a series of configurations is folded into a single graph which preserves concurrency information. Since the resulting graph may admit many different orderings of events, ranking conventions are defined to select a unique order. Though not completely equivalent, the pathway obtained is reminiscent of a Petri net that would have been filtered and ordered towards the chosen observable of interest.

Finally, some information about past dependency is lost by the folding operation. Future work will explore the possibility of recovering this information through an interactive use of concurrent biological pathways.

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