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Modelling patterns of gene regulation in the bond-calculus. (English) Zbl 1458.92039

Gupta, Ankit (ed.) et al., Proceedings of SASB 2018, the 9th international workshop on static analysis and systems biology, Freiburg, Germany, August 28, 2018. Amsterdam: Elsevier. Electron. Notes Theor. Comput. Sci. 350, 117-138 (2020).

Summary: The bond-calculus is a language for modelling interactions between continuous populations of biomolecular agents. The calculus combines process-algebra descriptions of individual agent behaviour with affinity patterns, which can specify a wide variety of patterns of interactions between the sites of different agents. These affinity patterns extend binary molecular affinities to multiway reactions, general kinetic laws, and cooperative interactions. In this paper we explore bond-calculus modelling of gene regulation at both the molecular and network levels. At the molecular level, we show how affinity patterns can succinctly describe the λ-switch, a prototypical example of cooperative regulation. Moving to the network level, we develop a general model of gene regulatory networks using affinity patterns and an expanded Hill kinetic law. We illustrate the approach with a specific example: the complex plant circadian clock. We analyse these models via the bond-calculus's differential equation and stochastic semantics, and validate our results against existing models from the literature.

For the entire collection see [Zbl 1448.92002].

MSC:

92C42 Systems biology, networks
92D10 Genetics and epigenetics

Keywords:

process algebra; gene regulation; biochemical networks; multiway

Software:

BIOCHAM; BioNetGen; Bio-PEPA; BlenX; PEPA; SpiCO; StochPy

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