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Quantitative Biology > Molecular Networks

Attribute Exploration of Gene Regulatory Processes

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(Submitted on 9 Apr 2012)

This thesis aims at the logical analysis of discrete processes, in particular of such generated by gene regulatory networks. States, transitions and operators from temporal logics are expressed in the language of Formal Concept Analysis. By the attribute exploration algorithm, an expert or a computer program is enabled to validate a minimal and complete set of implications, e.g. by comparison of predictions derived from literature with observed data. Here, these rules represent temporal dependencies within gene regulatory networks including coexpression of genes, reachability of states, invariants or possible causal relationships. This new approach is embedded into the theory of universal coalgebras, particularly automata, Kripke structures and Labelled Transition Systems. A comparison with the temporal expressivity of Description Logics is made. The main theoretical results concern the integration of background knowledge into the successive exploration of the defined data structures (formal contexts). Applying the method a Boolean network from literature modelling sporulation of Bacillus subtilis is examined. Finally, we developed an asynchronous Boolean network for extracellular matrix formation and destruction in the context of rheumatoid arthritis.

Comments:	111 pages, 9 figures, file size 2.1 MB, PhD thesis University of
	Jena, Germany, Faculty of Mathematics and Computer Science,
	2011. Online available at this http URL

- Subjects: **Molecular Networks (q-bio.MN)**; Computational Engineering, Finance, and Science (cs.CE); Logic in Computer Science (cs.LO); Logic (math.LO)
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