

AUTOMATIC BOOLEAN NETWORK SYNTHESIS TO MODEL CELL DIFFERENTIATION FROM SINGLE-CELL TRANSCRIPTOMICS

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Abstract: Our work addresses the synthesis of Boolean networks from constraints on their domain and emerging dynamical properties of the resulting network. The synthesis is expressed as a Boolean satisfiability problem, described as a logic program containing both the modelling formalism (Most Permissive Boolean network, MPBN) and the data on the biological process (static and dynamical knowledge : prior knowledge network, experimental measurement dynamics, observations on the reachable phenotypes depending on conditions?). We enable the modelling of processes implying bifurcations as in cell differentiation, thanks to the implementation of constraints in Answer-Set Programming that address the notion of trajectory (succession of changes in gene state), non-reachability (bifurcating event) and stability (differentiated cell). To illustrate the method, I present an application leveraging scRNA-seq data as dynamical knowledge for the modelling. This example notably shows that, by facing dynamical data with a large prior knowledge network, the method allows to retain the essential interactions to reproduce the behaviors.