ASSA-PBN: A Toolbox for Probabilistic Boolean Networks

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Abstract—As a well-established computational framework, probabilistic Boolean networks (PBNs) are widely used for modelling, simulation and analysis of biological systems. To analyse the steady-state dynamics of PBNs is of crucial importance to explore the characteristics of biological systems. However, large PBNs, which often arise in systems biology, may cause state-space explosion that will impede steady-state analysis. As a result, statistical methods remain the only feasible approach to solve such problems. We present ASSA-PBN, a software toolbox for modelling, simulation, and analysis of PBNs. ASSA-PBN provides efficient statistical methods with three parallel techniques to speed up the computation of steady-state probabilities. Moreover, particle swarm optimisation (PSO) and differential evolution (DE) for parameter estimation are employed to optimise the PBNs. In addition, in-depth analyses of PBNs, including parameter estimation, long-run influence analysis, long-run sensitivity analysis, and computation and visualisation of one-parameter profile likelihoods, are implemented in ASSA-PBN as well. The apoptosis PBN model is used as a case study to illustrate the main functionalities of ASSA-PBN and demonstrate its potentials on analysing biological systems modelled as PBNs.

Index Terms—Probabilistic Boolean networks, modelling, simulation and analysis of biological networks, discrete-time Markov chains, steady-state analysis, parameter estimation, long-run analysis.

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