

Demo Abstract

Software tools for analysing the chemical master equation

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I will demonstrate new software tools for analysing probabilistic properties of chemical systems. At Microsoft Research, we have been developing software built on domain-specific programming languages. A common modelling framework supports the Language for Biochemical Systems (LBS) and DNA strand displacement (DSD) programming languages. When models are specified such that low copy number variations are expected, analysis of the chemical master equation (CME) can describe the probability of the system being in a particular state over time. We have recently implemented a numerical solution algorithm for the CME, using adaptive step-size integration techniques (Runge-Kutta). In combination with a convenient graphical user interface, rapid probabilistic model exploration is possible, with visualizations for the stochastic mean and variance, and marginal distributions over time. I will introduce examples of approximate majority protocols and localized DNA strand displacement circuits.