Efficient stochastic sampling of first passage times for multi-scale simulations NAVODIT MISRA, RUSSELL SCHWARTZ, Carnegie Mellon University — Monte Carlo methods have become increasingly popular for simulating stochastic dynamics in biological systems. However, the standard Stochastic Simulation Algorithm (SSA) can become highly inefficient for multi-timescale problems, where important events occur in parallel and at a much slower rate than other relatively unimportant events. We present two new algorithms based on the spectral analysis of Continuous Time Markov Model (CTMM) graphs to accelerate sampling of rare events in SSA models. These methods are well suited for simulating a broad class of "stiff" reaction networks such as models of bond networks and nucleation-limited self-assembly in biological systems.

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