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"Error bound for piecewise deterministic processes modeling stochastic reaction systems"

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Review

This paper is concerned with numerical methods targeting continuous time Markov chains. This is the mathematical model of choice in computational systems biology when describing chemical kinetics and is a pure jump process over a certain discrete integer lattice which in continuous time keeps track of the number of molecules of each species.

The main tool used in the paper is the traditional description in terms of chemical master equations. The authors set out to prove an error estimate for certain piecewise deterministic approximations. The idea is that, when the molecule count is large, a certain deterministic approximation can be used, while species occurring in low copy numbers remain in the discrete and fully stochastic regime. The resulting description can then be understood as an approximate marginal distribution to the original master equation.

The main result of the paper is an error estimate which shows a linear convergence when measured in a certain scale parameter. As is usual with these types of considerations, a case not covered by the theory is when a low copy number species is affected by fast reactions since then the assumed scale separation does not hold. For practical

purposes, one should also note that the scaling parameter is a priori given for each problem and hence cannot be meaningfully changed.

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