

A new twist for the simulation of time varying chemical reactions and hybrid systems

Romain VELTZ, INRIA Sophia Antipolis, romain.veltz@inria.fr

Piecewise deterministic Markov processes (PDMP) [Dav84] are now heavily used in the modeling of biology [Bre14]. Yet, numerical methods rely on ad-hoc modifications [Rie13] of existing ODE solvers to cope with an integral equation. Solving this integral equation is indeed necessary to find the next jumping time. This is numerically inefficient especially in the case of stiff systems. Here, we report on a new trick to solve the integral equation by a change of time variable. This allows to use existing ODE solvers to simulate PDMP with great accuracy. Generalizations when the deterministic flow is generated by delay differential equations, PDE... or when jump process is delayed are provided. Several examples are given such as the forced Hodgkin-Huxley model with stochastic ion channels or the initiation of dendritic NMDA spikes.

References

- [Bre14] Paul C. Bressloff. *Stochastic processes in cell biology*. Springer, 2014.
- [Dav84] M. H. A. Davis. Piecewise-deterministic markov processes: A general class of non-diffusion stochastic models. *Journal of the Royal Statistical Society. Series B (Methodological)*, 46(3):353–388, January 1984.
- [Rie13] Martin G. Riedler. Almost sure convergence of numerical approximations for piecewise deterministic markov processes. *Journal of Computational and Applied Mathematics*, 239:50–71, February 2013.