Deterministic and stochastic models of circadian rhythms

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A simple model of circadian rhythms [3] is based on 16 chemical reactions involving genes, mRNA, and proteins. The standard deterministic model of chemical dynamics is based on the law of mass action and it yields a system of ordinary differential equations (ODEs) for concentrations. However, concentrations of certain species are often very low in biochemical systems. It is not exceptional to have just one or several molecules of a given species in the system. Consequently, the continuum description by ODEs fails and stochastic effects, such as the intrinsic noise, start to be significant.

Therefore, we model this biochemical system by stochastic simulation algorithms and compare it with the deterministic approach. We concentrate on the comparison of periods of oscillations. We investigate the system close to a Hopf bifurcation point and observe qualitative differences in the behavior of deterministic and stochastic models. Namely, in certain parameter regimes the stochastic models oscillates, but the deterministic one tends to a steady state. We analyze this phenomenon by tools developed in [1], [2].

References

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