

Modeling biological evolution using reaction networks

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Many biological experiments result in measurement data that describe the time evolution of certain processes, such as growth and decay. A common way to study such processes is to build a mathematical model in terms of differential equations. Certain classes of such models, mostly based on systems of ODEs can be obtained from chemical reaction networks using the mass action law. In such situations the reaction networks can be considered as a symbolic notation for the correspondent dynamical model. Such notation can be a helpful tool for the interpretation of the behavior of the biological process and for the understanding the intrinsic forces and interactions of the process. In this work we demonstrate this idea on several examples related to specific biological processes, notably bacterial growth and decay. The talk is based on joint work with colleagues R. Alt, M. Borisov, S. Dimitrov, A. Iliev and N. Kyurkchiev.

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