Multiscale Modelling and Simulation of Biological Processes

Chirstof Schütte *

The last decade of research has made it obvious that many cellular processes like gene expression and regulation or virus infection kinetics require stochastic chemical kinetics instead of deterministic descriptions. Experimental evidence indicates that significant stochastic fluctuations render deterministic models inadequate and require models and simulations based on the chemical master equation (CME). However, in many practical applications it is impossible to solve the CME directly due to its high dimensionality, and even Monte Carlo methods become tedious when the system dynamics include reaction processes on many different time scales or species with many different population levels. However, multiscale analysis shows that the evolution of species with high population levels can be approximated deterministically while very fast reactions can be averaged out. For this reason stochastic-deterministic hybrid algorithms have been constructed. The talk will report on recent development in this field. It will be outlined how such hybrid algorithms can be used in realistic scenarios including parameter estimation and how it may be possible to extend the approach to control problems in systems biology.

*Freie Universität Berlin