

Modeling and simulation of biological systems using stochastic algorithms

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Mathematical modeling and simulation methods are widely used to analyze the dynamics of biological systems. The square root law says that randomness or fluctuations is inversely proportional to square root of the number of particles regarded as an index of the system size. Biochemical species often occur in low copy numbers, participating in important processes such as cellular metabolism, regulation and signaling. The increase in randomness with reduction in number of these biochemical molecules is evident. Due to the occurrence of stochastic fluctuations of biochemical species in living systems, it is difficult to understand the biological systems. To analyze the stochastic dynamics of biological systems, user-friendly and effective tools are needed. Therefore, we have developed a java-based simulation environment for multi-time scale systems of which analytical solutions are not available without assumption or compromises. This work was supported by the Korean Systems Biology Research Program of the Ministry of Science and Technology and by the BK21 project.