Randomness is ubiquitous in nature. From single-molecule biochemical reactions to macroscale biological systems, stochasticity permeates individual interactions and often regulates emergent properties of the system. While such systems are regularly studied from a modeling viewpoint using stochastic simulation algorithms, numerous potential analytical tools can be inherited from...
statistical and quantum physics, replacing randomness due to quantum fluctuations with low-copy-number stochasticity. Nevertheless, classical studies remained limited to the abstract level, demonstrating a more general applicability and equivalence between systems in physics and biology rather than exploiting the physics tools to study biological systems. Here the Fock space representation, used in quantum mechanics, is combined with the symbolic algebra of creation and annihilation operators to consider explicit solutions for the chemical master equations describing small, well-mixed, biochemical, or biological systems. This is illustrated with an exact solution for a Michaelis-Menten single enzyme interacting with limited substrate, including a consideration of very short time scales, which emphasizes when stiffness is present even for small copy numbers. Furthermore, we present a general matrix representation for Michaelis-Menten kinetics with an arbitrary number of enzymes and substrates that, following diagonalization, leads to the solution of this ubiquitous, nonlinear enzyme kinetics problem. For this, a flexible symbolic maple code is provided, demonstrating the prospective advantages of this framework compared to stochastic simulation algorithms. This further highlights the possibilities for analytically based studies of stochastic systems in biology and chemistry using tools from theoretical quantum physics.

Data, horário e local:

19 de agosto de 2016, 16h

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