

Title: What is the correct Lagrangian description of stochastic gene dynamics?

Abstract:

Different Lagrangians have been used by quantitative biologists in computational studies of Waddington landscape dynamics—but only one of them should be correct, and identifying the correct Lagrangian is likely to provide a new theoretical way to view stochastic gene dynamics. In particular, Lagrangian descriptions of dynamical systems make explicit fundamental principles or symmetries; offer a number of powerful computational tools, including conservation laws and numerical schemes related to the least action principle; and, via Feynman's path integral, make the transition from deterministic to random dynamics intuitively clear. I will discuss some analytic and computational work attempting to reconcile some of the Lagrangians used in the literature, and describe how several consistency checks related to the Fokker-Planck equation suggest that none of them are completely correct. I propose a new Lagrangian as equivalent to stochastic differential equations-described dynamics, and explore its interpretation at both the average cell and single cell levels, as well as some possible underlying biological principles. Finally, I consider some ways that this proposed framework could be related to the chemical master equation, and sketch a possible grand analogy between physics and stochastic biology.