Stochastic Modeling in Single-Molecule Biophysics

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Abstract

Recent advances in nanotechnology allow scientists to follow a biological process on the individual molecule basis. These advances also raise many challenging stochastic modeling problems, because the experimental capability of zooming in on single molecules reveal that many classical models derived from oversimplified assumptions are no longer valid. In this talk we will look at two particular experimental discoveries: single-molecule Michaelis-Menten equations in enzymatic reactions, and subdiffusion in a single protein's conformational fluctuation; both strongly contradict the classical models. We will introduce models to explain these experimental findings, and explore the connection between the two phenomena.