Counting Photobleach Steps and the Dynamics of Bacterial Predators

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In this work, we develop a method based on MaxEnt that can be applied to FCS data from fluorophore-tagged proteins diffusing in the cell's complex environment. Although the FCS curves are often fit to anomalous diffusion models, we propose a biologically motivated alternative to explain how apparent anomalous diffusion arises in the cell. From our method we extract diffusion coefficient distributions which in turn let us determine how molecular crowding, fluorophore artifacts and affinity site binding contribute to the apparent anomalous behavior. We validate our method using actual experimental data from red fluorescent protein-tagged BZip transcription factor protein domains as they diffuse within different cellular environments. In addition, we explore the role of hydrodynamic interactions on the dynamics of bacterial predators. Our study shows that Bdellovibrio (BV) - a model predatory bacterium - is susceptible to self-generated hydrodynamic forces. Near surfaces and defects, these hydrodynamic interactions co-localize BV with its prey, and this may enhance BV's hunting efficiency