

Anomalous diffusion in biological crowded fluids: Stochastic modelling and first passage behaviors

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Over the past decades macromolecular diffusion in crowded cells has been investigated using various experimental methods. Recent advance of the single-particle tracking technique has enabled one to measure real-time trajectories of single molecules inside a cell. It has been shown by these experiments that at crowded circumstances particle diffusion often becomes anomalous, in which the mean-squared displacements (MSDs) of the particles grow nonlinearly with time. It is known that such anomalous diffusive motions can occur due to multiple physical origins, each of which producing a stochastically different diffusive process while sharing the same scaling law of MSD.

In this talk, I will explore recent theoretical studies combined with single-particle tracking experiments on anomalous diffusion in biological/artificial crowded fluids [1, 2, 3, 4]. By means of single-trajectory analysis tools, we study stochastic characters of experimentally obtained anomalous diffusive processes and identify an appropriate stochastic model for the process. It is shown that the stochastic characters of the crowding-induced anomalous diffusion are highly time-scale dependent as well as system-specific.

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