## Geometry-controlled fluctuation in obstructed diffusion

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Recent advance of the single-particle tracking technique has enabled one to access real-time trajectories of single molecules in various crowded fluids including the living cells. It has been shown that at such crowded circumstances usually the diffusion of particles not only becomes anomalous but also exhibits significant trajectory-to-trajectory fluctuation. It is a fundamental issue to quantify and to understand these fluctuation, in particular, for the purpose of establishing theoretical framework for the analysis of experimental data obtained from the single-particle tracking. In this talk, within this single-trajectory scheme, we deal with two distinct anomalous diffusion processes occurring in obstacle-crowded space. In the first part the diffusion on percolation clusters is discussed based on Monte Carlo simulation results. We show that the population of finite clusters gives rise to geometry-specific non-vanishing fluctuation in the time-averaged mean squared displacement (TA MSD) of individual trajectories and that the fractality of the accessible space at a percolation threshold renders the slow convergence to ergodicity for TA MSD. In the second part the lateral molecular diffusion in protein-crowded lipid membranes is studied based on molecular dynamics simulation results. We find that the membrane proteins completely change the stochastic character of lateral diffusion. Thus the correlated gaussian processes of the fractional Langevin equation model, identified as the stochastic mechanism behind lateral motion in protein-free membranes, no longer adequately describe the lateral diffusion in protein-crowded membranes. It is shown that individual lateral motion attains strong non-gaussianity as well as the significant spatiotemporal fluctuation due to the geometrical effect of the membrane proteins.