Abstract:

Conformational changes of biomolecules can be described as Markov processes on networks of discrete states representing minima of free energy landscapes. Network states for several types of membrane proteins and molecular motors are linked into cycles, and their reaction coordinates (represented by a "particle") jump between the cycle states predominantly in one direction with rare backward jumps occurring due to thermal fluctuations. Assuming that interactions of the particle with other degrees of freedom (other particles) cannot be neglected, we study times that it takes to complete one cycle. In particular, we compare mean times of cycle completion in and against the bias direction and show that they satisfy the universal inequality: Cycle-completion times in bias direction are never shorter than the ones against the bias. We discuss how the times depend on the interaction strength, cycle topology, quenched disorder, number of interacting particles, and check validity of our findings for two-dimensional models with canonical and grand-canonical particle reservoirs.