DNA flexibility at short length scales

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 Bending and twisting flexibility of the helix are essential to the DNA packaging in chromosomes, to the DNA-protein binding and to the formation of those transient local base pair openings along the chain which regulate DNA replication and transcription. Experimental advances in single molecule micro-manipulation techniques over the last decades have permitted achieving substantial knowledge of the DNA flexibility properties mostly by sampling the molecule response to applied mechanical deformations. Studies of DNA cyclization properties have also indicated that DNA maintains an intrinsic flexibility at length scales which are smaller than the typical persistence length thus questioning, at such scales, the applicability of traditional worm-like-chain models.

For short DNA molecules, all-atomistic simulations and mesoscopic models provide useful analytical tools as they can treat the helix at the level of the base pair and include those large fluctuational effects which shape the helix flexibility properties. We address these issues by reviewing a computational method, based on the path integral formalism, developed in the last years both for linear and circular helicoidal molecules [1-3]. The method is applied to a mesoscopic Hamiltonian which incorporates, for a helical molecule in a solvent potential, both the inter-strand hydrogen bond interactions and the intra-strand stacking interactions. The model also accounts for the bending and twisting fluctuations between adjacent base pairs along the molecules stack. The base pair separations are considered as trajectories in the path configuration space and the total partition function is computed by summing in the path space over a broad ensemble of base pair configurations consistent with the physical requirements of the model potential. Some recent results regarding the cyclization probabilities of molecules with about 100 base pairs [4] and the elastic response of short chains to external loads [5] are presented.

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