Polymer folding through active processes – implications for genome organization

The folding of polymers into specific conformations is a recurring theme among living cells. Equilibrium theories have long tackled this problem by invoking pairwise chemical affinities, which lead to relatively stable conformations with little thermal fluctuations. However, many processes in living cells and along the genome consume energy and are thus active. What are the implications of patterns of such active processes for polymer folding? To address this question, we idealize active processes as "athermal excitations": sequence-specific active random forces that can drive coherent polymer motion. Our analysis predicts that a local increase in activity (hence larger active forces) will induce bending and expansion of the polymer backbone, whereas decreased activity leads to straightening and contraction. Moreover, pairs of loci that exhibit correlated active (sub)diffusion will attract through effective long-ranged harmonic interactions, whereas anticorrelations lead to pairwise repulsion. Taken together, these nonequilibrium mechanisms can address a large shape space of steady-state polymer conformations, which show significant population heterogeneity and are only realized on average in the form of contact probabilities. These folding patterns could have important implications for the organization of chromatin—a large polymer consisting of DNA in complex with many proteins that can dissipate energy.