Complex Fluids Confined at the Nanometer Scale

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The goal of this NIRT is to develop a theoretical framework for describing the dynamics of fluids under extreme confinement; where the natural length scales become comparable to the confining dimensions. Such conditions are easily realized in biological systems where macromolecular fluids are naturally confined to nanoscales and in thin polymer films near the glass transition where the confinement length scales become comparable to the length scales of the dynamical heterogeneities. One of our aims is to explore the similarities between these two classes of systems.

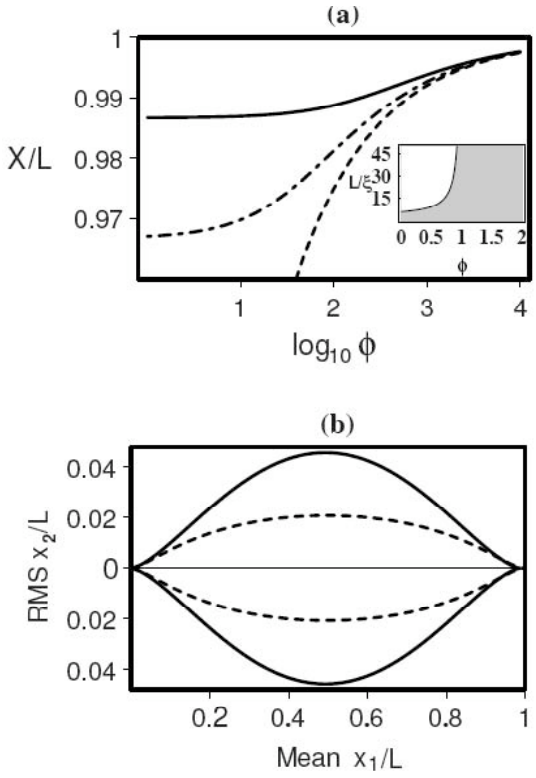

FIG. 1: (a)The relative extension of a polymer X/L pulled by a laser tweezer is plotted against reduced force $\phi = F\xi/kBT$ (ξ is the persistence length) for a short polymer (solid line). The dot-dashed line is the extension using a magnetic tweezer apparatus, while the dashed curve is the long chain result. The reduced polymer length is $L/\xi = 0.4$ (20 nm for DNA and 6μm for actin). In terms of force, $\phi = 1$ means 0.082 pN for DNA, and 0.27 fN for actin. (b) The shape of a polymer stretched with a laser tweezer is plotted parametrically in units of polymer contour length L for a short polymer ($L/\xi = 0.4$).

The project is currently focused on analyzing the properties of biomolecules under different conditions of confinement. A combination of analytical and numerical tools are being applied to study (a) the elasticity of DNA confined to two dimensions, (b) the mechanical properties of short, semiflexible polymers, (c) the dynamics of geometrically confined polymers, (d) the effect of hydrodynamic interactions on confined motion, and (e) developing models which can address the effects of cellular confinement on the polymerization dynamics of rigid polymers such as microtubules.

The mechanical properties of semi-flexible biopolymers are important for their biological functions. For example, DNA is packed tightly in eukaryotic chromosomes and in viruses, while acting and microtubules provide the scaffolding and structure for most animal cells.

In these cases the length scales at which the polymer properties of these macromolecules are of biological interest are comparable to their persistence length. Namely DNA packing typically involves loops of diameter less than its persistence length of 50 nm, and so does DNA looping induced by proteins such as the lac repressor, while actin is present in cells in the form of bundles and networks in which the typical length of the participating polymers is shorter

than its 15 μm persistence length. Experiments that probe the mechanical properties of semiflexible polymers usually involve stretching single molecules by means of laser tweezers, magnetic tweezers or by electric fields and hydrodynamic flows. These experiments differ in the way they treat the ends of the polymer molecule, which may be free or constrained in different ways. Using the worm-like-chain, the Kondev group has obtained exact results for the average end-to-end distance and shape of the polymer for boundary conditions that correspond to different single molecule stretching experiments. Their results demonstrate that differences in these boundary conditions produce measurable effects in the mechanical response of short polymers [2]. Hori, Prasad and Kondev have also computed exactly the force extension relationship for semiflexible polymers confined to two-dimensions. They have computed both the extension of the polymer due to an applied force at the chain end, and due to the influence of a nematic field [3].

Kondev's group has also proposed a theory of DNA diffusion when the polymer is confined to a supported lipid bilayer. The theory takes into account self-avoidance and hydrodynamic interactions between the chain monomers depending on the width of the supporting layer of diffusion. In the strong-screening regime the diffusion constant of DNA scales with the inverse of its length. This result is confirmed by experiments. In the weak-screening regime the diffusion constant is typically an order of magnitude larger and it scales only logarithmically with the DNA length. Prasad, Hori and Kondev have proposed experiments that would test the theory in this regime[4].

Using numerical simulations, the Chakraborty-Kondev group has been investigating the dynamics of a single polymer chain confined by rigid walls. In a Brownian dynamics simulation, a bead and spring model of a polymer has been confined to a sphere to mimic the effects of cellular confinement and the resultant dynamics has been explored. In this context, analytical results for a Gaussian chain confined by a parabolic potential is being used to predict the diffusion properties of individual monomers. This simple model, which is exactly solvable, can provide a framework for understanding simulation and experimental results. In collaboration with Claudio Chamon, the Brandeis group is in the process of constructing a field theory appropriate for describing the dynamics of a polymer confined by a parabolic potential when the self-avoidance property of a polymer is taken in to account.

Intuitively, one expects the effects of excluded volume (self-avoidance) to be enhanced by confinement. In order to explore the effects of self-avoidance, confinement and flexibility on the dynamics of a polymer, we have adopted the bond-fluctuation algorithm, which represents the polymer as a lattice walk but with fluctuating bond lengths. This algorithm proposed in 1988 by Carmesin and Kremer faithfully reproduces Rouse dynamics and has also been used to study the crossover from Rouse to reptation. Our emphasis is on using these simulations to provide the stepping stones for constructing effective theories of dynamics under crowding and confinement. One interesting question that we are currently investigating is whether the dynamics of a single polymer confined to a certain volume by rigid walls is similar to that of a polymer in a crowded environment where there is a certain ``effective'' volume available to it. The difference between dimensional reduction as for example a polymer confined between two parallel plates and confinement where the polymer is confined to a box of size comparable to its radius of gyration are also being investigated in order to develop a notion of weak and strong confinement

and to compare and contrast the situations relevant to glass transition in thin polymer films and the environment of a biological cell.

When an active biological entity moves through a cell, membrane or other confined region, it may use the hydrodynamic properties of the surrounding fluid to pull passive cargo with it. We aim to study how this "biological hydrodynamic entrainment" may occur. Reichman and collaborators have developed a method to simulate the full, many-body hydrodynamic forces that act on irregularly shaped bodies. As a first example, this approach has been applied to study the phase separation and gelation in colloidal systems and it has been shown that in the confined case (2d) cellular structures may be stabilized for long periods of time leading to transient gelation. Without the intervening fluid (namely without hydrodynamics) this effect is absent.

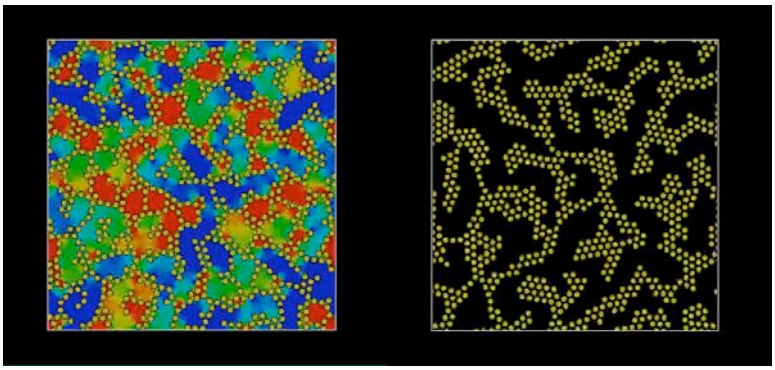

Fig 2. Snapshots of aggregating particles in a colloidal dispersion with (left) and without (right) hydrodynamic interactions. Here the volume fraction of particles is 0.338 (N=400). The background color in represents the pressure of the fluid. Blue and Red correspond to low and high pressure, respectively (Figure courtesy David Reichman).

The Chakraborty group has been investigating a microscopic model of microtubule dynamics. Microtubules are hollow cylindrical polymers that support the overall structure of cells and control fundamental cellular processes through a dynamical instability involving alternating polymerization and depolymerization. Preliminary results show a crossover from a bounded to an unbounded growth regime in the polymerization dynamics [5]. The distribution of microtubule breakup times broadens as one approaches the unbounded growth regime leading to a divergence of the average breakup time. The attractive aspect of this particular model is that it describes the dynamics at the protofilament level and, therefore, can investigate the impact on the microtubule dynamical instability of changes in structural properties such as the weakening of links between protofilaments and confinement as well as that of changes in external parameters such as temperature and tubulin concentration which can affect the dynamics in a single protofilament.

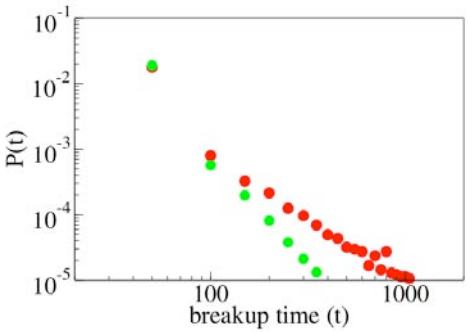

Fig 2. Distribution, P(t), of the time t between nucleation and breakup of a protofilament. The red circles represent data taken close to the phase boundary separating unbounded growth from bounded growth.

References

[1] For more information about this project email **bulbul@brandeis.edu**
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