their dysregulation in disease. However, the molecular mechanisms that drive these phase transitions, the biophysical properties of the resulting droplets, and the way their properties impact biological function, remain poorly understood. Here, we focus on LAF-1, an essential DEAD-box RNA helicase associated with P granules in the C. elegans germline. We find that purified LAF-1 can phase separate into liquid droplets at near physiological (low μM) concentrations. LAF-1 droplet formation is driven by its disordered N-terminal RGG domain, which is both necessary and sufficient for droplet formation. We combine microrheology, FRAP, and single molecule imaging approaches to reveal the local viscoelastic properties and molecular dynamics inside the droplets. Our results provide mechanistic and structural insight into the phase transition-driven assembly of liquid-like organelles, and suggest that the biophysics of intracellular phase separation can sensitively control molecular dynamics and function.

DNA Structure and Dynamics I

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Unfolding of Nanoconfined Circular DNA

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Nanofluidic channels have become a versatile tool to manipulate single DNA molecules. They allow investigation of confined single DNA molecules from a fundamental polymer physics perspective as well as for example in DNA barcoding techniques.

Circular DNA is of interest since it is found in many biologically relevant contexts, such as bacterial plasmids, viruses and eukaryotic mitochondrial DNA. Furthermore, the circular topology forces two strands in close proximity to each other in nanochannel, which changes the polymer physics compared to linear DNA. Circular DNA is difficult to study with traditional single molecule techniques because such techniques generally require the attachment of handles to the, but is readily accessed using nanofluidics.

Circular DNA has less entropy and higher conformational free energy than in its unfolded configuration. Therefore, as a double-strand break occurs and circular DNA opens up, it unfolds to its linear configuration inside the nanochannel. This study compares the static properties of confined linear and circular DNA as well as investigates the dynamics of the transition from circular to linear DNA as a double-strand break occurs.

We observe that the difference in extension between the circular and linear configurations depends on the degree of confinement, which we confirm with theoretical predictions. Our data for unfolding of the circular DNA to the linear configuration suggests that hydrodynamic friction between the DNA and the solvent is the main rate-determining factor but that DNA-DNA contacts are also important. Finally, by staining the DNA inhomogeneously, we can follow the local dynamics of the DNA as the folding occurs and conclude, for example, how the two different strands move relative to each other during the unfolding process. We are thus able to study the dynamics of confined DNA with unprecedented resolution and obtain completely new information about confined polymers.

1161-Pos Board B112

Supercoil Diffusion along Stretched DNA by Brownian Dynamics

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The dynamics of DNA supercoils are intimately connected to several fundamental cellular processes. Transcription is a prime example. While the rate of transcription is sensitive to the level of supercoiling, transcription produces positive (and negative) supercoils ahead of (and behind) RNA polymerase. Subject to thermal fluctuations and DNA-protein interactions, supercoils are dynamic structures which accumulate, rearrange, translocate, and dissipate. Recent single molecule studies have observed the dynamic formation, diffusion, hopping, and dissipation of supercoils. Here, we employ Brownian dynamics simulations of a discrete worm-like chain to build understanding beyond that provided by recent experimental efforts. Our computational model accounts for hydrodynamic interactions, thermal fluctuations, bending, torsion, extension, and electrostatics in stretched DNA. We perform many simulations including trajectories representing 21 kilobasepairs of supercoiled DNA over the course of about 500 ms. We observe several metrics describing the dynamics of supercoils, including: the average number of supercoils, their lifetime, first juxtaposition time, and diffusion constants. In addition, we explore the sensitivity of these quantities to DNA extension as well as sequence dependence (through the introduction of sites with elevated DNA flexibility).

1162-Pos Board B113

Analysing Small DNA Constructs via a Chromophore Model within the Point Dipole Approximation

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As all the genetic information contained within DNA is buried within the duplex helix, there must be a series of breathing fluctuations that expose the nucleic bases to aid roles like replication, transcription, and repair. The work presented here uses a classical chromophore model under the point dipole approximation to calculate the circular dichroism as well as the absorption spectra of oligonucleotides at individual conformational states. This analysis will aid in the evaluation of these breathing fluctuations by treating systems of dimers and small length oligonucleotides as local models of these fluctuations.

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CHARMM Drude Polarizable MD Simulations Reproduce Solution X-Ray Diffraction Patterns for B-DNA Sequences and Predict Differential Impact of the Li^+, Na^+, K^+ and Rb^+ Ions on DNA Conformational Properties

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Recently we have presented the first generation CHARMM Drude polarizable force field for DNA, which is capable of reproducing the main conformational features of DNA in solution, such as A-to-B equilibrium and transitions between BI and BII substates. Our current efforts are directed towards further model improvement, by achieving a proper balance of the interactions among surrounding mobile ions, water and DNA. Compared to the additive (non-polarizable) models, explicit treatment of the electronic polarizability in the Drude model leads to a markedly improved description of the interplay between the ionic atmosphere and DNA conformational behavior. In particular, the Drude model is shown to more accurately reproduce counterion condensation theory predictions of DNA charge neutralization by condensed ions, as well as the experimental data on the competitive binding of Li^+, Na^+, K^+ and Rb^+ ions to DNA. The most intriguing results is that the model predicts a differential impact of these seemingly similar monovalent cations on DNA conformational properties - a phenomenon not observed in the state-of-the-art CHARMM36 and AMBER atomistic additive models. In addition, the Drude model reproduces the solution X-ray diffraction patterns for a number of B form DNA sequences at a level of accuracy similar to, or exceeding that of the above mentioned additive models. The obtained results indicate that CHARMM Drude polarizable MD simulations provide a more realistic model of the physical forces involved in the interactions of DNA with its ionic environment, offering the potential to yield new insights into salt-mediated biological processes involving DNA, such as protein-DNA recognition and chromatin folding.

1164-Pos Board B115

Molecular Modeling and Simulations of DNA at Graphene-Water Interfaces towards Developing Biosensors and Drug Delivery Vehicles

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The biocompatibility of Graphene oxide (GO) surfaces and their preferential affinity to single stranded DNA (ssDNA) over double stranded DNA (dsDNA) make GO-ssDNA complexes an attractive target for drug delivery applications. GO-ssDNA complexes also hold promise as biosensors: fluorescence can be achieved by desorption of fluorescently tagged ssDNA from GO surfaces by their complementary strands or DNA-binding proteins in solution. To tune nucleic acid sequences for targeting specific molecules, and to achieve high sensing abilities, it is important to quantify the interaction of individual nucleobases (A, T, G & C) and small oligonucleotides with GO or graphene surfaces, and understand the molecular mechanisms involved. Although experimental studies in the past (ITC, AFM) have focused on graphene-nucleobase interaction in water, and a few theoretical studies have focused on the same interaction in vacuum, a quantitative understanding of graphene-nucleic acid interaction still remains elusive. To this end, we performed molecular dynamics simulations, guided by dispersion-corrected density functional theory (DFT) and ITC experiments, to accurately quantify and understand the molecular mechanism of nucleobases and nucleosides binding to graphene surfaces in water. As