substantial variations in intensity in our observed molecules at the higher ethanol concentrations are (i) suggestive of the higher order DNA conformations such as loops and toroids that have been observed in DNA dried on mica surfaces and (ii) in accord with the observation that the effective persistence length of DNA is reduced in ethanol solutions.

2426-Pos

Local Conformation of Confined DNA Studied using Emission Polarization Anisotropy

Fredrik Persson[1], Fredrik Westerlund[1], Anders Kristensen[2], Jonas O. Tegenfeldt[1].
[1]Gothenburg University, Gothenburg, Sweden, [2]Technical University of Denmark, Kongens Lyngby, Denmark.

When confined in nanochannels with dimensions smaller than the DNA radius of gyration, DNA will extend along the channel. We investigate long DNA confined in nanochannels, using fluorescence microscopy and intercalated dyes. Studies of the dynamics and statics of DNA in such nanoscale confinements as a function of e.g. degree of confinement and ionic strength have yielded new insights into the physical properties of DNA with relevance for applications in genomics as well as fundamental understanding of DNA packaging in vivo. Our work extends the field by not only studying the location of the emitting dyes along a confined DNA molecule but also monitoring the polarization of the emitted light. By measuring the emission polarized parallel and perpendicular to the extension axis of the stretched DNA, information on the local spatial distribution of the DNA backbone can be obtained. Comparing polarizations in two directions for DNA confined in channels of effective diameters of 85 nm and 170 nm reveals a striking difference. Whereas the DNA in the larger channels shows an isotropic polarization of the emitted light, the light is to a large extent polarized perpendicular to the elongation of the DNA in the smaller channels. We expect this technique to have a large impact on the studies of changes in DNA conformation induced by protein binding or during DNA compactation as well as in fundamental polymer physics studies of DNA in confined environments, for example in bacterial spores and viruses.

2427-Pos

Structure and Thermodynamics of ssDNA and dsDNA Near a Surface: a Coarse Grained Approach

Joaquin Ambia Garrido, Montgomery Pettitt.
University of Houston, Houston, TX, USA.

In the last two decades, new technologies have allowed us to measure properties of single DNA molecules in very accurate ways. At the same time, a number of theoretical models have been developed to understand the behavior of single stranded and double stranded DNA. These models have been shown to be accurate and relatively simple for very short systems of 6-8 base pairs. Comparatively less is known about the influence of a surface on the secondary structures of longer molecules important to many technologies. To gain insight into this situation we modeled DNA as a discretized worm-like chain; each link is considered a sphere of 6 base pairs in length for dsDNA and 1.5 bases for ssDNA. The chain is tethered to a surface by a fixed length, non-interactive 1 nm linker. Configurational sampling was achieved via Monte-Carlo sampling. Results on the average tilt are in agreement with all atom simulations. New insights into polyelectrolytes near surfaces are shown.

2428-Pos

Mechanical Constraints on Confined DNA

Benoît Knecht.
University of Heidelberg, Heidelberg, Germany.

A confined DNA molecule adopts various conformations, driven by entropy and constrained, in particular, by excluded volume interaction. But DNA also has some specific mechanical characteristics, such as twisting and bending elasticity. These properties influence the way DNA compacts itself inside the confined space, by favoring some conformations and impeding others. This situation is notably observed in E. Coli cells. Our model allows to simulate long polymer chains with given twist and bend elasticity constants, using the Monte Carlo method. Generating conformations with various twisting and bending rigidity gives detailed information on how DNA could be organized in such cells. By tuning the model with data from experiments on DNA mechanical properties, it becomes possible to make predictions on the DNA structure inside the cell nucleus.

2429-Pos

Self Organization in DNA-Loop-Extruding Enzymes

Elnaz Alipour-Assiabi, John F. Marko.
Northwestern University, Evanston, IL, USA.

We consider DNA-organizing molecular machines consisting of two coupled and oppositely directed motors which act to extrude loops from the double helix that they move along, while excluding one another sterically. In the case where these machines do not dissociate from the DNA (infinite processivity), the steady-state loop distribution is exponential and is described by an effective statistical-mechanical ensemble. However, if enzyme dissociation-rebinding occurs at any finite rate (finite processivity), the steady state qualitatively changes to a highly ordered "stacked" configuration with suppressed fluctuations, with tight hairpin-like condensation of the underlying DNA. This steady-state behavior can be understood via an approximate mapping to the restricted solid-on-solid model in an external field. Possible experimental realizations of these types of molecular machines are discussed, with a focus on type I restriction enzymes and condensin complexes.

2430-Pos

A Generalized Theory of DNA Cyclization and Loop Formation

David P. Wilson[1], Todd Lillian[1], Alexei Tkachenko[2], Noel C. Perkins[1], Jens-Christian Meiners[1].
[1]University of Michigan, Ann Arbor, MI, USA, [2]Brookhaven National Laboratory, Upton, NY, USA.

We have developed a semi-analytic method for calculating the Stockmayer Jacobson J-factor for protein mediated DNA loops, as well as DNA ring cyclization. The formation of DNA loops on the order of a few persistence lengths is a key component in many gene regulatory functions. The binding of LacI protein within the Lac Operon of E.coli serves as the canonical example in which loop regulated transcription is understood. This fundamental looping motif consists of one protein simultaneously bound to two DNA operator binding sites. We explore as inputs the effect of sequence-dependent curvature and elasticity on the formation of DNA loops by constructing a Hamiltonian describing thermal fluctuations about the open and looped states. These fluctuations allow us to compute the entropic cost of loop formation, and thus allow a full computation of the free energy. Our work demonstrates that even for short sequences of the order one persistence length, entropic contributions are required to correctly compute the J factor.

We determine the lowest energy shape of the inter-operator DNA loop using a non-linear mechanical rod model under prescribed binding topologies (e.g, parallel and anti-parallel binding). Expanding about this shape allows us to calculate the J factors associated with parallel and anti-parallel binding topologies within the Lac system, and thus how entropy influences the most energetically favorable topology. The J factor can be used to compare the relative loop lifetimes of various DNA sequences, making it a useful tool in sequence design. Our work also allows the computation of an effective torsional persistence length, which demonstrates how torsion bending coupling affects the conversion of writhe to twist.

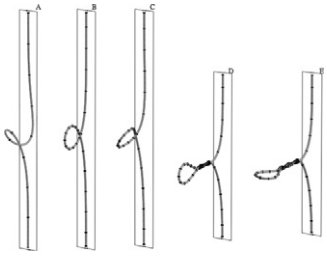
2431-Pos

Theory for the DNA Supercoiling Transition in Extension-Rotation Experiments

John F. Marko[1], **Sebastien Neukirch**[2].
[1]Northwestern University, Evanston, IL, USA, [2]UPMC Univ Paris 6, Paris, France.

Extension jumps were recently observed in single-molecule experiments where a DNA molecule (few kbp long) is held under tension while its ends are slowly rotated. For low rotation the molecule is believed to adopt (disordered) straight configurations and when a rotation threshold is reached the molecule jumps into a supercoiled phase: plectonemes arise. The transition is not continuous: the end-to-end extension of the molecule experiences an abrupt decrease.

We develop a theory where we compare the free-energies of the straight and supercoiled states. Care is taken with the energy of the supercoiled state where bending and twist energies for the plectonemes tip and the region joining the plectonemes and the ends of the molecules are included.



We find that the free energies of the straight and supercoiled states cross for a value n* of the imposed rotation. The extension jump is then given by the difference between the extension of the two states. Theoretically computed values compare well with experimental data.