BP 58: DNA & RNA

Time: Friday 9:30–10:45 Location: ZEU 250

BP 58.1 Fri 9:30 ZEU 250

Interactions between a short DNA oligonucleotide and urea in the light of Kirkwood-Buff theory: a Molecular Dynamics simulation study — •Ewa Anna Oprzeska-Zingrebe and Jens Smiatek — Institute for Computational Physics, University of Stuttgart, Stuttgart, Germany

In nature, a wide range of biological processes, such as transcription termination or intermolecular binding, is dependent on the formation of specific DNA secondary and tertiary structures. These structures can be both stabilized or destabilized by the osmolytes, coexisting with the nucleic acids in the cellular environment. In our study, we investigate a simple 7-nucleotide DNA hairpin with the sequence d(GCGAAGC) in the presence of varying concentrations of urea.

The interaction between DNA and urea in unbiased molecular dynamics simulations has been analysed according to Kirkwood-Buff theory. We implemented the local/bulk partitioning model, complemented by the analysis of preferential hydration and preferential interaction coefficients, to get insight into the distribution of the cosolute in the vicinity of the DNA oligonucleotide. The free energy landscape of unfolding has been approached via Metadynamics upon the addition of a bias potential. This study allows us to get a more comprehensive understanding of the stability of the DNA structures in the presence of urea.

BP 58.2 Fri 9:45 ZEU 250

Dynamic Organization of Bacterial Chromosome by SMC Condensin — •Christiaan Adrianus Miermans and Chase Broedersz — Arnold-Sommerfeld Center for Theoretical Physics, Ludwig-Maximilians Universität München

The bacterial chromosome is highly structured across a wide range of length-scales, extending up to the full length of the genome. Recent Hi-C experiments provide evidence for anomalously high contacts between opposite pairs of DNA loci – millions of basepairs apart – on the left and right chromosome arms. These striking long-range contacts in Hi-C contact maps have been attributed to a variety of nucleoid-associated proteins, including the highly conserved ATPase SMC condensin. Although the microscopic structure of these ATPases has been mapped in detail, how SMC condensins are able to effect these long-range chromosomal contacts in living cells remains an open question. We present a minimal model for the physical mechanisms for the large-scale DNA organization by SMC condensin. Our simulations indicate that condensin is not able to generate long-range DNA-DNA contacts under equilibrium conditions. In contrast, the inclusion of non-equilibrium dynamics in our model for condensin-DNA interactions gives rise to robust long-range chromosomal contacts. Taken together, our model suggests a novel mechanism for how protein-DNA interactions can dynamically drive chromosome organization in bacteria.

BP 58.3 Fri 10:00 ZEU 250

Chromosomal Organization by an Interplay of Loop Extrusion and Compartment Interaction — •Johannes Nuebler, Geoffrey Fudenberg, Maxim Imakaev, Carolyn Lu, Anton Goloborodko, Nezar Abdennur, and Leonid Mirny — Institute for Medical Engineering and Science, Massachusetts Institute of Technology (MIT), Cambridge, MA 02139, USA

The chromatin fiber in eukaryotic nuclei is far from being simply a confined but otherwise randomly arranged polymer. Rather, it shows a high degree of spatial organization on all length scales, from nucleosomes up to segregated chromosome territories. On intermediate scales, chromosome conformation capture techniques have revealed two ubiquitous modes of organization: an alternating compartment structure, where each type preferentially associates with other loci of its type, and topologically associating domains (TADs) with increased association within each domain but not across boundaries. The mechanisms behind this organization are only beginning to emerge. While a block-copolymer model is a natural starting point for the compartment structure, TADs may be more consistent with the active mechanism of loop extrusion. We review how this can explain in a unified way such diverse phenomena as TADs, DNA loops and mitotic compaction and segregation. We study in particular the interplay of active loop extrusion and a block-copolymer. We discuss consistency with recent experiments that interfere with the loading of the proposed loop extrusion factor cohesin.

BP 58.4 Fri 10:15 ZEU 250

A macromolecular crowding study of RNA folding and activity: polymer pore size matters! — •Richard Börner[1], Erica Fiorini[1], Michael Kovermann[2], and Roland K.O. Sigel[1] — [1]Department of Chemistry, University Zürich, Zürich, Switzerland — [2]Department of Chemistry, University Konstanz, Konstanz, Germany

Ribozymes are catalytic RNAs requiring a high magnesium(II) concentration to show folding and function in vitro (1,2). In contrast, in vivo conditions are characterized by a highly crowded cellular environment and much lower ion concentration. Molecular crowding agents are used to mimic the cellular crowding. However, particular physical/chemical properties explaining the crowders influence are poorly understood. In this study, we gain new insights on how polymer properties like viscosity, pore size etc. influence the activity and folding of a group II intron RNA (3,4). We combined bulk activity assays, sm-FRET experiments and NMR screening PEG volume fraction (%) and molecular weight (MW) and unveiled an optimal pore size in terms of the catalytic activity.

(1) Börner R, Kowerko D, Guisett-Miserach H, Schaffer MF, Sigel RKO. (2016) Coord .Chem. Rev. 327-328:123-142. (2) Steiner M, Karunatilaka KS, Sigel RKO, Rueda D. Proc. Natl. Acad. Sci. U.S.A. (2008) 105:13853. (3) Fiorini E, Börner R, Sigel RKO. (2015) Chimia. 69(4):207. (4) Fiorini E, Paudel B, Börner R, Rueda D, Sigel RKO. (2016) submitted.

BP 58.5 Fri 10:30 ZEU 250

Organization of Nucleotides in Different Environments: Implications for the Formation of First RNA under Prebiotic Conditions — •Sebastian Himbert[1,2] and Maikel Rheinstädter[1] — [1]Department of Physics and Astronomy, McMaster University, Hamilton, ON, Canada — [2]Department of Experimental Physics, Saarland University, Saarbrücken, Germany

How nucleic acids first assembled and then incorporated into the earliest forms of cellular life 4 billion years ago remains a fundamental question of biology. There has been no obvious way for RNA-like molecules to be produced and then encapsulated in cellular compartments in the absence of enzymes and metabolism. To support the hypothesis that environmental conditions in the neighbourhood of volcanic hydrothermal springs could act to organize monomeric nucleotides through various noncovalent interactions and chemical reactions in the prebiotic era, we investigated 5'-adenosine monophosphate (AMP) and 5'-uridine monophosphate (UMP) molecules captured in different matrices that have been proposed to promote polymerization [1]. Two nucleotides signals were observed in our X-ray diffraction experiments, one corresponding to a nearest neighbour distance of around 4.6 Å attributed to nucleotides that form a disordered, glassy structure. A second, smaller distance of 3.45 Å agrees well with the distance between stacked base pairs in the RNA backbone, and was assigned to the formation of pre-polymers, i.e., the organization of nucleotides into stacks of about 10 monomers. [1] S. Himbert et. al., Scientific Reports, 6, 31285 (2016).