BP 35: The Collapsed State of Polymers: From Physical Concepts to Applications and Biological Systems (Symposium SYCP, joint CPP/BP/DY)

Time: Thursday 9:30–12:15 Location: HSZ 02

Invited Talk BP 35.1 Thu 9:30 HSZ 02

Why do polymer collapse and polymer topology frustrate each other — •Alexander Y. Grosberg — Department of Physics and Center for Soft Matter Research, New York University, NY, USA

Polymer topology is most commonly studied in the context of a melt or concentrated solution. Here, the role of topological constraints is discussed in the context of a single chain swelling or collapse behavior, both in kinetics and in equilibrium (the latter in case topology is quenched, one way or another). Biological aspects are discussed in the context of both chromatin and proteins.

Invited Talk BP 35.2 Thu 10:00 HSZ 02

Nanoscopy of nuclear Genome Structure — •Christoph Cremer — Institute of Molecular Biology (IMB), D-55128 Mainz — Kirchhoff-Institute of Physics (KIP) University Heidelberg, D-69120 Heidelberg — Institute of Pharmacy and Molecular Biotechnology (IPMB) University Heidelberg, D-69120 Heidelberg

Numerical models as well biochemical data indicate a decisive functional role of genome nanostructure; but due to the conventional resolution limits of far-field light microscopy, direct light microscopic tests of such models were believed to be impossible. However, novel developments in optical technology and photophysics succeeded to radically overcome these conventional limits. With such"superresolution" techniques, it has become possible to analyze nuclear genome structure with a greatly enhanced light optical resolution down to a few tens of nanometer. Application examples will be presented on the use of such "nanoscopy" procedures to measure in cell nuclei the size of individual small chromatin domains, of replication and transcription complexes, as well as the spatial distribution of individual nuclear proteins and of short specifically labelled DNA sequences. It is anticipated that the wealth of nanoscale information on nuclear genome nanostructure accessible by the novel superresolution approaches will substantially contribute to the theoretical understanding of the folding in space and time of the huge polymers called chromosomes, and its functional consequences.

Invited Talk BP 35.3 Thu 10:30 HSZ 02

Blood Clotting Inspired Polymer Physics — •Alfredo Alexander-Katz — Massachusetts Institute of Technology

Nature has devised creative and efficient ways of solving complex problems, and one of these problems is that of blood clotting in flowing conditions. In fact, nature has used a novel combination of polymer physics and chemistry that enhances the self-healing propensity of a vessel when strong flows are present while avoiding coagulation when the flow is diminished, a rather counter-intuitive phenomenon. Underlying this process is a globular biopolymer, the so-called von Willebrand Factor, whose function is strongly regulated by flow. In this talk I will present our work on this macromolecule starting from the single molecule approach and building up to the multi component system that more closely resembles blood. I will emphasize how new concepts have emerged from trying to understand such a complex system, in particular I will show how these polymers can display giant non-monotonic response to shear, as well as a very large propensity to form polymer-colloid composites in flow while being a stable dispersed suspension in quiescent conditions. In fact, the aggregation behavior is universal and can be explained with simple scaling arguments. These novel concepts and results are in principle not unique to blood clotting and can have important ramifications in other areas.

15 min. break

Invited Talk BP 35.4 Thu 11:15 HSZ 02

Modeling dynamic spatial genome organization in yeast — •Christophe Zimmer — Institut Pasteur, 25 rue du Docteur Roux, 75015 Paris

The spatial organization and dynamics of chromosomes plays important roles for gene expression, DNA repair and replication, but its underlying principles remain poorly known. We will present quantitative experimental data and simulation results showing that the territorial organization the interphase yeast nucleus and the dynamics of chromosomes can be largely predicted by a model based on generic polymer physics with a minimal set of DNA sequence-specific constraints and assumptions. We will also discuss extensions of our budding yeast model to other organisms and address implications of this model for a quantitative understanding of DNA repair.

Invited Talk BP 35.5 Thu 11:45 HSZ 02

Ring polymers in the melt state: the physics of crumpling — •Ralf Everaers[1] and Angelo Rosa[2] — [1]Laboratoire de Physique et Centre Blaise Pascal, ENS Lyon, CNRS UMR5672, 46 allée d'Italie, 69364 Lyon, France — [2]SISSA - Scuola Internazionale Superiore di Studi Avanzati, Via Bonomea 265, 34136 Trieste (Italy)

The conformational statistics of ring polymers in melts or dense solutions is strongly affected by their quenched microscopic topological state. The effect is particularly strong for non-concatenated unknotted rings, which are known to crumple and segregate and which have been implicated as models for the generic behavior of interphase chromosomes. Here we use a computationally efficient multi-scale approach to identify the subtle physics underlying their behavior, where we combine massive Molecular Dynamics simulations on the fiber level with Monte Carlo simulations of a wide range of lattice models for the large scale structure. We show that (i) topological constraints may be neglected on scales below the standard entanglement length, L_e, (ii) that rings with a size $1 \leq L_r/L_e \leq 30$ exhibit nearly ideal lattice animal behavior characterized by primitive paths which are randomly branched on the entanglement scale, (iii) that larger rings are weakly swollen relative to ideal lattice animals with gyration radii $\langle R_g^2(L_r)\rangle \propto L_r^{2\nu}$ and $\nu \approx 1/d > 1/4$, and (iv) that ring melts can be *quantitatively* mapped to coarse-grained melts of *interacting* randomly branched primitive paths.