BP 7: Fibers and Bundles

Time: Monday 16:15–18:00 $\hspace{8cm}$ Location: H44

BP 7.1 Mon 16:15 H44

Finite bundle size in reconstituted cyotskeletal systems — •MIREILLE CLAESSENS and ANDREAS BAUSCH — TUM, Physik Department E22, James Franck Straße, D-85747, Garching

In the presence of non-adsorbing polymer and/or multivalent counterions charged biopolymers such as F-actin, microtubules, or DNA have been reported to form an equilibrium phase of bundles with a well defined thickness. Even in vivo actin bundles formed by specific actin binding proteins (ABPs) appear with well defined diameters. The stabilization mechanism of such bundles is proposed to be similar to that of equilibrium colloid clusters; steric and short range electrostatic interactions or frustration within the bundles probably prevent charge neutralization and force the equilibrium bundle size to be finite.

We show that in the presence of the specific actin binding protein fascin actin filaments organize into bundles with well defined number of filaments in vitro. The total thickness is defined by the concentration of fascin and limited to a maximal size of about 20 filaments - independent of electrostatic interactions. Geometrical considerations indicate that competition between binding energy and bundle bending rigidity controls the bundle diameter. We discuss how arising frustrations or packing defects in the bundles could cause the bundle thickness to saturate.

BP 7.2 Mon 16:30 H44

Dynamics and statistical mechanics of semiflexible polymer bundles — •CLAUS HEUSSINGER, MARK BATHE, and ERWIN FREY — Arnold-Sommerfeld-Center, Ludwig-Maximilians Universität, München

Bundles formed from semiflexible polymers are ubiquitous in nature (e.g. filopodia) and many areas of technology (e.g. carbon nanotube bundles). Despite their simple structure, their mechanical and dynamical properties are only poorly understood. We set up an elastic energy functional that allows characterizing the dynamical and statistical mechanical properties of polymer bundles, in much the same way as the standard worm-like chain model does for single polymers. The key result of our analysis is that bundles must be characterized by a wave-number dependent persistence length $l_p(q)$ instead of just a single q-independent value. This finding is shown to have dramatic consequences not only on the static and dynamic fluctuation spectrum of an isolated bundle but also on the scaling behaviour of their entangled solutions as well as their cross-linked networks.

BP 7.3 Mon 16:45 H44

Fluctuation Dynamics of Grafted Microtubules — •FRANCESCO PAMPALONI[1], KATJA TAUTE[2], GIANLUCA LATTANZI[3], and ERNST-LUDWIG FLORIN[2] — [1]EMBL Heidelberg - Cell Biology and Biophysics Unit - Heidelberg, Germany — [2]Center for Nonlinear Dynamics - University of Texas at Austin - Austin, USA — [3]Department of Medical Biochemistry, Biology and Physics, University of Bari - Bari, Italy

Microtubules (MTs) are tubular protein filaments that constitute one of the main components of the cellular cytoskeleton. MTs are composed by a variable number of protofilaments (most frequently 13) made by the dimeric protein tubulin. MTs are highly optimized to a maximum of mechanical performance: the hollow cylindrical shape allows high strength and stiffness combined with a minimum of structural elements (tubulin dimers). Such features of MTs - light, flexible, and stiff at once - make them similar to versatile composite structures investigated by material scientists. Recent studies have shown that one key mechanical parameter, the persistence length, is subject to an unexpected dependence on the overall MT length. This has been attributed to the MT's large mechanical anisotropy on the molecular level. We performed a dynamical analysis of the thermal fluctuations of grafted MTs obtaining first mode relaxation times. Single-particle tracking was employed to measure the fluctuations of the free end of the filament. We found that relaxation times follow an L^2 instead of an L^4 dependence for short microtubules. This relation is shown to result from the length dependence of the persistence length.

BP 7.4 Mon 17:00 H44

Force regulation of microtubule dynamics in living cells — •CHRISTIAN TISCHER[1], DAMIAN BRUNNER[2], and MARILEEN DOGTEROM[1] — [1]AMOLF, Amsterdam, Niederlande — [2]EMBL, Heidelberg, Deutschland

Microtubules are stiff biopolymers that self-assemble from tubulin proteins. Inside cells, microtubules are typically several micrometers long and form networks that are organized in a functional way. A unique property of microtubules is their ability to switch from a polymerizing to a depolymerizing state (so-called "catastrophes"). Investigating the intracellular regulation of this fascinating out-of-equilibrium behavior is crucial in order to understand how microtubules fulfill their important functions during cell division and cell morphogenesis. Here, we use the fission yeast (S. Pombe) to investigate regulation of microtubule catastrophes at the cell boundary. Fission yeast is an excellent model organism: it has a well defined cylindrical shape and contains only few microtubules whose dynamics can be readily followed with live-cell microscopy. Developing specialized image analysis methodology we were able to investigate the spatial and temporal distribution of microtubule catastrophes with unprecedented statistical accuracy. Analyzing thousands of catastrophes in hundreds of cells, we provide strong evidence that compressive polymerization forces, arising from growth of microtubules against the cell boundary, indeed enhance the rate of catastrophes. This effect had been predicted by measurements on purified microtubules growing against artificial boundaries.

BP 7.5 Mon 17:15 H44

Force generation by growing filament bundles — •JAN KIERFELD, TORSTEN KÜHNE, and REINHARD LIPOWSKY — Max-Planck-Institut für Kolloid- und Grenzflächenforschung, Science Park Golm, 14424 Potsdam

Force generation by polymerizing bundles of semiflexible filaments, which are formed due to attractive filament interactions, is investigated theoretically using Monte-Carlo simulations and analytical arguments. If a compressive force is applied to the end of a bundle it can undergo a force-induced unbundling transition. A polymerizing bundle can generate forces either by a zipping mechanism, which converts adhesive energy into force, or by a polymerization mechanism, which converts the energy gain upon adding monomers into force. Limitations from the buckling instability of the bundle are discussed for both mechanisms.

BP 7.6 Mon 17:30 H44

The Influence of internucleosomal interaction and local structure on the geometry of large chromatin fibers — •RENÉ STEHR[1], NICK KEPPER[2], KARSTEN RIPPE[2], and GERO WEDEMANN[1] — [1]Fachhochschule Stralsund, System Engineering and Information Management, Zur Schwedenschanze 15, D-18435 Stralsund, Germany — [2]Kirchhoff-Institut für Physik, Molecular Biophysics Group, Ruprecht-Karls-Universität Heidelberg, Im Neuenheimer Feld 227, D-69120 Heidelberg, Germany

The structure of the genetic material plays a major role in the regulation of gene expression. In eukaryotic cells the DNA is folded with histone proteins into chromatin. The internal structure of chromatin at physiological ionic strength is unknown.

We utilize computer simulations to study both the effect of different interaction potentials betweeen nucleosomes as well as changes to the nucleosome geometry. Our analysis revealed that the previously used potentials (e.g. Gay-Berne potential) are not compatible with the formation of stable chromatin fibers under physiological potential strengths while other geometries do. Furthermore, we extended the "two angle" model for the description of the DNA-nucleosoe geometry.

The results of our analysis identify the internucleosomal interaction and the local geometry at the nucleosomes as key determinants for the organization of the chromatin fiber. Modifications of these parameters by biological factors could be used to control the accessibility of DNA in the fiber in vivo.

BP 7.7 Mon 17:45 H44

The 30nm chromatin fiber: As dense as it gets — •MARTIN DEPKEN[1] and HELMUT SCHIESSEL[2] — [1]Max-Planck-Institut für Physik komplexer Systeme, Dresden, Germany — [2]Instituut-Lorentz for Theoretical Physics, Leiden, The Netherlands

We address the problem of the structure of the 30nm chromatin fiber. By considering the packing of nucleosomes at the periphery of the

fiber, together with their connections through the DNA linker backbone, we characterise the possible dense configurations without having to assume anything about the bending of the linker backbone. This results in a set of dense fiber configurations with properties that can be compared with experimental findings to determine possible structures.