BP 2: Computational Biophysics I

Time: Monday 9:30–12:45 Location: BAR/0106

BP 2.1 Mon 9:30 BAR/0106

Topology driven spatial organization of DNA-polymers in geometric confinement — •Debarshi Mitra[1], Shreerang Pande[2], and Apratim Chatterji[2] — [1]Leibniz Institute of Polymer Research Dresden, Hohe Strasse 6, 01069 Dresden, Germany — [2]Dept. of Physics, Indian Institute of Science, Education and Research-Pune (IISER-Pune), India-411008

The mechanism of chromosome segregation and organization in the bacterial cell cycle is one of its least understood aspects. The bacterial chromosome is often modeled as a bead spring ring polymer. We introduce cross-links in the DNA-ring polymer, resulting in the formation of loops within each replicating bacterial chromosome. We use simulations to show that the chosen polymer-topology ensures its self-organization along the cell long-axis, such that various chromosomal loci get spatially localized as seen in-vivo, in various growth conditions [1,2]. The organization arises only due to entropic repulsion between polymer loops of each daughter chromosome. We also reconcile observations from complementary experimental techniques probing the organization of the chromosome [1]. We further establish organizational principles for topologically modified polymers in various kinds of geometric confinement and discuss possible relevance to eukaryotic chromosomes.

[1] Debarshi Mitra Shreerang Pande, Apratim Chatterji. Soft Matter, 2022.

[2] Shreerang Pande, Debarshi Mitra, and Apratim Chatterji. Phys. Rev. E, 110(5), November 2024.

BP 2.2 Mon 9:45 BAR/0106

An extended boundary integral method for viscoelastic cells — •Thomas Mayr and Stephan Gekle — University Bayreuth, Bayreuth, Germany

The boundary integral method is a powerful method for modeling soft objects such as capsules, vesicles or red blood cells in flows at low Reynolds numbers. The beauty of this method lies in its effective two-dimensional description of the boundaries making fluid-structure interaction simple in comparison to other methods. So far, the boundary integral method is restricted to cells with a viscoelastic membrane and a purely viscous interior, whereas most biological cells contain a complex cytoskeleton and a nucleus in addition to their membrane. Here, we develop an extended three-dimensional boundary integral method, that can handle such cells, which are treated as a homogeneous viscoelastic material surrounded by a viscoelastic membrane. We use our method to study systematically the influence of bulk and membrane viscoelasticity on the dynamics of a cell in shear flow closely corresponding to recent experiments [1].

[1] Gerum et al., Elife 11, e78823 (2022)

BP 2.3 Mon 10:00 BAR/0106

Synchronization of both microtubule ends facilitates robust spindle length control — •Shane Fiorenza[1], Sheba Cheeran[2], Elena Doria[2], Iva Tolić[3], Patrick Meraldi[2], and Nenad Pavin[1] — [1]Faculty of Science, University of Zagreb — [2]Faculty of Medicine, University of Geneva — [3]Rudjer Bošković Institute, Zagreb

The mitotic spindle is a biomechanical structure that relies on a well-controlled geometry to accurately segregate genetic material, and so the mechanisms responsible for setting spindle length have been extensively studied both in vivo and in vitro. One of these myriad mechanisms, microtubule poleward flux, has proven difficult to characterize, with experiments showing that decreasing poleward flux can lead to spindle length increasing, decreasing, or remaining constant. How the spindle regulates its length and the role of poleward flux in this process remains unclear. Here we show that length-dependent regulation at both microtubule ends constitutes a fundamental mechanism of spindle length control through poleward flux. Our model demonstrates that length-dependent mechanisms at both microtubule ends allow plus- and minus-end dynamics to synchronize with one another, resulting in perturbations at either end having opposite effects on poleward flux for increasing spindle size. We predict that spindle length and poleward flux can be uncoupled via simultaneous perturbations, which we confirm with in vivo depletion experiments of KIF18A, KIF2A, and KATNB1 proteins. Our results provide a new way of understanding spindle length control and resolve a long-standing paradox of how poleward flux relates to spindle length.

BP 2.4 Mon 10:15 BAR/0106

A coarse-grained model for investigating the ejection of dsDNA from a viral capsid — •Adrian John Pinto[1], Klara Strobl[2], Carmen San Martin[3], Mar Alcazar Hutardo[2], Paul van der Schoot[4], Pedro J. de Pablo[2], Horacio V. Guzman[5], and Peter Virnau[1] — [1]Institute of Physics, JGU, Mainz, Germany — [2]Autonomous University of Madrid, Madrid, Spain — [3]Spanish National Center for Biotechnology, Madrid, Spain — [4]Eindhoven University of Technology, Eindhoven, Netherlands — [5]Institute of Material Science of Barcelona, Barcelona, Spain

Viruses are microscopic infectious agents that hijack the metabolic machinery of their hosts to replicate. They consist of genetic material, DNA for adenovirus, enclosed within a protein shell called a capsid. Adenoviruses are associated with respiratory diseases, gastroenteritis, conjunctivitis, and urinary tract infections. In this work, we investigate the denaturation of the viral capsid in the presence of urea as a chemical denaturant and analyze how increasing urea concentration affects capsid stability. To model the experimental system in simulations, we propose a coarse-grained representation of viral DNA based on a Kratky-Porod chain, which allows us to incorporate solvent conditions and obtain realistic length scales. Additionally, we model the capsid as a spherical confinement composed of discrete beads and introduce openings of various sizes to map changes in urea concentration to the simulation environment. Our findings indicate that the lag time observed in intensity curves can be explained by differences between partial and complete capsid opening.

BP 2.5 Mon 10:30 BAR/0106

Multi-Scale Computational Framework for Modeling Metabolic Pathways — •Miljan Dašić, Ashwathi Poolamanna, Mehrnoosh Khodam Hazrati, and Štěpán Timr — J. Heyrovský Institute of Physical Chemistry of the Czech Academy of Sciences, Dolejškova 2155/3, 182 00 Prague 8, Czech Republic

Spatial organization of enzymes (clustering, assemblies, and substrate channeling) has been increasingly recognized as a key determinant of metabolic efficiency. Recent studies suggest that non-specific enzyme-substrate interactions and molecular crowding can further impact the performance of metabolic pathways. However, the combined effect of these factors remains insufficiently quantified.

To address this gap, we developed a multi-scale computational framework connecting molecular-level enzyme-substrate interactions with emergent pathway-level kinetics. We first perform extensive coarse-grained Molecular Dynamics (MD) simulations with LAMMPS to quantify substrate transition kinetics at varying crowding levels. Resulting trajectories are analyzed using Markov State Models (MSMs) to extract the relevant states and transition rates. These kinetic parameters are then used to parameterize stochastic Reaction-Diffusion (RD) simulations in Smoldyn, enabling the study of large enzyme assemblies, different reaction orders, and multi-step metabolic pathways.

Our results reveal how molecular interaction strengths, crowding conditions as well as enzyme spatial organization impact pathway efficiency across scales: from nanometers and nanoseconds (MD) to micrometers and seconds (RD).

BP 2.6 Mon 10:45 BAR/0106

Coexistence in competition for shared resources with fluctuating fitness — •Angelique Burdinski and Dirk Brockmann — Center Synergy of Systems (Synosys), TUD Dresden University of Technology, 01069, Dresden, Germany

Understanding how species coexist in competitive scenarios has long been a central question in ecology and evolution. The contradiction between the competitive exclusion principle and the observed diversity of species has puzzled researchers for decades. Fluctuating environmental factors that selectively change species fitness have been proposed to stabilize coexistence, but theoretical results remain inconclusive. How competitive forces and temporal variability shape evolutionary outcomes remains debated, with model-specific results and few universal insights. We compare species dynamics under two generic but qualitatively different mechanisms. One model captures direct competition via the standard replicator equation; the other represents a consumer-resource system, yielding the adjusted replicator model. Under uniform fitness, both show identical asymptotics, diverging sharply when fitness fluctuates. The standard replicator leads to quasi-fixation of a single species, whereas the adjusted replicator exhibits stable coexistence below a critical timescale. We derive coexistence bounds based on the mean and variance of fitness, showing that higher mean and lower variability favor fixation, while coexistence may persist even in disadvantaged situations. This contrast reflects direct versus indirect competition and supports coexistence as a generic outcome of shared-resource interactions in temporally varying environments.

15 min. break

BP 2.7 Mon 11:15 BAR/0106

Dielectric response of graphene and MoS$_2$ nanopores in the detection of single amino acids — •Longlong Li and Maria Fyta — Computational Biotechnology, RWTH Aachen University, Germany

Recent advances in two-dimensional (2D) material nanopores have opened new opportunities for biosensing with single-molecule precision. In this work, we investigate the interaction of single amino acids with graphene and MoS$_2$ nanopores using density-functional theory (DFT), combined with dielectric response calculations and non-equilibrium Green's function (NEGF) transport simulations. After identifying the most stable conformations of selected amino acids residing inside the nanopores, we calculate both the electronic transport and optical response of the nanopores in the absence and presence of these biomolecules. While electronic current-voltage characteristics reveal only modest amino-acid-dependent variations, the optical response, characterized by frequency-dependent dielectric functions and optical absorption spectra, exhibits distinct material-specific signatures. In particular, MoS$_2$ nanopores exhibit strong and broadband optical sensitivities, which are significantly larger than those of graphene and thus enable more distinct discrimination of single amino acids across multiple photon energies. Our simulations reveal an enhancement in the optical read-out of nanopores and an even stronger signals in the case of MoS$_2$ nanopores highlighting the possibility of a broadband optical detection for protein detection platforms and biosensors.

BP 2.8 Mon 11:30 BAR/0106

From Bioanalytics to Neuromorphic Computing: Graphite-Based Nanopores for Protein Sequencing and Iontronic Memristors — •Chandan K. Das and Maria Fyta — Computational Biotechnology, RWTH Aachen University, Worringerweg 3, 52074 Aachen, Germany

Protein sequencing with single amino acid resolution using ionic current signatures is a rapidly advancing technique, yet challenges persist in maintaining protein linearity and controlling their translocation through solid state nanopores. We introduce a graphite-based nanopore featuring a constriction inspired by alpha-hemolysin. All atom MD simulations show that the positively charged pore lumen promotes strong anion selectivity and drives electro-osmotic flow (EOF), which generates hydrodynamic drag opposing the electrophoretic force (EPF). Balancing these forces straightens proteins during translocation and increases their residence time within the constriction, substantially improving sequencing accuracy. This design enables detection of all 20 proteinogenic amino acids and their post-translational modifications. Beyond sequencing, the graphite-based architecture supports diverse iontronic applications. In a graphite-hydrogel-graphite nanofluidic memristor, a neutral hydrogel selectively traps cations, inducing ion concentration polarization. Simulations reveal characteristic memristive behavior, including a hysteretic current-voltage response. Overall, graphite nanopores offer a versatile platform for sequencing and neuromorphic computing.

BP 2.9 Mon 11:45 BAR/0106

Protein Translocation in Two Dimensional Nanopores from Molecular Dynamics and Free Energy Calculations — •Peijia Wei, Mayukh Kansari, Santiago López Páramo, and Maria Fyta — Computational Biotechnology, RWTH Aachen University, Worringerweg 3, 52074 Aachen, Germany

Nanopores, nanometer scale openings in materials, offer strong potential for ultra fast, cost effective and real time next generation sequencing technologies. These pores can electrophoretically drive charged biomolecules through and detect them. Using computer simulations, we compare two dimensional nanopores, graphene and MoS$_2$, to evaluate their effectiveness in protein detection. Protein translocation and dynamics are being controlled by varying the surrounding solvent, using both a typical monovalent salt solution and a molecular solution. Atomistic simulations assess the ability of each nanopore to thread proteins, on the basis of the ionic current signals through the pore. We also perform free energy calculations to quantify the thermodynamic factors that influence protein entry and passage through the pores. Our results show that graphene nanopores interact strongly with proteins, which hinders translocation under physiological conditions. This can be overcome by adding a denaturant that forms a hydrophilic and cation rich layer on the surface and enables linearized threading. In contrast, MoS$_2$ nanopores allow protein passage even in physiological solutions and offer inherent control of the translocation. By combining molecular dynamics with free energy analysis, we reveal how the complex interactions among all components shape translocation behavior.

BP 2.10 Mon 12:00 BAR/0106

Extending quantum-mechanical benchmark accuracy to biological ligand-pocket interactions — •Mirela Puleva[1], Leonardo Medrano Sandonas[2], Balázs D. Lorincz[3], Jorge Charry[4], David M. Rogers[5], Péter R. Nagy[3], and Alexandre Tkatchenko[1] — [1]University of Luxembourg, Luxembourg — [2]TUD Dresden University of Technology, Germany — [3]Budapest University of Technology and Economics, Hungary — [4]Luxembourg Researchers Hub asbl, Luxembourg — [5]Oak Ridge National Laboratory, USA

Predicting the binding affinity of ligands to protein pockets is key in the drug design pipeline, yet accurate capture of interactions in the flexible ligand-pocket motifs requires robust quantum-mechanical (QM) benchmarks, which are scarce. Disagreement between "gold standard" Coupled Cluster (CC) and Quantum Monte Carlo (QMC) methods further challenges large non-covalent benchmarks. We introduce the QUantum Interacting Dimer (QUID) benchmark framework modeling diverse ligand-pocket motifs. CC and QMC agree within 0.5 kcal/mol for QUID, which spans key non-covalent binding motifs and energetic contributions from symmetry-adapted perturbation theory. Benchmark results shows several dispersion-inclusive density functional approximations predict energies accurately but differ in atomic van der Waals forces, while semiempirical and empirical methods need improvements for non-covalent interactions (NCIs) in out-of-equilibrium geometries. With a wide span of NCIs, highly accurate interaction energies, and further molecular properties, QUID goes beyond the "gold benchmark" QM benchmark of ligand-protein systems.

BP 2.11 Mon 12:15 BAR/0106

Insights into Quantum Decoherence in Biological Light Harvesting from First-Principles Simulations — Thomas Trepl, •Ingo Schelter, Johannes M. Foerster, and Stephan Kümmel — University of Bayreuth, Bayreuth, Germany

Photosynthesis is a fascinating process of outstanding importance since it provides the energy for most life on Earth. Considering the remarkable quantum efficiency with which the energy of absorbed photons is transferred in the initial light-harvesting step, there exists a longstanding speculation about the role of quantum coherence.

In this talk, I show the decoherence and localization of excitation energy that evolves from the coupled electron and nuclear dynamics in the B850 ring at room temperature after an initial Laser excitation as typically used in an experiment. The electron dynamics of the whole multichromophoric system is described by the real-time formulation of time-dependent density functional theory. The nuclear dynamics is treated by Ehrenfest dynamics, allowing for a non-adiabatic coupling between electrons and nuclei. The simulations show that nuclear dynamics starts to trigger quantum decoherence after only a few tens of femtoseconds.

BP 2.12 Mon 12:30 BAR/0106

Human breathing pattern dominates the effective diffusivity of droplets emitted while speaking — •Lars Natusch and Roland Netz — Fachbereich Physik, Forschungsgruppe Roland Netz, Freie Universität Berlin, Berlin, Germany

For understanding airborne viral infection pathways, the prediction of the effective diffusivity of saliva droplets emitted from a person while speaking and breathing is crucial.

In enclosed non-ventilated indoor spaces the diffusivity of tracer particles or molecules emitted by a person is governed by the complex interplay of various physical transport mechanisms. By comparison of lattice-based simulations of the three-dimensional compressible Navier-Stokes equation with experiments measuring the spreading of carbon-dioxide emitted from a person, we demonstrate that molecular diffusion and convection due to body heat and temperature gradients at walls and windows are present, but that the main spreading mechanism is related to the periodic breathing pattern of a person, which induces long-range advection.

Our results identify breathing as the dominant mechanism for particle transport in stagnant indoor air.