BP 16: Posters - Computational Biophysics

Time: Monday 17:30–19:30 Location: Poster C

BP 16.1 Mon 17:30 Poster C

Contact- and distance-based principal component analysis of protein dynamics — •Matthias Ernst and Gerhard Stock — University of Freiburg, 79104 Freiburg, Germany

To describe and understand protein dynamics, systematic dimensionality reduction is crucial. This can be accomplished by principal component analysis (PCA), a linear transformation which removes linear correlations of the coordinates by diagonalizing their covariance matrix. Different types of input coordinates can be used, like dihedral angles (dPCA[1]) or various kinds of distances (e.g. conPCA[2]) or cartesian atomic coordinates. Internal coordinates often provides higher resolution, especially for large-amplitude motion as found in folding systems[3]. In contrast to dihedral angles which mainly reflect the behaviour of neighbouring residues in a protein, distances between pairs of atoms also incorporate information about residues further apart in the primary sequence.

We employ PCA and classify the results based on distances between Ca atoms as well as distances between different residues (including side chains) for various types of well-known model problems, like folding of villin headpiece or functional dynamics of BPTI or lysozyme. We show that it can be advantageous to include only a selected set of coordinates for a PCA because the selection of input variables strongly influences the results of a PCA.

[1] Y. Mu, P. H. Nguyen, and G. Stock, Proteins 2005, 58, 45.

[2] M. Ernst, F. Sittel and G. Stock, submitted.

[3] F. Sittel, A. Jain and G. Stock, J. Chem. Phys. 2014, 141, 014111.

BP 16.2 Mon 17:30 Poster C

Structures and Processes in a Quantum Rattle — •Amanda Diez Fernandez, Molly Stevens, and Mike Finnis — Imperial College London, United Kingdom

Nanoparticles bring new possibilities to the field of drug delivery engineering. One of the properties nanoparticles for drug delivery must have is a large drug loading capacity and an extended and sustained release. This is necessary to ensure constant drug levels in the target tissue and improve drug efficiency. We recently developed a Quantum rattle based nanoparticle for drug loading and release [1] as well as multimodal imaging capabilities.

In order to understand the key features of the nanoparticle responsible for drug loading and release and to enable further optimisation of these parameters, we have taken a multiscale modelling approach. Firstly, a continuum mathematical model has been developed to describe drug diffusion and sorption in the nanoparticle. In the next phase of the project, Molecular Dynamics simulations are being done to obtain information from lower scales, such as the drug diffusion coefficient inside the pore channels.

REFERENCES:

[1] Gold silica quantum rattles for multimodal imaging and therapy M. Hembury, C. Chiappini, S Bertazzo, T. L. Kalberd, G. L. Driskoe, O. Ogunladed, S. Walker-Samueld, K.S. Krishnai, C. Jumeaux, P. Beard, C.S.S.R.Kumari, A. E. Porter, M.F.Lythgoe, C. Boissièree, C. Sanchez, and M. M. Stevens PNAS, February 17, 2015, vol. 112, no. 7, 1959 1964

BP 16.3 Mon 17:30 Poster C

Modelling and Controlling Electro-Hydrodynamics in Nanopore Translocation Experiments — •Andreas J Meyer and Peter Reimann — Universität Bielefeld

The translocation of biopolymers through nanopores is dominated by several competing effects, namely electrostatic forces resulting from an applied voltage difference, system-intrinsic charges, and the hence induced velocity field of the buffer solution. Since comprehensive molecular-dynamics simulations of translocation processes are practically infeasible, modelling the acting forces demands an effective description of nanoscopic structures and physical parameters. We employ a continuum description via Poisson-Nernst-Planck and Stokes equations for conducting numerical experiments and finding optimized parameter sets or new analysis techniques.

BP 16.4 Mon 17:30 Poster C

Phase Transitions and Defects in a Flocking Model at High Density — •Felix Kempf[1], Christoph A. Weber[2], and Erwin Frey[1] — [1]Arnold Sommerfeld Center for Theoretical Physics and Center for NanoScience, Department of Physics, Ludwig-Maximilians-Universität München, 80333 Munich, Germany — [2]Department of Biological Physics, Max Planck Institute for the Physics of Complex Systems, 01187 Dresden, Germany

To investigate active systems at high densities, we use computer simulations of a flocking model with repulsive interaction. Flocking models implement the core-features of active matter: self-propulsion and mutual alignment. At high densities, our model shows a transition reminiscent of melting in a 2d thermal crystal. Recently, the phase diagram was studied (C. Weber, C. Bock, and E. Frey, Phys. Rev. Lett. 112, 168301 (2014)), an open question was the role of defects in this transition. We now focus on the mutual interaction of dislocations in the crystaline phase. We explore phenomenology and statistics of the mutual interaction of two isolated dislocations in the ordered phase and compare the simulation results to a markovian model. The discrepancy between this simplified model and the statistics of the full simulations reveals that correlations are not negligible for defect interaction. We also observe a faster motion for short dislocation distances, which shows that the mechanisms governing the interactions in the near-range are fundamentally different compared to the far field.

In summary, our work elucidates phenomenology and statistics of the interaction of dislocation pairs in active high-density systems.

BP 16.5 Mon 17:30 Poster C

A mechanism for contraction of cytokinetic actin rings — •Fabian Hubertus Kreten, Christian Hoffmann, and Karsten Kruse — Universität des Saarlandes, Theoretische Physik, Campus E26, 66123 Saarbrücken

In the late stages of cell division, animal cells are cleaved by contraction of the cytokinetic ring. The ring consists of actin filaments, molecular motors, and other proteins. How this ring generates an average net contractile stress is still poorly understood.

Here, we study a mechanism involving the formation of bipolar filaments by joining polar actin filaments of opposite orientation at their barbed ends. We develop a continuum mean-field model for the dynamics of actin filaments and motors. A linear stability analysis shows that the homogenous distribution becomes unstable beyond a critical motor strength. Numerical solutions of the full dynamic equations exhibit a backward-bifurcating non-homogenous state with clustered filaments at distinct positions along the ring.

For sufficiently stable bipolar filaments, the distribution is stationary and reminiscent of muscle sarcomeres. In this state, the total stress is higher than in the homogenous state for the same parameters. If the bipolar filaments split fast enough into their polar constituting filaments, oscillatory states can be observed. We discuss these findings in terms of recent experiments.

BP 16.6 Mon 17:30 Poster C

Opposite Translocation of Long and Short Oligomers Through a Nanopore — •Thomas Töws, Sebastian Getfert, and Peter Reimann — Fakultät für Physik, Universität Bielefeld, 33615 Bielefeld, Germany

We consider elongated cylindrical particles, modeling e.g. DNA fragments or nanorods, while translocating under the action of an externally applied electric potential through a solid-state nanopore. Particular emphasis is put on the concomitant potential-energy landscape due to the complex interplay of various electrohydrodynamic effects beyond the realm of small Debye lengths. We find that the net potential energy difference across the membrane may be of opposite sign for short and long particles of equal diameters and charge densities (e.g. oligomers). Thermal noise thus leads to biased diffusion through the pore into opposite directions. The specific particle length at which this transport inversion occurs can be controlled by means of a membrane gate electrode.

BP 16.7 Mon 17:30 Poster C

New insights to the thermodynamic stability of DNA i-motif: A perspective from advanced computational sampling methods — •Raghvendra Pratap Singh, Vasileios Tatsis, and Andreas Heuer — Corrensstr. 30 , D-48149, Institute of Physical Chem-

istry, University of Münster, Germany

Under high temperature and low pH conditions, cytosine rich stretches of nucleic acids are able to fold in a novel localized tetrameric form via the protonation of N3 nitrogen of Cytosines. The protonation of N3 nitrogen facilitates the nucleic acids to form non Watson-Crick pairing (C+C). Recent studies suggest that this unique fold can be used as a template to create longer quadruplex nanowires for Bionanotechnology applications. The studies suggest that it could be a significant target for certain Cancer treatments. Here we present microsecond long MD simulation using advance-sampling technique of Metadynamics/Bias-exchange Metadynamics for protonated and deprotonated single stranded i-motif at ambient temperature (300K) and in high temperature (500K). Additionally, We studied unfolding simulations of experimentally solved crystal structures along with mutants of the base structure to study the impact of mutations on the thermodynamics of the DNA i-motif. A detailed comparative scenario on the stability and energetics of i-motif and induced mutants will be presented.

References [1] Guéron, M., Leroy, J.L, Current Opinion in Structural Biology 10(3),326-331(2000) [2] Ren, J., Qu, X., Trent, J.O., Chaires, J.B. Nucleic Acids Research 30, 2307*2315 (2002)

BP 16.8 Mon 17:30 Poster C

Interactions between Polyethylene Glycol and Proteins Investigated Using Molecular Dynamics Simulations — Jiajia Zhou[1], Friederike Schmid[1], and •Giovanni Settanni[1,2] — [1]Johannes Gutenberg University, Mainz, Germany — [2]Max-Planck Graduate Center with the University of Mainz

Polyethylene glycol (PEG) is a polymer with a vast range of applications, including medical and biochemical applications. Notwithstanding the widespread use of PEG to improve the therapeuthic efficacy of drugs, proteins, liposomes or nanoparticles through the PEGylation process, the molecular factors at the basis of this behaviour have not been clearly identified, yet. Here we use molecular dynamics simulations to investigate the non-covalent interactions taking place between PEG and several blood proteins. The simulations are used to measure the preferential binding coefficient of PEG for proteins, and reveal recurring patterns of interaction involving specific aminoacids. The latter could be used for the development of coarse grained representations of protein-PEG interactions and may provide the basis for understanding the properties of protein coronas formed around PEGylated nanoparticles.

BP 16.9 Mon 17:30 Poster C

Monte-Carlo-Simulations of Cellular Adhesion — •Filip Savić, Andreas Janshoff, and Burkhard Geil — Georg-August-Universität Göttingen, Institut für Physikalische Chemie, Tammannstraße 6, 37077 Göttingen, Germany

The adhesion of cells to the extracellular matrix is an important process in biology. To understand the physical processes involved in the on state of cellular adhesion, especially the lateral organization of adhesion molecules into clusters, we perform Monte-Carlo-Simulations based on a harmonic multi-spring model involving lipid membranes and their physical properties. Local deformation of the membrane in the vicinity of adhesion clusters facilitates cluster growth while a repulsive interaction between clusters arises due to an interplay of membrane bending rigidity and non-specific repulsion. Balance of this interaction governs cluster size and stability in our simulations.

BP 16.10 Mon 17:30 Poster C

Salting out Constants of Aromatic Compounds - Experiment, Simulation and Kirkwood-Buff Theory — •Jakub Polak, Pavel Vrbka, and Jan Heyda — Department of Physical Chemistry, University of Chemistry and Technology, Prague, Czech Republic

Fluctuation theory of solutions, also called Kirkwood-Buff theory (KB), can be used to determine salting out constants of sparingly soluble molecules, from computer simulation data.

In this contribution, we have experimentally determined the limiting activity coefficients for large set of aromatic compounds (benzene, toluene, ethylbenzen and xylenes) in salt solutions (NaCl, Na2SO4, NaSCN). Following a recent simulation study of alkali halides salting-out effect on benzene (dx.doi.org/10.1021/jp5011154), we gained microscopic insight into the role of salts via all-atom molecular dynamics simulations.

The KB analysis of simulation data provide a solid evidence that the preferential binding of salt over water is weakly negative (i.e., salt is weakly depleted) for NaSCN, negative for NaCl, and very negative for Na2SO4, in accord with experimentally determined salting out constants.

The applicability of, in the community frequent, partitioning concepts, as well as the arbitrariness of the selection of 'reference' salt are discussed.