BP 11: Transport Processes

Time: Tuesday 15:15–17:15 Location: C 243

BP 11.1 Tue 15:15 C 243

Subdiffusion as an efficient intracellular sampling strategy — •Matthias Weiss and Gernot Guigas — Cellular Biophysics Group, Deutsches Krebsforschungszentrum, Bioquant Center, Im Neuenheimer Feld 267, 69120 Heidelberg

Diffusion-mediated searching for interaction partners is an ubiquitous process in cell biology. Transcription factors, for example, search specific DNA sequences, signaling proteins aim at interacting with specific co-factors, and peripheral membrane proteins try to dock to membrane domains. Brownian motion, however, is affected by molecular crowding that induces subdiffusion of proteins and larger structures, thereby compromising diffusive transport and the associated sampling processes. Contrary to the naive expectation that subdiffusion obstructs cellular processes we show here by computer simulations that subdiffusion rather increases the probability of finding a nearby target. Consequently, important events like protein complex formation and signal propagation are enhanced as compared to normal diffusion. Hence, cells indeed benefit from their crowded internal state and the associated anomalous diffusion.

BP 11.2 Tue 15:30 C 243

How Nature beats the central limit theorem: non-Brownian search from gene control to animal foraging — •Ralf Metzler and Michael Lomholt — Technical University of Munich, Physics Department T30g, James Franck Strasse, D-85747 Garching

Simple chemical reactands search for each other by three-dimensional diffusion until encounter. At low concentrations of reactands, pure 3D search is quite inefficient. Nature has come up with various active and passive solutions to speed up search. I will discuss two examples.

Facilitated diffusion of regulatory proteins in search for their specific binding site on a DNA combines 3D volume diffusion with 1D motion along the DNA. The combination of these two mechanisms significantly speeds up the search. In addition, intersegmental transfers that occur at contact points of chemically remote segments of the DNA due to looping gives rise to Levy flights along the DNA that further optimise the search. While this model holds for diluted solutions, in the cell molecular crowding occurs, leading to the subdiffusion of larger molecules. Consequences of this effect include a weak ergodicity breaking, that could allow low regulatory protein concentrations (Phys Rev Lett 95, 260603 (2005); Phys Rev Lett 98, 200603 (2007)).

Bacteria or higher animals perform an active search for food. It turns out that long-tailed distributions, that help avoiding the spell of the central limit theorem, lead to significantly higher search efficiency and significantly reduced sensitivity to a changing environment (E-print arXiv:0709.2352; compare also Phys Rev Lett 99, 160602 (2007)).

BP 11.3 Tue 15:45 C 243

Target Search on a Dynamic Polymer — •Thomas Schötz[1], Richard Neher[2], and Ulrich Gerland[3] — [1]Arnold Sommerfeld Center (ASC), LMU München, Germany — [2]Kavli Institute for Theoretical Physics, University of California, Santa Barbara, USA — [3]Institute for Theoretical Physics, University of Cologne, Germany

The diffusive search of a particle (protein) for a specific site on a heterogeneous polymer (DNA) is an interesting physics problem posed by the molecular biology of gene regulation. In the relevant limit where the DNA is in a compact conformation and the generic (electrostatic) attraction between the protein and DNA is strong, this search proceeds predominantly by local 1D sliding along the DNA and "hopping"to a different segment of the DNA, which is closeby in 3D space but may be distant along the contour. If the time between two hopping events is sufficiently long, such that the DNA conformations at subsequent events are uncorrelated, the dynamics of this search process can be described with the fractional Fokker-Planck-equation approach [Lomholt et al. PRL (2005)]. However, outside of this "annealed limit", the search dynamics changes drastically, as has been demonstrated in a study of the "quenched limit", i.e. the frozen polymer case [Sokolov et al. PRL (1997)]. In biological systems, typically neither of these limits is realized. Here, we study the full problem of the target search on a dynamic polymer. We observe a non-trivial crossover between the two limits, which is due to the breakdown of the correlations in the polymer conformations. We characterize these correlations and their effect on the transport in detail.

BP 11.4 Tue 16:00 C 243

Stochastic models for bidirectional transport on biological networks — •Maximilian Ebbinghaus[1], Rosemary Harris[2], and Ludger Santen[1] — [1]Department of Theoretical Physics, Saarland University, 66041 Saarbruecken, Germany — [2]School of Mathematical Sciences, Queen Mary, University of London, Mile End Road, London E1 4NS, United Kingdom

The intracellular transport on the cytosceletal filament network is driven by molecular motors. They carry different kinds of cargo through the cell by performing a directed stochastic along the polarized filaments. Although the motion of a given molecular motor is unidirectional, it is possible to transport cargo in opposite direction along a filament, e.g., dyneins and kinesins move in opposite directions along microtubule filaments. We model the bidirectional transport by means of a one-dimensional stochastic lattice models. The model motor proteins interact by exclusion such that effective transport on a single track is possible only by detaching and reattaching moves from the microtubule. Simulations have been carried to investigate the influence of different hopping rates and densities on mean current, path lengths and cluster sizes on the filament. In addition, the influence of tau proteins that decorate the filament will be presented. These proteins intervene in the system by altering the attachment rate of kinesins only. Thus, spatial disorder is found in the system and the impact on measurable quantities have been studied. The results of these simulations can be used in order to elucidate general transport phenomena in elongated cells as, e.g., axons.

BP 11.5 Tue 16:15 C 243

Driven transport on parallel lanes with particle exclusion and obstruction — •Anna Melbinger, Tobias Reichenbach, Thomas Franosch, and Erwin Frey — Arnold Sommerfeld Center for Theoretical Physics (ASC) and Center for NanoScience (CeNS), Department of Physics, Ludwig-Maximilians-Universität, München, Germany

Traffic phenomena emerge in intracellular transport, where molecular motors move along parallel one-dimensional filaments, serving as biological engines. Recently, we have proposed a prototypical model for transport on parallel lanes [1]. Here, we consider the situation where motors on the same lane exclude each other, while a certain obstruction, stemming e.g. from the interaction of the bigger cargo particles, occurs between motors adjacent on parallel lanes. Depending on the strength of the obstruction, a rich phase behavior emerges, with density separation between the lanes as well as domain walls in the density profiles of the individual lanes being feasible. We rationalize our observations in an analytic approach, and show an intimate relation between the current-density relation and the systems' phase diagrams.

[1] T. Reichenbach, T. Franosch, E. Frey, Phys. Rev. Lett. 97, 050603 (2006)

BP 11.6 Tue 16:30 C 243

A Natural Molecule Trap — Dieter Braun[1], Franz Weinert[1], Stefan Duhr[1], Kono Lemke[2], Michael Russell[3], and •Dieter Braun[1] — [1]Biophysics, CENS, LMU München, Amalienstr. 54, 80799 München, Germany — [2]Institute for Mineralogy, ETH-Zürich, Switzerland — [3]Jet Propulsion Laboratory, CalTech, California, USA

We simulate molecular transport in elongated pores of rock near warm hydrothermal vents. We find extreme accumulation of molecules in a wide variety of plugged pores. The mechanism is able to provide highly concentrated single nucleotides, suitable for operations of an RNA world at the origin of life. It is driven solely by the thermal gradient across a pore. On the one hand the fluid is shuttled by thermal convection along the pore, whereas on the other hand, the molecules drift across the pore, driven by thermodiffusion. As a result, millimeter-sized pores accumulate even single nucleotides more than 10^8-fold into micrometer-sized regions. Since the accumulation depends exponentially on the pore length and temperature difference, it is considerably robust with respect to changes in the cleft geometry and the molecular dimensions. Our results indicate that for life to evolve, complicated active membrane transport is not required for the initial steps.

References:
PNAS 104, 9346-9351 (2007)
PNAS 103, 19678-19682 (2006)

BP 11.7 Tue 16:45 C 243

Protein Diffusion and Hydodynamic Interactions in Red Blood Cells — Wolfgang Doster[1] und •Stephane Longeville[2] — [1]Technische Universität München Physik E 13 — [2]CEA Saclay Paris

Die Konzentration von Makromolekülen in biologischen Zellen ist weit weg vom Ideal der verdünnten Lösung. Volumfraktionen um 0.3 sind typisch. Das *molecular crowding* beeinflusst Reaktionsraten, Dissoziations-Gleichgewichte und diffusiven Transport. Kann die Beweglichkeit der unterschiedlichen Komponenten einer Zelle auf der Basis von intermolekularen Wechselwirkungen verstanden werden? Der Transport von Sauerstoff in Muskelzellen und Erythrozyten wird durch Proteindiffusion unterstützt. In diesem Beitrag diskutieren wir Wechselwirkungen und Diffusion in konzentrierten Myoglobinlösungen und von Hämoglobin in Erythrozyten mit Neutronenspektroskopie [1]. Mit der Kombination von Kleinwinkestreuung und Spin-Echotechnik kann man die Diffusion auf der Skala der intermolekularen Kräfte untersuchen. Vor allem hydrodynamische Wechselwirkungen dominieren aus diesen Längenskalen. [1] W. Doster and S. Longeville Biophy.J. 93 1360 (2007).

BP 11.8 Tue 17:00 C 243

Anomalous diffusion of transmembrane proteins due to oligomerization — •Ulrich Schmidt[1], Markus Elsner[2], Maria Smedh[3], Tommy Nilsson[3], and Matthias Weiss[1] — [1]Cellular Biophysics Group, Deutsches Krebsforschungszentrum, Bioquant Center, Im Neuenheimer Feld 267, 69120 Heidelberg — [2]Cell Biology and Metabolism Branch, National Institutes of Health, USA — [3]Dept. of Medical and Clinical Genetics, Inst. of BioMedicine, Sahlgrenska Academy, Gothenburg University, Sweden

Membrane proteins frequently form higher-order structures, e.g. oligomers, to facilitate their function and to assume proper subcellular localization. Oligomerization, however, alters the diffusion properties of participating individual proteins. Here, we have tested this aspect for membrane proteins undergoing a dynamic oligomerization process by means of computer simulations. We find that the diffusion of individual proteins becomes anomalous on short time scales with the anomality depending on the underlying binding kinetics and the number of binding sites per protein. In support of these theoretical results, we find via fluorescence correlation spectroscopy that a fluorescently tagged transmembrane Golgi enzyme is highly anomalous in vivo. This observation is consistent with the notion that Golgi-resident proteins oligomerize, presumably to maintain correct cisternal localization and to enhance enzymatic reactions.