DY 5: Statistical Physics of Biological Systems II (organised by DY)

Time: Monday 14:00–17:00 Location: HÜL 186

Topical Talk DY 5.1 Mon 14:00 HÜL 186

Collective dynamics in the cytoskeleton and swimming bacteria — •Falko Ziebert[1,2], Sumanth Swaminathan[3], Shawn Ryan[4,5], Leonid Berlyand[4], and Igor Aranson[5] — [1]PCT - UMR CNRS Gulliver 7083, ESPCI, Paris, France — [2]Physikalisches Institut, Universität Freiburg — [3]Engineering Sciences and Applied Mathematics, Northwestern University, Evanston, U.S. — [4]Department of Mathematics, Pennsylvania State University, U.S. — [5]Materials Science Division, Argonne National Laboratory, Argonne, U.S.

Collective dynamics in active biological materials has attracted much attention in recent years. I will focus on select topics on two systems: i) semi-dilute cytoskeletal solutions where molecular motors induce self-organization of filaments and ii) collective swimming of bacteria solutions. In the first system I propose a model for the semi-dilute case, i.e. the regime of multi-filament interactions. I discuss the order of the isotropic-polar nematic transition - which can not be determined by macroscopic models - as well as the influence of motor fluctuations on the ordering and the respective defect patterns that form. In case of bacterial solutions, recent experimental studies evidenced a decrease in viscosity as a function of density/volume fraction of swimmers in case of pushers (e.g. B. subtilis). In contrast, pullers (e.g. chlamydomonas) lead to an increase in viscosity. To rationalize these findings we performed simulations and analytical work, demonstrating that the viscosity reduction in case of pushers is related to the onset of large-scale collective motion due to interactions between swimmers.

DY 5.2 Mon 14:30 HÜL 186

Stochastic amplification in an epidemic model with seasonal forcing — •Andrew Black and Alan McKane — Theoretical Physics Group, University of Manchester, UK

Stochastic models, subject to external forcing, can capture the regular oscillatory patterns of childhood epidemics, such as measles and whooping cough, but so far the mechanisms generating these pattens have not been well understood. We study the stochastic susceptible-infected-recovered (SIR) model with time-dependent forcing using analytic techniques which allow us to disentangle the interaction of stochasticity and external forcing. The model is formulated as a continuous time Markov process, which is decomposed into a deterministic dynamics together with stochastic corrections, by using an expansion in inverse system size. The forcing induces a limit cycle in the deterministic dynamics, and with the use of Floquet theory, a complete analysis of the fluctuations about this time-dependent solution is given. This analysis is applied when the limit cycle is annual, and after a period-doubling when it is biennial. The comprehensive nature of our approach allows us to give a coherent picture of the dynamics which unifies past work, but which also provides a systematic method for predicting the periods of oscillations seen in both whooping cough and measles epidemics.

DY 5.3 Mon 14:45 HÜL 186

Strong Noise Effects in one-dimensional Neutral Populations — •Luca Dall'Asta[1], Fabio Caccioli[2], and Deborah Beghè[3] — [1]ICTP, Trieste, Italy — [2]Santa Fe Institute, Santa Fe, NM — [3]Università di Parma, Parma, Italy

The dynamics of well-mixed biological populations is studied using mean-field methods and weak- noise expansions. Similar methods have been applied also in spatially extended problems, relying on the fact that these populations are organized in colonies with a large local density of individuals. We provide a counterexample discussing a one-dimensional neutral population with negative frequency- dependent selection. The system exhibits a continuous phase transition between genetic fixation and coexistence that is unexpected from weak-noise arguments. We show that the behavior is a non-perturbative effect of the internal noise that is amplified by presence of spatial correlations (strong- noise regime).

DY 5.4 Mon 15:00 HÜL 186

Active colloidal suspensions exhibit orientational order under gravity — •Mihaela Enculescu und Holger Stark — Technische Universität Berlin, Institut für Theoretische Physik, Hardenbergstr. 36, 10623 Berlin

Recently, the steady state of an active colloidal suspension under gravitational field was studied experimentally in [J.Palacci et al, Phys.Rev.Lett. 105, 088304 (2010)]. It was found that the sedimentation length depends strongly on the velocity of the active Brownian particles. We present a theoretical analysis for the sedimentation of an active colloidal suspension. We find that the change of the sedimentation length is coupled to a partial alignment of the suspension with the mean swimming direction oriented against the gravitational field. Our approach starts from Langevin equations of non-interacting active particles, from which a Smoluchowski equation for the particle distribution is derived. We determine the stationary particle distribution both numerically and by perturbation theory. It agrees very well with the experimental data. The predicted anisotropy in the particle orientational distribution is found to depend on the particle activity, as well as on the gravitational force.

DY 5.5 Mon 15:15 HÜL 186

Fluctuations of intracellular filaments — •Ines-Kristin Weber and Ludger Santen — Department of Theoretical Physics, Saarland University, 66041 Saarbrücken

The cytoskeleton is an inhomogeneous network of polar filaments consisting of, amongst others, microtubules. These highly dynamic biopolymer filaments are involved in a wide variety of biological processes such as cell division and intracellular transport. Although they are very rigid and form a stiff structural network, it has been shown that they typically exhibit significant bending on all length scales. In this work we describe microtubules as semi-flexible polymers and investigate their fluctuations under thermal and non-thermal forces by means of computer simulations and phenomenological approaches.

DY 5.6 Mon 15:30 HÜL 186

Modelling the African Trypanosome with stochastic rotation dynamics — •Sujin Babu and Holger Stark — Institut für Theoretische Physik Technische Universität Berlin

The dynamics of microorganisms in a viscous fluid has recently received considerable attention in the physics community. It has been reported that the African Trypanosome makes use of hydrodynamic flow fields to evade attack from antibodies in the blood stream. The spindle-shaped flexible cell body of the African Trypanosome possesses some bending rigidity due to its cytoskeleton. A single flagellum runs from the thicker posterior end to the thinner anterior end of the cell body and is firmly attached to it. By propagating a wave along the flagellum from the anterior to the posterior end, the trypanosome moves forward. However, the details of this propulsion mechanism is still under debate. Our goal is to study a model trypanosome in its viscous environment. We model the cell body and the flagellum as a net of vertices connected by springs and also include some resistance to bending. A bending wave passing through the flagellum propels the trypanosome. We simulate the flow field around the model trypanosome using the method of stochastic rotation dynamics, which is an effective solver for the Navier-Stokes equations but also includes thermal fluctuations. We will demonstrate how the model trypanosome is coupled to the effective fluid particles of stochastic rotation dynamics. We will also discuss the propulsion mechanism of the microorganism and demonstrate that our modeling reproduces different shape conformations observed in experiments.

DY 5.7 Mon 15:45 HÜL 186

Explicit Expressions for the Mean First Passage Time of a Diffusing Molecule in Different Two-Dimensional Geometries — •Ronny Straube — Systems Biology Group, Max Planck Institute for Dynamics of Complex Technical Systems, Magdeburg, Germany

The mean first passage time (MFPT) of a diffusing molecule is an important quantity that describes the first encounter between the molecule and a distant target site. For signaling molecules the MFPT can have a strong impact on the output of a signaling pathway and the inverse of the average MFPT can be used as the diffusion-limited association rate between the molecule and the target site. We have recently shown that in two dimensions the MFPT can be expressed in terms of an associated Neumann function [1] whose regular part can significantly contribute to the average MFPT. Here, I provide simple expressions for the average MFPT in different membrane patch geometries [2] including a square-shaped domain, a cylindrical domain and the surface of a sphere. I also discuss the impact of the presence of

multiple target sites on the MFPT. These results can be used to estimate the average MFPT, the foward rate constant or the time scale of receptor clustering for biological membranes of various shapes.

[1] D. Coombs, R. Straube, M. J. Ward, *SIAM J. Appl. Math.* **70**, 302–332 (2009). [2] F. Wei, D. Yang, R. Straube, J. Shuai, submitted to *Phys. Rev. E*

DY 5.8 Mon 16:00 HÜL 186

Perturbation analysis of a reduced model for collective motion: Effects of the initial condition — •Chiu Fan Lee — Max Planck Institute for the Physics of Complex Systems, Dresden, Germany

In a system of noisy self-propelled particles with interactions that favor directional alignment, collective motion will appear if the density of particles increases beyond a certain threshold. We argue here that such a threshold may depend also on the profiles of the initial perturbation in the particle directions. Specifically, we perform mean-field, linear stability, perturbative and numerical analyses on an approximated form of the Fokker-Planck equation describing the system. We find that if an angular perturbation to an initially homogeneous system is large in magnitude, it will be amplified even if the density of the system is below the threshold density obtained from mean-field approximation.

Reference: C.F. Lee. Fluctuation-induced collective motion: A single-particle density analysis. Physical Review E **81**, 031125 (2010).

DY 5.9 Mon 16:15 HÜL 186

Active Transport and Cluster Formation on Filament Networks — •Maren Westkott[1], Philip Greulich[2], and Ludger Santen[1] — [1]Department of Theoretical Physics, Saarland University, 66041 Saarbrücken, Germany — [2]Department of Physics & Astronomy, University of Edinburgh, Edinburgh EH9 3JZ, UK

We introduce a model for active transport on inhomogeneous networks embedded in a diffusive environment which is motivated by vesicular transport on actin filaments. In the presence of a hard-core interaction, particle clusters are observed that exhibit an algebraically decaying distribution in a large parameter regime, indicating the existence of clusters on all scales. The scale-free behavior can be understood by a mechanism promoting preferential attachment of particles to large clusters.

We also show that, by applying confining boundary conditions, a self-organization of the network toward a polarized structure is induced, even without explicit regulation and interactions. The polarity, can lead to separation of particle species adjusting to the enclosing geometry. The underlying mechanism can be understood by a linear theory similar to electrostatics. Finally we are discussing active transport phenomena on realistic cellular structures.

[1] P. Greulich and L. Santen, Eur. Phys. J. E 32, 191-208 (2010)

DY 5.10 Mon 16:30 HÜL 186

Modelling the adsorption of biofilms — •Olaf Leidinger and Ludger Santen — Department of Theoretical Physics, Saarland University, 66041 Saarbrücken, Germany

The very first step of the formation of a biofilm at a surface, the adsorption of proteins, is investigated. Therefore a colloidal model is used, in which proteins are described as polydisperse spheres interacting with each other via the framework of the DLVO theory – including steric repulsion, van der Waals and electrostatic interactions. Furthermore an internal degree of freedom, modelled as a change of geometry, is used to represent different conformations of a protein at the surface.

In qualitative agreement with experimental results, the adsorption kinetics of the initial biofilm formation was reproduced by means of Monte Carlo simulations [1,2]. The adsorption kinetics can be divided into three intervals: Initially the adsorption is limited by the flux of particles to the surface. At low concentrations the proteins spread at the surface in order to optimize the binding to the surface. At higher concentrations the adsorbed proteins are compacted due to particle-particle interactions and finally the surface coverage saturates. These dynamical regimes can be identified in experimental and theoretical investigations of the adsorbed amount. The comparison between experimentally and theoretically generated biofilms is completed by a detailed analysis of the point patterns connected to the adsorbed particles, which is carried out by means of integral measures.

[1] Y. Schmitt et al 2010 Biomicrofluidics 4, 032201
[2] A. Quinn et al 2008 EPL 81 56003

DY 5.11 Mon 16:45 HÜL 186

Thermally activated fragmentation of a homopolymer chain — •Simon Fugmann and Igor M. Sokolov — Humboldt-Universität zu Berlin, Department of Physics, Newtonstrasse 15, 12489 Berlin

We consider the thermally activated fragmentation of a homopolymer chain, which can exhibit strongly non-Markovian behavior on the timescale of interest. In our model the dynamics of the intact chain is a Rouse one until a bond breaks and bond breakdown is considered as a first passage problem over a barrier to an absorbing boundary. Using the framework of the Wilemski-Fixman approximation we calculate activation times of individual bonds for free and grafted polymer chains. We show that these times crucially depend on the length of the chain and the location of the bond yielding a minimum at the free chain ends. Going beyond the Wilemski-Fixman approximation we show that a generalized form of the renewal equation for barrier crossings serves to improve the quantitative agreement between numerical simulations and analytical predictions.