DY 53: Posters - Active Matter

Time: Thursday 17:00–19:30 Location: P1A

DY 53.1 Thu 17:00 P1A

Modelling the physical origin of bacterial biofilm morphotypes — •Horst-Holger Boltz and Stefan Klumpp — Institut für nichtlineare Dynamik, Fakultät Physik, Georg-August-Universität Göttingen, Göttingen, Deutschland

Microbial biofilms have been an important subject of study in the recent years due to their biological, medical and technological relevance. Biofilms are large multicellular structures of mi- croorganisms adherent to a substrate. The formation of these structures is usually accompanied by the production of an extracellular matrix formed by so-called extra-cellular polymeric substances (EPS). Thus, an elastic film is created that is growing due to the ongoing cell growth and division as well as the continued production of EPS. This growth leads to residual and dynamic stresses that are relieved by a non-planar pattern-formation (wrinkling). We present a reductionist model highlighting the physical origin of the different morphotypes observed.

DY 53.2 Thu 17:00 P1A

Bifurcations in a Model for Active Crystals: The Onset of Motion — •Lukas Ophaus, Svetlana Gurevich, and Uwe Thiele — Institut für Theoretische Physik, WWU, Münster, Germany

The conserved Swift-Hohenberg equation (or Phase-Field-Crystal [PFC] model) provides a simple microscopic description of the thermodynamic transition from a fluid to a crystalline state [1]. The model can be combined with the Toner-Tu theory for self-propelled particles to obtain a model for crystallization (swarm formation) in active systems [2]. Within the resulting active PFC model, resting and traveling crystals can be identified. Above a critical value of activity, crystals migrate with a well-defined velocity while keeping their spatial periodicity.

Like the passive PFC model [3], the active version describes a variety of localized clusters besides spatially extended crystals. We use a 1d model to explore how the bifurcation structure (slanted homoclinic snaking of localized states) is amended by activity. Numerical continuation is applied to follow resting and traveling localized states while varying the activity and mean concentration. In addition, we provide a general analytical criterion for the onset of motion in the nonlinear regime, that corresponds to a drift pitchfork bifurcation.

[1] M.J. Robbins et al., Phys Rev E 85, 061408 (2012)
[2] A.M. Menzel and H. Löwen, Phys. Rev. Lett. 110, 055702 (2013)
[3] U. Thiele et al., Phys Rev E 87, 042915 (2013)

DY 53.3 Thu 17:00 P1A

The growth and structural properties of microbial colonies in microfluidic devices — •Sebastian Mair — Max-Planck-Institut für Dynamik und Selbstorganisation, Am Faßberg 17, 37077 Göttingen, Deutschland

Microbial organisms are ubiquitous in nature. Escherichia coli bacteria serve as a model organism to study many phenomena pertaining to a large class of organisms. It is among the best understood microbes, yet relatively little is known about the colony growth mechanisms on a single-cell level. In the last decade the availability of microfluidic devices opened new pathways to experimental research. This facilitated the development of realistic simulation-schemes and related theory. We perform simulations of a growing microbial colony, where microbes are represented by mechanically interacting discrete elements, that incorporate the principles of reaction-diffusion systems. We study the microscale-growth, the dynamic properties and the emerging morphology of microbial colonies under the presence of convective flows. We compare our findings with experimental evidence.

DY 53.4 Thu 17:00 P1A

Dense Microswimmer Systems in Model Porous Media — •Jonathan Onody — DLR e.V. Köln, Deutschland, AG Prof. Thomas Voigtmann

We model the dynamics of active Brownian particles as model microswimmers in porous media by the mode-coupling theory of the glass transition.

The microswimmers are modeled as hard disks undergoing diffusive motion in both, translational and rotational direction. On top they have a constant velocity in a random direction. The particles are embedded in a porous background which is obtained by introducing a second species of particles that are not allowed to move and thus imitate obstacles for the microswimmers. We extend an approach by V. Krakoviack for passive particles without orientational degrees of freedom. The two-dimensional setting is described within the mode-coupling approach, such that an integro-differential equation for density fluctuations is obtained. The memory-kernel and first numerical results will be presented.

DY 53.5 Thu 17:00 P1A

Hot Brownian Nanoswimmers — •Romy Schachoff[1], Katrin Günther[2], Michael Mertig[2], and Frank Cichos[1] — [1]Universität Leipzig, Germany — [2]Technische Universität Dresden, Germany

Hot Brownian swimmers are thermally anisotropic Brownian particles driven by optical heating. Geometric asymmetry of the swimmers establishes an asymmetric temperature profile in the surrounding solvent upon particle heating. The thermo-osmotic flow along the surface of the swimmer leads to a phoretic self-propulsion. We studied hot Brownian swimmers that are synthesized from a gold nano particle of 50 nm in diameter and a tail of a DNA helix bundle (6HB) of a length of 400 nm. Here, the highly localized optical heating of the nanoparticles creates a steep temperature gradient over the DNA tail. The overall change in the diffusion coefficient for the chosen particle complex will be only in the per mille region, since rotational brownian motion randomizes the direction of propulsion. The ballistic propulsion is retained only for times shorter than the rotational diffusion time that scales with the radius cubed. We use our unique split focus geometry in twin-focus photothermal correlation spectroscopy to detect small flow velocities on small length and time scales (nm/ms) to show a clear swimmer characteristic of the gold nanoparticle DNA complex in dependence of the heating power that is clearly distinguishable from pure hot Brownian motion that is performed by heated gold nanoparticles themselves. Further, the split focus is arranged perpendicular to the optical axis to neglect flow velocities that are exerted by radiation pressure.

DY 53.6 Thu 17:00 P1A

Confined active Brownian particles: A comparison between simulations and analytical results — •Shibananda Das, Gerhard Gompper, and Roland G. Winkler — Theoretical Soft Matter and Biophysics (ICS 2/ IAS 2), Forschungszentrum Jülich, D-52425 Jülich, Germany

A thorough understanding of the relevant physical mechanisms of self-propelled objects, their collective behavior, and their properties in external fields and confinement, has promising applications in technology and health-care. This can be tackled with simplified and generic models of microswimmers such as the active Brownian particle (ABP) description. This model has been exploited to characterize the phase behavior and the non-equilibrium properties of active systems. We analyze the distribution function of active Brownian particles in confinement by computer simulations and analytical approach. We apply the well-known ABP model of a spherical colloid with a given propulsion direction which changes in a diffusive manner by an independent stochastic process. In addition, we study a somewhat more simplified theoretical model with independent stochastic processes along the Cartesian coordinates of the active velocity corresponding to a Gaussian, but non-Markovian, colored-noise process for the active velocity. Especially, we consider an ABP confined in a harmonic potential, which can be solved exactly. For non-harmonic potentials, we apply the Unified Colored Noise Approximation (UCNA) to find an approximate solution. The comparison between the simulation and analytical result reveals the applicability of the applied approximation schemes.

DY 53.7 Thu 17:00 P1A

DNA based molecular force sensors in reconstituted actin networks — •Christina Jayachandran[1], Max Wardetzky[2], Florian Rehfeldt[1], and Christoph Schmidt[2] — [1]Third Institute of Physics, Georg- August Universität — [2]Institute of Numerical and applied Mathematics, Georg- August Universität

Actin, among the other bio-polymers present in cells, is largely responsible for cellular shape and mechanical stability. The actin cytoskeleton which self-assembles into networks of crosslinked filaments and bundles is responsible for active cellular processes ranging from migration, di-

vision and intracellular transport to morphogenesis. Crucial for these processes is the spatial and temporal regulation of the structure and dynamics of the network and of the generation of forces, mostly by myosin motors.

To understand basic phenomena in such active networks, we investigate model networks comprised of semi-flexible actin filaments crosslinked by custom designed dsDNA constructs as flexible cross linkers. We also utilize these DNA constructs as force sensors in order to map stress distributions in the networks. We characterized the FRET-based stress sensors with a spectrophotometer. We study the macro- and micro-rheological properties of the actin/DNA networks, focusing on network failure mechanisms beyond a non-linear response.

DY 53.8 Thu 17:00 P1A

Phase behaviour of active Brownian particles — •Andreas Fischer and Thomas Speck — Institut für Physik, Johannes-Gutenberg-Universität Mainz, Germany

At sufficiently high densities and propulsion speeds, solutions of self-propelled colloidal particles can undergo a phase separation into large clusters and a dilute gas phase even without attractive interactions [1]. The same qualitative behaviour has been observed in simulations of 'active Brownian particles' - a minimal model capturing the main physical ingredients volume exclusion and persistence of motion. This motility induced phase separation is caused by a dynamical instability due to self-trapping of the particles and can be mapped onto that of passive fluids with attractive interactions via an effective free energy [2]. We extend this model to more general interactions and explore the phase behaviour combining analytic theory and numerical simulations.

[1] I. Buttinoni, J. Bialké, F. Kümmel, H. Löwen, C. Bechinger, and T. Speck, *Phys. Rev. Lett.* **110**, 238301 (2013)
[2] T. Speck, A.M. Menzel, J. Bialké, and H. Löwen, *J. Chem. Phys.* **142**, 224109 (2015)

DY 53.9 Thu 17:00 P1A

BD-Simulations on interfacially trapped active particles with long-ranged capillary interactions — •Jonathan Funk, Johannes Bleibel, and Martin Oettel — Institut für Angewandte Physik, Universität Tübingen, Deutschland

We study the dynamics of micron-sized colloidal particles trapped at a fluid interface. The particles deform the surface due to an external force (e.g. gravity), giving rise to long-ranged capillary interactions. Additionally the particles are self-propelled, with a constant velocity and changing direction due to rotational diffusion. In systems with a packing fraction ($\Phi > 0.3$) the active particles self-assemble in clusters even without an attractive potential by simply blocking each others motion. In systems with capillary interaction the ratio between the capillary force and an effective temperature is the determining factor for the clustering behavior. We study the movement in this capillary systems with lower densities, especially the active clustering effect and the diffusive characteristic of the active particles. Important observables of the system are the density distribution, the evolution of the Fourier modes of the density distribution, the average swimming speed and the persistence length of the active motion. With this observables, we can evaluate the phase behavior of the systems and establish a phase diagram.

DY 53.10 Thu 17:00 P1A

Highly Efficient Multivalent 2D Nanosystems for Inhibition of Orthopoxvirus Particles — Benjamin Ziem[1], Hendrik Thien[2,3], Katharina Achazi[1], Constanze Yue[3], Daniel Stern[3], Kim Silberreis[3], •Mohammad Fardin Gholami[4], Fabian Beckert[5], Dominic Gröger[1], Rolf Mülhaupt[5], Jürgen P. Rabe[4], Andreas Nitsche[3], and Rainer Haag[1] — [1]Institute of Chemistry and Biochemistry, Freie Universität Berlin — [2]Institute of Virology, University of Leipzig — [3]Robert Koch Institute, Center for Biological Threats and Special Pathogens, Berlin — [4]Department of Physics & IRIS Adlershof, Humboldt-Universität zu Berlin — [5]Institute for Macromolecular Chemistry, University of Freiburg

Efficient inhibition of cell-pathogen interaction to prevent subsequent infection is an urgent but yet unsolved problem. In this study, we developed a new 2D multivalent surface, functionalized with sulfated dendritic polyglycerol (dPG), to enable virus interaction. A simple "graft from" approach enhances the solubility of thermally reduced graphene oxide (TRGO) and provides a suitable 2D surface for multivalent ligand presentation. Polysulfation is used to mimic the heparan sulfate-containing surface of cells and to compete with this natural binding site of viruses. Here, orthopoxvirus strains are used as model viruses as they use heparan sulfate for cell entry. Scanning force microscopy (SFM) showed that the dPGs were successfully grafted to the TRGO sheets, resulting in abundant presence of dPG on the sheets. The newly designed graphene derivatives demonstrate excellent binding as well as efficient inhibition of orthopoxvirus infection.