DY 33: Statistical physics of biological systems I (joint session BP/DY)

Time: Wednesday 15:00–17:30 Location: H4

DY 33.1 Wed 15:00 H4

Active noise fuels the heterogeneous anomalous diffusion of inert nanoparticles in the cytoplasm — •Adal Sabri[1], Xinran Xu[2], Diego Krapf[2], and Matthias Weiss[1] — [1]Experimental Physics I, University of Bayreuth, Germany — [2]School of Biomedical Engineering, Colorado State University, CO, USA

Diffusive motion of inert particles in the cytoplasm of living cells is generally assumed to be driven by thermal noise. This assumption appears particularly justified for the frequently observed sublinear growth of the particles' mean square displacement ('subdiffusion').

In order to probe quantitatively to which extent also active noise contributes to (sub)diffusional motion in living matter, we have introduced inert quantum dots into the cytoplasm of living cells and performed extensive single-particle tracking experiments in untreated cells and after disrupting the cytoskeleton. In all cases a pronounced subdiffusive motion of the particles with a distinct anti-correlation of successive steps was observed. Yet, the degree of the diffusion anomaly and the generalized diffusion coefficients showed marked changes when the integrity of the cytoskeleton was compromised, i.e. particles moved less vivid when cytoskeleton-associated active transport was erased. This observation highlights that cytoplasmic subdiffusion is partially fueled by active noise. In line with this notion, several measures of the trajectories, e.g. the gaussianity, highlight a strongly heterogeneous random walk with a temporally and/or spatially varying noisy driving.

DY 33.2 Wed 15:15 H4

Self-organised segregation of bacterial chromosomal origins — •Sean Murray — Max Planck Institute for Terrestrial Microbiology, Marburg, Germany

In spite of much effort, many aspects of chromosome segregation in bacteria remain unclear. Like many other bacteria, the chromosomal origin of replication in Escherichia coli is dynamically positioned throughout the cell cycle. Initially maintained at mid-cell, where replication occurs, origins are subsequently partitioned to opposite quarter positions. However the mechanism underlying this is unknown. Here, we provide an explanation based on the self-organisation of the Structural Maintenance of Chromosomes complex, MukBEF. We propose that a non-trivial feedback between the self-organising MukBEF gradient and the origins leads to accurate positioning and partitioning as an emergent property. We find excellent agreement with quantitative experimental measurements and confirm key predictions. In particular, we show that origins exhibit biased motion towards MukBEF, rather than mid-cell, consistent with the model. Overall, our findings suggest that MukBEF and origins act together as a self-organising system for chromosome segregation and introduces protein self-organisation as an important consideration for future studies of chromosome dynamics.

DY 33.3 Wed 15:30 H4

Perfect anomalous transport of subdiffusive cargos by molecular motors in viscoelastic cytosol — •Igor Goychuk — Institute for Physics and Astronomy, University of Potsdam, Karl-Liebknecht-Str. 24/25, 14476 Potsdam-Golm, Germany

Multiple experiments show that various submicron particles such as magnetosomes, RNA messengers, viruses, and even much smaller nanoparticles such as globular proteins diffuse anomalously slow in the viscoelastic cytosol of living cells. Hence, their sufficiently fast directional transport by molecular motors such as kinesins is crucial for the cell operation. It has been shown recently that the traditional flashing Brownian ratchet models of molecular motors are capable to describe both normal and anomalous transport of such subdiffusing cargos by molecular motors with a very high efficiency. This work elucidates further an important role of mechanochemical coupling in such an anomalous transport. It shows a natural emergence of a perfect subdiffusive ratchet regime due to allosteric effects, where the random rotations of a "catalytic wheel" at the heart of the motor operation become perfectly synchronized with the random stepping of a heavily loaded motor, so that only one ATP molecule is consumed on average at each motor step along microtubule. However, the number of rotations made by the catalytic engine and the traveling distance both scale sublinearly in time. Nevertheless, this anomalous transport can be very fast in absolute terms.

[1] I. Goychuk, Biosystems, in press, arXiv:1809.08032 [physics.bio-ph]

Invited Talk DY 33.4 Wed 15:45 H4

Chaos in self-propelled droplets — •Annette Zippelius and Reiner Kree — Georg-August-Universität Göttingen, Institut für Theoretische Physik, Friedrich-Hund Platz 1, 37077 Göttingen

Intracellular flow can be generated by a variety of active mechanisms, such as motors transporting cargo. The actively generated flow has at least two effects: it can drive cell locomotion and simultaneously play a central role for intracellular transport. We develop increasingly more complex, but analytically solvable models, starting from a simple fluid droplet or a biphasic droplet, consisting of a fluid and a rigid gel. Active forces or stresses, which are co-localised on the gel, generate internal flow. The trajectories of tracer particles which are advected by the internal flow, are shown to display the full richness of dynamical systems, ranging from closed orbits to quasiperiodic motion and chaotic trajectories in general. We discuss the mixing properties of the internal flow as well as its significance in comparison to diffusive transport. Despite chaos inside the droplet, locomotion of the droplet as a whole remains simple and regular, e.g. motion on a straight line or a spiral.

DY 33.5 Wed 16:15 H4

Three-dimensional membrane confinement and geometry dictate excitable signaling dynamics in Dictyostelium cells. — •Marcel Hörning[1,2,3] and Tatsuo Shibata[2] — [1]Institute of Biomaterials and Biomolecular Systems, University of Stuttgart, 70569 Stuttgart, Germany — [2]Laboratory for Physical Biology, RIKEN Center for Biosystems Dynamics Research, Kobe 650-0047, Japan — [3]Institute for Integrated Cell-Material Sciences, Kyoto University, 606-8501, Kyoto, Japan

Propagating waves on the plasma membrane mediate the membrane protrusive activities in Dictyostelium and mammalian cells. Most studies focus on the dynamics extracted from single focal planes only. Thus, the relation between the dynamics and three-dimensional cell shape remains elusive, due to the lack of signaling information about the unobserved part of the membrane.

We show that PtdInsP3 wave dynamics are directly regulated by the three-dimensional geometry - size and shape - of the plasma membrane. By introducing an analysis method that extracts the three-dimensional spatiotemporal activities on the entire cell membrane, we show that PtdInsP3 oscillatory waves self-regulate their dynamics within the confined membrane area. This leads to changes in speed, orientation and pattern evolution, following the underlying excitability of the signal transduction system. This findings emphasize the role of the plasma membrane topology in reaction-diffusion driven biological systems and indicate its importance in other mammalian systems.

DY 33.6 Wed 16:30 H4

Non-equilibrium spatial scaling reveals intrinsic features of the active driving — •Federica Mura, Grzegorz Gradziuk, and Chase Broedersz — Arnold-Sommerfeld-Center for Theoretical Physics and Center for NanoScience, Ludwig-Maximilians-Universität München

Recent experiments indicate non-equilibrium activity in a host of biological systems, including chromosomes, cell membranes, and the cytoplasm. Measuring and quantifying non-equilibrium dynamics in such systems is a major challenge in biophysics, due to their many-body nature and the limited number of variables accessible in an experiment. We investigate what information concerning the system's non-equilibrium state can be extracted by non-invasively tracking a subset of degrees of freedom. To this end, we develop a general, yet simple stochastic model of soft elastic networks with spatially-varying internal driving, representing internal enzymatic force generation. With this model, we determine the scaling behavior of non-equilibrium dynamics from the phase space currents of tracer particles with varying spatial separations in the system. Finally, we will discuss how the non-equilibrium dynamics measured on different length scales can reflect the intrinsic microscopic features of the internal active driving.

DY 33.7 Wed 16:45 H4

Dynamical states of a living network — •Philipp Fleig, Mirna

Kramar, Michael Wilczek, and Karen Alim — Max-Planck-Institut für Dynamik und Selbstorganisation, Göttingen, Germany

Understanding the emergence of behaviour in living systems from underlying physical mechanisms is a major goal of biophysics. Even very simple, non-neural organisms like the slime mould *Physarum polycephalum* show remarkably complex behaviour including growth, adaptation of the network morphology and foraging for food - despite only being a single, giant, network-shaped cell.

Behavioural dynamics, here, emerge directly from living matter, namely the coordinated contractions of the cell's tubular shaped actomyosin cortex undergoing rhythmic contraction every 100 seconds. We decompose this spatiotemporal dynamics into principal components and identify a reduced set of characteristic large-scale contraction patterns spanning the network. Based on this dictionary of patterns we are able to determine the typical sequence of the network's response patterns to a controlled stimulus, mimicking a natural response scenario. We also find spontaneously occurring breaking of coherent contraction dynamics into decoherent patterns over short time-scales. Finally, we note a power law distribution of the relative amplitudes of the principal components. This may be key in explaining the observed dynamical features from the underlying biomechanics. Our findings connect behaviour with characteristic states of living matter.

DY 33.8 Wed 17:00 H4

Active droplets can center internal particles — •David Zwicker[1,2], Anthony Hyman[3], and Frank Jülicher[2] — [1]Max Planck Institute for Dynamics and Self-Organization, Göttingen — [2]Max Planck Institute for the Physics of Complex Systems, Dresden — [3]Max Planck Institute of Cell Biological and Genetics, Dresden

Active droplets are non-equilibrium systems where chemical reactions drive fluxes of the droplet material. These fluxes can control the droplet nucleation as well as the droplet size and thereby stabilize many droplets against the typical coarsening observed in passive systems. Here, we study how the non-equilibrium fluxes affect solid particles inside such active droplets. We find that particles get centered when the droplet is maintained externally, while particles are expelled in the opposite case of autocatalytic droplets. In this case, only catalytically active particles can be centered. An example of such a situation are centrosomes in biological cells. Our theory thus accounts for the observed central positioning of centrioles and it generally provides a mechanism for controlling the morphology of active droplets.

DY 33.9 Wed 17:15 H4

Mesoscopic roughness analysis of propagating cell fronts: physical statistics as an in-vitro phenotype probe — •Guillaume Rapin[1], Audrey Rawleigh[2], Aziza Merzouki[3], Ermano Moriggi[2], Bastien Chopard[3], Thierry Giamarchi[1], Steven A. Brown[2], and Patrycja Paruch[1] — [1]DQMP, University of Geneva, Switzerland — [2]IST, Universtiy of Zurich, Switzerland — [3]CSD, University of Geneva, Switzerland

The competition between elasticity and disorder governs the geometry and dynamics of interfaces in many systems, from ferroic domain walls to bacterial colonies. In the latter case, it has been used as a framework to explore cell front evolution, with local mapping of displacements and forces, and the origin of the cell front roughness.

Here, we report on the geometry and dynamics of propagating rat epithelial cell fronts in artificial wound healing assays over 72 hours, studied over 5 orders of magnitude in length scale ranging from $1\mu m$ to $2cm$. Under standard conditions, they present 3 distinct regimes: power law growth of the roughness with characteristic roughness exponent values of $\zeta = 0.55$ at sub-cell length scales, and of $\zeta \approx 0.3$ at few-cell length scales, reaching a scale-independent maximum beyond $400\mu m$. Exposure to a selection of chemical inhibitors targeting cell division rates, mobility, or intercellular communications changes this roughening behaviour, as well as the initial and steady-state dynamics of the cell front. Our results suggest that collective motion on the order of 4-10 cells plays a key role in the roughness evolution of the front. These experimental results will be compared to numerical simulations.