BP 20: Poster IIIa

Active Matter, Statistical Physics in Biological Systems, Systems and Network Biophysics

Time: Wednesday 11:00–14:30 Location: Poster B

BP 20.1 Wed 11:00 Poster B

Influence of Environmental Inhomogeneity on Active Particle Dynamics in Obstacle Parks: A Numerical Study — •Zeinab Sadjadi[1] and Heiko Rieger[1,2] — [1]Department of Theoretical Physics & Center for Biophysics, Saarland University, 66123 Saarbrücken, Germany — [2]Leibniz Institute for New Materials INM, 66123 Saarbrücken, Germany

Biological microorganisms have the ability to detect external fields and environmental signals, and they can adjust their dynamics accordingly. The redirected motion in response to a gradient of a stimulus, called taxis, is a vital navigation mechanism in many biological systems. Our focus lies on topotaxis, the ability of particles to sense the geometrical and topographical features of their surroundings. We numerically study the dynamic behavior of active particles moving in pillar parks. First, by introducing a disorder in the diameter size as well as the position of pillars, we investigate the influence of environmental inhomogeneity on particle dynamics. we also demonstrate how imposing a gradient in the disorder in geometrical characteristics could bias the direction of active agents and induce a topotaxis in the pillar park. Our results are of technological importance for design of efficient taxis devices.

BP 20.2 Wed 11:00 Poster B

Order from disorder: active particles with random alignment interactions — •Eloise Lardet and Thibault Bertrand — Imperial College London, London, UK

In 1995, Vicsek et al. wrote a seminal paper describing a simple model that displays a transition from disorder to collective ordered behaviour. It describes a system of self-propelled point particles that align with their neighbours within a certain radius. This minimal model displays rich nonequilibrium behaviours such as flocking and banding. Inspired by the random couplings of spin glass models, I present numerical findings of introducing Gaussian distributed pairwise couplings into a self-propelled particle system. Through adding further disorder by increasing the standard deviation of the Gaussian distribution that the couplings are drawn from, we are able to observe the emergence of global polar order in systems where the majority of couplings are anti-aligning.

BP 20.3 Wed 11:00 Poster B

Design and manufacture of self-propelled particles driven by light — •Jannis Fischer, Alejandro Jurado Jiménez, and Timo Betz — Third Institute of Physics, University of Göttingen, Göttingen, Germany

In all living things, biochemical processes take place on scales that are not visible to the naked human eye. However, when compared to forces we encounter in our daily lives, other forces tend to be more dominant: Frictional forces have a considerable influence on the movements of particles while inertial forces can often be neglected [1]. Therefore, it is of great interest and also a challenge to create particles that can actively move on such scales. Getting micrometer-sized particles to move in a controlled manner within living tissue would prove to be a great advantage for specific drug delivery or the design of micro-robots. A fundamental part of movement is propulsion. If the particles themselves can generate active movement, they are called self-propelled particles. One recently proposed method is to use homogeneous light illumination in conjunction with transparent particles that demonstrate a gradient of refractive index. Here the refraction of the light leads to a momentum transfer, which then drives the active movement. In this work, both a simulation and the production of the corresponding particles are used to investigate which particle shape leads to the greatest forces and thus to the highest velocities.

[1] E.M. Purcell, American Journal of Physics, 45(1) (1977).

BP 20.4 Wed 11:00 Poster B

Simulating a field-theoretic model of transcription condensates — •Kathrin Hertäg[1], Joshua Robinson[2,3], and Thomas Speck[1] — [1]ITP4, Stuttgart, Deutschland — [2]Institut für Physik, Johannes Gutenberg-Universität Mainz, Deutschland — [3]H.H. Wills Physics Laboratory, University of Bristol

Phase separation of macromolecules has recently attracted substantial interest, in particular in the context of membrane-less organelles in the cell. These organelles are typically modeled as condensates. Instead of coarsening to a fully phase separated state, such protein condensates form stable droplets of finite size in vivo. Therefore, an important question is the role of non-equilibrium processes since the physical processes underlying stable droplet behavior are not yet resolved. Here we study active model B+, a scalar field theory developed in the context of motile active matter, and employ methods of active liquid theory to explore activity as the underlying mechanism for condensate stabilization.

BP 20.5 Wed 11:00 Poster B

Learning in slime molds? — Adrian Büchl, •Lisa Schick, and Karen Alim — School of Natural Sciences, Technical University of Munich, Germany

Learning and adapting to changing environments is crucial for the survival for living organisms. Generally, learning involves the formation of memory by gathering and storing information and applying this memory in novel contexts. In neuronal organisms, learning can be directly mapped to adaptations in the neuronal network. However, information processing and memory formation can also be found in non-neuronal organisms like slime molds that lack a central nervous system. The slime mold *Physarum polycephalum* is well known for its network adaption processes as a response to environmental cues. Can we consider this complex behavior learning? Using bright-field microscopy observations, we investigate how *P. polycephalum* networks react to repetitive negative blue light stimuli. We observe migratory behavior persisting much longer than network adaptation, and by this, establish memory of environmental stimuli in the slime molds migration dynamics. By looking at flow patterns and response times to different stimuli, we set out to unravel if learning exists in organisms without a nervous systems.

BP 20.6 Wed 11:00 Poster B

Mesoscopic hydrodynamic modeling of *Trypanosoma brucei* — •Zihan Tan, Julian Isaac Ufoma Peters, and Holger Stark — Institut für Theoretische Physik, Technische Universität Berlin, 10623 Berlin, Germany

Trypanosoma brucei is notorious for causing African trypanosomiasis also known as sleeping sickness. Due to significant challenges in experimentation, a physical understanding of how *T. brucei* interacts with fluid environments and navigates through confinements, typically in blood vessels but also in tissue, remains largely elusive. To this end, mesoscopic hydrodynamic modeling can provide additional insights. Through elaborate comparison with experiments, our group has developed an in-silico *T. brucei* model coupled with a viscous solvent, simulated by multiparticle collision dynamics (MPCD). The *T. brucei* body is discretized into vertices and facets, allowing for adequate bending and torsion while satisfying surface and volume constraints. Moreover, a flagellum, starting from a pocket at the thicker posterior end of the body, is laterally attached. A sinusoidal bending wave is imposed along the flagellum. It deforms the whole cell body and through the interaction with the ambient fluid generates propulsion. Since the dynamics of MPCD solvents is independently computed inside each cubic collision unit, we could considerably accelerate our simulations using GPU parallel computing. Our model has been validated to exhibit realistic hydrodynamic and mechanical properties of *T. brucei*. In particular, we focus on how the model *T. brucei* navigates through a microchannel with constrictions or containing hard or soft obstacles.

BP 20.7 Wed 11:00 Poster B

Evaluating the cell-cell interactions of swimming flagellated microbes — •Henrik Groh[1], Alexandros A. Fragkopoulos[1], Colin-Marius Koch[2], Michael Wilczek[2], and Oliver Bäumchen[1] — [1]University of Bayreuth, Experimental Physics V, 95447 Bayreuth, Germany — [2]University of Bayreuth, Theoretical Physics I, 95447 Bayreuth, Germany

In suspensions of living microorganisms individual cells often interact leading to larger-scale emergent effects. Such collective phenomena

are studied more extensively than the single-cell behaviour and the interactions that lead to the overall effect. However, understanding their mutual interactions is necessary to fully understand the emergence of their collective behaviour. For example, the aggregation of *Chlamydomonas reinhardtii*, a swimming unicellular microbe, in the presence of self-generated oxygen gradients has been investigated [1], but the cell-cell interactions in this system have yet to be explored. Here, we investigate the mutual interactions of microswimmers in a quasi-2D suspension of *C. reinhardtii* with high temporal and spatial resolution. This involves the determination of an effective potential between two cells via the relationship between the incoming and outgoing cell motility of a collision event. A particular challenge in this context is to identify the influence of the flagella on the contact process. With our investigations we gain more detailed insights into the swimming behavior of *C. reinhardtii* and, thus, better understand their population-level properties.
[1] A.A. Fragkopoulos et al., *J. R. Soc. Interface* **18**, 20210553 (2021).

BP 20.8 Wed 11:00 Poster B

Quantifying vascular morphology on a chip — •Leonie Karr, Fatemeh Mirzapour, and Karen Alim — Technische Universität München

Our human vasculature is dynamic, growing and re-organizing not only in development but continuously adapting its morphology. Yet, what determines vessel formation and branching in healthy and disease state seems complex given the multitude of contributing factors.

Our focus lies in growing a human vasculature within the controlled environment of a chip, with the goal of quantifying the flow properties of self-organized in vitro networks. Additionally, we are examining the interplay of various cell types on these self-organized morphologies. Employing image analysis techniques alongside flow simulation methods, our objective is to accurately quantify how flow and cell types determine network architecture. The results obtained from our analyses will significantly contribute to the development of next-generation therapeutics aimed at targeting vessel development.

BP 20.9 Wed 11:00 Poster B

Metabolically controlled bioconvection in suspensions of photoactive microbes — •Florian Böhme[1], Alexandros Fragkopoulos[1,2], Nicole Drewes[2], and Oliver Bäumchen[1,2] — [1]University of Bayreuth, Experimental Physics V, 95447 Bayreuth, Germany — [2]Max Planck Institute for Dynamics and Self-Organization (MPIDS), 37077 Göttingen, Germany

Photosynthetic microbes have evolved and successfully adapted to environmental changes of their habitat. In the abscence of light, they can still sustain their biological functionality and metabolic activity through aerobic respiration. However, for the soil-dwelling microalga *Chlamydomonas reinhardtii*, their environment is often deprived of both oxygen and light, resulting in a significant reduction of their swimming velocity [1]. Here, we investigate the effect of these motility changes on the emergence of bioconvection, a collective phenomenon that arises due to the natural tedency of the bottom-heavy cells to move against gravity. We show that the motility change that is associated to the metabolic switch between photosynthesis and anaerobic respiration is sufficient to induce or prevent the formation of bioconvective plumes. Our experiments use a side-view perspective allowing us to extract the local cell density and flow fields of single bioconvection plumes, in addition to the wavelength and the spatiotemporal evolution of the pattern. In particular, we extract how these parameters depend on the single-cell motility.
[1] A.A. Fragkopoulos et al., *J. R. Soc. Interface* **18**, 20210553 (2021).

BP 20.10 Wed 11:00 Poster B

Effect of flagella length on the motility of confined microbes — •Tom Sosniok, Alexandros Fragkopoulos, and Oliver Bäumchen — University of Bayreuth, Experimental Physics V, 95447 Bayreuth, Germany

Many microorganisms utilize flagella to propel and navigate through their surrounding liquid environment. Often times though, the natural habitats of such microswimmers comprise confined spaces, and therefore, cell interactions with boundaries play an important role on their navigation. *Chlamydomonas reinhardtii*, a biflagellated, green microalga that is commonly found in soil, typically swims in close proximity to curved boundaries [1]. We found that this near-wall swimming motility is controlled by gradients of wall curvature and steric interactions between the flagella and the surface [2]. Here we explore the effect of the flagella length on the motility and surface interactions of the cells using two different *C. reinhardtii* strains with different flagella lenghts in quasi-2D circular confinement. We extract information about their motion from their mean squared displacements and visualize the wall-guided swimming via relative and radial probability densities. By comparing the results for both strains we can directly analyse the influnce of the flagella lenght on their motility and find that steric interactions alone are insufficient to describe our observations.
[1] T. Ostapenko et al., *Phys. Rev. Lett.* **120**, 068002 (2018).
[2] J. Cammann et al., *PNAS* **118**, e2024752118 (2021).

BP 20.11 Wed 11:00 Poster B

Tracking and analysis of active droplet dynamics: from image processing to synthetic biology — •Roberto Menichetti[1,2], Matteo Scandola[1], and Raffaello Potestio[1,2] — [1]Physics Department, University of Trento, Trento, Italy — [2]INFN-TIFPA - Trento Institute for Fundamental Physics and Applications, Trento, Italy

Active matter can harness energy from its surroundings and propel itself away from equilibrium, with its constituents absorbing energy from the environment and dissipating it, e.g. through motion or the exertion of mechanical forces. The investigation of these systems offers promising new perspectives on the field of non-equilibrium statistical physics, further paving the way for the design of innovative life-like materials and devices. In this work, we analyse the behaviour of a synthetic active matter system consisting of liquid droplet surfers whose self-propulsion decays over time [1]. By relying on a synergistic combination of techniques, such as computer vision algorithms for accurate droplet detection and analyses grounded on non-equilibrium statistical mechanics and graph theory, we quantitatively characterise all the stages of the dynamic evolution of the system, from its initial diffusive regime up to the generation of large clusters of droplets that appear as the activity wanes. The presented work showcases a comprehensive analysis of an actively evolving system, offering not only a general pipeline for the investigation of analogous problems, but also a deep perspective at the intersection between physics and synthetic biology. [1] Tanaka, S. et al., Phys. Rev. E 91, 032406 (2015).

BP 20.12 Wed 11:00 Poster B

Entropy production of active crystals — •Connor Roberts and Gunnar Pruessner — Imperial College London, United Kingdom

We consider a two-dimensional triangular lattice of active particles that interact with their nearest neighbours through a general pair potential. We study this “active crystal” as a means of characterising the dense phase of active matter at high packing fraction. By approximating the interactions to leading order, we obtain exactly the fully time-dependent two-point position correlation and position-self-propulsion cross-correlation matrices for an active harmonic crystal. Importantly, our approximation retains non-trivial terms that are often neglected despite capturing the essential geometry of a particle’s local potential. From our expressions of the correlation matrices, we subsequently derive the entropy production, covariance, and mean square displacement. The entropy production is found to have a general form akin to that of non-interacting active particles in external potentials. This may suggest a universal expression for the entropy production that is valid for any system of active particles subject to linear forces, regardless of the forces’ origins.

BP 20.13 Wed 11:00 Poster B

Quantification and model-based classification of the aging dynamics of single endothelial cells under confluent conditions — •Anselm Hohlstamm, Andreas Deussen, Stephan Speier, and Peter Dieterich — Institut für Physiologie, TU Dresden

Endothelial cells, which are grown into a two-dimensional, confluent layer, exhibit intricate movement patterns and aging processes. While maintaining dynamic cell-cell contacts, individual cells perform a continuous, correlated motion. It is the objective of this study to quantify and classify these dynamics. Therefore, we studied the migration of human umbilical vein endothelial cells. Their nuclei were marked using a fluorescent dye and observed for 48 hours, with data collected at 10-minute intervals. We were able to monitor several 10.000 cells in each of the 10 experiments. The mean squared velocity of the cells decreased as a function of time, which could be characterized with two temporal scales. In addition, the mean squared displacement revealed a temporal transition of scaling $\sim t^{\alpha}$ from more directional movements with $\alpha \sim 1.6$ for short times towards a subdiffusive behavior with $\alpha \sim 0.4$ for long times. Based on the analysis of the temporal velocity autocorrelation, we constructed different stochastic models as combinations of

Ornstein-Uhlenbeck and fractional processes that were supplemented by aging contributions. Bayesian inference allowed selecting the best model given the experimental data. In summary, the movement of cells under confluent conditions can be characterized as an aging dynamics in a non-thermal environment.

BP 20.14 Wed 11:00 Poster B

Reinforcement Learning in Active Colloidal Reservoir Computing — •Jonas Scheunemann, Samuel Tovey, and Christian Holm — Institute for Computational Physics, Stuttgart, Germany

The capacity to process information through a physical system can be exploited and further understood by using the recently introduced framework of physical reservoir computing. The concept involves utilizing the dynamics of nonlinear physical systems for time series forecasting, speech recognition, or classification tasks. The characteristics of an effective reservoir are still under discussion, and we use reinforcement learning to delve deeper into this question. Our reservoir substrate consists of a swarm system of active matter colloids, which has recently been demonstrated to work using a modified Reynolds boids model. We train the swarm by rewarding the colloidal agents through a concentration field approach, inspired by the behaviour of E. coli, and tested by forecasting a chaotic time series with a Lorenz attractor input. As the swarm reservoir's memory depends on the colloids' correlation time, we employ the Langevin equation to set up the system at diverse temperatures. We identify a potential connection between temperature and prediction accuracy, opening up research on the advantages of temperature-induced noise in the reservoir.

BP 20.15 Wed 11:00 Poster B

Radius-Dependent Dynamics of Active Spot — •Arghavan Partovifard and Holger Stark — Institut für Theoretische Physik, Technische Universität Berlin, Berlin, Germany

Active nematics exhibit distinctive behavior for a spatially varying activity [1,2]. Utilizing the Doi-Edwards theory supplemented by an active stress tensor [1], we investicate an active nematics solely confined to a circular spot by switching off activity outside of the spot. Depending on the spot radius, we observe different emerging dynamics. At very small radii, two $+1/2$ defects form a spiral and rotate synchronously, while the velocity field displays a single vortex. As the radius of the activity spot increases, the two $+1/2$ defects gradually separate from each other, while circling around each other. When the $+1/2$ defects approach the border of the spot, a third $+1/2$ defect forms. Subsequently, one of the original $+1/2$ defects leaves the spot, and the two remaining $+1/2$ In this regime, the velocity field exhibits two or three vortices moving within the spot. With further increase of the spot radius, pairs of $\pm1/2$ defects are constantly generated and they annihilate with other defects. The corresponding velocity field consists of many vortices moving chaotically, similar to what is observed in active turbulence. We thoroughly investigate and classify the occuring dynamics.

[1] Partovifard *et al.*, submitted (2023).

[2] Rønning *et al.*, R. Soc. Open Sci. **10**, 221229 (2023).

BP 20.16 Wed 11:00 Poster B

Efficient Bayesian Inference of Active Brownian Motion using Reinforcement-learned Brownian Bridges — •Sascha Lambert and Stefan Klumpp — Georg-August-Universität Göttingen, Institut für Dynamik Komplexer Systeme

Active Brownian Particles (ABPs) describe microswimmers by a Langevin equation that combines stochastic fluctuations and deterministic forces, including the swimmer's active propulsion and the interactions with obstacles.

Full Bayesian inference of the parameters of the Langevin equation can be achieved within the framework of Particle Pseudo-Marginal Metropolis-Hastings algorithms (PMMH). These algorithms sample from the full posterior of the model parameters, conditioned on experimental observations. A key strategy in these algorithms is using a particle filter for resampling the trajectories between observations.

The sampling efficiency is largely determined by uncertainties of the experimental measurements, with lower uncertainties resulting in reduced acceptance rates of newly generated samples. The rotational degrees of freedom and the resulting memory of ABPs produce strong temporal correlations that are not easily resolved using particle filters, as they only filter based on individual observations. We construct an approximative Brownian Bridge to increase the particle swarm's coherence and to guide the swarm between the observations. This approach increases the resampling efficiency by several orders of magnitude.

The exact guidance parameters depend on the full non-linear system and can be learned through reinforcement learning.

BP 20.17 Wed 11:00 Poster B

Self-organized criticality in animal collectives: the effects of network topology and heterogeneities — •Bianca Pacini[2,4], Yunus Sevinchan[1,2], Carla Vollmoeller[1,2], David Bierbach[1,3], Jens Krause[1,3], and Pawel Romanczuk[1,2] — [1]Science of Intelligence, TU Berlin, Berlin, Germany — [2]Institute for Theoretical Biology, HU Berlin, Berlin, Germany — [3]Leibniz-Institute of Freshwater Ecology and Inland Fisheries, Berlin, Germany — [4]Department of applied science and technology, Politecnico di Torino, Torino, Italy

Large-scale collective biological systems – such as large animal groups – have been suggested to operate at or near so-called critical points, at which they show maximum sensitivity towards environmental signals [1]. We have studied large fish shoals of sulphur mollies (*Poecilia sulphuraria*) in Southern Mexico, which perform collective diving cascades as a response to predation. Through agent-based numerical simulations and analyzing videos and images, we investigated the structure and role of the underlying social interaction network. As changes in spatial structure are strictly local, the resulting network and its changes will strongly depend on the spatial wiring mechanism. Important question remain unanswered: How do local heterogeneities affect how behaviour spreads? What are the effects of changes in the network on the behavioural contagion and discrimination ability of the system? Our results contribute to a better understanding of mechanisms of self-organization and how collectives may self-tune their distance to criticality. [1]Gomez-Nava et al. *Fish shoals resemble a stochastic excitable system*, Nature Physics 19, 2023

BP 20.18 Wed 11:00 Poster B

Controlling Droplet Formation and Dissolution with Chemical Reactions — •Gerrit Wellecke, Jan Kirschbaum, and David Zwicker — Max Planck Institute for Dynamics and Self-Organization, Göttingen, Germany

Droplets formed by phase separation are vital for intracellular organization and function. Chemical reactions can generally control the formation and dissolution of such droplets. To understand how cells can influence droplets in space and time, we here consider a ternary system that displays bistabilities between homogeneous and phase-separated states. We use a thermodynamically consistent approach to describe the reactions, which allows us to quantify the energy dissipation during transitions in such a system. We identify optimal protocols for reaction-controlled droplet formation and dissolution in the bistable regime. Our model identifies plausible mechanisms for how cells control their droplets and suggests paths for controlling synthetic soft matter systems.

BP 20.19 Wed 11:00 Poster B

Clonal dynamics of surface-driven growing tissues — •Ruslan Mukhamadiarov[1,2], Matteo Ciarchi[1,2], Fabrizio Olmeda[1,2], and Steffen Rulands[1,2] — [1]LMU, München, Germany — [2]Max Planck Institute for the Physics of Complex Systems, Dresden, Germany

The self-organization of cells into complex tissues relies on a tight coordination of cell behavior. Identifying the cellular processes driving tissue growth is key for understanding the emergence of tissue forms and for devising targeted therapies for aberrant growth, such as in cancer. Inferring the mode of tissue growth, whether it is driven by cells on the surface or cells in the bulk, is possible in cell culture experiments, but difficult in most tissues in living organisms (in vivo). Genetic tracing experiments, where a subset of cells is labelled with inheritable markers have become important experimental tools to study cell fate in vivo. Here, we show that the mode of tissue growth is reflected in the size distribution of the progeny of marked cells. To this end, we derive the clone-size distributions using analytical calculations and an agent-based stochastic sampling technique in the limit of negligible cell migration an cell death. We show that for surface-driven growth the clone-size distribution takes a characteristic power-law form with an exponent determined by fluctuations of the tissue surface. Our results allow for the inference of the mode of tissue growth from genetic tracing experiments.

BP 20.20 Wed 11:00 Poster B

Measuring activity from particle trajectories — •Lukas Abegg[1], Till M. Muenker[1], Gabriel Knotz[2], Anna-Lotta Höper[2], Matthias Krüger[2], and Timo Betz[1] — [1]Third Institute of Physics, Georg August Universität Göttingen — [2]Institute of Theoretical Physics, Georg August Universität Göttingen

Is it possible to distinguish activity from thermal fluctuations just from observed trajectories? The newly introduced statistical quantity mean back relaxation aims to achieve exactly this by using three-point correlation functions. This non-dimensional function yields a measure for deviation from equilibrium within a confined system. It is calculated as the average displacement of a tracer particle under the condition of having moved the distance d in advance. For an equilibrium process this quantity results in a long time value of $\frac{1}{2}$. However, deviation from this value is a marker for broken detailed balance. To gain deeper inside into this new statistical measure, we investigate this quantity inside a controlled system, namely a viscoelastic polyacrylamide gel. This probe was tuned to imitate the mechanical properties of cells, containing polystyrene particles with size of one micron. To drive this system out of equilibrium, we use a movable optical tweezer to simulate active motion of the particle. The mean back relaxation is calculated for all trajectories and fitted with an analytical solution for a viscoelastic system. The results are used to quantify the diffusion coefficient of the trapping laser and thus, the activity of the system tuned by our experimental realisation. Additionally, we can calculate the shear modulus $G^\star$ from this result.

BP 20.21 Wed 11:00 Poster B

Phase separation on membranes with matter exchange and dimerization — •Riccardo Rossetto[1], Kueyoung Kim[2], and David Zwicker[1] — [1]Max Planck Institute for Dynamics and Self-Organization — [2]Department of Chemistry, The Pennsylvania State University

Patterns form on membranes in a large variety of biological contexts. In many cases, the patterns are affected by material exchange between the membrane and the bulk. Moreover, the involved biomolecules often also form short polymers and interact unspecifically. We describe this situation with a thermodynamically consistent minimal model, which accounts for phase separation, dimerization, and material exchange between the membrane and the bulk. While these mechanisms are understood individually, interesting nonlinear effects emerge from their combination. We illustrate this by explaining experimental data from the PAR patterning system, which exhibits dimerization and membrane binding. The general conclusions from our model unveil fundamental mechanisms of pattern formation on membranes and will help us explain more biological observations in the future.

BP 20.22 Wed 11:00 Poster B

Unraveling the Role of Physical Interactions in Multicomponent Phase Separation — •Yicheng Qiang, Chengjie Luo, and David Zwicker — Max Planck Institute for Dynamics and Self-Organization, Am Faßberg 17, 37077 Göttingen, Germany

Phase separation is a crucial phenomenon in soft matter and biophysics, e.g., for forming biomolecular condensates. Yet, our understanding of how the physical interactions between components affect phase separation remains limited, particularly in systems with many components. Investigations are often restricted to systems with very few species, are focused on pair interactions, or only consider the stability of the homogeneous state. We developed a powerful method to study coexisting phases in multicomponent fluids and used it to analyze two cases. First, we concentrate on the equilibrium behavior of a many-component system with pair interactions. We demonstrate that the number of coexisting phases can significantly differ from the number of unstable modes identified through stability analysis. Second, we explore the impact of higher-order interactions on phase separation. Our findings reveal that three-body interactions can trigger additional phases compared to pair interactions, underscoring the crucial role of higher-order interactions in phase separation. In summary, our study elucidates the nuanced role of physical interactions in phase separation, offering valuable insights for investigating biomolecular condensates in cells.

BP 20.23 Wed 11:00 Poster B

Probing Neuronal Dendrites by First-Passage Properties — •Fabian Hubertus Kreten[1,2], Ludger Santen[1,2], and Reza Shaebani[1,2] — [1]Department of Theoretical Physics, Saarland University, Saarbrücken, Germany — [2]Center for Biophysics, Saarland University, Saarbrücken, Germany

Probing Neuronal Dendrites by First-Passage Properties

Part of the neuronal signal transmission mechanism is the dendritic tree, an arborous structure of gradually thickening channels leading to the soma. Along these channels bulbous protrusions (spines) are located at which synapses can form.

Neurodegenerative diseases alter the structure of the dendritic tree and by that perturb this finely tuned machinery. Probing the structure of a patient's dendrites could thereby give insight into the progression of the disease in question.

Previously, studies of how the structural parameters of dendritic trees influence their transport properties and how these structural properties might be regained from measurements of tracer particles have been undertaken. [1,2] In the present work we extend these studies to hypothetical tracer particles which spontaneously enter the dendritic tree, perform a random walk on the dendritic tree and when reaching the soma spontaneously decay while emitting a signal.

[1] M. Reza Shaebani et al., Phys. Rev. E 98 (4 2018)

[2] Robin Jose, Ludger Santen and M. Reza Shaebani, Biophysical Journal 115.10 (2018)

BP 20.24 Wed 11:00 Poster B

Spherical harmonics and the morphology of red blood cells — •Thomas John, Felix Maurer, and Christian Wagner — Campus E26, 66123 Saarbrücken

Red blood cells are highly flexible and, at rest (without flow), exhibit a biconcave shape. Under flow conditions, altered environmental parameters, or due to diseases, this shape can deviate significantly from its resting state. Using 3D images obtained through confocal microscopy, we demonstrate how the shape, and thus the surface, can be represented as an expansion in spherical harmonics. This parameterization is rotationally invariant and can be utilized to distinguish between various cell shapes. This, in turn, can be done conventionally or through AI-based methods.

BP 20.25 Wed 11:00 Poster B

General motifs of flagella number control and cellular counting — •Richard Swiderski, Florian Rasshofer, and Erwin Frey — LMU, Munich, Germany

Monopolarly flagellated bacteria tightly control the flagellum assembly in order to construct only a single flagellum. Building upon models of the highly conserved C-ring assembly machinery, we present a theoretical study which identifies key motifs for number control in stochastic reaction networks. These findings not only help us to better understand the counting mechanism behind flagellum assembly, but can also be applied to more general processes which require the control of particle numbers. In the future this might be applied in medical treatments which rely on precise dosage on a cellular level.

BP 20.26 Wed 11:00 Poster B

Mean-filed theory for fibrillar aggregation and nematic-isotropic phase separation — •Kafa Alameh[1,2] and Christoph Weber[1] — [1]Mesoscopic Physics of Life, Institute of Physics, Universitätsstr. 1, Augsburg, Germany — [2]Center for Systems Biology Dresden, Pfotenhauerstr. 108, 01307 Dresden, Germany

Cells use droplet-like compartments to spatially organize their interior into sub-compartments, known as membrane-less organelles. Such organelles are liquid condensates and provide distinct physical environments for chemical processes. Recently, it has been shown that various proteins with beta-sheet structures, such as FUS, are involved in protein aggregation diseases such as ALS and Alzheimer's. Moreover, FUS-rich condensates were shown to undergo aberrant "phase transition," leading to fibrillar, solid-like aggregates. Several theoretical studies have focused on how phase-separated compartments affect the irreversible aggregation of dilute monomers; however, the interplay between aggregation and phase separation at non-dilute conditions remains elusive. Such conditions are particularly relevant at the condensate interface, where aggregates are often nucleated and enriched. Here, we propose a mean-field theory accounting for the interplay between aggregation, condensate formation, and phase transition at condensate interfaces. We find a rich phase behavior; three coexisting phases differing in density and the degree of order: disordered-dilute, disordered-dense, and nematic-dense phases. Our theory suggests the possibility of finding ordered membrane-less organelles in regulatory pathways of neurodegenerative diseases.

BP 20.27 Wed 11:00 Poster B

Tangential diffusion and motility-induced mixing transition in growing spheroidal cell colonies — •Torben Sunkel[1,2], Lukas Hupe[1,2], and Philip Bittihn[1,2] — [1]MPI for Dynamics and Self-Organization, Göttingen, Germany — [2]Institute for the Dynamics of

Complex Systems, Göttingen University, Göttingen, Germany

Growth is a known driver of cellular dynamics in a range of dense aggregates from bacterial colonies to developing tissues to tumors. Hence, universal physical principles underlying these dynamics are of great interdisciplinary interest. Here, we study the emergent dynamics arising from the interplay of growth, steric repulsion and motility in a minimal agent-based model of exponentially growing three-dimensional spheroids. Our results show that, without cell motility, deterministic motion caused by overall volume expansion dominates the dynamics of individual cells in the radial direction, while growth and division lead to cellular-scale diffusive motion in the tangential direction, whose magnitude is largely independent of expansion velocity. Despite this small-scale diffusion, we show that cell lineages are subject to confinement in their local environment, quenching weak cell motility. At higher motility, we find a transient regime of tangential superdiffusivity, accompanied by global mixing of cells. Reminiscent of glassy dynamics, we find a diverging mixing time scale at the transition. We also explore the influence of passive components like extracellular matrix. Our observations highlight the complex mechanical interaction between global expansion and local cell activity and may serve as a baseline to identify additional biological mechanisms in experiments.

BP 20.28 Wed 11:00 Poster B

A Study on Tradeoffs Induced Landscapes Model — •Muna Turki[1], Suman Das[2], Muhittin Mungan[3], Rotem Gross[4], and Joachim Krug[5] — [1]Institute of Biological Physics - University of Cologne — [2]Institute of Ecology and Evolution - University of Bern — [3]Institute of Biological Physics - University of Cologne — [4]Institute of Biological Physics - University of Cologne — [5]Institute of Biological Physics - University of Cologne

Effects mutations have on the fitness of a genotype are environment dependent. The endangering pressure of antibiotics directs bacterial cultures towards the selection of resistant mutants. These resistant mutants are equipped with mutations that increase the fitness of bacteria in the presence of antibiotics allowing for adaptation, however they come with a cost in the form of decreasing fitness in absence of antibiotics as the resistant mechanisms the mutant bacteria develop tend to be energy-costly, which is a tradeoff the mutant has to endure.

Tradeoff Induced Landscape (TIL) is a mathematical model that was motivated by antibiotic dose-response curves of Ciprofloxacin resistance in Escherichia coli strains which model evolution in a changing environment through adaptation-cost tradeoffs. The model assumes a non-epistatic accumulative effect of mutations on the fitness parameters, generating fitness landscapes with exceptionally smooth topology and high accessibility.

Recent experimental data on evolution of Escherichia coli in the context of β-lactam resistance are available through which the model could be tested and modified.

BP 20.29 Wed 11:00 Poster B

A Wang-Landau-based approach to sample the configurational space of complex biomolecules — •Camilla Spreti[1,2], Raffaello Potestio[1,2], and Roberto Menichetti[1,2] — [1]Physics Department, University of Trento, via Sommarive, 14 I-38123 Trento, Italy — [2]INFN-TIFPA - Trento Institute for Fundamental Physics and Applications,Trento, Italy

The Wang-Landau algorithm is a Monte Carlo (MC) method commonly employed to estimate the density of states (DoS) of a system through a random walk exploring the available energy space. This allows access to the thermodynamic properties of the system at all temperatures by means of a transformation from the microcanonical to the canonical ensemble. Although the algorithm was originally developed to study discrete systems, we propose a modified version of the method for sampling continuous systems, such as polymers, proteins and complex molecules. The implementation of the method is described and showcased with simple examples of liquid and polymeric systems.

BP 20.30 Wed 11:00 Poster B

Data-driven, ecosystem-based approach to cancer development — Alessandra Accettola, •Margherita Mele, and Raffaello Potestio — Physics Department, University of Trento, via Sommarive, 14 I-38123 Trento, Italy

Cancer cells exhibit a heterogeneous genetic and phenotypic landscape that evolves over time. Within this complexity lies the challenge of distinguishing critical driver mutations from less important ones.

Our approach, inspired by a minimalist model of microbial communities, explores hierarchically structured ecosystems to mimic the dynamics of resource competition. Using HiC data from different tumour stages, we model interactions to unravel the systematic differences that characterise evolutionary transitions from healthy to tumour cells.

Through this data-driven effort, we aim to achieve a dual goal: to delineate the systematic differences that drive evolutionary dynamics; and to identify critical features that drive such dynamics, ultimately providing the research community with a practical and useful instrument to comprehend and possibly hinder cancer development

BP 20.31 Wed 11:00 Poster B

Evolution on fitness landscapes with universal negative epistasis — •Daniel Oros and Joachim Krug — University of Cologne, Institute for Biological Physics, Germany

An approach to model evolution is by describing it as a process that selects viable genotypes from the space of all possible ones. Each genotype is assigned a fitness value, corresponding to its reproductive success. The search process then takes place in the landscape defined by the genotype and their corresponding fitness, referred to as fitness landscape. The notion of epistasis refers to the interaction between different mutations in the genotype and their effect on fitness. We investigate certain fitness landscapes that are structured [1]. The concept of universal negative epistasis (UNE) imposes short and long ranged effects on genotype interactions. A way to sample UNE landscapes and an analysis of them is presented together with a connection to the tradeoff induced landscapes (TIL) model [2]. This leads to a lower bound on the number of genotypes from which a peak is accessible from, already known from the TIL-Model. Recent experiments, see [1], highlight the importance of highly accessible landscapes. How their basins of attraction, meaning all genotypes from which a peak is accessible by increasing its fitness by mutations, differ is discussed along with general mathematical properties of UNE.

[1] Krug, J. and Oros, D. (2023) Evolutionary accessibility of random and structured fitness landscapes, https://arxiv.org/abs/2311.17432

[2] Suman G Das et al. Predictable properties of fitness landscapes induced by adaptational tradeoffs. In: eLife 9 (May 2020)

BP 20.32 Wed 11:00 Poster B

Modelling host-pathogen interactions: combining population dynamics with behavioural analysis — •Soham Mukhopadhyay[1], Jonathan Pollock[2], Ben Fabry[3], David Voehringer[2], and Vasily Zaburdaev[1] — [1]Max-Planck-Zentrum für Physik und Medizin, Erlangen, Germany — [2]Department of Infection Biology, University Hospital Erlangen, Friedrich-Alexander University Erlangen, Germany — [3]Biophysics Group, Department of Physics, Friedrich-Alexander-University Erlangen

Helminth infections affect a large proportion of the world's population and cause significant morbidity. There are no vaccines against helminths, and the factors shaping how these parasites migrate through their hosts require further elaboration. To better understand the immune system response we develop a mathematical model describing the helminth load in different organs of the host as a function of time. We use the rodent helminth *N.brasiliensis* as a model to contrast migration dynamics in immunocompetent and susceptible mice during primary and secondary infection. We model the progression of infection as a system of coupled, time-delayed equations which allow us to link the initial infective dose to the number of eggs shed to the environment by adult worms and compare model predictions with experimental data. For a more microscopic insight into the behavior of larvae at different developmental stages, we carry out biophysical characterization of larval motility in in-vitro settings. Combining these results we aim to achieve a quantitative description of the infection progression in the host.

BP 20.33 Wed 11:00 Poster B

Mechanics of decision-making in light-trapped slime mold — •Lisa Schick, Emily Eichenlaub, Fabian Drexel, Siyu Chen, and Karen Alim — School of Natural Sciences, Technical University of Munich, Germany

The human brain continuously makes conscious and unconscious decisions to navigate everyday life's complexity. Lacking a central nervous system, complex behavior and remarkable decision-making abilities have been reported for non-neuronal organisms like unicellular slime molds. Yet, decision-making is solely described as a response to processed information of the environment and focusing on the outcome rather than the decision-making process. We, here, trap the unicellular slime mold *Physarum polycephalum* in blue light shapes and follow its decision-making process to find an escape route. We find that decision-making is established by a dynamic adaptation of the flow pattern inside the tubular structure of the organism inducing a pressure buildup for overall mass reallocation.

BP 20.34 Wed 11:00 Poster B

Quantification of the network morphology of *Physarum polycephalum* under environmental effects — •Valentin Pauli, Lisa Schick, and Karen Alim — School of Natural Sciences, Technical University of Munich, Germany

To fully understand an organism, one must consider both its intrinsic properties and its environmental interactions. Network-forming organisms, such as fungi and slime molds, continuously reorganize their networks. *Physarum polycephalum*, a unicellular slime mold, shows a remarkable adaptability in response to various environmental factors. In this study, we investigate environmental factors which lead to specific changes in network architecture and dynamics. By systematically altering the environment, we aim to decipher the factors that influence network adaptations in *Physarum polycephalum* and understand what functions underlie the observed adaptations. Understanding how the environment shapes *Physarum polycephalum* not only provides a better insight into the mechanisms of this extraordinary organism, but also contributes to a broader knowledge of adaptive behaviors in biological systems.

BP 20.35 Wed 11:00 Poster B

Periodic impulse response of ERK signaling in HeLa cells — •Stefan Köstler[1], Thoma Itoh[2], and Kazuhiro Aoki[2] — [1]Max Planck Institute for Dynamics and Self-Organization, Göttingen, Germany — [2]National Institute for Basic Biology, National Institutes of Natural Sciences, Okazaki, Japan

The Extracellular-signal Regulated Kinase (ERK) signaling pathway is one of the most important signaling pathways controlling the cell cycle and survival of most cells. Defects in this pathway are a critical step in the development of many cancers, making it a valuable target for treatment strategies. To gain insight into its response behavior, we activate ERK from different layers of the pathway by impulse stimulation. The ERK activity is quantified by using the fluorescent biosensor ERK-KTR-iRFP, which is exported from the nucleus upon phosphorylation. We show that impulse stimulation of two different layers of the pathway, either by EGF or the optogenetic tool Opto-RAF, both lead to a repeated activation of ERK with a characteristic period of about 65 minutes.

BP 20.36 Wed 11:00 Poster B

Dynamical Network Remodeling of Physarum polycephalum — •Mathieu Le Verge-Serandour and Karen Alim — School of Natural Sciences, Technical University of Munich, Germany

Remodeling of a network is one of the hallmarks of biological flow networks, ensuring their optimal morphology. Due to limited building costs, the removal of vessels allows these networks to reallocate matter to minimize dissipation while ensuring maximum coverage,. *Physarum polycephalum* is a unicellular slime mold organized as a two-dimensional tubular network that evolves drastically over a few hours, evacuating a large zone of a few millimeters squared. Unfavorable competing parallel veins are first removed to form a tree-like structure, where veins prune sequentially until complete evacuation of the zone. Analyzing time-lapses of the slime mold, we find an exponential decrease in the number of tubes reproduced by our model based on the network hierarchy. We explore the dynamics of simulated networks by looking at the influence of the global outlets, tube length distribution, and network hierarchy. Our approach to flow networks may be generalized to pruning flow networks, as during embryonic development, stroke events, or information encoding.

BP 20.37 Wed 11:00 Poster B

Systematic Classification and Quantification of Microbial Interactions — •Timon Wittenstein, Gerrit Ansmann, Adriana Espinosa-Cantú, and Tobias Bollenbach — Institute for Biological Physics, University of Cologne, Germany

Microbial communities play a vital role in Earth's ecosystems, yet understanding how individual interactions shape the emergent properties of such communities remains a challenge. In a simplified laboratory system, we integrate theory and experiment to explore microbial interactions, focusing on a gut bacteria collection of the model organism *C. elegans.*

Informed by theoretical considerations, we employ a conditioned media approach to quantify pairwise interactions between individuals, aiming to differentiate various interaction types beyond just positive and negative classifications. We are able to identify trophic behaviours, such as resource competition or the exchange of nutrients, as well as more direct 'strong' interactions, like the transfer of toxins or vitamins.

The resulting interaction data unveils relationships among ecological interactions. For instance, competing populations exhibit more negative strong interactions, while more complex environments foster increased syntrophic interactions. Furthermore, these insights allow us to build a dynamical model and then quantitatively test its predictions in an experiment, offering a comprehensive approach for a deeper understanding of microbial ecology.