DY 54: Active Matter V (joint session BP/DY)

Time: Friday 9:30–13:00   Location: H 1028

DY 54.1 Fri 9:30 H 1028
Noise reduction with droplets of many components — •TYLER HARMON — Leibniz Institute for Polymer Research, Dresden, Germany

Noise control is critical for cell homeostasis and decision making. We previously showed that phase separation could be used to robustly reduce noise in phase separating systems. Others have suggested that noise buffering has the strongest suppression of noise parallel to the co-existence tie lines. They proposed that correlations from features such as coupled transcription could align the noise with the tie lines, significantly reducing the noise. Here we show how the kinetics associated with phase diagrams naturally aligns the noise to the tie lines. This helps optimize the noise reduction in systems with many components.

DY 54.2 Fri 9:45 H 1028
Pulsatile Control of Actomyosin Contraction — •JAMES CLARKE and JOSÉ ALVARADO — Department of Physics, The University of Texas at Austin, Austin, Texas, USA

Cells are always under control and tightly control their mechanics. The actomyosin cytoskeleton is one important cellular structure which receives control signals and turns that into contraction. Existing research has investigated the mechanical properties of actomyosin materials. However, these are usually in terms of responses to external stresses, which may be absent in living systems. Here we instead measure response to biochemical control signals. We apply a control-theoretical framework and investigate quasistatic actomyosin contractility in response to external pulsatile signals of UV light that release ATP molecules from light-sensitive NPE-cages. Across all experimental conditions, we report statistically indistinguishable maximum strains achieved by the gel. We find that the coupling from energy input to contractile strain is weakly nonlinear, with a s^{-2} dependence in Laplace space. Our novel characterization is not only an essential first step in a better understanding of how cells control cytoskeletal contractions via internal control signals. It is also an essential first step towards using biomimetic actomyosin active gels for microrobotic applications.

DY 54.3 Fri 10:00 H 1028
Self-assembly of myofibrils in muscle cells — FRANCINE KOLLEY[1], IAN D. ESTABROOK[1], CLARA SIDOR[2], CLEMENT RODIER[2], FRANK SCHNORRER[2], and •BENJAMIN M. FRIEDRICH[1] — [1]Physics of Life, TU Dresden, Germany — [2]IBDM, Marseilles, France

Voluntary motions and heartbeat in animals is driven by contractions of myofibrils, millimeter-long acto-myosin bundles with characteristic periodic patterns of micrometer-sized sarcomeres. Yet, the physical mechanisms that drive the self-assembly of these "cytoskeletal crystals" are not understood. Here, we report data demonstrating that myosin molecular motors and actin-crosslinking Z-disc proteins form sarcomeric patterns first, while actin becomes polarity-sorted only hours later [1]. This data informs mathematical models of sarcomere self-assembly that are able to replicate periodic sarcomeric patterns, either through (i) non-local interactions between spatially-extended myosin filaments and Z-disc proteins, which bind to an actin scaffold, or (ii) catch-bond behavior of the prominent Z-protein α-actinin in response to active myosin forces. Both models are robust to small-number fluctuations for a wide parameter range in agent-based simulations, providing plausible mechanisms of early sarcomere self-assembly.
Next, even after the establishment of sarcomeric patterns, new sarcomeres are added to myofibrils, despite these being under mechanical tension. We report a new mechanism of controlled "self-rupture" in which a mother sarcomere divides into two daughter sarcomeres by splitting its myosin stack, and establishing a new Z-disc in between. [1] https://www.biorxiv.org/content/10.1101/2023.08.01.551279v1

DY 54.4 Fri 10:15 H 1028
Size-coordination trade-off in Trichoplax adhaerens, an animal lacking a central nervous system — MIRCEA R. DAVIDESCU[1], •PAWEL ROMANCZUK[2,3], THOMAS GREGOR[4], and IAIN D. COUZIN[5,6,7] — [1]Dept. of Ecology and Evolutionary Biology, Princeton University, USA — [2]Dept. of Biology, Humboldt Universität zu Berlin, Germany — [3]Excellence cluster "Science of Intelligence", Berlin, Germany — [4]Lewis-Sigler Institute for Integrative Genomics, Joseph Henry Laboratories of Physics, Princeton University, USA — [5]Dept. of Collective Behaviour, Max Planck Institute for Animal Behavior, Konstanz, Germany — [6]Dept. of Biology, Chair of Biodiversity and Collective Behaviour, University of Konstanz, Germany — [7]Centre for the Advanced Study of Collective Behavior, University of Konstanz, Germany

Coordination with increasing size is a fundamental challenge affecting collective systems from biofilms to governments. The earliest multicellular organisms were decentralized, with indeterminate sizes and morphologies, as exemplified by Trichoplax adhaerens, arguably the earliest-diverged and simplest motile animal. We investigated the coordination in T. adhaerens by observing the degree of collective order in locomotion across animals of differing sizes and found that larger individuals exhibit increasingly disordered locomotion. We reproduced this effect using an active elastic cellular sheets model and show that this relationship is best recapitulated across all body sizes when the simulation parameters are tuned to criticality. We discuss possible implications of this on the evolution hierarchical structures such as nervous systems in larger organisms.

DY 54.5 Fri 10:30 H 1028
SwarmRL: Lowering the entry barrier to reinforcement learning for active matter research — •SAMUEL TOVEY, CHRISTOPH LOHRMANN, and CHRISTIAN HOLM — Institute for Computational Physics, University of Stuttgart, Stuttgart, Germany

As scientists learn to better design and control devices at a microscopic scale, so too must the tools used to control these devices develop. Multi-agent reinforcement learning (MARL) is a powerful machine learning paradigm for learning control strategies in agents at all scales. Recent work has applied MARL to controlling microscopic agents, whether in learning chemo-taxis behaviour, object manipulation, or swarming.
This talk introduces SwarmRL, a powerful open-source library for applying MARL to microscopic environments. We demonstrate how SwarmRL is used in our group to control micro-scale agents in simulation and experiments and how to interpret the learned policies. The talk introduces the library broadly before looking into results from our recent work using SwarmRL, including a better understanding of the role of temperature on learned strategy and the emergence of chemotactic behaviour in unstable regimes. Finally, we discuss our vision for the future of the library and its integration into experiments and simulations.

DY 54.6 Fri 10:45 H 1028
Sensitive shape dependence in agent-based simulations of growth — •JONAS ISENSEE[1,2], LUKAS HUPE[1,2], RAMIN GOLESTANIAN[1,2,3], and PHILIP BITTIHN[1,2] — [1]Max Planck Institute for Dynamics and Self-Organization, Göttingen, Germany — [2]Institute for the Dynamics of Complex Systems, Faculty of Physics, University of Göttingen, Germany — [3]Rudolf Peierls Centre for Theoretical Physics, University of Oxford, United Kingdom

We consider purely sterically interacting particles that grow and divide in two-dimensional confinement. Such models have been used to study cell dynamics in tissues and bacterial aggregates. A common feature in these is the rich emergent orientation dynamics due to anisotropic shapes, directed growth, and confinement. By introducing continuously tuneable tip variations around a common rod shape and characterizing the resulting orientation dynamics in space and time, we identify trends in the collective dynamics caused by certain shape features. In particular, we find a strong effect of small deviations from the traditional rod shape. Our results separate the effects of aspect ratio and particle shape, contribute to the characterization of the effective dynamics at large and intermediate length scales, and thereby also provide strategies for the design of future artificial systems.

15 min. break

Invited Talk DY 54.7 Fri 11:15 H 1028
Large scale collective dynamics of bacteria suspensions — •ERIC CLEMENT[1], BENJAMIN PEREZ ESTAY[1], ANKE LINDNER[1], CARINE DOUARCHE[2], JOCHEN ARLT[3], VINCENT MARTINEZ[3], WILSON POON[3], and ALEXANDER MOROSOV[3] — [1]PMMH-ESPCI, Sorbonne University, Paris , France — [2]FAST, University Paris-Saclay —

[3]School of Physics & Astronomy, University of Edinburgh

Fluids laden with swimming micro-organisms have become a rich domain of applications and a conceptual playground for the statistical physics of active matter. Such active bacterial fluids display original emergent phases as well as unconventional macroscopic transport properties, hence leading to revisit standard concepts in the physics and hydrodynamics of suspensions.

Here, I will present and discuss some recent advances on the spontaneous emergence of a "critical fluid" state for dense bacteria suspensions, characterized by a vanishing viscosity and and a divergent "active turbulence" scale controlled by the confinement. Close to the transition I will also describe a novel collective state leading to very large scale coherent motion of the bacteria.

DY 54.8   Fri 11:45   H 1028

Analysis techniques for active matter simulations — •Lukas Hecht, Kay-Robert Dormann, Aritra Mukhopadhyay, Kai Spanheimer, Mahdieh Ebrahimi, Suvendu Mandal, and Benno Liebchen — Institut für Physik kondensierter Materie, Technische Universität Darmstadt, Hochschulstr. 8, D-64289 Darmstadt, Germany

Simulations of active matter systems provide a promising route to understand collective phenomena and the non-equilibrium physics of active matter. Prominent models for active matter systems comprise particle-based models such as the active Brownian particle model and continuum models such as the active model B+. To analyze the data obtained from the numerical solution of these models, currently, many researchers develop in-house code. Here, we present the Active Matter Evaluation Package (AMEP), a unified framework to analyze active matter simulations. This Python library is easy to use and provides a powerful and simple interface for handling large data sets. The package features various methods for calculating observables, visualizing results, and analyzing data from molecular-dynamics, Brownian-dynamics, and continuum simulations. These features allow the user, for example, to easily calculate spatial and temporal correlation functions, to perform cluster analyses, to visualize simulation results, and to study phase separation, pattern formation, and critical phenomena in active matter systems.

DY 54.9   Fri 12:00   H 1028

Unveiling Active Fluctuations in Cellular Aggregates through Derivation of Hydrodynamic Transport — •Subhadip Chakraborti[1,2] and Vasily Zaburdaev[1,2] — [1]Friedrich-Alexander-Universität Erlangen-Nürnberg, Erlangen, Germany — [2]Max-Planck-Zentrum für Physik und Medizin, Erlangen, Germany

The biological functionality of cellular aggregates is a collective result of the activities and displacements of individual constituent cells. The theoretical characterization of this activity involves hydrodynamic transport coefficients, such as diffusivity and conductivity. Motivated by the clustering dynamics in bacterial microcolonies, we propose a model for active multicellular aggregates on 1D lattice. Employing macroscopic fluctuation theory, we derive a fluctuating hydrodynamics framework for this model system. Both semi-analytical theory and microscopic simulations reveal that non-equilibrium microscopic parameters exert a significant influence on the hydrodynamic transport coefficients, causing a notable decrease within the clusters. Additionally, we illustrate how the active nature of intercellular interactions disrupts the conventional Einstein relation that establishes a connection between transport coefficients and fluctuations. This study not only provides a comprehensive understanding of the hydrodynamic transport in bacterial microcolonies but also offers valuable tools for experimental investigations in other systems involving active cellular aggregates, such as tumor spheroids and organoids.

DY 54.10   Fri 12:15   H 1028

Expansion-flow driven orientation patterns in systems of growing rods — •Lukas Hupe[1,2], Jonas Isensee[1,2], Ramin Golestanian[1,2,3], and Philip Bittihn[1,2] — [1]Max Planck Institute for Dynamics and Self-Organization, Göttingen, Germany — [2]Institute for the Dynamics of Complex Systems, Faculty of Physics, University of Göttingen, Germany — [3]Rudolf Peierls Centre for Theoretical Physics, University of Oxford, United Kingdom

In densely-packed two-dimensional systems of growing rods, such as bacteria, a number of experimental and numerical studies report long-range nematic alignment in the presence of confinement. In some geometries, spatially heterogeneous preferred orientations are observed. So far, these effects have been qualitatively explained using continuum theories of growing active nematics adapted to the specific geometry under investigation.

Here, we first show how the shear rate tensor of the expansion flow alone can be used to qualitatively predict time-averaged orientation patterns from the geometry of the confinement. We apply this method to a series of example geometries and compare with results from agent-based simulations. To quantitatively describe alignment strength, we then develop a simple model which takes into account advection and explore its potential for cross-prediction across different geometries.

Our results provide a unifying theoretical framework and highlight the role of domain geometry in shaping nematic order of growing systems.

DY 54.11   Fri 12:30   H 1028

Walking the Road to Active Nematic Turbulence — •Malcolm Hillebrand[1,2] and Ricard Alert[1,2] — [1]Max-Planck-Institut für Physik komplexer Systeme, Nöthnitzerstr 38, Dresden 01187 — [2]Center for Systems Biology Dresden, Pfotenhauerstr 108, 01307 Dresden, Germany

Active matter, where internal energy consumption drives motion, exhibits a richly complex array of behaviours. In particular, the appearance of turbulent-like flows at very low Reynolds number, termed active turbulence, provides possibilities for chaotic fluid motion at scales as small as the surface of a cell. Here, in a hydrodynamic model of an active nematic, we thoroughly investigate the transition from smooth shear flow all the way to fully developed active turbulence. We utilise tools from dynamical systems theory, including Lyapunov exponents and time series analysis of velocity fields, as well as energy spectra and scaling laws, to describe the series of changes in dynamics that occur as we increase the activity. We find a sequence of increasingly unpredictable rearrangements between steady flow states that eventually give rise to continuously unstable chaos via a regime of apparent multistability. In addition, intermittent flow characteristics of fully active turbulent flows from simulations are compared to data from kinesin-microtubule experiments.

DY 54.12   Fri 12:45   H 1028

Activation fronts, fluctuations and criticality in the initiation of collective motion — •Parisa Rahmani[1], Hadrien-Matthieu Gascuel[2,3], Richard Bon[2], and Fernando Peruani[1,3] — [1]LPTM, UMR 8089, CY Cergy Paris Universite, 95302 Cergy-Pontoise, France — [2]CNRS, Centre de Recherches sur la Cognition Animale, F-31062 Toulouse Cedex 9, France — [3]Universite Cote d'Azur, Laboratoire J. A. Dieudonne, UMR 7351 CNRS, F-06108 Nice Cedex 02, France

Collective motion is generally not a continuous process, and collectives display repeated transitions from static to moving phases. The initiation of collective motion – of an initially static group – is a crucial process to ensure group cohesion and behavioral synchrony that remains largely unexplored. Here, we investigate the statistical properties of the initiation of collective motion. We find that the information propagates as an activation wave, whose speed is modulated by the velocity of the active agents, where both, the magnitude and direction of the agents' velocity play a crucial role. The analysis reveals a series of distinct dynamic regimes, including a selfish regimes that allow the first informed individuals to avoid predation by swapping position with uninformed individuals. Furthermore, we unravel the existence of a generic and intimate connection between the initiation of collective motion and critical phenomena in systems with an absorbing phase, showing that in a range of agents' velocities the initiation process displays criticality. The obtained results provide an insight in the way collectives distribute, process, and respond to the local environmental cues.