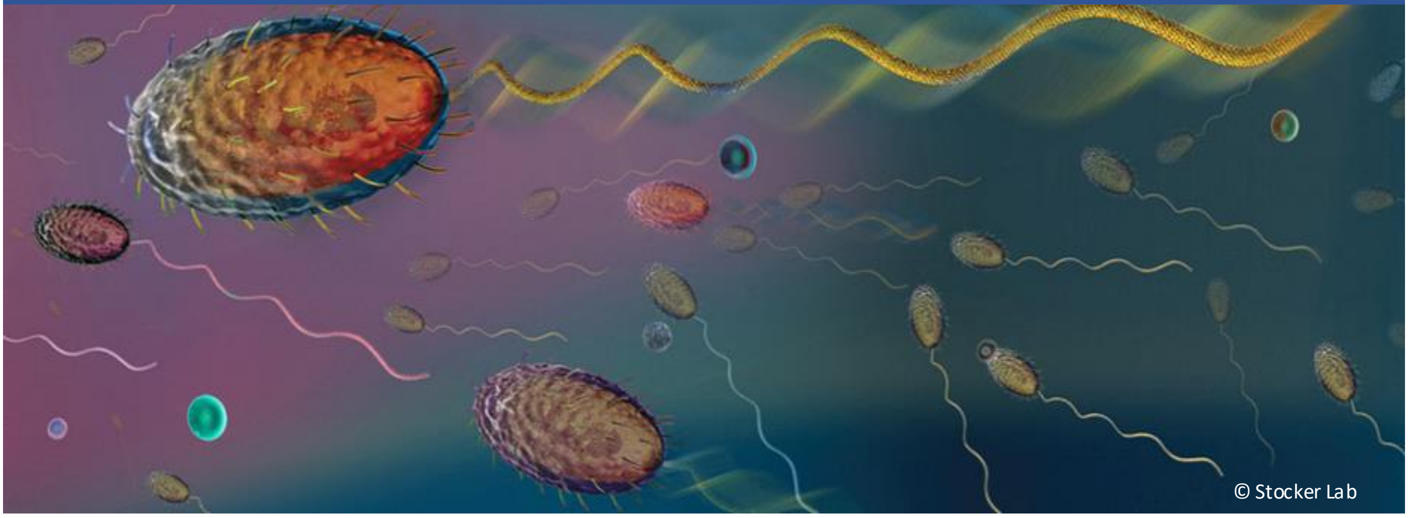
International Conference

MOTILE ACTIVE MATTER 2024

November 18-21, 2024, Gustav-Stresemann-Institut, Bonn, Germany



© Stocker Lab

This project has received funding from the European Union’s Horizon 2020 research and innovation program under the Marie Skłodowska-Curie grant agreement No 955910.

The latest electronic version of this booklet can be found at:
https://etn-phymot.eu/phymot-workshop/

The open-source LATEX template, AMCOS_booklet, used to generate this booklet is available at
`https://github.com/maximelucas/AMCOS_booklet`

Contents

About

PHYMOT

PHYMOT is a European Consortium of Universities, Research institutes and industrial Partners located in Denmark, France, Germany, Israel, Italy, Spain, Switzerland and the United Kingdom.

Beneficiaries		
Forschungszentrum Jülich	Gerhard Gompper	Shubham Anand
		Bohan Zhang
IMEDEA/UIB Esporles	Marco Polin	Luc Zorrilla
	Idan Tuval	Medea Zanoli
Technical University Denmark	Thomas Kiørboe	Federica Miano
ETH Zürich	Roman Stocker	Riccardo Foffi
Uni. Claude Bernard Lyon 1	Cecile Cottin-Bizonne	Tommaso Pietrangeli
University Rome La Sapienza	Roberto Di Leonardo	Farnoosh Joulaeian
University Basel	Knut Drescher	Eva Jiménez Siebert
University Würzburg	Markus Engstler	Nargesh Jamshidi
Synoptics LTD	Allen Donald	Morten Kals
University of Cambridge	Pietro Cicuta	Erika Causa
ESPCI Paris	Anke Lindner	Peixin Zhang
	Eric Clément	Benjamín Pérez
Lyncée Tec SA	Yves Emery	Patryk Nienałtowski
Partners		
Ben Gurion University	Avraham Be'er	
CAIRN	Jeremy Graham	
IMC/CSIC	Esther Garcés	
IFPEN	Valentin Guillon	
University of Warwick	Vasily Kantsler	

PHYMOT's broad scientific objective is to understand the physics of cell motility, from single cells to collective behavior. Research on cell motility is flourishing, driven by new experimental, theoretical, and numerical tools from mathematics, engineering, and physics. Within PHYMOT, young researchers will be trained at the interface between physics, biology, and engineering to face core challenges of a modern society such as food production, disease treatment strategies, sustainable and ecological development.

The workshop "Physics of Microbial Motility" aims to bring together theoretical and experimental researchers working on biological active matter at the microscale. The main topics of the workshop are a) Motility and Sensing, b) Collective Motion and c) Geometry and Motility

Timetable

IS: Invited Speaker, CT: Contributed Talk, ST: Short Talk

Monday Nov. 18

08:30-09:15	**Registration**			
09:15-09:20	**Welcome remarks Gerhard Gompper**			
09:20-09:45	CT	**Christophe Ybert** Univ. Claude Bernard Lyon1	France	Study of bacterial magneto-aerotactic behaviour in a controlled environment
09.45-10:10	CT	**Axel Voigt** TU Dresden	Germany	Asymmetry in bacterial swarming - a continuous modeling approach
10.10-10:20	ST	**Narges Jamshidi** University of Würzburg	Germany	Evolution of micro-swimmer designs in distinct microenvironments
10:20-11:00	**Coffee**			
11:00-11:35	IS	**Antoine Deblais** University of Amsterdam	Netherlands	Locomotion and transport of Active Polymerlike Worms in Porous Media
11:35-11:45	ST	**Isabelle Wielert** University of Cologne	Germany	Antigenic variation impacts gonococcal lifestyle and antibiotic tolerance by modulating interbacterial forces
11:45-11:55	ST	**Pierre Martin** TU Berlin	Germany	Tumbling bacteria in bulk and close to surfaces
11:15-12:15	CT	**Quentin Martinet** ISTTA	Austria	Static and dynamic properties of an active rod
12:15-12:25	ST	**Riccardo Foffi** ETH Zürich	Switzerland	Chemotactic encounters between bacteria and phytoplankton
12:25-14:00	**Lunch**			
14:00-14:35	IS	**Navish Wadhwa** Arizona State University	USA	How physical forces regulate bacterial motility across scales
14:35-14:55	CT	**Rajesh Singh** IIT Madras	India	Emergent dynamics of chemically active polymers
14:55-15:15	CT	**Thomas Kiørboe** DTU	Denmark	The functional diversity of the flagella of free-living flagellates
15:15-15:25	ST	**Diana Coroiu** University of Edinburgh	UK	Engineering of motility-based whole-cell biosensors
15:25-16:00	**Coffee**			
16:00-16:35	IS	**Eleonora Secchi** ETH Zürich	Switzerland	Formation Dynamics And Rheology of Bacterial Biofilms under Fluid Flow
16:35-16:55	CT	**Lucas Le Nagard** University of Edinburgh	UK	Non-linear dependency of the bacterial flagellar motor speed on proton motive force and its consequences for swimming
16:55-17:15	CT	**Anke Lindner** PMMH-ESPCI, Paris	France	Scale-free active turbulence in bacterial suspensions
17:15-17:25	ST	**Benjamín Pérez** ESPCI, Paris	France	Accessing microscopic details in a 3D Lagrangian perspective of active turbulence
18:00-22.00	**Dinner at the GSI**			

Tuesday Nov. 19

09:00-09:40	IS	**Lucio Isa** ETH Zürich	Switzerland	Designing Active Particles: From Optical Control to Shape Adaptation
09.40-10:05	CT	**Yves Emery** Lyncee Tech, Lausanne	Switzerland	4D tracking by DHM: current status and future direction
10:05-10:15	ST	**Tommaso Pietrangeli** Univ. Claude Bernard Lyon1	France	Run-and-tumble in Porous Media: Universal Law for Dispersal
10.15-10:25	ST	**Hyorin Nam** ETH Zürich	Switzerland	Bacterial sedimentation: Effects of activity?
10:25-11:00	**Coffee**			
11:00-11:35	IS	**Avraham Be'er** Ben Gurion Univ. of the Negev	Israel	Topological defects in multi-layered swarming bacteria
11:35-11:55	CT	**Stefano Ugolini** ETH Zürich	Switzerland	Thin water film environments facilitate bacterial chemotaxis
11:55-12:15	CT	**Gerhard Gompper** Forschungszentrum Jülich	Germany	Viscotaxis of Self-Propelling Flagella near Surfaces
12:15-12:25	ST	**Alexandre Morin** Leiden University	Netherlands	Spontaneous Demixing of Binary Colloidal Flocks
12:25-14:00	**Lunch**			
14:00-14:35	IS	**Pablo Sartori** IGC Oeiras	Portugal	From mechanical control to behavioral variability
14:35-14:45	ST	**James Cass** University of Bristol	UK	The Reaction-Diffusion Regime of Eukaryotic Flagella
14:45-14:55	ST	**Priyanka Iyer** Forschungszentrum Jülich	Germany	Cognitive Flocks: Order-Disorder Transitions and Threat Evasion
14:55-15:15	CT	**Benjamin Friedrich** TU Dresden	Germany	Information theory of chemotactic agents using both spatial and temporal comparison
15:15-15:25	ST	**Horacio Serna** Univ. Complutense de Madrid	Spain	Effects of gravitational fields and confinement on the collective behavior of biological microswimmers
15:25-16:00	**Coffee**			
16:00-16:35	IS	**Antonio De Simone** SSS, Pisa	Italy	Motility and self-propulsion in biological and bio-inspired systems
16:35-16:45	ST	**Giacomo Di Dio** MPI Marburg	Germany	Active segregation in binary mixtures under flow
16:45-16:55	ST	**Bappaditya Roy** AIST-Tohoku, Sendai	Japan	Learning hydrodynamic equations from microscopic Langevin simulations of self-propelled particles dynamics
16:55-17:15	CT	**Pierre Illien** Sorbonne Université,Paris	France	Microscopic and stochastic simulations of chemically active droplets
18:00-	**Poster session**			

Wednesday Nov. 20

09:00-09:35	IS	**Roberto Di Leonardo** Univ. Rome La Sapienza	Italy	Boundary shape engineering for the spatial control of confined microswimmers
09:35-09:45	ST	**Veit-Lorenz Heuthe** University of Konstanz	Germany	Counterfactual rewards promote collective transport using individually controlled swarm microrobots
09:45-09:55	ST	**Yihong Shi** MPI Göttingen	Germany	Mutual information as a measure of mixing efficiency in viscous fluids
09.55-10:15	CT	**Douglas Brumley** University of Melbourne	Australia	The role of chemotaxis in bacterial interactions
10.15-10:25	ST	**Joscha Mecke** Shenzhen University	PR China	Vortex formation and odd viscosity in a chiral active fluid
10:25-11:00		**Coffee**		
11:00-11:35	IS	**Victor Sourjik** MPI Marburg	Germany	Engineering Bacterial Microswimmers for Targeted Delivery
11:35-11:55	CT	**Knut Drescher** University Basel	Switzerland	Spatiotemporal dynamics of bacterial swarm development
11:55-12:15	CT	**Markus Engstler** University Würzburg	Germany	Mechanical Strategies to Avoid Interspecies Competition in Parasites
12:15-12:25	ST	**Timo Knippenberg** University of Konstanz	Germany	Reentrant cluster formation in active baths under soft confinement
12:25-14:00		**Lunch**		
14:00-14:35	IS	**Andreas Zöttl** University of Vienna	Austria	Modeling active motion in complex fluids
14:35-14:45	ST	**Ajesh Jose** Ben Gurion Univ. of the Negev	Israel	Immobility of swarmer cells due to local liquid depletion
14:45-14:55	ST	**Regis Turuban** Scuola Superiore Sant'Anna, Pisa	Italy	Chaotic collective mixing by a S. Lemnae feeding cluster
14:55-15:15	CT	**Marco Polin** IMEDEA, Esporles	Spain	Single cell death triggers local avoidance response in the cosmopolitan picoeukaryote Micromonas
15:15-15:25	ST	**Peixin Zhang** PMMH, ESPCI, Paris	France	E-coli transport along microfluidic edges determined by trajectory chirality and confinement
15:25-16:00		**Coffee**		
16:00-16:35	IS	**Gerard Wong** UCLA	USA	Motility as communication in bacterial active matter
16:35-16:55	CT	**Sebastien Michelin** LadHyX, Palaiseau	France	Self-propulsion of confined active droplets
16:55-17:05	ST	**Luc Zorrila** IMEDEA, Esporles	Spain	Mechanical coupling is sufficient to synchronize C. Reinhardtii flagella
17:05-17:15	ST	**Gaurav Gardi** MPI Stuttgart	Germany	On-Demand Breaking of Action-Reaction Reciprocity between Magnetic Microdisks Using Global Stimuli
19:00-22:00		**Conference dinner**		

Thursday Nov. 21

09:00-09:35	IS	**Manu Prakash** Stanford University	USA	Behavioral cartography: Mapping cellular behavior in the wild
09:35-09:55	CT	**Raphaël Jeanneret** Sorbonne Université, Paris	France	Swimming behavior of Chlamydomonas reinhardtii cells in complex photonic environments
09.55-10:15	CT	**Dmitry Fedosov** Forschungszentrum Jülich	Germany	E. coli steering and interaction with surfaces
10.15-10:25	ST	**Shubham Anand** Forschungszentrum Jülich	Germany	Viscotaxis of Beating Flagella at Surfaces
10:25-11:00	**Coffee**			
11:00-11:35	IS	**Katja Taute** Leipzig University	Germany	Adaptation in flagellar architecture improves chemotaxis in complex environments
11:35-11:45	CT	**Kristian Stølevik Olsen** Heinrich-Heine-Universität Düsseldorf	Germany	Intermittent active motion for enhanced spatial exploration
11:45-12:20	IS	**Heiko Rieger** Saarland University	Germany	Capillary action and stationary currents in scalar active matter
12:20-12:25	**Closing remarks**			
12:25-14:00	**Lunch**			

List of Abstracts – Talks

Monday Nov. 18

CT - Study of bacterial magneto-aerotactic behaviour in a controlled environment

V. Poncet[1], **M. Marmol**[2], **F. Detcheverry**[1], **C. Cottin-Bizonne**[1], **A. Cebers**[3], **D. Faivre**[2], **C. Ybert**[1]

[1] Universite Claude Bernard Lyon 1, CNRS, Institut Lumière Matière, UMR5306, F-69100, Villeurbanne, France
[2] BIAM Aix-Marseille University, CEA and CNRS, Cadarache, France
[3] MMML Latvia University, Riga, Latvia

Motile micro-organisms have developed numerous and elaborated strategies to adapt and navigate their environment. The ability to respond to various external cues -be it chemical, light, gravity, ...- through so-called taxis, has immediate consequences on the individual dynamics such as the run-and-tumble swimming strategy, but also bears significance at a collective level where for instance bioconvection is shaped by different taxis [1]: gravitaxis, gyrotaxis, etc. Here, we focus our attention on magnetotactic bacteria, capable of responding to external magnetic fields, together with more classical cues such as oxygen concentration. This offers an appealing system at the frontier between biological and artificial matter with such bacteria sharing properties with magnetic colloids, known to offer rich dynamics on their own [2]. In this presentation, we will discuss how control of the chemical and magnetic environment in microsystems can be used to bring new insights into either the individual or the collective dynamics of such bacteria. First, in their natural environment, magnetotactic bacteria are found at the oxic-anoxic transition zone for which the magnetic field should offer an assistance to aerotaxis [3]. Controlling chemical gradients, magnetic field orientation together with capturing the individual dynamics of many bacteria allows us to get detailed insight into the swimming strategy of the bacterial strain SS-5 and how it relates to the different cues and yield to a band formation at a specific oxygen level. In a second part, we will discuss collective motion that can arise in concentrated aerotactic band as a result of an imposed homogeneous magnetic field. This motion takes the form of a shear-flow along the band whose properties can be regulated by the field strength and orientation. This novel phenomenon where flows can be triggered and controlled externally in active systems can be quantitatively rationalized with a simple model of active fluids where heterogeneous bacteria distribution and imposed orientation combine to generate active stresses.

References

[1] M.A. Bees, Annu. Rev. Fluid Mech. **52**, 449 (2020)
[2] D. Jin and L. Zhang, Acc. Chem. Res. **55**, 98 (2022)
[3] M. Marmol, E. Gachon and D. Faivre, Rev. Mod. Phys. **96**, 021001 (2024)

CT - Asymmetry in bacterial swarming - a continuous modeling approach

R. Backofen[1], **A. Voigt**[1,2]

[1] Institute of Scientific Computing, TU Dresden, Dresden, Germany
[2] Center for Systems Biology Dresden, Dresden, Germany

In [1] active flows in bacterial swarms are considered using a generalized Navier–Stokes (GNS) equation. This GNS equation describes internally driven flows through higher-order hyper- viscosity-like terms in the stress tensor. This model is used to consider different active turbulence regimes and a turnover from low activity, featuring hyperuniform (HU) characteristics, to high activity featuring "anti-hyperuniformity" is found. The transition from HU to "anti-HU" could be shown to be related to a transition from non-inertial to inertial scaling behavior in active turbulence. We extend this investigation to two-phase flow systems, for mixtures of active and passive fluids. One phase thereby will be described by the GNS and the other by classical incompressible Navier-Stokes (NS) equations. Coupling is achieved via an auxiliary phase field variable leading to the so-called model H, but with a phase-dependent (hyper)viscosity. We analyse the non-equilibrium properties of the interface by measuring the angle of the interface normal and considering its time-averaged power spectrum to quantify the interface fluctuations. We are also concerned with the effect on phase separation and coarsening. The model can be related to active field theories, such as active model B (AMB), active model B+ (AMB+) or active model H. Except for the last HU characters of the phase separation patterns for these models have recently been analyses [2,3]. A significant difference with these models is the incorporation of activity. At least conceptionally activity is incorporated at the interface in these models (all activity terms are related to $\nabla \phi$, if ϕ is the phase field variable). In our approach activity is a bulk phenomenon of the active fluid and the emerging chaotic flows in the active fluid give rise to interface fluctuations, see Fig. 1.

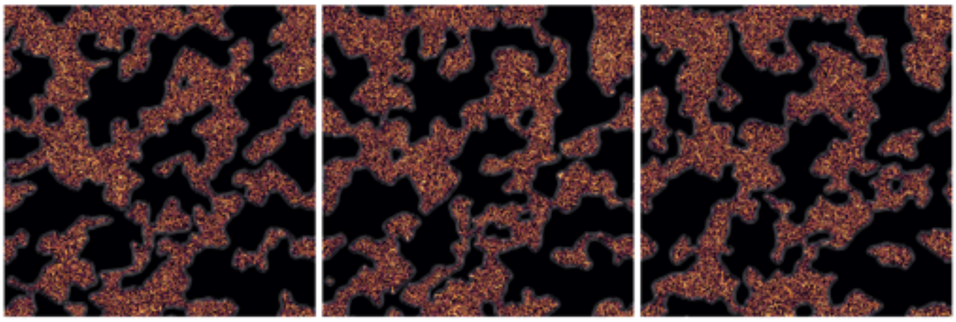


Figure 1: Dynamics of mixture of active and passive (black) phase. The vorticity in the active phase is color codes together with LIC visualisation. The figures show consecutive time instances and indicate asymmetric fluctuations of the interface.

References

[1] R. Backofen, A. A. Altawil, M. Salvalaglio, A. Voigt, Proc. Nat. Acad. Sci. (USA) **121**, e2320719121, (2024)
[2] Y. Zheng, M. A. Klatt, H. Löwen. arXiv:2310.03107 (2023)
[3] F. De Luca, X. Ma, C. Nardini, M. E. Cates. arXiv:2405.00508 (2024)

ST - Evolution of micro-swimmer designs in distinct microenvironments

N. Jamshidi, T. Krüger, M. Engstler

Department of Cell and Developmental Biology, Biocentre, University of Würzburg, 97074 Würzburg, Germany

Trypanosoma brucei, a flagellate parasite transmitted by tsetse flies, causes sleeping sickness in humans and infects various vertebrates. Throughout its life cycle, *T. brucei* adapts to diverse environments in its hosts, such as blood and skin, each with different mechanical properties like viscosity and physical constraints such as spatial confinement [1]. *T. brucei* has an elastic, spindle-shaped body with a helically attached flagellum [2]. Cell movement initiates with a planar bending wave on the flagellum at the anterior end of the cell, followed by a longitudinal rotation due to the helical attachment of the flagellum to the cell body [3].However, a detailed quantitative understanding of *T. brucei*'s single-cell dynamics and adaptive behaviors across different microenvironments remain insufficiently quantified. This study examined *Trypanosoma brucei*'s motility in various viscosities and collagen gels using high-resolution and digital holographic microscopy, allowing for the elucidation of 2D and 3D motility data of single-cell movement. Results show the adaptation of rotational behavior and its crucial role in maintaining swimming speed in different viscosities. At higher viscosities and in dense collagen, cells exhibit altered paths, such as circular swimming, suggesting that mechanical properties of the environment significantly impact motility.

References

[1] Krüger, Timothy, Sarah Schuster, and Markus Engstler. Trends in parasitology **34**.12 (2018)
[2] Bargul, Joel L., et al. PLoS pathogens **12**.2 (2016)
[3] Heddergott, Niko, et al. PLoS pathogens **8**.11 (2012)

IS - Locomotion and transport of Active Polymerlike Worms in Porous Media

R. Sinaasappel, T. Heeremans, M. Fazelzadeh, T. Hooijschuur, D. Bonn, S. Woutersen, S. Jabbari-Farouji, A. Deblais

Soft Matter Group, van der Waals-Zeeman Institute, Institute of Physics, University of Amsterdam, Amsterdam.

I will discuss our recent investigation into the locomotion of thin, living *T. Tubifex* worms, which exhibit active polymer-like behavior, within quasi-2D pillar arrays of varying spatial arrangements and densities. Our findings show that worm dynamics in these crowded environments strongly depend on both obstacle concentration and configuration. Notably, in disordered pillar arrays, increasing pillar density enhances long-term diffusion, while in ordered arrays, diffusion is hindered. In disordered media, the worms reptate through curvilinear pathways, whereas in ordered media, they become trapped in pores. Interestingly, reducing worm activity significantly enhances their spread, enabling passive sorting by activity level. These observations are supported by simulations of the tangentially driven polymer model. In a second experiment, we apply a chromatography approach to investigate the transport and separation of active polymer mixtures based on activity. The transport rate through the channel correlates strongly with activity, which we attribute to the distinct conformations adopted by worms of different activity levels. Our results offer a novel method to sort active polymers by activity and provide a versatile system for studying the hydrodynamics of active polymers.

ST - Antigenic variation impacts gonococcal lifestyle and antibiotic tolerance by modulating interbacterial forces

I. Wielert[1,2], **S. Kraus-Römer**[1,2], **T.E. Volkman**[1,2], **L. Crai**[3], **P.G. Higgin**[2,4,5], **B. Maier**[1]

[1] Institute for Biological Physics, University of Cologne, Germany
[2] Center for Molecular Medicine Cologne
[3] Department of Molecular Biology and Biochemistry, Simon Fraser University, Burnaby, British Columbia, Canada
[4] Institute for Medical Microbiology, Immunology and Hygiene, Faculty of Medicine and University Hospital Cologne, University of Cologne, Cologne, Germany
[5] German Centre for Infection Research, Partner site Bonn-Cologne, Cologne, Germany

Type 4 pili (T4P) are multifunctional filaments involved in adhesion, surface motility, biofilm formation, and horizontal gene transfer. By cycles of retraction, attachment and elongation, T4P mediate motility at surfaces and within colonies. As T4P are surface-exposed, *Neisseria gonorrhoeae* uses pilin antigenic variation to escape immune surveillance, yet it is unclear how antigenic variation impacts other functions of T4P. Here, we address this question by replacing the major pilin of a laboratory strain with pilins from clinical isolates. We reveal that the resulting strains vary in velocity and persistence of twitching motility. Furthermore, we show that pilin antigenic variation substantially affects pilus:pilus mediated attractive forces between neighbouring bacteria. Strongly interacting bacteria form microcolonies while weakly interacting bacteria retain a planktonic lifestyle. In mixed microcolonies different variant strains segregate in agreement with the differential strength of adhesion hypothesis. By combining structural predictions and laser tweezers experiments, we show that the C-terminal region of the pilin is crucial for attraction. The lifestyle affects growth kinetics and antibiotic tolerance. In the presence of ceftriaxone or ciprofloxacin, the killing kinetics indicate strongly increased tolerance of aggregating strains. We propose that pilin antigenic variation produces a mixed population containing variants optimized for growth, colonization, or survivability under external stress. Different environments select different variants, ensuring the survival and reproduction of the population as a whole.

References

[1] I. Wielert, bioRxiv: 2023.07.06.548055. (2023)
Available: https://www.biorxiv.org/content/10.1101/2023.07.06.548055v1

ST - Tumbling bacteria in bulk and close to surfaces

P. Martin[1], T.C. Adhyapak[2], D.C. Gomes[2], H. Stark[1]

[1] Institut für Theoretische Physik, Technische Universität Berlin, Germany
[2] Indian insitute of science education and research (IISER), Tirupati, India

Escherichia coli (*E. coli*) swims by rotating multiple flagella, which are randomly distributed on the surface of its cell body and connected via flexible hooks. These hooks act as universal joints, transferring motor torque to the flagellar filaments. When all the motors rotate in the same direction, the filaments wrap together and form a bundle. This bundle is stabilized by a combination of hydrodynamic and steric interactions, turning the bacterium into a straight swimmer. To change direction, *E. coli* performs tumble events by reversing the rotation of one or more flagella. The involved filaments undergo a series of polymorphic transformations, altering both their helicity and handedness [1, 2]. Although this process has been known for decades, the physical understanding remains incomplete. This complex phenomenon involves the interplay of semiflexible filaments and hydrodynamic interactions, most of which have been studied without fully resolving flagellar dynamics. Here, we have developed a detailed numerical framework to simulate *E. coli*, capturing the dynamics of flexible flagella and their hydrodynamic interactions. The flagellar elasticity is effectively modeled by an extended Kirchhoff free energy. The filaments and the cell body are embedded in a fluid, which we model using multi-particle collision dynamics, an efficient solver for the Navier-Stokes equations [3]. We analyzed a large number of tumble events, focusing on the roles of hook and flagellar flexibility as well as flagellar polymorphism. We find that they strongly influence the distribution of tumble angles. Finally, we also show that close to a flat surface the mean tumble angle is strongly shifted to smaller values. This indicates that tumble events may not be recognized, which could give the impression of suppressed tumbling near surfaces as reported in [4].

References

[1] L. Turner, W. S. Ryu and H. C. Berg, J. Bacteriol.,**182**, 2793, (2000)
[2] T. Adhyapak and H. Stark, Soft Matter, **12**, 5621, (2016)
[3] A. Malevanets and R. Kapral, J. Chem. Phys., **110**, 8605, (1999)
[4] M. Molaei, M.Barry, R. Stocker and J.Sheng , PRL, **113**, 068103, (2014)

CT - Static and dynamic properties of an active rod

Q. Martinet[1], Y. Li[1], A. Aubret[2], E. Hannezo[1], J. Palacci[1]

[1] ISTA Institute of Science and Technology Austria, Klosterneuburg, Austria
[2] LOMA CNRS, Bordeaux, France

The engineering of machines at microscale is a challenge, owing to difficult assembly and reconfigurability at this size. We previously demonstrated a novel approach, templated assembly, which exploits optical forces and the activity of the colloids to create autonomous, mobile, stable reprogrammable [1] and self-positioning [2] metamachines, or machines made of machines. Those metamachines however lack the ability to reconfigure and adapt their shape to their environment. It would be desirable to achieve machines with more sophisticated mechanical or dynamical response, such as responsive and flexible parts to go through a constriction. In a step in that direction, we investigate the static and dynamical properties of an active rod: a micromachine made of 20-50 active colloids [3]. We first study the mechanical properties of the active rod, seen as a material, and estimate the Young modulus of the active rod through a micro tensile test with optical tweezers. This mechanical property is also independently validated with the persistence length measurements. We show the importance of the coupling of the individual active colloids with the hydrodynamic flow on the persistence of the motion of these active rods. We furthermore observe a complex dynamics of the rods clamped on one hand with optical tweezer. We show that the dynamics arise from the coupling between motion and hydrodynamic alignment and describe our experiments with an analytical model of an elastic beam driven by an active particle. The model notably unveils the emergence of self-oscillations in this internal driven material.

References

References
[1] A. Aubret, Q. Martinet, et J. Palacci, « Metamachines of pluripotent colloids », Nat Commun, vol. **12**, no 1, p. 6398, nov. 2021, doi: 10.1038/s41467-021-26699-6
[2] Q. Martinet, A. Aubret, et J. Palacci, « Rotation Control, Interlocking, and Self-Positioning of Active Cogwheels », Advanced Intelligent Systems, vol. **5**, no 1, p. 2200129, janv. 2023, doi: 10.1002/aisy.202200129
[3] Q. martinet, Y. Li, A. Aubret, E. Hannezo, et J. Palacci, « Static and dynamic properties of an active rod », (in prep.)

ST - Chemotactic encounters between bacteria and phytoplankton

R. Foffi[1], **D.B. Brumley**[2], **F.J. Peaudecerf**[3], **R. Stocker**[1], **J. Słomka**[1]

[1] Institute of Environmental Engineering, ETH Zürich, Zürich, Switzerland
[2] School of Mathematics and Statistics, The University of Melbourne, Victoria, Australia
[3] Univ Rennes, CNRS, IPR (Institut de Physique de Rennes) - UMR 6251, Rennes, France

Chemotaxis enables marine bacteria to increase encounters with phytoplankton cells by reducing their search times, provided that bacteria detect noisy chemical gradients around phyto-plankton. Gradient detection depends on bacterial phenotypes and phytoplankton size: large phytoplankton produce spatially extended but shallow gradients, whereas small phytoplankton produce steeper but spatially more confined gradients. To date, it has remained unclear how phytoplankton size and bacterial swimming speed affect bacteria's gradient detection ability and search times for phytoplankton [1]. We computed an upper bound on the increase in bacterial encounter rate with phytoplankton due to chemotaxis over random motility alone. We found that chemotaxis can substantially decrease search times for small phytoplankton, but this advantage is highly sensitive to variations in bacterial phenotypes or phytoplankton leakage rates. By contrast, chemotaxis towards large phytoplankton cells reduces the search time more modestly, but this benefit is more robust to variations in search or environmental parameters [2]. Applying our findings to marine phytoplankton communities, we found that, in productive waters, chemotaxis towards phytoplankton smaller than 2 μm provides little to no benefit, but can decrease average search times for large phytoplankton ($\sim$ 20 μm) from two weeks to two days, an advantage that is robust to variations and favors bacteria with higher swimming speeds. By contrast, in oligotrophic waters, chemotaxis can reduce search times for picophytoplankton ($\sim$ 1 μm) up to ten-fold, from a week to half a day, but only for bacteria with low swimming speeds and long sensory timescales. We propose that this asymmetry may promote the coexistence of diverse search phenotypes in marine bacterial populations.

References

[1] Seymour et al., Trends Microbiol. **32**, 640-649, (2024)
[2] Foffi et al. (under review)

IS - How physical forces regulate bacterial motility across scales

N. Wadhwa[1,2]

[1] Biodesign Center for Mechanisms of Evolution, Arizona State University, USA
[2] Center for Biological Physics and Department of Physics, Arizona State University, USA

Physical forces play a crucial role in bacterial behavior, from single cells to entire communities. For free-swimming bacteria, the hydrodynamics of flagellar propulsion govern motility, while on surfaces, physical interactions are complex but equally important. In this talk, I will present our lab's recent findings on how physical forces shape bacterial motility across molecular to community scales. First, I will discuss how bacterial flagellar motors adapt to changes in viscous load through molecular remodeling, revealing that bacterial motility machinery is not static but highly dynamic and responsive. Next, I will introduce "swashing," a mode of motility where bacteria migrate across surfaces without active propulsion, instead harnessing fluid flows generated by metabolic activity. Remarkably, *Salmonella* and *Escherichia coli* mutants lacking functional flagella still migrate at rates comparable to wild-type strains, challenging the assumption that flagellar propulsion is essential for surface motility in these bacteria. This passive form of migration could have significant implications for medical and environmental microbiology, providing new insights into how bacteria colonize surfaces.

CT - Emergent dynamics of chemically active polymers: rigid flocks, undulatory gaits, and chiral foldamers

R. Singh

Department of Physics, Indian Institute of Technology Madras, Chennai, India

Active matter systems - such as a suspension of microorganisms or synthetic microswimmers - dissipate energy and maintain exciting collective dynamics. This talk will discuss three distinct experimental active matter systems. The first part of the talk will be about the emergence of rigidity from phoretic self-interactions in an active polymer [1]. I will then show that non-reciprocal trail-mediated interactions between monomers of the polymer give rise to novel phenomena, such as chiral molecules with tunable dynamics, sustained undulatory gaits and reversal of the direction of motion [2]. Our results provide a novel interpretation of the role of trail-mediated interactions, in addition to providing active self-assembly principles arising due to non-reciprocal interactions.

References

[1] M. Kumar, A. Murali, A.G. Subramaniam, R. Singh, S. Thutupalli. Nature Communications **15**, 4903, (2024)
[2] A.G. Subramaniam, M. Kumar, S. Thutupalli, R. Singh. New J. Phys. **26** 083009, (2024)

CT - The functional diversity of the flagella of free-living flagellates

T. Kiørboe

Centre for Ocean Life, DTU Aqua, Kgs Lyngby, Denmark

Flagellates, unicellular organisms equipped with one or a few flagella, play a key role in ocean biogeochemistry. They are functionally hugely diverse [1]. Yet, most studies have focused on a few model organisms and on the role of the flagellum in propulsion, ignoring its fundamental role in foraging. The number and position of flagella vary, the flagella may be equipped with vanes or hairs, the kinematics and wave patterns vary, and the flagellum may be embedded in a groove on the cell surface. All these features impact the fluid dynamics and functioning of the flagellum. I will consider two cases: (A) Flagella equipped with rigid hairs oriented in the beat plane reverse the direction of the force compared to a naked flagellum, and thus pulls the cell through the water. When feeding, the cell attaches and in many species switches to beating the flagellum in a 3-dimensional pattern, which generates an incoming feeding current. I will demonstrate the very different mechanisms of force production between the two flagella configurations. (B) Other flagella are equipped with a vane oriented perpendicular to the beat plane. While a vane increases the ability of the flagellum to 'shovel' water, this effect is limited. However, when the vaned flagellum is embedded in a groove, the effect is substantial and an energy-efficient way of generating a feeding current. I will demonstrate several other flagellar arrangements in quantitatively important species, where the functioning and fluid mechanics remain to be explored.

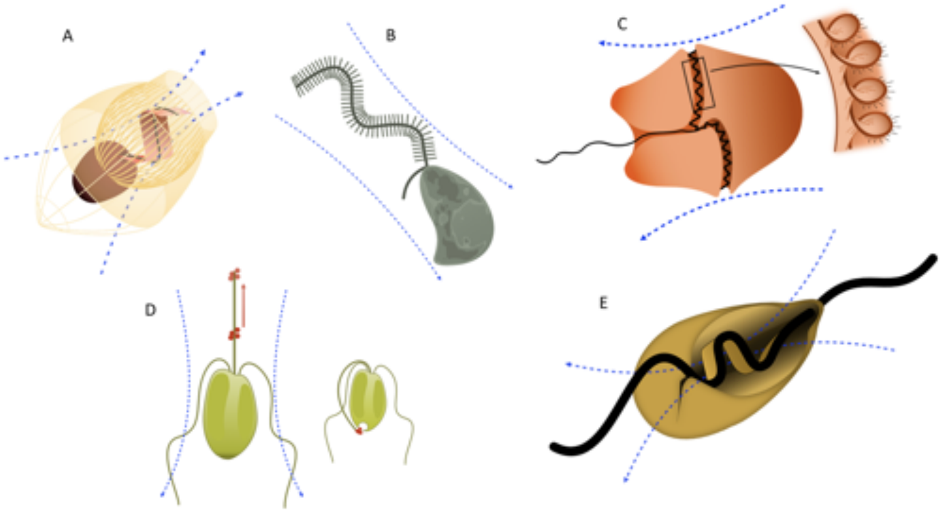


Figure 1: Schematic illustrating some of the diversity of flagellates. From [1].

References

[1] T. Kiørboe, Ann Rev Mar Sci **16**: 361–81 (2024)

ST - Engineering of motility-based whole-cell biosensors

D. Coroiu[1], **J. Broughton**[2], **T. Pilizota**[1,2]

[1] School of Biological Sciences, The University of Edinburgh, United Kingdom
[2] Institute of Cell Biology, The University of Edinburgh, United Kingdom

Many bacteria possess motility systems and associated regulatory networks that enable them to navigate their environment. *Escherichia coli* swims using its flagella, which are protein complexes mainly composed of a 10-micron extracellular filament that rotates powered by the (bacterial) flagellar motor (BFM). This rotation can be tracked either optically, using tethered cells or bead assays, or electrically, using impedance measurements. As the latter can be achieved in small integrated circuits, we aim to engineer *E. coli* strains that change the rotational direction of their flagellar motor in response to specific analytes in the environment, and thus obtain whole-cell biosensors that could be used in situ. To obtain *E. coli*-derived biosensors, we rewired the chemotactic pathway, a signalling network which *E. coli* has evolved to sense chemical gradients and thus navigate towards favourable environments. Normally, transmembrane chemotactic receptors relay information about the cell's surroundings to the motor by a series of feedback loops that end with the phosphorylation of the CheY protein, which, when active, interacts with the BFM and switches its direction from counterclockwise to clockwise [1]. Our biosensor uses a mutant form of CheY, CheY**, which is always active [2], as a reporter, and thus responds to chemicals by increasing the fraction of time the BFM spends rotating clockwise. We have created sensors to L-rhamnose and zinc, which are up to 100 times more sensitive than their GFP-based equivalents. We have also investigated the response dynamics and detection limits through mathematical modelling and further experimental characterisation.

References

[1] Welch, M. et al. (1993) 'Phosphorylation-dependent binding of a signal molecule to the flagellar switch of bacteria.', Proceedings of the National Academy of Sciences, **90**(19), pp. 8787–8791. doi:10.1073/pnas.90.19.8787

[2] Scharf, B.E. et al. (1998) 'Control of direction of flagellar rotation in bacterial chemotaxis', Proceedings of the National Academy of Sciences, **95**(1), pp. 201– 206. doi:10.1073/pnas.95.1.201

IS - Formation Dynamics And Rheology of Bacterial Biofilms under Fluid Flow

E. Secchi

Institute of Environmental Engineering, ETH Zurich, Switzerland

Biofilms are aggregates of microorganisms embedded in a self-secreted matrix of polymeric substances, which protect the microbial community from chemical and mechanical insults, thereby enhancing their survival and evolutionary success. Due to their resilience, biofilms significantly impact environmental, industrial, and medical settings1,2. Typically, biofilms develop in moist environments where fluids are in motion—a ubiquitous environmental factor that regulates chemical transport and exerts mechanical forces on biofilms3. However, a mechanistic understanding of how fluid dynamics shape biofilm properties remains limited. In our research, we investigate how fluid dynamic conditions drive biofilm assembly and the emergence of distinctive morphological and rheological properties. Our findings reveal that during biofilm formation in porous structures, the interplay between biological functions and fluid flow controls biofilm morphology and rheology, ultimately affecting the biofilm's physiological protective functions4–6. Specifically, we explore the role of fluid dynamics in the formation of biofilm streamers—filamentous biofilm structures suspended in the flow—which often initiate clogging. Utilizing a newly developed microfluidic platform, we examine how flow conditions determine the mechanical properties of these streamers7,8. For the first time, we demonstrate that biofilm streamers exhibit stress-hardening behavior, a property with profound implications for their flow adaptation. By elucidating the relationship between flow dynamics and biofilm development, our research not only deepens the physical understanding of biofilm formation but also advances biofilm engineering and eradication.

References

[1] M. Caldara, C. Belgiovine, E. Secchi and R. Rusconi, Clin. Microbiol. Infect., **35**, e00221-20 (2022)

[2] D. Marra, T. Karapantsios, S. Caserta, E. Secchi, M. Holynska, S. Labarthe, B. Polizzi, S. Ortega, M. Kostoglou, C. Lasseur, I. Karapanagiotis, S. Lecuyer, A. Bridier, M. Noirot-gros and R. Briandet, Biofilm, **5**, 100109 (2023)

[3] J. D. Wheeler, E. Secchi, R. Rusconi and R. Stocker, Annu. Rev. Cell Dev. Biol., **35**, 213–237 (2019)

[4] S. H. Lee, E. Secchi and P. K. Kang, Proc. Natl. Acad. Sci., **120**, e2204466120 (2023)

[5] D. L. Kurz, E. Secchi, F. J. Carrillo, I. C. Bourg, R. Stocker and J. Jimenez-Martınez, Proc. Natl. Acad. Sci., **119**, e2122202119 (2022)

[6] D. L. Kurz, E. Secchi, R. Stocker and J. Jimenez-martinez, Environ. Sci. Technol., , DOI:10.1021/acs.est.2c08890

[7] E. Secchi, G. Savorana, A. Vitale, L. Eberl, R. Stocker and R. Rusconi, Proc. Natl. Acad. Sci., **119**, e2113723119 (2022)

[8] G. Savorana, J. Slomka, R. Stocker, R. Rusconi and E. Secchi, Soft Matter, **18**, 3878–3890 (2022)

CT - Non-linear dependency of the bacterial flagellar motor speed on proton motive force and its consequences for swimming

E. Krasnopeeva[1], **L. Le Nagard**[2], **W.C.K. Poon**[3], **C.-J. Lo**[4,5], **T. Pilizota**[2]

[1] Institute of Science and Technology Austria, Am Campus 1, 3400 Klosterneuburg, Austria
[2] Centre for Synthetic and Systems Biology, King's Buildings, EH9 3FF, University of Edinburgh, Edinburgh, UK
[3] School of Physics and Astronomy, King's Buildings, EH9 3FD, University of Edinburgh, Edinburgh, UK
[4] Department of Physics and Center for Complex Systems, National Central University, Jhongli 32001, Taiwan
[5] Institute of Physics, Academia Sinica, Taipei 11529, Taiwan

The bacterial flagellar motor (BFM) enables bacteria to swim by rotating helical flagellar filaments that often form a bundle at the back of the cell. In *Escherichia coli*, the BFM uses the energy stored in the proton motive force (PMF) to produce the torque driving this rotation. Until now, the rotation speed of the motor was thought to be proportional to the magnitude of the PMF, irrespective of the viscous load [1, 2, 3]. Here, we show that this linear relationship does not hold universally. We measured the rotation speed of the BFM across a wide range of physiologically achievable PMF values, while subjecting the motor to different viscous loads. By exploring the entire PMF-torque space available to *E. coli* we find, contrary to previous thoughts, that the PMF-speed proportionality saturates when the motor reaches its maximum torque, typically at high PMF and/or under high viscous load. We then show that fully energised free-swimming cells experience this saturation in aqueous environments, where even small increases in viscosity result in a swimming speed that is independent of the PMF. Finally, we combine those results to estimate the mechanical load under which the flagellar motors operate in free-swimming *E. coli*.

References

[1] D. C. Fung, & H.C. Berg, Nature **375**, 6534, (1995)
[2] C.V. Gabel, & H.C. Berg, PNAS **100**, 15, (2003)
[3] A. Biquet-Bisquert, G. Labesse, F. Pedaci, & A.L. Nord, Frontiers in Microbiology **12**, 659464, (2021)

CT - Scale-free active turbulence in bacterial suspensions

B. Pérez-Estay[1], A. Morozov[2], E. Clément[1], A. Lindner[1]

[1] PMMH-ESPCI, Paris, France
[2] School of Physics and Astronomy, University of Edinburgh, UK

Dense suspensions of motile bacteria display at low Reynolds number fascinating collective motion with swirls and jets, reminiscent of inertial fluid turbulence. Recently, an intense endeavor aimed at understanding the fundamental concepts behind the spontaneous emergence of collective motion displayed by biological objects of many different kinds and sizes, such as cells, insects, birds, fishes or mammal populations. Macroscopic theories, mostly based on phenomenological symmetry arguments, categorize such dynamical structures featuring a preferred mesoscopic length scale that expresses the interplay between microscopic activity and fluid constitutive properties. Here, we show that contrary to those generic predictions, motile *E. coli* suspensions display scale-free turbulence that is at least 1000 times a single cell size. The maximal extent of the turbulent vortices scales proportionally to the externally imposed confinement height. We also reveal the existence of a long transient state featuring an extremely large vortex (ELV), whose coherence over time and space defies any theoretical prediction so far. This work provides novel indications that the conceptual picture of momentum-conserving active bacteria suspensions still needs to be completed.

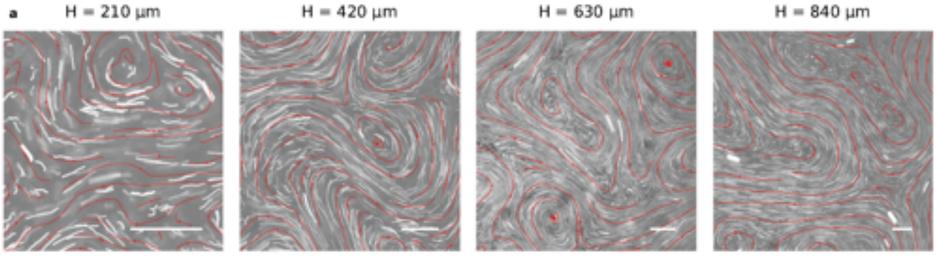


Figure 1: Scale free turbulence in a suspension of *E. coli* bacteria in a bath with varying height H.

ST - Accessing microscopic details in a 3D Lagrangian perspective of active turbulence

B. Pérez-Estay[1], **J. Savoye**[1], **A. Lindner**[1,2], **E. Clément**[1,2]

[1] PMMH-UMR 7636 of the CNRS, ESPCI-PSL-Sorbonne University, Univ. Paris Cite, 7 quai Saint-Bernard, Paris, 75005, France
[2] Institut Universitaire de France (IUF, Paris, France

Bacteria produce a flow when swimming, leading to hydrodynamic interactions between bacteria and the environment. These hydrodynamic bacteria-bacteria interactions at high densities of bacteria create a hydrodynamic instability that leads to active turbulence. In collective motion, we observe correlations in the swimming orientation that can be 1000 times bigger than bacteria [1] (see Fig 1 a). Although much work has focused on this system, not much is known of the 3D structure of the flow. In this work, we use a Lagrangian tracking setup controlled by an AI model to precisely follow a fluorescent particle's motion inside the bacteria bath. The tracks are longer than 10 min giving significant statistics of the bath. In parallel, we observed bacteria motion in a different fluorescent channel. This allows us to compare the motion of the surrounding bacteria to the bead itself, giving us information about the order in the bacteria suspensions. We quantify how the order changes as a function of the distance to the surface and the bacteria bath's properties.

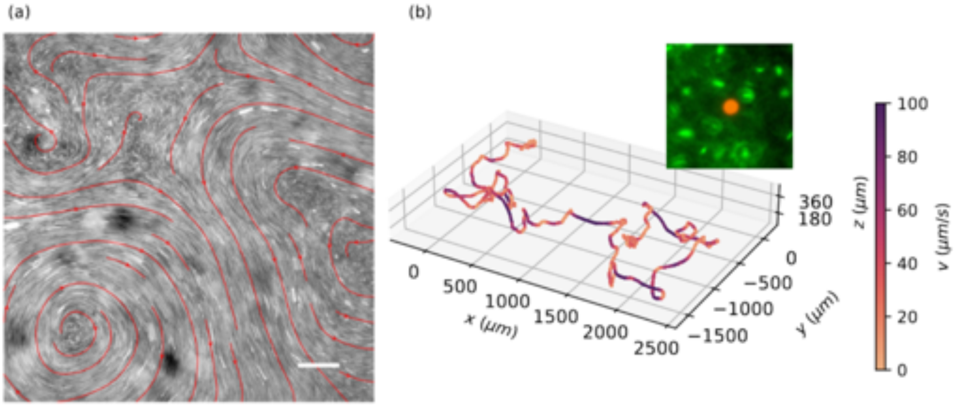


Figure 1: (a) Superposition of fluorescent beads tracks advected by the bacteria turbulence (60 images at 20 FPS) with streamline obtained from PIV measurement. Scale bar is 100m. (b) 3D reconstruction of the trajectory of a passive bead inside a bacteria bath. The particle is tracked for about 10 min. The inset shows a typical image acquired with the microscope, showing the passive fluorescent particle in red and the surrounding bacteria in green.

References

[1] Martinez, Vincent A., et al. Proceedings of the National Academy of Sciences **117**.5 2326-2331 (2020)

Tuesday Nov. 19

IS - Designing Active Particles: From Optical Control to Shape Adaptation

L. Isa

ETH - Zürich

Synthetic microswimmers, or active particles, are micro-scale objects that are capable of converting available energy, e.g., stored in chemical "fuel" or harvested from external sources, into directed motion. They are often thought as model systems for biological microscopic swimmers and have been offering new insights in the behavior of matter out of thermodynamic equilibrium. However, most synthetic microswimmers to date have been obtained from a very limited space of design parameters, and hence exhibit a limited range of functions compared to biological entities or larger machines. The challenge to expand the design space is then coupled to the incorporation of new materials and the development of new fabrication strategies, which enable programming and controlling the response of active particles under different conditions.

After a general introduction, I will propose two strategies that we are currently exploring in our laboratory. First, I will show that by choosing a photo-conductive coating that changes electrical conductivity under UV illumination, we can obtain Janus swimmers with programmable motility within light patterns. I will then show that the incorporation of thermo-responsive polymers, combined with the precise positioning of adaptive elements in the design of microswimmers, i.e., via directed assembly or nanoscale printing, enables the realization of reconfigurable microswimmers with multiple dynamical states, which are programmed during fabrication.

The rapid advancement in micro and nanoscale fabrication techniques and the ever-growing palette of available functional materials reveal an exciting future to develop complex active systems with programmable responses.

References

[1] L Alvarez et al., Nature Communications, **12**:4762 (2021)
[2] S van Kesteren et al., Proceedings of the National Academy of Sciences USA, **120** (11) e2213481120 (2023)
[2] S van Kesteren et al., Advanced Materials, 2207101 (2023)

CT - 4D tracking by DHM: current status and future direction

Y. Emery[1], **P. Nienaltowski**[1,2]

[1] Lyncee Tec SA, Lausanne
[2] ETH Zürich, Switzerland

This presentation will showcase the capabilities of Digital Holographic Microscopy (DHM) for 4D tracking of micro swimmers, highlighting its submicron spatial precision in detecting both micro swimmer bodies and the dynamics of flagella. Comparison with alternative techniques will be provided to highlight the strengths and limitations of DHM, along with its broad range of applications. Beyond 4D tracking, DHM provides invaluable insights into microorganism behavior, physiological health, and life cycle, along with the gradients and geometric characteristics of their surrounding medium. These additional layers of information, crucial for understanding the microenvironment, will be demonstrated through various real-world applications. We hope this presentation will inspire future collaborations and open new avenues of research into microbial motility and its interactions with complex environments.

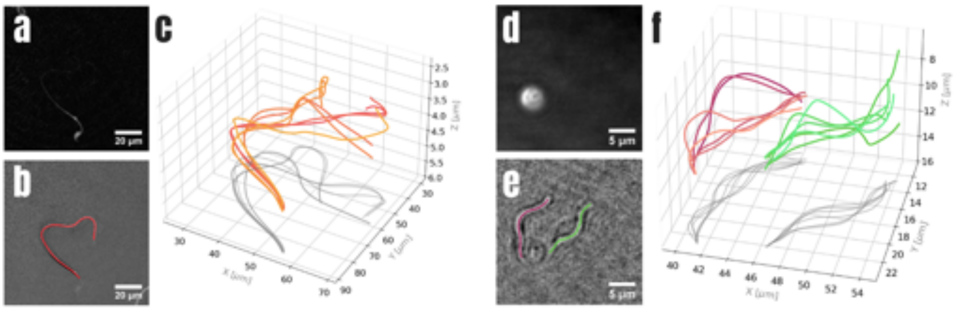


Figure 1: Results of 4D tracking using digital holographic microscopy for the mouse sperm cell and Chrysochromulina simplex flagella. (a) Phase reconstruction of a single z plane showing the mouse sperm cell. (b) Outcome of 3D temporal filtering with the overlaid result of the flagellum core detection algorithm, highlighted in red. (c) Three-dimensional spatial reconstruction of the mouse sperm cell flagellum. (d) Phase reconstruction of a single z plane with Chrysochromulina simplex visible. (e) Effect of 3D temporal filtering on a single z plane, showing lateral localization of the left flagellum (red) and right flagellum (green). (f) Three-dimensional spatial reconstruction of the Chrysochromulina simplex flagella.

References

[1] P. Nienaltowski, Precise, label-free 4D tracking of eukaryotic flagella using digital holographic microscopy [Manuscript in preparation] (2024)

[2] F. Miano, P. Nienaltowski, Capturing the beat: quantification of flagellar kinematics and 3D beat patterns in Pseudobodo sp. using Digital Holographic Microscopy [Manuscript in preparation] (2024)

ST - Run-and-tumble in Porous Media: Universal Law for Dispersal

T. Pietrangeli

University Claude Bernard Lyon 1, France

Dispersal is a key process for many motile microorganisms living in porous environments such as rocks, soils, and tissues. However, the relationship between dispersal, movement strategies, and pore space structure remains an open question. This work investigates, through numerical simulations, the long-time dispersal of run-and-tumble microorganisms that become trapped at solid surfaces and escape by tumbling. The results demonstrate a universal connection between dispersal and mean run time, applicable across various porous structures and swimming strategies. Using a simple model for orientational decorrelation, the study reveals that this behavior arises from the invariance of the mean free path, regardless of the movement strategy. The optimal strategy for maximizing dispersal is discussed, and the approach is extended to microorganisms that move along surfaces. This work provides a general framework for quantifying dispersal across diverse movement patterns and porous environments.

ST - Bacterial sedimentation: Effects of activity?

H. Nam[1], **E. Secchi**[2], **J. Vermant**[1]

[1] Laboratory for Soft Materials, Department of Materials, ETH Zürich, Switzerland
[2] Department of Civil, Environmental and Geomatic Engineering, ETH Zürich, Switzerland

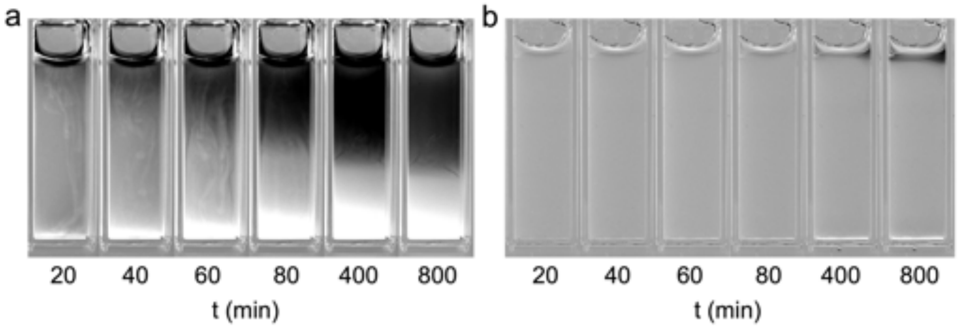


Figure 1: Bacterial sedimentation of (a) motile and (b) non-motile *Vibrio anguillarum*.

Swimming bacteria, a well-known and extensively studied form of living active matter, exhibit a remarkable property: they are self-propelled organisms. This activity presents a challenging problem in the theoretical understanding of the complex dynamical behaviors within the realm of out-of-equilibrium statistical physics of soft matter. The sedimentation of active matter suspensions is a relevant subject due to the pervasive presence of swimming microorganisms in natural and industrial processes. Till now, some studies have explored simulations of squirmer sedimentation [1] and experimentally examined the behavior of dilute artificial swimmer suspensions [2], but a full understanding on live bacterial sedimentation has not yet been carried out. Apart from the result that the presence of swimming bacteria significantly slows the sedimentation front of passive particles [3], we investigated motile bacterial suspensions which, surprisingly, exhibit a much higher settling velocity compared to non-motile (passive) bacterial suspensions, displaying a vortex-shaped instability during sedimentation (Figure 1). We must acknowledge that the both suspensions have a volume fraction of $\phi \approx 0.00057$, which should be in a dilute regime. In the present research, we will focus on studying the origins of this instability and its link to the high settling velocity, particularly in relation to the dilute limit and the excluded volume of swimming bacteria. Prior to this phase, *Vibrio anguillarum* was selected based on the criteria that they produce minimum extracellular polymeric substance which leads to biofilm, possess exceptionally high speed ($\sim 5 \mu m/s$), and have constant growth kinetics over an extended duration. Preliminary image analysis has been conducted to extract parameters that describe the properties of the selected bacteria such as the run-reverse-flick swimming pattern, the distribution of angle change, swim speed, and reorientation time.

References

[1] Scagliarini, Andrea, and Ignacio Pagonabarraga. Soft Matter **18**.12, 2407-2413 (2022)
[2] Palacci, Jérémie, et al. Physical Review Letters **105**.8 088304 (2010)
[3] Singh, Jaspreet, et al. Soft Matter **17**.15, 4151-4160 (2021)

IS - Topological defects in multi-layered swarming bacteria

V. Yashunsky[1], **D.J.G. Pearce**[2], **G. Ariel**[3], **A. Be'er**[4]

[1] The Jacob Blaustein Institutes for Desert Research, Ben-Gurion University of the Negev, SedeBoqer Campus, 84990 Midreshet Ben-Gurion, Israel.
[2] Department of Theoretical Physics, University of Geneva, 1211 Geneva, Switzerland.
[3] Department of Mathematics, Bar-Ilan University, 52900 Ramat-Gan, Israel.
[4] The Department of Physics, Ben-Gurion University of the Negev, 84105 Beer-Sheva, Israel.

Topological defects, which are singular points in a director field, play a major role in shaping active systems. Here, we experimentally study topological defects and the flow patterns around them, that are formed during the highly rapid dynamics of swarming bacteria. The results are compared to the predictions of two-dimensional active nematics. We show that, even though some of the assumptions underlying the theory do not hold, the swarm dynamics is in agreement with two-dimensional nematic theory. In particular, we look into the multi-layered structure of the swarm, which is an important feature of real, natural colonies, and find a strong coupling between layers. Our results suggest that the defect-charge density is hyperuniform, i.e., that long range density-fluctuations are suppressed.

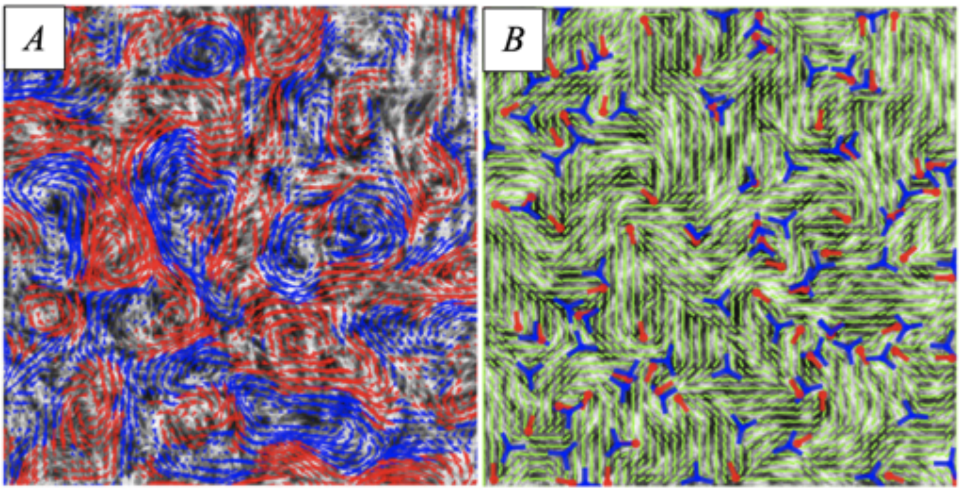


Figure 1: (A) Velocity field (in the background of the cells) calculated using an optical flow method, demonstrating chaotic collective swirling motion. Blue and red colors indicate clockwise and counterclockwise rotating regions. (B) The nematic director field extracted from (A) with positive (red) and negative (blue) locations and orientations of half-integer defects.

References

[1] V. Yashunsky, D.J.G. Pearce, G. Ariel and A. Be'er, Soft Matter **20**, 4237-4245 (2024)

CT - Thin water film environments facilitate bacterial chemotaxis

G. Ugolini[1], **R. Foffi**[1], **B. Daniel**[2], **J. Vorholt**[2], **R. Stocker**[1]

[1] Institute of Environmental Engineering, Department of Civil, Environmental and Geomatic Engineering, ETH Zurich, Switzerland
[2] Institute of Microbiology, Department of Biology, ETH Zurich, Switzerland

Many environments on Earth harbor microbiomes and bacterial communities confined within thin water films, bounded by various physical and biological surfaces such as plant surfaces and soil particles. While motility and chemotaxis are well recognized as critical processes enabling bacterial life and shaping ecological niches, they become increasingly complex in confined environments, as they are hindered by hydrodynamic interactions with the surrounding surfaces. Natural bacteria isolates from the leaf microbiome were found to express genes associated with flagellar motility and chemotaxis [1], however, it remains unclear how, and under what specific hydration conditions, they can effectively perform these functions. We employ microfabricated chambers and video microscopy to investigate the efficiency of chemotaxis towards chemoattractant pulses in thin water films confined by solid surfaces, as well as in micron-thin films bounded by a solid surface and an air interface. In the former case, we observe enhanced chemotaxis due to the reduced dimensionality of the system. For the latter case, we demonstrate that efficient motility and chemotaxis occur in thin water films only when a protein layer adsorbed at the air-water interface restores favorable hydrodynamic conditions for swimming [2]. In particular, we show that natural compounds present on the leaves of *Arabidopsis thaliana* can provide these favorable hydrodynamic conditions, allowing bacteria to perform chemotaxis even in films whose thickness is comparable to the cell size.

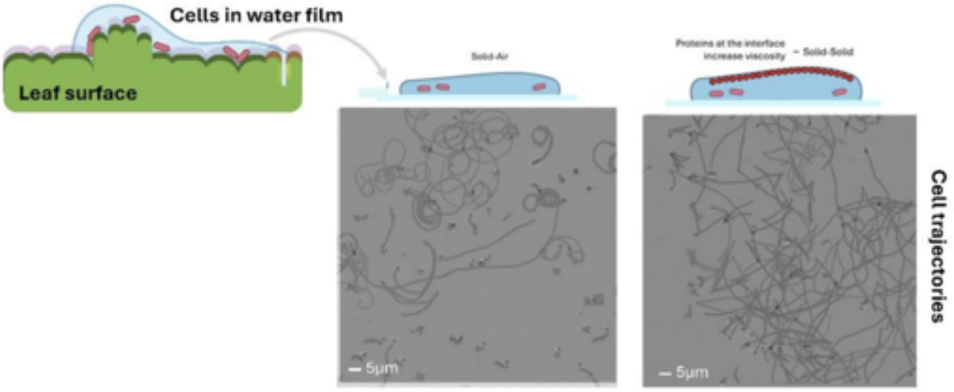


Figure 1: Sample trajectories from tracking bacteria in thin water films without or with the presence of interfacial protein layers.

References

[1] J. Vorholt, Nat Rev Microbiol **10**(12), 828-840 (2012)
[2] Morse et al., Biophys. J. **105**, 21–28, (2013)

CT - Viscotaxis of Self-Propelling Flagella near Surfaces

S. Anand, J. Elgeti, G. Gompper

Forschungszentrum Jülich, Institute for Advanced Simulation, 52425 Jülich, Germany

The motion of microswimmers can be strongly affected by variations of the physical properties of their environment [1]. Well-known examples are rheotaxis (the upstream swimming in microchannel flows) and gravitaxis (swimming against the gravitational field). Unidirectional external signals can also induce biochemical processes in biological microswimmers, which result in steering and directional motion, such as photo- or chemotaxis. We focus here on the direct physical mechanisms. We are interested in the motion of beating flagella in fluids with a viscosity gradient. Such a situation is often encountered by sperm on their way to the female egg. Here, the unique propulsion mechanism of sperm, with its sinusoidally beating flagellum, distinguishes its behavior from those of other microswimmers, such as those modelled by squirmers [2]. Our combined simulation and theoretical modelling study [3] is based on a flagellum, which is described by a semiflexible filament with a travelling bending wave [4, 5]. The simulations show that the behavior strongly depends on the beat amplitude, the average (spontaneous) curvature and the flexibility of the flagellum. In general, we find positive viscotaxis (motion toward regions of higher viscosity), but there are also cases where sperm swims in drifting circles perpendicular to the gradient direction[3] – see. Fig. 1. The effect of flexibility is descibed by a scaling function, which depends only a single dimensionsless parameter, the Sperm number. Viscotaxis decreases with increasing Sperm number, e.g. with decreasing bending rigidity or increasing beat frequency [3]. Our results can be useful for controlling sperm motion in microfluidic devices [6].

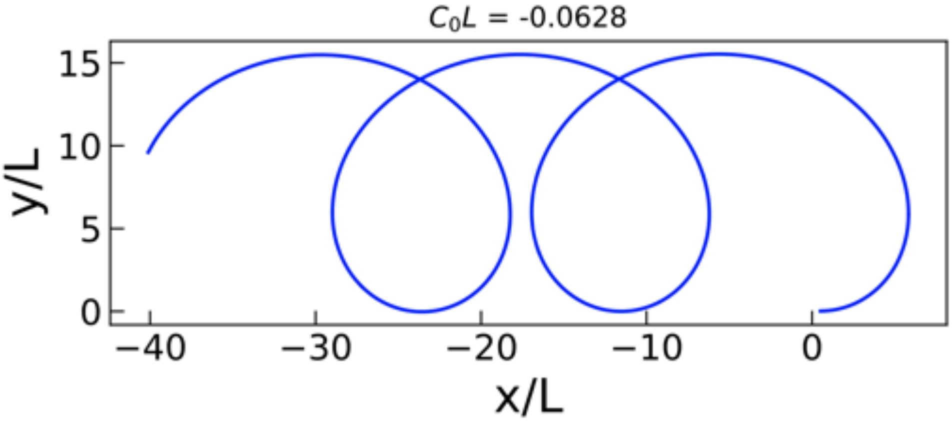


Figure 1: Trajectory of a flagellum with spontaneous curvature in a viscosity gradient (in y-direction).

References

[1] J. Elgeti, R.G. Winkler, and G. Gompper, Rep. Prog. Phys. **78**, 056601 (2015)
[2] V.A. Shaik and G.J. Elfring, Phys. Rev. Fluids **6**, 103103 (2021)
[3] S. Anand, J. Elgeti, and G. Gompper, arXiv (2024)
[4] Y. Yang, J. Elgeti, and G. Gompper, Phys. Rev. E **78**, 061903 (2008)
[5] J. Elgeti, U.B. Kaupp, and G. Gompper, Biophys. J. **99**, 1018 (2010)
[6] S. Rode, J. Elgeti, and G. Gompper, New. J. Phys. **21**, 013016 (2019)

ST - Spontaneous Demixing of Binary Colloidal Flocks

S. Maity, A. Morin

Insitute of Physics, Leiden University, Netherlands

Population heterogeneity is ubiquitous among active living systems, but little is known about its role in determining their spatial organization and large-scale dynamics. Combining evidence from synthetic active fluids assembled from self-propelled colloidal particles along with theoretical predictions at the continuum scale, we demonstrate the spontaneous demixing of binary polar liquids within circular confinement. Our analysis reveals how both active speed heterogeneity and nonreciprocal repulsive interactions lead to self-sorting behavior. By establishing general principles for the self-organization of binary polar liquids, our findings highlight the specificity of multicomponent active systems [1].

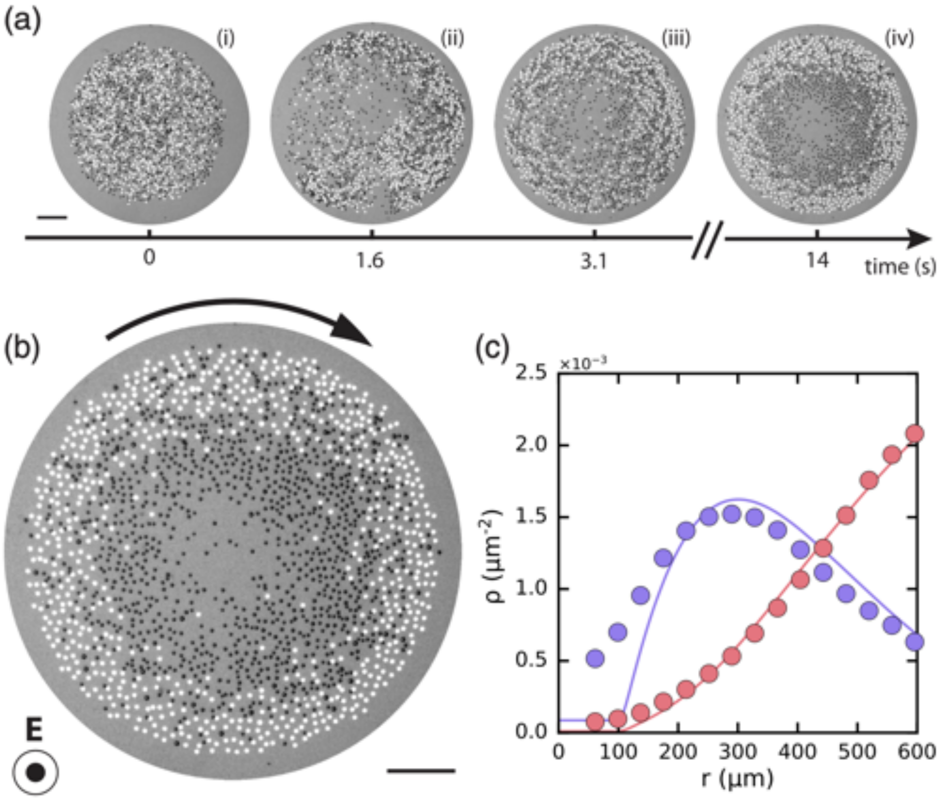


Figure 1: Spontaneous demixing of binary colloidal flocks — (a) Spontaneous demixing of an initially homogeneous binary mixture. Scale bar: 200 μm. (b) Steady-state configuration of a binary colloidal flock. Scale bar: 200 μm. (c) Radial density profiles of the two species. Red: fluorescent 7 μm diameter colloids. Mauve: non-fluorescent 5 μm-diameter colloids. Dots: experimental data. Lines: hydrodynamic theory.

References

[1] S. Maity, A. Morin, Physical Review Letters **131**, 178304, (2023)

IS - From mechanical control to behavioral variability

P. Sartori

Instituto Gulbenkian de Ciência, Oeiras, Portugal

Swimming is a behavior that is widespread among microbes. One of the key evolutionary conserved structures underlaying microbial swimming is the cilium. This mechanical system is capable of generating a variety of precisely orchestrated bending waves that powers microbial locomotion. In this talk I will give an overview of our past efforts to understand the mechanical basis behind ciliary motion, taking the unicellular algae *Chlamydomonas reinhardtii* as a model system. I will then discuss recent work in which we show how from this mechanical control a large variety of beating patterns emerge. Finally, I will present ongoing efforts to relate this variability in ciliary waveforms to variability at the level of organismal swimming.

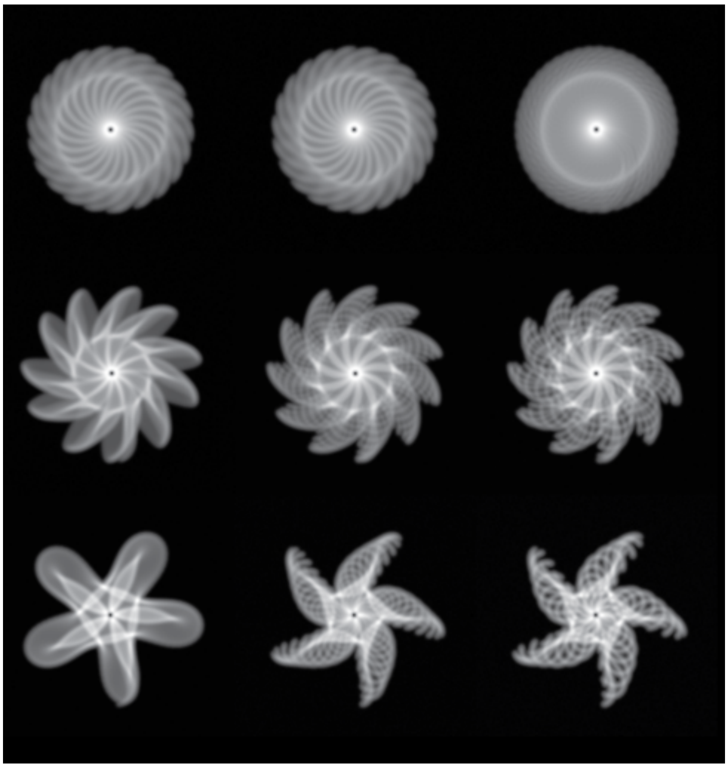


Figure 1: Time-trace of beating cilia display striking regular patterns, arising from tight mechanical control. Yet, like snowflakes, each pattern is unique, revealing the variability across species, conditions, and individuals. (Adapted from Ref 3).

References

[1] Sartori, Geyer, Scholich, Jülicher, Howard. Elife (2016)
[2] Sartori, Geyer, Scholich, Jülicher, Howard. Phys Rev E (2016)
[3] Geyer, Howard, Sartori. Nature Physics, (2022)

ST - The Reaction-Diffusion Regime of Eukaryotic Flagella

J.F. Cass, H. Bloomfield-Gadêlha

School of Engineering Mathematics and Technology, University of Bristol, Bristol, UK

Eukaryotic cilia and flagella are cellular appendages used to propel organisms through fluid or drive flows. Dynein motor proteins power beating of the flagellum by exerting axial forces on the doublet microtubules of the internal flagellar structure known as the axoneme. Research is ongoing to understand how the collective activity of individual dyneins can result in the self-sustaining stable oscillations that propagate along the flagellum enabling locomotion. Here we present a perspective on flagellar dynamics which decouples the intrinsic beat-patterning mechanism from the interaction of the flagellum with the surrounding fluid. We derive a minimal sliding-controlled reaction-diffusion system, employing tug-of-war reaction kinetics of dynein motors coupled to a planar elastic axoneme. Our system displays spatio-temporal animated patterns akin to classical reaction-diffusion systems [1]. Inspired by experimental work, our model eschews the assumption that energy supplied by motor proteins is primarily dissipated in the surrounding fluid [2]. Instead, we show that it is sufficient for producing a diverse range of flagellar waveforms that energy is mostly lost to internal friction. The model is able to fit quantitatively the beating patterns of bull sperm and the green alga *C. Reinhardtii*, distant eukaryotic species which vary in the length of their flagella/cilia, their axonemal structure, ultrastructure and cell morphology (see Fig. 1). We reveal a novel mechanism of non-reciprocal flagellar wave generation that may be crucial for low viscosity aquatic microswimmers. A weakly nonlinear analysis provides analytical solutions for the amplitude, frequency and propulsive force generated by the system, with surprising accuracy relative to simulations even far from the onset of oscillations [3].

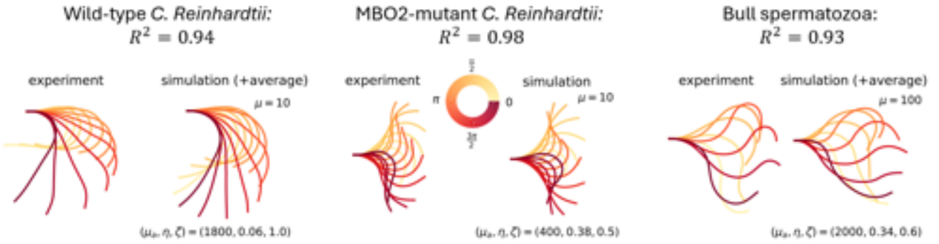


Figure 1: A simple reaction-diffusion model fits the beating patterns of diverse eukaryotic species.

References

[1] J.F. Cass and H. Bloomfield-Gadêlha, Nature Communications, **14**(1), (2023)
[2] D. Mondal, R. Adhikari, P. Sharma, Sci. Adv. **6**(33), (2020)
[3] J.F. Cass and H. Bloomfield-Gadêlha, biorxiv.org/content/10.1101/2024.08.14.607876v1, (2024)

ST - Cognitive Flocks: Order-Disorder Transitions and Threat Evasion

P. Iyer[1], C. Soroco[1,2], G. Gompper[1]

[1] Forschungszentrum Jülich, Institute for Advanced Simulation, 52425 Jülich, Germany
[2] University of British Columbia, Vancouver, BC V6T 1Z4, Canada

Directed self-propulsion is ubiquitous in living organisms. Ranging from *E. Coli* dispersing in biofilms to bird flocks migrating across oceans, living organisms are constantly out-of equilibrium. By sensing their environment and adjusting their movement, organisms can exhibit emergent patterns and collective behaviors, such as self-organization in human crowds [1, 2], bird flocks, and fish schools. The Inertial Spin Model (ISM) was introduced to explain the fast and robust propagation of information in bird flocks [3], when only alignment interactions are considered. However, more generally, agents exhibit a variety of interactions like local avoidance, cohesion and threat evasion [4]. We show how such behaviours can be incorporated within the framework of the ISM. It is found that local avoidance introduces emergent noise in the system, triggering an order-disorder transition. Exploring the flock dynamics near this transition reveals a complex interplay between cohesion, alignment, and local avoidance, resulting in a diverse array of behaviors such as pronounced shape fluctuations and the diffusive motion of the flock. Building on this understanding, we apply our flocking model to a simple scenario of stationary threat avoidance, where only the edges of the group can detect the threat. We explore how various flock properties, such as speed, local avoidance, and signal damping, influence the way the threat information propagates across the flock. This illuminates the physical mechanisms that govern collective motion in flocks, providing valuable insights that can be leveraged to design effective navigation strategies.

Figure 1: (a) Increasing local avoidance (left to right) leads to increased disorder and shape changes in the flock. (b) A flock avoiding a threat that is directly ahead of it (black bullet). Trajectory lines shown for the agents at the front of the flock.

References

[1] Negi, R. S. et al. , Sci. Rep. **14**, 9443, (2024)
[2] Iyer, P. et al. , arXiv, 2405.18528, (2024)
[3] Attanasi, A. et al. , Nat. Phys. **10**, 691-696, (2014)
[4] Negi, R. S. et al. , Phys. Rev. Res. **6**, 013118, (2024)

CT - Information theory of chemotactic agents using both spatial and temporal comparison

J. Rode[1], **M. Novak**[2], **B. M. Friedrich**[1]

[1] Cluster of Excellence Physics of Life, TU Dresden, Dresden Germany
[2] Department of Physics, University of Zagreb, Zagreb, Croatia

Biological cells and small organisms navigate in concentration fields of signaling molecules using two fundamental gradient-sensing strategies: spatial comparison of concentrations measured at different positions on their surface and temporal comparison of concentrations measured at different locations visited along their motion path. It is believed that size and speed dictate which gradient-sensing strategy cells choose, yet only heuristic notions exist to explain this evolutionary choice. We present an information theory of an ideal agent that combines both strategies to quantify 'chemotaxis in bits' [1,2]. This enables us to predict when each strategy provides more information as function of a powerlaw that combines agent size, motility noise and sensing noise. We demonstrate our theory with a bio-inspired search robot.

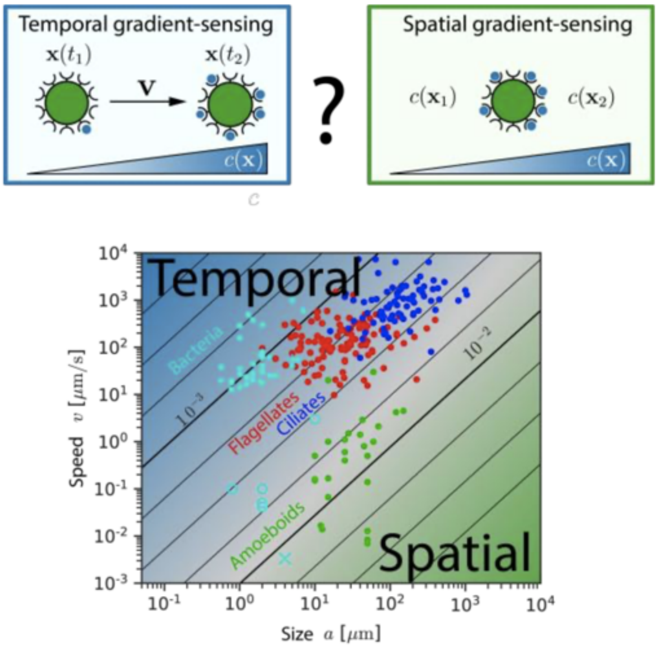


Figure 1: Small and fast bacteria sense concentration gradients in time while moving actively (left), where as large and slow eukaryotic cells with crawling motility sense concentration gradients across their diameter in space (right). Using information theory [1], we predict which gradient-sensing strategy provides more information as function of a powerlaw, which can account for the evolutionary choice of gradient-sensing strategy of biological cells as function of size and speed [2] (bottom).

References

[1] A. Auconi et al., EPL **138**, 12001 (2023)
[2] J. Rode et al., PRX Life **2**, 023012 (2024)

ST - Effects of gravitational fields and confinement on the collective behavior of biological microswimmers

H. Serna[1], **C. M. Barriuso Gutierrez**[1], **M. Polin**[2], **I. Pagonabarraga**[3], **C. Valeriani**[1]

[1] Universidad Complutense de Madrid, Spain
[2] Mediterranean Institute for Advanced Studies IMEDEA-UIB-CSIC, Spain
[3] Universidad de Barcelona, Spain

Biological Microswimmers (BM) have evolved mechanisms to self-propel. The interactions between different types of BM (hydrodynamic, chemical, among others) are relevant in natural processes such as the regulation of carbon and oxygen biogeochemical cycles and the release of toxins by phytoplankton blooms under certain environmental conditions. On the other hand, interactions between BM's and passive objects are crucial to design processes with potential technological applications such as activity-induced sorting (separation) and cargo delivery. Apart from that, in both natural and controlled scenarios, BM's swim through complex environments where their motion is affected by external fields and different types of confinement. In particular, the combined effect of hydrodynamics, external fields, and confinement not only plays a role in natural processes like bio-convection, but also is key to understand and control the BM's collective motion, aiming to design new technologies in active and smart materials. In this work, we use computational simulations to study the structural and dynamical properties of suspensions of squirmer-like BM's under the influence of a gravitational field. Also, we present a preliminary study on activity-induced transport of passive colloids confined in micro-channels.

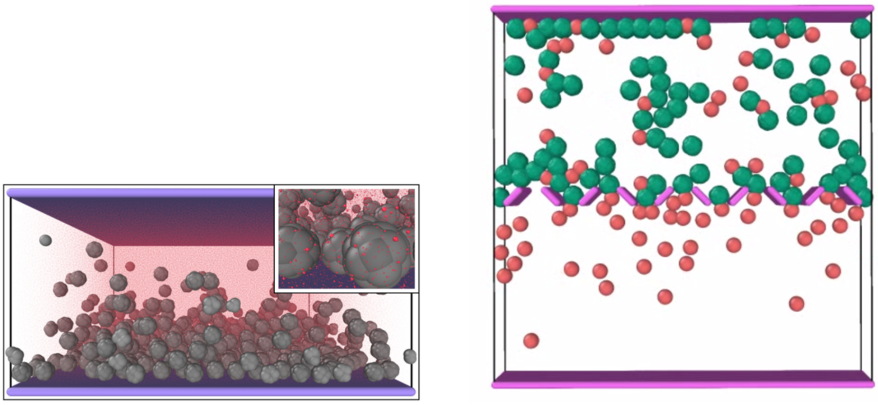


Figure 1: Left: snapshot of microswimmers during sedimentation. Right: snapshot of a designed micro-channel to promote the separation of a mixture of microswimmers and passive colloids.

References

[1] J. Seymour, S. Amin, J. Raina, R. Stocker, Nat. Microbiol., **2**, 17065 (2017)
[2] E. Ehrlich, U. Thygesen, T. Kiørboe, Proc. R. Soc. B., **289**, (2022)
[3] C. Bechinger, R. Di Leonardo, H. Löwen, C. Reichhardt, G. Volpe, G. Volpe, Rev. Mod. Phys., **88**, 045006 (2016)
[4] S. Williams, R. Jeanneret, I. Tuval, M. Polin, Nat. Commun., **13**, 4776 (2022)
[5] R. Martinez, F. Alarcon, J. Aragones, C. Valeriani, Soft Matter, **16**, 4739-4745 (2020)
[6] O. Yasa, P. Erkoc, Y. Alapan, M. Sitti, Advanced Materials, **30**, (2018)
[7] J. Kuhr, F. Rühle, H. Stark, Soft Matter, **15**, 5685-5694 (2019)

IS - Motility and self-propulsion in biological and bio-inspired systems

A. De Simone[1,2]

[1] The Biorobotics Institute, Scuola Superiore Santanna, Pisa
[2] SISSA-Mathlab, Trieste

Active matter is a broad field with many potential applications. A common thread underlying many of the current research lines is the study of systems powered by some internal energy source, as in the case of organisms moving thanks to food metabolism. In fact, self-propelling systems need to overcome the resistance of the surrounding medium, drawing the required energy from their environment. The study of locomotion and self-propulsion in biological and bio-inspired artificial system appears, therefore, as an ideal testing ground to put the concepts and tools of active matter at work. We will report on recent progress coming from case-studies on the motility of biological organisms and bio-inspired micro-robots, with special emphasis on swimming and collective feeding of unicellular organisms (flagellates and ciliates), studied from the point of view of the mechanics of active matter.

ST - Active segregation in binary mixtures under flow

G. Di Dio, R. Colin

Max Planck Institute for Terrestrial Microbiology and Center for Synthetic Microbiology, Marburg

In nature, from the gut to the soil, bacteria form complex heterogeneous communities, the organization of which is essential to their functioning, with broad impacts on natural and industrial processes. In these porous environments, shear flow is a ubiquitous external physical constraint that can influence the swimming behavior of active bacteria and the structures of communities. However, how the physics of shear flow contributes to the structuring of complex, phenotypically heterogeneous communities still remains poorly understood. Here, we investigate experimentally how a model heterogeneous bacterial community of motile and non-motile *Escherichia coli* organizes in a confined environment under shear flow. We discovered that the mixture actively segregates under flow, with the non-motile population accumulating on the "left" side of the channel (i.e. opposite to the vorticity direction) at low shear rates. We demonstrate experimentally and in simulation that this segregation, which depends on motile cell density and flow rate, originates from the backflow generated from the collective rheotactic drift of motile cells. We also show that non-motile cell accumulation requires sedimentation, which counters the incompressibility of the conveyer-belt-like backflow, to take effect. Finally, the segregation of non-motile cells under flow leads at long times to asymmetric co-biofilm formation in the channel. Our findings reveal a novel mechanism by which physical interactions in flowing environments can drive the spatial organization and long-term dynamics of complex microbial communities.

ST - Learning hydrodynamic equations from microscopic Langevin simulations of self-propelled particles dynamics

B. Roy[1], **N. Yoshinaga**[2]

[1] AIST-TohokuU Mathematics for Advanced Materials-OIL, Katahira 2-1-1, Aoba-Ku, Sendai, 980-8577 JAPAN
[2] Future University Hakodate, 116-2 Kamedanakano-cho, Hakodate, Hokkaido 041-8655, Japan

In nonequilibrium systems, a collective movement of microscopic active particles often displays several common emerging properties, such as swarming, motility-induced phase separation, nonequilibrium disorder-order transitions, anomalous density fluctuation, spatiotemporal patterning, and unusual rheological properties. However, those universal aspects of collective behaviors are hardly captured from microscopic particle-based simulation methods. The macroscopic properties obtained from nonlinear hydrodynamic equations are useful for understanding those aspects. Therefore, we start from the numerical Langevin simulations of the microscopic particle dynamics and present a data-driven strategy for the collection of self-propelled particles to develop the hydrodynamics equations[1]. In our method, microscopic particle data is our input. Hence, the hydrodynamics fields are obtained by coarse-graining from the discrete description of particle dynamics. For partial differential equation (PDE) learning [2], the spectral representation gives the efficient and accurate computation of spatial and temporal derivatives of density and polarization density fields. Using sparse regression on the fields, we generate hydrodynamic equations. The estimated PDEs from microscopic models are beneficial to understanding the universal features of the system in comparison to standard supervised learning. Hence, the macroscopic features will be shared both by microscopic models and hydrodynamic equations.

References

[1] R. Supekar, B. Song, A. Hastewell, J. Dunkel, PNAS **120** (7), e2206994120 (2023)
[2] S. H. Rudy, S. L. Brunton, J. L. Proctor, J. N. Kutz, Science Advances **3**, e160261 (2017)

CT - Microscopic and stochastic simulations of chemically active droplets

R. Berthin, J. Fries, M. Jardat, V. Dahirel, P. Illien

Sorbonne Université, CNRS, Physical Chemistry of Electrolytes and Interfacial Nanosystems (PHENIX), 4 Place Jussieu, 75005 Paris, France

Biomolecular condensates play a central role in the spatial organization of living matter. Their formation is now well understood as a form of liquid-liquid phase separation that occurs very far from equilibrium. For instance, they can be modeled as active droplets, where the combination of molecular interactions and chemical reactions result in microphase separation. However, so far, models of chemically active droplets are spatially continuous and deterministic. Therefore, the relationship between the microscopic parameters of the models and some crucial properties of active droplets (such as their polydispersity, their shape anisotropy, or their typical lifetime) is yet to be established. In this work, we address this question computationally, using Brownian dynamics simulations of chemically active droplets: the building blocks are represented explicitly as particles that interact with attractive or repulsive interactions, depending on whether they are in a droplet-forming state or not. Thanks to this microscopic and stochastic view of the problem, we reveal how driving the system away from equilibrium in a controlled way determines the fluctuations and dynamics of active emulsions.

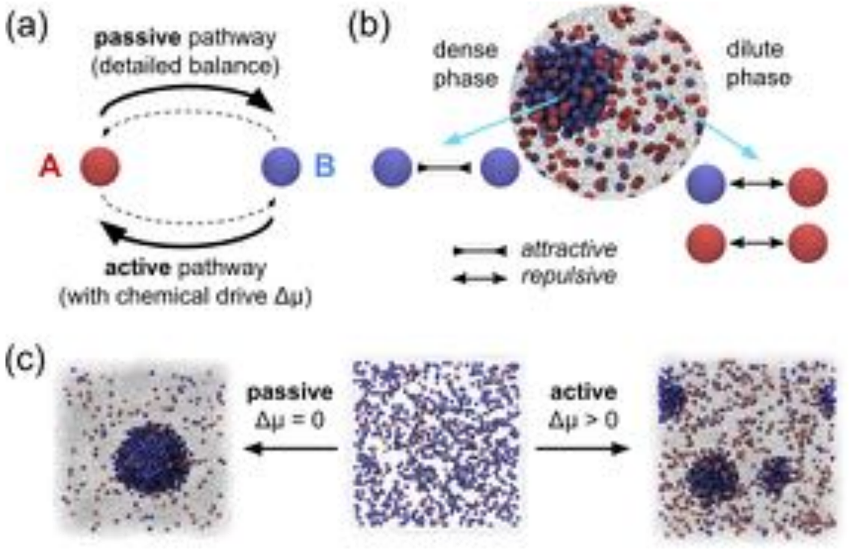


Figure 1: (a) Two chemical pathways for the interconversions $A \rightleftharpoons B$: a passive pathway, which fulfils detailed balance, and an active pathway, which violates it, because of a constant chemical drive $\Delta\mu$. (b) System under study: chemically active species (A and B) and inert particles (C, represented as grey dots for readability). See text for details on the interaction potentials. (c) Typical snapshots: starting from the same initial configuration, an equilibrium simulation, where species interconversions only follow the passive pathway ($\Delta\mu = 0$), leads to macroscopic phase separation, whereas a nonequilibrium simulation ($\Delta\mu > 0$) leads to interrupted phase separation and selection of a finite droplet size.

References

[1] R. Berthin, J. Fries, M. Jardat, V. Dahirel, P. Illien, arXiv:2406.14256 (2024)

IS - Boundary shape engineering for the spatial control of confined microswimmers

R. Di Leonardo[1], **A. Búzás**[2], **L. Kelemen**[2], **D. Tóth**[3], **S. Z. Tóth**[3], **P. Ormos**[2], **G. Vizsnyiczai**[2]

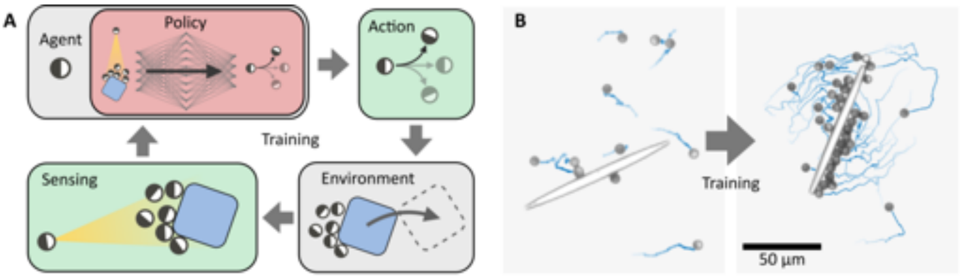
[1] Dipartimento di Fisica, Sapienza Universita di Roma, Piazzale A. Moro 5, I-00185, Rome, Italy
[2] Institute of Biophysics, HUN-REN Biological Research Centre Szeged, Temesvari krt. 62, H-6726, Szeged, Hungary
[3] Laboratory for Molecular Photobioenergetics, Institute of Plant Biology, HUN-REN Biological Research Centre, Szeged, Temesvári krt 62, H-6726 Szeged, Hungary

Unlike an equilibrium gas, the distribution of active particles can be very sensitive to what happens at the boundaries of their container. Experiments and simulations have previously highlighted the possibility of exploiting this behavior for the geometric control of active particles, although a general theoretical framework is lacking. Here we propose a boundary method based on the flux transfer formalism typical of radiometry problems, where surface elements transmit and receive "rays" of active particles with infinite persistence length. As in the case of blackbody radiation, a Lambert scattering law results in a uniform distribution of active particles within the cavity, while other scattering laws result in specific patterns of particle accumulation in the bulk or over the boundary walls. We validate the predictions of our method with numerical simulations and experimentally demonstrate its practical utility for spatially organising swimming microalgae confined by light-defined arenas. The presented boundary method provides a simple and efficient way to predict particle distributions when both the boundary geometry and the scattering law are known. It also provides a general design principle for engineering container shapes optimized for the transport, accumulation and sorting of self-propelled colloids and microorganisms.

ST - Counterfactual rewards promote collective transport using individually controlled swarm microrobots

V. -L. Heuthe[1,2], **E. Panizon**[3,4], **H. Gu**[1], **C. Bechinger**[1,2]

[1] University of Konstanz, Department of Physics, Universtaetsstrasse 10, 2 Konstanz, 78464, Germany
[2] Centre for the Advanced Study of Collective Behaviour, Universtaetsstrasse 10, Konstanz, 78464, Germany
[3] The Abdus Salam International Centre for Theoretical Physics (ICTP), Strada Costiera 11 4 Trieste, 34151, Italy
[4] Area Science Park, Data Engineering Laboratory, Località Padriciano 99, Trieste, 34149, Italy



Swarm robotics explores the potential of collective behavior for robotic systems, reminiscent of ants working together to move large objects. Efficient control schemes for robot swarms require that all robots have an equal contribution to the task. Therefore, a major challenge in swarm control is to estimate the contribution of each unit, which becomes particularly difficult at the microscale where the dominant noise introduces high stochasticity. In this study, we address these challenges by implementing Multi-Agent Reinforcement Learning (MARL, illustrated in panel A) to individually control up to 200 microrobots using laser spots. These microrobots collectively manipulate and transport large cargo objects, much like an ant swarm. By employing counterfactual rewards, our approach efficiently assigns credit to individual microrobots, enabling unbiased training with high flexibility regarding different tasks. The resulting control strategy is highly scalable, and robust, capable of adapting to variations in group size, malfunctioning units, and environmental noise. This demonstration marks a significant step forward in the development of micro-robot swarms as tools for manipulating microscopic objects. Our system's ability to perform complex tasks, such as simultaneous manipulation of multiple objects, suggests promising applications in automated assembly of mobile micromachines, programmable drug delivery capsules, and advanced lab-on-a-chip technologies.

ST - Mutual information as a measure of mixing efficiency in viscous fluids

Y. Shi[1], **R. Golestanian**[1,2], **A. Vilfan**[1,3]

[1] Max Planck Institute for Dynamics and Self-Organization (MPI-DS), Goettingen, Germany
[2] Rudolf Peierls Centre for Theoretical Physics, University of Oxford, Oxford, UK
[3] Jožef Stefan Institute, Ljubljana, Slovenia

Fluid mixing at the microscale is of paramount importance in biological organisms and in artificial systems. Examples range from the the uptake of oxygen, nutrients or chemical signals in aquatic organisms to microreactors and “lab on a chip” applications. In biology, mixing is frequently accomplished by cilia which drive long-range flows, but also localized regions of chaotic advection. A particular challenge to microscale mixing is posed by the time-reversibility of flows at low Reynolds numbers. Mixing therefore requires an interplay between advection (stirring) and diffusion. Here we introduce mutual information between particle positions before and after mixing as a measure of mixing efficiency. We demonstrate its application in a Couette flow in an annulus and show that the mixing efficiency depends in a non-trivial way on the time sequence of rotation. We show that under this measure, the mixing efficiency is symmetric upon time reversal of the actuation sequence. Among all sequences with the same rotation angle, the ones with optimal mixing consist of a fast rotation in the middle of the time interval, or in some cases two symmetrically arranged. We also determine mutual information from Brownian dynamics simulations using data compression algorithms and demonstrate that advanced neural network based compression algorithms can be applied to estimate mutual information to a high accuracy. Our results show that mutual information provides a universal and assumption-free measure of mixing efficiency in microscale flows. Furthermore, we expect that our formalism will also be applicable to more complex mixing situations, for example by active swimmers, natural or artificial cilia or in active materials. Our current work is to apply mutual information in studying mixing caused by different types of microswimmers.

References

[1] Y. Shi, R. Golestanian and A. Vilfan, Phys. Rev. Research, **6**, L022050 (2024)

CT - The role of chemotaxis in bacterial interactions

D.R. Brumley

School of Mathematics and Statistics, The University of Melbourne, Parkville 3010, Victoria, Australia

Bacterial motility, symbioses, and marine nutrient cycling unfold at the scale of individual microorganisms and are inherently dynamic. Moreover, microorganisms are routinely exposed to microscopic fluid flows, which have the capacity to influence motility and redistribute chemical cues. This talk will outline recent work, which uses video-microscopy, image processing and mathematical modelling to resolve dynamic microscale processes which underpin the ecology of microorganisms. This reveals that marine bacteria exhibit heighted chemotactic sensitivity [1] compared to the well-studied bacterium *E. coli*, providing a conspicuous advantage for targeting microscale nutrient hotspots commonly found in the ocean. This level of chemotactic precision allows for nutrient exchange and symbioses between organisms which were previously considered to be too small to find one another [2]. In conjunction with microfluidic experiments, cell tracking, and direct measurement of nutrient exchange between individual cells, we develop a mathematical model which fully resolves the movement of co-moving cells, and the release, transport and uptake of dissolved organic matter. This demonstrates how highly resolved processes at the scale of individual cells can be connected to bulk measurements at the population-level through an interplay between experiments and mathematical modelling. The capacity for individual bacteria to target one another through chemotaxis points to an important, but largely overlooked phenotype within inter-bacterial interactions [3].

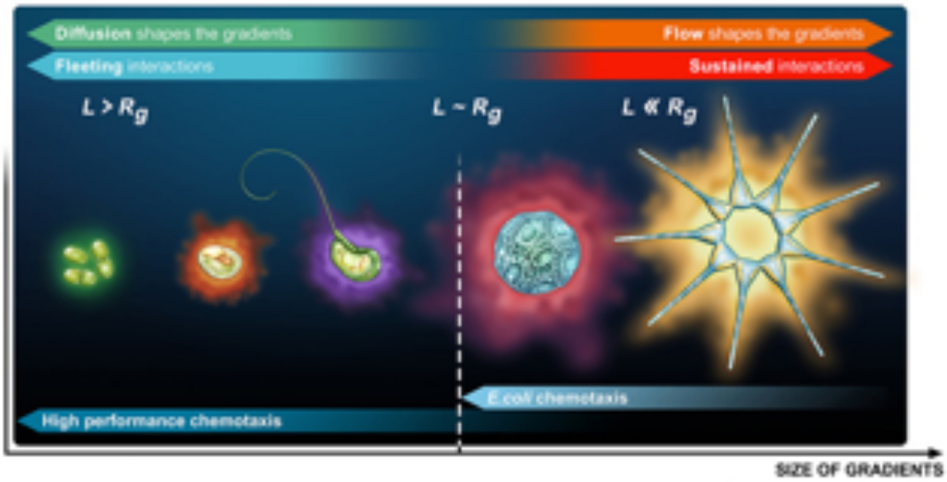


Figure 1: The capacity for bacteria to detect microscale chemical gradients around individual picophytoplankton cells facilitates "transient symbiosis". In this case, the reciprocal exchange of nutrients occurs through fleeting interactions which are underpinned by cell chemotaxis. Figure modified from Ref [3].

References

[1] D.R. Brumley et al., PNAS USA **116**, 10792-10797 (2019)

[2] J-B. Raina, M. Giardina, D.R. Brumley et al., Nature Microbiology **8**, 510-521 (2023)

[3] J.R. Seymour, D.R. Brumley, R. Stocker, J-B. Raina, Trends in Microbiology **32**, 640-649 (2024)

ST - Vortex formation and odd viscosity in a chiral active fluid

J. Mecke[1,2], **Y. Gao**[1], **G. Gompper**[2], **M. Ripoll**[2]

[1] Institute for Advanced Study, Shenzhen University, Shenzhen, PR China
[2] nstitute of Advanced Simulation, Forschungszentrum Jülich, Germany

Materials consisting of active particles with an intrinsic rotation can be considered as chiral active matter. Related systems can be observed in biology and also in synthetic materials, e.g., by use of rotating fields on particles carrying a dipole moment [1]. We study a colloidal chiral active system, consisting of magnetic microrotors of diameter 0.8 μm in an externally applied rotating magnetic field. The stabilised rotating colloids solely interact via steric and hydrodynamic interactions, granting active stresses already at low densities and large colloidal separations. We address the system by means of experiments as well as particle based hydrodynamics simulations (MPC) of the active colloidal suspension. The rotors' transverse, anti-symmetric, and non-reciprocal interactions lead to a pair-rotation about the centre of mass and subsequently to the formation of multiscale vortices (see Fig.1). The energy is injected on the particle level and is transported to the largest scales in the system, unless it is dissipated into the substrate or adjacent fluid layers [2], a process reminiscent of turbulence, even in the absence of dominant inertial contributions. We introduce the influence of momentum leakage in the MPC fluid, which can be thought of as a frictious substrate below the 2D active fluid layer, leading to the emergence of a hydrodynamic damping length due to the fluid friction, which limits the size of the emergent vortices. The rich phenomenology of our system additionally includes correlations between vorticity and density which allow for a measurement of the system's odd viscosity [3], enhancement of effective diffusive transport by the introduction of obstruction, or directed transport by virtue of symmetry breaking at confining walls.

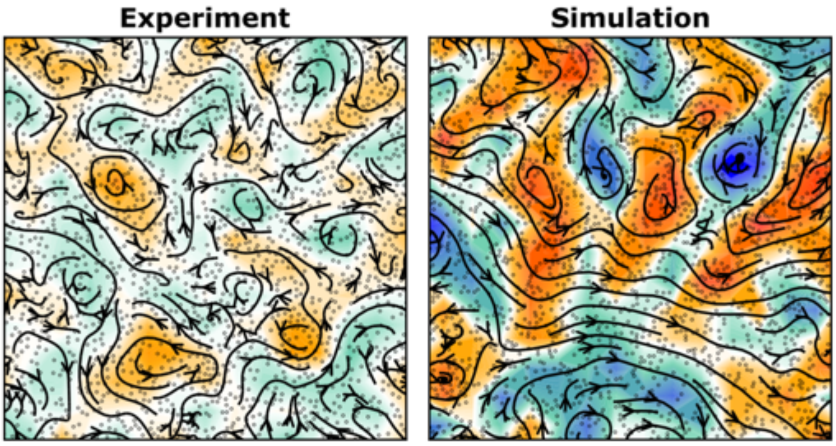


Figure 1: Vortex formation in the colloidal chiral active system obtained from experiments (left) and simulation (right). Red, white, blue areas correspond to positive, zero, negative vorticity, respectively.

References

[1] J. Mecke, J.O. Nketsiah, R. Li, Y. Gao, Natl. Sci. Open 3(4):20230086 (2024)
[2] J. Mecke, Y. Gao, G. Gompper, and Marisol Ripoll, https://arxiv.org/abs/2408.12820 (2024)
[3] J. Mecke, Y. Gao, C.A. Ramírez Medina, D.G.A.L. Aarts, G. Gompper, and M. Ripoll , Commun. Phys. **6**, 324 (2023)

IS - Engineering Bacterial Microswimmers for Targeted Delivery

V. Sourjik

Max Planck Institute for Terrestrial Microbiology, Marburg, Germany

The swimming motility and chemotaxis exhibited by bacteria are among the most well-understood biological behaviors. These phenomena have long served as exemplars of how physics can determine the performance of biological systems. Here we apply our biological and physical understanding of motility and chemotaxis in *Escherichia coli* to engineer bacterial microswimmers that could be used for biodelivery, including various biotherapeutic applications. I will discuss our progress on the engineering of two types of microswimmers: cargo-carrying *E. coli* “bacteriabots” and chromosome-less minicells. These microswimmers have different hydrodynamic properties compared to the normal *E. coli* cells, which must be taken into account for the rational engineering and optimization of their motility.

CT - Spatiotemporal dynamics of bacterial swarm development

K. Drescher

University of Basel

Development of microbial communities is a complex multi-scale phenomenon with wide-ranging biomedical and ecological implications. How biological and physical processes determine emergent spatial structures in microbial communities remains poorly understood due to a lack of simultaneous measurements of gene expression and cellular behaviour in space and time. Here, we combined live-cell microscopy with a robotic arm for spatiotemporal sampling, which enabled us to simultaneously acquire phenotypic imaging data and spatiotemporal transcriptomes during Bacillus subtilis swarm development. Quantitative characterization of the spatiotemporal gene expression patterns revealed correlations with cellular and collective properties, and phenotypic subpopulations. By integrating these data with spatiotemporal metabolome measurements, we discovered a spatiotemporal cross-feeding mechanism fueling swarm development: during their migration, earlier generations deposit metabolites which are consumed by later generations that swarm across the same location. These results highlight the importance of spatiotemporal effects during the emergence of phenotypic subpopulations and their interactions in bacterial communities.

CT - Mechanical Strategies to Avoid Interspecies Competition in Parasites

M. Engstler

Biozentrum, Uni. Würzburg, Germany

Parasites, like all organisms, must adapt to their ecological niche, which in their case is inherently hostile due to the host's defence mechanisms. Hosts are often infected by multiple parasites, leading to interspecific competition for the same niche. Avoiding such competition is crucial for the evolutionary success of parasitism. We hypothesise that adaptations to the physical properties of the microenvironment play a key role in this process.

African trypanosomes, unicellular flagellate parasites, colonise the body fluids of their host. Two closely related species, *T. brucei* and *T. congolense*, occupy distinct niches within the same host—*T. brucei* in tissue interstitial spaces and *T. congolense* in the peripheral capillary system. Despite similar body structures, they differ significantly in swimming behaviour, attachment to host cells, and their ability to navigate crowded, confined, and flowing environments. We propose that these differences in locomotion are crucial for avoiding interspecies competition.

In my presentation, I will highlight four key insights: (1) The two trypanosome species exert different mechanical forces on their surroundings. (2) Their body stiffness varies—*T. brucei* is highly elastic, stretching in high-viscosity environments, which alters its flagellar beating without affecting swimming speed. (3) While *T. brucei* navigates through tissue interstitium, it cannot traverse in vitro collagen networks of similar or lower density. (4) In contrast, *T. congolense* attaches to red blood cells, underscoring how mechanical strategies have evolved differently to avoid interspecies competition.

These discoveries have significantly reshaped our understanding of trypanosome behaviour.

ST P21 - Reentrant cluster formation in active baths under soft confinement

T. Knippenberg, C. Bechinger

University of Konstanz, Department of Physics, Universtaetsstrasse 10, 2 Konstanz, 78464, Germany

The behavior of active particles (APs) is known to be strongly influenced by their environment, particularly when they come in contact with boundaries, giving rise to numerous non-trivial phenomena absent in passive fluids. A well-studied example is an increase of pressure due to the accumulation of particles at concave boundaries [1]. Because of the persistence of the APs' motion, the presence and the shape of a boundary can exert a far-reaching impact on their density distribution and flow dynamics [2]. Here, we present an experimental method to study the influence of boundaries on the behavior of APs. This method is based on the local modulation of the APs' velocity in a feedback-controlled setup, to mimic the presence of an arbitrary shaped external potential. We use this to investigate the structural and dynamic properties of APs confined within a soft annulus-shaped channel [3]. Depending on the strength of the confinement and the Péclet number, we observe a reentrant behavior that is not present in unconfined systems. Our findings are substantiated by numerical simulations and analytical considerations, revealing that this behavior arises from the strong coupling between the Péclet number and the effective confining dimensionality of the APs. Our work highlights the peculiarities of soft boundaries for APs and how clogging can be avoided under such conditions.

References

[1] Y. Fily, Phys. Rev. E. **91**, 012125 (2015)
[2] O. Granek et al, arXiv preprint arXiv:2310.00079 (2023)
[3] T. Knippenberg et al, Phys. Rev. Lett. **133**, 048301 (2024)

IS - Modeling active motion in complex fluids

A. Zöttl

Faculty of Physics, University of Vienna, Boltzmanngasse 5, 1090 Vienna, Austria

The active transport of microswimmers through complex fluids is of great importance for biological and potential technological applications. Here we use the well-known squirmer microswimmer model to show the importance of the local fluid microstructure and non-continuum effects which determine the swimming speed of squirmers in different polymeric and filamentous fluids (see snapshot in Fig. 1(left)). Surprisingly, we find in our numerical simulations that different squirmer types (contractile/extensile) move at considerably different speed in filamentous fluids (Fig. 1(right)) which cannot be explained by existing continuum models, but by considering the local fluid and polymer properties around the squirmers. Furthermore, neglecting hydrodynamic flow fields by using a simple Active Brownian Particle (ABP) model strongly decreases the speed compared to squirmers [1]. We demonstrate that for sufficiently large polymers both local hydrodynamic flows and steric swimmer-polymer interactions significantly contribute to the swimming speed of the squirmers. Our approach allows us to disentangle hydrodynamic from steric hindrance effects, which enables to bridge the gap between commonly used continuum hydrodynamic models and ABP models. Our results are expected to be of experimental relevance to better understand microswimmer locomotion in heterogeneous and filamentous polymeric environments, as they typically appear in real biological situations.

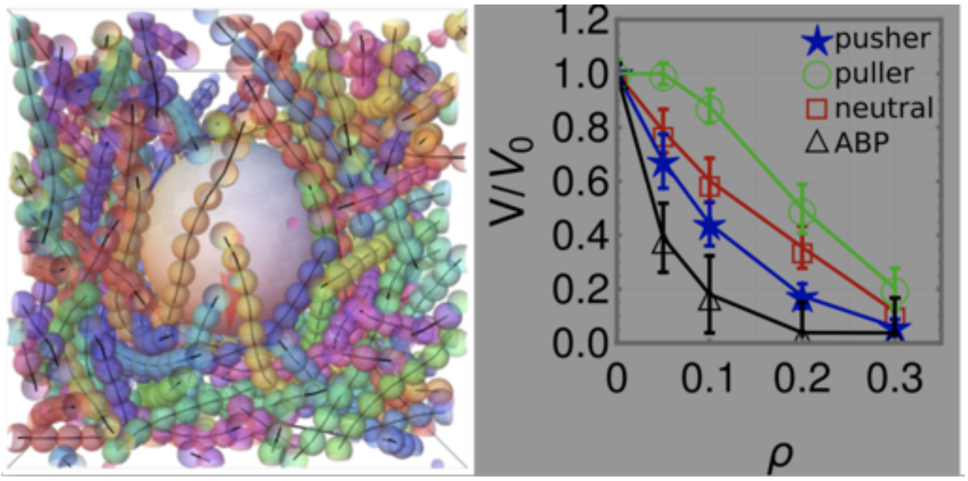


Figure 1: (left) snapshot of a spherical microswimmer (squirmer) surrounded by explicitly modeled semi-flexible filaments embedded in a Newtonian background fluid (not shown). (right) Comparison of Polymer-density dependent swimming speed for different swimmers

ST - Immobility of swarmer cells due to local liquid depletion

A. Jose[1], B. Pérez-Estay[2], S. Omer Bendori[3], A. Eldar[3], D.B. Kearns[4], G. Ariel[5], A. Be'er[6,7]

[1] The Albert Katz International School for Desert Studies, The Jacob Blaustein Institutes for Desert Research, Ben-Gurion University of the Negev, SedeBoqer Campus, 84990 Midreshet Ben-Gurion, Israel.
[2] Laboratoire PMMH-ESPCI Paris, PSL Research University, Sorbonne University, University Paris-Diderot, 7, Quai Saint-Bernard, Paris, 75005, France.
[3] The Shmunis School of Biomedicine and Cancer Research, Faculty of Life Sciences, Tel Aviv University, Tel Aviv, 69978 Israel.
[4] Department of Biology, Indiana University, Bloomington, Indiana 47405, USA
[5] Department of Mathematics, Bar-Ilan University, 52900 Ramat-Gan, Israel.
[6] Zuckerberg Institute for Water Research, The Jacob Blaustein Institutes for Desert Research, Ben-Gurion University of the Negev, Sede Boqer Campus 84990, Midreshet Ben-Gurion, Israel
[7] The Department of Physics, Ben-Gurion University of the Negev, 84105 Beer-Sheva, Israel.

Bacterial swarming is a complex phenomenon in which thousands of self-propelled rod-shaped cells move coherently on surfaces, providing an excellent example of active matter. However, bacterial swarming is different from most studied examples of active systems because single isolated cells do not move, while clusters do. The biophysical aspects underlying this behavior is unclear. This talk explores the case of low local cell densities, where single cells become temporarily immobile. We show that immobility is related to local depletion of liquid. In addition, it is also associated with the state of the flagella. Specifically, the flagellar bundles at (temporarily) liquid depleted regions are completely spread-out. Our results suggest that dry models of self-propelled agents, which only consider steric alignments and neglect hydrodynamic effect, are oversimplified and are not sufficient to describe swarming bacteria.

ST - Chaotic collective mixing by a S. Lemnae feeding cluster

R. Turuban[1,2], **G. Noselli**[2], **A. Beran**[3], **A. De Simone**[1,2]

[1] The BioRobotics Institute, Scuola Superiore Sant'Anna, Pisa, Italy
[2] SISSA–International School for Advanced Studies, Trieste, Italy
[3] OGS–Istituto Nazionale di Oceanografia e di Geofisica Sperimentale, Trieste, Italy

Although it is an efficient swimmer, the suspension feeder *Stylonychia Lemnae* greatly prefers to crawl on solid surfaces. Whenever sensing food, the cells change their locomotion behavior in order to remain in the most favorable area, mostly by reducing their crawling speed. In the meantime, anchored cells apply a net force on the fluid, thereby generating a long-range feeding current. As cells progressively gather around food, they become close enough so that the multiple feeding flows interact hydrodynamically: a collective chaotic flow has emerged, at the scale of the whole feeding cells cluster, with new striking fluid dispersion and mixing properties. Here, we measure experimentally the collective feeding flow using PIV, and show that we can entirely predict this unstationary 3D flow with an analytical model consisting in the superposition of regular forces over a non-slip boundary, with each force representing a feeding cell with evolving orientation and position. From the analytical flow, we provide first a numerical quantification of the fluid dispersion coefficient which reveals that, at equivalent population density, the collective feeding flow is at least 40 times more efficient at spreading fluid than a suspension of squirmers, based on the model proposed by [1]. Second, we compute the Lyapunov exponent, which is shown to compare well even with non-active chaotic laminar flows such as porous media flows or sheared particulate suspensions. We will finally discuss about the biological benefits potentially granted by the active collective flow, as well as its possible cooperative nature.

References

[1] Z. Lin, Journal of Fluid Mechanics **669**, 167-177, (2011)

CT - Single cell death triggers local avoidance response in the cosmopolitan picoeukaryote Micromonas

M. Polin

Mediterranean Institute for Advanced Studies IMEDEA (UIB-CSIC) C/ Miquel Marqués 21 07190 Esporles, Balearic Islands, Spain

Phytoplankton cell death has been identified as contributing to the largest carbon transfers on the planet moving 109 tonnes of carbon in the oceans every day. During a cell death organic matter is released into the local environment which can act as both a food source and a warning signal for nearby organisms. Here we present a novel motility response in populations of the cosmopolitan pico-eukaryote Micromonas sp., where the death of a single cell triggers the escape of cells in the surrounding area. These so-called "burst events" follow a simple model based on the release of a diffusive species with an estimated diffusion constant typical of molecules. Laser ablation of single cells reproduces the observed avoidance response, confirming that Micromonas sp. has evolved a motility allowing it to escape from regions where cell lysis takes place. This behaviour has potential implications for the spread of viral infections in Micromonas communities.

ST - E-coli transport along microfluidic edges determined by trajectory chirality and confinement

P. Zhang[1], **S. M. Köhler**[2], **F. Goio Castro**[1], **E. Clément**[1], **A. Zöttl**[2], **A. Lindner**[1]

[1] PMMH, CNRS, ESPCI Paris, Université PSL, Sorbonne Université, Université de Paris, F-75005, Paris, France
[2] Faculty of Physics, University of Vienna, 1090 Wien, Austria

Swimming of bacteria near surfaces is of high biological and medical relevance, for example, in the formation of biofilms [1] or their transport through medical conducts. Such near-surface accumulation, has been attributed to hydrodynamic attraction and collisions between the cells and the surface. The motion of E.coli bacteria near surfaces is related to their asymmetric shape and chiral flagella, leading to the well-known chiral clock-wise circular trajectories in the presence of the counter-rotation body and flagella [2]. It has been reported that such chirality of E.coli trajectories can lead to navigation of the swimming bacteria along a preferential direction along confined microfluidic channels [3, 4]. However, the exact mechanism behind these observations remain to be fully understood.

In this work we study the relationship between the chirality of bacteria trajectories at flat surfaces and their swimming direction along the edge region of a rectangular channel formed by two perpendicular sections of channel surfaces. We measure the orientation directions of smooth runner E.coli bacteria approaching the edges. Interestingly, we identified a preferential approaching orientation which is reversed from swimming to the right to swimming to the left for increasing confinement. This observation is consistent with both our numerical simulations and analytical results in two dimensions. To understand the mechanism hidden behind this general observation, we explore the distribution of the incoming angle at the edges and it shows strong correlation with the subsequent swimming direction along the edges. Finally we show that this angle distribution is a function of the channel confinement and explains the preferential confinement-dependent orientations. To understand transport along all four edges of a rectangular channel we also obtained individual bacterial 3D lagrangain-tracking trajectories suggesting the presence of competing effects of different channel surfaces. These results coupled with our two-dimensional observations will give a more complete understanding of the role of chirality in bacteria transport near the edges of rectangular channels. This work will shed light on performing targeted transport in lab-on-chip devices and other medical applications.

References

[1] Paula Watnick and Roberto Kolter. “Biofilm, city of microbes”. In: Journal of bacteriology **182**.10 pp. 2675–2679 (2000)
[2] Eric Lauga et al. “Swimming in circles: motion of bacteria near solid boundaries”. In: Biophysical journal **90**.2 pp. 400–412 (2006)
[3] Mite Mijalkov and Giovanni Volpe. “Sorting of chiral microswimmers”. In: Soft Matter **9**.28 pp. 6376–6381 (2013)
[4] Willow R DiLuzio et al. “Escherichia coli swim on the right-hand side”. In: Nature **435**.7046 pp. 1271–1274 (2005)

IS - Motility as communication in bacterial active matter

G. Wong

UCLA, LosAngeles, USA

Figure 1:

CT - Self-propulsion of confined active droplets

S. Michelin[1], **N. Desai**[1,2]

[1] LadHyX, CNRS – Ecole Polytechnique, Institut Polytechnique de Paris, Palaiseau, France
[2] DAMTP, University of Cambridge, Cambridge, United Kingdom

Chemically-active droplets are intriguingly simple systems that can swim at micron scale as a result of their physico-chemical activity. In particular, self-solubilising droplets can self-propel spontaneously in surfactant-laden solutions as a result of the non-linear transport of surfactant molecules and micellar compounds by the interfacial flows induced at their surface by gradients of such species. Many recent experiments have reported the complex individual behaviour of these droplets and the onset of propulsion is now relatively well understood conceptually and modelled [1]. Yet, almost all modeling theoretical and numerical analyses of such fascinating systems focus exclusively on the case of an isolated self-propelled droplet in an unbounded and quiescent fluid. These assumptions are in fact particularly restrictive as they ignore an intrinsic feature of the experimental systems, namely the immediate vicinity of one or more confining boundaries, as a result of the relative buoyancy of the droplet. The presence of a nearby wall or free surface is not anecdotal, since the instability and propulsion could well be hindered or suppressed as a result of the the strong and dissipative lubrication stresses within the thin fluid layers separating the droplets from the inactive substrate. In this work, we resolve this major shortcoming and analyse for the first time the stability and onset of propulsion of isotropic active droplets close to a rigid boundary, using the canonical fully-coupled hydro-chemical model of active droplets for arbitrary distance to the wall. We demonstrate how confinement, far from preventing propulsion, can actually promote and enhance it, and explain the underlying physical mechanisms [2,3].

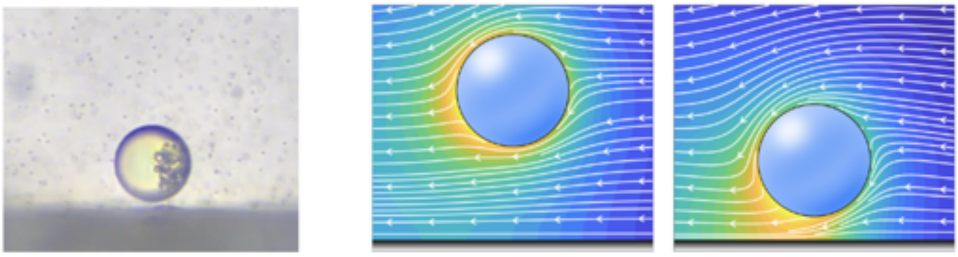


Figure 1: (Left) Side view of a self-propelled chemically-active droplet (Cheon et al., 2021) (Right) Solute distribution and streamlines around a moving droplet for two different buoyancy ratios [3].

References

[1] S. Michelin, Self-propulsion of chemically-active droplets, Ann. Rev. Fluid Mech., **55**, 77-101 (2023)

[2] N. Desai & S. Michelin, Instabilities and self-propulsion of active droplets along a wall, Phys. Rev. Fluids, **6**, 114103 (2021)

[3] N. Desai & S. Michelin, Steady state propulsion of isotropic active colloids along a wall, Phys. Rev. Fluids, **7**, 100501 (2022)

ST - Mechanical coupling is sufficient to synchronize C. Reinhardtii flagella

L. Zorrila[1], K. Desai[2], A. Allard[3], M. Polin[1]

[1] IMEDEA (UIB-CSIC), Esporles, Spain
[2] University of Warwick
[3] LOMA, University of Bordeaux

Physical laws apply differently at the microscale than at the macroscale, therefore constraining microorganisms' biological functions. A key instance of this is that microbes perceive their surrounding medium as extremely viscous, constraining them to adopt non-symmetric motion to be able to propel forward. Some bacteria (*E. coli*) and unicellular algae (*C. reinhardtii*) have evolved different asymmetric motions in order to propel. *C. reinhardtii* has two flagella, mechanically connected from inside the cell, that beat synchronously in a "breaststroke" pattern. Flagellar synchronization is necessary to propel forward but is not fully understood. More generally, many microorganisms, including human epithelial cells or multiciliate microbes display flagellar synchronization. Experiments on isolated pairs of flagella from multicellular alga Volvox have shown that hydrodynamic coupling alone is sufficient for metachronal synchronization. But *C. reinhardtii* also displays internal mechanical coupling that has been shown to be necessary to synchronize its flagella in a breaststroke movement. What is the respective nature of hydrodynamic and mechanical coupling in flagellar synchronization of these unicellular alga? To find out, we separate their two flagella by a cantilever to prevent inter-flagellar hydrodynamic interactions, while holding the cell with a micropipette. We observe that flagella stay synchronized without hydrodynamic interactions, including when subject to stress. We further investigate the quantitative and qualitative contribution of hydrodynamic coupling to synchronization with the use of anti-phase synchronized (ptx1) cell mutants.

ST - On-Demand Breaking of Action-Reaction Reciprocity between Magnetic Microdisks Using Global Stimuli

G. Gardi[1], **M. Sitti**[1,2]

[1] Physical Intelligence Department, Max Planck Institute for Intelligent Systems, 70569 Stuttgart, Germany
[2] School of Medicine and College of Engineering, Koç University, 34450 Istanbul, Turkey

Coupled physical interactions induce emergent collective behaviours of many interacting objects. Nonreciprocity in the interactions generates unexpected behaviours. There is a lack of experimental model system that switches between the reciprocal and nonreciprocal regime on demand. Here, we study a system of magnetic microdisks that breaks action-reaction reciprocity via fluid-mediated hydrodynamic interactions, on demand. Via experiments and simulations, we demonstrate that nonreciprocal interactions generate self-propulsion-like behaviours of a pair of disks; group separation in collective of magnetically nonidentical disks; and decouples a part of the group from the rest. Our results could help in developing controllable microrobot collectives. Our approach highlights the effect of global stimuli in generating nonreciprocal interactions.

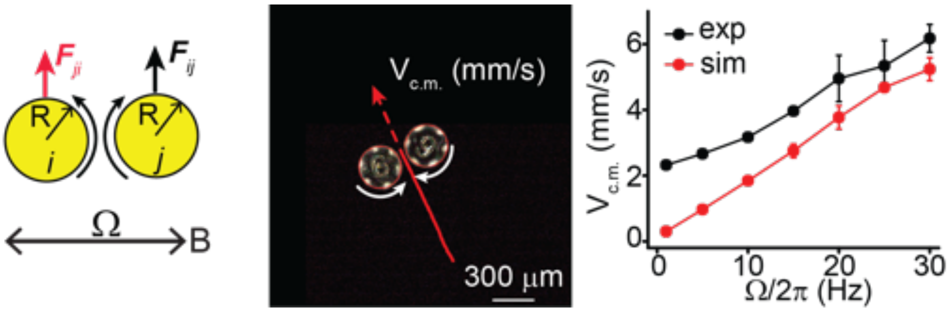


Figure 1: Left: schematic of non-reciprocal interaction between counter-rotating disks under oscillating magnetic field. Middle: experimental image showing translation of a counter-rotating disk pair. Right: Translation speed of centre of mass of disks vs frequency of magnetic field.

References

[1] G. Gardi, and M. Sitti, Physical review letters, **131**(5), 058301 (2023)

IS - Behavioral cartography: Mapping cellular behavior in the wild

M. Prakash

Department of BioengineeringBiology (courtesy) and Oceans (courtesy)School of Engineering, School of Sustainability, School of Medicine, Stanford University

It is difficult to understand living systems without ecological context in which they live. Ecology shapes every aspect of a cell including cellular behavior, metabolism, growth and development. Here we present a new framework for mapping single cell behavior in an unbounded context of an aquatic environment (marine and fresh water). We share instrumentation and software tools that enable a unique class of behavioral assay capable of "free swimming" motility of a living cell in an unbounded landscape. Creating a virtual reality arena for a cell by modulating light, pressure, gravitational orientation, salinity and other chemical cues - we can collect unbiased behavioral datasets in the field. Here we share our efforts over the last few years to build a global cell motility atlas - from the Arctic to Antarctica, in Pacific, and Atlantic Ocean and marine and fresh water species. The database represents largest collection of behavioral data collected over more than 10 expeditions with partners in US and Europe. We will further describe our framework to scale these technologies and platforms to broaden our understanding of cell behavior in the wild.

CT - Swimming behavior of Chlamydomonas reinhardtii cells in complex photonic environments

G. Jacucci[1], J.-F. Allemand[1], S. Gigan[2], R. Jeanneret[1]

[1] Laboratoire de Physique de l'Ecole normale supérieure, ENS, Université PSL, CNRS, Sorbonne Université, Université Paris Cité, F-75005 Paris, France
[2] Laboratoire Kastler Brossel, Sorbonne Université, Ecole Normale Supérieure-Paris Sciences et Lettres (PSL) Research University, CNRS, Collége de France, 75005 Paris, France

Chlamydomonas reinhardtii cells have the ability to orient themselves in light fields, a property called phototaxis. As opposed to chemotaxis which has been extensively studied in the past 50 years, this phenomenon is still poorly understood. In *Chlamydomonas* phototaxis is mediated by a specialized organelle called the eyespot, that is thought to provide direct information about the direction of light propagation to the cells. However, recent experiments suggest that *Chlamydomonas* cells can also use light gradients to navigate light fields [1]. In this work, we studied the swimming behavior of micro-algae in tailored laser illuminations in confined microfluidic chambers. By tracking individual cells, we demonstrated that the run-and-tumble motion of *Chlamydomonas* is influenced by both local light intensity and gradient. Notably, under a ring-shaped illumination, micro-algae quickly climb up the light gradients and accumulate inside the ring (Fig. 1). We rationalized this phenomenon thanks to a thorough characterization of the motility of the cells within such illumination pattern. Our findings offer new insights into how *Chlamydomonas* modulates its motility in response to light, adapting to both its direction and gradient. Our experiments also suggest novel strategies for controlling and redirecting their movement.

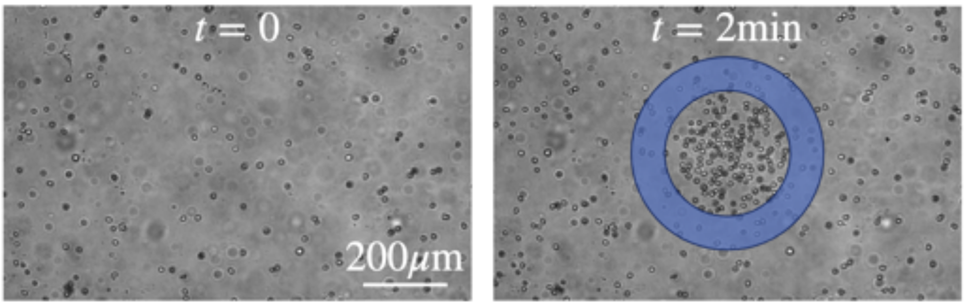


Figure 1: When confined to a quasi-2D chamber (20 μm-thick) and illuminated by a ring-shaped beam, Chlamydomonas cells quickly get trapped and accumulate inside the ring. We rationalized this phe- nomenon by studying the modulation of the motility of the cells within the different regions of the illumination pattern, providing new insights into the swimming behavior of these important micro-organisms in light fields.

References

[1] A. Ramamonjy et al, PRL **128**, 258101 (2022)

CT - E. coli steering and interaction with surfaces

B. Wu-Zhang, G. Gompper, D. A. Fedosov

Theoretical Physics of Living Matter, Institute for Advanced Simulation, Forschungszentrum Jülich, 52425 Jülich, Germany

A huge variety of existing microorganisms motivates fundamental studies of their behavior with a possibility to construct their mimics. A prominent example is *E. coli* bacterium which employs several helical flagella for propulsion to explore the environment and seek for nutrition. This type of bacteria alternates between run (direct swimming) and tumble (change in the swimming direction) phases to steer within a fluidic environment. Even though the run-and-tumble behavior of *E. coli* seems to be simple, physical properties and mechanisms that enable this dynamics are still poorly understood. We establish a detailed *E. coli* model (see Fig. 1), which is coupled to fluid flow described by the dissipative particle dynamics method, and investigate its run-and-tumble behavior. Various *E. coli* characteristics, including body and flagella geometry, flagella bending rigidity, and the number of flagella and their arrangement at the body, are considered. Furthermore, we investigate the interaction of E. coli with surfaces. Interestingly, *E. coli* also employs tumbling to escape from a surface, and the orientation of the body after tumbling mainly determines surface-escape success. In conclusion, the developed model helps us better understand physical mechanisms which govern *E. coli* dynamics, and can further be used to explore the behavior of *E. coli* in more complex realistic environments.

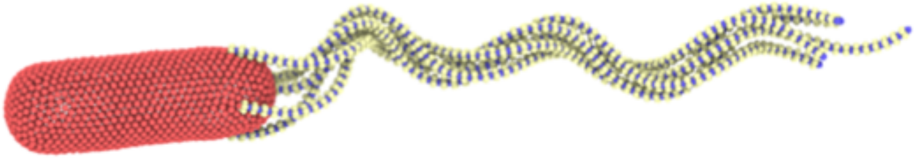


Figure 1: *E. coli* model that consists of a sphero-cylindrical cell body (red) and five left-handed helical flagella (yellow).

ST - Viscotaxis of Beating Flagella at Surfaces

S. Anand, J. Elgeti, G. Gompper

Theoretical Physics of Living Matter, Institute for Biological Information Processing and Institute for Advanced Simulation, Forschungszentrum Jülich, 52425, Germany

Understanding how microorganisms steer, change their swimming direction, and achieve directional motion in complex environments is crucial for many biological processes, including egg fertilization[1,2,3]. In some cases, eukaryotic flagellated microswimmers, like sperm, navigate their surroundings by responding to environmental gradients, such as chemical, temperature, gravitational fields, and light. These external cues trigger specific behavioral responses that enable the microswimmers to adjust their swimming direction, helping them reach their targets[4,5]. This ability to respond and adapt their motion to environmental stimuli is known as taxis, which plays a fundamental role in guiding microswimmers in complex biological processes. A well-known example is chemotaxis, where concentration gradients of a chemo-attractant are sensed and guide the sperm cell towards the egg cell. We investigate another potentially relevant physical mechanism, viscotaxis, in which a beating flagellum reacts to gradients of fluid viscosity. Various kinds of microswimmers have been found to respond to viscosity gradients depending on their shape or hydrodynamic propulsion mechanisms [6,7]. We investigate viscosity gradient effects on flagellum motion. Our flagellum model is represented by a semi-flexible filament with a traveling wave of spontaneous curvature, to investigate viscotaxis in two-dimensional space. Through a combination of numerical simulations and analytical approaches, we show that actively beating flagellum exhibits positive viscotaxis, orienting toward regions with higher viscosity. This behavior is characterized by analyzing the relationship between rotational velocity and parameters such as beat amplitude, swimming speed, and wavelength. Furthermore, we explore the effects of asymmetric flagella waveforms and flagella elasticity. The asymmetric flagellar waveforms result in linear or trochoid-like trajectories, with large asymmetry causing drifting circles perpendicular to the gradient. Deformability of the flagella significantly reduces both the beat amplitude and viscotactic response, which is captured by a universal function based on the sperm number. We have also studied the role of a head, where the viscotactic response is found to decrease with increase in head size.

References

[1] J. Elgeti et al., Rep. Prog. Phys.**78**, 056601, (2015)
[2] L. Alverez et al., Trends Cell Biol. **24**, 198, (2014)
[3] A. Gong et al., 2020 Phil. Trans. R. Soc. B37520190149 (2020)
[4] G. Saggiorato et al., Nat. Commun **8**, 1415 (2017)
[5] A. Gong et al., Phil. Trans. R. Soc. B **375**, 20190149 (2019)
[6] V. A. Shaik et al., Phys. Rev. Fluids **6**, 103103 (2021)
[7] B. Liebchen et al., Phys. Rev. Lett. **120**, 208002 (2018)

IS - Adaptation in flagellar architecture improves chemotaxis in complex environments

K. Taute

Peter Debye Institute for Soft Matter Physics, Leipzig University

Abstract: Flagellar motility enables bacteria to navigate natural habitats with a wide range of mechanical properties, from the ocean to the digestive tract and soil. Species differ in the number, position, and shape of their flagella, but the adaptive value of these flagellar architectures is unclear. Many species traverse multiple types of environments, such as pathogens inside and outside a host. We investigated the hypothesis that flagellar architectures mediate environment-specific benefits in the marine pathogen *Vibrio alginolyticus* which exhibits physiological adaptation to the mechanical environment. In addition to its single polar flagellum, the bacterium produces lateral flagella in environments that differ mechanically from water. These are known to facilitate surface motility and attachment. We used high-throughput 3D bacterial tracking to quantify chemotactic performance of both flagellar architectures in three archetypes of mechanical environments relevant to the bacterium's native habitats: water, polymer solutions, and hydrogels. We reveal that lateral flagella impede chemotaxis in water by lowering the swimming speed but improve chemotaxis in both types of complex environments. Statistical trajectory analysis reveals two distinct underlying behavioral mechanisms: In viscous solutions of the polymer PVP K90, lateral flagella increase the swimming speed. In agar hydrogels, lateral flagella improve overall chemotactic performance, despite lowering the swimming speed, by preventing trapping in pores. Our findings [1] show that lateral flagella are multi-purpose tools with a wide range of applications beyond surfaces. They implicate flagellar architecture as a mediator of environment-specific benefits and point to a rich space of bacterial navigation behaviors in complex environments.

References

[1] Grognot et al., PNAS 2023, doi:10.1073/pnas.230187312

CT - Intermittent active motion for enhanced spatial exploration

K.S. Olsen, **H. Löwen**

Institute for Theoretical Physics II: Soft Matter, Heinrich Heine University Düsseldorf, D-40225 Düsseldorf, Germany

When does stopping make you go faster? While counterintuitive at first glance, intermittent pauses in the dynamics can have a range of benefits, and even facilitate rapid spatial exploration. Intermittent dynamics is a ubiquitous phenomenon in nature, with examples including nano-tracers in heterogeneous media, the motility patterns of cells, and foraging strategies observed in macroscopic living animals. Recently, there is an increased interest in intermittent active motion, where self-propelled particles stochastically switches between a mobile and an immobile phase, illustrated in Fig. 1. Here, we present recent results showcasing the conditions under which intermittent motion serves as a beneficial strategy of motion. In particular, we consider a chiral active particle that intermittently interrupts its chiral trajectories by reorientations. Both instantaneous reorientations and finite-time dynamical reorientations are studied, and explicit expressions for the effective diffusion coefficient are derived in each scenario. Optimal intermittency strategies that enhance diffusion are identified. Potential generalisations to the case of directed motion are discussed, and connections are made to composite dynamical processes and stochastic resetting processes [2,3].

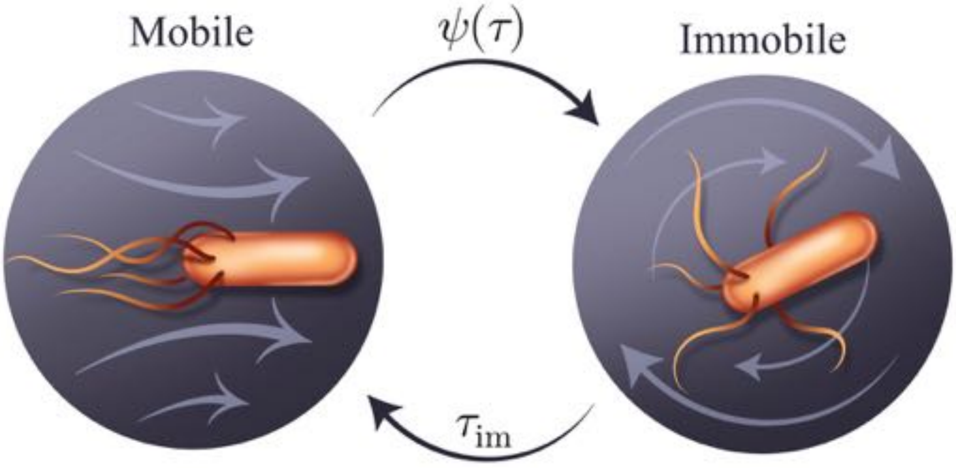


Figure 1: A self-propelled particle (e.g. a bacterium) intermittently enters a phase of rapid reorientations ("immobile"), before continuing its active motion ("mobile"). The 2-phase dynamics continues intermittently.

References

[1] K. S. Olsen and H. Löwen, Optimal diffusion of chiral active particles with strategic reorientations, arXiv:2405.14326, (2024)

[2] K. S. Olsen and H. Löwen, Dynamics of inertial particles under velocity resetting, Journal of Statistical Mechanics: Theory and Experiment, 2024, 033210 (2024)

[3] I. Santra, K. S. Olsen and D. Gupta, Dynamics of switching processes: general results and applications to intermittent active dynamics, arXiv:2408.16643, (2024)

IS - Capillary action and stationary currents in scalar active matter

A. Wysocki[1], A. Fins Carreira[2], M. Leocmach[2], M. Mangeat[1], C. Ybert[2], C. Cottin Bizonne[2], H. Rieger[1,3]

[1] Department of Physics & Center for Biophysics, Saarland University, D-66123 Saarbrücken, Germany
[2] Université de Lyon, Université Claude Bernard Lyon 1, CNRS, Institut Lumière Matière, Villeurbanne, France
[3] Leibniz Institute for New Materials INM, Campus D2 2, D-66123 Saarbrücken, Germany

Recently it was theoretically predicted that scalar active matter in a gravitational field would rise against gravity up a confining wall or inside a thin capillary, in spite of repulsive particle-wall interactions [1]. Using an active Brownian particle (ABP) model, we elucidate the mechanism leading to the formation of a meniscus rising above the bulk of the sedimentation region, whose height increases algebraically with the Péclet number. The formation of the meniscus is accompanied by a stationary circular particle current, a vortex, centered at the base of the meniscus, whose size and strength increase with the ABP activity [2]. These predictions are tested experimentally by considering a non-phase separated sediment of self-propelled Janus colloids in contact with a vertical wall [3]. We provide experimental evidence of an unexpected and dynamic adsorption layer at the wall. Our ABP model recapitulates quantitatively the experimental observations. We show that an adhesive and aligning wall enhances the pre-existing polarity heterogeneity within the bulk, enabling polar active particles to climb up a wall against gravity, effectively powering a global flux. Such steady-state flux has no equivalent in a passive wetting layer.

References

[1] Adam Wysocki and Heiko Rieger, Phys. Rev. Lett. **124**, 048001 (2020)
[2] Matthieu Mangeat, Adam Wysocki, Heiko Rieger, Phys. Rev. E **109**, 014616 (2024)
[3] Adérito Fins Carreira, Adam Wysocki, Christophe Ybert, Mathieu Leocmach, Heiko Rieger, Cécile Cottin-Bizonne, Nat. Comm. **15**, 1710 (2024)

List of Posters

P01 - Collective behavior of squirmers in thin films

B. Wu-Zhang, G. Gompper, D. Fedosov

Forschungszentrum Jülich, Germany

Bacteria are able to migrate collectively over wet surfaces and form stable and highly motile aggregates, which are often referred to as biofilms. Collective locomotion of bacteria within aggregates is called swarming [1], and is affected by interactions between bacteria, their shape and the strength of propulsion, and the density of bacteria packing within a biofilm [2,3]. To better understand the collective behavior of bacteria, numerical simulations of a large number of swimmers are performed. The swimmers are represented by the so-called squirmer model, in which bacteria propulsion is imposed by a prescribed slip velocity field at the surface of the swimmer [4]. This model allows the simulation of swimmers with different propulsion properties, including various motility types (e.g., pusher, puller) and propulsion strengths. We find that local interactions between swimmers mediated by the fluid environment determine their swarming behavior and the formation of clusters, see an example in Fig. 1. In particular, swarming generally takes place at moderate volume fractions of swimmers, while at high swimmer densities, large non-motile clusters prevail [5]. These results advance our understanding of bacterial film formation and the connection between the collective swarming behavior and the internal properties of individual swimmers.

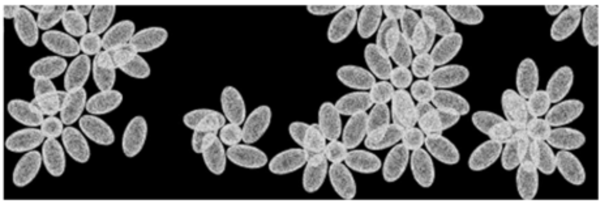


Figure 1: Snapshot of a simulation of pullers at a volume fraction of $\phi = 0.18$. Pullers tend to form flower-like clusters consisting of several swimmers.

References
[1] J. Elgeti et al., Rep. Prog. Phys. **78**, 056601, (2015)
[2] M. Theers et al., Soft matter **14**, 8590-8603, (2018)
[3] K. Qi et al., Commun. Phys. **5**, 49, (2022)
[4] M. Theers et al., Soft Matter **12**, 7372-7385, (2016)
[5] Wu-Zhang et al., Soft Matter **20**, 5687-5702, (2024)

P02 - Intrinsic Curvatures of the Volvox carteri

J. Y. Y. Chui, M. Vona, A. Srinivasan, R.E. Goldstein

University of Cambridge, Cambridge, United Kingdom

Extracellular matrix (ECM) is common across living systems and is integral to many cellular processes, as well as a means of providing structure to an organism. The colonial green alga *Volvox carteri* is one such organism, where ciliated somatic cells produce ECM throughout their lifecycle to generate an expanding spherical colony that is capable of phototaxing through the water column. In these experiments where *Volvox carteri* is broken into pieces using a homogenizer, we discover that these thin sheets of cells embedded in ECM have an intrinsic curvature different to that of the initial spheroid, and depending on the characteristic shape and size of these broken-off pieces we can infer residual stresses in ECM of a volvox colony as it expands over its lifecycle. We use confocal imaging techniques to observe how changes in the number of cells, boundary conditions, and age of the tissue changes the final shape of the piece, as well as how the cilia interact and synchronize with each other to propel a piece with a very different shape factor. Using our experimental data as a guide, we then propose a general theoretical framework that recovers these unique shapes and curvatures, and also determines the extent of influence the number of ECM producing neighbours has on the intrinsic curvature of a piece. The sum of this will help answer important questions regarding shape, structural integrity, and aging as it relates to ECM in general.

P03 - Buoyancy regulation in diatoms : an indirect motility mechanism in response to shear stress?

C. Fronda[1], **I. Tuval**[2], **R. Jeanneret**[1]

[1] Laboratoire de Physique de l'Ecole normale supérieure, ENS, Université PSL, CNRS, Sorbonne Université, Université Paris Cité, F-75005 Paris, France
[2] Institut Mediterrani d'Estudis Avançats, IMEDEA (UIB-CSIC), 07190 Esporles, Mallorca, Spain

Diatoms are one of the main phytoplankton species contributing to the ocean carbon sink and playing a key role in the marine ecosystems foodchains (40 % of total marine primary production). Even though they do not possess any flagella, different studies have challenged the previous paradigm of considering diatoms as passive drifters, showing that they can exhibit an indirect form of motility, by controlling their buoyancy in the water column. Such buoyancy control involves complex biochemical mechanisms spanning distinct timescales (seconds to days): changes in silicification [1], carbohydrates accumulation/release [2] or ions exchange in vacuoles [3]. In particular, recent preliminaries studies have evidenced rapid changes in diatoms sinking speeds induced by viscous shear stress, suggesting that there exist an active mechano-transduction mechanism for buoyancy control in diatoms [4]. In this poster I will present the experimental set up we have built to track diatoms species in millifluidic channels and to get detailed statistical analysis of single cell behaviours under controlled shear rates (Poiseuille flow). First measurements on the species *Ditylum brightwellii* have notably shown that these cells experience a transition to a regime of lower sinking speeds when repeatedly exposed to shear stresses (Fig. 1), demonstrating mechano-transduction and active buoyancy regulation in this species.

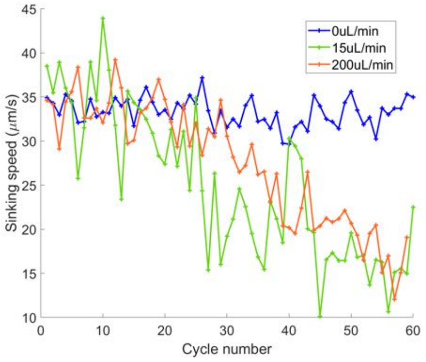


Figure 1: Mean sinking speed of the population of cells as a function of cycle number. A cycle corresponds to a phase of flow advection followed by a phase of sedimentation without any external flow (during which sinking speeds are measured). A clear decrease in sinking speed is observed as cells experience shear stresses (green and orange markers), demonstrating active buoyancy regulation. The effect is absent when cells are not stimulated by flows (blue markers).

References

[1] Raven J.A., Doblin M.A., Journal of Experimental Botany **65**, (2014)
[2] Fisher A.E., J. Phycol. **32**, (1996)
[3] Boyd, C. M., Gradmann, D., Mar. Biol. **141**, (2002)
[4] Arrieta, J. et al., Phil. Trans. R. Soc. **378**, (2020)

P04 - Emergent spatiotemporal structures in bacterial binary mixtures

S. Espada Burriel, R. Colin

Max Planck Institute for Terrestrial Microbiology, Marburg, Germany

Microbial communities often exhibit complex spatial structures that are important for their functioning, ecology and evolution. While the role of biochemical interactions has been extensively studied, it is unclear how physical interactions contribute to the structuring of multispecies and phenotypically diverse bacterial communities. Here, we investigate the physical effect of motility, a key bacterial trait, on the spatial organization of complex communities, using binary bacterial mixtures as a minimal model system, where one component is motile and the other is not. We observe that the activity of the motile cells enhances the aggregation of non-motile bacteria and that adhesive motile cells promote the formation of complex, three-dimensional biofilm structures, suggesting that motility, together with the ability of motile cells to aggregate, is important for the early stages of biofilm formation. These results show how the activity of motile species can shape the spatial organization of complex microbial communities.

P05 - Different Wobbling Gaits and Their Role in Bacterial Mobility

W. Feng[1], **P. Zhang**[2], **Y. Liu**[1], **H. Luo**[1], **A. Lindner**[2], **E. Clément**[2], **G. Jing**[1]

[1] School of Physics, Northwest University, 710127, Xi'an, China
[2] Laboratoire PMMH-ESPCI, UMR 7636 CNRS-PSL-Research University, Sorbonne Université, Université Paris Cité, 7-9 quai Saint-Bernard, 75005 Paris, France

Wobbling is a common gait in bacterial swimming, reflecting responsive mechanisms that navigation from bulk fluids to confined spaces [1, 2, 3]. Whether this wobbling gait remains consistent as bacteria swim and how speed may correlate with the degree of wobbling are both very curious. In our study, we experimentally observed bacteria exhibiting gaits with wildly varying wobbling angles while swimming steadily near a surface. These variations in wobbling angles corresponded to shifts in the off-axis position of the flagellar bundle, and the flagellar bundle did not unbundle during the whole process. Remarkably, despite notable differences in wobbling intensity, the bacteria maintained a smooth trajectory. This experiment provides unique visual insights into the mechanisms underlying bacterial swimming.

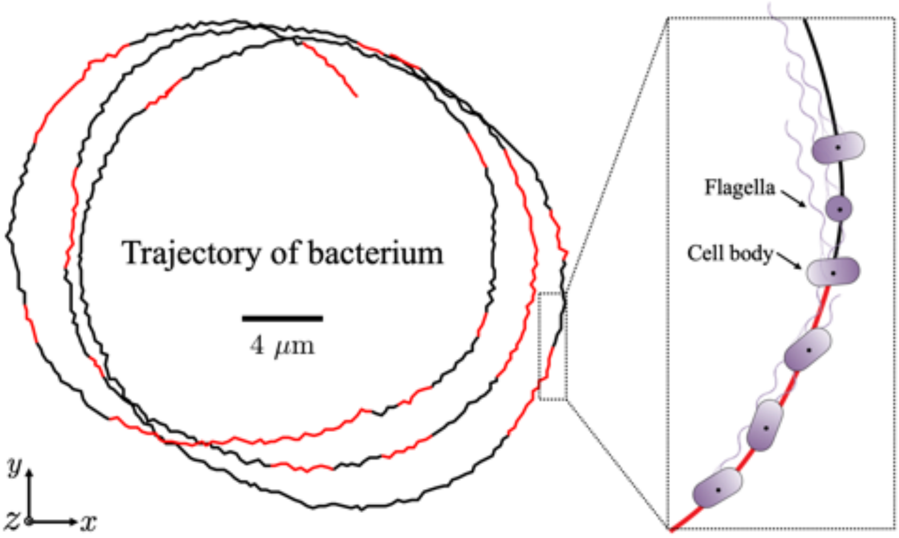


Figure 1: *Escherichia coli* swimming near the surface.

References

[1] Bianchi, S., Saglimbeni, F., Frangipane, G., Dell'Arciprete, D., Di Leonardo, R., Soft Matter, **15**(16), 3397–3406, (2019)
[2] Mousavi, S. M., Gompper, G., Winkler, R. G., Soft Matter, **16**(20), 4866–4875, (2020)
[3] Hu, J., Gui, C., Mao, M., Feng, P., Liu, Y., Gong, X., Gompper, G., in arXiv preprint arXiv:2409.13350, (2024)

P06 - Motility and pairwise interactions of chemically active droplets

P. Kumar, R. Mangal

Department of Chemical Engineering, Indian Institute of Technology Kanpur, Kanpur, India

Self-propelled droplets serve as ideal model systems to delve deeper into understanding the motion of biological microswimmers by simulating their motility. Biological microorganisms are renowned for showcasing a diverse array of dynamic swimming behaviors when confronted with physical constraints. This study aims to elucidate the impact of physical constraints on swimming characteristics of biological microorganisms. To achieve this, we present observations on the individual and pairwise behavior of micellar solubilized self-propelled 4-cyano-4-pentyl-biphenyl (5CB) oil droplets in a square capillary channel filled with a surfactant trimethyl ammonium bromide (TTAB) aqueous solution. To explore the effect of the underlying Péclet number of the swimming droplets, the study is also performed in the presence of additives such as high molecular weight polymer polyethylene oxide (PEO) and molecular solute glycerol. The capillary confinement restricts droplet to predominantly one-dimensional motion, albeit with noticeable differences in their motion across the three scenarios. Through a characterization of the chemical and hydrodynamic flow fields surrounding the droplets, we illustrate that the modification of the droplets' chemical field due to confinement varies significantly based on the underlying differences in the Péclet number in these cases. This alteration in the chemical field distribution notably affects the individual droplets' motion. Moreover, these distinct chemical and flow field field interactions between the droplets also lead to variations in their pairwise motion, ranging from behaviors like chasing to scattering.

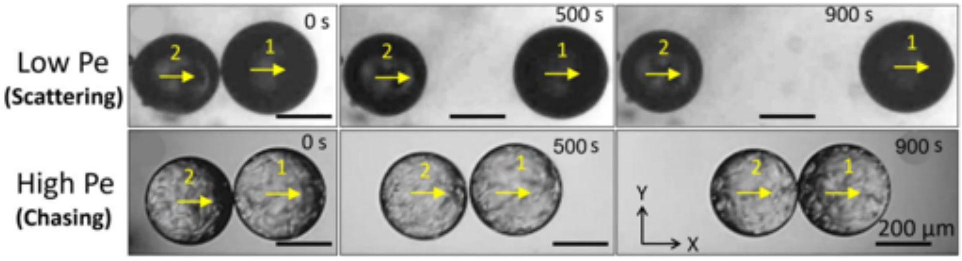


Figure 1: Scattering and chasing behavior of 5CB swimming droplet in a capillary channel in 6 wt.% TTAB aqueous solution with additives as PEO (upper panel) and glycerol (lower panel).

P07 - Growth under Tension - is Motility Necessary?

C. Yao, J. Elgeti

Forschungszentrum Jülich, Jülich, Germany

Ever since the ground breaking work of Trepat et al. in 2009 [1], we know that cell colonies growing on a substrate can be under tensile mechanical stress. The origin of tension has so far been attributed to cellular motility forces being oriented outward of the colony. Works in the field mainly revolve around how this orientation of the forces can be explained, ranging from velocity alignment, self-sorting due to self-propulsion, to kenotaxis. In this work, we demonstrate that tension in growing colonies can also be explained without cellular motility forces! Using a combination of well established tissue growth simulation technique and analytical modelling [2, 3], we show how tension can arise as a consequence of simple mechanics of growing tissues. Combining these models with a minimalistic motility model [4] shows how colonies can expand while under even larger tension. Furthermore, our results and analytical models provide novel analysis procedures to identify the underlying mechanics. phase transition.

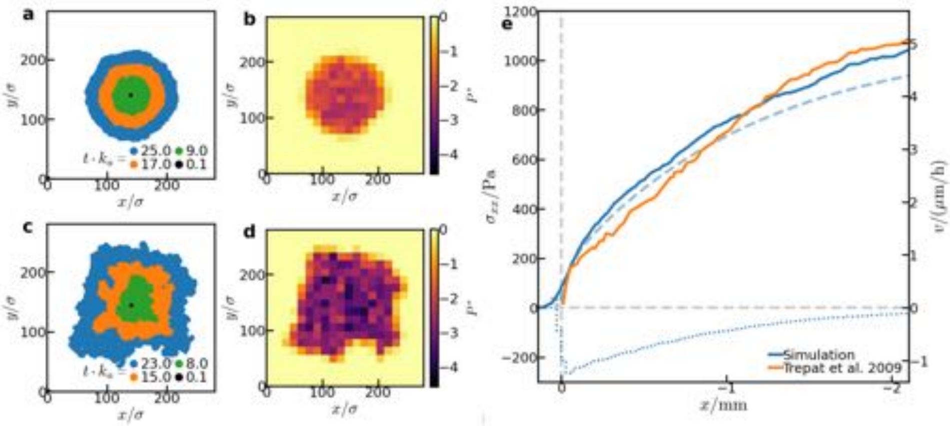


Figure 1: Growth of tensile colonies. (a) Superimposed snapshots of a growing colony of non-motile cells at various times. It grows indefinitely in a roughly circular shape, but remains under tension. (b) The local stress profile corresponding to the last snapshot (blue) of (a). (c) Superimposed snapshots of a growing colony of motile cells at various times. It grows indefinitely, displaying fingering at the edge and large tension inside. (d) The local stress profile corresponding to the last snapshot (blue) of (c). Both colonies are under tension, which is built up from the boundary to the center. (e) The stress profile of an expanding quasi-1d motilie colony (blue solid) with suitable parameters matches those from Trepat et al. 2009 [1]. The dashed and dotted lines are the corresponding theory prediction and veloicty profile.

References

[1] Trepat, X. et al. Nat. Phys. **5**, 426–430 (2009)
[2] Podewitz, N., Delarue, M. & Elgeti, J. EPL **109**, 58005 (2015)
[3] Büscher, T., Diez, A. L., Gompper, G. & Elgeti, J. New J. Phys. **22**, 083005 (2020)
[4] Sarkar, D., Gompper, G. & Elgeti, J. Commun. Phys. **4**, 1–8 (2021)

P08 - Motility and adhesion collectively determine the collective phase behavior of cells in viscoelastic medium

S. Das, D. Parashar, S. Dutta

Department of Chemical Engineering, Indian Institute of Technology Bombay, Mumbai, India-400076

In natural biological systems, cells organize into tissues through a combination of processes, including cellular signaling [1-3], collective migration[4-5], contractile activity of cytoskeletal elements[6], and interactions with their surroundings [7]. In recent decades, advancements in microscopy, genetic engineering, biochemistry, and computational modeling have enabled a more quantitative understanding of these processes. In this work, we present an integrated computational software that accounts for various physical mechanisms that influence cellular assembly and collective behavior and predict the final structure starting from an initial configuration. Specifically, we use this framework to study how cell-cell adhesion and cellular motility collectively interact to determine the phase behavior of cellular collective starting from a random as well as a specified bio-printed structure. Moreover, we observe how the phase behavior depends on the mechanical properties of the medium. Altogether, this work leads to a computational framework that allows us to design phase behavior of collective of cells tuning their interaction as well as motility.

References

[1] Grimm, O. et al. Torso RTK controls Capicua degradation by changing its subcellular localiization. Development **139**, 3962–3968 (2012)

[2]Houchmandzadeh, B., Wieschaus, E. Leibler, S. Establishment of developmental precision and proportions in the early Drosophila embryo. Nature **415**, 798–802 (2002)

[3] Klipp, E., and LiebeKlipp, E., and Liebermeister, W. Mathematical modeling of intracellular signaling pathways. BMC Neurosci **7**(Suppl. 1), S10 (2006)

[4] Friedl, P., Gilmour, D. Collective cell migration in morphogenesis, regeneration and cancer. Nat Rev Mol Cell Biol **10**, 445–457 (2009)

[5] Haeger,A. et. al. Collective cell migration: guidance principles and hierarchies,Trends in Cell Biology, **25**(9), 556-566 (2015)

[6] Shinar, T. et. al. A model of cytoplasmically driven microtubule-based motion in the single-celled Caenorhabditis elegans embryo. Proc. Nat. Acad. Sci. USA 108, 10508–10513 (2011)

[7] Lo, C. M., Wang, H. B., Dembo, M. Wang, Y. L. Cell movement is guided by the rigidity of the substrate. Biophys. J. **79**, 144-152 (2000)

P09 - Effects of gravitational fields and confinement on the collective behavior of biological

L. Parkavousi[1], **N. Rana**[1], **R. Golestanian**[1,2], **S. Saha**[1]

[1] Max Planck Institute for Dynamics and Self-Organization (MPI-DS), D-37077 Göttingen, Germany
[2] Rudolf Peierls Centre for Theoretical Physics, University of Oxford, Oxford OX1 3PU, United Kingdom

Random non-reciprocal interactions between a large number of conserved densities are shown to enhance the stability of the system towards pattern formation. The enhanced stability is an exact result when the number of species approaches infinity and is confirmed numerically by simulations of the multi-species non-reciprocal Cahn-Hilliard model. Furthermore, the diversity in dynamical patterns increases with increasing number of components and novel steady states such as pulsating or spatiotemporally chaotic condensates are observed. Our results may help to unravel the mechanisms by which living systems self-organise via metabolism. We have studied the multicomponent NRCH model for a large number of species and illustrated the role of non-reciprocity in regulating complex phase behaviour. The self-averaging nature of the most unstable eigenvalues in our application of RMT has enabled us to make robust predictions.

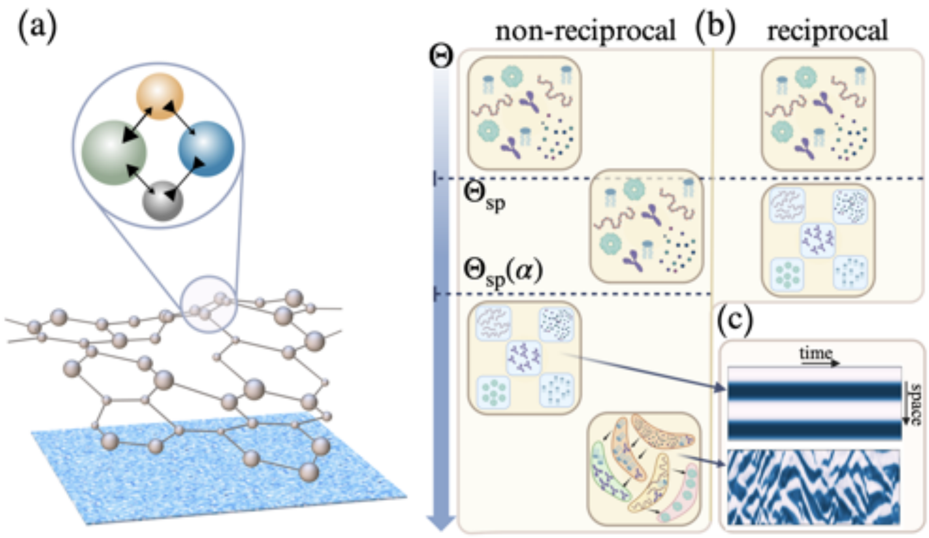


Figure 1: (a) Schematic representation of a minimal living cell, which we define as a collection of a large number of bio-molecular building blocks with random interactions. (b) Non-reciprocity is a reliable way to control LLPS, as it always lowers the phase separation temperature . (c) Activity stirs the mixture while simultaneously stabilising it, leading to chaotic dynamics as shown in the representative kymographs.

References

[1] L. Parkavousi, N. Rana, R. Golestanian, and S. Saha, Enhanced stability and chaotic condensates in multi-species non-reciprocal mixtures (2024), arXiv:2408.06242 [cond-mat.soft]

P10 - Pure hydrodynamic instabilities in active jets of motile micro-algae

I. Eisenmann[1], **M. Vona**[2], **N. Desprat**[1], **T. Ishikawa**[3], **E. Lauga**[2], **R. Jeanneret**[1]

[1] LPENS, Paris, France
[2] DAMTP, Cambridge, UK
[3] Department of Biomedical Engineering, Sendai, Japan

Hydrodynamic instabilities in active jets of micro-swimmers have been predicted in simulations and 1D models but never observed . Here, we harness phototaxis to control millions of swimming *C.reinhardtii* cells and show how a cell jet can spontaneously break up into droplets or buckle into a zigzag structure depending on the cells preferential orientation. Experiments are in excellent agreement with a newly developed continuum description of the system as well as numerical simulations, proving that these instabilities are of purely hydrodynamic nature. To our knowledge these are the first experimental observations of collective behaviors mediated by self-generated flows in "puller" micro-swimmers.

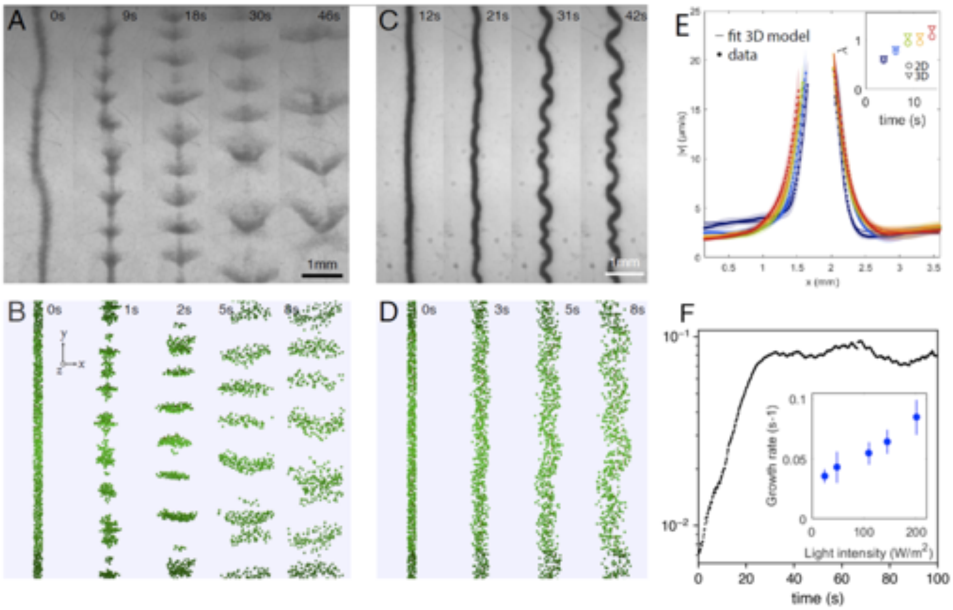


Figure 1: Droplet instability: experiments (A) and simulations (B). Buckling instability: experiments (C) and simulations (D). E: Flow decay around the jet. Inset: fitting with the 3D model gives reasonable wavelengths. F: Exponential growth of the droplet instability. Inset: growth rate increases with light intensity.

References

[1] T.Ishikawa, PRL **100**, 088103, (2008)
[2] L.Jibuti, PRE **90**, 063019, (2014)
[3] E.Lauga, EPL **116**, 64004, (2017)
[4] T.Ishikawa, PRF **7**, 093102, (2022)

P11 - Bio-Convective Transport for Selective Particle Sorting

V. Nicolazo Crach[1], **T. Laroussi**[2], **J. Bouvard**[2], **G. Amselem**[2], **M. Jarrahi**[1]

[1] Laboratoire FAST, Université Paris-Saclay, Orsay, France
[2] Laboratoire LadHyX, École polytechnique, Palaiseau, France

Active particles are inherently out-of-equilibrium systems, able to uptake energy from their environment and convert it to motion. Potential applications of active particles such as microswimmers and micro-robots in bio-medicine are developing rapidly [1]. For example, *Chlamydomonas reinhardtii* (CR) is a micro-swimmer whose orientation can be dictated by a light gradient in its environment (phototaxis). It is known that a collective motion, triggered due to the phototaxis of a population of CR, generates bioconvective structures that affect the fluid medium [2]. The purpose of this study is to control the motion of algae swarms and resulted bioconvection in order to achieve a guided transportation of microscopic objects submerged in the algal suspension. High concentrations of algae and microparticles were confined in a small square Hele-Shaw cell surrounded by a series of LED allowing us to apply different well-controlled gradients of light in a quasi-2D horizontal domain. It was shown that the microparticles can be effectively transported to a target zone while being sorted based on density (Fig.1 (Left)) or their friction against the walls (Fig.1 (Right)).

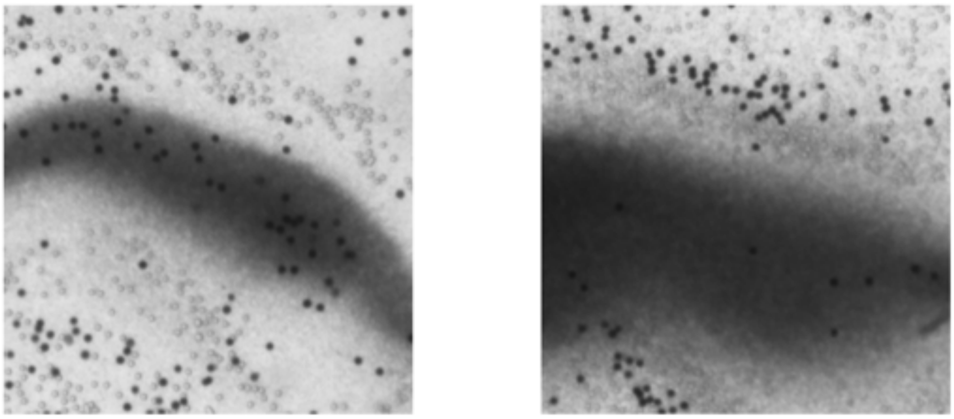


Figure 1: Snapshots of a CR bath containing various beads. The dark regions in both snapshots are regions of high CR concentration. (Left) Black floating beads of density 0.99 g.mL^{-1} are gathered at the center of the CR swarm while the sedimented white beads of density 1.05 g.mL^{-1} are repelled by it. (Right) Black sedimented beads of density 1.01 g.mL^{-}1 are repelled further than the white beads of density 1.05 g.mL^{-1}

References

[1] A. I. Bunea, D. Martella, S. Nocentini, C. Parmeggiani, R. Taboryski, and D. S. Wiersma, Adv. Intell. Syst. **3**, 2000256 (2021)
[2] J. Dervaux, M. Capellazzi Resta, and P. Brunet, Nature Phys **13**, 306–312 (2017)

P12 - Bacterial motility effects on leaf surface exploration

E. M. Mollica[1], **G. S. Ugolini**[1], **B. Daniel**[2], **C. Pestalozzi**[2], **F. Carrara**[1], **E. Secchi**[1], **J. Vorholt**[2], **R. Stocker**[2]

[1] Institute of Microbiology, ETH Zürich, Zürich, Switzerland
[2] Institute for Environmental Engineering, ETH Zürich, Zürich, Switzerland

Plants, like most living organisms, host a wide diversity of microbial life. The aerial part of the plant — the Phyllosphere — which consists of leaves, stems, and flowers, harbors a variety of microbial communities crucial for plant health [1]. Current research aims to understand their adaptations and distribution on leaves. While extensive studies have elucidated late-stage colony distribution and composition, the mechanisms governing initial bacterial distribution remain unknown. We show that hydrodynamic attraction to the surface guides the initial distribution of bacterial colonies inducing trapping on the epidermal grooves. To probe the physical interactions between bacteria and leaf surfaces, we developed a model system of leaf morphology, allowing experimental study of microorganisms with single-cell resolution. Combining laser scanning microscopy and two-photon nanolithography, we replicate real leaf surfaces in microfluidic PDMS chips, isolating their morphological and physical properties from chemical/biological variables. We explore the interplay between motile bacteria and leaf topography, observing surface exploration and initial colony development. On a timescale of hours, bacteria exhibit preferential attachment within the grooves between epidermal cells, giving rise to small colonies, as evidenced by microscopy imaging and previous research [2]. Our data indicates that bacterial surface interactions leading to trapping during surface exploration happen more frequently in grooves than in other leaf regions. This observation underscores the preferential attachment observed during colony development and is supported by the findings of a 2-dimensional mathematical model of near-surface swimming on curved surfaces [3]. We expect our results to shed light on the effects of motility and hydrodynamics in the Phyllosphere and provide a deeper understanding of the mechanisms guiding bacterial distribution during plant growth. These outcomes could also be a step towards characterizing the effects of topographical roughness of living systems on their respective microbiomes.

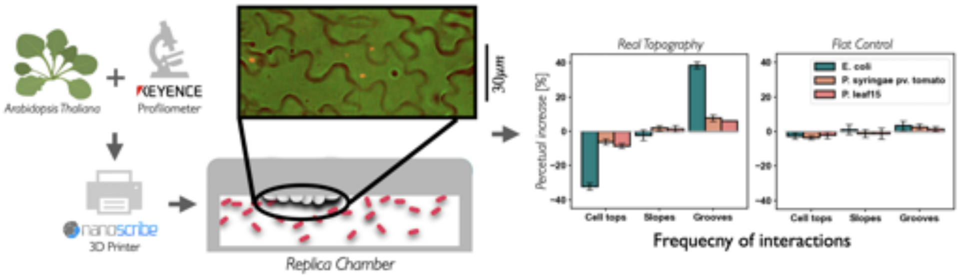


Figure 1: (left) Schematics of the experimental procedures. (right) interaction frequencies for three bacterial strains on the leaf topography and on a flat control surface.

References
[1] Julia A. Vorholt, Nature Reviews Microbiology **10**(12), 828–840, (2012)
[2] Steven E. Lindow and Maria T. Brandl, Applied and Environmental Microbiology **69**(4), 1875–1883, (2003)
[3] Orsolya Sipos, Katalin Nagy, R Di Leonardo, Peter Galajda, American Physical Society, **114**(25), 258104, (2015)

P13 - E. coli in motion in clay environments

A. Le Guen[1], **A. Akanno**[2], **J.O. Fossum**[2], **E. Clément**[1]

[1] PMMH-ESPCI, Sorbonne Université, Paris, France
[2] Norwegian University of Science and Technology, NTNU, Trondheim, Norway

Motion of microorganisms in Newtonian fluids is extensively studied, yet understanding their motility in environments of complex rheology remains quite challenging. This study investigates the swimming dynamics of *E. coli* in clay suspensions (Laponite RD) across different physical states— isotropic liquid, gel, and glass phases— achieved by varying mass concentrations. In Newtonian fluids, the exploration kinematics of *E. coli* results in the compound of run and tumble phases. Our measurements based on a 3D Lagrangian tracking technique that allows to follow a single bacterium over several minutes, reveals that the mechanical constraints disrupt the typical swimming dynamics and the bacteria exhibit a specific "stop go" process due to the medium entrapment. Visualization of both the body and the flagella points on a link between tumbling and stopping frequency. Remarkably in Laponite solutions, with a pH of approximately 10, *E. coli* remains motile despite their usual inability to swim at such high pH hence suggesting a protective effect of the clay on the bacteria.

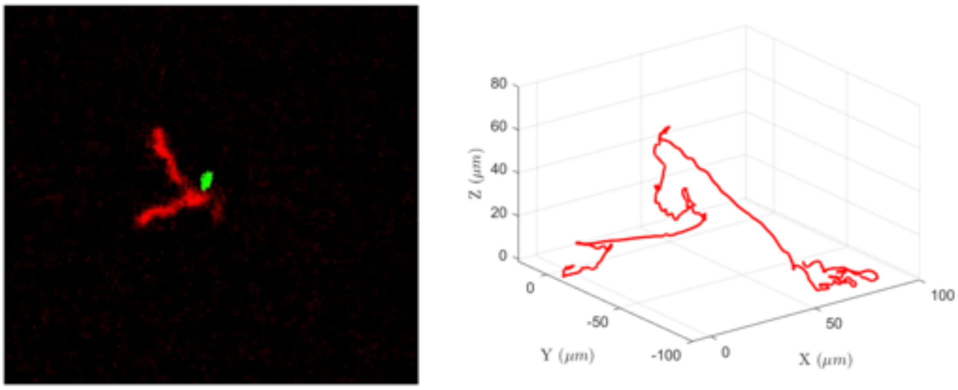


Figure 1: 3D tracking of *E. coli* in 3 wt % clay

P14 - Controlling the transport of passive beads in a suspension of phototactic microalgae

T. Laroussi[1], **J. Bouvard**[1], **M. Jarrahi**[2], **G. Amselem**[1]

[1] Laboratoire d'Hydrodynamique (LadHyX), CNRS, Ecole Polytechnique, Institut Polytechnique de Paris, 91120 Palaiseau, France
[2] Université Paris-Saclay, CNRS, FAST, 91405 Orsay, France

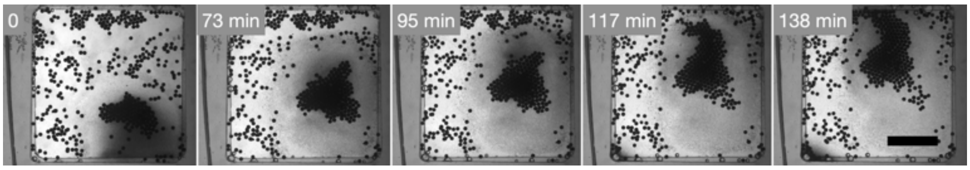


Figure 1: Raft of plastic beads assembled and transported directionally to the top of a centimetric well by swimming microalgae. Scale bar: 3 mm.

When passive beads are placed in a suspension of active particles, such as swimming microorganisms, they undergo a random motion with an effective diffusion coefficient orders of magnitude larger than that given by the traditional Stokes-Einstein relationship. Here we show how to rectify this random motion of passive beads into a directed one, by controlling the motion of the microorganisms in the suspension. We enclose plastic beads (size $50 - 450$ μm) and a suspension of the model microalga *Chlamydomonas reinhardtii* (size $\propto 10\mu$m) in a centimetric well. The algae are phototactic and swim away from strong light stimuli. In the presence of a single source of light, *C. reinhardtii* accumulate at the boundary of the well away from the light and create photo-bioconvection rolls [1,2]. These rolls displace beads denser than the surrounding medium away from the algae, while lighter beads are drawn towards the accumulated algae. We then focus the algae in a region of a couple mm within the well, using two opposing light sources with two different light intensities. By gradually varying the two light intensities, the region of accumulated algae is progressively shifted towards one side of the well. The dense algal region attracts beads lighter than the fluid, creating a raft of beads that is transported directionally over ~ 1 cm, see figure.

References

[1] Dervaux, J, Capellazzi Resta M, Brunet P, Light-controlled flows in active fluids, Nat. Phys. **13**, 306-313, (2017)
[2] Arrieta, J, Polin M, Saleta-Piersanti, R, Tuval, I, Light Control of Localized Photobioconvection, PRL **123**, 158101, (2019)

P15 - Bayesian inference of wall torques for active Brownian particles

S. Lambert, M. Duchêne, S. Klumpp

University of Göttingen, Institute for the Dynamics of Complex Systems, Göttingen, Germany

The motility of living things and synthetic self-propelled objects is often described using Active Brownian particles (ABP). To capture the interaction of these particles with their often complex environment, this model can be augmented with empirical forces or torques, for example, to describe their alignment with an obstacle or wall after a collision. Here, we assess the quality of these empirical models by comparing their output predictions with trajectories of rod-shaped active particles that scatter sterically at a flat wall. We employ a classical least-squares method to evaluate the instantaneous torque. In addition, we lay out a Bayesian inference procedure to construct the posterior distribution of plausible model parameters. In contrast to the least squares fit, the Bayesian approach does not require orientational data of the active particle and can readily be applied to experimental tracking data.

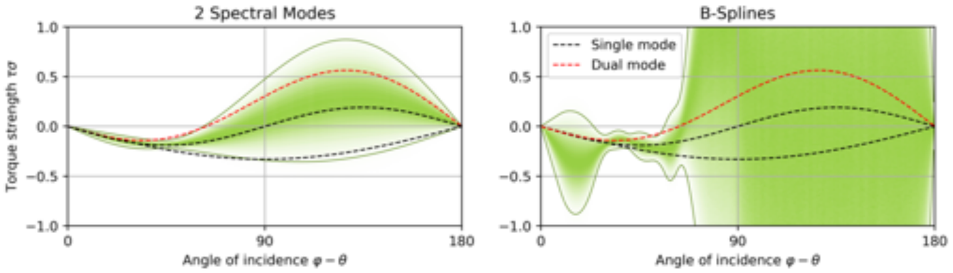


Figure 1: Posterior densities of the empirical torque model of an ABP tracking an active rods' tip. The x-axis denotes the angle of incidence of the ABP with the wall normal, the vertical axis is the empirical torque it get's subjected to. We use 10 simulated trajectories of rods, sterically interacting with a wall. We then perform a Bayesian inference of an ABP model on the trajectories, resulting in the posterior distribution of plausible torques that best describe the trajectories. The posterior is parametrized using two spectral mode amplitudes on the left and 10 B-spline knots on the right. The green shaded area is the density of the posterior. It is enveloped by its 99% credible interval, indicated by green lines. The dashed lines are the result of a classical least-squares fitting approach using a single angular frequency (black) and two frequencies (red).

References

[1] Andrieu C. and Roberts G. O., The Annals of Statistics, **37** 697 (2009)
[2] von Toussaint U., Rev. Mod. Phys., **83** 943 (2011)

P16 - Active Breathing Particles: Unjamming and Rheology

S. Ghosh[1,2], **M. Le Goff**[3], **P. Chaudhuri**[1,2], **K. Martens**[4]

[1] The Institute of Mathematical Sciences, Chennai, India
[2] Homi Bhabha National Institute, Training School Complex, Anushakti Nagar, Mumbai, 400094, India
[3] Institut für Theoretische Physik, Universität Innsbruck, Innsbruck, Austria
[4] Laboratoire Interdisciplinaire de Physique, Grenoble, France

We investigate the behaviour of "active breathing particles", i.e. particles with actively deforming radii, using microscopic simulations. In the absence of an external drive, there exists a threshold breathing amplitude for large-scale plasticity in the system. The overall elastoplastic behaviour of the system is similar to cyclically sheared systems. Observations on the memory of activity stored in the system have analogies with memory retention in amorphous solids under macroscopically applied cyclic shear. In the presence of an external shear, the mechanical response confirms loss of rigidity around the aforementioned threshold amplitude, and hence we observe two different branches of the flow-curves above and below the threshold amplitude, one pertaining to a yield stress solid and the other a fluid.

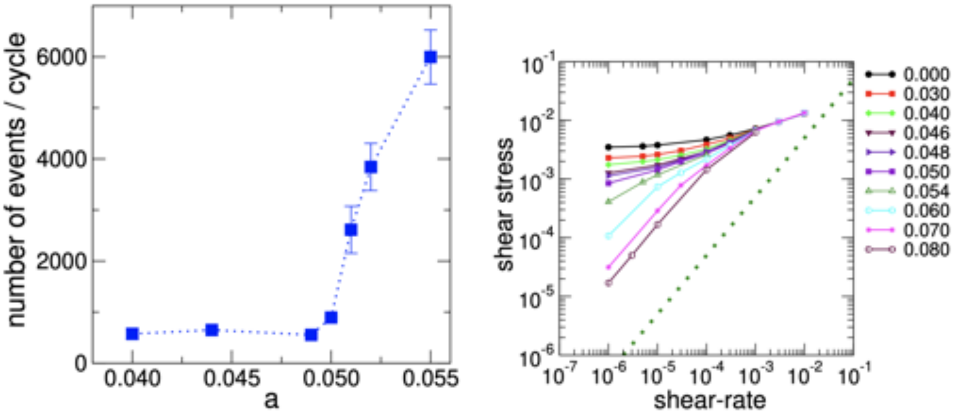


Figure 1: Left sub-figure: Number of nearest neighbour rearrangement events observed between two frames separated by one cycle of breathing plotted against the breathing amplitude "a". Right sub- figure: Plot of steady state shear stress vs shear-rate for different values of the breathing amplitude. The green dotted line represents Newtonian behaviour.

P17 - Bayesian Model Inference for Biological Tracking Data

J. Albrecht[1], **M. Opper**[2,3], **R. Grossmann**[1]

[1] Institute of Physics and Astronomy, University of Potsdam, 14476 Potsdam, Germany
[2] TU Berlin, Fakultät IV-MAR 4-2, Marchstraße 23, 10587 Berlin, Germany
[3] Centre for Systems Modelling and Quantitative Biomedicine, University of Birmingham, B15 2TT, United Kingdom

In order to understand and predict the motion patterns of microorganisms, robust methods to infer motility models from time discrete experimental data are required. Due to the internal complexity of the organisms, their movements appear to have random components which motility models need to account for. Bayesian statistical methods provide a way to efficiently extract information from the trajectory data and provide model parameter estimates together with a measure of uncertainty. We showcase that Bayesian methods are especially well suited when the models contain additional layers of stochasticity, for example population heterogeneity or temporal dependence of parameters. Furthermore, we demonstrate how challenges that arise when multidimensional dynamics is only partially observed, e.g. second order dynamics, colored noise or non-observed internal degrees of freedom, can be addressed.

P18 - Motility and chemotaxis of bacterial minicells

I. Kalita, R. Colin, S. Hoch, V. Sourjik

Max Planck Institute for Terrestrial Microbiology and Center for Synthetic Microbiology (SYNMIKRO), Marburg, Germany

Bacterial minicells are submicron-sized spherical cells that are produced as a result of aberrant division cycles. While cellular composition is similar to parental bacteria, minicells lack genomic DNA and therefore cannot reproduce themselves. Because of their inability to proliferate and small size, bacteria-derived minicells have attracted attention of targeted drug delivery where severe toxicity of drugs could be significantly reduced by developing more precise and efficient chemotaxis-based delivery methods. Here, we engineered *Escherichia coli* strains generating motile minicells and further enhanced their swimming speed and chemotaxis response by introducing genetic modifications specifically targeting flagella number, length, and rotation speed. With an additional insertion of a biotinylated autotransporter on cell surface, we attached streptavidin-coated submicron particles to the minicells and showed that such minibots are able to carry the particles (Fig. 1) and deliver them towards a chemoattractant source. Furthermore, we found that minicells and minibots tend to improve their swimming in the medium with intermediate viscosity. We hypothesized that slightly increased viscosity stabilizes the direction of active motion by reducing reorientations due to rotational diffusion.

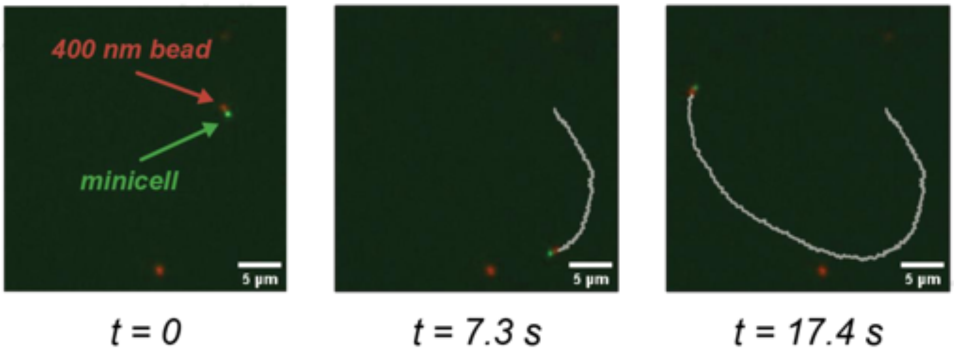


Figure 1: A time-lapse wide-field fluorescence series with a bacterial minicell (*shown in green*) actively moving an attached 400 nm bead (*shown in red*).

P19 - Motility and chemotaxis of bacterial minicells

F.A. Overberg, G. Gompper, D.A. Fedosov

Theoretical Physics of Living Matter, Institute for Advanced Simulation, Forschungszentrum Jülich, 52428 Jülich, Germany

We investigate the motility of the protozoan *Trypanosoma brucei* (*T. brucei*) via numerical simulations and a trypanosome model (Fig. 1) that is based on experimental observations [1, 2]. The cell body is represented by a set of vertices distributed homogeneously on a pre-defined elongated surface, forming a triangulated elastic network of springs. This network model incorporates bending rigidity, area conservation, and volume conservation constraints. For the purpose of propulsion generation, a flagellum is attached to the cell body. The flagellum consists of four parallel filaments, two of which are embedded in the body and used for generating a propagating bending wave [3]. Flagellar beating also leads to body deformation. We examine the model's behavior for various conditions, including different flagellum and body stiffnesses, beating frequencies, actuation wavelengths, and amplitudes. Our simulations yield swimming velocities and rotation frequencies around the swimming axis which are in a good agreement with experimental measurements. Additionally, this model enables the investigation of the importance of various actuation details, such as orientation of the beating plane and the relaxed conformation of the flagellum. Next, this model will be used to investigate trypanosome locomotion in a stationary blood suspension and in blood flow.

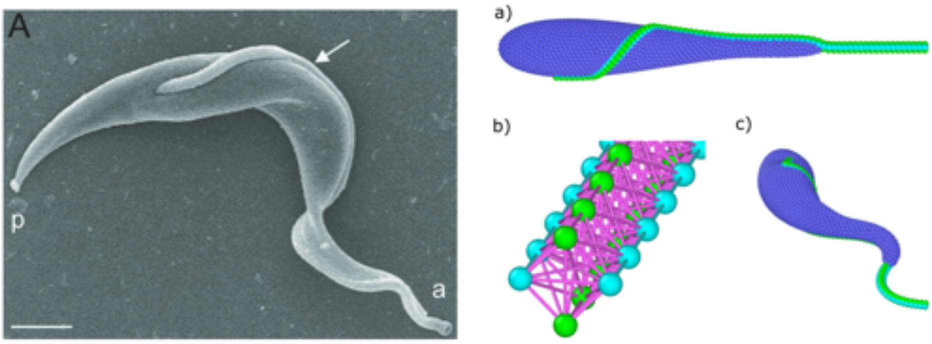


Figure 1: Left: Scanning electron micrograph of T. brucei from [4]., Right: Visualisations of the try- panosome model. Blue indicates body particles and cyan as well as green flagellum particles. The cyan particles are also part of the membrane. a) Side view of a trypanosome with an unactuated flagellum. b) Flagellum without an attached body with four filaments. The passive connecting bonds are pink and the active bonds that are affected by the actuation wave are cyan. c) Active beating of the flagellum which deforms the body.

References

[1] J. L. Bargul et al., PLoS pathogens, **12**, e1005448, (2016)
[2] N.Hedergott et al., PLoS pathogens, **8**, e1003023, (2012)
[3] S. Rode et al., New J. Phys., **21**, 013016, (2019)
[4] K. L. Hill, Eukaryotic Cell, **2**, p.200-208, (2003)

P20 - Active drops with autocatalytic surfactants: from simple self-propulsion to chaotic motion

F. Voss, **U. Thiele**

Institute for Theoretical Physics, University of Münster, Münster, Germany

Due to the interplay of advection and chemical reactions, chemically active drops are able generate and maintain surface tension gradients and can thus self-propel [1]. We here consider partially wetting drops on a flat substrate that are covered by two species of surfactants which can engage in an autocatalytic reaction. Starting from a free energy functional, we derive a simple thermodynamically consistent model that encapsulates the physics of wetting, Marangoni fluxes and chemical reactions (see also [2]). By allowing the surfactants to adsorb onto/desorb from the drop surface the system is rendered active. We clarify the role of the nonlinear chemical reaction in the generation and maintenance of surface tension gradients and study the emerging self-propulsion. For two-dimensional drops, besides simple modes of motion, we find for example direction reversing (shuttling) drops (Fig.1, left panel) that are connected to simpler states via global bifurcations. Three-dimensional drops show chaotic motion (Fig.1, right panel) which collapses to shuttling motion as the drop volume is decreased.

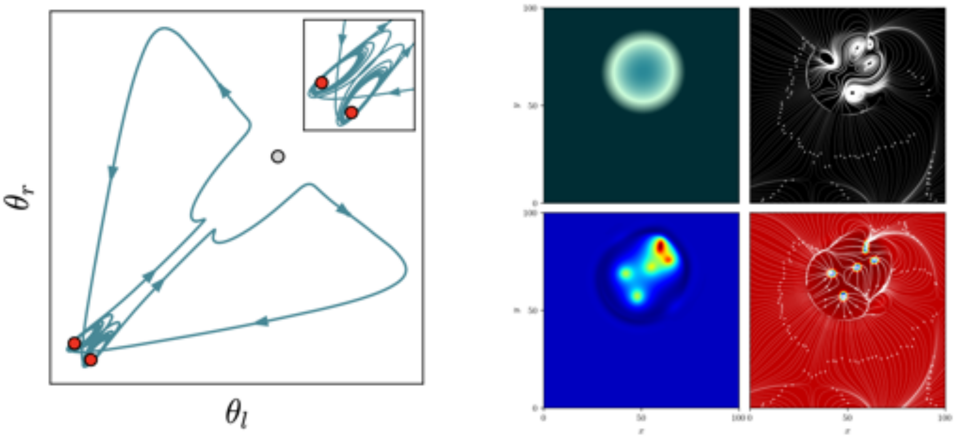


Figure 1: Left panel: Trajectory of a two dimensional shuttling drop in the contact angle plane. The trajectory 'winds itself' around the simple self-propelled states (red dots) in a Shilnikov-like mechanism [3] and then passes by a left-right symmetric resting state (gray dot). Right panel: Snapshot of a three-dimensional drop during chaotic motion. Upper left: local film-height (color-coded), upper right: streamlines of the liquid flux, lower left: surface tension distribution, lower right: streamlines of the surfactant flux and local surfactant mass gain/loss due to the reaction system (color coded).

References

[1] S. Michelin. Self-propulsion of chemically active droplets. Annu. Rev. Fluid Mech., **55**: 77–101, (2023) doi: 10.1146/annurev-fluid-120720-012204

[2] F. Voss and U. Thiele. Gradient dynamics approach to reactive thin-film hydrodynamics. arXiv:2403.10295, 2024. doi: 10.48550/arXiv.2403.10295

[3] P. Glendinning. and C. Sparrow. Local and global behavior near homoclinic orbits. J. Stat. Phys., **35**:645–696, 1984. doi: 10.1007/BF01010828

P21 - Reentrant cluster formation in active baths under soft confinement

T. Knippenberg, C. Bechinger

University of Konstanz, Department of Physics, Universtaetsstrasse 10, 2 Konstanz, 78464, Germany

The behavior of active particles (APs) is known to be strongly influenced by their environment, particularly when they come in contact with boundaries, giving rise to numerous non-trivial phenomena absent in passive fluids. A well-studied example is an increase of pressure due to the accumulation of particles at concave boundaries [1]. Because of the persistence of the APs' motion, the presence and the shape of a boundary can exert a far-reaching impact on their density distribution and flow dynamics [2]. Here, we present an experimental method to study the influence of boundaries on the behavior of APs. This method is based on the local modulation of the APs' velocity in a feedback-controlled setup, to mimic the presence of an arbitrary shaped external potential. We use this to investigate the structural and dynamic properties of APs confined within a soft annulus-shaped channel [3]. Depending on the strength of the confinement and the Péclet number, we observe a reentrant behavior that is not present in unconfined systems. Our findings are substantiated by numerical simulations and analytical considerations, revealing that this behavior arises from the strong coupling between the Péclet number and the effective confining dimensionality of the APs. Our work highlights the peculiarities of soft boundaries for APs and how clogging can be avoided under such conditions.

References

[1] Y. Fily, Phys. Rev. E. **91**, 012125 (2015)
[2] O. Granek et al, arXiv preprint arXiv:2310.00079 (2023)
[3] T. Knippenberg et al, Phys. Rev. Lett. **133**, 048301 (2024)

P22 - (Bio-) dynamics of yeasts inside wasps' guts

F. Font Verdera[1,2], **M. Polin**[1,2]

[1] Instituto Mediterráneo de Estudios Avanzados (IMEDEA, UIB-CSIC), Esporles, Spain.
[2] Departament de Física, Universitat de les Illes Balears, Palma de Mallorca, Spain.

Saccharomyces cerevisiae is one of the best characterized eukaryotic model organisms. Its life cycle includes both haploid and diploid phases, the latter leading to sporulation as main developmental process e.g. when experiencing lack of nutrients. During sporulation, a single diploid cell generates four haploid cells -a tetrad- which are tightly enclosed within a structure called the ascus. Confinement within the ascus is thought to enforce mating between products of the same meiotic division, generating clones and thus minimizing outbreeding. As a result, outcrossing has been commonly considered extremely rare in nature. This rarity contrasts with the ecological importance of outcrossing as an accelerator of *S. cerevisiae* evolution. Recent studies, however, have started to shed light on this puzzle by uncovering a surprising ecological niche for the outbreeding of wild yeast: the guts of various insects and in particular wasps. The peculiar physicochemical environment experienced by yeast within wasps' guts, together with its biological response, results in a very high probability of outbreeding compared to inbreeding [1, 2]. Wasps' digestive tracts can maintain *S. cerevisiae* across seasons and even for years [2, 3], and can lead to the generation of completely new strains, by promoting both intraspecific and interspecific mating between *Saccharomyces* spp. [2]. Unfortunately, the specific mechanism(s) promoting yeast outbreeding are currently unknown. Here we investigate the dynamical process that allows yeasts' spores to find each other and mate via outcrossing, rather than inbreeding within single ascii. Our results indicate ascus breakage resulting from a combination of mechanical stresses (in our case rotational motion mimicking mixing within the gut) and enzymatic digestion. Additionally, the mixing which mimics movement at the gut-level can promote the formation of multi-strain aggregates which favour to physical proximity between spores of different strains, therefore increasing the chances of outbreeding. Understanding the natural mechanisms leading to yeast outbreeding in nature will lead us to a better understanding of the *S. cerevisiae* evolution and its adaptation capability. This project is a part of a HFSP grant entitled "The aphrodisiac gut", in collaboration with research groups specialized in Chemistry from the University of Sydney (Australia), in Biology from University of Turin (Italy) and Mathematics from Boston University (United States).

References

[1] D. Cavalieri, In Current Opinion in Genetics and Development, Volume **75**, August 2022, 101922 (2022)
[2] I. Stefanini, Proceedings of the National Academy of Sciences of the United States of America, **113**(8), 2247 (2016)
[3] I. Stefanini, Proceedings of the National Academy of Sciences of the United States of America, **109**(33), 13398 (2012)

P23 - Optically driven thermofluidic assembly of passive and active bacteria

D. Quinn[1], S. Hanisch[2], R. Karande[2,3], F. Cichos[1]

[1] Peter Debye Institute for Soft Matter Physics, Faculty of Physics and Earth Sciences, Leipzig 2 University, Leipzig, Germany
[2] Helmholtz Center for Environmental Research (UFZ), Leipzig, Germany
[3] Biophysical Chemistry, Leipzig University, Leipzig, Germany

Bacteria in their planktonic state are known to assemble into biofilms in the vicinity of a solid surface. The complex cascade that results in the adhesion of the bacteria to the surface is usually triggered by the diffusion of bacteria to its vicinity. We propose a method that makes use of temperature induced flow fields and depletion interactions for the localized assembly and manipulation of bacteria. In addition to the physical interactions that contribute to the assembly process, the motility of the bacteria affects the assembly and can be altered by the induced temperature and altered distribution of molecules. We try to disentangle these effects by studying passive and active bacteria independently and look at how motility parameters change in response to the fields induced by the laser. By looking at the development of the cluster over time, our proposed method provides a way to probe the role of motility in biofilm formation. In addition, such controlled assembly of bacteria could be useful for technological applications in bioreactors.

References

[1] Desmond Quinn and Frank Cichos, Frontiers in Nanotechnology **5**, 1135408 (2023)
[2] Martin Fränzl and Frank Cichos, Nature communications **13**.1, 656 (2022)

P24 - Unusual motility behavior of dominant marine pico-eukaryote Mircomonas Pusilla

S.K. Choudhary[1], **R.J. Henshaw**[2], **M. Polin**[1]

[1] Mediterranean Institute for Advanced Studies (IMEDEA UIB-CSIC), Illes Balears, Spain
[2] ETH Zurich, Switzerland

Micromonas pusilla is a motile unicellular photosynthetic pico-eukaryote found globally in marine ecosystems. It is considered to be one of the most abundant pico-eukaryotes in marine environments and serves as a model system for interaction between viruses and unicellular hosts [1]. *M. pusilla* of body size 1 μm propel itself in liquid medium using a single flagellum of length 3-5 μmm with a highly peculiar structure and follow a novel motility strategy of stop-run or reverse. Interestingly, based on the flagellar orientation cells can swim as either puller or "pusher". Except for a few rare attempts [2], its motility in general is largely uncharacterized. Here we report an unusual motility behavior of *M. pusilla* wherein the cell's velocity during the "run" event undergoes a rapid significant initial increase, followed by a longer period of constant decrease leading the cell to eventually stop. We will characterise this peculiar behaviour and discuss its potential origin, which could include a combination of decay in the metabolic activity of cells and conformal changes in the flagellum during the "run" event.

References

[1] J. Mayer, F. Taylor, Nature **281**, 299–301 (1979) https://doi.org/10.1038/281299a0
[2] R. Henshaw, R. Jeanneret, M. Polin, bioRxiv 740571; doi: https://doi.org/10.1101/740571

P25 - Biophysical self-organizations in heterogeneous bacterial populations

S. Espada Burriel, G. Di Dio, A. Nadig, P. Unriza Siaucho, R. Colin

Max Planck Institute for Terrestrial Microbiology, Marburg, Germany

In wild environments, phenotypically diverse microorganisms interact both physically and chemically to give rise to complex community organization [1]. We are interested in the role of physical interactions arising from flagellar motility, a major bacterial trait, in the structuration of such complex communities. Multiple out-of-equilibrium mechanisms offer potential routes for structure emergence. We recently developed minimal systems for complex microorganism communities, binary mixtures of motile and non-motile *Escherichia coli* [2] and *B. subtilis* bacteria, with which we notably highlighted the importance of the fluid flows induced by the swimmers in structuring the non-motile cells. I will show some of the consequences we are currently investigating of these short-term effects at long time on the structure of biofilms, on the ability to survive abiotic and biotic stress factors, and on how the swimmer-induced fluid flows interact with biochemical effects to further reshape the community.

References

[1] C. D. Nadell, K. Drescher and K. Foster, Nature Reviews Microbiology **14**, 589-600 (2016)
[2] S. Espada Burriel and R. Colin, PRX Life, **2**, 023002 (2023)

P26 - Interplay of flow and swimming in porous media

P. Das[1,2], **M. Residori**[1], **A. Voigt**[3,4,5], **S. Mandal**[2], **C. Kurzthaler**[1,4,5]

[1] Max Planck Institute for the Physics of Complex Systems, Dresden, Germany
[2] Technische Universität Darmstadt, Darmstadt, Germany
[3] Institute of Scientific Computing, Technische Universität,Dresden, Germany
[4] Center for Systems Biology Dresden, Dresden, Germany
[5] Cluster of Excellence, Physics of Life, TU Dresden, Dresden, Germany
[6] Max Planck Institute for Terrestrial Microbiology, Marburg, Germany

Transport of active agents through complex media is of interest for various technological applications, such as filtration, bioremediation, and oil recovery processes, and in the context of microorganisms moving in their natural habitats, such as wet soil or mucus. The geometrical aspects of these complex environments such as the porosity [1] or the shape of the constituents significantly alter the dynamics. The coupling of the swimmers with the hydrodynamic flows has been shown to play a crucial role in their dynamics [2,3]. Here, We model porous channels using the two-dimensional random Lorentz gas, and study the transport behaviour of active Brownian particles (ABP), in the presence of pressure-driven flow across the channel. The flow velocity is highly heterogeneous [4] in such systems and the interplay of these complex flows with the swimming dynamics of active agents varies at different density limits and flow strengths. We characterize the transport of ABPs by the exit time distributions from the porous channel and study the underlying mechanisms, such as shear flows or changes in motility resulting in different transport behaviours.

References

[1] Zeitz et al., The European Physical Journal E **40** 1-10 (2017)
[2] Rusconi et al. Nature Physics **10**.3 212-217 (2014)
[3] Creppy et al. Physical Review Fluids **4**.1 01310 (2019)
[4] Residori et al. arXiv preprint arXiv:2405.12381 (2024)

P27 - Study of bacterial magneto-aerotactic behaviour in a controlled environment

V. Poncet, T. Pietrangeli, C. Cottin-Bizonne, F. Detcheverry, C. Ybert

Universite Claude Bernard Lyon 1, CNRS, Institut Lumière Matière, UMR5306, F-69100, Villeurbanne, France

How motile bacteria navigate their environment in response to various cues has far reaching implications from health science to climate studies, the understanding of these navigation strategies is however incomplete and thus a very active field of research. In this study, we focus on the response of a motile magneto-tactic bacteria strain to two external cues: magnetic field and oxygen concentration. Indeed the strain we use is a special sort of swimming bacteria from the fact that it synthesizes a magnet to take benefit of the magnetic field of the earth to navigate its environment, especially its oxic environment. Our study stands out from the fact that we have developed the microfluidic tools to accurately control the oxygen environment in the very low concentration regime; in addition to the Helmoltz coils that allow us to dynamically control the magnetic field in the experiment and the image analysis techniques from which we extract thousands of individual trajectories. Benefiting from this set of tools, we can finely control the stimuli the bacteria are exposed to and study the individual response to it. It is well known that magneto-tactic bacteria in an oxygen gradient will gather in a dense band at their preferred oxygen concentration when exposed to a magnetic field. However, the underlying mechanism of this so-called « magneto-aerotactic » behaviour is not known: we will present preliminary results that unveil a part of it.

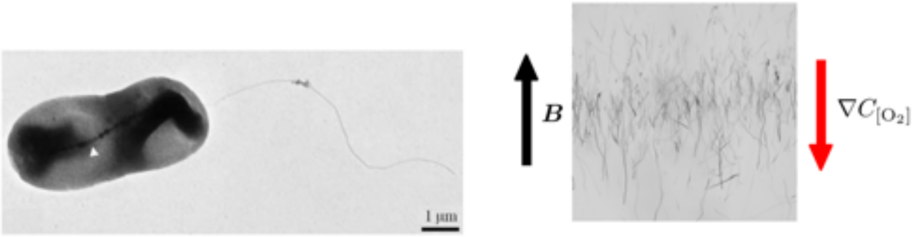


Figure 1: (Left) Electron microscopy image of a cell of the SS-5 bacteria strain used at our lab, adapted from [1]. (Right) Visualisation of bacteria tracks in a magneto-aerotaxis experiment with the direction of the imposed magnetic field and oxygen gradient represented in black and red respectiveley.

References

[1] Christopher T. Lefévre et al.“Diversity of Magneto-Aerotactic Behaviors and Oxygen Sensing Mechanisms in Cultured Magnetotactic Bacteria”. In: Biophysical Journal **107**.2 (July 15, 2014). Publisher: Elsevier, pp. 527–538. ISSN: 0006-3495. DOI: 10.1016/j. bpj.2014.05.043.

[2] M. Marmol, E. Gachon, and D. Faivre. “Colloquium: Magnetotactic bacteria: From flagellar motor to collective effects”. In: Reviews of Modern Physics **96**.2 (Apr. 4, 2024). Publisher: American Physical Society, p. 021001. DOI: 10.1103/RevModPhys.96. 021001.

P28 - Collective response of prey agents to attacks by multiple persistent predators

S. Mohapatra, P.S. Mahapatra

Indian Institute of Technology Madras, Chennai, India

Collective behaviour is a ubiquitous phenomenon entailing the emergence of fascinating pattern formations in organisms. Dilution of predation risk is presumed to be a major factor contributing towards the evolution of such behaviour. However, the effect of persistent attacks by multiple predators on the behavioural response of the prey remains largely unexplored. The current work aims to address this issue using an agent-based approach employing an underdamped Langevin model [1]. The effect of predation is found to be non-additive in the presence of multiple predators (see Fig. 1(a)), even if they are competing and non-interacting [2]. The transition in prey response from a cohesive escape to split-and-escape (refer Fig. 1(b)) and an associated region of bistability is discussed with respect to the angular configuration of the predators before the attack (see Fig. 1(c)). The impact of the frequency of the predator attacks and the target preference of the predators [3] is also examined in the purview of the success of the collective escape response. The statistics show the attack on the nearest prey to be the most successful pursuit strategy, while alternative strategies such as attacking the centre of the group have conspicuous ancillary effects, such as group splitting. A long-term temporal study of the system indicates a counter-intuitive faster decay of prey numbers at higher intensity of prey coordination χ, hinting at possible superfluous alignment and its detrimental effects in case of successive predator attacks.

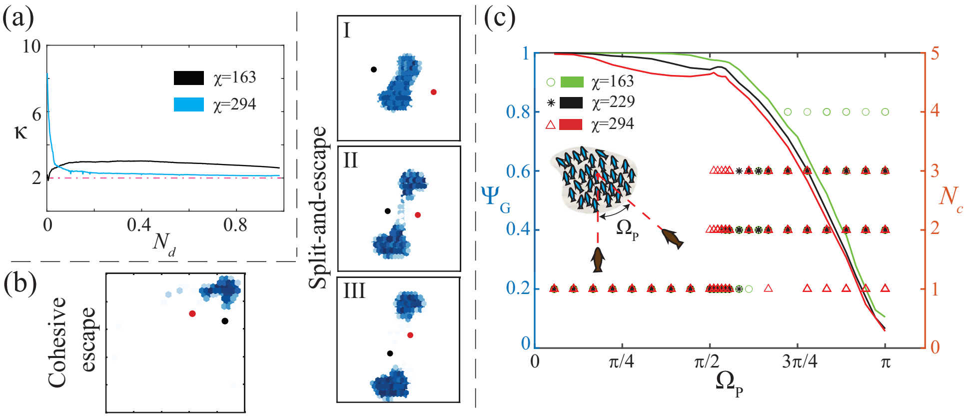


Figure 1: Panel (a) illustrates the non-additive nature of the predation effect through , the ratio of average time taken to capture a fraction of the prey N_d for a solitary predator ($N_p = 1$) compared to that required of two non-coordinating predators ($N_p = 2$) at different prey coordination strengths χ. Panel (b) demonstrates the collective response of the prey to the predator attacks: split-and-escape (I-III), or cohesive escape; while panel (c) displays the variation in global order after the prey response Ψ_G and the corresponding number of prey groups in the system N_c, with the relative angle of the predators' attackΩ_P (schematic inset).

References

[1] S. Mohapatra, and P. S. Mahapatra, Scientific Reports **9**(1), 11258, (2019)
[2] S. Mohapatra, and P. S. Mahapatra, bioRxiv 2023-11, (2023)
[3] S. I. Nishimura, Biosystems **65**(1), 25–35, (2002)

P29 - Coexistence of uniform and oscillatory states resulting from nonreciprocity and conservation laws

D. Greve[1], **U. Thiele**[1,2]

[1] Institut für Theoretische Physik, Universität Münster, Wilhelm-Klemm-Str. 9, 48149 Münster, Germany
[2] Center for Nonlinear Science (CeNoS), Universität Münster, Corrensstr. 2, 48149 Münster, Germany

The interplay of nonreciprocity and conservation laws results in the coexistence of uniform stationary and oscillatory phases [1, 2]. For nonequilibrium models with a spurious gradient dynamics structure [3] the coexistence between nonequilibrium phases can nevertheless be predicted by a Maxwell double-tangent construction including phases with sustained out-of-equilibrium dynamics [4]. This is corroborated by bifurcation studies and time simulations for a nonreciprocal Cahn-Hilliard model. In passing we also discuss the related emergence of active solids and their coexistence with a uniform state.

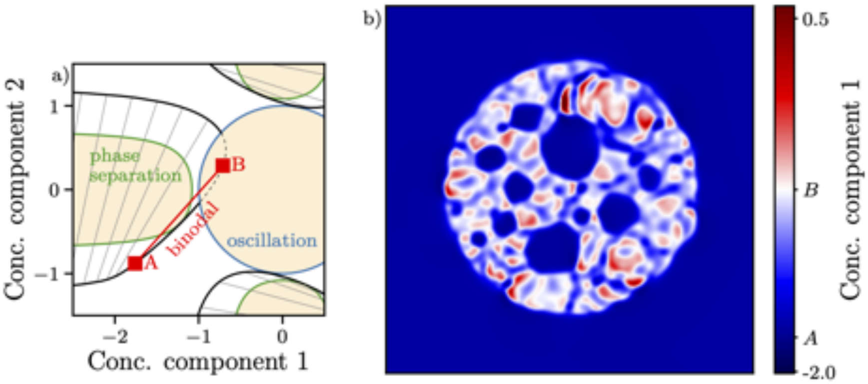


Figure 1: Panel (a) shows a phase diagram including a binodal (red line) that connects a uniform stable phase to an oscillatory unstable uniform phase. Panel (b) shows a corresponding phase separated state in two dimensions, where irregular oscillations coexist with a uniform background.

References

[1] A. Dinelli et al., Nat. Commun. **14**, 7035 (2023)
[2] Y. Duan et al., Phys. Rev. Lett. **131**, 148301 (2023)
[3] T. Frohoff-Hülsmann et al., Phys. Rev. E **107**, 64210 (2023)
[4] D. Greve et al., arxiv, 2402.08634, (2023)

P30 - Synchronization driven flows and motility of spherical ciliates

A. Ravi[1], **B. Chakrabarti**[2,3], **S. Fürthauer**[1]

[1] Theory of Living Matter Group, Institute for Applied Physics, TU Wien, Vienna 1040
[2] Center for Computational Biology, Flatiron Institute, New York 10010
[3] Fluid Dynamics and Biophysics Group, ICTS-TIFR, Bengaluru 560089

Cilia are actively driven, hair-like membrane bound organelles in eukaryotic cells. They exert forces on their surrounding fluid medium and detect chemical and mechanical cues from their environment. In a world where viscous forces dominates inertial forces, cilia need to execute a non-reciprocal "beat pattern" to pump fluid. Collectives of cilia are observed to synchronize their beat patterns through hydrodynamic interactions to increase the efficiency of fluid transport by coordinating into metachronal waves [1]. While this problem has been extensively studied in flat periodic systems [2][3][4], most ciliated tissues in biology are topologically and geometrically more complex. As an example, most microorganisms are homeomorphic to a 2-sphere, and have curved surfaces along which cilia are distributed. Yet, the effects of topology and geometry on the synchronization remain unclear. Here, we present a theoretical study of ciliary synchronization on spherical topologies. Our approach is to coarse grain the microscopic physics of a minimal model of non-reciprocally beating cilia into a continuum theory following [4]. Doing so we arrive at predictions for synchronization behavior of a spherical swimmer, which will also help us understand its trajectories. Further, our description generalizes to arbitrary surface geometries and topologies, and thus will allow us to investigate fluid transport in a plethora of living systems.

References

[1] Chakrabarti, Brato, et al. "A multiscale biophysical model gives quantized metachronal waves in a lattice of beating cilia." Proceedings of the National Academy of Sciences **119**.4 e2113539119 (2022)
[2] Kanale, Anup V., et al. "Spontaneous phase coordination and fluid pumping in model ciliary carpets." Proceedings of the National Academy of Sciences **119**.45 : e2214413119 (2022)
[3] Solovev, Anton, and Benjamin M. Friedrich. "Synchronization in cilia carpets: multiple metachronal waves are stable, but one wave dominates." New Journal of Physics **24**.1 013015 (2022)
[4] Meng, Fanlong, et al. "Conditions for metachronal coordination in arrays of model cilia." Proceedings of the National Academy of Sciences **118**.32 : e2102828118 (2021)

P31 - Microswimmers to displace large particles

T. Laroussi[1], J. Bouvard[1], V. Nicolazo-Crach[2], M. Jarrahi[2], G. Amselem[1]

[1] LadHyX, CNRS, École Polytechnique, Institut Polytechnique de Paris, 91120 Palaiseau, France
[2] Université Paris-Saclay, CNRS, FAST, 91405, Orsay, France

Small passive particles immersed in an active bath of microswimmers, either artificial swimmers or living microorganisms, may be displaced due to the activity of the suspension [1,2]. This enhanced motion can lead to rich phenomena such as aggregation or phase separation. In this experimental work, we study how large beads are moved by randomly swimming microalgae. Plastic beads of diameter $d = 50\mu m$ are introduced in an algal suspension of *Chlamydomonas reinhardtii* ($\sim 10\mu m$) where they quickly sediment. Those passive beads are displaced by the swimming microalgae, with an intensity depending on the algal concentration. The exhibited diffusive behaviour is characterised by an effective diffusion coefficient D 10 to 10^3 higher than the one of Brownian motion, consistently with previous works with smaller beads and lower algal concentration [3]. The rescaled probability distribution functions seem to collapse onto a single curve, but it is not entirely clear whether it is self-similar or if it converges to a Gaussian at large times and large optical densities. Surprisingly, important jump-like motions were observed. Previous work had highlighted similar behaviours [4], but with much smaller beads ($d = 1\mu m$). These observations could help us having a better understanding of the interactions between swimming micro-organisms and their environment.

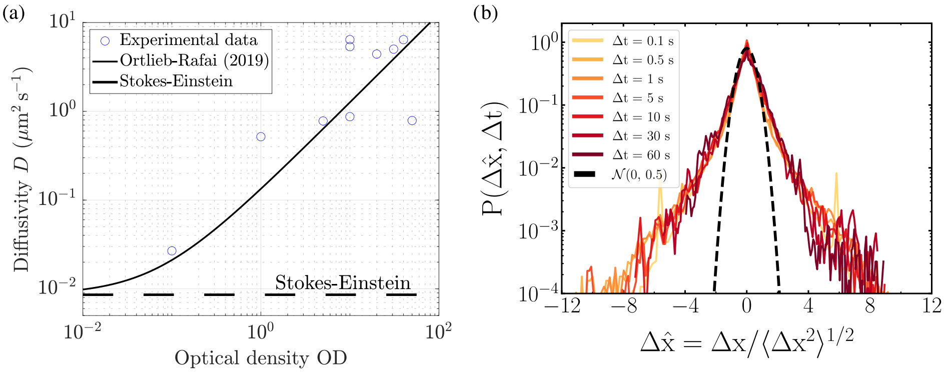


Figure 1: (a) Effective diffusivity D of $d = 50\mu m$ diameter beads in a concentrated algal suspension.
(b) Probability distribution functions of rescaled displacements for different times Δt

References

[1] X. Wu and A. Libchaber, Phys. Rev. Lett. **84**, 13, (2000)
[2] J. C. Leptos, J. S. Guasto, J. P. Gollub, A. I. Pesci and R. E. Goldstein, Physical Review Letters, **103**(19), 198103, (2009)
[3] L. Ortlieb, S. Rafaï, P. Peyla, C. Wagner, T. John, Physical Review Letters, **122**(14), 148101, (2019)
[4] R. Jeanneret, D. O. Pushkin, V. Kantsler and M. Polin, Nat. Comm., **7**(1), 12518, (2016)

P32 - 2-TIPS (2 Temperature Induced Phase Separation) in confined geometries

J. Mandal, **P.K. Maiti**

Department of Physics, Indian Institute of Science, Bangalore, India

We studied the effect of confinement on a binary mixture of active and passive particles of various shapes, using computer simulations. Such mixtures are studied using the 2-temperature model, where half of the particles are connected to a thermostat with higher temperature (particles termed 'hot' or 'active') and the other half to a lower temperature (particles termed 'cold' or 'passive'). Such scalar model of active-passive mixtures lacks the vector 'motility' for active systems but manifests a phase separation scenario which is termed as '2-Temperature Induced Phase Separation' (2-TIPS)[1,2]. For spherical particles, in 2 dimensions or for systems confined with walls, the phase separation is incomplete, and the resulting structures corresponds to a dense-dilute phase coexistence, a situation which is observed for the purely active systems (termed MIPS or Motility Induced Phase Separation). Further investigation shows that similar phenomena are observed for a system confined on the surface of the sphere (Fig 1A and 1B). For shape anisotropic spherocylindrical particles, the equilibrium configuration on the surface of the sphere at intermediate packing fractions results in a nematic structure with four +1/2 defects (Fig 1C). For such systems, when activity is introduced using 2-temperature model, we observe a dense dilute phase coexistence, in which the dense region captures a large fraction of the particles. At low activity, the dense region has nematic structure with a +1 defect. When activity is increased, it forms smectic layering with the +1 defect still being intact. The charge and nature of the defect changes from equilibrium to 2TIPS.

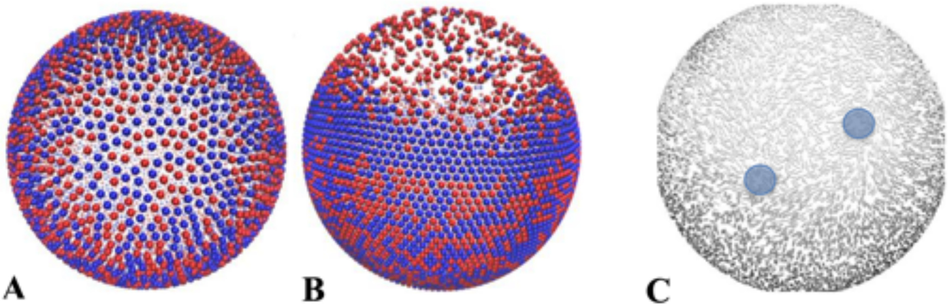


Figure 1: A) The equilibrium configuration of the Lennard Jones particles on a sphere, B) 2-TIPS on sphere at high enough activity. C) Two of the four +1/2 defects observed for an equilibrium spherical nematic shell, indicated by blue circles.

References

[1] Venkatareddy, N., Mandal, J., & Maiti, P. K., Soft Matter, **19**(44), 8561-8576 (2023)
[2] Chari, S. S. N., Dasgupta, C., & Maiti, P. K., Soft matter, **15**(36), 7275-7285, (2019)

P33 - Characterisation of swimming phenotypes using parallel microscopy

Y. Bhasin, C. Costa, P. Sartori

Instituto Gulbenkian de Ciência (IGC), Oeiras, Portugal

Chlamydomonas reinhardtii (CR) cells exhibit a fascinating ability to navigate towards light. Other important phenotypic traits like growth and cell division number are also strongly correlated with light. We aim to explore the diversity and dynamics of phenotypes expressed by CR cells by systematically perturbing the genetic background and light environment of these cells. To achieve this, we embark on a microscopy marathon that will encompass a total of 900 days of microscopy time. Here, we present the experimental methodology behind our study which combines microfluidics and a custom built parallel microscopy system. With this approach we are able to isolate single cells and track them for their entire lifetime. Our preliminary data shows the existence of multiple timescales in the dynamics of CR swimming.

P34 - Effect of change in micellar structure of bath in liquid crystal droplet self-propulsion

S. Kar, S. Dutta, M. Chowdhury

IIT Bombay, Mumbai, India

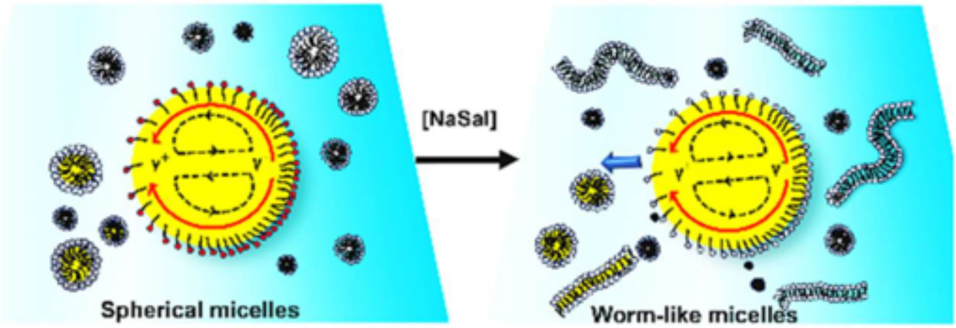


Figure 1: Schematic showing possible mechanism behind propelling of the LC oil droplet in the aqueous media containing (a) spherical micelles and (b) worm-like micelle (WLM).

Self-propulsion of oil droplets in surfactant media primarily occurs through molecular or micellar solubilization mechanism1. Both mechanisms comprise some common and essential characteristics for self-propulsion, like asymmetry in the stress tensor created in the droplet due to the chemical field or surface tension gradient that eventually leads to an interfacial flow and the convective chemical transport associated with this flow, further enhancing the initial inhomogeneity. To sustain the initiated droplet motion, convective transport of the field must dominate over diffusion-driven relaxation towards concentration homogeneity. Our study explores the dynamic behavior of liquid crystal (LC) droplets within a medium (CTAB) undergoing a morphological transformation of micelles from spherical to worm-like structures (WLM). Sodium salicylate-induced morphological transition of CTAB micelles from spherical to worm-like structures can significantly modify hydrophobic droplet solubilization as the elongated cores of wormlike micelles offer distinct solubilization capacities and interactive environments compared to spherical counterparts. The correlation between micellar structure and liquid crystal droplet transport was investigated in CTAB/Sodium Salicylate (NaSal) systems. Increasing worm-like micelle (WLM) fraction2, induced by varying NaSal concentration, significantly enhanced droplet velocity. Our analysis of mean squared displacement of the droplet reveals an increasingly super-diffusive motion with increase of WLM content. This work sets the platform for further studies on motional behavior, Péclet number, surfactant kinetics, and flow field dynamics are necessary to elucidate the underlying mechanism.

References

[1] S. Michelin, Annu. Rev. Fluid Mech. **55**, 77-101 (2022)
[2] N. Subba, N. Das, P. Sen, Langmuir, **38**, 2486-2494 (2022)

P35 - Evolution of micro-swimmer designs in distinct microenvironments

N. Jamshidi, T. Krüger, M. Engstler

Department of Cell and Developmental Biology, Biocentre, University of Würzburg, 97074 Würzburg, Germany

Trypanosoma brucei, a flagellate parasite transmitted by tsetse flies, causes sleeping sickness in humans and infects various vertebrates. Throughout its life cycle, *T. brucei* adapts to diverse environments in its hosts, such as blood and skin, each with different mechanical properties like viscosity and physical constraints such as spatial confinement [1]. T. brucei has an elastic, spindle-shaped body with a helically attached flagellum [2]. Cell movement initiates with a planar bending wave on the flagellum at the anterior end of the cell, followed by a longitudinal rotation due to the helical attachment of the flagellum to the cell body [3].However, a detailed quantitative understanding of *T. brucei*'s single-cell dynamics and adaptive behaviors across different microenvironments remain insufficiently quantified. This study examined *Trypanosoma brucei*'s motility in various viscosities and collagen gels using high-resolution and digital holographic microscopy, allowing for the elucidation of 2D and 3D motility data of single-cell movement. Results show the adaptation of rotational behavior and its crucial role in maintaining swimming speed in different viscosities. At higher viscosities and in dense collagen, cells exhibit altered paths, such as circular swimming, suggesting that mechanical properties of the environment significantly impact motility.

References

[1] Krüger, Timothy, Sarah Schuster, and Markus Engstler. Trends in parasitology **34**.12 (2018)
[2] Bargul, Joel L., et al. PLoS pathogens **12**.2 (2016)
[3] Heddergott, Niko, et al. PLoS pathogens **8**.11 (2012)

P36 - Antigenic variation impacts gonococcal lifestyle and antibiotic tolerance by modulating

I. Wielert[1,2], **S. Kraus-Römer**[1,2], **T.E. Volkman**[1,2], **L. Crai**[3], **P.G. Higgin**[2,4,5], **B. Maier**[1]

[1] Institute for Biological Physics, University of Cologne, Germany
[2] Center for Molecular Medicine Cologne
[3] Department of Molecular Biology and Biochemistry, Simon Fraser University, Burnaby, British Columbia, Canada
[4] Institute for Medical Microbiology, Immunology and Hygiene, Faculty of Medicine and University Hospital Cologne, University of Cologne, Cologne, Germany
[5] German Centre for Infection Research, Partner site Bonn-Cologne, Cologne, Germany

Type 4 pili (T4P) are multifunctional filaments involved in adhesion, surface motility, biofilm formation, and horizontal gene transfer. By cycles of retraction, attachment and elongation, T4P mediate motility at surfaces and within colonies. As T4P are surface-exposed, *Neisseria gonorrhoeae* uses pilin antigenic variation to escape immune surveillance, yet it is unclear how antigenic variation impacts other functions of T4P. Here, we address this question by replacing the major pilin of a laboratory strain with pilins from clinical isolates. We reveal that the resulting strains vary in velocity and persistence of twitching motility. Furthermore, we show that pilin antigenic variation substantially affects pilus:pilus mediated attractive forces between neighbouring bacteria. Strongly interacting bacteria form microcolonies while weakly interacting bacteria retain a planktonic lifestyle. In mixed microcolonies different variant strains segregate in agreement with the differential strength of adhesion hypothesis. By combining structural predictions and laser tweezers experiments, we show that the C-terminal region of the pilin is crucial for attraction. The lifestyle affects growth kinetics and antibiotic tolerance. In the presence of ceftriaxone or ciprofloxacin, the killing kinetics indicate strongly increased tolerance of aggregating strains. We propose that pilin antigenic variation produces a mixed population containing variants optimized for growth, colonization, or survivability under external stress. Different environments select different variants, ensuring the survival and reproduction of the population as a whole.

References

[1] I. Wielert, bioRxiv: 2023.07.06.548055. (2023)
Available: https://www.biorxiv.org/content/10.1101/2023.07.06.548055v1

P37 - Tumbling bacteria in bulk and close to surfaces

P. Martin[1], **T.C. Adhyapak**[2], **D.C. Gomes**[2], **H. Stark**[1]

[1] Institut für Theoretische Physik, Technische Universität Berlin, Germany
[2] Indian insitute of science education and research (IISER), Tirupati, India

Escherichia coli (*E. coli*) swims by rotating multiple flagella, which are randomly distributed on the surface of its cell body and connected via flexible hooks. These hooks act as universal joints, transferring motor torque to the flagellar filaments. When all the motors rotate in the same direction, the filaments wrap together and form a bundle. This bundle is stabilized by a combination of hydrodynamic and steric interactions, turning the bacterium into a straight swimmer. To change direction, *E. coli* performs tumble events by reversing the rotation of one or more flagella. The involved filaments undergo a series of polymorphic transformations, altering both their helicity and handedness [1, 2]. Although this process has been known for decades, the physical understanding remains incomplete. This complex phenomenon involves the interplay of semiflexible filaments and hydrodynamic interactions, most of which have been studied without fully resolving flagellar dynamics. Here, we have developed a detailed numerical framework to simulate *E. coli*, capturing the dynamics of flexible flagella and their hydrodynamic interactions. The flagellar elasticity is effectively modeled by an extended Kirchhoff free energy. The filaments and the cell body are embedded in a fluid, which we model using multi-particle collision dynamics, an efficient solver for the Navier-Stokes equations [3]. We analyzed a large number of tumble events, focusing on the roles of hook and flagellar flexibility as well as flagellar polymorphism. We find that they strongly influence the distribution of tumble angles. Finally, we also show that close to a flat surface the mean tumble angle is strongly shifted to smaller values. This indicates that tumble events may not be recognized, which could give the impression of suppressed tumbling near surfaces as reported in [4].

References

[1] L. Turner, W. S. Ryu and H. C. Berg, J. Bacteriol.,**182**, 2793, (2000)
[2] T. Adhyapak and H. Stark, Soft Matter, **12**, 5621, (2016)
[3] A. Malevanets and R. Kapral, J. Chem. Phys., **110**, 8605, (1999)
[4] M. Molaei, M.Barry, R. Stocker and J.Sheng , PRL, **113**, 068103, (2014)

P38 - Accessing microscopic details in a 3D Lagrangian perspective of active turbulence

B. Pérez-Estay[1], **J. Savoye**[1], **A. Lindner**[1,2], **E. Clément**[1,2]

[1] PMMH-UMR 7636 of the CNRS, ESPCI-PSL-Sorbonne University, Univ. Paris Cite, 7 quai Saint-Bernard, Paris, 75005, France
[2] Institut Universitaire de France (IUF, Paris, France

Bacteria produce a flow when swimming, leading to hydrodynamic interactions between bacteria and the environment. These hydrodynamic bacteria-bacteria interactions at high densities of bacteria create a hydrodynamic instability that leads to active turbulence. In collective motion, we observe correlations in the swimming orientation that can be 1000 times bigger than bacteria [1] (see Fig 1 a). Although much work has focused on this system, not much is known of the 3D structure of the flow. In this work, we use a Lagrangian tracking setup controlled by an AI model to precisely follow a fluorescent particle's motion inside the bacteria bath. The tracks are longer than 10 min giving significant statistics of the bath. In parallel, we observed bacteria motion in a different fluorescent channel. This allows us to compare the motion of the surrounding bacteria to the bead itself, giving us information about the order in the bacteria suspensions. We quantify how the order changes as a function of the distance to the surface and the bacteria bath's properties.

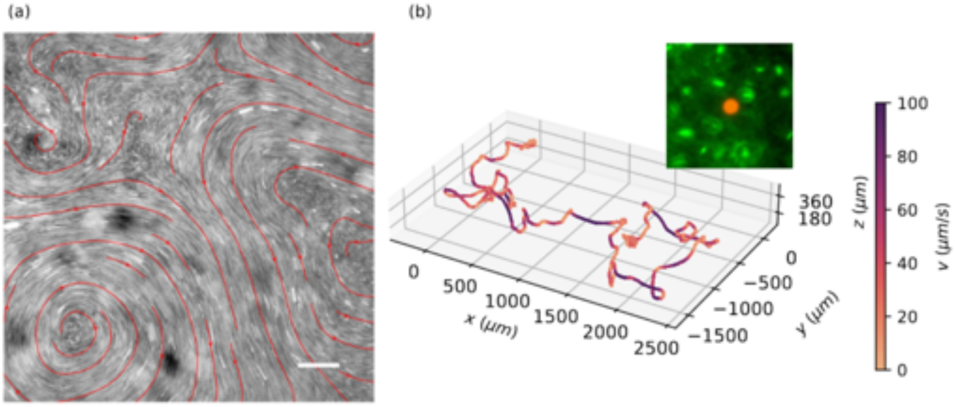


Figure 1: (a) Superposition of fluorescent beads tracks advected by the bacteria turbulence (60 images at 20 FPS) with streamline obtained from PIV measurement. Scale bar is 100m. (b) 3D reconstruction of the trajectory of a passive bead inside a bacteria bath. The particle is tracked for about 10 min. The inset shows a typical image acquired with the microscope, showing the passive fluorescent particle in red and the surrounding bacteria in green.

References

[1] Martinez, Vincent A., et al. Proceedings of the National Academy of Sciences **117**.5 2326-2331 (2020)

P39 - Engineering of motility-based whole-cell biosensors

D. Coroiu[1], **J. Broughton**[2], **T. Pilizota**[1,2]

[1] School of Biological Sciences, The University of Edinburgh, United Kingdom
[2] Institute of Cell Biology, The University of Edinburgh, United Kingdom

Many bacteria possess motility systems and associated regulatory networks that enable them to navigate their environment. *Escherichia coli* swims using its flagella, which are protein complexes mainly composed of a 10-micron extracellular filament that rotates powered by the (bacterial) flagellar motor (BFM). This rotation can be tracked either optically, using tethered cells or bead assays, or electrically, using impedance measurements. As the latter can be achieved in small integrated circuits, we aim to engineer *E. coli* strains that change the rotational direction of their flagellar motor in response to specific analytes in the environment, and thus obtain whole-cell biosensors that could be used in situ. To obtain *E. coli*-derived biosensors, we rewired the chemotactic pathway, a signalling network which *E. coli* has evolved to sense chemical gradients and thus navigate towards favourable environments. Normally, transmembrane chemotactic receptors relay information about the cell's surroundings to the motor by a series of feedback loops that end with the phosphorylation of the CheY protein, which, when active, interacts with the BFM and switches its direction from counterclockwise to clockwise [1]. Our biosensor uses a mutant form of CheY, CheY**, which is always active [2], as a reporter, and thus responds to chemicals by increasing the fraction of time the BFM spends rotating clockwise. We have created sensors to L-rhamnose and zinc, which are up to 100 times more sensitive than their GFP-based equivalents. We have also investigated the response dynamics and detection limits through mathematical modelling and further experimental characterisation.

References

[1] Welch, M. et al. (1993) 'Phosphorylation-dependent binding of a signal molecule to the flagellar switch of bacteria.', Proceedings of the National Academy of Sciences, **90**(19), pp. 8787–8791. doi:10.1073/pnas.90.19.8787

[2] Scharf, B.E. et al. (1998) 'Control of direction of flagellar rotation in bacterial chemotaxis', Proceedings of the National Academy of Sciences, **95**(1), pp. 201– 206. doi:10.1073/pnas.95.1.201

P40 - Chemotactic encounters between bacteria and phytoplankton

R. Foffi[1], **D.B. Brumley**[2], **F.J. Peaudecerf**[3], **R. Stocker**[1], **J. Słomka**[1]

[1] Institute of Environmental Engineering, ETH Zürich, Zürich, Switzerland
[2] School of Mathematics and Statistics, The University of Melbourne, Victoria, Australia
[3] Univ Rennes, CNRS, IPR (Institut de Physique de Rennes) - UMR 6251, Rennes, France

Chemotaxis enables marine bacteria to increase encounters with phytoplankton cells by reducing their search times, provided that bacteria detect noisy chemical gradients around phyto-plankton. Gradient detection depends on bacterial phenotypes and phytoplankton size: large phytoplankton produce spatially extended but shallow gradients, whereas small phytoplankton produce steeper but spatially more confined gradients. To date, it has remained unclear how phytoplankton size and bacterial swimming speed affect bacteria's gradient detection ability and search times for phytoplankton [1]. We computed an upper bound on the increase in bacterial encounter rate with phytoplankton due to chemotaxis over random motility alone. We found that chemotaxis can substantially decrease search times for small phytoplankton, but this advantage is highly sensitive to variations in bacterial phenotypes or phytoplankton leakage rates. By contrast, chemotaxis towards large phytoplankton cells reduces the search time more modestly, but this benefit is more robust to variations in search or environmental parameters [2]. Applying our findings to marine phytoplankton communities, we found that, in productive waters, chemotaxis towards phytoplankton smaller than 2 μm provides little to no benefit, but can decrease average search times for large phytoplankton ($\sim 20\ \mu m$) from two weeks to two days, an advantage that is robust to variations and favors bacteria with higher swimming speeds. By contrast, in oligotrophic waters, chemotaxis can reduce search times for picophytoplankton ($\sim 1\ \mu m$) up to ten-fold, from a week to half a day, but only for bacteria with low swimming speeds and long sensory timescales. We propose that this asymmetry may promote the coexistence of diverse search phenotypes in marine bacterial populations.

References

[1] Seymour et al., Trends Microbiol. **32**, 640-649, (2024)
[2] Foffi et al. (under review)

P41 - Spontaneous Demixing of Binary Colloidal Flocks

S. Maity, A. Morin

Insitute of Physics, Leiden University, Netherlands

Population heterogeneity is ubiquitous among active living systems, but little is known about its role in determining their spatial organization and large-scale dynamics. Combining evidence from synthetic active fluids assembled from self-propelled colloidal particles along with theoretical predictions at the continuum scale, we demonstrate the spontaneous demixing of binary polar liquids within circular confinement. Our analysis reveals how both active speed heterogeneity and nonreciprocal repulsive interactions lead to self-sorting behavior. By establishing general principles for the self-organization of binary polar liquids, our findings highlight the specificity of multicomponent active systems [1].

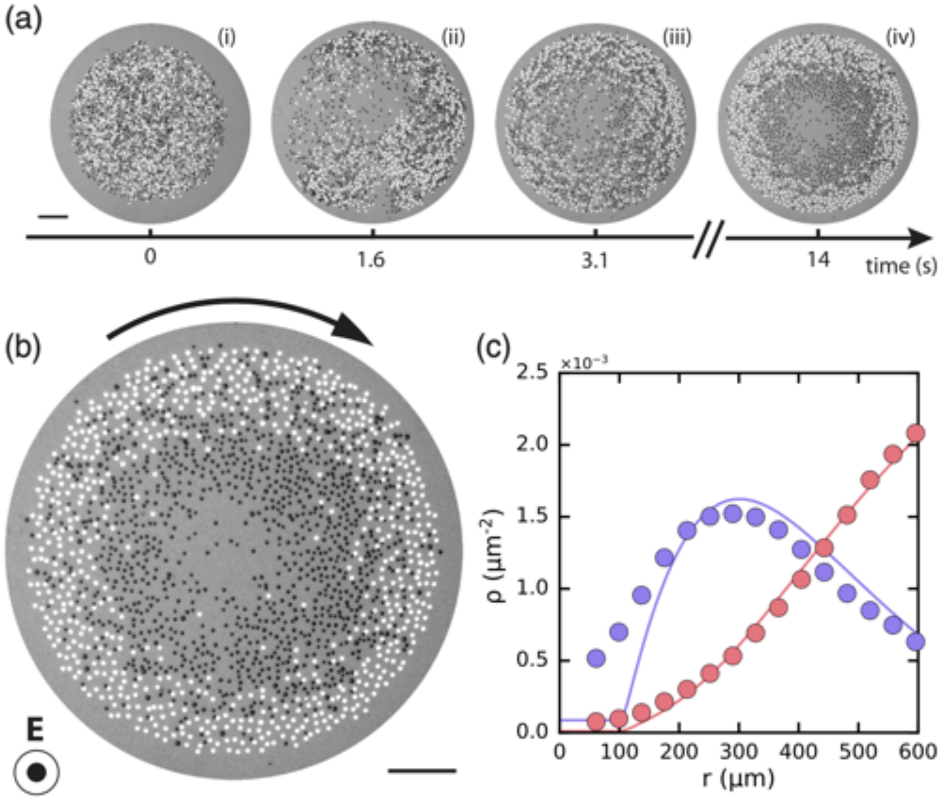


Figure 1: Spontaneous demixing of binary colloidal flocks — (a) Spontaneous demixing of an initially homogeneous binary mixture. Scale bar: 200 μm. (b) Steady-state configuration of a binary colloidal flock. Scale bar: 200 μm. (c) Radial density profiles of the two species. Red: fluorescent 7 μm diameter colloids. Mauve: non-fluorescent 5 μm-diameter colloids. Dots: experimental data. Lines: hydrodynamic theory.

References

[1] S. Maity, A. Morin, Physical Review Letters **131**, 178304, (2023)

P42 - The Reaction-Diffusion Regime of Eukaryotic Flagella

J.F. Cass, **H. Bloomfield-Gadêlha**

School of Engineering Mathematics and Technology, University of Bristol, Bristol, UK

Eukaryotic cilia and flagella are cellular appendages used to propel organisms through fluid or drive flows. Dynein motor proteins power beating of the flagellum by exerting axial forces on the doublet microtubules of the internal flagellar structure known as the axoneme. Research is ongoing to understand how the collective activity of individual dyneins can result in the self-sustaining stable oscillations that propagate along the flagellum enabling locomotion. Here we present a perspective on flagellar dynamics which decouples the intrinsic beat-patterning mechanism from the interaction of the flagellum with the surrounding fluid. We derive a minimal sliding-controlled reaction-diffusion system, employing tug-of-war reaction kinetics of dynein motors coupled to a planar elastic axoneme. Our system displays spatio-temporal animated patterns akin to classical reaction-diffusion systems [1]. Inspired by experimental work, our model eschews the assumption that energy supplied by motor proteins is primarily dissipated in the surrounding fluid [2]. Instead, we show that it is sufficient for producing a diverse range of flagellar waveforms that energy is mostly lost to internal friction. The model is able to fit quantitatively the beating patterns of bull sperm and the green alga *C. Reinhardtii*, distant eukaryotic species which vary in the length of their flagella/cilia, their axonemal structure, ultrastructure and cell morphology (see Fig. 1). We reveal a novel mechanism of non-reciprocal flagellar wave generation that may be crucial for low viscosity aquatic microswimmers. A weakly nonlinear analysis provides analytical solutions for the amplitude, frequency and propulsive force generated by the system, with surprising accuracy relative to simulations even far from the onset of oscillations [3].

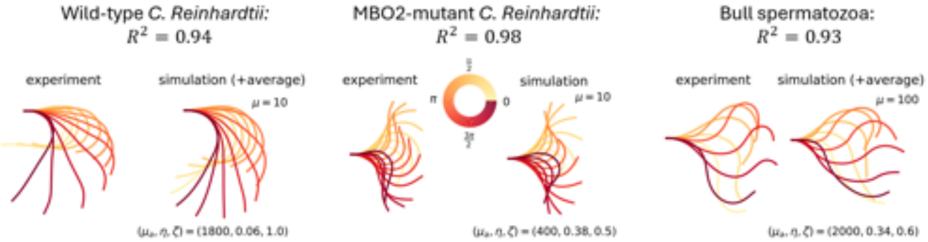


Figure 1: A simple reaction-diffusion model fits the beating patterns of diverse eukaryotic species.

References

[1] J.F. Cass and H. Bloomfield-Gadêlha, Nature Communications, **14**(1), (2023)
[2] D. Mondal, R. Adhikari, P. Sharma, Sci. Adv. **6**(33), (2020)
[3] J.F. Cass and H. Bloomfield-Gadêlha, biorxiv.org/content/10.1101/2024.08.14.607876v1, (2024)

P43 - Cognitive Flocks: Order-Disorder Transitions and Threat Evasion

P. Iyer[1], **C. Soroco**[1,2], **G. Gompper**[1]

[1] Forschungszentrum Jülich, Institute for Advanced Simulation, 52425 Jülich, Germany
[2] University of British Columbia, Vancouver, BC V6T 1Z4, Canada

Directed self-propulsion is ubiquitous in living organisms. Ranging from *E. Coli* dispersing in biofilms to bird flocks migrating across oceans, living organisms are constantly out-of equilibrium. By sensing their environment and adjusting their movement, organisms can exhibit emergent patterns and collective behaviors, such as self-organization in human crowds [1, 2], bird flocks, and fish schools. The Inertial Spin Model (ISM) was introduced to explain the fast and robust propagation of information in bird flocks [3], when only alignment interactions are considered. However, more generally, agents exhibit a variety of interactions like local avoidance, cohesion and threat evasion [4]. We show how such behaviours can be incorporated within the framework of the ISM. It is found that local avoidance introduces emergent noise in the system, triggering an order-disorder transition. Exploring the flock dynamics near this transition reveals a complex interplay between cohesion, alignment, and local avoidance, resulting in a diverse array of behaviors such as pronounced shape fluctuations and the diffusive motion of the flock. Building on this understanding, we apply our flocking model to a simple scenario of stationary threat avoidance, where only the edges of the group can detect the threat. We explore how various flock properties, such as speed, local avoidance, and signal damping, influence the way the threat information propagates across the flock. This illuminates the physical mechanisms that govern collective motion in flocks, providing valuable insights that can be leveraged to design effective navigation strategies.

Figure 1: (a) Increasing local avoidance (left to right) leads to increased disorder and shape changes in the flock. (b) A flock avoiding a threat that is directly ahead of it (black bullet). Trajectory lines shown for the agents at the front of the flock.

References

[1] Negi, R. S. et al. , Sci. Rep. **14**, 9443, (2024)
[2] Iyer, P. et al. , arXiv, 2405.18528, (2024)
[3] Attanasi, A. et al. , Nat. Phys. **10**, 691-696, (2014)
[4] Negi, R. S. et al. , Phys. Rev. Res. **6**, 013118, (2024)

P44 - Effects of gravitational fields and confinement on the collective behavior of biological microswimmers

H. Serna[1], **C. M. Barriuso Gutierrez**[1], **M. Polin**[2], **I. Pagonabarraga**[3], **C. Valeriani**[1]

[1] Universidad Complutense de Madrid, Spain
[2] Mediterranean Institute for Advanced Studies IMEDEA-UIB-CSIC, Spain
[3] Universidad de Barcelona, Spain

Biological Microswimmers (BM) have evolved mechanisms to self-propel. The interactions between different types of BM (hydrodynamic, chemical, among others) are relevant in natural processes such as the regulation of carbon and oxygen biogeochemical cycles and the release of toxins by phytoplankton blooms under certain environmental conditions. On the other hand, interactions between BM's and passive objects are crucial to design processes with potential technological applications such as activity-induced sorting (separation) and cargo delivery. Apart from that, in both natural and controlled scenarios, BM's swim through complex environments where their motion is affected by external fields and different types of confinement. In particular, the combined effect of hydrodynamics, external fields, and confinement not only plays a role in natural processes like bio-convection, but also is key to understand and control the BM's collective motion, aiming to design new technologies in active and smart materials. In this work, we use computational simulations to study the structural and dynamical properties of suspensions of squirmer-like BM's under the influence of a gravitational field. Also, we present a preliminary study on activity-induced transport of passive colloids confined in micro-channels.

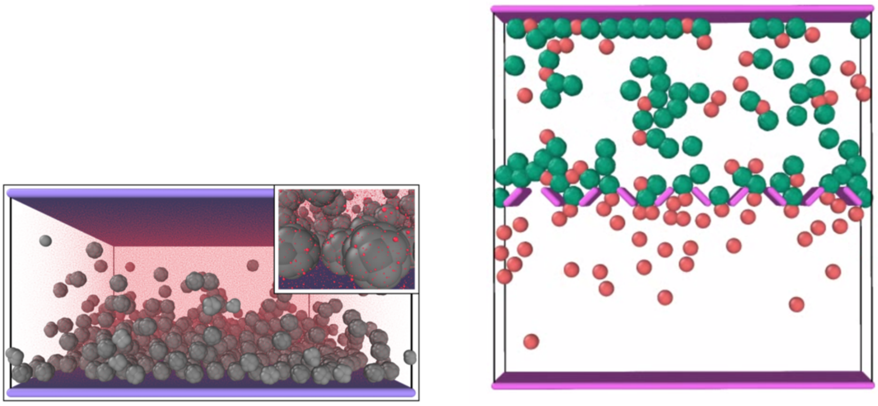


Figure 1: Left: snapshot of microswimmers during sedimentation. Right: snapshot of a designed micro-channel to promote the separation of a mixture of microswimmers and passive colloids.

References

[1] J. Seymour, S. Amin, J. Raina, R. Stocker, Nat. Microbiol., **2**, 17065 (2017)
[2] E. Ehrlich, U. Thygesen, T. Kiørboe, Proc. R. Soc. B., **289**, (2022)
[3] C. Bechinger, R. Di Leonardo, H. Löwen, C. Reichhardt, G. Volpe, G. Volpe, Rev. Mod. Phys., **88**, 045006 (2016)
[4] S. Williams, R. Jeanneret, I. Tuval, M. Polin, Nat. Commun., **13**, 4776 (2022)
[5] R. Martinez, F. Alarcon, J. Aragones, C. Valeriani, Soft Matter, **16**, 4739-4745 (2020)
[6] O. Yasa, P. Erkoc, Y. Alapan, M. Sitti, Advanced Materials, **30**, (2018)
[7] J. Kuhr, F. Rühle, H. Stark, Soft Matter, **15**, 5685-5694 (2019)

P45 - Active segregation in binary mixtures under flow

G. Di Dio, R. Colin

Max Planck Institute for Terrestrial Microbiology and Center for Synthetic Microbiology, Marburg

In nature, from the gut to the soil, bacteria form complex heterogeneous communities, the organization of which is essential to their functioning, with broad impacts on natural and industrial processes. In these porous environments, shear flow is a ubiquitous external physical constraint that can influence the swimming behavior of active bacteria and the structures of communities. However, how the physics of shear flow contributes to the structuring of complex, phenotypically heterogeneous communities still remains poorly understood. Here, we investigate experimentally how a model heterogeneous bacterial community of motile and non-motile *Escherichia coli* organizes in a confined environment under shear flow. We discovered that the mixture actively segregates under flow, with the non-motile population accumulating on the “left” side of the channel (i.e. opposite to the vorticity direction) at low shear rates. We demonstrate experimentally and in simulation that this segregation, which depends on motile cell density and flow rate, originates from the backflow generated from the collective rheotactic drift of motile cells. We also show that non-motile cell accumulation requires sedimentation, which counters the incompressibility of the conveyer-belt-like backflow, to take effect. Finally, the segregation of non-motile cells under flow leads at long times to asymmetric co-biofilm formation in the channel. Our findings reveal a novel mechanism by which physical interactions in flowing environments can drive the spatial organization and long-term dynamics of complex microbial communities.

P46 - Learning hydrodynamic equations from microscopic Langevin simulations of self-propelled particles dynamics

B. Roy[1], **N. Yoshinaga**[2]

[1] AIST-TohokuU Mathematics for Advanced Materials-OIL, Katahira 2-1-1, Aoba-Ku, Sendai, 980-8577 JAPAN
[2] Future University Hakodate, 116-2 Kamedanakano-cho, Hakodate, Hokkaido 041-8655, Japan

In nonequilibrium systems, a collective movement of microscopic active particles often displays several common emerging properties, such as swarming, motility-induced phase separation, nonequilibrium disorder-order transitions, anomalous density fluctuation, spatiotemporal patterning, and unusual rheological properties. However, those universal aspects of collective behaviors are hardly captured from microscopic particle-based simulation methods. The macroscopic properties obtained from nonlinear hydrodynamic equations are useful for understanding those aspects. Therefore, we start from the numerical Langevin simulations of the microscopic particle dynamics and present a data-driven strategy for the collection of self-propelled particles to develop the hydrodynamics equations[1]. In our method, microscopic particle data is our input. Hence, the hydrodynamics fields are obtained by coarse-graining from the discrete description of particle dynamics. For partial differential equation (PDE) learning [2], the spectral representation gives the efficient and accurate computation of spatial and temporal derivatives of density and polarization density fields. Using sparse regression on the fields, we generate hydrodynamic equations. The estimated PDEs from microscopic models are beneficial to understanding the universal features of the system in comparison to standard supervised learning. Hence, the macroscopic features will be shared both by microscopic models and hydrodynamic equations.

References

[1] R. Supekar, B. Song, A. Hastewell, J. Dunkel, PNAS **120** (7), e2206994120 (2023)
[2] S. H. Rudy, S. L. Brunton, J. L. Proctor, J. N. Kutz, Science Advances **3**, e160261 (2017)

P47 - Run-and-tumble in Porous Media: Universal Law for Dispersal

T. Pietrangeli

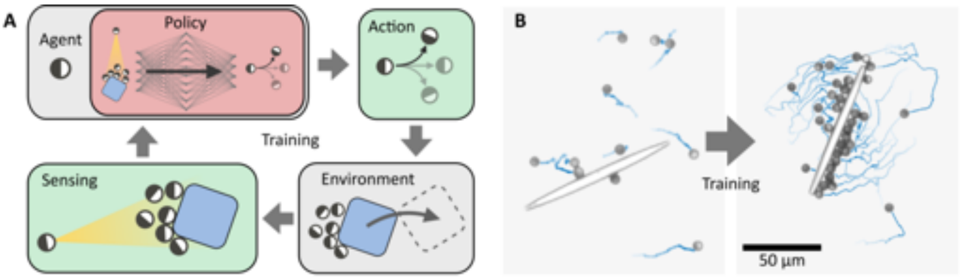
University Claude Bernard Lyon 1, France

Dispersal is a key process for many motile microorganisms living in porous environments such as rocks, soils, and tissues. However, the relationship between dispersal, movement strategies, and pore space structure remains an open question. This work investigates, through numerical simulations, the long-time dispersal of run-and-tumble microorganisms that become trapped at solid surfaces and escape by tumbling. The results demonstrate a universal connection between dispersal and mean run time, applicable across various porous structures and swimming strategies. Using a simple model for orientational decorrelation, the study reveals that this behavior arises from the invariance of the mean free path, regardless of the movement strategy. The optimal strategy for maximizing dispersal is discussed, and the approach is extended to microorganisms that move along surfaces. This work provides a general framework for quantifying dispersal across diverse movement patterns and porous environments.

P48 - Counterfactual rewards promote collective transport using individually controlled swarm microrobots

V. -L. Heuthe[1,2], **E. Panizon**[3,4], **H. Gu**[1], **C. Bechinger**[1,2]

[1] University of Konstanz, Department of Physics, Universtaetsstrasse 10, 2 Konstanz, 78464, Germany
[2] Centre for the Advanced Study of Collective Behaviour, Universtaetsstrasse 10, Konstanz, 78464, Germany
[3] The Abdus Salam International Centre for Theoretical Physics (ICTP), Strada Costiera 11 4 Trieste, 34151, Italy
[4] Area Science Park, Data Engineering Laboratory, Località Padriciano 99, Trieste, 34149, Italy



Swarm robotics explores the potential of collective behavior for robotic systems, reminiscent of ants working together to move large objects. Efficient control schemes for robot swarms require that all robots have an equal contribution to the task. Therefore, a major challenge in swarm control is to estimate the contribution of each unit, which becomes particularly difficult at the microscale where the dominant noise introduces high stochasticity. In this study, we address these challenges by implementing Multi-Agent Reinforcement Learning (MARL, illustrated in panel A) to individually control up to 200 microrobots using laser spots. These microrobots collectively manipulate and transport large cargo objects, much like an ant swarm. By employing counterfactual rewards, our approach efficiently assigns credit to individual microrobots, enabling unbiased training with high flexibility regarding different tasks. The resulting control strategy is highly scalable, and robust, capable of adapting to variations in group size, malfunctioning units, and environmental noise. This demonstration marks a significant step forward in the development of micro-robot swarms as tools for manipulating microscopic objects. Our system's ability to perform complex tasks, such as simultaneous manipulation of multiple objects, suggests promising applications in automated assembly of mobile micromachines, programmable drug delivery capsules, and advanced lab-on-a-chip technologies.

P49 - Mutual information as a measure of mixing efficiency in viscous fluids

Y. Shi[1], **R. Golestanian**[1,2], **A. Vilfan**[1,3]

[1] Max Planck Institute for Dynamics and Self-Organization (MPI-DS), Goettingen, Germany
[2] Rudolf Peierls Centre for Theoretical Physics, University of Oxford, Oxford, UK
[3] Jožef Stefan Institute, Ljubljana, Slovenia

Fluid mixing at the microscale is of paramount importance in biological organisms and in artificial systems. Examples range from the the uptake of oxygen, nutrients or chemical signals in aquatic organisms to microreactors and "lab on a chip" applications. In biology, mixing is frequently accomplished by cilia which drive long-range flows, but also localized regions of chaotic advection. A particular challenge to microscale mixing is posed by the time-reversibility of flows at low Reynolds numbers. Mixing therefore requires an interplay between advection (stirring) and diffusion. Here we introduce mutual information between particle positions before and after mixing as a measure of mixing efficiency. We demonstrate its application in a Couette flow in an annulus and show that the mixing efficiency depends in a non-trivial way on the time sequence of rotation. We show that under this measure, the mixing efficiency is symmetric upon time reversal of the actuation sequence. Among all sequences with the same rotation angle, the ones with optimal mixing consist of a fast rotation in the middle of the time interval, or in some cases two symmetrically arranged. We also determine mutual information from Brownian dynamics simulations using data compression algorithms and demonstrate that advanced neural network based compression algorithms can be applied to estimate mutual information to a high accuracy. Our results show that mutual information provides a universal and assumption-free measure of mixing efficiency in microscale flows. Furthermore, we expect that our formalism will also be applicable to more complex mixing situations, for example by active swimmers, natural or artificial cilia or in active materials. Our current work is to apply mutual information in studying mixing caused by different types of microswimmers.

References

[1] Y. Shi, R. Golestanian and A. Vilfan, Phys. Rev. Research, **6**, L022050 (2024)

P50 - Vortex formation and odd viscosity in a chiral active fluid

J. Mecke[1,2], **Y. Gao**[1], **G. Gompper**[2], **M. Ripoll**[2]

[1] Institute for Advanced Study, Shenzhen University, Shenzhen, PR China
[2] nstitute of Advanced Simulation, Forschungszentrum Jülich, Germany

Materials consisting of active particles with an intrinsic rotation can be considered as chiral active matter. Related systems can be observed in biology and also in synthetic materials, e.g., by use of rotating fields on particles carrying a dipole moment [1]. We study a colloidal chiral active system, consisting of magnetic microrotors of diameter 0.8 μm in an externally applied rotating magnetic field. The stabilised rotating colloids solely interact via steric and hydrodynamic interactions, granting active stresses already at low densities and large colloidal separations. We address the system by means of experiments as well as particle based hydrodynamics simulations (MPC) of the active colloidal suspension. The rotors' transverse, anti-symmetric, and non-reciprocal interactions lead to a pair-rotation about the centre of mass and subsequently to the formation of multiscale vortices (see Fig.1). The energy is injected on the particle level and is transported to the largest scales in the system, unless it is dissipated into the substrate or adjacent fluid layers [2], a process reminiscent of turbulence, even in the absence of dominant inertial contributions. We introduce the influence of momentum leakage in the MPC fluid, which can be thought of as a frictious substrate below the 2D active fluid layer, leading to the emergence of a hydrodynamic damping length due to the fluid friction, which limits the size of the emergent vortices. The rich phenomenology of our system additionally includes correlations between vorticity and density which allow for a measurement of the system's odd viscosity [3], enhancement of effective diffusive transport by the introduction of obstruction, or directed transport by virtue of symmetry breaking at confining walls.

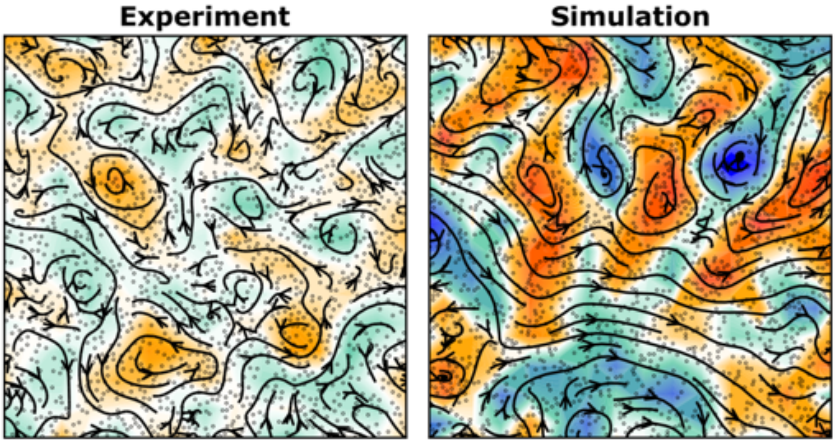


Figure 1: Vortex formation in the colloidal chiral active system obtained from experiments (left) and simulation (right). Red, white, blue areas correspond to positive, zero, negative vorticity, respectively.

References

[1] J. Mecke, J.O. Nketsiah, R. Li, Y. Gao, Natl. Sci. Open 3(4):20230086 (2024)
[2] J. Mecke, Y. Gao, G. Gompper, and Marisol Ripoll, https://arxiv.org/abs/2408.12820 (2024)
[3] J. Mecke, Y. Gao, C.A. Ramírez Medina, D.G.A.L. Aarts, G. Gompper, and M. Ripoll , Commun. Phys. **6**, 324 (2023)

P51 - Immobility of swarmer cells due to local liquid depletion

A. Jose[1], B. Pérez-Estay[2], S. Omer Bendori[3], A. Eldar[3], D.B. Kearns[4], G. Ariel[5], A. Beér[6,7]

[1] The Albert Katz International School for Desert Studies, The Jacob Blaustein Institutes for Desert Research, Ben-Gurion University of the Negev, SedeBoqer Campus, 84990 Midreshet Ben-Gurion, Israel.
[2] Laboratoire PMMH-ESPCI Paris, PSL Research University, Sorbonne University, University Paris-Diderot, 7, Quai Saint-Bernard, Paris, 75005, France.
[3] The Shmunis School of Biomedicine and Cancer Research, Faculty of Life Sciences, Tel Aviv University, Tel Aviv, 69978 Israel.
[4] Department of Biology, Indiana University, Bloomington, Indiana 47405, USA
[5] Department of Mathematics, Bar-Ilan University, 52900 Ramat-Gan, Israel.
[6] Zuckerberg Institute for Water Research, The Jacob Blaustein Institutes for Desert Research, Ben-Gurion University of the Negev, Sede Boqer Campus 84990, Midreshet Ben-Gurion, Israel
[7] The Department of Physics, Ben-Gurion University of the Negev, 84105 Beer-Sheva, Israel.

Bacterial swarming is a complex phenomenon in which thousands of self-propelled rod-shaped cells move coherently on surfaces, providing an excellent example of active matter. However, bacterial swarming is different from most studied examples of active systems because single isolated cells do not move, while clusters do. The biophysical aspects underlying this behavior is unclear. This talk explores the case of low local cell densities, where single cells become temporarily immobile. We show that immobility is related to local depletion of liquid. In addition, it is also associated with the state of the flagella. Specifically, the flagellar bundles at (temporarily) liquid depleted regions are completely spread-out. Our results suggest that dry models of self-propelled agents, which only consider steric alignments and neglect hydrodynamic effect, are oversimplified and are not sufficient to describe swarming bacteria.

P52 - Chaotic collective mixing by a S. Lemnae feeding cluster

R. Turuban[1,2], **G. Noselli**[2], **A. Beran**[3], **A. De Simone**[1,2]

[1] The BioRobotics Institute, Scuola Superiore Sant'Anna, Pisa, Italy
[2] SISSA–International School for Advanced Studies, Trieste, Italy
[3] OGS–Istituto Nazionale di Oceanografia e di Geofisica Sperimentale, Trieste, Italy

Although it is an efficient swimmer, the suspension feeder *Stylonychia Lemnae* greatly prefers to crawl on solid surfaces. Whenever sensing food, the cells change their locomotion behavior in order to remain in the most favorable area, mostly by reducing their crawling speed. In the meantime, anchored cells apply a net force on the fluid, thereby generating a long-range feeding current. As cells progressively gather around food, they become close enough so that the multiple feeding flows interact hydrodynamically: a collective chaotic flow has emerged, at the scale of the whole feeding cells cluster, with new striking fluid dispersion and mixing properties. Here, we measure experimentally the collective feeding flow using PIV, and show that we can entirely predict this unstationary 3D flow with an analytical model consisting in the superposition of regular forces over a non-slip boundary, with each force representing a feeding cell with evolving orientation and position. From the analytical flow, we provide first a numerical quantification of the fluid dispersion coefficient which reveals that, at equivalent population density, the collective feeding flow is at least 40 times more efficient at spreading fluid than a suspension of squirmers, based on the model proposed by [1]. Second, we compute the Lyapunov exponent, which is shown to compare well even with non-active chaotic laminar flows such as porous media flows or sheared particulate suspensions. We will finally discuss about the biological benefits potentially granted by the active collective flow, as well as its possible cooperative nature.

References

[1] Z. Lin, Journal of Fluid Mechanics **669**, 167-177, (2011)

P53 - E-coli transport along microfluidic edges determined by trajectory chirality and confinement

P. Zhang[1], **S. M. Köhler**[2], **F. Goio Castro**[1], **E. Clément**[1], **A. Zöttl**[2], **A. Lindner**[1]

[1] PMMH, CNRS, ESPCI Paris, Université PSL, Sorbonne Université, Université de Paris, F-75005, Paris, France
[2] Faculty of Physics, University of Vienna, 1090 Wien, Austria

Swimming of bacteria near surfaces is of high biological and medical relevance, for example, in the formation of biofilms [1] or their transport through medical conducts. Such near-surface accumulation, has been attributed to hydrodynamic attraction and collisions between the cells and the surface. The motion of *E.coli* bacteria near surfaces is related to their asymmetric shape and chiral flagella, leading to the well-known chiral clock-wise circular trajectories in the presence of the counter-rotation body and flagella [2]. It has been reported that such chirality of *E.coli* trajectories can lead to navigation of the swimming bacteria along a preferential direction along confined microfluidic channels [3, 4]. However, the exact mechanism behind these observations remain to be fully understood.

In this work we study the relationship between the chirality of bacteria trajectories at flat surfaces and their swimming direction along the edge region of a rectangular channel formed by two perpendicular sections of channel surfaces. We measure the orientation directions of smooth runner *E.coli* bacteria approaching the edges. Interestingly, we identified a preferential approaching orientation which is reversed from swimming to the right to swimming to the left for increasing confinement. This observation is consistent with both our numerical simulations and analytical results in two dimensions. To understand the mechanism hidden behind this general observation, we explore the distribution of the incoming angle at the edges and it shows strong correlation with the subsequent swimming direction along the edges. Finally we show that this angle distribution is a function of the channel confinement and explains the preferential confinement-dependent orientations. To understand transport along all four edges of a rectangular channel we also obtained individual bacterial 3D lagrangain-tracking trajectories suggesting the presence of competing effects of different channel surfaces. These results coupled with our two-dimensional observations will give a more complete understanding of the role of chirality in bacteria transport near the edges of rectangular channels. This work will shed light on performing targeted transport in lab-on-chip devices and other medical applications.

References

[1] Paula Watnick and Roberto Kolter. “Biofilm, city of microbes”. In: Journal of bacteriology **182**.10 pp. 2675–2679 (2000)
[2] Eric Lauga et al. “Swimming in circles: motion of bacteria near solid boundaries”. In: Biophysical journal **90**.2 pp. 400–412 (2006)
[3] Mite Mijalkov and Giovanni Volpe. “Sorting of chiral microswimmers”. In: Soft Matter **9**.28 pp. 6376–6381 (2013)
[4] Willow R DiLuzio et al. “Escherichia coli swim on the right-hand side”. In: Nature **435**.7046 pp. 1271–1274 (2005)

P54 - Mechanical coupling is sufficient to synchronize C. Reinhardtii flagella

L. Zorrila[1], **K. Desai**[2], **A. Allard**[3], **M. Polin**[1]

[1] IMEDEA (UIB-CSIC), Esporles, Spain
[2] University of Warwick
[3] LOMA, University of Bordeaux

Physical laws apply differently at the microscale than at the macroscale, therefore constraining microorganisms' biological functions. A key instance of this is that microbes perceive their surrounding medium as extremely viscous, constraining them to adopt non-symmetric motion to be able to propel forward. Some bacteria (*E. coli*) and unicellular algae (*C. reinhardtii*) have evolved different asymmetric motions in order to propel. *C. reinhardtii* has two flagella, mechanically connected from inside the cell, that beat synchronously in a "breaststroke" pattern. Flagellar synchronization is necessary to propel forward but is not fully understood. More generally, many microorganisms, including human epithelial cells or multiciliate microbes display flagellar synchronization. Experiments on isolated pairs of flagella from multicellular alga Volvox have shown that hydrodynamic coupling alone is sufficient for metachronal synchronization. But *C. reinhardtii* also displays internal mechanical coupling that has been shown to be necessary to synchronize its flagella in a breaststroke movement. What is the respective nature of hydrodynamic and mechanical coupling in flagellar synchronization of these unicellular alga? To find out, we separate their two flagella by a cantilever to prevent inter-flagellar hydrodynamic interactions, while holding the cell with a micropipette. We observe that flagella stay synchronized without hydrodynamic interactions, including when subject to stress. We further investigate the quantitative and qualitative contribution of hydrodynamic coupling to synchronization with the use of anti-phase synchronized (ptx1) cell mutants.

P55 - Viscotaxis of Beating Flagella at Surfaces

S. Anand, J. Elgeti, G. Gompper

Theoretical Physics of Living Matter, Institute for Biological Information Processing and Institute for Advanced Simulation, Forschungszentrum Jülich, 52425, Germany

Understanding how microorganisms steer, change their swimming direction, and achieve directional motion in complex environments is crucial for many biological processes, including egg fertilization[1,2,3]. In some cases, eukaryotic flagellated microswimmers, like sperm, navigate their surroundings by responding to environmental gradients, such as chemical, temperature, gravitational fields, and light. These external cues trigger specific behavioral responses that enable the microswimmers to adjust their swimming direction, helping them reach their targets[4,5]. This ability to respond and adapt their motion to environmental stimuli is known as taxis, which plays a fundamental role in guiding microswimmers in complex biological processes. A well-known example is chemotaxis, where concentration gradients of a chemo-attractant are sensed and guide the sperm cell towards the egg cell. We investigate another potentially relevant physical mechanism, viscotaxis, in which a beating flagellum reacts to gradients of fluid viscosity. Various kinds of microswimmers have been found to respond to viscosity gradients depending on their shape or hydrodynamic propulsion mechanisms [6,7]. We investigate viscosity gradient effects on flagellum motion. Our flagellum model is represented by a semi-flexible filament with a traveling wave of spontaneous curvature, to investigate viscotaxis in two-dimensional space. Through a combination of numerical simulations and analytical approaches, we show that actively beating flagellum exhibits positive viscotaxis, orienting toward regions with higher viscosity. This behavior is characterized by analyzing the relationship between rotational velocity and parameters such as beat amplitude, swimming speed, and wavelength. Furthermore, we explore the effects of asymmetric flagella waveforms and flagella elasticity. The asymmetric flagellar waveforms result in linear or trochoid-like trajectories, with large asymmetry causing drifting circles perpendicular to the gradient. Deformability of the flagella significantly reduces both the beat amplitude and viscotactic response, which is captured by a universal function based on the sperm number. We have also studied the role of a head, where the viscotactic response is found to decrease with increase in head size.

References

[1] J. Elgeti et al., Rep. Prog. Phys.**78**, 056601, (2015)
[2] L. Alverez et al., Trends Cell Biol. **24**, 198, (2014)
[3] A. Gong et al., 2020 Phil. Trans. R. Soc. B37520190149 (2020)
[4] G. Saggiorato et al., Nat. Commun **8**, 1415 (2017)
[5] A. Gong et al., Phil. Trans. R. Soc. B **375**, 20190149 (2019)
[6] V. A. Shaik et al., Phys. Rev. Fluids **6**, 103103 (2021)
[7] B. Liebchen et al., Phys. Rev. Lett. **120**, 208002 (2018)

P56 - On-Demand Breaking of Action-Reaction Reciprocity between Magnetic Microdisks Using Global Stimuli

G. Gardi[1], **M. Sitti**[1,2]

[1] Physical Intelligence Department, Max Planck Institute for Intelligent Systems, 70569 Stuttgart, Germany
[2] School of Medicine and College of Engineering, Koç University, 34450 Istanbul, Turkey

Coupled physical interactions induce emergent collective behaviours of many interacting objects. Nonreciprocity in the interactions generates unexpected behaviours. There is a lack of experimental model system that switches between the reciprocal and nonreciprocal regime on demand. Here, we study a system of magnetic microdisks that breaks action-reaction reciprocity via fluid-mediated hydrodynamic interactions, on demand. Via experiments and simulations, we demonstrate that nonreciprocal interactions generate self-propulsion-like behaviours of a pair of disks; group separation in collective of magnetically nonidentical disks; and decouples a part of the group from the rest. Our results could help in developing controllable microrobot collectives. Our approach highlights the effect of global stimuli in generating nonreciprocal interactions.

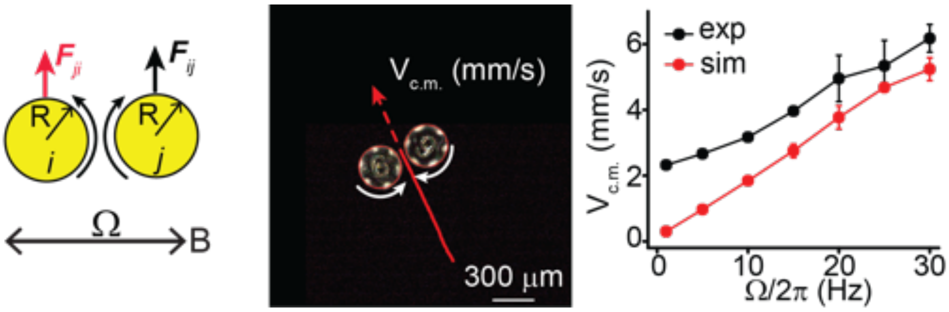


Figure 1: Left: schematic of non-reciprocal interaction between counter-rotating disks under oscillating magnetic field. Middle: experimental image showing translation of a counter-rotating disk pair. Right: Translation speed of centre of mass of disks vs frequency of magnetic field.

References

[1] G. Gardi, and M. Sitti, Physical review letters, **131**(5), 058301 (2023)

List of Participants

Name	Page	Email Address
Jan Albrecht	83	jan.albrecht@uni-potsdam.de
Shubham Anand	31, 63, 121	s.anand@fz-juelich.de
Avraham Be'er	29, 52, 117	beera@bgu.ac.il
Yatharth Bhasin	99	byatharth@igc.gulbenkian.pt
Julien Bouvard	77, 80, 97	bouvard.julien@gmail.com
Douglas Brumley	16, 45	d.brumley@unimelb.edu.au
James Cass	34, 108	james.cass@bristol.ac.uk
Andreea-Oana Chelban		andreea.chelban@unibas.ch
Sujeet Kumar Choudhary	90	sujeet@imedea.uib-csic.es
Mithun Chowdhury	100	mithunc@iitb.ac.in
Jane Chui	68	yyjc2@cam.ac.uk
Eric Clement		eric.clement@upmc.fr
Remy Colin	39, 70, 84, 111	remy.colin@synmikro.mpi-marburg.mpg.de
Diana Coroiu	20, 105	d.coroiu@sms.ed.ac.uk
Pallabi Das	92	pallabi@pks.mpg.de
Antoine Deblais	12	a.deblais@uva.nl
Antonio De Simone	38, 53, 118	desimone@sissa.it
Giacomo Di Dio	39, 91, 111	giacomo.dio@synmikro.mpi-marburg.mpg.de
Roberto Di Leonardo	42	roberto.dileonardo@uniroma1.it
Knut Drescher	48	knut.drescher@unibas.ch
Sayantan Dutta	74, 100	sayantan.dutta@iitb.ac.in
Isabelle Eisenmann	76	ieisenmann31@gmail.com
Jens Elgeti	31, 63, 73, 121	j.elgeti@fz-juelich.de
Yves Emery	26	yves.emery@lynceetec.com
Markus Engstler	11, 49, 101	markus.engstler@biozentrum.uni-wuerzburg.de
Silvia Espada Burriel	70, 91	silvia.burriel@mpi-marburg.mpg.de
Dmitry Fedosov	62, 67, 85	d.fedosov@fz-juelich.de
Wei Feng	71	im.will.feng@gmail.com
Riccardo Foffi	16, 30, 106	rfoffi@ethz.ch
Francesca Font	88	xfont@imedea.uib-csic.es
Benjamin Friedrich	36	benjamin.m.friedrich@tu-dresden.de
Clara Fronda	69	clara.fronda@phys.ens.fr
Gaurav Gardi	59, 122	gardi@is.mpg.de

Name	Page	Email Address
Sayantan Ghosh	82	saagey@gmail.com
Gerhard Gompper	31, 35, 46, 62, 63 67, 85, 109, 116, 121	g.gompper@fz-juelich.de
Daniel Greve	95	daniel.greve@uni-muenster.de
Veit-Lorenz Heuthe	43, 114	veit-lorenz.heuthe@uni.kn
Pierre Illien	41	pierre.illien@sorbonne-universite.fr
Lucio Isa	25	lucio.isa@mat.ethz.ch
Priyanka Iyer	35, 109	p.iyer@fz-juelich.de
Narges Jamshidi	11, 101	narges.jamshidi-khameneh@uni-wuerzburg.de
Raphaël Jeanneret	61, 69, 76	raphael.jeanneret@phys.ens.fr
Ajesh Jose	52, 117	ajesh@post.bgu.ac.il
Irina Kalita	84	irina.kalita@synmikro.mpi-marburg.mpg.de
Thomas Ki	19	tk@aqua.dtu.dk
Meike Kleinen		m.kleinen@fz-juelich.de
Timo Knippenberg	50, 86	timo.knippenberg@uni-konstanz.de
Pawan Kumar	72	pawandahiya4@gmail.com
Sascha Lambert	81	sascha.lambert@phys.uni-goettingen.de
Taha Laroussi	77, 80, 97	taha.laroussi@polytechnique.edu
Alex Le Guen	79	alex.le-guen@espci.fr
Lucas Le Nagard	22	llenaga@exseed.ed.ac.uk
Anke Lindner	23, 24, 55, 71 104, 119	anke.lindner@espci.fr
Jaydeep Mandal	92, 98	jaydeepm@iisc.ac.in
Pierre Martin	14, 103	p.martin@campus.tu-berlin.de
Quentin Martinet	15	quentin.martinet@ist.ac.at
Joscha Mecke	46, 116	j.mecke@fz-juelich.de
Sebastien Michelin	57	sebastien.michelin@polytechnique.edu
Siddhant Mohapatra	94	siddhant@smail.iitm.ac.in
Edoardo Maria Mollica	78	emollica@ethz.ch
Alexandre Morin	32, 107	morin@physics.leidenuniv.nl
Hyorin Nam	28	hyorin.nam@mat.ethz.ch
Luke Neville		luke.neville@bristol.ac.uk
Victoria Nicolazo-Crach	77	victoria.nicolazo-crach@universite-paris-saclay.fr
Kristian Olsen	65	kristian.olsen@hhu.de
Florian Overberg	85	f.overberg@fz-juelich.de
Laya Parkavousi	75	laya.parkavousi@ds.mpg.de
Benjamín Pérez Estay	23, 24, 52, 104, 117	benjamin.perez-estay@espci.fr
Tommaso Pietrangeli	27, 93, 113	tomm.pietrangeli@gmail.com
Marco Polin	37, 54, 58, 88 91, 110, 120	mpolin@imedea.uib-csic.es
Valentin Poncet	9, 93	valentin.poncet@univ-lyon1.fr
Manu Prakash	60	manup@stanford.edu
Desmond Joseph Quinn	89	desmond_joseph.quinn@uni-leipzig.de
Harishwar Raman		harishw8r@gmail.com
Arun Ravi	96	arun.ravi@tuwien.ac.at
Heiko Rieger	66	heiko.rieger@uni-saarland.de
Bappaditya Roy	40, 112	physicsbapai@gmail.com
Pablo Sartori	33, 99	psartori@igc.gulbenkian.pt

Name	Page	Email Address
Eleonora Secchi	21, 28, 78	secchi@ifu.baug.ethz.ch
Horacio Antonio Serna Serna	37, 110	hoserna@ucm.es
Yihong Shi	44, 115	yihong.shi@ds.mpg.de
Rajesh Singh	18	rsingh@physics.iitm.ac.in
Victor Sourjik	47, 84	victor.sourjik@mpi-marburg.mpg.de
Katja Taute	64	katja.taute@uni-leipzig.de
Regis Turuban	53, 118	regis.turuban@gmail.com
Giovanni Stefano Ugolini	30, 78	gugolini@ethz.ch
Gerrit Vliegenthart		g.vliegenthart@fz-juelich.de
Axel Voigt	10, 92	axel.voigt@tu-dresden.de
Florian Voss	86	f_voss09@uni-muenster.de
Navish Wadhwa	17	navish.wadhwa@asu.edu
Isabelle Wielert	13, 102	iwielert@smail.uni-koeln.de
Chenyun Yao	73	c.yao@fz-juelich.de
Christophe Ybert	9, 66, 93	christophe.ybert@univ-lyon1.fr
Bohan Zhang	62, 67,	b.zhang@fz-juelich.de
Peixin Zhang	55, 71, 119	peixinzhang.phy@gmail.com
Luc Zorrilla	58, 120	lzorrilla@imedea.uib-csic.es
Andreas Zšttl	51, 55, 119	andreas.zoettl@univie.ac.at

Useful Information

Venue, poster session, conference dinner

The conference will take place at the Gustav-Stresemann Institut in Bonn.
Langer Grabenweg 68, 53175 Bonn

The **poster session** will take place Tuesday from 18.00 to 20.00. Posters are numbered and listed in the book of abstracts. The (maximum) poster format is A0, portrait. All presenters of a short talk are invited to present a poster.

At the poster session there will be fingerfood and drinks. For dinner afterwards, visit one of the restaurants in the neighbourhood or take the tram to downtown Bonn.

The **conference dinner** will be held on Wednesday night from 19.00 on, at restaurant Rheinaue, Ludwig-Erhard-Allee 20 53175 Bonn. (https://rheinaue.de) We will walk here all together after the last talk of the day. You are invited for the conference dinner if you indicated so at time of registration.