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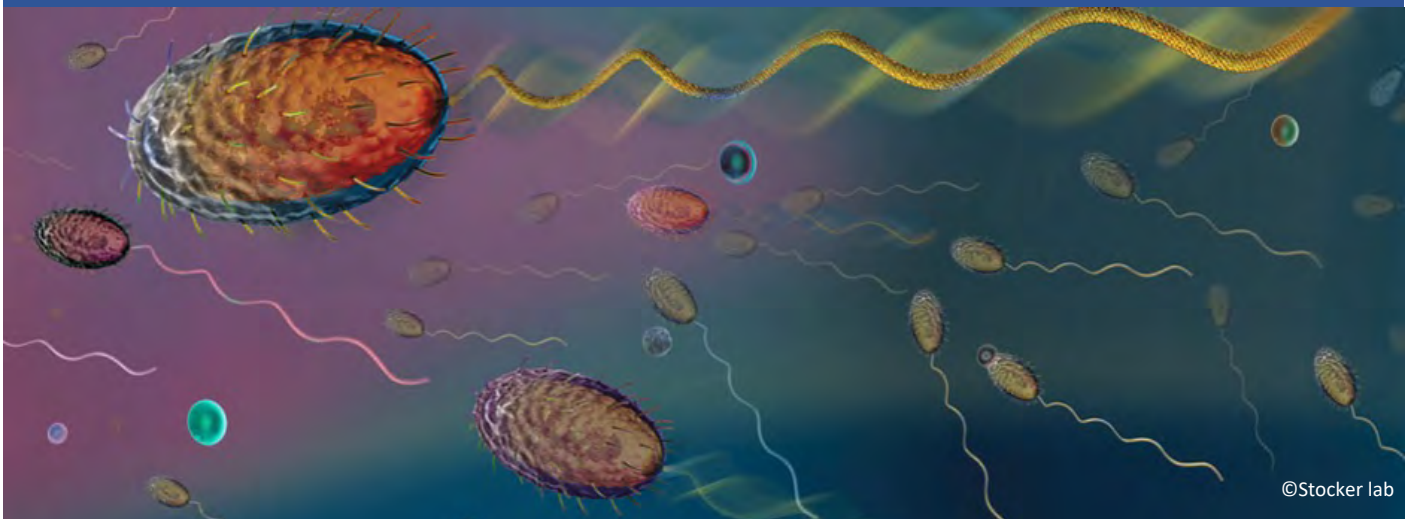
PHYMOT
Physics of Microbial Motility

JÜLICH
FORSCHUNGSZENTRUM

International Workshop

PHYSICS OF MICROBIAL MOTILITY

November 2-4, 2022, ESPCI Paris, France



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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.

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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

Wednesday Nov. 2

11:00–13:45	**Registration**		
13:50–14:00	**Welcome remarks Lindner & Gompper**		
14:00–14:30	IS	**Daniel Tam** TU Delft, The Netherlands	Experimental characterization of the dynamics of motile suspensions
14:30–14:50	CT	**Reza Shaebani** Saarland University, Germany	Optimal search strategies of active random searchers in crowded environments
14:50–15:10	CT	**Jonasz Słomka** ETH Zürich, Switzerland	Pushing the boundaries of cell tracking
15:10–15:30	CT	**Knut Drescher** Basel University, Switzerland	Physiological differentiation during bacterial swarm development
15:30–16:00	**Coffee**		
16:00–16:20	CT	**Silvia Espada Burriel** MPI Terrestrial Microbiology, Marburg, Germany	Density fluctuations in bacterial binary mixtures
16:20–16:40	CT	**Thomas Kiørboe** Technical University Denmark	Foraging trade-offs in flagellates, and the role of flagella in foraging
16:40–17:00	CT	**Raphaël Jeanneret** ENS Paris, France	Phototaxis of the dominant marine pico-eukaryote Micromonas sp.: from population to single cell
17:00–17:20	CT	**Jerko Rosko** University of Warwick, UK	Evidence for rotary-motor powered gliding motility in a filamentous cyanobacterium
17:30–19:30	**Poster session with fingerfood & drinks**		

Thursday Nov. 3

09:00-09:30	IS	**Kirsty Wan** University of Exeter, UK	On the origins of ciliary metachronism
09:30-09:50	CT	**Alberto Dinelli** Université Paris Cité, Paris	Self-organization of bacterial mixtures interacting via quorum-sensing
09.50-10:10	CT	**Maria Tătulea-Codrean** University of Cambridge, UK	Bacterial Olympics: Multiflagellarity allows bacteria to maintain constant motility across cell size
10.10-10:30	CT	**Pietro Cicuta** University of Cambridge, UK	Motile cilia waves: creating and responding to flow
10:30-11:00	**Coffee**		
11:00-11:30	IS	**Ingmar Riedel-Kruse** University of Arizona, USA	Synthetic adhesion logic, self-assembly of bacterial swarms, and multicellular tiling patterns
11:30-11:50	CT	**Antoine Deblais** University of Amsterdam, The Netherlands	Chromatographic Separation of Active Polymer-like Worm Mixtures by Contour Length and Activity
11:50-12:10	CT	**Yves Emery** LyncéeTec, Switzerland	Digital Holographic Microscopy 4D tracking – and much more
12:10-12:30	CT	**Isabelle Eisenmann** LPENS, Paris, France	Collective photoprotection through light-induced phase separation in a phototactic micro-algae
12:30-14:00	**Lunch**		
14:00-14:30	IS	**Teresa López León** ESPCI, Paris, France	Motility in anisotropic media
14:30-14:50	CT	**Steffen Lange** TU Dresden, Germany	Sperm chemotaxis in marine species is optimal for physiological flow rates according to the theory of filament surfing
14:50-15:10	CT	**Giacomo Frangipane** La Sapienza University, Rome, Italy	Interplay between phototaxis and photokinesis in light-driven E. coli
15:10-15:30	CT	**Eric Grelet** Université de Bordeaux, France	Bacterial micro-swimmers in colloidal liquid crystals
15:30–16:00	**Coffee**		
16:00-16:20	CT	**Jason Lewis** Lund University, Sweden	Active turbulence in bacterial suspensions under the effect of an external chemical gradient
16:20-16:40	CT	**Eric Clément** ESPCI, Paris, France	Emergence and scaling of collective flow patterns in active bacteria suspensions
16:40-17:00	CT	**Eric Climent** Université de Toulouse, France	Gyrotactic plankton cells in turbulence: the effects of motility, shape and fluid inertia
17:00-17:20	CT	**Avraham Be'er** Ben Gurion University, Israel	Mixed-species bacterial swarms – an interplay of mixing and segregation across scales
18:00-22.00	**Conference Dinner**		

Friday Nov. 4

09:00–09:30	IS	**Mike Shelley** Flatiron Institute, New York, USA	Self-organization and flow in living cells
09:30– 09.50:20	CT	**Markus Engstler** University of Würzburg, Germany	Evolution of microswimmer designs in distinct micro-environments
09:50–10:10	CT	**Cecile Cottin-Bizonne** ILM, University Lyon, France	Driven motion in complex environment
10:10–10:30	CT	**Helene de Maleprade** Sorbonne Université, Paris, France	Light control of bioconvective dynamics
10:30–11:00	**Coffee**		
11:00–11:30	IS	**Lisa Fauci** Tulane University, New Orleans, USA	Explorations of motile helices at the microscale
11:30–11:50	CT	**Jens Elgeti** Forschungszentrum Jülich, Germany	Swimming by Axonemal Beating
11:50–12:10	CT	**Dmitry Fedosov** Forschungszentrum Jülich, Germany	Behavior of microswimmers under confinement
12:10–12:30	CT	**Francseco Pedaci** CNRS Montpellier, France	Dynamic stiffening of the flagellar hook
12:30–14:00	**Lunch**		
14:00–14:30	IS	**Philippe Bastin** Institut Pasteur, Paris, France	Motility from within: molecular trafficking in the trypanosome flagellum
14:30–14:50	CT	**Blaise Delmotte** LadHyX, Paris, France	Understanding and modeling the intriguing motion of the diatom chain B. Paxillifer
14:50–15:10	CT	**Roberto Di Leonardo** La Sapienza University, Rome, Italy	Programming micro-motility with light
15:10–15:30	CT	**Anke Lindner** ESPCI, Paris, France	Bacteria transport close to surfaces: from rheotaxis to upstream contamination
15:30–15:45	**Closing remarks Lindner & Gompper**		
15:45	**End of workshop & departure**		

List of Abstracts – Talks

Wednesday Nov. 2

Experimental characterization of the dynamics of motile suspensions

D. Tam, A. Buchner, K. Muller IS

TU Delft, Fluid Mechanics, The Netherlands

Mechanical interactions in suspensions of motile microorganisms give rise to complex dynamics observed in both biological systems and industrial bioreactors. Several theoretical studies have focused on characterizing the role of hydrodynamic interactions, while experimental work has highlighted the importance of steric interactions. Here, we describe an experimental approach that enables the three-dimensional tracking of a large number of microorganisms in a millimetre-sized flow cell. We use a multi-view microscope and develop a tracking algorithm to record cell trajectories, which we use to resolve the interactions governing the dynamics of motile suspensions. We report recent results on the dynamics of swimming microorganisms accumulating near solid surfaces. For bacteria-like extensile swimmers, long-range hydrodynamic interactions have been shown to play a role in governing this near-surface accumulation. In this study, we investigate the roles of surface scattering and long-range interactions in the near-surface accumulation of a model contractile swimmer. A population of C. reinhardtii, swimming within a large volume, is recorded simultaneously by four cameras, and yields a large sample of 3D cell trajectories. We derive statistics of the isotropically diffusive swimming kinematics as well as their surface scattering dynamics, and observe a long-range cell-surface interaction. These statistics are sampled to build an empirically-driven Markov Chain Monte-Carlo simulation. In this way, we directly link the population near-surface accumulation to the swimming, scattering and surface interaction dynamics. We find that the experimentally observed population distribution can only be accounted for by including, in the model, the long-range cell-surface interaction characterised experimentally.

Optimal search strategies of active random searchers in crowded environments

R. Shaebani

Department of Theoretical Physics and Center for Biophysics, Saarland University, 66123 Saarbrücken, Germany

Biological active agents, such as bacteria and migrating cells, exhibit various motility patterns, resulting from diverse mechanisms of motion and from their interactions with the environment. How they should adjust their complex dynamics to optimally fulfil functions, such as navigation and search, is an intriguing problem. Velocity autocorrelation functions have been widely served as a measure of diffusivity and spreading and to reflect the complexity of the dynamics. We numerically investigate the influence of speed and direction autocorrelation functions as well as the direction-speed cross-correlation on the first-passage time of active searchers to find randomly located targets in confinement. We show that optimizing the direction memory and direction-speed coupling plays the major role; however, adopting an optimal speed memory can also reduce the search time compared to uncorrelated spontaneous speeds. Our results suggest that active searchers can improve their search efficiency, especially in crowded environments, through the directional or speed persistence or the speed-direction correlation.

References

[1] M. R. Shaebani, M. Piel, and F. Lautenschlager. Distinct speed and direction memories of migrating cells diversify their possible search strategies. To appear in Biophys. J., (2022)
[2] M. R. Shaebani et al. Effects of vimentin on the migration, search efficiency, and mechanical resilience of dendritic cells. To appear in Biophys. J., (2022)
[3] M. R. Shaebani, R. Jose, L. Santen, L. Stankevicins, F. Lautenschlager. Persistence-speed coupling enhances the search efficiency of migrating immune cells. Phys Rev Lett **125** 268102, (2020)
[4] J. Najafi, M. R. Shaebani, T. John, F. Altegoer, G. Bange, C. Wagner. Flagellar number governs bacterial spreading and transport efficiency. Science Advances **4**, eaar6425, (2018)

Pushing the boundaries of cell tracking

J. Słomka[1], **R. Foffi**[1], **P. Nienałtowski**[1,2], **R. Stocker**[1]

[1] ETH Zürich, Insitute of Environmental Engineering, Zürich, Switzerland
[2] Lyncée Tec SA, Innovation Park of EPFL, Lausanne, Switzerland

Understanding of how bacteria tune their energy investment towards motility in nutrient-deplete conditions and how the nutrient encounter history matters for individual movement decisions requires long-term tracking of cells over large spatial domains. Inspired by the Argos satellite system, used to track animal movements at the planetary scale, we are developing a microfluidic platform to perform long-term observations (∼6 hours) of hundreds of individual bacteria over a centimeter-scale domain. This new approach, based on low-resolution multi-band fluorescence imaging, where a moving stage microscope scans over a microfluidic arena, will help us understand the decision-making strategies of individual bacteria in ecologically relevant scenarios. Similarly,

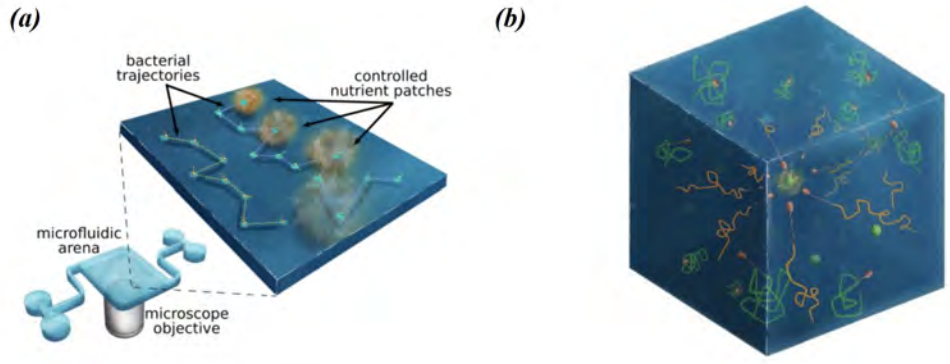

Figure 1: (a) microArgos: a novel platform for long-term cell tracking over a centimeter-scale domain. (b) 4D tracking of swimming microorganisms using digital holographic microscopy.

despite the importance of tracking microbes in 3D, we still lack intervention-free tools that would enable tracking without the use of markers or pre-existing libraries. We developed a label-free method, based on a combination of digital holographic microscopy with a point 3D detection method, to track swimming microorganisms and biological microstructures in 3D space and time. The approach is characterized by high precision (0,1μm lateral and 0,2μm axial resolution) and enables measurement of complex 3D structures such as sperm cell flagella.

Physiological differentiation during bacterial swarm development

K. Drescher[1], H. Jeckel[1], K. Nosho[1], K. Neuhaus[1], D. Saha[1], D.J. Skinner[2], A.D. Hastewell[2], J. Dunkel[2]

[1] Biozentrum, University of Basel, Switzerland
[2] Department of Mathematics, Massachusetts Institute of Technology, USA

Microbial life on earth primarily exists in the context of structured communities, which, even when comprised of genetically identical cells, often exhibit distinct microenvironments and phenotypic heterogeneity among its members. Identifying subpopulations and disentangling the complexity of interactions between them requires spatiotemporal readouts, which are challenging to experimentally acquire due to the destructive nature of most spatial sampling methods. In this study, we introduce an approach to repeatedly sample from the same developing Bacillus subtilis swarm in a non-destructive manner, obtaining a detailed map of spatiotemporal physiology in addition to bright-field microscopy and metabolite measurements. The combination of these different datasets allows us to identify distinct subpopulations within the swarm and reveals, among other insights into swarm development, a cross-feeding of metabolites in space and time.

Density fluctuations in bacterial binary mixtures

S. Espada Burriel, V. Sourjik, R. Colin

Max Planck Institute for Terrestrial Microbiology, Marburg, Germany

In wild environments, bacteria are found as mixtures of motile and sessile species, which interact physically and chemically to give rise to complex community organization. Very little is understood of the role of physical interactions in these processes: Numerical works on dry active matter and experiments on colloidal systems have shown that the activity of the active particles may affect the spatial distribution of passive particles with which they are mixed. However, the physical behavior of binary mixtures of bacteria remains largely unexplored. In our study, we present a novel phenomenon in which non-motile bacteria form large density fluctuations when mixed with motile bacteria, distinct from the aforementioned behaviors (Fig. 1). We systematically explored the phase diagram of the mixtures in experiments combining microfluidics, fluorescence (confocal) microscopy, quantitative image analysis and parameter tuning by genetic engineering. Our experimental results show that the emergence of these large density fluctuations of the non-motile cells in presence of motile cells is controlled by hydrodynamic interactions between the motile and non-motile cells and by the sedimentation of the non-motile cells, possibly because it breaks the systems symmetry.

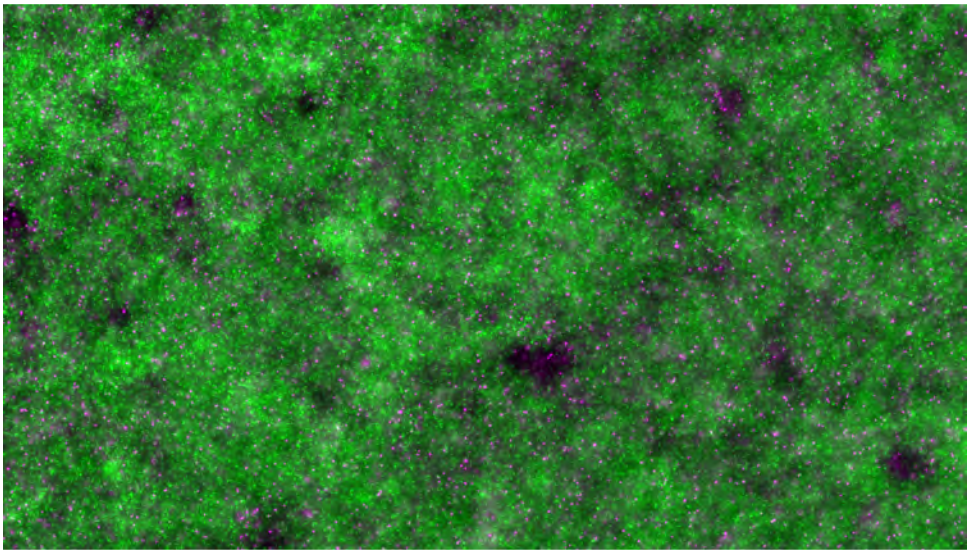

Figure 1: Density fluctuations on the non-motile strain in binary mixtures of motile and non-motile cells in bacterial binary mixtures.

Foraging trade-offs in flagellates, and the role of flagella in foraging

T. Kiørboe[1], **S. Suzuki-Tellier**[1], **F. Miano**[1], **S. S. Asadzadeh**[1], **A. Andersen**[1], **R. Schuech**[2]

[1] Centre for Ocean Life, DTU Aqua, Technical University of Denmark
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Flagellated unicellular protists play a key role in shaping the structure and function of marine microbial communities. They are the main consumers of bacteria and other picoplankton in the ocean and are themselves prey to zooplankton. They are equipped with one or a few flagella that may propel the cell through the water and – maybe more important – generate a feeding current that facilitates prey encounter. The flagella also perceive prey cells and capture and handle the prey. At the same time the feeding current generates a fluid disturbance that may be perceived by the flagellates' flow-sensing predators, hence the foraging trade-off. In this project we examine the fluid dynamics of foraging and the associated trade-offs for flagellates that are distributed across the eukaryotic tree of life. This encompasses a huge diversity in flagellar kinematics, beat shape, and morphology (naked, hairy, with vane). We use a combination of high-speed video-microscopy, flow visualisation, and CFD (Fig. 1) to describe foraging, understand the underlying fluid dynamics, and quantify the trade-offs. The presentation will summarize our main recent findings, including the role of hairs and vanes and the significance of beat shape and kinematics for generating a feeding current and 'noise' [1–3], the role of the flagella in perceiving and handling prey [4], and the ability of some flagellates to escape predators through high-speed escape jumps propelled by the flagella.

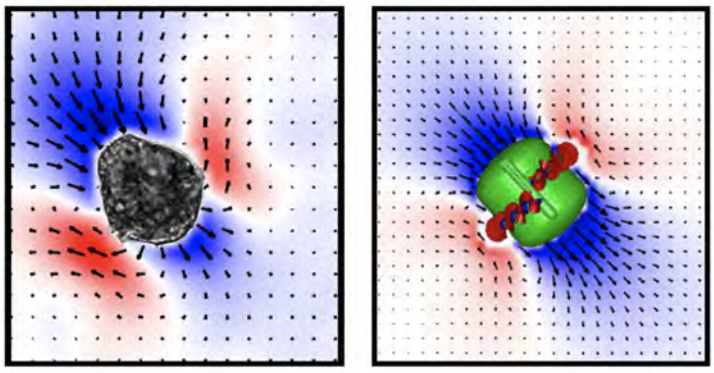

Figure 1: Observed (left) and simulated (right) flow (arrows) and vorticity (colour) fields generated by a swimming dinoflagellate. Schuech et al. in preparation.

References

[1] S. S. Asadzadeh, J. H. Walther, A. Andersen, and T. Kiørboe, Hydrodynamic Interactions Are Key in Thrust-Generation of Hairy Flagella, Physical Review Fluids **7**, 073101 (2022).
[2] L. T. Nielsen, S. S. Asadzadeh, J. Dölger, J. H. Walther, T. Kiørboe, and A. Andersen, Hydrodynamics of Microbial Filter Feeding, Proc Natl Acad Sci USA **114**, (2017).
[3] L. T. Nielsen and T. Kiørboe, Foraging Trade-Offs, Flagellar Arrangements, and Flow Architecture of Planktonic Protists, Proceedings of the National Academy of Sciences **118**, e2009930118 (2021).
[4] S. Suzuki-Tellier, A. Andersen, and T. Kiørboe, Mechanisms and Fluid Dynamics of Foraging in Heterotrophic Nanoflagellates, Limnology and Oceanography **67**, 1287 (2022).

Phototaxis of the dominant marine pico-eukaryote Micromonas sp.: from population to single cell

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Micromonas is a unicellular photosynthetic pico-eukaryote globally dominant in marine ecosystems. Although previously been described as strongly phototactic, its phototactic strategy and indeed its motility are currently poorly understood. It is also unclear how light is detected, given that the tiny cells do not possess the eyespot typical of larger unicellular green algae: the organism is essentially blind. Here we first perform population-scale phototactic experiments to show that this organism actively responds to a wide range of light wavelengths and intensities. These population responses follow a simple drift-diffusion framework displaying a all-or-none-type response to light. Single-cell tracking experiments detail thoroughly the way Micromonas sp. explore its environment. The extracted motility resembles the run-and-reverse styles of motion commonly observed in marine prokaryotes but with long stopping periods between runs and no specific pattern in the sequence of reversals. The associated peculiar microscopic changes upon photostimulation are finally described and integrating those into jump-diffusion simulations produces phototactic drifts that are quantitatively compatible with those obtained experimentally at the population level. These drifts match the natural sedimentation speed of cells, providing the cells with a mechanism to stay within the photic zone. We conclude with a perspective on the possible mechanism that the cells might utilize to recognise where the light is coming from.

Evidence for rotary-motor powered gliding motility in a filamentous cyanobacterium

J. Rosko, S. Duxbury, M. Coates, O. Soyer

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Several species of filamentous cyanobacteria are able to glide over surfaces. This mode of motility does not require the presence of flagella and always comes in tandem with slime secretion. However, the exact mechanism is poorly understood and it may depend on the species, as some species rotate during motion, while others do not. We studied a novel cyanobacterium isolated from a local water body. Similar species were previously thought to move using pores to generates propulsive "slime jets" or glide using type IV pili. We combined light microscopy with analytical techniques and found evidence for a completely different model where, similar to Myxobacteria, molecular motors generate contact forces at the cell-substrate interface.

Thursday Nov. 3

On the origins of ciliary metachronism

K. Wan IS

University of Exeter, UK

Cilia are ubiquitous, hair-like protrusions attached to cells. Interactions between cilia and ciliated tissues mediate a variety of physiological flows that may be external (directed outside of the organism), or internal (to facilitate internal processes such as feeding or mucociliary clearance). Whenever multiple cilia exist in close proximity they will invariably interact, leading to the emergence of many types of local and global coordination patterns. Often, the mechanism of this interaction or coupling is mysterious and highly system-dependent. Adjacent appendages can communicate hydrodynamically through the fluid, but they can also do so via mechanical interactions between cilia, or via basal elastic or cytoskeletal linkages through the cell or tissue surface. In this talk we will explore manifestations of ciliary metachronism in diverse organisms ranging from single-celled eukaryotes to the larvae of marine invertebrates. Travelling waves of ciliary activity are common in both natural and artificial ciliary arrays, where typically a robust direction is maintained between the polarised ciliary beat and the wave propagation direction. We focus here on the origins and functional consequences of diaplectic metachrony - wave direction transverse to the main beat direction – a form of coordination that is least well-understood, despite being highly prevalent in biological microswimmers.

Self-organization of bacterial mixtures interacting via quorum-sensing

A. Dinelli[1], J. O'Byrne[1,2], A. Curatolo[3], Y. Zhao[4], P. Sollich[5,6], J. Tailleur[1,7]

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[7] Department of Physics, Massachusetts Institute of Technology, Cambridge, Massachusetts, USA

Understanding the self-organization of motile entities is a key problem in active matter, with applications ranging from pattern formation in biological systems to the engineering of soft active materials. Recently, the regulation of motility in bacteria via quorum sensing interactions (QS), i.e. by the local density of their peers, has shown to be a promsing pathway to spatial structuring in these systems. So far, the literature on the topic has mostly focused on single-component active systems; however, in order to obtain more complex structures like the ones encountered in biology, heterogeneity should be accounted for. Here we propose an analytical and numerical study of the self-organization of mixtures of QS run-and-tumble particles. We show the emergence of a rich large-scale phenomenology, including static and dynamic patterns. First, we derive a microscopic condition for restoring action-reaction at the macroscopic scale, which endows the system with an effective free energy functional. The latter allows us to rationalize the static patterns observed in our simulations and to predict the corresponding phase diagram. On the contrary, in the presence of non-reciprocal interactions we derive a sufficient condition to observe the emergence of travelling patterns, from steady travelling waves to intermittency and band chaos.

References

[1] A. Dinelli, J. O'Byrne, A. Curatolo, Y. Zhao, P. Sollich, J. Tailleur, Self-organization of bacterial mixtures in the presence of quorum-sensing interactions (submitted to PRL). Preprint: arXiv:2203.07757
[2] A. Curatolo, N. Zhou, Y. Zhao, C. Liu, A. Daerr, J. Tailleur, J.-D.Huang, Nature Physics **16**, 1152-1157, (2020)

Bacterial Olympics: Multiflagellarity allows bacteria to maintain constant motility across cell size

S. Kamdar[3], D. Ghosh[3], W. Lee[2], M. Tatulea-Codrean[1], Y. Kim[4], S. Ghosh[3], Y. Kim[3], T. Cheepuru[3], E. Lauga[1], S. Lim[5], X. Cheng[3]

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In Olympic swimming, size typically matters: podiums are occupied by the tallest swimmers who use their long limbs to push the fluid and move faster. In contrast to olympic athletes who swim at high Reynolds numbers of Re $\sim 10^6$, bacteria swim at Re $\sim 10^{-5}$, where viscous drag dominates the hydrodynamics and suggests a decrease in swimming speed of bacteria of large sizes due to the elevated drag on their bodies. Here, we measure the swimming speed of E. coli, a model multiflagellar bacteria, and we find that the population-averaged swimming speed of bacteria is constant over a three-fold increase in their body length. We show how bacteria utilize the increasing number of flagella to regulate flagellar motor load, which results in higher rotational speeds as well as a constant swimming speed for large cell sizes. We perform simulations that reveal the role of interflagellar interactions in controlling the increase of rotational speeds. Our mechanism predicts that the swimming speed of uniflagellar species decreases with increasing cell size, which we verify directly through experiments on several strains of uniflagellar bacteria. Until now, it is believed that the presence of additional flagella does not confer strong benefits for swimming speed. The stark difference between the uniflagellar and multiflagellar swimming demonstrated in our study provides new insight into the crucial role of multiflagellarity in maintaining optimum motility for navigation and survival of bacteria in their native habitats.

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Motile cilia waves: creating and responding to flow

P. Cicuta, N. Pellicciotta, E. Causa, D. Liu, B. Meadowcroft

University of Cambridge, Cambridge, UK

Motile cilia are active filaments present on the surface of various human organs, where they perform crucial functions by driving surface flows. Structurally, they are conserved across the eukaryotes. Cilia can affect each other, for example leading to phase locking of their beating, by the forces they exert on each other through the fluid and in some cases through the cell cytoskeleton. Some beautiful physics has been developed by various teams in the last decade to understand how the details of beating on each cilium can lead to specific phase locking, and to the emergence of collective waves. In recent work we have explored the role of external flows, both oscillatory and constant. Analogies can be drawn between these flows and the effect of external magnetic fields in magnetic systems. We present both experimental results, and numerical explorations of a simple class of "rower" models of motile cilia.

Synthetic adhesion logic, self-assembly of bacterial swarms, and multicellular tiling patterns

I. Riedel-Kruse IS

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Multicellular systems, from bacterial biofilms to human organs, form spatial patterns and interfaces to achieve complex functionality, promising applications like programmable biomaterials, artificial tissues, and metabolic consortia [1]. Our ability to rationally engineer such active matter is still limited. My lab recently developed the first synthetic and optogenetic approaches to control cell-cell and cell- surface adhesion for bacterial self-assembly [2] and patterning ('Biofilm Lithography') [3]. I will discuss the biophysical characterization of these tools and their applications to investigate cooperative antibiotic responses in biofilms. I will then demonstrate a synthetic 4-bit cell-cell adhesin logic to experimentally program and mathematically model universal two-dimensional interface patterns [4]. These interfaces are generated through a swarming adhesion mechanism that enables precise control over interface geometry as well as adhesion-mediated analogs of developmental organizers and morphogen fields. Utilizing tiling and four-color mapping concepts, I present algorithms for creating versatile target patterns. Remarkably, a minimal set of four adhesins suffices to program arbitrary tessellation patterns, implying a low critical threshold for the engineering and evolution of complex multicellular systems.

References

[1] Kim H, Jin X, Glass DS, Riedel-Kruse IH, Engineering and modeling of spatio-temporal patterns and morphologies in multicellular systems Current Opinion in Genetics & Development; 2020, **63**, 95.
[2] Glass D, Riedel-Kruse IH. A genetically encoded adhesin toolbox for programming multicellular morphologies and patterns. Cell; 2018. 174 (3) 649–658.
[3] Jin X, Riedel-Kruse IH. Biofilm Lithography: High-resolution cell patterning via optogenetic adhesin expression. PNAS; 2018. **115** (14) 3698-3703.
[4] Kim H, Skinner DJ, Glass DS, Hamby AE, Stuart BAR, Dunkel J, Riedel-Kruse IH* Synthetic 4-bit adhesion logic and universal multicellular interface patterning Nature; 2022. **608**, 324-329.

Chromatographic Separation of Active Polymer-like Worm Mixtures by Contour Length and Activity

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The convective transport rate of polymers through confined geometries depends on their size, allowing for size-based separation of polymer mixtures (chromatography) [1-2]. Here, we investigate if mixtures of active polymers can be separated in a similar manner based on their activity. We use thin living worms T. tubifex [3-4] as a model system for active polymers and study the transport of these worms by an imposed flow through a channel filled with a hexagonal-pillar array. The transport rate through the channel depends strongly on the degree of activity, an effect that we assign to the different distribution of conformations sampled by the worms depending on their activity. Our results demonstrate a unique way to sort mixtures of active polymers based on their activity and provide a versatile and convenient experimental system to investigate the hydrodynamics of active polymers.

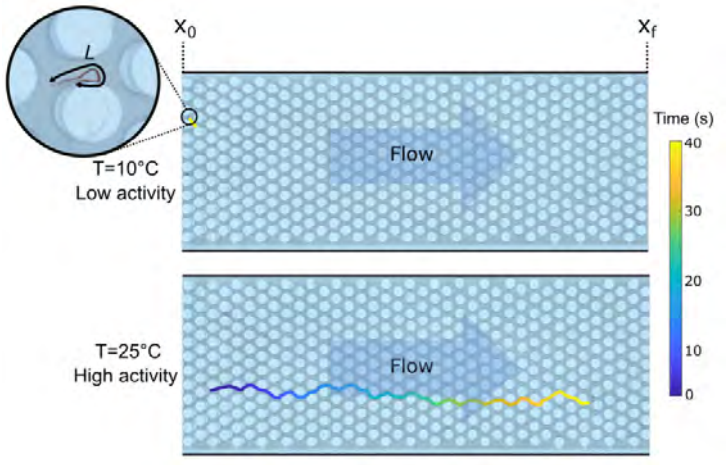

Figure 1: Hydrodynamic pillar array experiment with active polymerlike worms. Trajectories in the channel for the same worms at two different temperatures (top, T = 10^0C and bottom, 2^0C) in time (color gradient). The continuous line shows the tracked paths along the channel at the two different temperatures for the same amount of time (40 s); decreasing temperature increases the elution time.

References

[1] M. C. VandeSande, D. J. Pasut, and H. W. de Haan, Electrophoresis **38**, 2488 (2017).
[2] D. Berek, Journal of separation science **33**, 315 (2010).
[3] A. Deblais, S. Woutersen, and D. Bonn, Physical Review Letters **124**, 188002 (2020).
[4] A. Deblais, A. C. Maggs, D. Bonn, and S. Woutersen, Physical Review Letters **124**, 208006 (2020).

Digital Holographic Microscopy 4D tracking – and much more

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Digital Holography Microscopes (DHM) are well known in the field of micro swimmers motility for their ability to measure motions in 3D (4D tracking). But additionally, the DHM can provides much more information on the organisms activity, health, and morphology. This presentation

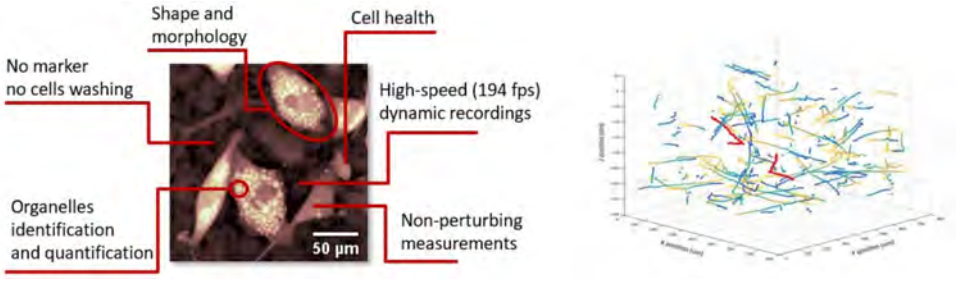

Figure 1: Liquid droplet in adipocytes quantification and 4D bacteria tracking by DHM.

reviews DHM applications in life sciences that could be exploited simultaneously to 4D tracking to provide physio pathological information on microorganisms. Cell cycle quantification, cytotoxicity assays, high content screening, and cell dynamics will be presented [1-4].

References

[1] Rappaz B, Cano E, Colomb T, et al. Noninvasive characterization of the fission yeast cell cycle by monitoring dry mass with digital holographic microscopy. J Biomed Opt. 2009;14(3):034049. doi:10.1117/1.3147385

[2] J. Kühn J, Label-free cytotoxicity screening assay by digital holographic microscopy. Assay Drug Dev Technol. 2013 Mar;11(2):101-7. doi: 10.1089/adt.2012.476. Epub 2012 Oct 12. PMID: 23062077; PMCID: PMC3593696.

[3] Pavillon N, Kühn J, Moratal C, et al. Early cell death detection with digital holographic microscopy. PLoS One. 2012;7(1):e30912. doi:10.1371/journal.pone.0030912

[4] Rappaz B, Barbul A, Emery Y, et al. Comparative study of human erythrocytes by digital holographic microscopy, confocal microscopy, and impedance volume analyzer. Cytometry A. 2008;73(10):895-903. doi:10.1002/cyto.a.20605

Collective photoprotection through light-induced phase separation in a phototactic micro-algae

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Excess of light can be hazardous for photosynthetic organisms. When intensity is too high, the motile micro-algae Chlamydomonas reinhardtii therefore reorients itself to swim away from the incident light. We recently discovered that a suspension of such migrating cells can be unstable, whereby small spatial fluctuations in cell density can quickly trigger the phase separation of the system and the formation of dynamic branching patterns, whose features depend on the global cell density, light intensity and medium viscosity. This new kind of instability can be understood from the strong coupling between cell density and light fields through both negative phototaxis and light absorption by the individual cells. Our model shows the destabilization of the system for critical control parameters and finely reproduces the experimental data. On the physiological side, algae inside the dense phase are protected from the light stress, showing that on short timescales, phototaxis efficiently contributes to photoprotection through non-trivial reponses at the population level.

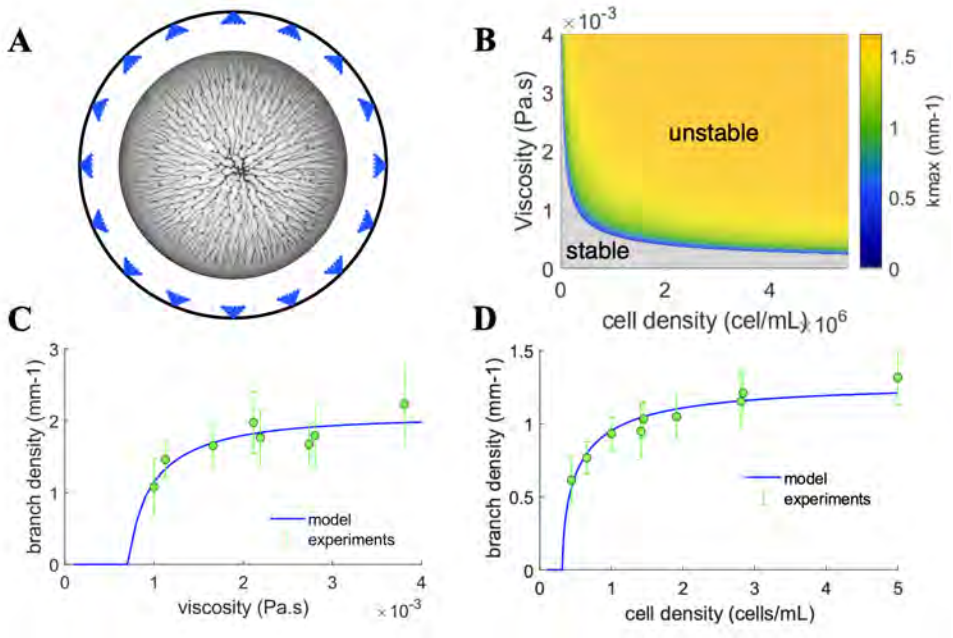

Figure 1: A: a small Petri dish (3.5cm diameter) is illuminated by a ring of LED. A suspension of negatively phototactic algae is unstable, leading to branch formation within $\sim$ 1min. B : phase diagram of the system. C and D: branch density at the onset of destabilization as a function of cell density (C) or viscosity (D)

Motility in anisotropic media

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Bacteria motility depends on genetic and biochemical factors, but also on the physical parameters of the medium in which they swim, including viscosity or the presence of walls. In water, Escherichia coli (E-coli) bacteria exhibit a "run and tumble" mechanism that yield random trajectories reminiscent of a Brownian walk. This mechanism can be dramatically modified in biological media, such as the human body, where the local environment of the bacterium can be strongly anisotropic, enhancing motion in one preferential direction. Liquid crystals have recently emerged as an in-vitro model system where to study fundamental questions regarding how bacteria swim in those complex biological conditions [1]. In this talk, I will show you the swimming mechanism of a single E-coli bacterium constrained to move along the director field of a lyotropic chromonic liquid crystal that is confined to a planar cell. In such an environment, the spontaneous "run and tumble" motion of the bacterium is frustrated by the elasticity of the liquid crystal, which prevents flagella from unbundling. Interestingly, in order to change direction, bacteria execute a reversal motion along the director field, driven by the relocation of a single flagellum to the other side of the bacterial body [2]. Because of the aligning effect of the liquid crystal, bacteria collectively behave as a "living liquid crystal", exhibiting fascinating structural and dynamical properties [3, 4]. Some of these properties can also be found in active nematics, where bundles of microtubules are set into motion by the action of molecular motors [5]. In the second part of my talk, I will show you how we can control the dynamics of these anisotropic active media using confining walls [6, 7].

References

[1] A. Kumar et al., Mol. Cryst. Liq. Cryst. **574**, 33 (2013)
[2] M. Goral et al., J. R. Soc. Interface, arXiv:2206.10316 (2022) [3] S. Zhou et al., PNAS **111**, 1265 (2014)
[4] C. Peng et al., Science **354**, 882 (2016)
[5] T. Sanchez et al., Nature **491**, 431 (2012)
[6] J. Hardoüin et al., Commun. Phys. **2**, 121 (2019)
[7] J. Hardoüin et al., Soft Matt **16**, 9230 (2020)

Sperm chemotaxis in marine species is optimal for physiological flow rates according to the theory of filament surfing

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Many motile cells navigate in complex environments along concentration gradients of signaling molecules. This chemotaxis has been studied extensively both experimentally and theoretically, yet mostly for idealized conditions of perfect chemical gradients. But under physiological conditions, concentration fields are subject to distortions, e.g., by turbulent flows in the ocean. Recent experiments with bacteria[1] and sperm cells from marine invertebrates[2,3] have surprisingly revealed the existence of an optimal turbulence strength at which the chemotaxis is more effective than for still water conditions with perfect gradients. Yet to date, the mechanistic cause for this optimum is not known. We present a general theory of chemotactic navigation of sperm cells in external flow. We characterize how external flow distorts concentration fields into long filaments, and show how chemotaxing cells can subsequently 'surf' along these filaments towards a chemoattractant source. Stronger flows make concentration filaments longer, but also thinner; together, these two counter-acting effects set an optimal flow strength. The optimum predicted by our theory matches flow measurements in shallow coastal waters. Our theory quantitatively agrees with two previous fertilization experiments in Taylor-Couette chambers[2,3] and provides a mechanistic understanding of these early experiments. 'Surfing along concentration filaments' could be a paradigm for navigation in complex environments in the presence of turbulent flow.

References

[1] J. R. Taylor & R. Stocker, Science **338**, 675, (2012)
[2] R. K. Zimmer & J. A. Riffell, PNAS **108**, 13200, (2011)
[3] K. S. Mead, M. W. Denny, Biol. Bull. **188**, 46, (1995)

Interplay between phototaxis and photokinesis in light-driven E. coli

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From theory [1] we know that if the speed of non-interacting swimmers varies spatially, $v(r)$, then their density $\rho(r)$ satisfies $\rho(r) \propto 1/v(r)$. Recently, this relation was confirmed in experiments using a smooth swimming photokinetic E. coli strain [2]. These bacteria express the protein proteorhodopsin that allows through light stimuli to control the energy to drive the flagellar motor [3]. Furthermore, it was also observed that if proteorhodopsin is expressed in a strain with an intact chemotaxis pathway the density modulation was completely different from the theory [2]. We study the origin of this deviation, and we observe that these bacteria are phototactic and they tend to reduce their tumbling rate when they experience an increasing light intensity. In the same strain we observe that the swimming speed is higher at higher light intensity (photokinesis). The combination of these effects results in an interplay between a photophilic and photophobic behavior. We study this phenomenology in sinusoidal light intensity landscapes, and we observe that the spatial frequency of the pattern affects the fate of the cell's density profile (Fig.1). For "slowly" changing patterns bacteria tend to behave as if photophilic, while for high spatial frequency modulation is the photokinetic mechanism to dominate resulting higher concentration in the dark. We develop a 1D run-and-tumble model including phototaxis and photokinesis that describe experimental data. Moreover, by also deleting the chemotaxis receptor Aer we can obtain a purely photokinetic run-and-tumble strain without any phototaxis.

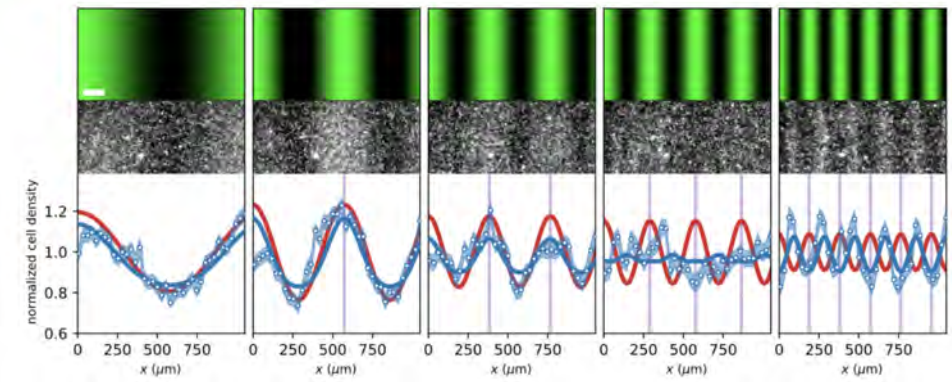

Figure 1: Bacterial density modulation under sinusoidal light patterns at different spatial frequency. The relation between velocity profiles (red) and density profiles (blue) is affected by the pattern.

References

[1] Tailleur, J. & Cates, M. Phys. Rev. Lett. **100**, 218103 (2008)
[2] Arlt, J. et al. Nat Commun **10**, 2321 (2019)
[3] Frangipane, G. et al. eLife **7**:e36608 (2018)

Bacterial micro-swimmers in colloidal liquid crystals

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Active matter are systems whose constituents are able to harvest energy from their environment to generate self-propelled motion. Such out-of-equilibrium systems exist in the Nature at different scale ranging from macroscopic (bird flocks, school of fish ...) to microscopic (bacteria, spermatozoa ...) scale. Motion of bacteria in a complex fluid is a common occurrence in life and happens, for example, when they are moving through the human body to infect it. Although it is a common occurrence, little is known about the dynamics of such active particles in complex fluids. To tackle this problem, we have been studying the swimming of the bacteria Bacillius Subtilis in a complex fluid of colloidal liquid crystal through optical microscopy and single particle tracking. The liquid crystalline phase used in our work is formed by suspensions of fd viruses, widely used for many years in soft matter as a model system of rod-like particle [1]. In addition to the visualization of the bacteria body, our experimental system allows us to have a direct observation of every key component labelled with "orthogonal" fluorescent dyes: bacteria flagella which generate the motion, as well as the viral rod-shaped colloids. Single particle tracking of the micro-swimmers allows to determine both the velocity and the wobbling motion of the bacteria in presence of colloidal particles. Recent work done on bacteria with molecular liquid crystal has shown the possibility to monitor the swimming direction [2] thanks to the liquid crystal orientation. We will address this question in the case of colloidal liquid crystal, and we will also show the importance of the colloidal scale for the swimming speed of the bacteria [3].

Acknowledgments We would like to thank Professor Daniel Kearns from the Indiana University Bloomington for providing us with the bacteria strain. This project has been funded by the french national research agency (ANR).

References

[1] Barry, E. et al. "A Model Liquid Crystalline System Based on Rodlike Viruses with Variable Chirality and Persistence Length." Soft Matter, vol. 5, no. 13, June 2009, pp. 2563–70.
[2] Zhou, S. et al. "Living Liquid Crystals." Proceedings of the National Academy of Sciences, vol. 111, no. 4, Jan. 2014, pp. 1265–70.
[3] Kamdar, S. et al. "The Colloidal Nature of Complex Fluids Enhances Bacterial Motility." Nature, vol. 603, no. 7903, Mar. 2022, pp. 819–23.

Active turbulence in bacterial suspensions under the effect of an external chemical gradient

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Collective motion is an emergent phenomena observed in myriad biological systems across many length scales from birds to bacteria. The active constituents in the group provide energy to the system at the individual level via self-propulsion. An archetypal example of this is so-called "active turbulence" observed in dense suspensions of microscopic swimming bacteria such as Escherichia coli [1] (Figure 1, left). This emerges due to hydrodynamic interactions between the microswimmers and takes the form of high-speed jets and large-scale vorticies [2]. In isolation, an individual microswimmer travels ballistically ("runs") until it randomly reorients ("tumbles"). In their typical environment, bacteria such as E. coli direct their movement by sensing their surroundings, specifically following chemical gradients, known as "chemotaxis". This is done by extending the effective length of runs that happen to orient in the direction of the chemical gradient, which causes a net drift of the swimmer toward the chemoattractant [3, 4]. Here we investigate the impact of chemotactic behaviour on the presence of the active turbulent state in a bacterial suspension using large-scale, particle-resolved, three-dimensional lattice Boltzmann simulations of model microswimmers. We find that chemotaxis is disrupted by the active turbulent state, inhibiting chemically directed motility at high densities, in agreement with previous experimental observations [5]. Furthermore, we investigate strategies to circumvent this suppression of bacterial motility and improve chemotactic efficiency.

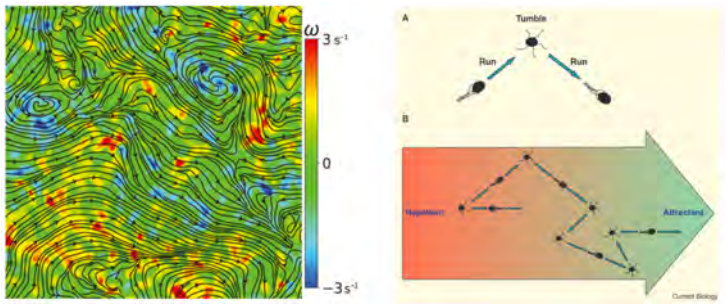

Figure 1: Left: active turbulence in E. coli showing fluid streamlines and vorticity ω [1]. Right: chemotaxis of run-and-tumble bacterium in chemical gradient [6].

References

[1] Y. Peng, Z. Liu, X. Cheng, Sci. Adv. 7, eabd1240 (2021).
[2] D. Bárdfalvy, et. al., Soft Matter 15, 7747–7756 (2019).
[3] G. Subramanian, D. L. Koch, and S. R. Fitzgibbon, Phys. Fluids 23, 041901 (2011).
[4] T. V. Kasyap and D. L. Koch, Phys. Rev. Lett. 108, 038101 (2012).
[5] R. Colin, K. Drescher and V. Sourjik, Nat. Commun. 10, 5329 (2019).
[6] D. J. Webre, P. M. Wolanin and J. B. Stock, Curr. Bio. 13, R47–R49 (2003).

Emergence and scaling of collective flow patterns in active bacteria suspensions

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Understanding individual and collective macroscopic transport properties of motile micro-organisms in various environments is a timely question, relevant to many ecological, medical and technological situations.The existence of microscopic sources of energy borne by the motile character of these micro-swimmers is driving self-organization processes at the origin of original emergent phases and unconventional macroscopic properties leading to revisit many standard concepts in the physics of suspensions. In this presentation, I will discuss a recent exploration on the question of spontaneous formation of large scale collective motion in relation with the rheological response of active suspensions [1]. The question of the maximal spatial extension that can be reached by spontaneously forming vortical structures will be addressed and related to the generic predictions of active fluid hydrodynamics.

References

[1] Vincent A. Martinez et al. "A combined rheometry and imaging study of viscosity reduction in bacterial suspensions". In: Proc. Natl. Acad. Sci. (USA) **117**.5 (2020), pp. 2326–2331.

Gyrotactic plankton cells in turbulence: the effects of motility, shape and fluid inertia

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A detailed understanding of the physical mechanisms driving motile species to migrate vertically towards the surface allows better quantification of biogeochemical fluxes across the ocean. We focus on marine phytoplankton cells that are motile under gyrotactic forcing. Some species spontaneously swim in the direction opposite to gravity [1]. Gyrotaxis is originating either from morphological properties (elongated shape, density heterogeneity) [2] or the coupled effect of swimming and settling which results in a torque induced by fluid inertia on such swimmers [3]. We analysed the equilibrium orientation of swimmers in quiescent fluid (fig.1a - they spontaneously swim in the direction opposite to gravity) and the mean orientation in turbulent flows using direct numerical simulations. Similar to well-known gyrotaxis mechanisms, the effect of fluid inertial torque can be quantified by an effective reorientation time scale which is close to Kolmogorov time scale when preferential vertical alignment is strong. Based on numerical simulations of hundreds of thousands of micro-organisms swimming in homogeneous isotropic turbulence, we will comment on the different sources of gyrotactic induced spatial clustering [2,3] and vertical migration [4]. Our findings suggest that the fluid inertial torque is a new mechanism of gyrotaxis that stabilizes the upward orientation of micro-swimmers such as plankton. Some specific configurations lead to the accumulation of elongated cells in upwelling flow regions (fig. 1b) enhancing their ability to move across turbulence towards the ocean surface.

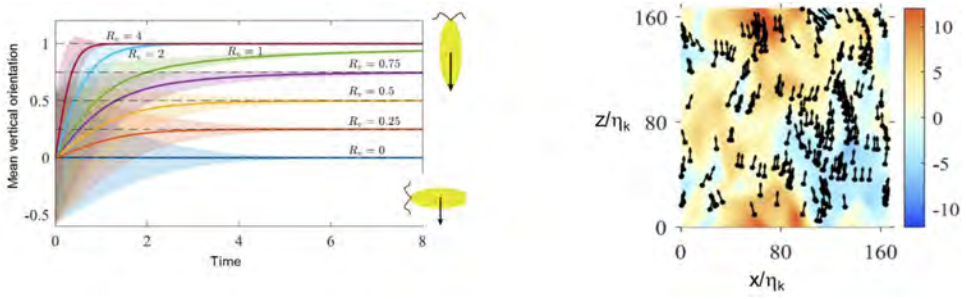

Figure 1: a) Mean orientation of swimmers in quiescent water for different ratios of swimming to settling speed. b) Snapshot of elongated swimmers in turbulence (colorbar corresponds to local vertical fluid velocity).

References

[1] Kessler J.O. (1985), Nature - 313, 218–220.
[2] Durham W. M., Climent E., Barry M., De Lillo F., Boffetta G., Cencini M. and Stocker R., (2013) Nature Communications - 4, 2148.
[3] Qiu J., Z. Cui, E. Climent, and L. Zhao. (2022) Phys. Rev. Research 4, 023094.
[4] Lovecchio S., Climent E., Stocker R. and Durham W. M. (2019) Sci. Adv. - 5: eaaw7879.

Mixed-species bacterial swarms – an interplay of mixing and segregation across scales

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Ben Gurion University of the Negev, Israel

Bacterial swarms are a highly-researched example of natural active matter. In particular, the interplay between biological interactions and the physics underlying the swarming dynamics is of both biological and physical interest. We study mixed swarms of Bacillus subtilis and Pseudomonas aeruginosa, and Bacillus subtilis and Serratia marcescens. We find intricate interactions between the species, showing both cooperation and segregation across different spatial and temporal scales. On one hand, even though axenic colonies grow on disparate time scale, an order of magnitude apart, the two-species swarm together, forming a single, combined colony. However, the rapidly moving populations are locally segregated, with different characteristic speeds and lengths (or cluster sizes) that depend on the ratio between the species. Comparison with controlled mutant strains suggest that both the physical and known biological differences in species characteristics may not be enough to explain the segregation between the species in the mixed swarm. We hypothesize that the heterogeneous spatial distribution is due to some mechanism that enables bacteria to recognize their own kind, whose precise origin we could not identify.

References

[1] Jose et al. Phys Rev E **105**, 064404 (2022)
[2] Natan et al. Sci Rep, in press (2022)

Friday Nov. 4

Self-organization and flow in living cells

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Flows in the fluidic interior of living cells can serve function, and by their structure shed light on how forces are exerted within the cell. Some of these flows can arise through novel collective instabilities of the cytoskeleton, that set of polymers, cross-linkers, and molecular motors that underlie much of the mechanics within and between cells. I'll discuss experiments, mathematical modeling and analysis, and simulations of two such cases. One is understanding the emergence of cell-spanning vortical flows in developing egg cells, while the other arises from studying the nature of force transduction in the dynamics of microtubule arrays inside of synthetic cells. Both show the importance of polymer density in determining dynamics and time-scales, and have required the development of new coarse-grained models and simulation methods.

Evolution of microswimmer designs in distinct micro-environments

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An enormous range of parasitic trypanosome species infect virtually all animals, and in humans they cause fatal diseases. African trypanosomes, transmitted by the notorious tsetse fly, cause sleeping sickness in humans. These trypanosomes go through several genetically programmed stage transitions in the mammalian host and in the insect vector. All life cycle stages are basically variations of the same design principle, having a single flagellum uniquely attached to the spindle-shaped cell body. However, the movement possibilities and characteristics differ considerably between the trypanosome forms. We therefore hypothesise that evolution has shaped the individual parasite stages to manoeuvre in different microenvironments, such as the tissue spaces of human skin [1] and adipose tissue, the bloodstream [2] and brain, and the complex digestive system of the tsetse fly [3]. Here we present experimental evidence supporting our hypothesis and highlight current challenges.

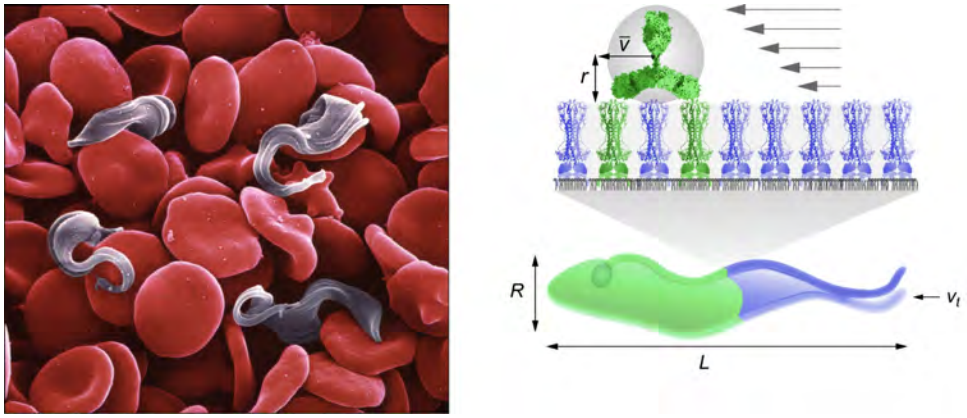

Figure 1: Trypanosomes (grey) actively and incessantly swim in extremely crowed environments, such as mammalian blood or tissue spaces [2]. In the host's bloodstream this directed motion is exploited for the hydrodynamic removal of host antibodies from the parasite's cell surface [4].

References

[1] C. Reuter, bioRxiv 2021.05.13.443986; doi: doi.org/10.1101/2021.05.13.443986
[2] J. Bargul, PloS Pathogens 12, doi: 10.1371/journal.ppat.1005448 (2014)
[3] S. Schuster, eLife 6, doi: 10.7554/eLife.27656 (2017)
[4] M. Engstler, Cell 131, doi: 10.1016/j.cell.2007.08.046 (2007)

Driven motion in complex environment

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Many bacteria have the ability to move in their environment in order to respond to their needs, be they nutrients or oxygen. Strikingly, bacteria exhibit a rich repertoire of swimming patterns, from run-and-tumble to run-reverse-flick. Which benefits come with a particular pattern is still an open question. Besides bacteria often have to move under mechanical constraints such as hydrodynamics or geometric constraints. Our understanding of their motion under such constraint is currently limited. Our goal is to explore those issues, using both a theoretical approach and an experimental investigation of magnetotactic bacteria. Those bacteria can be remotely oriented, so as to define a preferred direction of propulsion, making their transport properties extremely rich.

Collective swimming to the light

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Microscopic algae are commonly found in mud, puddles or lakes, and show great diversity in structural complexity. One of the simplest algae encountered is the unicellular Chlamydomonas, exhibiting two flagella whose beating enables them to swim in a breast stroke. One also finds Gonium pectorale, a colony made of 16 Chlamydomonas-like cells arranged in two concentric squares, with all flagella on one side of the plate. These colonies are among the first multicellular algae and their study offers an insight into the evolution from unicellular to coherent multicellular behaviour. Algae, like plants, get energy from photosynthesis: Gonium colonies take advantage of their motility to swim towards light, efficiently reorienting within a couple of seconds. However, the mechanism of this phototactic behaviour is not straightforward: how do 16 cells individually produce a coherent collective response? How are the flagella modulated to create an asymmetry in the swimming pattern, and how does it lead to reorientation? We experimentally investigate the phototaxis of Gonium, analysing their reorientation trajectory towards light. We compare those results to an analytical model and numerical simulations, describing with high precision the reorientation process.

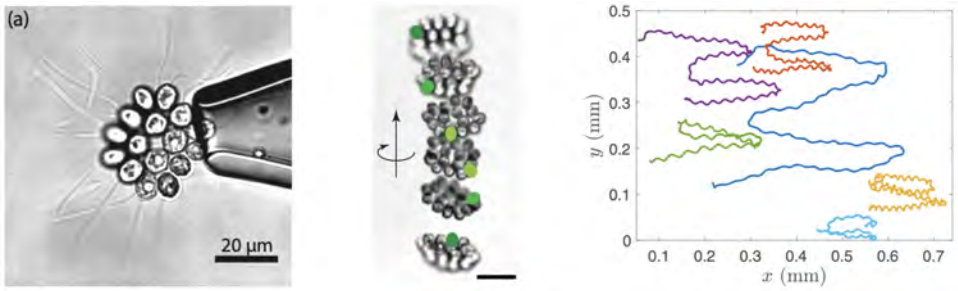

Figure 1: (left) Gonium colony isolated on a micropipette. (center) Colony swimming to the top, while rotating on itself as highlighted by the green spot following a specific cell.0.4$sbetweeneachimage.Scalebar$: 20μm. (right) Typical reorientation trajectories when light is shown on Gonium alternatively from the right and left sides every 20 s.

References

[1] H. de Maleprade, F. Moisy, T. Ishikawa and R.E. Goldstein. Motility and phototaxis of Gonium, the simplest differentiated alga, PRE **101**, 022416 (2020).

Explorations of motile helices at the microscale

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The motion of actuated elastic filaments in a fluid environment is a common element in motility at the microscale - both in biological and engineered systems. Examples include bacterial flagella propelling a cell body and engineered helical nano-propellers designed to penetrate mucosal tissue for drug delivery. Complex fluid environments and geometries, such as polymeric networks or confinement, can have dramatic effects upon the dynamics of filaments, whether rigid or flexible. In this talk we will present computational models of two intriguing systems: flexible helical filaments whose swimming performance improve when confined to a narrow tube, and rigid helical filaments that penetrate a polymeric network with the ability to remodel the material properties of the network as they move through it.

Swimming by Axonemal Beating

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From sperm cells to green Algae, propulsion of eukaryotic microswimmers[1] is commonly enabled by the same cytoskeletal structure called the Axoneme. It generates the sinusoidal beat that allow sperm cells to swim as well as the whip like motion of cilia on the surface of our lungs or green algae. In this talk, we explore the role of hydrodynamic interactions on axoneme enabeled swimming. As first example we look at sperm cells. It is the time-irreversibility of the flagellar beat and the interaction with the surrounding fluid that allows the sperm cell move forward and to navigate in complex environments [1,2]. The flagellar beat is usually planar and symmetric. However, the flagellum can have some time-averaged curvature or the beat pattern can contain a temporal second-harmonic component [3], and the beat-shape can become three-dimensional [4]. The planar or non-planar beat, as well as the average flagellung curvature have important consequences for the swimming behavior of sperm near surfaces [5] and in structured microchannels [6,7], as they strongly affect the ability of sperm to attach to surfaces, follow curved walls, or detach from walls with high curvature. Next, we turn our attention to a multiciliated microswimmer[8], where several cilia cover the surface of a spherical swimmer. We find that the resulting swimming speed is a highly non-trivial function of cilia number, arrangement, and coordination. As predicted from planar arrays of cilia, we find that metachronal coordination is key to enhancing propulsion, however the spherical topology does not allow for the simple most wave solution. We furthermore explore the propulsive speed stemming from self-organized coordination and find that small variations of cilia positioning has strong effects on propulsive speed.

References

[1] J. Elgeti et al., Rep. Prog. Phys. **78**, 056601 (2015)
[2] A. Gong et al., Phil. Trans. R. Soc. B37520190149 (2020)
[3] G. Sagiorato et al., Nat. Commun. **8**, 1415 (2017)
[4] A. Gong et al., EPJE **44**, 87 (2021)
[5] J. Elgeti et al., Biophys. J. **99**, 1018 (2010)
[6] S. Rode et al., New J. Phys. **19**, 013016 (2019)
[7] A. Wysocki et al., Phys. Rev. E **91**, 050302 (2015)
[8] S. Rode et al., EPJE **44**, 76 (2021)

Behavior of microswimmers under confinement

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Locomotion of microswimmers often takes place in a fluid environment under complex confinement conditions [1, 2]. Examples include bacteria within a cellular environment and parasites in a host organism. In such cases, steric and hydrodynamic interactions of swimmers with their surroundings play an important role, and may significantly affect their behavior. One interesting model is bacteria confined within a soft membrane (e.g., a vesicle), which is a dynamically deformable active system that partially resembles biological cells. Due to the forces exerted by microswimmers on the membrane, this system exhibits a variety of different non -equilibrium shapes with tether-like protrusions and highly branched, dendritic structures [3, 4]. Within tethers, microswimmers become tightly wrapped by the membrane, but are still able to propel forward. We employ theoretical analysis and mesoscopic simulations to better understand physical mechanisms of microswimmer propulsion under strong confinements. Our model shows that the force generation of swimmers under a strong confinement is localized around them, which should not result in pulling of long tethers as the generated force cannot propagate far enough toward the vesicle. Therefore, the formation of tethers in active vesicles by microswimmers does not rely only on the hydrodynamic force generation by the swimmers.

References

[1] J. Elgeti et al., Rep. Prog. Phys. **78**, 056601 (2015)
[2] G. Gompper et al., J. Phys. Condens. Matter **32**, 193001 (2020) [3] H.R. Vutukuri et al., Nature 586, 52 (2020)
[4] P. Iyer et al., Soft Matter **18**, 6868 (2022)

Dynamic stiffening of the flagellar hook

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For many bacteria, motility stems from one or more flagella, each rotated by the bacterial flagellar motor, a powerful rotary molecular machine. The hook, a soft polymer at the base of each flagellum, acts as a universal joint, coupling rotation between the rigid membrane-spanning rotor and rigid flagellum. In multi-flagellated species, where thrust arises from a hydrodynamically coordinated flagellar bundle, hook flexibility is crucial, as flagella rotate significantly off-axis. However, consequently, the thrust applies a significant bending moment. Therefore, the hook must simultaneously be compliant to enable bundle formation yet rigid to withstand large hydrodynamical forces. Here, we run high-resolution “bead assays" where we can follow the rotational speed of micron size beads tethered to individual motors of living immobilized E.coli cells with ms-resolution. Based on a simplified geometrical model for the system, we develop a novel analysis of hook fluctuations under dynamical conditions. This allows us to elucidate how the hook fulfills such double functionality: the hook shows a dynamic increase in bending stiffness (of one order of magnitude) under increasing torsional stress. Such strain-stiffening allows the system to be flexible when needed yet to reduce deformation under high loads, enabling high speed motility.

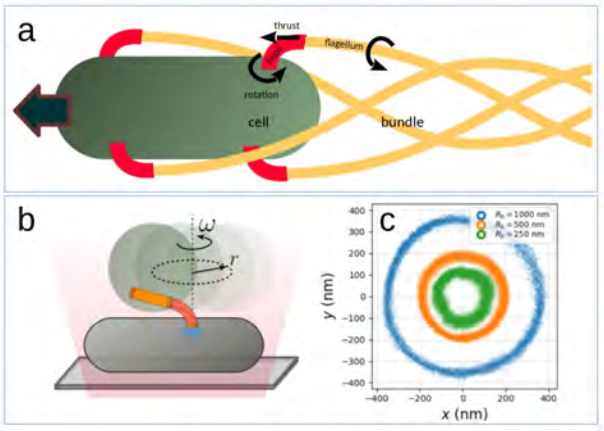

Figure 1: Schematic of a E.coli cell swimming via bundle formation. b) Schematic of a bead assay, where the rotation of a bead tethered to a flagellar stub is tracked to provide information of the activity of the motor. c) x, y trajectories of beads of different radius R_b, rotated by one flagellar motor.

Motility from within: molecular trafficking in the trypanosome flagellum

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The trypanosome flagellum is a complex organelle composed of a cylinder of 9 doublet microtubules flanked on one side by a lattice-like structure called the paraflagellar rod. It is constructed by addition of new elements at the distal end. These building blocks are delivered by Intraflagellar transport (IFT), the movement of large protein particles called trains driven by kinesin (from base to tip) and dynein (from tip to base) molecular motors. These display amazing high speed (2-5 µm per second) and high frequency (1-3 trains per second), yet collisions are extremely rare. We revealed that, intriguingly, only 4 out of the 9 microtubule doublets are used for IFT. This feature could have important consequences in terms of trafficking but also in terms of evolution. In this presentation, I will present our efforts to decipher how trains move bidirectionally within the flagellum, how they are assembled and how they are recycled using 3D-electron microscopy, in vivo and in vitro imaging.

Understanding and modeling the intriguing motion of the diatom chain B. Paxillifer

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Diatom chains are cohesive assemblies of unicellular microorganisms that are found in still and fresh waters. Some species move passively with the ambient flow while others use various strategies to move or self-propel. One species in particular, called Bacillaria Paxillifer, forms colonies of stacked rectangular cells that slide along each other. Their intriguing coordinated motion leads to beautiful and nontrivial trajectories at the scale of the colony. So far, little is known about the purpose of these movements, their swimming efficiency and the underlying (fluid) mechanics. We have

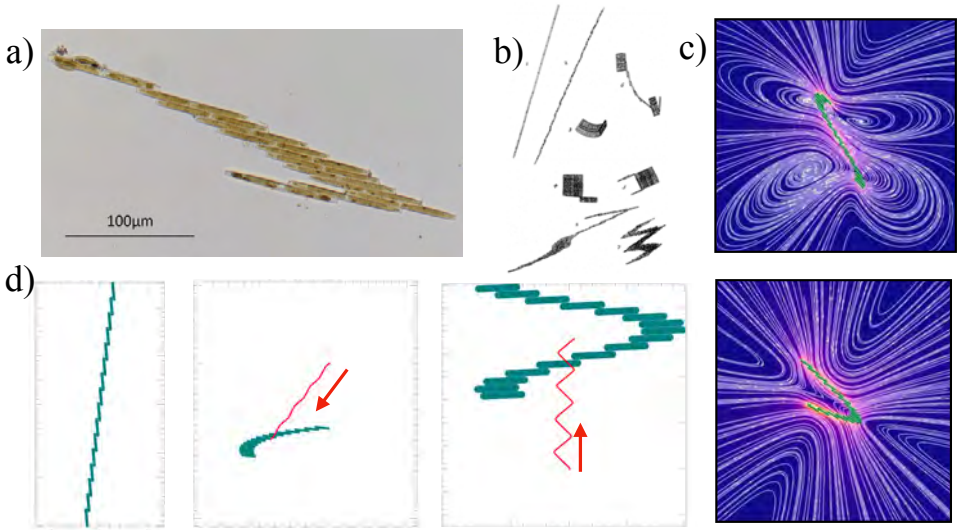

Figure 1: a) Microscope view of B. Paxillifer. b) Various cooordinated motions of a colony observed under a microscope [1]. c) Simulated flow fields around two colonies with different conformations. d) Simulated trajectories of a colony with increasing sliding phase shift between cells (left to right).

developed a numerical method to model Bacillaria Paxillifer as an assembly of rigid rods that are constrained to remain parallel relative to each other with a prescribed sliding motion [2]. Our preliminary simulations show that the direction and the swimming speed of such micro-organism change non-monotonically with the sliding phase shift between pairs of cells. We find that the most efficient swimming mode, in terms of swimming efficiency [3], is obtained for a unique phase shift regardless of the colony length. If time allows, I might also present ongoing microfluidic experiments carried out at LadHyX with G. Amselem.

References

[1] Müller, O. F. Kleine Schriften aus der Naturhistorie (Vol. 1). Buchhandlung der Gelehrten (1782).

[2] Usabiaga, F. B., and Delmotte, B. A numerical method for suspensions of articulated bodies in viscous flows. Journal of Computational Physics, 111365, (2022).

[3] Lighthill, S. J. Mathematical biofluiddynamics. Society for Industrial and Applied Mathematics, (1975).

Programming micro-motility with light

R. Di Leonardo

The flagellar motility of bacteria is a prime example of the engineering power of evolution. It consists of an electric rotary nanomotor, an optimally crafted propeller and a simple and robust sensing and control network. The discovery of light-driven proton pumps in bacteria adds to this toolbox of biological components a solar nano-cell, proteorodopsin, which allows optical control of swimming speed with high spatial and temporal resolution [1]. Using light for rapid and precise remote control, we can establish feedback loops in which computer programs can dynamically modulate micromotility. With this approach, we can stably confine clouds of active bacteria with independently adjustable concentration and activity [2]. Colloidal cargoes can be transported by shaping the pressure field in the surrounding active fluid. Finally, we demonstrate that it is possible to program biohybrid, self-driving microshuttles to move along a predefined path.

References

[1] G. Frangipane et al. Elife **7**, e36608, (2018)
[2] H. Massana-Cid et al. Nature Communications **13**, 2740, (2022)

Bacteria transport close to surfaces: from rheotaxis to upstream contamination

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Individual bacteria transported in viscous flows, show complex interactions with flows and bounding surfaces resulting from their complex shape as well as their activity. Understanding these transport dynamics is crucial, as they impact soil contamination, transport in biological conducts or catheters, and constitute thus a serious health thread. Here we investigate the trajectories of individual E-coli bacteria in confined geometries under flow, using microfluidic model systems in bulk flows [1,5] as well as close to surfaces [2] using a novel Langrangian 3D tracking method [4]. Combining experimental observations and modeling we elucidate the origin of upstream swimming, lateral drift or persistent transport along corners [4,6].

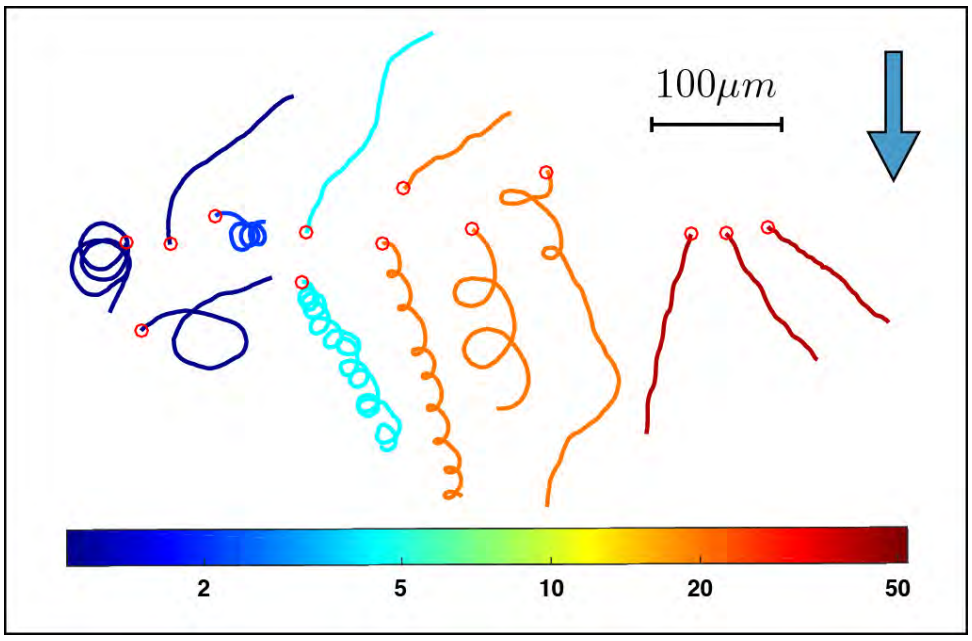

Figure 1: Collage of various surface dynamics types, obtained from 3D tracking of E-coli bacteria at increasing shear rates, shown in the lab frame at a distance from 2-5 μm from the bottom surface (from [2])

References

[1] Junot et al, EPL, **126** (2019) 44003
[2] Mathijssen et al. **10**:3 (2019) Nature Comm.
[3] Figueroa-Morales et al., Soft Matter, 2015,**11**, 6284-6293
[4] Darnige et al. Review of Scientific Instruments **88**, 055106 (2017
[5] Jing et al, Science Advances, 2020; **6** : eabb2012
[6] Figueroa-Morales et al, Sci. Adv. 2020; **6** : eaay0155, 2020, 10.1126/sciadv.aay0155

List of Posters

P01: High Throughput Single Cell Bacterial Imaging

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Antibiotic resistance is a growing issue in healthcare around the world, and is currently responsible for over one million deaths annually. Tackling this issue will require many different strategies, one of which will be using the antibiotics we have more strategically. This will require the development of more efficient tools for determining the most effective antibiotic type and dosage for a given infection. Currently, the most widely used method for antibiotic susceptibility testing is based on determining minimum inhibitory concentration (MIC) using Kirby-Bauer (KB) disk diffusion. This project seeks to develop a more rapid, higher throughput system for antibiotic susceptibility testing. In support of this goal, we developed a platform where samples are placed on a series of 60 agarose pads with different antibiotics present at varying concentrations. The bacteria are confined to a single imaging plane using a glass coverslip and imaged for four hours under a microscope. An image processing toolchain is employed to analyse the resulting images and determine which conditions inhibit the growth of bacteria. A series of prototypes were developed to work with existing microscope infrastructure, and a customised image analysis pipeline was produced. Testing the system included capturing brightfield and fluorescent images of bacteria to generate training datasets for the image segmentation algorithm. Temporally maintaining the cells in focus across the different pads was one of the most significant challenges. Multiple experiments were carried out to characterise and develop techniques to overcome this issue. The ability to measure different colony growth rates have, in addition, been tested using variations in growth media. This platform has the potential to drastically cut testing time, leading to more targeted utilisation of antibiotics.

P02: Collective Dynamics in A Dense Suspension of Self-Propelling Pseudomonas Aeruginosa Bacteria

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Bacterial motility has multiple functions. In bacterial colonies on agar gel, it allows for enhanced expansion speed through swarming. Bacteria such as P. aeruginosa swarm for up to ten fold enhanced expansion speed [1]. While it is known that flagellar motility is crucial for swarming, it remains an open challenge to understand how microscopic motility gives rise to enhanced colony expansion rate [2]. To make progress in this direction, I simulate the collective dynamics in dense monolayers of P. aeruginosa. Bacteria are modelled by spherocylinders which actively move according to run and tumble motion. Figure 1 shows a dense monolayer of bacteria from experimental data and simulation data. We test our model by comparing the mesoscopic dynamics using quantities such as velocity correlations and vorticity. Modelling still faces some challenges. The model lacks the observed behaviour of stalled local regions. There are three reasons for this discrepancy: 1) the motility pattern on agar is not yet experimentally characterized, 2) we neglect hydrodynamics, 3) we neglect cell-cell friction. Experiments at lower bacteria density will allow tracking bacteria motility without interruption by collisions, hence solving point 1). The role of point 2) remains unclear, as including hydrodynamics remains computationally challenging. Next, to tackle point 3), we will introduce a simple model for cell-cell friction and investigate its role. Modelling the effect of cell-cell friction will aid in future studies of bacterial colony formation.

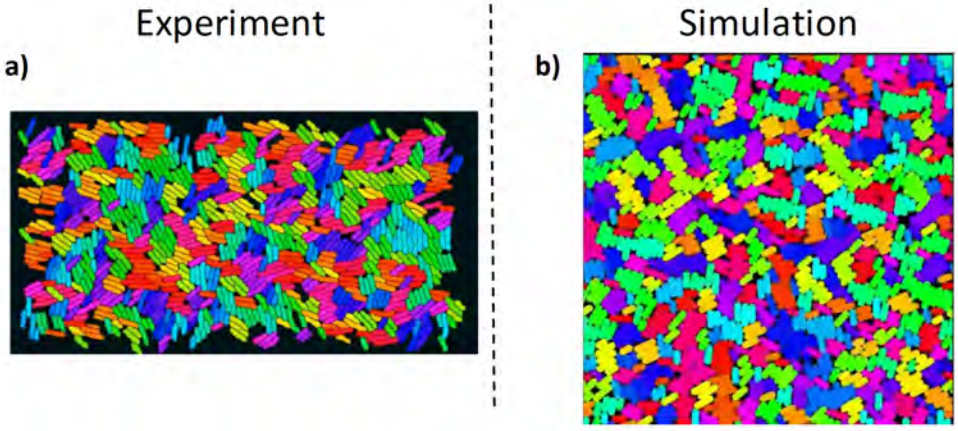

Figure 1: **a)** Experimental data of the monolayer at the edge of the colony. 870 bacteria at approximately 90% area fraction in a region of width 70 micron and height 30 micron. Colour indicates orientation with respect to the x-axis. **b)** Snapshot of my simulation of 1000 bacteria.

References

[1] J. Yan, et al., Annual Review of Microbiology **73**, 293-312, (2019)
[2] N. C. Darnton, et al., Biophysical Journal **98**, 2082-2090, (2010)

P03: Optimal swimming strategy in confinement

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Bacteria have colonised a large diversity of habitats and have evolved different swimming patterns, which raise many open questions. In particular, it is still unclear what the benefits of a specific swimming strategy are with respect to others. We address this issue from a physical point of view and investigate which swimming strategies results in optimal transport in confined environments. We employ numerical simulations of a minimal model describing bacterial motion within a planar slit. Complementing other works on this topic [1, 2], we focus on transport properties parallel to the confinement and quantify the long-time diffusion coefficient. We find that a pronounced maximum is reached when the average run length is 10-20 times the channel width. Such results open the way to exploration of the more complex environments found in porous media.

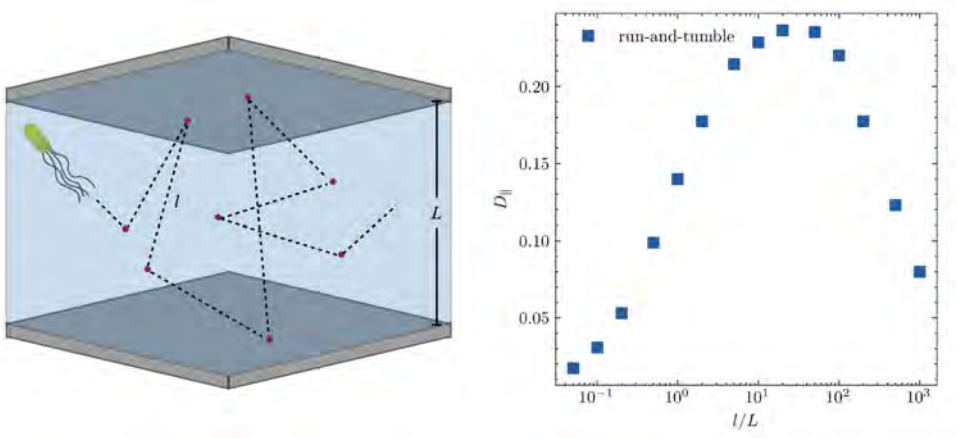

Figure 1: (left) Example of trajectory for bacteria swimming in a planar slit. (right) Lateral diffusion coefficient for run-and-tumble swimming strategy within a planar slit, as a function of mean run length (l)

References

[1] J. Elgeti & G. Gompper, EPL **109**, 58003 (2015)
[2] G. Junot et al., PRL **128**, 248101 (2022)

P04: Screening for genetic determinants of Vibrio cholerae biofilm architecture

E. Jiménez Siebert[1], **M. Bayer**[1], **N. Netter**[1], **K. Neuhaus**[1], **H. Jeckel**[1], **K. Strenger**[1], **K. Drescher**[1]

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Most of the bacterial biomass on Earth is found in three-dimensional communities, termed biofilms [1], which confer protection against many forms of physical, chemical, and biological stress. In this work we overcome previous limitations by developing a novel microfluidic high-throughput biofilm cultivation approach, as well as an automatized adaptive fluorescence microscopy screening procedure, to obtain single-cell resolution, three-dimensional biofilm images of a V. cholerae genome-wide transposon mutant library. Extraction of high-dimensional architectural data with the image analysis pipeline BiofilmQ [2] and examination of the overall biofilm formation capabilities of each strain enabled us to establish the biofilm lifestyle in V. cholerae as a highly regulated one in which half of the V. cholerae genome plays an important role, most of its genes affecting either the temporal development of biofilm formation or the three-dimensional structure of the biofilm. Interestingly, we found that genes encoding motility- and chemotaxis-related proteins have an impact on biofilm structure, their absence leading to an exacerbated biofilm seeding density, biofilm size and cell packing in some cases, but also to a complete incapability to form three-dimensional biofilm structures.

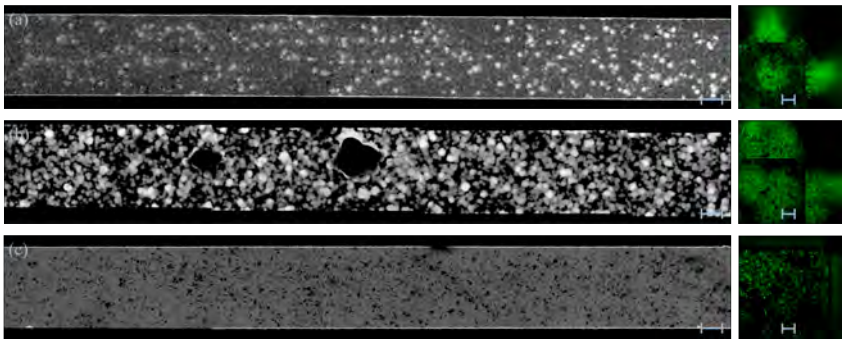

Figure 1: Comparison of biofilm formation in microfluidic chambers between a V. cholera WT (a), the flagellar mutant ΔfliQ (b) and the chemotaxis mutant ΔVCA0658 (c). Images show a large channel-overview at low resolution (left, scale bar: 100μm) and a high-resolution bottom- and side-view of one of the colonies in the channel (right, scale bar: 10μm).

References

[1] Flemming, HC., Wuertz, S. Bacteria and archaea on Earth and their abundance in biofilms. Nat Rev Microbiol **17**, 247-260 (2019).

[2] Hartmann, R. Jeckel, H. Jelli, E. et al., Quantitative image analysis of microbial communities with BiofilmQ. Nat Microbiol **6**, 151-156 (2021).

P05: Glassy dynamics in bacterial monolayers

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Motile bacteria have the possibility to organize in numerous collective phases, such as orientationally ordered phase or swarming state. These collective phases often result from properties and activities at the single cell scale, such as growth rate, swimming speed and cell-cell interactions. Understanding how individual properties can trigger emergence of long range order is a crucial aspect of biological and physical studies on bacteria, and can lead to better understanding of the mechanisms of colony and biofilm formation. Here the properties of the 2D swarming state of Pseudomonas aeruginosa, a motile bacteria, in growing colonies are studied. We are able to obtain large and dense monolayers of bacteria at the edge of 3D colonies expanding on agar gels. The detection of bacterial trajectories from high-speed movies is fulfilled through the use of an innovative deep learning technique that performs segmentation and tracking together. We show that the swarming state of P. aeruginosa exhibits short range orientational order, in the form of alignment clustering, and that this order is unstable in time and decays in the order of less than a second. Furthermore, the increase of surface fraction triggers the emergence of two distinct phases : a fluid phase, with rapidly evolving motile cells, and a jammed glassy phase, where cells are unable to move and orientational order is conserved in time. This points to glass transition, which has already been observed in dense populations of bacteria. Bacteria are shown to oscillate between the two states (jammed and fluid), and the movement of phases is not correlated with the actual migration of motile bacteria, but rather with an activity transfer from one bacterium to another. Nonetheless, the mechanisms behind this transfer of activity are still not entirely understood.

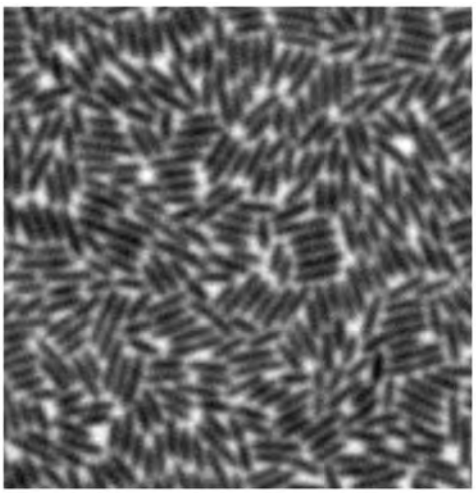

Figure 1: Monolayer organization at the colony edge, displaying nearly jammed phase (average cell length = 2μm).

P06: Evolution of microswimmer designs in distinct micro-environments

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Trypanosoma brucei are uniflagellate parasites that infect a wide range of vertebrate species and cause deadly diseases. T. brucei's life cycle alternates between tsetse flies and vertebrates. Throughout their life cycle, they encounter a variety of microenvironments with different features, e.g., flow, viscosity, pressure and confinement [1]. The parasites have been shown to possess a high ability to adapt in these environments, by adopting various complex morphologies and developing effective motion mechanisms, which is crucial for survival facing the host's immune system [2]. Their motion initiates with a planar bending wave of the flagellum at the anterior end and continues with a longitudinal rotation due to the helical attachment of the flagellum to the cell body (Fig. 1) [3]. It has been shown that changes in microenvironment properties can affect trypanosomes swimming patterns, speed, and flagellar motility [2,3]. Although trypanosome motility has been described to some extent, there is still a lack of quantitative knowledge on the single cell motility and motion pattern. This project aims to quantitatively describe the trypanosomes mechanisms of motility in different viscosities, by using high-speed microscopy and 4D analysis. This study demonstrates how T. brucei parasites become faster swimmers in high viscosity media. It indicates that different cell lines adapt similar morphological modifications to obtain their maximum speed in the same medium. Further, comparing behavior in different viscosities, interesting correlations of rotational cell translocation and frequency of flagellar beating are shown. These lead us to define experiments to measure mechanical cell properties that could help to elucidate the underlying morphological basis of adaptations in motility patterns.

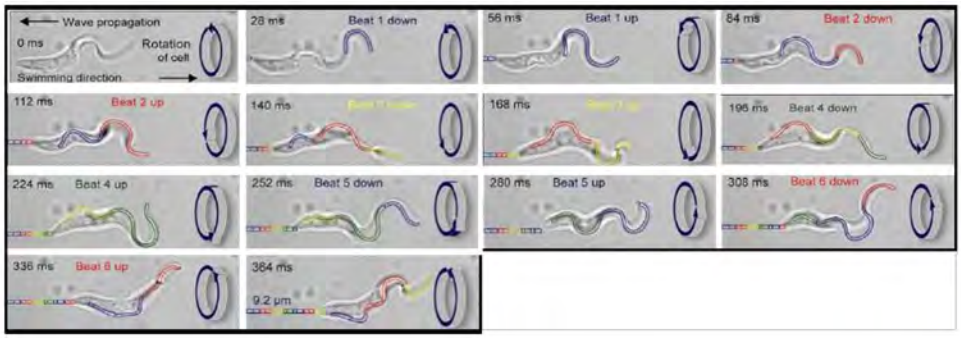

Figure 1: Brightfield images from a xyt-series acquired with 500 fps. Each image shows the beginning of successive up- or down-strokes of the flagellar tip, meaning a new wave starts at the anterior end of the flagellum every two images. Every single up- and down-stroke causes forward motion in the opposite direction of wave propagation, due to the helical path of the body, cell rotates about 25 degrees counter-clockwise in each beat.

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).

P07: Escape jumps in flagellates

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Some flagellates can sense approaching predators and perform rapid escape jumps [1]. For a range of flagellates with diverse flagellar arrangements [2], we examined their ability to perceive predators, the characteristics and threshold magnitude of fluid and mechanical signals, and the mechanisms that allow flagellates to increase their escape speed by more than one order of magnitude. We used microfluidics to characterize escapes and escape-eliciting fluid signals. The flagellate suspension was made flowing inside a convergent channel where a constant flow rate was imposed through a flow rate controller connected to a pressure pump. By identifying the starting point of many jump events and the associated values of maximum deformation and rate of change of maximum deformation (evaluated by CFD), we were able to identify the threshold value of the escape-eliciting fluid signal.

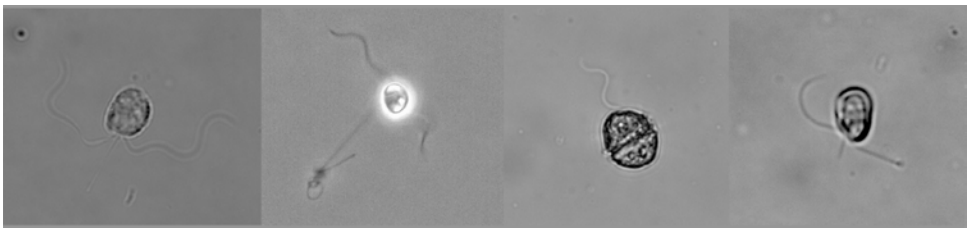

Figure 1: Diversity of flagellates among the eukaryotic tree of life.

References

[1] Escape response of planktonic protists to fluid mechanical signals. Jakobsen, H. Mar. Ecol. Prog. Ser., **214**, 67–78 (2001).

[2] Foraging trade-offs, flagellar arrangements, and flow architecture of planktonic protists. Nielsen, L.T. & Kiørboe, T. Proc. Natl. Acad. Sci., **118**, e2009930118 (2021).

P08: Suppression of bacterial rheotaxis in wavy channels

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Controlling the swimming behavior of bacteria is crucial, for example, to prevent contamination of ducts and catheters. We show that bacteria modeled by deformable microswimmers can accumulate in flows through straight microchannels either in their center or on previously unknown attractors near the channel walls. In flows through wavy microchannels we predict a novel resonance effect for semiflexible microswimmers. As a result, microswimmers can be deflected in a controlled manner so that they swim in modulated channels distributed over the channel cross-section rather than localized near the wall or the channel center. Thus, depending on the flow amplitude, both upstream orientation of swimmers and their accumulation at the boundaries, which can promote surface rheotaxis, are suppressed. Our results suggest new strategies for controlling the behavior of live and synthetic swimmers in microchannels.

P09: Amoeboid Cell Migration under Lateral and Vertical Confinement

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Motile biological agents, e.g. migrating cells, exist in environments with complex topographical features. Amoeboid migration through extracellular matrices and confined tissue plays a crucial role in various physiological processes, e.g. the immune response. Cells and other organisms are capable of sensing the topographical cues of the environment and adapt their migration accordingly; this ability is called topotaxis [1, 2, 3, 4, 5]. Here, we study the topographical influence of the environment on amoeboid migration in vitro in regular pillar forests[6]. We have designed a microfluidic device and tracked HL-60 cells differentiated into neutrophils in quasi- 2D spaces confined between two parallel plates. We demonstrate how migration and search efficiency of the cells are influenced by the lateral and vertical confinement, spatial arrangement of micropillars, and cell-pillar interactions. We find that at each cell-pillar contact event, the cell spends a finite time near the pillar surface, which is independent of the height of the chamber and the interpillar spacing. We observe that by decreasing the vertical confinement h, the persistence of cells decreases, without a significant change in the velocity. Our simulations reveal that the interplay between cell persistence and cell-pillar interactions can dramatically affect cell diffusivity and, thus, its first-passage properties.

References

[1] Park,J.-S.,D.-H.Kim,andA.Levchenko.2018.Topotaxis:Anewmechanismofdirected cell migration in topographic ECM gradients. Biophys. J. **114**:1257-1263.
[2] Reversat A. et al. 2020. Cellular locomotion using environmental topography. Nature. 582:582-585.
[3] Gorelashvili, M., M. Emmert, K. F. Hodeck, D. Heinrich. 2014. Amoeboid migration mode adaption in quasi-3D spatial density gradients of varying lattice geometry. New J. Phys. **16**:075012.
[4] Frey,M.T.,I.Y.Tsai,T.P.Russell,S.K.Hanks,andY.-L.Wang.2006.Cellularresponses to substrate topography: Role of myosin II and focal adhesion kinase. Biophys. J. **90**:3774- 3782.
[5] Kaiser, J.-P., A. Reinmann, and A. Bruinink. 2006. The effect of topographic characteristics on cell migration velocity. Biomaterials **27**:5230-5241.
[6] Z. Sadjadi, et al. 2022. Amoeboid Cell Migration through Regular Arrays of Micropillars under Confinement. doi: https://doi.org/10.1101/2022.04.08.487483

P10: Torque output and dynamics of the bacterial flagellar motor in Campylobacterota

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The pathogenicity of bacteria is often governed by the ability of the bacteria to move using chemotaxis to navigate its environment. Most bacteria have flagella which propel their movement and are driven by an intricately structured molecular machine called the bacterial flagellar motor. The structure and function of the bacterial flagellar motor are well understood for enteric bacteria, e.g. Escherichia coli, but recently, motors with additional protein structures have been discovered in the phylum Campylobacterota [1]. The evolutionary reason for these additional proteins remains an open question, and the relationship between the dynamics of the bacterial flagellar motor and the motility of these bacteria remains poorly understood. Single particle biophysical microscopy techniques, specifically tethered cell and bead assays [2], provide the means to probe torque output and dynamics of the bacteria flagellar motor. With this poster, I will present our efforts towards studying the motor of Campylobacter jejuni, a member of Campylobacterota and a major cause of diarrhoeal disease in humans [3]. I will show results from tethered cell assays of C. jejuni, a first for this bacterium. I will also describe the development of a robust protocol for bead assays of C. jejuni. This protocol will overcome complications of imaging polar-flagellated bacteria, which may occur due to surface-induced drag. These results will aid the determination of the evolutionary advantage, if any, that additional proteins in the bacterial flagellar motors of Campylobacterota provide.

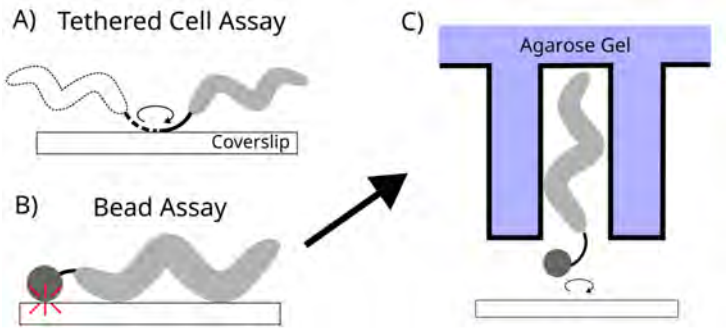

Figure 1: Biophysical microscopy to investigate the bacterial flagellar motor of C. jejuni. A) In a tethered cell assay, the flagellum of a bacterium is attached to a glass coverslip, and the rotation of the cell is monitored. B) In a bead assay, a microscopic bead is attached to a truncated flagella which is then monitored. In the case of polarw -flagellated bacteria, there is potential for surface effects on bead rotation. C) Our proposed method of centrifuging bacteria into holes in agarose gel [4] where attached beads can freely rotate.

References

[1] M. Beeby et al., Proc. Natl. Acad. Sci. U. S. A. **113** E1917–E1926, (2016)
[2] P. P. Lele, B. G. Hosu, and H. C. Berg, Proc. Natl. Acad. Sci. U. S. A. **110**, 11839-11844, (2013)
[3] P. Lertsethtakarn, K. M. Ottemann, and D.R. Hendrixson, Annu. Rev. Microbiol. **65**, 389-410, (2011)
[4] K. D. Whitley et al., Nat. Protoc. **17**, 847-869, (2022)

P11: Bacteria propulsion and interactions in thin biofilms

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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. These results advance our understanding of bacterial film formation and the connection between the collective swarming behavior and the internal properties of individual swimmers.

References

[1] J. Elgeti et al., Rep. Prog. Phys. **78**, 056601 (2015)
[2] M. Theers et al., Soft matter **14** (42), 8590-8603 (2018)
[3] K. Qi et al., Commun. Phys. **5**, 49 (2022)
[4] M. Theers et al., Soft Matter **12**, 7372 (2016)

P12: Anomalous bacterial transport in confined geometries

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Motile bacteria are known to interact with flows exhibiting in the bulk active Betherton-Jeffery trajectories [1] or rheotactic drift [2] due to the helical flagella shapes. In the vicinity of bounding surfaces, one also observes specific trajectories [3] including persistent upstream swimming, an effect enhanced by the presence of edges [4]. Statistically, the combination of hydrodynamic interactions and flow-induced orientation, leads to a strong density increase in the surface vicinity, inducing a boundary layer of around 10 μm in extension [5]. In disordered and complex environments, the presence of surface and flow make large-scale dispersion properties of active bacteria a challenging issue [6]. To elucidate the combined role of flow and the presence of surfaces, we developed experimental model systems suited to observe individual trajectories and to assess the emerging dispersion processes in confined microfluidic channels presenting various complex geometries using motile E.coli bacteria. In previous studies, the transport of E.coli suspensions flowing through very confined microfluidic channels presenting a constriction[7], revealed anomalous spatial density distributions due a strong surface retention effect present after the constriction. In order to understand the relation between the boundary layer and the geometrical parameters (ie.,confinement height), we studied the transport in such a geometry varying the channel height. Changing the confinement we found: (1) a sharp density increase downstream close to surfaces at the same shear rate as in previous work; (2) the accumulation effect persists even for decreasing confinement, within the surface layer but disappears in the bulk. In the future, we will extend this work to multiple constrictions and pillar-arrays of varying symmetries. The present work will help to understand motility-dependent surface/bulk exchange mechanisms and to obtain a complete description of bacteria transport in the presence of confining surfaces of different geometry.

References

[1] Gaspard Junot et al. "Swimming bacteria in Poiseuille flow: The quest for active Bretherton-Jeffery trajectories". In: EPL (Europhysics Letters) **126**.4 (2019), p. 44003.
[2] Guangyin Jing et al. "Chirality-induced bacterial rheotaxis in bulk shear flows". In: Science advances **6**.28 (2020), eabb2012.
[3] Arnold JTM Mathijssen et al. "Oscillatory surface rheotaxis of swimming E. coli bacteria". In: Nature communications **10**.1 (2019), pp. 1–12.
[4] Nuris Figueroa-Morales et al. "E. coli "super-contaminates" narrow ducts fostered by broad run-time distribution". In: Science advances **6**.11 (2020), eaay0155.
[5] Jérémie Gachelin et al. "Non-Newtonian viscosity of Escherichia coli suspensions". In: Physical review letters **110**.26 (2013), p. 268103.
[6] Adama Creppy et al. "Effect of motility on the transport of bacteria populations through a porous medium". In: Physical Review Fluids **4**.1 (2019), p. 013102.
[7] E Altshuler et al. "Flow-controlled densification and anomalous dispersion of E. coli through a constriction". In: Soft Matter **9**.6 (2013), pp. 1864–1870.

P13: Tracking of passive E. coli inside collective motion

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We investigate the motion of passive tracers in the bulk of an active suspension of E. coli. Normally passive tracers are subject to Brownian motion which diffuses the particles in the media. Nevertheless, in an active suspension dense enough to be above the critical density of collective motion the behaviour is different [1]. The collective motion produces flows that have a correlation length considerably larger than the bacteria size as can be seen on the large structures of figure 1. Also, the velocity has a correlation time in the order of seconds. For times lower than this characteristic time, the tracers follow ballistic motion and for larger times diffusive behaviour is observed with a diffusion coefficient which is orders of magnitudes larger than the Brownian diffusion coefficient.

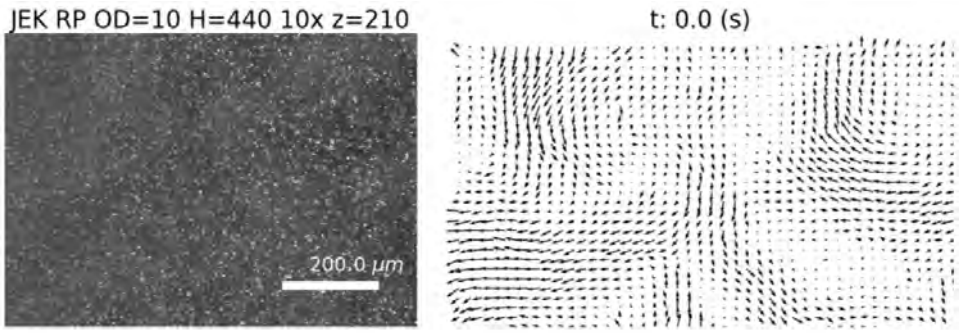

Figure 1: Picture of a layer inside collective motion of E. coli taken with a confocal microscope and on the right the corresponding velocity field obtained with PIV. The sample is a mixture of JEK1036 (non-fluorescent) and RP437 (fluorescent) tumbling E. coli in a confinement of 440 micrometers.

References

[1] Martinez, Vincent A., et al. A combined rheometry and imaging study of viscosity reduction in bacterial suspensions. Proceedings of the National Academy of Sciences, 2020, **117**, no 5, p. 2326-2331.

P14: Viscoelastic properties of Chlamydomonas R. flagella

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Flagella and cilia are ubiquitous organelles in eukaryotic organisms with a highly conserved structure [1]. They perform a variety of functions such as motility and mechano-chemical sensing [2]. To understand the link between structure and function, mechanical properties are an essential puzzle piece [3]. In particular, the axoneme – the inner scaffold of flagella – plays a crucial role in the collective motion of flagellar beating [4]. We know that flagella and cilia axonemes exhibit bending resistance in an elastic regime [5]. But so far, most experiments probe static properties only while there could also be internal dissipations during beating [6]. Other types of elasticity [7] and non-elastic regimes [8] have also been found. We thus designed an experiment that aims to probe the response of eukaryotic flagella of Chlamydomonas R. to a periodic flow [Figure 1]. Amplitude and frequency of the flow, flagellar length - by suction and subsequent regrowth of flagella - and use of mutants are control parameters we aim at using to untangle the link between axoneme structure and viscoelastic properties. On one hand image analysis is used on experimental data to extract flagellar shape over time and flow field, while on the other hand a coarse-grained model is developed including internal viscosity and different kinds of elasticity, based on [9]. Figure 1. Schema of the experimental setup. A micropipette holds a Chlamydomonas cell in a flow chamber, moved by a piezo-stage. A point force can be exerted by the use of a microneedle while flagellar length is controlled by suction using a micropipette and subsequent regrowth of flagella.

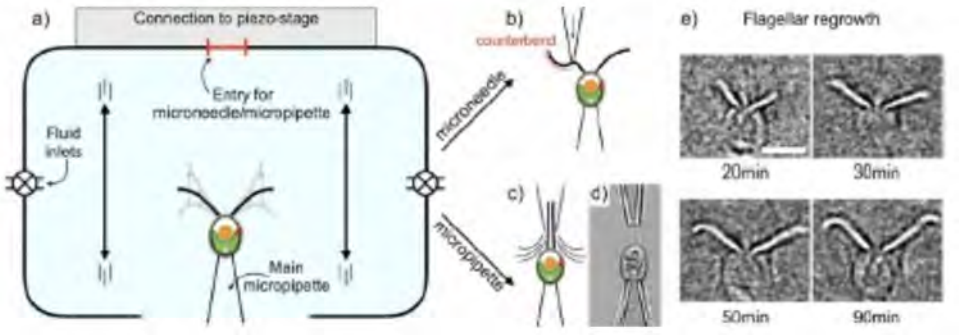

Figure 1: Schema of the experimental setup. A micropipette holds a Chlamydomonas cell in a flow chamber, moved by a piezo-stage. A point force can be exerted by the use of a microneedle while flagellar length is controlled by suction using a micropipette and subsequent regrowth of flagella.

References

[1] N. Klena & G. Pigino, Annual Review of Cell and Developmental Biology, **38**, 2022
[2] H.A. Praetorius & K.R. Spring, The Journal of Membrane Biology, **184**:71-79, 2001
[3] S. Prosser & L. Pelletier, Nature Reviews Molecular Cell Biology, **18**(3):187-201, 2017
[4] P. Satir, J. Cell. Biol., **39**(1):77-94, 1968
[5] A. Baba, J. Exp. Biol., **56**(2):459-467, 1972
[6] D. Mondal, P. Sharma, Science Advances, **6**:33:eabb0503, 2020
[7] I. Minoura, R. Kamiya, Cell Structure and Function, **24**:1:27-33, 1999
[8] Y.-N. Young & M. Downs, Biophysical Journal, **103**:4:629-639, 2012
[9] C. Moreau, H. Gadêlha, J. R. Soc. Interface, **15**:20180235, 2018

P15: Bacterial exploration in confined environment

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From experiments of 3D lagrangian tracking of fluorescent E. coli, we can access the trajectory of a single bacterium. E. coli, a model bacterium, performs the so called run & tumble motion in a 3D newtonian fluid at a constant speed V. When close to a surface, bacteria change their motion from straight to circular run of radius R due to hydrodynamic interaction. I study the XY

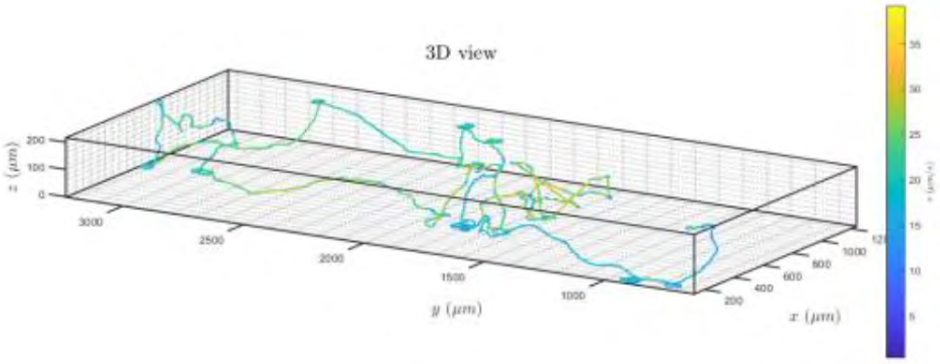

Figure 1: 3D-trajectory of a bacterium.

exploration of bacteria confined between two plates separated by a height H. The exploration of a bacterium is characterized by the effective diffusion coefficient D emerging from the MSD at large time. Experiments are compared to numerical simulations and confronted to a simple theory D=f(V,R,H) mixing bulk and surface behaviours. Experiments agree with numerics and deviations

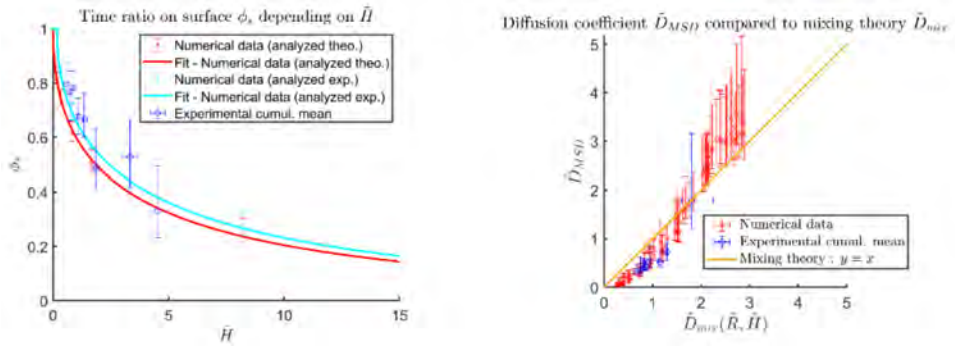

Figure 2: Time spent on surface and diffusion coefficient from experiments are well reproduced by the numerical simulations. There exists some deviations from the theory.

from theory come from well-understood but non-trivial correlations between bulk and surface.

References

[1] N. Figueroa-Morales, Phys. Rev. X **10**, 021004 (2020)
[2] G. Junot, Phys. Rev. Lett. **128**, 248101 (2022)

P16: Spatio-temporal dynamics of the proton motive force on single bacteria cells

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The proton motive force (PMF) is the electro-chemical potential established during cellular respiration across the membranes of bacteria and mitochondria. It regulates a wide range of important physiological processes, in particular powering, via a proton flux, ATP synthesis and bacterial motility. In bacteria, the dynamical behavior of this out of equilibrium potential difference (often only characterized by a population average) is still not completely understood, especially at the single cell level. The possibility of a dynamic behavior of the PMF was opened by the observations of single cell voltage depolarizations in Escherichia coli, using a novel voltage sensitive fluorescent probe (PROPS) [1]. Also, polar clustering of respiratory complexes observed in E.coli could be an indication of a spatial heterogeneity of the PMF [2]. Such heterogeneity has been recently shown along the inner membrane of individual mitochondria [3], but it remains to be probed in single bacteria. Technically, given the micron scale of bacteria, it is still very challenging to directly interrogate the PMF on single cells without perturbations, and for this reason the main employed techniques rely on fluorescence, which adds the complexity given by the fluorophore response. Here, we probe the dynamics of the PMF on single E.coli cells, using their flagellar motors as local probes on the membrane, taking advantage from the linearity between their rotational speed and the potential. Expanding previous works, we also use laser illumination on single bacteria expressing the light-driven proton pump proteorhodopsin, to trigger the production of an excess of PMF which is capable to power and accelerate the flagellar motor [4, 5]. We explain our observations with a circuit model that includes the relevant cellular electric components and explains the observed dynamics at the millisecond time scale. Furthermore, locally and periodically illuminating long filamentous cells, we find that the response of a flagellar motor is the same irrespective to the distance from the local laser-controlled proton source. Proton diffusion cannot explain our observations, even considering it proceeding in 2D along the membrane with the fastest diffusion coefficient for ions. These findings suggest that in single bacteria an excess of local membrane voltage can propagate quickly and at long distances (tens of μm, ms), as on electrical wires, effectively homogenizing the PMF of the bacterium.

References

[1] Kralj, J. M., Hochbaum, D. R., Douglass, A. D., & Cohen, A. E. (2011). Electrical spiking in Escherichia coli probed with a fluorescent voltage-indicating protein. Science, **333**(6040), 345-348.
[2] Magalon, A., & Alberge, F. (2016). Distribution and dynamics of OXPHOS complexes in the bacterial cytoplasmic membrane. Biochimica et Biophysica Acta (BBA)-Bioenergetics, 1857(3), 198-213.
[3] Wolf, D. M., Segawa, M., Kondadi, A. K., Anand, R., Bailey, S. T., Reichert, A. S., ... & Shirihai, O. S. (2019). Individual cristae within the same mitochondrion display different membrane potentials and are functionally independent. The EMBO journal, **38**(22), e101056.
[4] Walter, J. M., Greenfield, D., Bustamante, C., & Liphardt, J. (2007). Light-powering Escherichia coli with proteorhodopsin. Proceedings of the National Academy of Sciences, **104**(7), 2408-2412.
[5] Tipping, M. J., Steel, B. C., Delalez, N. J., Berry, R. M., & Armitage, J. P. (2013). Quantification of flagellar motor stator dynamics through in vivo proton-motive force control. Molecular microbiology, **87**(2), 338-347.

P17: Chemotaxis in marine protists: The role of dimethylated sulfur compounds (DMSCs) in predation

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How does a micro-scale predator find its micro-scale prey in the patchy, turbulent marine environment? For some, predation is a matter of chemical cues. In the last decade, multiple studies have suggested that the chemoresponse of marine predators to dimethylated sulfur compounds (DMSCs) shapes the interaction between predators and prey at different trophic chain levels [1,2,3,4,5,6]. However, the exact function of DMSCs remains unclear. Some studies showed evidence of a chemoattraction of marine predators towards these compounds [2,5,6] and some, on the contrary, found evidence of chemorepulsion [1,3,4]. This study investigated the chemoresponse of some model marine herbivore protists to different concentrations of different DMSCs (DMSP, DMS, Acrylate). A traditional capillary asset set up made of two capillaries, one DMSCs- filled and one of control, was inserted in a homogenous predators culture. The system was then filmed for 5 to 10 minutes. Individual cells' trajectories were then tracked using the Python library Trackpy. Our preliminary results suggest a clear chemoattraction of Gyrodonium d. and Oxyrris m. towards DMSP and DMS at all concentrations. No significant chemoresponse was detected for Acrylate. In the case of Gyrodinium d., the chemoresponse also lead to a change in the swimming behavior of the organism, in terms of speeds (increased speed in presence of DMSP), and orientation (straighter trajectories).

References

[1] Breckels, M. Journal of Plankton Research, **33** (2011)
[2] Shemi, A. Nature Microbiology **6** (2021)
[3] Wolfe, G Nature (1997)
[4] Teng Z., Nature Microbiology **6**(11) 1351-1356 (2021)
[5] Seymour J 329(5989) 342-345 (2010)
[6] Lewis N. Ecological Complexity **16** 41-50 (2013)

P18: Frustrated run and tumble of swimming E-coli bacteria in nematic liquid crystals

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In many situations, bacteria move in complex environments, as soils, oceans or the human gut-track, where carrier fluids show complex structures associated with non-Newtonian rheology. Many fundamental questions concerning the ability to navigate in such environments remain unsolved. Recently, it has been shown that the kinetics of bacterial motion in structured fluids as liquid crystals (LCs) is constrained by the orientational molecular order (or director field) and that novel spatio-temporal patterns arise [1,2]. A question unaddressed so far is how bacteria change swimming direction in such an environment. In this work, we study the swimming mechanism of a single bacterium, E. coli, constrained to move along the director field of a lyotropic chromonic liquid crystal confined to a planar cell. Here, the spontaneous 'run and tumble' motion of the bacterium gets frustrated: the elasticity of the LC prevents flagella from unbundling. Interestingly, to change direction, bacteria execute a reversal motion along the director field, driven by the relocation of a single flagellum, a 'frustrated tumble'. We characterize this phenomenon in detail experimentally, exploiting exceptional spatial and temporal resolution of bacterial and flagellar dynamics, using a two colour Lagrangian tracking technique. We suggest a possible mechanism accounting for these observations.

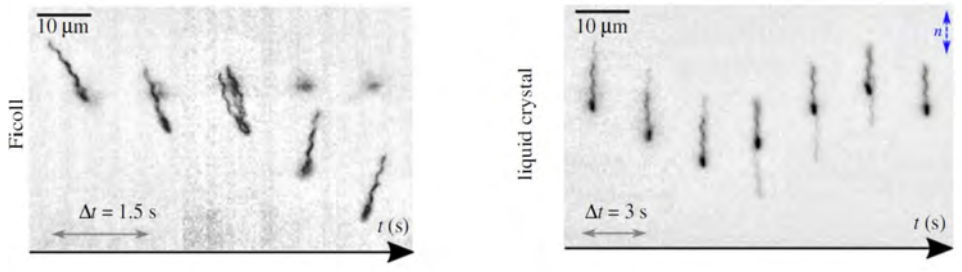

Figure 1: Snapshots of a swimming E. coli bacterium performing a run and tumble motion in a 20 μm high observation chamber, at room temperature, in a Ficoll solution of viscosity 18 mPa s and in a liquid crystal (DSCG 12 wt%, 18 mPa s)

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References

[1] S. Zhou, A. Sokolov, O.D. Lavrentovich, and I.S. Aranson, Proc. Natl. Acad. Sci. U.S.A. **111**(4), 1265-1270 (2014)
[2] M.M. Genkin, A. Sokolov, O.D. Lavrentovich, and I.S. Aranson, Phys. Rev. X 011029 (2017)

P19: Microswimmers in viscosity gradients

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Viscosity gradients are abundant in the habitat of microorganisms like bacteria or algae cells. These species had to develop strategies to navigate through such complex environments and adapt their swimming to the local viscosity or to its variations. Identifying principles of self-propulsion is consequently a key first step to understand the viscotactic behavior of biological microswimmers. Therefore, significant effort has been invested in the field with a focus on model systems in which the swimming stroke is fixed. The disadvantage of these models is that their swimming strategy is unresponsive to changes in the surroundings. We circumvent this issue by studying a swimmer model made of beads and springs where we prescribe the driving forces. Consequently, our swimmer "perceives" the change in viscosity and the associated drag, thus adjusting its stroke, i.e. the bead motions. Furthermore, we postulate that the swimmer can measure the viscosity gradient through hydrodynamic interactions between the beads, i.e. its body parts. To model this effect, we first derive a general expression for hydrodynamic interactions and the corrections to the mobility matrix in weak viscosity gradients. We apply this result to linear viscosity gradients, where we unveil the existence of radially constant flows induced by the beads. We elaborate on this effect with respect to the particle position within the finite-size gradient [1]. Integrating these properties into our model, we reveal the rich properties of self-propulsion. In contrast to recent swimmer models with either viscophilic [2] or -phobic [3] behavior, our swimmer can be tuned between those two modes by changing the driving frequency applied. We also employ these results to construct a simple swimmer inspired by the Chlamydomonas algae and compare its viscotactic behavior to our swimmer's. Notably, we obtain a good agreement between Chlamydomonas and our model swimmer in terms of swimming velocity, flow field and rotation in a viscosity gradient.

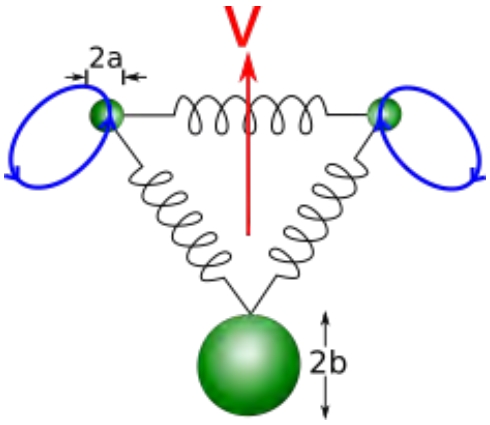

Figure 1: Model swimmer for Chlamydomonas reinhardtii.

References

[1] S. Ziegler et al, JFM, **943**, A29 (2022)
[2] B. Liebchen et al, PRL **120**, 208002 (2018)
[3] C. Datt & G. Elfring, PRL **123**, 158006 (2019)

P20: Emergent structures in binary mixtures under flow

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Bacteria are often found in heterogeneous communities organized thorough physical interaction with their surrounding environment. Although external physical constraints like shear flow are frequent in natural situations and have been shown to influence the swimming behavior of bacteria [1], little is still known about their effect on the distribution of bacteria within complex communities. Under no flow condition, previous experiments have shown the emergence of large density fluctuations of passive bacterial cells driven by the activity of motile bacteria with which they are mixed. Through microfluidic experiments, we investigate how the spatiotemporal organization and the density distribution of a binary mixture of active and passive E. coli bacteria react under different configurations of shear flow. Our initial focus is on the effect of Poiseuille flow (linear shear profile) on the mixture, but we also plan to study the behavior under Couette flow. We notably focus on possible transport effects emerging from the combined action of external shear and active swimming on the non-motile species of the mixture. Our experiments aim at understanding the physical roles of flow and shear in the spatiotemporal organization of multispecies bacterial communities.

References

[1] Jing G, Zöttl A, Clément E, Lindner A. Sci Adv. 2020 Jul 10

P21: Cell motility: A particle-based mesoscopic modeling approach

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Cell motility is essential in many biological processes such as wound healing, immune response, etc. The motility is a complex process, primarily modulated by actin cytoskeleton and cell membrane properties. As it is extremely vital process, it has attracted lot of attention in last few decades on both experimental and modelling side. Majority of computational models for cell motility are based on continuum models which makes incorporation of different cytoskeleton elements such as microtubules or motors non-trivial. However, particle-based models provide flexibility to incorporate various cytoskeletal elements. In this presentation, I will present our mesoscopic particle-based cell motility model. Cell membrane is modelled as a triangulated surface. The actin dynamics are employed by discretizing and solving the continuum actin polarization field on the membrane. We present discrete keratocyte cell like motility modes by varying model parameters that are related to actin dynamics. Some of the dynamical states agree with experiments and continuum modeling approaches. The speed of the moving cell depends on the cell morphology and adhesion strength with substrate. We also discuss how these dynamical states depend on membrane properties such as membrane viscosity and membrane tension.

P22: Characterizing collective motion transition for suspensions of pusher microswimmers

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Active matter is any system in which the constituents are capable of transforming energy to self-propel or exert mechanical force. Numerous examples of such systems exists such as flocks of birds, bacteria, and Janus particles. At sufficiently high densities, spontaneous phenomena emerge as a resultant of the interactions between these self-propelled particles. An example of this class of phenomena is the chaotic collective behavior that appears in bacterial suspensions and manifest in the form of low Reynolds numbers turbulences [1], more commonly known as active turbulence. Using large-scale particle resolved Lattice Boltzmann simulations, we simulate suspensions of pusher microswimmers e.g., E. coli. Active turbulence emerges naturally as a result of mere long-range hydrodynamic interactions. We aim to characterize this transition by exploring different potential order parameters. We observe large number fluctuations at the transition, a marker of out-of-equilibrium systems. These anomalous fluctuations have been mostly studied in dry active matter dominated by short-range interactions, and is unprecedented for systems with only long-range interactions, such as ours.

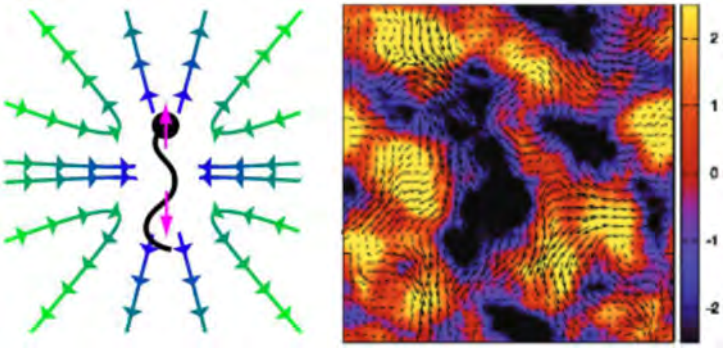

Figure 1: Left: Schematic image of the flow field induced by pusher swimmers [2]. Right: Snapshot of a slice of the fluid velocity field at the turbulent regime. Vectors show the velocity field in the xy-plane and the colours indicate it's z-component [3].

References

[1] A. Creppy, O. Praud, X. Druart, P. L. Kohnke and F. Plouraboue. Phys. Rev. E: Stat., Nonlinear, Soft Matter Phys., **92**, 032722. (2015)

[2] Elgeti, Jens Winkler, R. Gompper, Gerhard. Reports on Progress in Physics. 78, 056601. (2015)

[3] Dóra Bárdfalvy, Henrik Nordanger, Cesare Nardini, Alexander Morozovc, Joakim Stenhammar. Soft Matter, **15**, 7747-7756. (2019)

P23: microArgos: a novel approach to long-term cell tracking

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Classical cell tracking techniques can be generally separated into two classes: lagrangian techniques allow high-frequency observation of the trajectory of a single cell over fundamentally unlimited space-time windows [1], while eulerian approaches (such as defocused imaging methods [2]) allow population-level observations, collecting brief trajectories of a multitude of cells inside a fixed spatial region. For certain types of applications, however, we would like to to follow individual cells continuously over long timescales (hours) and large spatial domains (at least hundreds of millimeters), while still having access to population-level statistics within the same biological sample. Inspired by the Argos satellite system [3], now a cornerstone of macroscopic behavioral ecology, used to track animal movements at the planetary scale, we are developing a microfluidic platform to perform long-term observations (6 hours) of hundreds of individual bacteria over a centimeter-scale domain. This new approach, based on low-resolution multi-band fluorescence imaging, where a moving-stage microscope scans over a microfluidic arena, will help us understand the decision-making strategies of individual bacteria in ecologically relevant scenarios, e.g: how different bacteria tune their energy investment towards motility in nutrient-deplete conditions, and how the history of nutrient encounters can affect the future behavior of individuals.

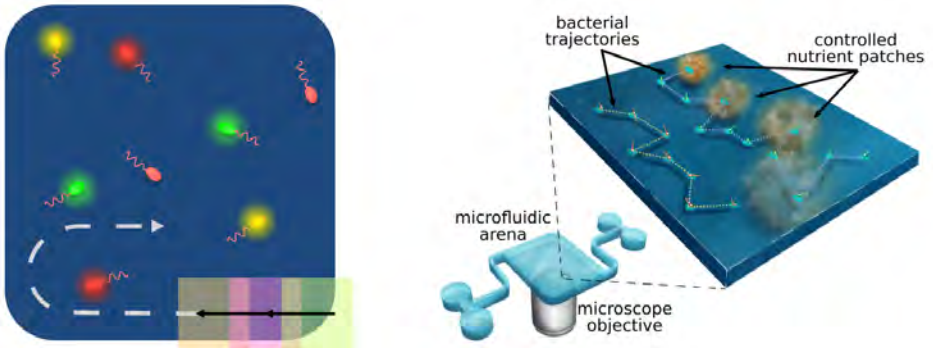

Figure 1: (Left) Operating principle of the microArgosplatform: a moving-stage microscope scans over a centimeter-scale domain to collect low-resolution images of bacteria with locally unique fluorescent barcodes. (Right) Individual bacteria are tracked for hours in controlled chemical landscapes to correlate foraging behavior with their individual nutrient encounter history.

References

[1] T. Darnige et al., Review of Scientific Instruments **88**.5, 055106, (2017)
[2] K.M. Taute et al., Nature Communications **6**.1, 1–9, (2015)
[3] B.A. Block et al., Nature **475**.7354, 86–90, (2011)

P24: Motile cilia induce velocity and diffusion within the Periciliary Layer

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The ciliated epithelium of the human respiratory tract is lined by a thin stratified fluid. This airway surface liquid (ASL) serves as a protective barrier and is essential for maintaining normal respiratory mechanics. However, our understanding on how it is propelled by cilia and how flow is coupled between the two ASL compartments is still fragmentary. Mucus transport can be measured experimentally via various techniques, but the complex and impenetrable structure of the Periciliary Layer (PCL), occupied by cilia-tethered mucins which create a brush with nanometric mesh size [1], is more challenging as for example it interferes with the conventional use of tracer beads. Earlier studies have measured the average displacement of fluorescent dyes localised in the PCL [2], but have not managed to extract a clear velocity profile in this layer. Moreover, while [2] found extremely reduced transport after removal of the mucus layer, the same result was not observed in more recent studies on mucus-washed explanted tracheae [3],[4]. In the last decades, great effort has also been put in understanding cilia-driven flows from a theoretical perspective. However, given the complexity of the system, many studies simulated the problem by introducing one or several approximations, commonly producing contrasting results [5],[6]. We tackled the constrains posed by the PCL structure with the use of caged-fluorescent compound and high-speed imaging of airway epithelium from a side view. Briefly, we photoactivated the dye in a localised region within the PCL and followed its translation and diffusion over time. We believe that activating the compound at different distances from the apical surface of the epithelium and extracting the velocity for each position provides an effective method to experimentally determine the flow profile in the PCL.

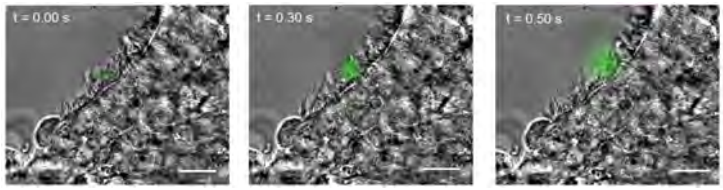

Figure 1: Fig. 1: PCL transport can be measured following the displacement of a fluorescent dye uncaged within the cilia layer. Scale bar = 20μm.

References

[1] B. Button et al., Science, **337**, 6097, (2012).
[2] H. Matsui et al., The Journal of clinical investigation, **102**, 6 (1998).
[3] J. Hussong et al., Journal of biomechanics, **46**, 3, (2013).
[4] S. Bermbach et al., American journal of respiratory cell and molecular biology, **51**, 1, (2014).
[5] P. G. Jayathilake et al., Computers Fluids, **67**, (2012).
[6] D. J. Smith et al., Bulletin of mathematical biology, **69**, 3, (2007).

P25: Viscotaxis of Swimming Sperm Cells

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How do sperm steer? How do they change their swimming direction? How is directional motion achieved in complex environments? These are important issues to be clarified in order to understand how sperm can negotiate their tortuous journey toward the egg [1,2,3]. Here, external fields and gradients can play an important role. A well-known and well-investigated is chemotaxis, where concentration gradients of a chemo-attractant are sensed and guide sperm toward the egg. We investigate here another potentially relevant mechanism, viscotaxis, in which sperm reacts to gradients of fluid viscosity. Our model employs the slender-body approximation for the flagellum in combination with resistive force theory for the hydrodynamics of propulsion [4,5]. Preliminary simulation results indicate that sperm reorients in the direction of increasing viscosity.

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] J. Gray and G.J. Hancock, J. Exp. Biol. **32**, 802 (1955)
[5] J. Elgeti et al., Biophys. J. **99**, 1018 (2010).

P26: Bio-hybrid microshuttels remotely controlled by light

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Active particles can apply forces on passive structures and generate mechanical work [1]. Using light-driven bacteria [2] as propellers we can steer 3-D printed microshuttles by unbalancing light intensity over different shuttles parts. We show that by a dynamic feedback loop that couples position and orientation to the projected light pattern we can independently guide multiple micro-shuttles through a series of checkpoints distributed in space. These bio-hybrid micro-machines are very efficient in converting light power, so that in principle hundreds of such systems could be controlled simultaneously with optical powers in the milliwatts range. The microstructures are produced by two-photon polymerization and are designed to capture individual bacteria within their compartmentalised structure in order to optimally harness their propulsion mechanism. This remote control micro shuttles can provide a powerful microrobotic tool for lab-on-chip applications.

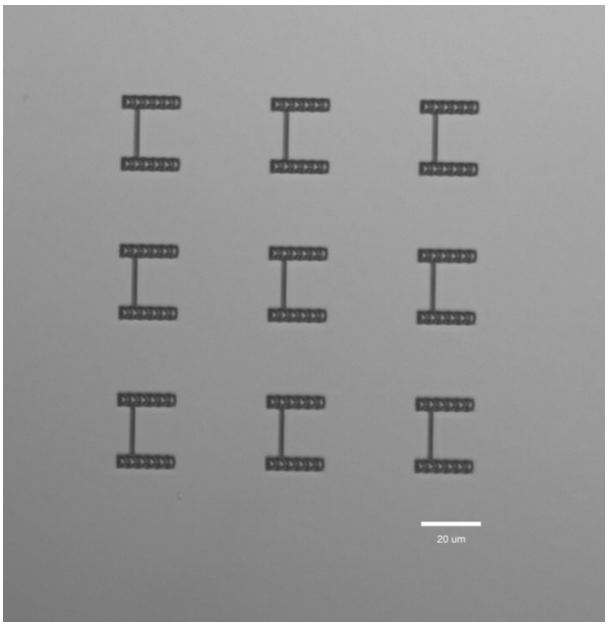

Figure 1: An array of fabricated microstructures (without bacteria).

References

[1] Vizsnyiczai,G.et al. Light-controlled 3D micromotors powered by bacteria. Nat Commun **8**, 15974 (2017).

[2] Frangipane G. et al. Dynamic density shaping of photokinetic E. coli eLife **7**:e36608. (2018).

P27: Automatic 4D tracking of swimming microorganisms using digital holographic microscopy

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Observing and measuring motility on a microscale is a difficult task, necessary to understand the basic processes governing the world of aquatic microorganisms [1]. Despite its importance, there is still a lack of easy to use intervention-free tools that would allow insight into this fascinating world without the need to use markers or pre-existing libraries. Digital holographic microscopy (DHM) is a technique that is ideally suited for microscale 3D measurement and tracking at high speed [2]. Herein, we report a label-free method that allows for precise 3D localization of a single point inside a microorganism. We developed an algorithm that combines a point 3D detection method with digital holographic microscopy to track swimming microorganisms and biological microstructures. The proposed approach is characterized by high precision (0,1 m lateral resolution and 0,2 m axial resolution) and the ability to measure 3D the shape of complex structures such as the flagellum of sperm cells. The presented results prove the practicality and metrological potential of the method for observing the motility of bacteria and biophysical parameters or for automatic 3D detection of the flagella shape.

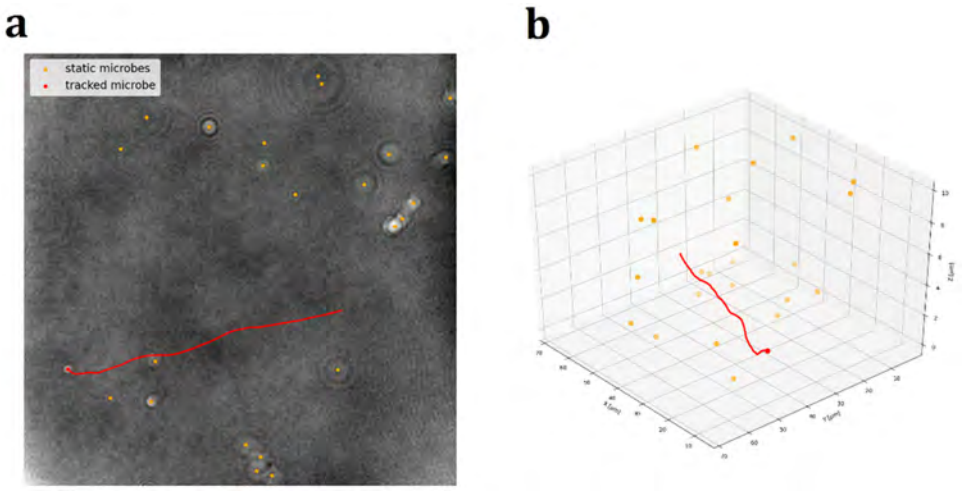

Figure 2: Result of the 3D tracking algorithm of Paraglaciecola sp. (a) 2D trajectory of the tracked microbe (red) with the static background microbes marked (orange). (b) the 3D trajectory of the tracked microbe (red) with marked 3D positions of static background microbes (orange)

References

[1] K. Son, D. Brumley, R. Stocker, “Live from under the lens: exploring microbial motility with dynamic imaging and microfluidics,” Nat Rev Microbiol **13**, 761-775 (2015)
[2] J. Sheng, E. Malkiel, and J. Katz, "Digital holographic microscope for measuring three-dimensional particle distributions and motions," Appl. Opt. **45**(16), 3893-3901 (2006)

P28: Large variability in the motility of spiroplasmas in media of different viscosities

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Spiroplasmas are bacteria that do not possess flagella and their motility is linked to kink propagation coupled to changes in the cell body helicity. While the motility of bacteria with flagellar motion has been studied extensively, less work has been devoted to the motility of spiroplasmas. We first show that the motility of such bacteria has large variability from individual to individual as well as large fluctuations in time. The Brownian motion of such bacteria both in orientation and translation is also highlighted. We propose a simple model to disentangle the different components of this motility by examining trajectories of single bacteria in different viscosity solvents. The mean velocity of the bacteria turns out to depend on the viscosity of the medium as it increases with viscosity. Further, the temporal fluctuations of the bacteria motility turn out to be very strong with a direct link to tumbling events particular to this bacteria.

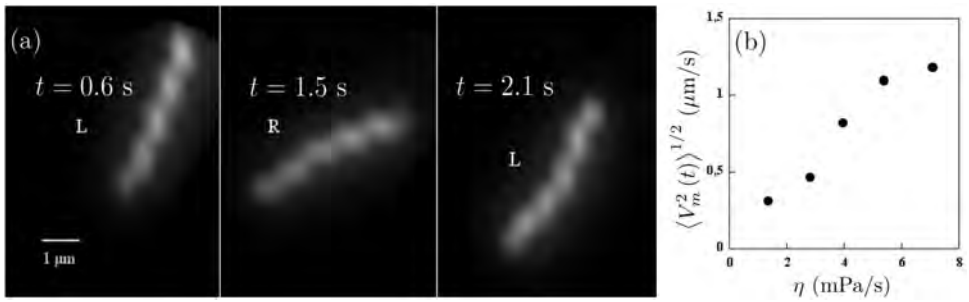

Figure 1: (a) Sequence of dark-field microscopy images of a Spiroplasma citri bacterium with several changes from left (L) and right (R) helicity after kink propagation along the cell body (adapted from [1]). (b) Motor velocity of the bacteria as a function of the solution viscosity η.

References

[1] J.F. Boudet et al., Scientific Reports **8**(1), 1-14, (2018)

P29: A study of bacteria entrapment using multiparticle collision dynamics

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The purpose of the current study is to investigate entrapment of bacteria near surfaces. Mechanisms to control trapping of bacteria near solid surfaces is of utmost interest to many medical and biotechnological applications. Trapping leads to enhanced attachement, facilitates the proliferation of cells and ultimately the formation of bacterial biofilms on the surface. Bacteria such as Escherichia coli (E. coli) propel themselves by rotating a bundle of helical flagella. They can change direction by reversing the rotation of a flagella, a process known as tumbling. The motion of bacteria near surfaces induces hydrodynamic interactions with the substract, aligning the cell almost parallel to the surface. This creates an attractive force from the bacteria to the surface, moving and trapping the bacteria along it [1, 2, 3]. We currently implement a realistic model of E. coli including its tumbling motion within a computer code where we couple it to fluid flow at low Reynolds numbers. The fluid flow is simulated using the method of multi-particle collision dynamics, an efficient solver of the Navier-Stokes equations. Our first goal is to simulate non-tumbling numerical strain of E.coli under shear flow. We will analyse the importance of rheotaxis and Jefferey orbits for near surfaces motility and trapping.

References

[1] A. P. Berke, L. Turner, H. C. Berg, and E. Lauga, Phys. Rev. Lett. **101**, 038102 (2008).
[2] C. Bechinger, R. Di Leonardo, H. Löwen, C. Reichhardt, G. Volpe, and G. Volpe, Rev. Mod. Phys. **88**, 045006 (2016).
[3] E. Lauga, W. R. DiLuzio, G. M Whitesides, and H. A. Stone, Biophys. J. **90**, 400 (2006).

P30: Oxygen mediated algae-bacteria interaction controlled with light

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The algae Chlamydomonas reinhardtii (C.R.) is a photosynthetic microorganism able to produce oxygen using light, with a rate dependent on intensity and wavelength. This oxygen is fundamental for bacteria to fuel their metabolism. In fact, highly concentrated suspensions of E. coli deplete oxygen in a few minutes and when this happens they stop to swim. However, by introducing C.R. to the suspension and shining red light on the sample, we can restore E. coli motility through algae photosynthesis. Another possible way to restore their motility (photokinesis) is using a genetically modified strain expressing the light-driven proton pump proteorhodopsin [1] and shining green light on them. Furthermore, both bacteria and algae respond to blue light: E. coli increase their tumble rate [2] while C.R. adhere to the surface [3]. By using a digital light projector we will shine tailored patterns of different colors with high precision in space and time to stimulate these responses independently. In this way, we want to introduce a new strategy to control the motility of E. coli with light. The complex interplay of photosynthesis, phototaxis, and photokinesis will produce new interesting phenomena challenging current theories of active matter while providing novel insights into the collective dynamics of marine ecosystems.

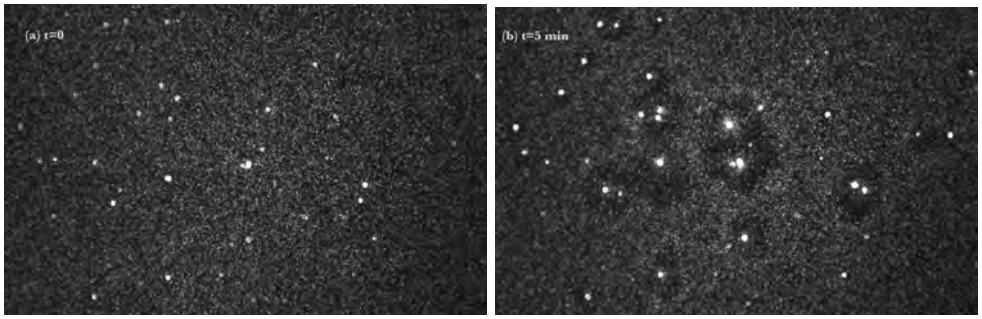

Figure 1: Fig. 1: The effect of green light on the sample in (a) t=0 and (b) t=5 min.

References

[1] Jessica M Walter, Derek Greenfield, Carlos Bustamante, and Jan Liphardt. Light-powering escherichia coli with proteorhodopsin. Proceedings of the National Academy of Sciences, **104**(7):2408–2412, 2007.

[2] Tatyana Perlova, Martin Gruebele, and Yann R Chemla. Blue light is a universal signal for escherichia coli chemoreceptors. Journal of bacteriology, **201**(11):e00762–18, 2019.

[3] Christian Titus Kreis, Marine Le Blay, Christine Linne, Marcin Michal Makowski, and Oliver Bäumchen. Adhesion of chlamydomonas microalgae to surfaces is switchable by light. Nature Physics, **14**(1):45–49, 2018.

P31: Neutral swimmer moves upstream

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A hydrodynamic model for microswimmers, squirmer model, categorizes flow fields around swimming cells into three patterns: pusher, puller and neutral swimmer. While, in the past decade, pusher (e.g., mammalian sperm, bacteria) and puller (e.g., Chlamydomonas, Euglena) have been focused on, we studied swimming behaviours of neutral swimmer (e.g., Paramecium, Tetrahymena) in hydrodynamic experiment and theory [1,2]. Rheotaxis, a property of aquatic organisms to move against an external flow, plays a crucial role to stay in living environments. For instance, freshwater fishes in rivers swim upstream to avoid being swept away to the sea. We elucidated the rheotaxis of the ciliate, Tetrahymena, a well-known single-celled freshwater microorganism swimming by cilia (Fig.1-left) [3]. While that microorganism does not have a sensor to detect flow direction and micrometer-sized particles are swept away downstream in a viscous flow, what dynamics underlie the rheotaxis of the ciliate? Our experiments revealed that the ciliate slid upstream along a wall, which indicates that the cells receive rotational torque from shear flow to align swimming orientation. To evaluate the shear torque, we performed a numerical simulation with a hydrodynamic model swimmer adopting cilia dynamics in a shear flow (Fig.1-right). The result suggests that the ciliate automatically slides upstream by using cilia-sensing mechanics.

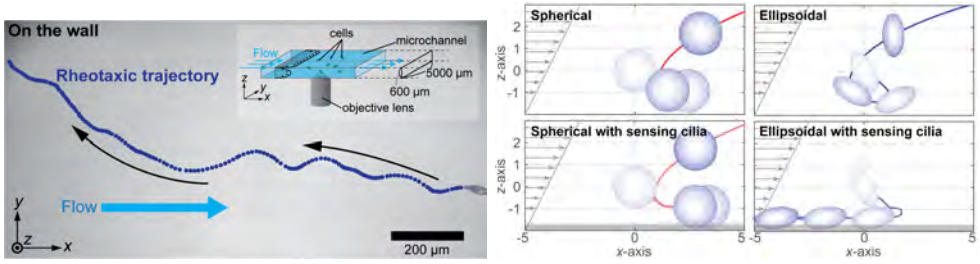

Figure 1: (left) Rheotaxis of ciliates on a wall. (right) Numerical calculation

References

[1] T. Ohmura, Y. Nishigami, A. Taniguchi, S. Nonaka, J. Manabe, T. Ishikawa, M. Ichikawa, PNAS **115**, 3231–3236 (2018)
[2] Y. Nishigami, T. Ohmura, A. Taniguchi, S. Nonaka, J. Manabe, T. Ishikawa, M. Ichikawa, Commun. Integr. Biol. **11**, e1506666 (2018)
[3] T. Ohmura, Y. Nishigami, A. Taniguchi, S. Nonaka, T. Ishikawa, M. Ichikawa, Sci. Adv. **7**, eabi5878 (2021)

P32: Excitable gait control in a sperm-like marine quadriflagellate

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Eukaryotic microorganisms typically display a range of motile behaviours characterised by the dynamic actuation of cilia. The ecological role of any given motility pattern includes environment exploration, energy conservation, and escape dynamics in response to external stimuli. Producing these behaviours requires the contortion of the cilium into a remarkable range of waveforms highlighting the versatility of the cilium as a propulsion device. A vast array of cilium-driven locomotion strategies and behaviours exist in diverse marine flagellates but full scale quantification of these is lacking. This makes broader parallels about the shared propulsion characteristics hard to clearly identify. Here we focus on the unicellular marine alga Pterosperma. This organism consists of a cell body with a typical size of 8 μm and four cilia that can extend to 80 μm in length. The cell displays highly excitable behaviour with the capacity to operate its cilia independently in a quiescent state or by bundling these into a single compound cilium in order to drive swimming behaviour, reminiscent of spermatozoa, as well as ultrafast re-orientations that are capable of turning the cell through 180^0. We present the first biophysical characterisation of the motility of this marine alga. This incorporates population-wide motility phenotyping, swimming mode selection at the single-cell level, and single-cilium dynamics that drive cell locomotion. We compute residency times and transition rates between discrete swimming modes and demonstrate how these are indicative of the ecological role played by these behaviours. We extract ciliary waveforms from high-speed imaging data, and use these to directly quantify and make theoretical predictions about the resulting fluid-structure interactions and swimming dynamics observed. Finally, we apply our novel multi-scale characterisation to study how cells respond to environmental stimuli focusing on the function of the cilium as a key sensory organelle.

P33: Multiscale analysis of colony expansion in a run-reverse motile bacteria

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A colony of motile bacteria is a good experimental example of coupling between single-cell motility behaviour and large scale colony expansion. To which extent does the behaviour of each cell control the spreading dynamics of the whole colony? An answer could lie at an intermediate scale: collective motility and long-range correlation (typically 100 μm) emerge from cell-cell interactions (typically 1 μm), and yield to colony morphogenetic patterns (typically 10 cm, Figure 1, left). I investigate this multiscale coupling in the bacterium Pseudomonas aeruginosa. Each cell can move forward or backward by spinning its single corkscrew-shaped flagellum clockwise or counterclockwise. These motile cells are so densely packed within a colony growing on an agar gel that collective migration naturally emerges. I focus on two regions: at the very edge of the colony, cells are organised as a monolayer and run-reverse swimming mode translates into a nearly jammed 2D phase (Figure 1, right). A few millimetres from the edge, the colony gets thicker (20 μm) and cells display active turbulence, with long-range nematic ordering and topological defects. I characterise cell trajectories and emergence of long-range alignment, with the aid of an innovative Deep-Learning model for segmentation and tracking, and I correlate these physical quantities to colony shapes in various motility mutants.

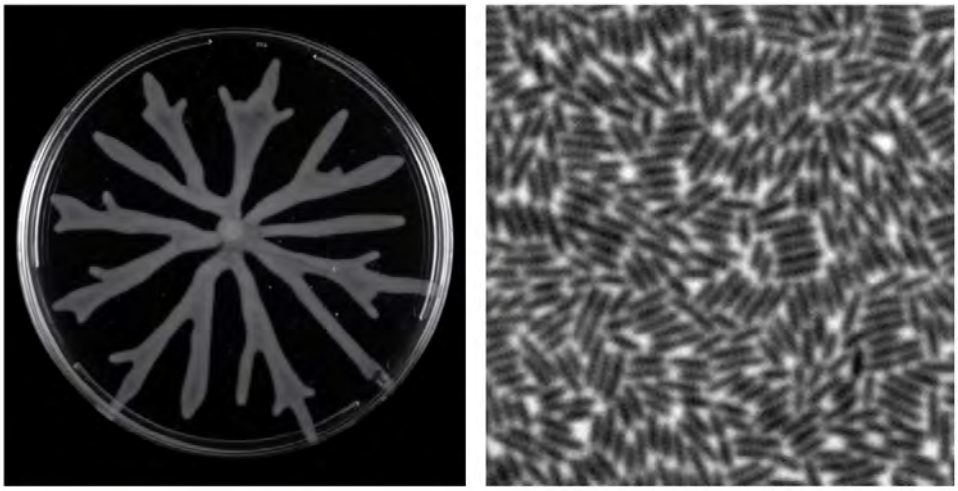

Figure 1: Left: Pseudomonas aeruginosa swarming colony growing on an agar gel (10 cm in diameter). Right: monolayer organization at the colony edge, displaying nearly jammed phase (average cell length = 2 μm).

P34: Elastohydrodynamic origins of viscosity-related flagellar beat transitions in sperm

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Sperm flagella are driven by an internal 'engine' known as the axoneme. Flagella exhibit complex beating waveforms and the mechanism by which these beat patterns are regulated remains largely unknown. It is observed that environmental factors such as external fluid viscosity and the presence of walls cause transitions in these patterns [1]. For instance, sea urchin sperm [2] switch from planar to helical beating and back again to planar beating when viscosity of the ambient fluid is increased. It is currently thought that such beat transitions are biochemically regulated [3]. We demonstrate an elastohydrodynamic origin for changes in beating patterns. Recent models have shown that spontaneous flagellar oscillations can emerge due to elastohydrodynamic instabilities [4]. In our simulations, a preferred-curvature travelling wave is imposed in the material frame of every cross-section of the inextensible and unshearable Kirchhoff rod that is suspended in a Newtonian fluid. Non-local hydrodynamic interactions are included through Rotne-Prager-Yamakawa tensors. We also compare our simulation results to experimental data obtained with freely-swimming bull sperm in fluids of different viscosities. Our results show, for the first time, beat transitions qualitatively similar to those observed in experiments. As viscosity is increased, planar-helical-planar transitions are observed. Stability analysis suggests that the transitions emerge from a linear instability. We also observe more complex irregular beating in certain regions of the parameter space. Furthermore, the beat patterns in some regions of the parameter space are modified by the presence of an infinite plane wall.

References

[1] E. A. Gaffney, H. Gadelha, D. J. Smith, J. R. Blake and J. C. Kirkman-Brown, Annual Review of Fluid Mechanics **43**, 501–528 (2011)
[2] D. Woolley and G. Vernon, J. Exp. Biol. **204**(7), 1333–1345 (2001)
[3] C. B. Lindemann and K. A. Lesich, Cytoskeleton **78**(2), 36–51 (2021)
[4] B. Chakrabarti and D. Saintillan, Phys. Rev. Fluids **4**, 043102 (2019)

P35: Interacting particles in an activity landscape

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We study interacting active Brownian particles (ABPs) with a space-dependent swim velocity. We find that, although an equation of state exists, a mechanical equilibrium does not apply to ABPs in activity landscapes. The pressure imbalance originates in the flux of polar order across the interface between regions of different activity. An active-passive patch system is mainly controlled by the smallest global density for which the passive patch can be close packed. Below this density a critical point does not exist and the system splits continuously into a dense passive and a dilute active phase with increasing activity, see Fig. 1(a). Above this density and for sufficiently high activity the active phase may start to phase separate into a gas and a liquid phase caused by the same mechanism as motility-induced phase separation of ABPs with a homogeneous swim velocity, see Fig. 1(b).

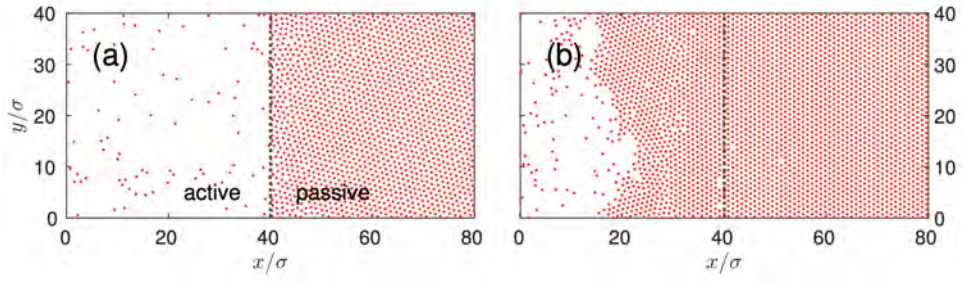

Figure 1: Snapshots of active Brownian particles in an active-passive patch system for two different global packing fractions $\phi_0 = 0.4$ (a) and $\phi_0 = 0.7$ (b) but for the same activity Pe = 30. Only half of the simulation box is shown and the dotted vertical line indicates the interface between the active (left) and the passive region (right). Lengths are scaled by the particle diameter σ

References

[1] A. Wysocki, A. K. Dasanna, and H. Rieger, arXiv:2204.01029, (2022).

P36: Collective effects in auto-chemorepulsive particles : band formation and search strategies

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Autochemotaxis refers to the ability of organisms to produce a chemical cue to which their motility behavior is sensitive. From ants to immune cells, this phenomenon is observed in nature at different scales and is often used as a communication channel between organisms of the same species, in particular for the collective search of preys (food, toxic cells, ...). Here, we present results on the collective effects of auto-chemorepulsive particles using a lattice model. While a strong chemotactic coupling acts as a propeling force that makes particles move in straight lines in the low density regime, this complex interaction may lead to the formation of bands of particles traveling at constant speed in the transverse direction as density increases. Such bands form if fluctuations allow a high concentration of particles in a localized region, which results in an intense chemotactic field that traps other particles in its vicinity and grow even larger. We will here describe the conditions and mechanisms for these bands to form and how the efficiency of a collective search is negatively impacted by them.

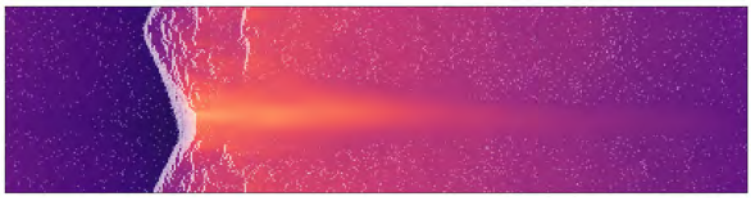

Figure 1: Band formed by auto-chemorepulsive particles. The color represents the intensity of the chemical field while the white dots indicate the position of the particles.

References

[1] H. Meyer, H. Rieger, Physical Review Letters **127**(7), 070601 (2021).

P37: Run and Tumble is not good enough: Bacterial motility in tight porous confinement

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Bacteria and other motile microorganisms are often encountered in porous media with pore sizes ranging down to the diameter of a single cell. Such tight confinement imposes challenges for swimmers when they navigate their environment. To investigate what makes a swimmer successful at this task, we developed a model of micro-swimmers based on rod-shaped Brownian particles with various types of motility such as straight swimming, run-and-tumble or run-and-reverse[1]. Here we present the application of the model to geometries inspired by recent experiments[2] and the analysis of the resulting trajectories with emphasis on long-time effective diffusivity. This allows us to establish a ranking of motility types with regard to their ability to explore porous media.

References

[1] M. Lee, J. Chem. Phys. **150**, 174111 (2019)
[2] T. Bhattacharjee, Nat Commun **10**, 2075 (2019)

P38: Locomotion of Active Polymerlike Worms in Porous Media

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There have been many recent advancement in our understanding of active matter as a framework to study microbial motility. However, most of these studies focus on the motility of rigid shapes in free environments, while in nature microbes tend to be elongated, flexible and live in very complex and crowded environments. We investigate the locomotion of thin, living T. Tubifex worms that behave as active polymers in model quasi-2D porous media made of an array of 3D-printed pillars. Active worms spread in the crowded environment with dynamics that depend on the concentration of obstacles and on whether the lattice exhibit a random or an ordered phase. Our findings show that the motion of active polymers can be optimized by tuning these parameters and rationalized using well-known reptation concepts borrowed from classical polymer dynamics. Interestingly, we found that the spread of the active worm can be strongly enhanced by decreasing the worm's activity, allowing us to passively sort the worms by activity.

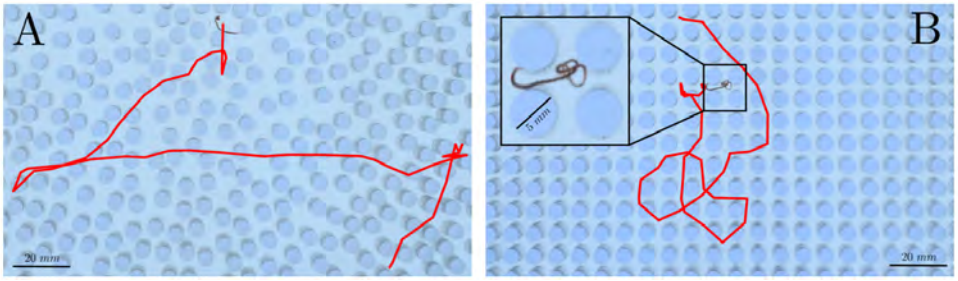

Figure 1: Trajectory of the same T. Tubifex worm in both an ordered and disordered porous medium. Both trajectories took 3.2 minutes.

P39: Changing bacterial swimmers' locomotion strategy under flow conditions

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We report on changes in the swimming strategy of rod-shaped bacteria under flow conditions. To swim bacteria utilise special lash-like organelles on the cell body, flagella. The model organism for this study is the soil bacterium Pseudomonas putida, which has a rod-shaped body and multiple flagella located at one pole of the cell (lophotrichous flagellation), so they can act in concert to drive the bacterium in a single direction. The strategy of switching between different swimming modes (push-pull-wrap) in bulk was already well described.1,2 Here, we increase the complexity of the system and study the cells' locomotion strategy under flow to better understand the processes of infection spreading in capillaries and biofilm formation in a natural environment. The creation of hydrodynamic flows in sub-millimetre dimensions is mostly carried out by microfluidic devices, in our study, we use the advantages of this kind of approach to create different shear stress conditions in the bulk fluid and close to the surface. For varying the geometry of flow patterns on the micron-scale we also use light-induced flow technics (in particular thermo-osmosis on a gold surface3) to create flow locally and to advect or trap swimming bacteria. To analyse the well-known "run-and-turn" strategy performs under flow conditions, we concentrate on characteristic features of the swimming pattern, such as changes in the swimming modes distribution, concentration and also orientation with respect to the flow. By tracking the position of the cell body and the configuration of its flagella at same time, we observe that run modes show different flow responses. We also study a mutant cell line under flow conditions (cells with total deficiency in motor function) to elucidate the role of the cell geometry in this process.

References

[1] Z. Alirezaeizanjani, R. Großmann, V. Pfeifer, M. Hintsche, and C. Beta, Sci. Adv. **6**,(2020).
[2] M. Hintsche, V. Waljor, R. Großmann, M.J. Kühn, K.M. Thormann, F. Peruani, and C. Beta, Sci. Rep. **7**, 1 (2017).
[3] V. Muraveva, M. Bekir, N. Lomadze, R. Großmann, C. Beta, and S. Santer, Appl. Phys. Lett. **120**, 231905 (2022).

P40: Active particles in optical fields

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Active matter labels systems that take energy from the environment to perform an action. Bacteria colonies, bird flocks, and human crowds are just a few examples of systems described as active matter. Conversely to their passive counterpart, active systems exhibit collective behaviours, e.g., swarming. The study of active matter is an interdisciplinary task of primary importance in modern science to understand, for example, the formation of biofilms and the spread of infections. Moreover, artificial active particles hold the potential for many applications, e.g., in personalised healthcare. However, an understanding of the behaviour of active systems in realistic (spatially complex and time-varying) environments is missing [1]—hindering their use in practical and fundamental problems. Here, we exploit light fields to create topographies with high control of both their spatial and temporal properties. Our model system consists of silica colloids half-coated with a carbon layer, suspended in a critical mixture of water and 2,6-lutidine [2] and under the illumination of a complex light field (speckle). We show that a speckle field influences the dynamics of a single active particle by modifying the step size and velocity-autocorrelation of its motion.

References

[1] C. Bechinger, R. Di Leonardo, H. Löwen, C. Reichhardt, G. Volpe, G. Volpe, Reviews of Modern Physics 88, 1, (2016).
[2] C. Lozano, B. ten Hagen, H. Löwen, C. Bechinger, Nature Communications 7, 1, (2016).

P41: Rectification and confinement of photokinetic bacteria in an optical feedback loop

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Active particles can self-propel by exploiting locally available energy resources. When powered by light [1], these resources can be distributed with high resolution allowing spatio-temporal modulation of motility [2, 3]. Here we show that the random walks of light-driven bacteria are rectified when they swim in a structured light field that is obtained by a simple geometric transformation of a previous system snapshot [4]. The obtained currents achieve an optimal value that we establish by general theoretical arguments. This optical feedback is used to gather and confine bacteria in high-density and high-activity regions that can be dynamically relocated and reconfigured. Moving away from the boundaries of these optically confined states, the density decays to zero in a few tens of micrometers, exhibiting steep exponential tails that suppress cell escape and ensure long-term stability (Fig. 1). Our method is general and scalable, providing a versatile tool to produce localized and tunable active baths for micro-engineering applications and systematic studies of non-equilibrium phenomena in active systems.

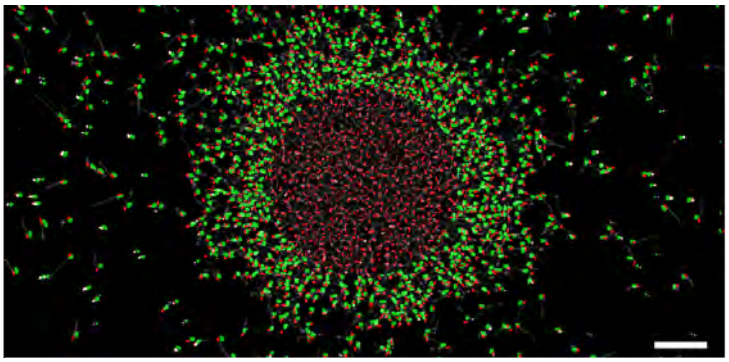

Figure 1: Confined bacteria with the optical feedback loop. Dark-field microscope image of the bacteria (red) superimposed with the bright regions in projected dynamic light pattern (green). White traces represent bacterial trajectories of the previous 2s. Scale bar is 50μm.

References

[1] J. M. Walter, D. Greenfield, C. Bustamante and J. Liphardt, Proc. Natl. Acad. Sci. U. S. A., **104**, 2408–2412 (2007)
[2] G. Frangipane et al., eLife, **7**, e36608 (2018)
[3] J. Arlt, V.A. Martinez, A. Dawson, T. Pilizota and W.C. K. Poon, Nat. Commun, **9**, 768 (2018)
[4] H. Massana-Cid, C.Maggi, G. Frangipane, R. Di Leonardo, Nat. Commun **13**, 2740, (2022)

P42: Clustering dynamics of passive particles induced by swimming bacteria

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Passive particles immersed in an active bath of micro-swimmers, either artificial swimmers or living microorganisms, may be displaced due to the activity of the suspension. This enhanced motion can lead to interesting phenomena, *e.g.* aggregation or phase separation. In this study, we highlight experimentally for the first time an aggregation dynamics for such a system. We add fluorescent beads to a bacterial suspension of *Burkholderia contaminans* [1]. When suspended in the bacterial bath, the beads display an effective diffusive motion, as previously described [2,3]. On a larger scale, they gather in dense zones which are growing in time. One important feature of these clusters is their dynamics: particles are constantly exchanged from one cluster to another. We measure the characteristic lengthscale L_c of these clusters for various bead diameters D_B, surface fractions Φ_B and bacterial concentrations. We show that this characteristic lengthscale is well described by the self-similar growth

$$\frac{L_c}{R_B} = \beta\left(1+\alpha\frac{t}{\tau}\right)^{1/3} \quad ; \quad \tau = \frac{R_B^2}{\Phi_B \mu_B}, \tag{0.1}$$

with $R_B = D_B/2$ the bead radius, μ_B the effective diffusion coefficient and τ the characteristic aggregation time. Measurements of bead-bead relative velocity allow us to reconstruct the short-range attractive force ($\sim 10\,\mu$m) induced by the bacterial swimming motion and responsible of this cluster formation.

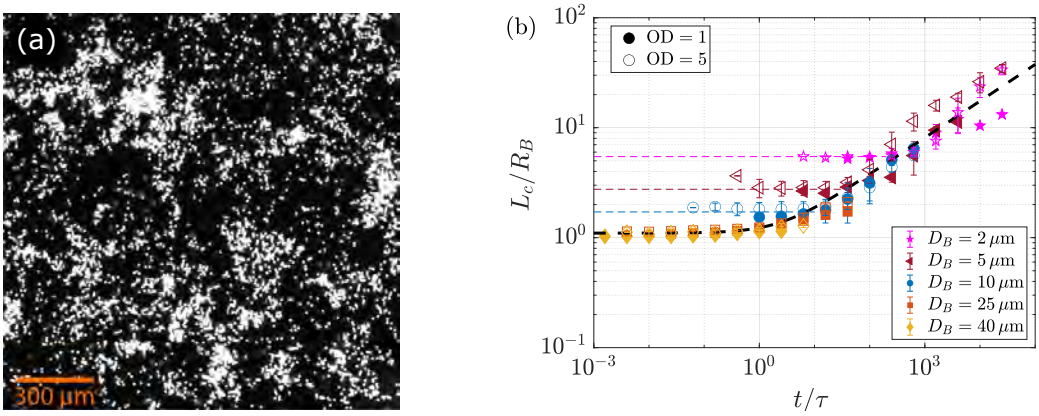

Figure 1: (a) Fluorescent image of beads of diameter $D_B = 10\,\mu$m, at $\Phi_B = 0.3$, in a bacterial suspension at an optical density OD = 5. (b) Evolution of the normalized cluster size L_c/R_B as a function of the normalized time t/τ for various bead diameters D_B and bacterial concentrations.

References

[1] J. Bouvard et al., accepted in Physical Review E (2022)
[2] X. L. Wu and A. Libchaber, Physical review letters **84**(13), 3017, (2000)
[3] A. E. Patteson et al., Soft matter **12**, 2365, (2016)

P43: Implications on Aquatic Environments of Active-Passive Particles' interaction

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In recent years, the study of systems composed of a mix of active and passive elements has become a burgeoning research field, with a focus on the subtleties of their interactions and the richness and potential control of their emergent properties. These have mostly been analyzed by means of theoretical and numerical models, although recent advances in experimental techniques and, in particular, suitable model systems have started to boost its empirical study. Potential applications for the control of active-passive systems in technological settings abound, but their implications in the natural world (e.g., for ecological interactions) might not be that obvious. For instance: what happens when a fish swims on/through/near the sediments? Maybe not much unexpected. But now imagine motile micro-algae... What happens when a microscopic single-cell organism interacts with a single grain of sand? How should we take into account the correct fluid dynamics? And the alga's microbial motility? What's the dynamics of the passive component in a dense bath of actively swimming microbes?
In this case, what happens is an active-passive matter!

P44: Flows induced by a capsule of microalgae

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When active particles are encapsulated in a droplet, the droplet exhibits a random motion. To rectify this random motion and obtain a directional trajectory of the droplet, the only current means is to place the droplet in an anisotropic solution of liquid crystals. Here, we encapsulate the microalgae Chlamydomonas reinhardtii in aqueous droplets and place them in oil. The oil is seeded with microparticles, enabling to track the oil flow induced by the encapsulated microalgae. When the microalgae are illuminated from below with a strong white light, they form dynamic patterns of photobioconvection. This leads to flows outside the droplet. Our results will help understand under which condition it is possible to make move directionally a droplet filled with microalgae, and how to steer it with light.

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Useful Information

Venue

The workshop will take place at the Pierre Gilles de Gennes Institute for Microfluidics at 6 Rue Jean Calvin, 75005 Paris.

Talks will be held at the **Amphitheatre** of IPGG. It is situated at the ground floor strairs down towards your right when you enter the building.

The **poster session** will be held on Wednesday night from 18.00 on, right in front of the amphitheatre of the IPGG.

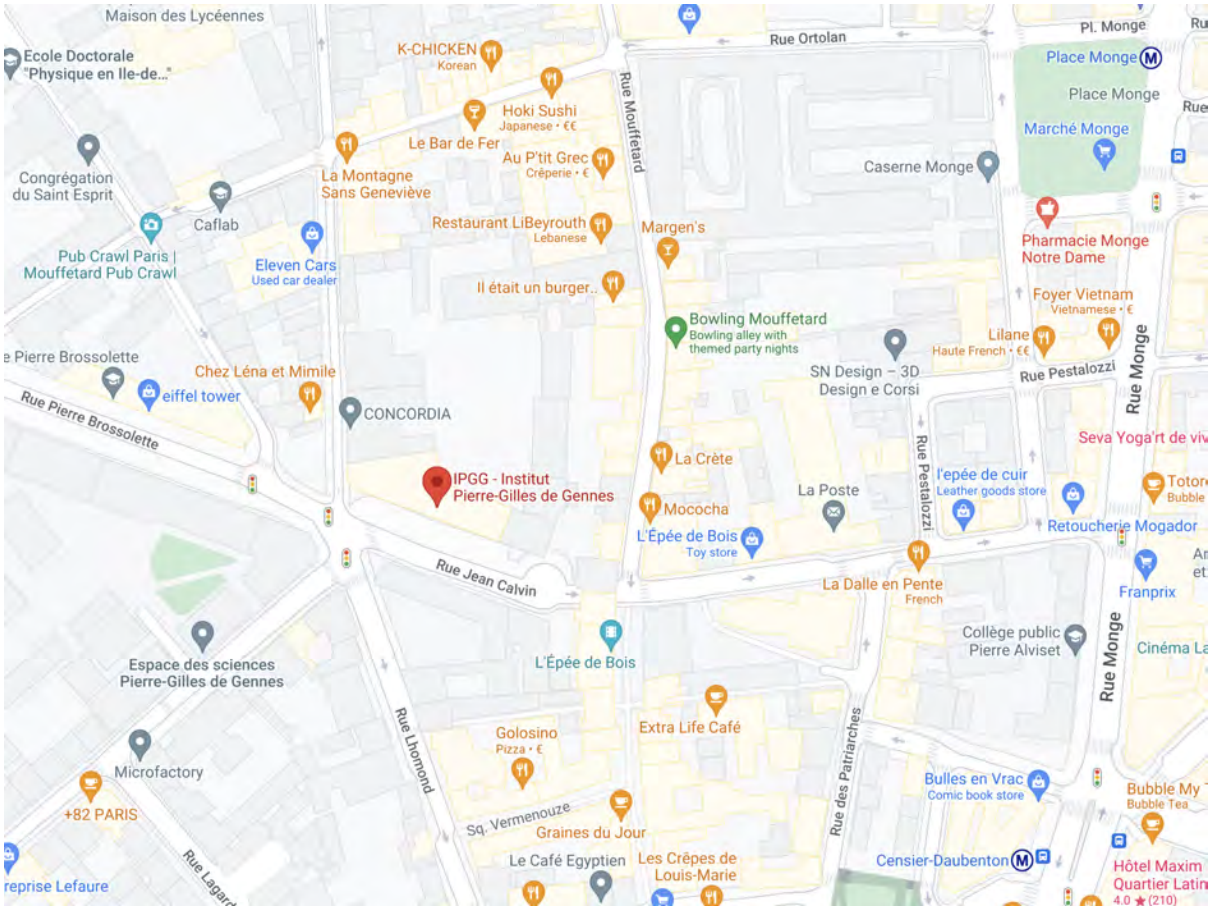
The **conference dinner** will be held on Thursday night from 18.00 on, at the Salle Panoramique, Tour Zémanski, 24th floor Campus Jussieu, Sorbonne Université, 4, place Jussieu, 75005 We will walk here all together after the last talk of the day.

How to get to the IPGG?

The Institut Pierre-Gilles de Gennes located at 6 Rue Jean Calvin, 75005 Paris, can be reached by:

- **Metro:** Line 7 “Censier – Daubenton”
- **Metro:** Line 7 “Place Monge”
- **RER:** Line B "Luxembourg"

see also the map at the next page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Lebanese
Il était un burger..
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Graines du Jour
Rue des Patriarches
Bulles en Vrac
Comic book store
Bubble My
Bubble Tea
Le Café Egyptien
Les Crêpes de Louis-Marie
Censier-Daubenton
Hôtel Maxim Quartier Latin
4.0 ★ (210)
reprise Lefaure
Rue Lagarde