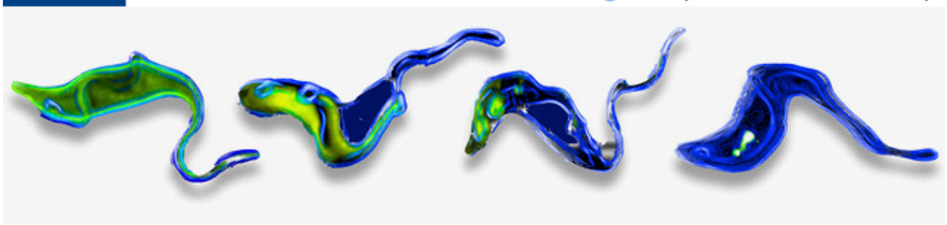
Physics of Microbial Motility



Report of Contributions

https://events.hifis.net/e/phymot_W2

Contribution ID: **9** Type: **not specified**

Welcome: Marcus Engstler & Gerhard Gompper

Wednesday 4 October 2023 13:50 (10 minutes)

Contribution ID: **13** Type: **Poster**

Colloidal transport by light-induced gradients of active pressure

Active fluids, like all other fluids, exert mechanical pressure on confining walls. Unlike equilibrium, this pressure is generally not a function of the fluid state in the bulk and displays some peculiar properties. For example, when activity is not uniform, fluid regions with different activity may exert different pressures on the container walls but they can coexist side by side in mechanical equilibrium.
Here we show that by spatially modulating bacterial motility with light, we can generate active pressure gradients capable of transporting passive probe particles in controlled directions. Although bacteria swim faster in the brighter side, we find that bacteria in the dark side apply a stronger pressure resulting in a net drift motion that points away from the low activity region.
Using a combination of experiments and numerical simulations, we show that this drift originates mainly from an interaction pressure term that builds up due to the compression exerted by a layer of polarized cells surrounding the slow region.
In addition to providing new insights into the generalization of pressure for interacting systems with non-uniform activity, our results demonstrate the possibility of exploiting active pressure for the controlled transport of microscopic objects.

Primary author: PELLICCIOTTA, Nicola (Sapienza University of Rome)

Co-authors: Mr BUONOMO, Dario (La Sapienza University of Rome); Dr FRANGIPANE, Giacomo (Sapienza University of Rome); Dr ANGELANI, Luca (ISC-CNR); Dr PAULUZZI, Matteo (Departament de Física de la Matèria Condensada); Prof. DI LEONARDO, Roberto (Sapienza University of Rome)

Presenter: PELLICCIOTTA, Nicola (Sapienza University of Rome)

Contribution ID: **14** Type: **PHYMOT contributed talk (20 min)**

Control of bacteria turbulence through surfaces

Hydrodynamic instabilities appear in E. coli suspensions at high enough concentrations. Controlling such instabilities could allow extracting energies at the microscales. We achieved control of the collective motion size in a sample confined between two parallel solid surfaces at a distance of H. By measuring the velocity correlation function in the center of the sample, we determined that the decay length scales increase linearly with the value of H up to $800\mu m$. We also tracked passive beads inside the bacteria turbulence and determined the impact of this scaling in the mixing properties of the bath. These results show that controlling the size of the collective motion is possible even at larger scales, revealing the importance of surface effects in the properties of the active suspension.

Primary authors: Prof. LINDNER, Anke (PMMH - ESPCI); PEREZ ESTAY, Benjamin (PMMH - ESPCI); Prof. CLEMENT, Eric (PMMH - Sorbonne Universite)

Presenter: Prof. LINDNER, Anke (PMMH - ESPCI)

Contribution ID: **15** Type: **Contributed talk (20 min)**

Bacterial glass transition in Pseudomonas aeruginosa

Motile bacteria self-organize in numerous collective phases, such as orientationally ordered phase or swarming state. These collective phases 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 colonies and biofilms formation. Here we study the properties of the 2D swarming state of an elongated motile bacteria, Pseudomonas aeruginosa, in growing colonies. We are able to obtain large and dense bacterial monolayers at the edge of 3D colonies expanding on agar gels. We perform the detection of bacterial trajectories from high-speed movies through the use of an innovative deep learning technique that compute segmentation and tracking altogether, taking advantage of temporal information. As density increases in bacterial monolayers, P. aeruginosa undergoes kinetic arrest, and collectively transitions from a liquidlike state to a glassy state. We show that this transition does not only affect the scales of the system's relaxation times, but also the very nature of the dynamics at play. We reproduce the analysis to several P. aeruginosa mutants of different shapes and single-cell motion properties, and show that all flagellated mutants exhibit a similar glass transition. The critical surface density to trigger the transition does not depend on single-cell motion properties, and seems to only depend on the aspect ratio of cells.

Primary author: MALIET, Martin (Sorbonne University)

Co-author: Dr DEFORET, Maxime (Sorbonne University)

Presenter: MALIET, Martin (Sorbonne University)

Contribution ID: **16** Type: **Poster**

Chemotaxis quantification methods with a three channel microfluidic chip

Bacteria and plants communicate via chemical signals to establish symbiotic interaction. The chemosensory system of the bacteria receives chemical inputs that biases the random motility of the bacteria.
Microfluidic technologies now make it possible to produce chips in which the chemical environment can be controlled. The model I use is a chip with three parallel channels on an agarose layer. Fluids containing known concentrations of the chemical species are placed in the outer channels. This generates a gradient of the chemical species across the agar layer. After a few minutes, we inject a suspension of bacteria into the central channel.
The cell is placed under a microscope, allowing us to film the bacterial population regularly. The first series of studies we carried out aimed to characterize the method's limitations for determining the chemotactic response of bacteria. In particular, we looked at the influence of channel surfaces on the measurement. To this end, we used fluorescent *E. coli* bacteria and placed them in Casaminoacid gradients.
By taking measurements at different heights over the 80-micron height of the channel, we have shown that the chemotactic response is not the same on the surfaces and in the middle of the channel. We will propose a model including this effect. We also want to characterize the influence of viscosity on chemotaxis by adding PVP to our suspension. We will conclude by applying this method to Sinorhizobia meliloti.

Primary author: Mr GARGASSON, Adam (FAST)

Co-authors: Dr DOUARCHE, Carine (FAST); AURADOU, Harold (FAST, CNRS, Université Paris-Saclay); Prof. MERGAERT, Peter (I2BC)

Presenter: Mr GARGASSON, Adam (FAST)

Contribution ID: **17** Type: **Poster**

Influence of motility and hydrodynamics on phage-bacteria encounters

Bacteriophages - or “phages” for short - are viruses that can infect and kill bacteria. They are small particles that rely on thermal diffusion to find target cells, but are also advected in the flow-field generated by motile bacteria. We use coupled lattice-Boltzmann and coarse-grained molecular dynamics simulations to investigate the encounter between phages and bacteria. We find that while motility increases the encounter rate, the effect is much smaller than what would be predicted if hydrodynamic interactions were neglected. This has important implications for our understanding of the evolutionary cost that bacteria have to pay for their motility.

Primary author: LOHRMANN, Christoph (University of Stuttgart, Institute for Computational Physics)

Co-authors: Prof. DATTA, Sujit (Princeton University, Department of Chemical and Biological Engineering); Prof. HOLM, Christian (University of Stuttgart, Institute for Computational Physics)

Presenter: LOHRMANN, Christoph (University of Stuttgart, Institute for Computational Physics)

Contribution ID: **18** Type: **PHYMOT contributed talk (20 min)**

Optimal run-and-tumble in confinement

Run-and-tumble is a basic model of persistent motion and a widespread moving strategy in micro-organisms and individuals cells. In many natural settings, motion occurs in the presence of surfaces and confinement~[1]. While accumulation at the wall has been extensively studied~[2,3], the transport along the surfaces has received less attention. We consider a run-and-tumble particle confined in a slit, and which may move, or not, at the wall. We first propose a four-direction model that is fully tractable and obtain analytically the long-time diffusion coefficient along the slit. Second, we show using numerical simulations of more realistic motions that our prediction is to a large extent valid more generally. Third, we find that lateral transport might be maximized by an optimal mean run time and identify the conditions for the existence of an optimum. Our results should help to assess the advantages of micro-organisms moving strategies in confined environments.

Primary authors: COTTIN-BIZONNE, Cecile (University Claude Bernard Lyon 1); Mr YBERT, Christophe (Université Claude Bernard Lyon 1); DETCHEVERRY, Francois (Université Claude Bernard Lyon 1); Mr PIETRANGELI, Tommaso (Université Claude Bernard Lyon 1)

Presenter: DETCHEVERRY, Francois (Université Claude Bernard Lyon 1)

Contribution ID: **19** Type: **Invited Talk (30 min)**

Elastic Bistability and the Geometry of Cellular Neighbourhoods in Choanoflagellates and Green Algae

Elastic Bistability and the Geometry of Cellular Neighbourhoods in Choanoflagellates and Green Algae

Raymond E. Goldstein
DAMTP, University of Cambridge, Cambridge, United Kingdom
E-mail: R.E.Goldstein@damtp.cam.ac.uk

This talk will describe two recent advances in understanding the physics of cellular organization in simple multicellular organisms. The first part concerns the fluid dynamical and elastic properties of the recently discovered [1] multicellular choanoflagellate *C. flexa*, which dynamically interconverts between two hemispherical forms of opposite curvature. The swimming and filter-feeding properties are described [2] within a simple model of a raft of spheres with associated stokeslets to represent the action of the flagella. An elastic model based on linear elasticity of the microvilli of adjacent cells that adhere to each other is shown to support bistability at the organism level as a consequence of the presence of numerous pentagonal neighbourhoods in the raft. In the second part I will first review the recent findings [3] that the cellular neighbourhood volumes in both lab-evolved and extant multicellular species, obtained by Voronoi tessellations based on the cell locations, are accurately described by gamma distributions, suggesting a hitherto unrecognized "universal"aspect of noise in cellular packing. Here we propose an explanation [4] of those observations by considering the very simplest models for stochastic ECM generation by somatic cells and show that they define Poisson point processes whose Voronoi tesselations are demonstrably governed by gamma distributions. I summarize by proposing a link between the two parts of the talk.

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Primary author: GOLDSTEIN, Raymond (University of Cambridge)

Presenter: GOLDSTEIN, Raymond (University of Cambridge)

Contribution ID: **20** Type: **Contributed talk (20 min)**

Structural Colour from Bacteria Collective Motion

We report a type of marine, non-pathogenic bacteria, Flavobacterium Iridescent 1 (IR1), that grows into a colony in active liquid crystal phase with intense structural colour. We show that these rod-like gliding bacteria organize hierarchically, from bacteria clusters, to monolayer, multi-layers and finally into large scale chiral vortices up to one millimeter in diameter. We demonstrate that the bacteria motility gives rise to three-dimensional ordered nanostructure that constructively reflects incident light, resulting in the bright iridescent colour observed in the colony [1-2]. We also illustrate how the bacteria colony adapts to confinement of different geometries.

Primary author: WANG, Junwei (University of Cambridge)

Presenter: WANG, Junwei (University of Cambridge)

Contribution ID: **21** Type: **Contributed talk (20 min)**

Droplet and waving instabilities of an active fluid jet

Micro-algae in relatively dense suspensions modify their environment by absorbing light, consuming and releasing chemical compounds or generating flows. Instabilities that appear in those systems can in turn give biological insight regarding the way this critically important class of micro-organisms navigate their environment.

Here we harness phototaxis to precisely control millions of swimming Chlamydomonas reinhardtii cells and experimentally test theoretical predictions regarding the behavior of dense suspensions, in which they interact via their self-generated flows [1,2,3,4,5]. Starting from a straight cell jet, we show for the first time the two kind of instabilities that were predicted : its breaking into drops and its buckling into waves, depending on the cells preferential orientation. The instabilities wavelength and growth rate can be controlled notably by light intensity.

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Primary author: EISENMANN, Isabelle (LPENS, Ecole Normale Superieure)

Co-authors: Mr LAUGA, Eric (DAMTP); Mr DESPRAT, Nicolas (LPENS); Mr JEANNERET, Raphaël (LPENS); Mr ISHIKAWA, Takuji (BFSL)

Presenter: EISENMANN, Isabelle (LPENS, Ecole Normale Superieure)

Contribution ID: **22** Type: **Poster**

Bacterial chemotaxis considering memory effects

The ability of motile microorganisms to sense and migrate along due to a chemical or ligand gradient is known as Chemotaxis. This process is a key ingredient in some biological performances, like the acting of immune systems or tumoral migration in metastasis. This mechanism is used also for bacteria to find places to proliferate. The first relevant theoretical model to describe this phenomenon at a macroscopic scale came at the hands of the Keller and Segel article **[1]**. They introduce a macroscopic equation that couples a diffusion-drift equation for bacterial density with a reaction-diffusion equation for the chemoattractant concentration. Over the years, chemotaxis has been increasingly understood. For example, a bacterium like *E. coli*,
orients itself through run-and-tumble movements, altering its tumble rate when moving in the direction of the ligand gradient. The variation of this magnitude depends on fluctuations in the concentration of phosphorylated CheY protein (CheY-P) **[2]**. Tracking *E. coli* bacteria,it was found that these fluctuations have large amplitude and present long memory times (tens of seconds) **[3]**. These new performances are not taken into account in the Keller-Segel model and fails to predict some experimental results. The objective of this work is to obtain new macroscopic equations that can perform the phenomena precisely. Considering a stochastic differential model for CheY-P concentration with memory effects **[4]**, we use a kinetic equation that presents the memory relaxation time and changes in tumble rate **[5]**. By identifying different scales of memory time, we derive a Keller–Segel type chemotaxis model by applying the Chapman-Enskog method in each case. For short memory times, we can only consider the bacteria's density as a conserved field. We deduce the equation, which allows us to obtain the diffusion coefficient and mobility. The results are in agreement with Keller-Segel's predictions for the memoryless time limit. When we consider long memory times, the density of CheY-P protein is a quasi-conserved field. In this case, macroscopic equations of bacteria's density and CheY-P density are derived, together with the associated transport coefficients. In this case, macroscopic equations of bacteria's density and CheY-P density are derived, together with the
associated transport coefficients. An Onsager's relation is obtained for the transport coefficients. We validate these equations by analyzing the stationary regime and linear response to a spatiotemporal signal and compare them with simulations.

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Primary authors: MAYO LEON, MANUEL (Universidad de Sevilla, Universidad de Chile); Dr SOTO, Rodrigo (Universidad de Chile)

Presenter: MAYO LEON, MANUEL (Universidad de Sevilla, Universidad de Chile)

Contribution ID: **23** Type: **Invited Talk (30 min)**

Active density patterns formation in bacterial binary mixtures

In wild environments, phenotypically diverse microorganisms interact both physically and chemically to give rise to complex community organization [1]. We are interested in the role of physical interactions arising from flagellar motility, a major bacterial trait, in the structuration of such complex communities. This aspect, contrary to biochemical interactions, remains less studied in experiments, despite out-of-equilibrium mechanisms such as motility-induced phase separation (MIPS) offering potential routes for structure emergence [2].
We focused on a minimal system for complex microorganism communities, a binary mixture of motile and non-motile Escherichia coli bacteria. We report a novel non-equilibrium phenomenon by which strong large-scale density heterogeneity patterns of the non-motile bacteria emerge when mixed with motile ones, in a wide physiologically relevant range of concentrations. Experimental results together with quantitative modeling and numerical simulations show that circular swimming of motile cells at surfaces generate recirculation flows that advect the non-motile cells through hydrodynamic interactions, and that sedimentation, by breaking the vertical symmetry of the system, is essential for local non-motile cell accumulation and the emergence of the large-scale density fluctuations. This behavior represents a new type of non-equilibrium self-organization in active bacterial populations, distinct from MIPS-like phenomena, which appears crucial for complex microbial community structuration [3]. We also find that similar physical constraints govern non-motile segregation to the left-hand side when the binary mixture is under flow.

Primary authors: ESPADA BURRIEL, Silvia; DIDIO, Giacomo; COLIN, Remy

Presenter: COLIN, Remy

Contribution ID: **24** Type: **Poster**

Local curvature steers the self-organization of active particles in confinement

The impact of confinement on the self-organization of active particles has gained much attention1,2,3. Previous investigations have primarily focused on circular or square/rectangular geometric constraint. However, to explore more realistic scenarios, like particles enclosed in a membrane, confinement in curved geometry is essential 4. A suitable and simple geometry for such a case happens to be the ellipse. Consequently, we present simulations (in Julia5) of active Brownian particles in hard elliptical confinement. The particles interact via hard sphere correction and experience reflection upon reaching the boundary6. We found curvature-dependent organization of the particles, wherein more particles tend accumulate at high curvature (equators) of the ellipse. Moreover, the extent of curvature induced collection depends on various factors, including on the eccentricity of the ellipse, packing fraction, particle size, and velocity. Furthermore, we are actively looking for experimental evidence of this collective dynamics based on active Janus particles (Pt/silica) confined inside elliptical micro wells. To have the necessary confining structure, we successfully implemented a novel yet simple drop cast method allowing formation of a few microns sized elliptical wells in a PDMS film. These wells were able to confine the Janus particles, aiding observation. We anticipate our results might be applicable to the design of active particles-based microrobots, where environment-induced curvature of the membrane boundary could guide encapsulated active particles.

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5) https://julialang.org/

Primary author: Dr SHARMA, Jyoti (The Biorobotics Institute, Sant'Anna, Pisa, Italy)

Co-authors: Mr BIANCIARDI, Francesco (The Biorobotics Institute, Scuola Superiore Sant'Anna, Pontedera (Pisa), Italy); Mr CORTI, Lapo (University of Pisa, Pisa, Italy); Prof. PALAGI, Stefano () The Biorobotics Institute, Scuola Superiore Sant'Anna, Pontedera (Pisa), Italy)

Presenter: Dr SHARMA, Jyoti (The Biorobotics Institute, Sant'Anna, Pisa, Italy)

Contribution ID: **25** Type: **Contributed talk (20 min)**

Controlling bacterial swimming in wavy channels

The navigation of swimming microorganisms, such as bacteria, is guided by rheotaxis, their re-orientation with respect to flow gradients. While recent investigations focused on the con- trol of passive particles, such as red blood cells, in spatially modulated and time-dependent flows [1–3], less is known about the behavior of swimming agents in such flows. 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, a wavy-induced swinging motion is revealed which can become resonant. As a consequence swimmers are distributed across the channel instead of accumulating at its center. We show that wavy-induced tumbling exhibits a much larger ampli- tude compared to tumbling in planar flows and is characterized by rapid, oscillatory patterns of motion along the lateral direction. Our results suggest new strategies for controlling the behav- ior of live and synthetic swimmers in microchannels. For example, the wavy channel provides a means for the separation of bacteria according to their properties, such as size or swimming speed, potentially aiding their selective elimination [4].

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Primary author: SCHMIDT, Winfried (Universität Bayreuth)

Co-authors: ARANSON, Igor S.; ZIMMERMANN, Walter

Presenter: SCHMIDT, Winfried (Universität Bayreuth)

Contribution ID: **27** Type: **Poster**

Anomalous bacterial transport in confined geometries

Motile bacteria are known to interact with flows exhibiting in the bulk active Betherton-Jeffery trajectories or rheotactic drift due to the helical flagella shapes. In the vicinity of bound- ing surfaces, one also observes specific trajectories including persistent upstream swimming, an effect enhanced by the presence of edges. 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⊠ in extension. In disordered and complex environments, the presence of surface and flow make large-scale dispersion properties of active bacteria a challenging issue.

Based on the previous study, here we developed experimental model systems suited to observe individual trajectories and to assess the emerging dispersion processes in funnel-shape microfluidic device(figure(a)) varying the flow velocity using motile bacteria. We found: (1) a sharp density increases downstream close to surfaces at the same shear rate as in previous work(figure(a)); (2) the concentration difference indicator (⊠1) increase with time and then reach a steady state. This work will help to understand the role of flow on the transport of motile bacteria, in the presence of geometrically complex surfaces and surface.

Primary author: ZHANG, Peixin (PMMH, ESPCI)

Co-authors: LINDNER, Anke (PMMH - ESPCI); Prof. CLEMENT, Eric (ESPCI)

Presenter: Prof. CLEMENT, Eric (ESPCI)

Contribution ID: **28** Type: **Poster**

Flow structures around a microswimmer at fluid-fluid interface

Living organisms such as bacteria and algae often form biofilms at air-liquid and/or liquid-liquid interfaces. Therefore, it is important to understand the hydrodynamic interaction between the fluid-fluid interface and microorganisms. In this study, the flow field structures around a symmetrically trapped spherical microswimmer at an interface separating two fluids with different viscosities are investigated using lattice Boltzmann (LB) simulations. In these simulations, Reynolds (Re) and Capillary (Ca) numbers are very small, and hence the contribution of inertia and interface deformations are neglected. Simulations of different types of microswimmers (pusher, puller, and neutral) are achieved by varying the squirmer parameter (β). It is observed that the flow structure and vorticity distribution around the microswimmers are strongly influenced by the squirmer parameter (β) and viscosity contrast (λ). Furthermore, the interplay between force-dipole and source-dipole along with viscosity contrast leads to a range of flow structures such as symmetric four-lobe, and asymmetric quadrupolar flow fields. Flow structure asymmetry is quantified for swimmer with different steady state orientations. Finally, the hydrodynamic interaction between microswimmer and passive tracer particles are presented in terms of trajectories.

Primary author: MISHRA, RISHISH (Indian Institute of Technology Jammu, India)

Co-authors: Dr GIDITURI, Harinadha (Basque Centre for Applied Mathematics, Bilbao, Spain); Dr POTHUKUCHI, Harish (Indian Institute of Technology Jammu, India)

Presenter: MISHRA, RISHISH (Indian Institute of Technology Jammu, India)

Contribution ID: **29** Type: **Poster**

Chemotactic swimming of two chiral squirmers

Please find the attachment.

Primary author: Dr MAITY, Ruma (TU Wien)

Co-author: Dr BURADA, P. S. (IIT Kharagpur)

Presenter: Dr MAITY, Ruma (TU Wien)

Contribution ID: **30** Type: **Poster**

Simulating Trypanosome Motility

We investigate motility of the protozoan Trypanosoma, using numerical simulations. We have established a trypanosome model (see Fig. 1), which is motivated by experimental observations [1, 2] and builds upon the previously proposed model [3, 4]. The cell body is represented by a set of vertices which are distributed homogeneously on a pre-defined elongated surface and form a triangulated elastic network of springs. The network model also incorporates bending rigidity, and area and volume conservation constraints. For parasite propulsion, a flagellum is attached to the cell body. The flagellum is constructed from four parallely placed filaments, two of which are embedded into the body, and the other two are used for the generation of a propagating bending wave [5]. Flagellum beating leads to a deformation of the body and generates propulsion. We study the behavior of this model for different body stiffnesses, beating frequencies,wavelengths, and amplitudes. The simulations achieve values for the swimming velocity
and the body rotation around its swimming axis, which are at the same order of magnitude as experimental measurements. The trypanosome model is flexible enough and can be adapted to reproduce the behavior of different trypanosome species. This model will be used to investigatetrypanosome locomotion in blood stream.

Primary author: OVERBERG, Florian

Co-authors: FEDOSOV, Dmitry (Institute of Biological Information Processing, Forschungszentrum Juelich); GOMPPER, Gerhard (Forschungszentrum Jülich)

Presenter: OVERBERG, Florian

Contribution ID: **31** Type: **PHYMOT contributed talk (20 min)**

Dispersion of motile bacteria in confined and geometrically complex channels

In the laboratory, we built via soft lithography , geometrically controlled micro-fluidic environments of various complexity. We monitor trajectories of motile wild-type E.coli to characterize the mean transport and dispersion processes under flow. We show that the swimming activity of motile species and in particular their specific trajectories in a flow, their interaction with the walls and well as the internal statistical features driving the run-and-tumble process, lead to emerging transport phenomena different from the classical Taylor-Aris dispersion processes for molecular and colloidal species

Primary authors: LINDNER, Anke (PMMH - ESPCI); Prof. CLEMENT, Eric (ESPCI); Dr JUNOT, Gaspard (Dept of Condensed Matter Physics, University of Barcelona, Barcelona, Spain); ZHANG, Peixin (PMMH, ESPCI); DARNIGE, Thierry (ESPCI-Sorbonne Université)

Presenter: Prof. CLEMENT, Eric (ESPCI)

Contribution ID: **33** Type: **Contributed talk (20 min)**

Transport of passive beads by random and directed motion of swimming micro-organisms

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 [1]. This enhanced motion can lead to rich phenomena such as aggregation or phase separation. In this experimental work, we study how passive beads are moved by randomly swimming bacteria and directionnaly swimming micro-algae.

First, in a uniform environment, we highlight the aggregation dynamics of the beads in a bacterial bath of *Burkholderia contaminans* [2]. Unexpectedly, the passive beads display a dynamic clustering similar to Ostwald rippening: clusters are slowly growing in time as a $t^{1/3}$ power-law, dynamically as beads are constantly getting exchanged from one cluster to another.

Second, we bring our experiment closer to a natural environment by adding biases to the swimming motion of the microorganisms. This time, we use micro-algae *Chlamydomonas reinhardtii* considering their quick reaction to light [3]. As their local concentration grows, the algae push away the passive beads in a steric fashion. By varying the incoming light direction, we manage to create complex patterns of passive particles, and even direct them towards precise locations. Such directed motion of micro-particles open up exciting perspectives, for instance in medicine.

References

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Primary authors: BOUVARD, Julien (LadHyX, Institut Polytechnique de Paris); Mr LAROUSSI, Taha (LadHyX, Institut Polytechnique de Paris)

Co-authors: Prof. MOISY, Frédéric (FAST, Université Paris-Saclay); Prof. AMSELEM, Gabriel (LadHyX, Institut Polytechnique de Paris); AURADOU, Harold (FAST, CNRS, Université Paris-Saclay); Prof. JARRAHI, Mojtaba (FAST, Université Paris-Saclay)

Presenter: BOUVARD, Julien (LadHyX, Institut Polytechnique de Paris)

Contribution ID: **34** Type: **Contributed talk (20 min)**

Quantifying gliding forces of filamentous cyanobacteria

Filamentous cyanobacteria are one of the oldest and today still most abundant lifeforms on earth, with manifold implications in ecology and economics. Their flexible filaments, often several hundred cells long, exhibit gliding motility in contact with solid surfaces. The underlying force generating mechanism is not yet understood. Here, we demonstrate that propulsion forces and friction coefficients are strongly coupled in the gliding motility of filamentous cyanobacteria. We directly measure their bending moduli using micropipette force sensors, and quantify propulsion and friction forces by analyzing their self-buckling behavior, complemented with analytical theory and simulations. The results indicate that slime extrusion unlikely generates the gliding forces, but support adhesion-based hypotheses, similar to the better-studied single-celled myxobacteria. The critical self-buckling lengths align well with the peaks of natural length distributions, indicating the importance of self-buckling for the organization of their collective in natural and artificial settings.

Primary author: KARPITSCHKA, Stefan (Universität Konstanz)

Presenter: KARPITSCHKA, Stefan (Universität Konstanz)

Contribution ID: **35** Type: **PHYMOT contributed talk (20 min)**

Evolution of micro-swimmer designs in distinct microenvironments

Trypanosoma brucei, a eukaryotic parasite with a single flagellum, is transmitted by tsetse flies and thrives across a broad range of vertebrate species. These parasites cause several diseases in their hosts, exemplified by sleeping sickness in humans. Throughout their life cycle, these cells encounter diverse microenvironments with different physical attributes, such as viscosity [1]. These cells have demonstrated a notable capacity to adapt within these microenvironments. Cell morphology and propulsion are highly dependent on flagellar motion [2]. The cell movement initiates with a planar bending wave on the flagellum in the anterior end of the cell, followed by a longitudinal rotation due to the helical attachment of the flagellum to the cell body [3]. However, the details of the motion behavior and morphological cell changes remain insufficiently quantified.
In this study, we acquired live cells at high temporal resolution. This allowed us to elucidate the single-cell movement of Trypanosoma brucei, particularly within different viscosities. This investigation involves quantitatively comparing cell behavior in different viscosities, revealing interesting correlations of rotational cell translocation, and frequency of flagellar beating. Further, the characterization of the environment's rheological properties is underway in order to determine how the environmental properties affect cell behavior. These prompted us to carry out experiments aimed at quantifying the mechanical properties of the cells, explaining the underlying morphological basis for changes in motility patterns.

Primary authors: Prof. ENGSTLER, Markus (Würzburg university, Würburg, Germany); JAMSHIDI KHAMENEH, Narges; Dr KRÜGER, Timothy (Würzburg university, Würburg, Germany)

Presenter: JAMSHIDI KHAMENEH, Narges

Contribution ID: **36** Type: **Contributed talk (20 min)**

Utility of information in chemotaxis

Living cells improve their fitness by sensing noisy environmental signals and tuning their behavior in response in a seemingly modular fashion. Yet these two processes often occur simultaneously, and behavioral response affects future signal values. Whether a cell is aware of and able to efficiently use the information it itself generates, is an open question. A complete understanding of the design of sensing and response motifs, in terms of the *usability* of sensed information, has so far been limited to perturbative regimes without accounting for the information feedback from the cell to the environment (Mattingly et al., 2021).

We address this gap by studying the dynamics of chemotaxis of *Escherichia coli* in a steady chemoattractor gradient, with a coarse-grained model (Long et al., 2017) for sensory receptors and run-and-tumble motion in the seconds timescale. For computing the mutual information between signal and response trajectories, we extend a recently developed numerical algorithm, Path Weight Sampling (PWS) (Reinhardt et al., 2022), to achieve exact computation of mutual information rate in the presence of nonlinear coupling and feedback. We find that there exist distinct optima in terms of cell's behavioral parameters for maximum performance, measured by the chemotactic drift speed, and maximum mutual information rate. Further, irrespective of the cellular environment, sensed information and its *usability* independently constrain chemotactic performance. With analytical theory, we rationalize our findings in terms of the design and interdependence of the sensing and response motifs in *E. coli* and the bimodal nature of a run-and-tumble response.

Primary author: Dr DAS, Avishek (AMOLF, Amsterdam)

Co-author: Prof. TEN WOLDE, Pieter Rein (AMOLF, Amsterdam)

Presenter: Dr DAS, Avishek (AMOLF, Amsterdam)

Contribution ID: **37** Type: **PHYMOT contributed talk (20 min)**

FUNCTIONAL MORPHOLOGY AND FLUID DYNAMICS OF FORAGING IN 'TYPICAL EXCAVATES'

Excavates are phagotrophic flagellates characterized by a ventral groove and two flagella. The anterior flagellum is naked, and its beating creates a feeding current directed towards the groove, while the posterior flagellum is equipped with a vane and beats within the groove. We combined flow visualization and observations of prey capture in three clades of excavates with computational fluid dynamic modelling to understand the functional significance of this arrangement. We estimated clearance rate magnitudes from flow visualization and CFD modelling. We found that a vaned flagellum beating in a confined groove produces a very efficient feeding current at low energy costs, irrespective of the beat plane and the orientation of the vane and of all other morphological variations.

Primary author: MIANO, Federica (Technical University of Denmark)

Presenter: MIANO, Federica (Technical University of Denmark)

Contribution ID: **39** Type: **Contributed talk (20 min)**

Signature of (anti)cooperativity in the stochastic fluctuations of small systems: application to the mechano-sensitive assembly of the bacterial flagellar motor

The cooperative binding of molecular agents onto a substrate is pervasive in living systems, particularly stochastic processes inside cells. When the number of binding sites is small enough, we can rely on a fluctuation analysis of the number of substrate-bound units, an experimentally accessible quantity, to study whether a system shows cooperativity.

First, we present a general-purpose grand canonical Hamiltonian description of a small one-dimensional (1D) lattice gas with either nearest-neighbor or long-range interactions as prototypical examples of cooperativity-influenced adsorption processes. We propose 1) a criterion to determine whether a given adsorption system exhibits cooperative or anti-cooperative behavior and 2) a method to quantify the amplitude of the ligand-ligand interaction potential.

Second, we compare the theoretical predictions of our model to bead assay measurements of the bacterial flagellar motors (BFM) of *E. coli*. In this way, we find evidence that cooperativity controls the mechano-sensitive dynamical assembly of the torque-generating units, the so-called stator units, onto the BFM. Finally, we estimate the stator-stator interaction potential and attempt to quantify the *adaptability* of the BFM.

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Primary authors: PALMERI, John (Laboratoire Charles Coulomb (L2C), Université de Montpellier); FRANCO-OÑATE, María-José (Laboratoire Charles Coulomb (L2C), Université de Montpellier); WALLISER, Nils-Ole (Laboratoire Charles Coulomb (L2C), Université de Montpellier)

Presenter: WALLISER, Nils-Ole (Laboratoire Charles Coulomb (L2C), Université de Montpellier)

Contribution ID: **40** Type: **Poster**

Changes in the phototactic behavior of Chlamydomonas reinhardtii resulting from the integration of past light stimuli

Organisms such as *Chlamydomonas reinhardtii* use phototaxis to explore their environment and find the best conditions for photosynthesis. In our work, we study the phototactic behavior of suspensions of *C. reinhardtii* confined within shallow cylindrical wells, and exposed to directional light stimuli of various intensities. We recover known results: at low light intensities, the algae exhibit positive phototaxis, at high light intensities, negative phototaxis and at intermediate light intensities, we find that the behavior depends on past phototactic stimuli, in a way that is the opposite of an adaptive behavior 1, 2 and [3].

It is known that cells adapt to previous stimuli, and that stimulating *C. reinhardtii* multiple times with an identical high light intensity leads to different responses; the first stimulus leads to negative phototaxis, while after several stimuli, the algae exhibit positive phototaxis, as if they sensed a lower stimulus [4] and [5]. In our experiments at intermediate light intensities, we highlight a behavior that is the opposite of adaptation: cells integrate the signal over time. Applying the same stimulus twice at a couple minutes interval leads to a change in phototactic response, from positive phototaxis to negative phototaxis, such that the response to the second stimulus is the same as if the light was of higher intensity. Waiting a couple hours between the experiments allows to recover the original positive phototactic behavior. A simplified model of phototaxis is introduced, where the time-integration of light stimuli results from the interplay between the underlying biological time scales and the time scales of the light stimuli. The outcome of the model captures qualitatively our experimental results.

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Primary author: LAROUSSI, Taha (LadHyX, Institut Polytechnique de Paris)

Co-authors: AMSELEM, Gabriel (LadHyX, Institut Polytechnique de Paris); JARRAHI, Mojtaba (FAST, Université Paris-Saclay); LAROUSSI, Taha (Ecole Polytechnique)

Presenter: LAROUSSI, Taha (LadHyX, Institut Polytechnique de Paris)

Contribution ID: **41** Type: **PHYMOT contributed talk (20 min)**

HoloV3C: unveiling eukaryotic flagella in 3D with holographic microscopy

The flagellum is pivotal in the survival mechanisms of eukaryotic cells and measuring its three-dimensional shape is essential to understanding these key mechanisms. However, accurately assessing the intricate structure of flagella has been challenging due to the lack of a reliable method for determining the 3D position of individual points. Our digital holographic microscopy (DHM) method overcomes this hurdle, enabling dynamic 3D tracking of eukaryotic cell flagella shape and motility. We harness holographic microscopy benefits, including high-speed imaging of large sample volumes, for 4D tracking (X, Y, Z, and time) of microorganisms and their flagella. This technique offers precise 3D localization of nanometer-sized, unlabeled structures and is robust against changes in reconstruction parameters. We reconstructed for the first time the shape of a 200 nm diameter *Chrysochromulina simplex* flagellum and measured mouse sperm flagella over time, capturing approximately 800 points along a single flagellum. Our proposed method unleashes the full potential of digital holography, enabling high-speed and precise 3D tracking of microorganisms and their flagella at the nanoscale across depths that are beyond the reach of other existing techniques. This opens new avenues for studying flagella's roles in cellular functions and survival strategies.

Primary author: NIENALTOWSKI, Patryk Kamil (Lyncée Tec SA)

Co-authors: Dr MARTINEZ-PEREZ, Clara (Institute of Environmental Engineering, ETH Zurich); Dr SLOMKA, Jonasz (Institute of Environmental Engineering, ETH Zurich); Prof. STOCKER, Roman (Institute of Environmental Engineering, ETH Zurich); Dr COLOMB, Tristan (Lyncée Tec SA); Dr EMERY, Yves (Lyncée Tec SA)

Presenter: NIENALTOWSKI, Patryk Kamil (Lyncée Tec SA)

Contribution ID: **42** Type: **Poster**

Geometry and Motility: Ratcheting, Autonomous Pumping, Guidance and Filtering

The interplay of motility and geometry can lead to a variety of striking effects such as rectification of motion of motile particles and autonomous pumping of passive particles in a ratchet channel 1, trapping and release of motile and immotile particles assisted by motile species 2, guidance and transient rectification of motion of motile particles due to the directional locking in presence of immotile species [3], and guidance of motion of motile particles by soft "boundaries"on a topographically flat surface of distinct chemical patterns allowing reflection, crossing and filtering of motile particles [4].
The mechanism of rectification of motion of motile particles in an asymmetric channel is different from that for the Brownian motion. It essentially involves the memory effect related to motility and the finite persistence length 1. The direction locking leads to the increase of the persistence length and occurs due to the transient "embedding"of motile particles in clusters of immotile species [3].
An electrokinetic motile Janus particle can sense boundaries between distinct chemical patterns with different Zeta-potentials, via the feedback modification of the electroosmotic flows generated by the motile particle by these soft boundaries, resulting in gentle guidance of motile particles on topographically flat surfaces [4].

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Primary authors: Dr MISKO, Vyacheslav (Vrije Universiteit Brussel (VUB)); Dr BARABAN, Larysa (HZDR); Dr MAKAROV, Denys (HZDR); Prof. DE MALSCHE, Wim (Vrije Universiteit Brussel (VUB))

Presenter: Dr MISKO, Vyacheslav (Vrije Universiteit Brussel (VUB))

Contribution ID: **43** Type: **Contributed talk (20 min)**

Microfluidics Approaches for Selection and Enhancement of Sperm Motility for Improved Fertilization

Motility of sperm refers to its ability to swim in a forward direction to reach the oocyte and fertilize it. Normal sperm motility plays a crucial role in couple's reproductive health. Low motility of sperm cells could lead to issues with fertilization. Medical assisted reproduction (MAR) technologies are used to improve fertilization in this case. These imply selecting sperm with the highest motility using various techniques. However, it can occur that the selected sperm does not have the capacity of successful fertilization, due to reduced motility. In this case, it would be desirable to enhance their motility. Thus, it was shown that adding species of higher motility to other species of lower motility could result in an effect called "motility transfer"1. The motility transfer was demonstrated in a binary system of artificial microswimmers, i.e., synthetic Janus particles whose motility is caused by the catalytic chemical reactions at the surface of asymmetric microspheres (e.g., recently synthesized high-motility Ag/AgCl Janus particles active in bio-compatible environments [2, 3]). The proposed technique of motility control 1 can be implemented in various biological and medical systems, where one wishes to enhance the motility of insufficiently active nano- or micro-particles. In case of weakly motile sperm cells, this technique has advantages over other similar proposals (e.g., using self-propelled metallic rotors trapping sperm cells), whereby it is substantially less damaging to living sperms and much easier to implement, as it does not require the fast guest swimmers to localize and trap individual sperms one by one. We will also discuss our recent experimental advances in motility sperm selection techniques (with human sperm) using an acoustic microfluidic setup [4].

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Primary authors: Dr MISKO, Vyacheslav (Vrije Universiteit Brussel (VUB)); Dr BARABAN, Larysa (HZDR); Dr MAKAROV, Denys (HZDR); Prof. DE MALSCHE, Wim (Vrije Universiteit Brussel (VUB))

Presenter: Dr MISKO, Vyacheslav (Vrije Universiteit Brussel (VUB))

Contribution ID: **44** Type: **Poster**

Characterising the motility of the novel SS-5 strain of Magnetotactic bacteria

Magnetotactic bacteria (MTB) have garnered significant interest due to their unique ability to align with magnetic fields and respond to environmental stimuli. Currently, the well-studied species of MTBs exhibit complex cell morphologies and propulsion mechanisms, making them poorly suitable for physics modelling. In this project, we study the aerotaxis and magnetic alignment of the novel SS-5 strain of MTB, which features a simple rod shape similar to E.coli and performs run-reverse motion using a single flagellum. To achieve this, we have developed a custom experimental setup enabling precise tuning of both oxygen concentration and magnetic field within a microfluidic device. Our initial results provide an insightful understanding of the magnetic response of the SS-5 bacteria, indicating a strong ability to align with magnetic fields. Ongoing research focuses on how the SS-5 strain reacts to oxygen gradients, with preliminary results showing a significant aerotactic response to very low oxygen concentrations. These results lead towards a comprehensive modelling of MTB motion, with potential applications in employing their motility responses as navigation tools through complex and confined environments.

Primary authors: COTTIN-BIZONNE, Cecille (University Claude Bernard Lyon 1); DETCHEVERRY, Francois (Université Claude Bernard Lyon 1); PIETRANGELI, Tommaso (Universitè Claude Bernard Lyon 1)

Presenter: PIETRANGELI, Tommaso (Universitè Claude Bernard Lyon 1)

Contribution ID: **46** Type: **Poster**

Run and Tumble Behavior of E. Coli

E. coli is a multi-flagellated bacterium with a prolate spheroidally-shaped body and several left-handed helical flagella (typically between 2 and 5). The helical flagella are rotated by a motor, enabling the bacterium to propel forward. E. coli generally has two modes of swimming: (i) 'run' with a straight swimming direction, and (ii) 'tumble'during which the bacterium can change its swimming direction [1-3]. During the run stage, all flagella rotate anticlockwise, such that they bundle into a single propeller. During the tumble stage, one or more flagella switch to the clockwise rotation, so that they leave the bundle and facilitate E. coli to change its swimming direction. In our work, we investigate how different E. coli properties, including body and flagella geometry, flagella stiffness and the strength of actuation, govern the run-and-tumble behavior of these bacteria. We establish a realistic E. coli model (see Fig. 1) and validate it using available experimental observations [1-3]. The model properly captures the running speed of E. coli, rotational frequency of the head and flagella, tumbling time and angle in comparison to experimental measurements [1-5]. Furthermore, our simulations show that the stiffness of a hook (the short part of a flagellum which connects it directly to the motor) plays an important role in the run-and-tumble behavior, which has also been suggested in experimental studies [6-7]. This detailed model of E. coli helps us better understand its swimming behavior, and allows the exploration of E. coli locomotion in more complex realistic environments such as with walls [8].

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Primary authors: ZHANG, Bohan (IBI-5/IAS-2, Forschungszentrum Juelich); Dr FEDOSOV, Dmitry (IBI-5/IAS-2, Forschungszentrum Juelich); Prof. GOMPPER, Gerhard (IBI-5/IAS-2, Forschungszentrum Juelich)

Presenter: ZHANG, Bohan (IBI-5/IAS-2, Forschungszentrum Juelich)

Contribution ID: **47** Type: **Contributed talk (20 min)**

Hydrodynamic near field effects give rise to fast synchronisation in finite groups of cilia

When many cilia are located on the surface of a microorganism, their beating can synchronise such that their phases form metachronal waves. To understand the process of synchronisation, we study a model where each cilium is represented as a spherical particle, moving along a tilted trajectory with a position-dependent active driving force and a position-dependent internal drag coefficient. The model thus takes into account all the essential broken symmetries of the ciliary beat. We show that taking into account the near-field hydrodynamic interactions, the effective coupling between cilia can become nonreciprocal: the phase of a cilium is more strongly affected by an adjacent cilium on one side than by a cilium at the same distance in the opposite direction. As a result, synchronisation starts from a seed at the edge of a group of cilia and propagates rapidly across the system, leading to a synchronisation time that scales proportionally to the linear dimension of the system. A ciliated surface is thus characterised by three different velocities: the velocity of fluid transport, the phase velocity of metachronal waves and the group velocity of order propagation. Unlike in systems with reciprocal coupling, boundary effects are not detrimental for synchronisation, but rather help to initiate the wave.

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Primary author: VILFAN, Andrej (Max Planck Institute for Dynamics and Self-Organization)

Co-authors: Dr HICKEY, David; GOLESTANIAN, Ramin (Max Planck Institute for Dynamics and Self-Organization)

Presenter: VILFAN, Andrej (Max Planck Institute for Dynamics and Self-Organization)

Contribution ID: **48** Type: **PHYMOT contributed talk (20 min)**

microArgos: a new tool for bacterial movement ecology

Abstract enclosed

Primary author: FOFFI, Riccardo (ETH Zürich)

Co-authors: Prof. PEAUDECERF, François (Université de Rennes); Dr HENSHAW, Richard (ETH Zürich); Prof. STOCKER, Roman (ETH Zürich)

Presenter: FOFFI, Riccardo (ETH Zürich)

Contribution ID: **49** Type: **Contributed talk (20 min)**

Swimming vs gliding: Exploring the first steps of biofilm formation of motile microbes

Cilia and flagella are cellular appendages that enable microorganisms to propel themselves and interact with surfaces. Particularly, the unicellular microalga *Chlamydomonas reinhardtii* swims by actuating its two flagella, but it can also use them to attach to surfaces and perform gliding motility. Its flagellar adhesiveness can be switched on and off by blue and red light, re- spectively 1. This makes *C. reinhardtii* ideal to study surface colonization and aggregation of photoactive microorganisms; the first steps towards biofilm formation. We employ single-cell micropipette force spectroscopy 2 on model substrates and find that flagellar adhesion is of around 1-2 nN in blue light, surface-unspecific, and mediated by electrostatic interactions [3]. We also use bright-field microscopy and a Langmuir-type model to quantify the adsorption and desorption kinetics of a confined suspension of motile *C. reinhardtii* cells under controlled light conditions [4]. Finally, we discovered that populations of surface-associated cells transition from local clusters to interconnected networks with increasing surface coverage by means of their gliding motility in conjunction with flagella mechanosensing [5].

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Primary author: CATALAN, R (Max Planck Institute for Dynamics and Self-Organization (MPIDS), Göttingen, Germany, Chair of Experimental Physics V, University of Bayreuth, Bayreuth, Germany)

Co-authors: FRAGKOPOULOS, A (Max Planck Institute for Dynamics and Self-Organization (MPIDS), Göttingen, Germany, Chair of Experimental Physics V, University of Bayreuth, Bayreuth, Germany); GIROT, A (Max Planck Institute for Dynamics and Self-Organization (MPIDS), Göttingen, Germany, Chair of Experimental Physics V, University of Bayreuth, Bayreuth, Germany); MAZZA, M (Interdisciplinary Centre for Mathematical Modelling, Loughborough University, UK.); BAIDUKOVA, O (Institute of Biology, Humboldt-Universität, Berlin, Germany); BÄUMCHEN, O (Max Planck Institute for Dynamics and Self-Organization (MPIDS), Göttingen, Germany, Chair of Experimental Physics V, University of Bayreuth, Bayreuth, Germany); HEGEMANN, P (Institute of Biology, Humboldt-Universität, Berlin, Germany)

Presenter: CATALAN, R (Max Planck Institute for Dynamics and Self-Organization (MPIDS), Göttingen, Germany, Chair of Experimental Physics V, University of Bayreuth, Bayreuth, Germany)

Contribution ID: **50** Type: **Invited Talk (30 min)**

Swimming and Rheology of Active Suspensions in Viscoelastic Fluids

The natural habitat of microorganisms are non-Newtonian fluids, which besides shear viscosity also have an elastic response. Using a second-order model fluid, we present an analysis, how weak viscoelasticity affects the rheology of a dilute suspension of microswimmers 1. Starting with modifications of the well-known Jeffery orbits and the orientational distribution due to tumbling and rotational diffusion, we show how the effective shear viscosity is influenced. In particular, for pushers such as E.coli bacteria, the shear viscosity is further reduced due to elastic stresses. In the end, we also comment on swimming in a viscoelastic fluid with a reciprocal stroke pattern 2.

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Primary author: STARK, H (Institute of Theoretical Physics, Technische Universität Berlin , D-10623 Berlin, Germany)

Co-authors: CHOUDHARY, A (Department of Chemical Engineering, Indian Institute of Technology Kanpur, Kanpur, India, Institute of Theoretical Physics, Technische Universität Berlin , D-10623 Berlin, Germany); EBERHARD, M (Institute of Theoretical Physics, Technische Universität Berlin , D-10623 Berlin, Germany); NAMBIAR, S (KTH Royal Institute of Technology and Stockholm University, Stockholm 10691, Sweden)

Presenter: STARK, H (Institute of Theoretical Physics, Technische Universität Berlin , D-10623 Berlin, Germany)

Contribution ID: **51** Type: **Contributed talk (20 min)**

Phase separation of passive particles in active liquids

The transport properties of colloidal particles in active liquids have been studied extensively. It has led to a deeper understanding of the interactions between passive and active particles. However, the phase behavior of colloidal particles in active media has received little attention. We have studied passive colloids dispersed in suspensions of active particles in experiments and simulations. Our study reveals dynamic clustering of colloids in active media due to an interplay of active noise and an attractive effective potential between the colloids. The size-ratio of colloidal particles to the bacteria sets the strength of the interaction. As the relative size of the colloids increases, the effective potential becomes stronger and the average size of the clusters grows. The simulations reveal a macroscopic phase separation of passive colloids at sufficiently large size-ratios. We will also present some recent results on the coarsening of passive particles.

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Primary author: CHIKKADI, V (Indian Institute of Science Education and Research Pune, Pune, India 411008)

Co-authors: KUSHAWAHA, P (Indian Institute of Science Education and Research Pune, Pune, India 411008); MAITY, S (Indian Institute of Science Education and Research Pune, Pune, India 411008); MISHRA, S (Indian Institute of Technology (BHU), Varanasi, India 221005); SEMWAL, V (Indian Institute of Technology (BHU), Varanasi, India 221005)

Presenter: CHIKKADI, V (Indian Institute of Science Education and Research Pune, Pune, India 411008)

Contribution ID: **52** Type: **Poster**

Chemotactic swimming of two chiral squirmers

In this work, we investigate the synchronous swimming of a pair of self-propelled low Reynolds number swimmers in a chemical field 1. We observe that the hydrodynamic interaction be- tween the swimmers helps them to reach the chemical target quicker than a single swimmer [1, 2].
We have used the chiral squirmer model [2, 4] to understand the dynamics of the swimmers. The former model swimmer possesses a translational V and an angular velocity Ω. Chiral squirmers exhibit synchronized bounded motion apart from the regular monotonic attraction and repulsion depending on its nature, i.e., puller or pusher type. In bounded motion, they synchronize, approach each other, and separate from each other in a periodic manner [2, 4]. We observe that in a chemical landscape the former synchronized swimming mechanism helps them to reach the chemical target faster. This study is helpful in understanding the collective dynamics of swimmers in a complex environment.

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Primary author: MAITY, R (Institute for Theoretical Physics, Technische Universität Wien, Wien, Austria, Department of Physics, Indian Institute of Technology Kharagpur, Kharagpur, India)

Co-author: BURADA, P. S (Department of Physics, Indian Institute of Technology Kharagpur, Kharagpur, India)

Presenter: MAITY, R (Institute for Theoretical Physics, Technische Universität Wien, Wien, Austria, Department of Physics, Indian Institute of Technology Kharagpur, Kharagpur, India)

Contribution ID: **54** Type: **Poster**

A metabolic switch controls bioconvection in a microbial suspension

Photosynthesis is an essential process for life that converts light into energy for higher-level plants and also phototrophic microbes. Even in the absence of light, these microbes can produce energy through other metabolic processes, such as aerobic and anaerobic respiration. In the case of the unicellular microalga Chlamydomonas reinhardtii, the cell's swimming motility is affected by a number of parameters, e.g. the geometry of the confinement [1,2], but also by the cell's metabolic state. Under unfavourable light conditions for photosynthesis, the deprivation of oxygen severely reduces the cell's swimming velocity. In 2D compartments, the switch from photosynthesis to oxygen respiration causes the emergence of self-generated oxygen gradients and, ultimately, the formation of microbial aggregates [3].
In 3D, density patterns in Chlamydomonas suspensions may also form through bioconvection, a phenomenon that rises due to a natural tendency of bottom-heavy cells to move against gravity [4]. Here, we show that the formation of bioconvection patterns can be reversibly triggered by a metabolic switch of the cells. The intensity of light is employed to control the metabolic pathways. We quantify the bioconvection using top- and side-view experiments that allow to access a plethora of characteristic quantities, such as the wavelength, flow-field, and relative cell density. Finally, we directly link the single cell motility at different metabolic states to the spatio-temporal characteristics of the instability.

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Primary author: FRAGKOPOULOS, A. A (Chair of Experimental Physics V, University of Bayreuth, 95447 Bayreuth, Germany, Max Planck Institute for Dynamics and Self-Organization, 37077 Göttingen, Germany)

Co-authors: BÖHME, F (Chair of Experimental Physics V, University of Bayreuth, 95447 Bayreuth, Germany); DREWES, N (Max Planck Institute for Dynamics and Self-Organization, 37077 Göttingen, Germany); BÄUMCHEN, O (1Chair of Experimental Physics V, University of Bayreuth, 95447 Bayreuth, Germany, Max Planck Institute for Dynamics and Self-Organization, 37077 Göttingen, Germany)

Presenter: FRAGKOPOULOS, A. A (Chair of Experimental Physics V, University of Bayreuth, 95447 Bayreuth, Germany, Max Planck Institute for Dynamics and Self-Organization, 37077 Göttingen, Germany)

Contribution ID: **55** Type: **Poster**

Bacterial motility differs on slippery and non-slipper surfaces

Many microorganisms form sessile communities, called biofilms, in self-secreted extracellular polymeric substances (EPS), which often attach to solid surfaces. Biofilm-associated infections have dramatic economic and societal impacts. Recently, slippery surfaces based on liquid infused surfaces have been developed to prevent biofilm formation 1. However, their antibiofilm performance can decay in hydrodynamic conditions due to shear induced oil depletion 2. Therefore, another slippery surfaces (i.e. liquid-like solid surfaces) have been proposed as an alternative antibiofilm strategy 2. For both liquid infused surfaces and liquid- like solid surfaces, they can significantly inhibit initial bacterial attachment and biofilm formation which is possibly due low contact angle hysteresis. It has been reported that various surface parameters such as surface roughness, surface wettability and surface charge could affect bacterial attachment and motility [3]. We hypothesized that these slippery surfaces can significantly affect how bacteria sense the surfaces and the subsequent bacterial motility.
In this work, we have designed flow cells, co-registered to microscope with high-speed camera, to enable the in-situ capture of bacterial movement. We have demonstrated that *P. aeruginosa* PAO1 and its mutant (e.g. type B Flagellin mutant, fliC) are much more motile on those slippery surfaces compared to non-slippery surfaces such as glass and Polydimethylsiloxane (PDMS). Furthermore, bacterial motility patterns have also significantly differed between slippery and non-slippery surfaces. This may advance our understanding about how bacteria sense the surfaces for better biofilm control.

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Primary author: DAWSON, J (School of Engineering, Newcastle University, United Kingdom)

Co-author: CHEN, J (School of Engineering, Newcastle University, United Kingdom)

Presenter: DAWSON, J (School of Engineering, Newcastle University, United Kingdom)

Contribution ID: **56** Type: **Poster**

Viscotaxis for Symmetric and Asymmetric Flagellar beat patterns

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 navigate their tortuous journey towards the egg [1,2,3]. The sperm flagellum besides propelling the cell also acts as a sensory antenna, detects environmental cues, enabling steering adjustments and beat pattern modifications for egg localization during fertilization [4,5].
Microswimmers in general often reside in gradients of temperature, chemicals, gravitation field and light [6], and can reorient and navigate along the gradients by a mechanism known as taxis. A well-known example is chemotaxis, where concentration gradients of a chemo-attractant are sensed and guide the sperm cell towards the egg cell. We investigate here another potentially relevant mechanism, viscotaxis, in which sperm reacts to gradients of fluid viscosity [6,7]. In previous research, different kinds of microswimmers have been found to respond to the vis- cosity gradients depending on their shape or hydrodynamic multipole strengths [6,7]. We use numerical simulations to investigate viscosity gradient effects on flagellum motion. Represent- ing sperm cells through a bead-spring model experiencing anisotropic, space-dependent drag, our simulations reveal positive viscotaxis, where sperm cells reorient towards areas of higher viscosity. We quantify this behaviour in form of the rotational velocity and its dependencies on various factors. Furthermore, we explore the effects of asymmetric flagella waveforms and flagella elasticity.

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Primary author: ANAND, S (Theoretical Physics of Living Matter, Institute for Biological Information Processing and Institute for Advanced Simulation, Forschungszentrum Jülich, 52425 Jülich, Germany)

Presenter: ANAND, S (Theoretical Physics of Living Matter, Institute for Biological Information Processing and Institute for Advanced Simulation, Forschungszentrum Jülich, 52425 Jülich, Germany)

Contribution ID: **57** Type: **Poster**

Run and Tumble Behavior of E. Coli

E. coli is a multi-flagellated bacterium with a prolate spheroidally-shaped body and several left-handed helical flagella (typically between 2 and 5). The helical flagella are rotated by a motor, enabling the bacterium to propel forward. E. coli generally has two modes of swimming: (i) 'run' with a straight swimming direction, and (ii) 'tumble'during which the bacterium can change its swimming direction [1-3]. During the run stage, all flagella rotate anticlockwise, such that they bundle into a single propeller. During the tumble stage, one or more flagella switch to the clockwise rotation, so that they leave the bundle and facilitate E. coli to change its swimming direction. In our work, we investigate how different E. coli properties, including body and flagella geometry, flagella stiffness and the strength of actuation, govern the run-and-tumble behavior of these bacteria. We establish a realistic E. coli model and validate it using available experimental observations [1-3]. The model properly captures the running speed of E. coli, rotational frequency of the head and flagella, tumbling time and angle in comparison to experimental measurements [1-5]. Furthermore, our simulations show that the stiffness of a hook (the short part of a flagellum which connects it directly to the motor) plays an important role in the run-and-tumble behavior, which has also been suggested in experimental studies [6-7]. This detailed model of E. coli helps us better understand its swimming behavior, and allows the exploration of E. coli locomotion in more complex realistic environments such as with walls [8].

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Primary authors: ZHANG, Bohan (IBI-5/IAS-2, Forschungszentrum Juelich); Dr FEDOSOV, Dmitry (IBI-5/IAS-2, Forschungszentrum Juelich); Prof. GOMPPER, Gerhard (IBI-5/IAS-2, Forschungszentrum Juelich)

Presenter: ZHANG, Bohan (IBI-5/IAS-2, Forschungszentrum Juelich)

Contribution ID: **58** Type: **PHYMOT contributed talk (20 min)**

Bacteria Propulsion and Interactions in Thin Biofilms

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. In particular, swarming generally takes place at moderate volume fractions of swimmers, while at high swimmer densities, large non-motile clusters prevail. These results advance our understanding of bacterial film formation and the connection between the collective swarming behavior and the internal properties of individual swimmers.

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Primary authors: ZHANG, Bohan (IBI-5/IAS-2, Forschungszentrum Juelich); Dr FEDOSOV, Dmitry (IBI-5/IAS-2, Forschungszentrum Juelich); Prof. GOMPPER, Gerhard (IBI-5/IAS-2, Forschungszentrum Juelich)

Presenter: Dr FEDOSOV, Dmitry (IBI-5/IAS-2, Forschungszentrum Juelich)

Contribution ID: **60** Type: **Poster**

P. sineare in confinement: breaking free through narrow escapes

The microbial ecosystem is full of narrow constrictions that microorganisms need to learn to navigate in order to survive. Here, we study a Nature example of a "microorganism billiard": a system composed of a population of microorganisms packed in a closed space, with only a few narrow apertures to escape from. This situation occurs when the marine parasite Parvilucifera sinerae infects and replicates inside a dinoflagellate host, and the newly born parasites find themselves in the closed and extremely packed space represented by the dead host body (the "sporangium"). In order to start a new successful infection cycle, the parasite's zoospores must find their way out of this closed structure. Which strategies are deployed by the parasites to manage a successful escape? A particular interaction with the boundaries might help them navigate this structure, and collective behaviours between individual parasites might be key in "finding the way out". Here, we present the preliminary results of an experiment aimed at reconstructing the 3D orientation of the zoospores inside the sporangium during the emptying process, to investigate the possible emergence of an ordered phase.

Primary authors: ZANOLI, Medea (Mediterranean Institute for Advanced Studies (IMEDEA) , Esporles, Spain); Mrs CASTILLO, Sara (Mediterranean Institute for Advanced Studies (IMEDEA) , Esporles, Spain); Dr TUVAL, Idan (Mediterranean Institute for Advanced Studies (IMEDEA) , Esporles, Spain)

Presenter: ZANOLI, Medea (Mediterranean Institute for Advanced Studies (IMEDEA) , Esporles, Spain)

Contribution ID: **61** Type: **PHYMOT contributed talk (20 min)**

Multipad Agarose Plate (MAP): A Rapid and High-Throughput Approach for Antibiotic Susceptibility Testing

Antibiotic resistance is a growing issue in healthcare worldwide and is currently responsible for over one million deaths annually. We seek to develop a new method for antibiotic susceptibility testing (AST) using single-cell microscopy. The assay is based on a multi-pad agarose plate (MAP), where one or more bacteria samples are placed on 96 small agarose pads. Each pad provides a growth environment where media, nutrients, and toxins can be added independently. The bacteria are confined to a single imaging plane using a glass coverslip and imaged for two hours with single-cell microscopy. We then analyse the image sets with a fully automated segmentation pipeline that outputs statistics for colony growth and single-cell characteristics. We demonstrate how, by adding concentration gradients of antibiotics to the pads, the minimum inhibitory concentration (MIC) can be consistently determined. Additional experiments were also conducted to demonstrate that the pads on the MAP are not affected by their neighbours and that the method is not sensitive to agarose concentration and seeding density.

Primary authors: Dr DONALD, Allen (Synoptics); Dr MANCINI, Leonardo (University of Cambridge); KALS, Morten (Synoptics + Univeristy of Cambridge); Prof. CICUTA, Pietro (University of Cambridge)

Presenter: KALS, Morten (Synoptics + Univeristy of Cambridge)

Contribution ID: **62** Type: **PHYMOT contributed talk (20 min)**

Motile cilia induce Periciliary transport.

The ciliated epithelium of the human respiratory tract is lined by a thin stratified fluid. The 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, 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, but have not managed to extract a clear velocity profile in this layer. 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.
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 micrometric region within the PCL and followed its translation over time along lines parallel to the epithelium. The compound is activated at different distances from the cell apical surface to measure the transport as a function of the position within the PCL. Our findings show that the dye displacement is generally segmented, suggesting that the compound is transported with two prominent speeds for short (< 1 s) and long-times. The two speeds appear almost constant along the cilium length, with the first one being almost four time bigger than the second one. Moreover, we found that decreasing the temperature from 37℃ to room temperature reduces PCL transport and has its major effects on the short-time speed.

Primary authors: CAUSA, Erika (University of Cambridge, Physics Department); Mr KOTAR, Jurij (University of Cambridge, Physics Department); Mr FERIANI, Luigi (University of Cambridge, Physics Department); CICUTA, Pietro (University of Cambridge)

Presenter: CAUSA, Erika (University of Cambridge, Physics Department)

Contribution ID: **63** Type: **Contributed talk (20 min)**

Microfluidics to emulate the behavior of biological microswimmers using artificial alternatives

A key feature of biological microswimmers is their ability to navigate away from or toward a certain stimuli, and this skill is termed as 'taxis'. Tactic behavior can be induced by physicochemical changes in the environment such as light (phototaxis), chemical (chemotaxis), temperature (thermotaxis) and fluid flow (rheotaxis). In the last few years, a lot of research has been done for mimicking the behavior of the biological organisms in a fully synthetic way. Hence, artificial microswimmers were developed which have the same basic trait i.e. they are able to autonomously move at microscale. While these artificial devices lack any sensing and signaling capabilities, it is worth investigating if they can also mimic the taxis character of the biological organisms. In order to mimic the taxis behavior, one of the most crucial challenge is creating changes in the environment in a controlled manner. Here, microfluidics offers great solutions due to its excellent fluid manipulation abilities at the microscale 1. Using microfluidics, we were able to create an otherwise technically challenging chemical gradients and fluid flow and study the chemotaxis 2 and rheotaxis [3] response of catalytically active Janus spheres. We also studied the phototaxis response of artificial microswimmers which did not require microfluidic setup and could be built using simple platform [4].

Here, I describe rheotaxis behavior in artificial microswimmers in detail: many motile microorganisms respond to the presence of the water currents by either migrating up or down the flow and this behavior is termed as rheotaxis. Similar to their biological counterparts, artificial microswimmers have also been shown to respond to fluid flows [5]. To deepen the understanding of how different microswimmers behave in an externally imposed flow, it is crucial to understand the influence played by their swimming patterns. Experimentally, pusher-type Pt@SiO2 Janus microswimmers have been shown to exhibit cross-stream migration in flow conditions. Whereas, theoretical studies have predicted an upstream response for puller-type microswimmers. In this work, we introduce Cu@SiO2 Janus spheres that swim towards their catalytic cap, quite differently from Pt@SiO2 which move towards SiO2. Using theoretical flow field calculations, we hypothesize that they behave as a puller-type system. Indeed, when placed in an externally imposed flow, these swimmers show a steady upstream response, which supports our hypothesis. Using a simple squirmer model for puller-type system, we reproduce all the experimental observations. To conclude, our study highlights the relevance of the flow field pattern around the microswimmers to comprehend the rheotactic behavior in motile systems.

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Primary author: SHARAN, P (Physical Chemistry, TU Dresden, Dresden 01069, Germany)

Co-author: SIMMCHEN, J (Physical Chemistry, TU Dresden, Dresden 01069, Germany and Pure and applied chemistry, University of Strathclyde, Cathedral Street, Glasgow G1 1XL, UK)

Presenter: SHARAN, P (Physical Chemistry, TU Dresden, Dresden 01069, Germany)

Contribution ID: **64** Type: **PHYMOT contributed talk (20 min)**

MECHANICAL COUPLING IS SUFFICIENT TO SYNCHRONIZE C. REINHARDTII FLAGELLA

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

Primary author: ZORRILLA, Luc (IMEDEA (UIB-CSIC))

Co-authors: Dr ALLARD, Antoine (Université de Bordeaux); Mr DESAI, Krish (University of Warwick); Dr POLIN, Marco (IMEDEA (UIB-CSIC), University of Warwick)

Presenter: ZORRILLA, Luc (IMEDEA (UIB-CSIC))

Contribution ID: **65** Type: **Invited Talk (30 min)**

The physics of bacterial transport in dilute and porous environments

Unraveling the motion of microorganisms in dilute and porous media is important for our understanding of both the molecular basis of their swim gait and their survival strategies in microbial habitats. First, I will show that by using renewal processes to analyze experimental measurements of wild-type *E. Coli*, we can provide a quantitative spatiotemporal characterization of their run-and-tumble dynamics in bulk [1,2]. We further demonstrate quantitatively how the persistence length of an engineered strain can be controlled by a chemical inducer and characterize a transition from perpetual tumbling to smooth swimming. Second, I will address how this run-and-tumble gait evolves towards a hop-and-trap motility pattern of agents moving in a porous environment [3]. Using computer simulations, we discover a geometric criterion for their optimal spreading, which emerges when their persistence lengths are comparable to the longest straight path available in the porous medium. Our criterion provides a fundamental principle for optimal transport in densely-packed environments, which could be tested experimentally by using engineered cells and may provide insights into microbial adaption mechanisms.

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Primary author: KURZTHALER, C (Max Planck Institute for the Physics of Complex Systems, Dresden, Germany)

Presenter: KURZTHALER, C (Max Planck Institute for the Physics of Complex Systems, Dresden, Germany)

Contribution ID: **68** Type: **Poster**

Chlamydomonas Reinhardtii 3D Motion Captured by Holographic Microscopy

Motility of microscopic entities is a central question in biology. In an idealization attempt, the problem could be reduced to four key elements: viscous flow, soft confinement, thermal fluctuations and activity.
To address this matter, a novel method based on Mie holography and stochastic inference was developed in the group 1. In a nutshell, this method allows to track particles in 3 dimensions, with a resolution of 10 nm. Over the past years, it led to quantify experimentally and theoretically how a Brownian sphere is affected by complex confined situations, such as rigid and charged walls, elastomeric ones or liquid interfaces. Specifically, in the case of a sphere diffusing in salted walter on top of a glass wall, fine deviations from the bulk Gaussian statistics of displacements were quantified theoretically and numerically and measured experimentally 2. Also, surface forces are measured down to a few femtonewtons. Thus, the method is a promising contactless and gentle probe, since it is only driven by thermal fluctuations.
After that robust calibration of the technique, more complex situations can be studied. The first one is the motion ofthe active alga Chlamydomonas *reinhardtii*. Its 3D motion was successfully tracked, which paves the way for tackling questions concerning the alga's behavior in confinement, or even gliding properties.

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Primary authors: Mr FARES, Nicolas (Univ. Bordeaux, CNRS, LOMA, UMR 5798); Mr LAVAUD, Maxime (Univ. Bordeaux, CNRS, LOMA, UMR 5798); Mr ALLARD, Antoine (Univ. Bordeaux, CNRS, LOMA, UMR 5798); Prof. BÄUMCHEN, Oliver (Experimental Physics V, University of Bayreuth, Germany); Mr AMAROUCHENE, Yacine (Univ. Bordeaux, CNRS, LOMA, UMR 5798); Mr SALEZ, Thomas (Univ. Bordeaux, CNRS, LOMA, UMR 5798)

Presenter: Mr FARES, Nicolas (Univ. Bordeaux, CNRS, LOMA, UMR 5798)

Contribution ID: **69** Type: **Poster**

ThirdPeak –a software to process, visualize and analyze tracks in two and three dimensions

Life, as we know it, is sustained but also constrained by Brownian motion and the diffusion of vital nutrients and proteins required for cell growth and survival. The advent of super-resolution microscopy techniques has revolutionized our ability to observe molecular dynamics within cells with improved temporal and spatial resolution. Although tools exist for localizing 1 and connecting tracks 2 in two and three dimensions, visualization and analysis software often only cater to two-dimensional data [3].
To simplify the exploration and analysis of three-dimensional track data, we developed ThirdPeak —a MATLAB-based software with a user-friendly graphical interface. This software offers flexibility by supporting various data formats, accommodating track or localization data from diverse sources and length scales. During preprocessing, users can apply quality filters and correct for drift. Once the results are validated, in-depth analysis becomes possible.
ThirdPeak enables users to select individual tracks, focus on tracks within specific regions of interest, or analyze multiple files concurrently. We have successfully utilized this software to uncover the dynamics within the endosomal system of Trypanosoma brucei. We believe that ThirdPeak can serve as a valuable addition to the workflow of researchers studying similar systems or conducting three-dimensional track analysis.

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Primary authors: ENGSTLER, Markus (Würzburg university, Würburg, Germany); MUELLER, Thomas

Presenter: MUELLER, Thomas

Contribution ID: **70** Type: **Poster**

Screening for genetic determinants of Vibrio cholerae biofilm architecture

Most of the bacterial biomass on Earth is found in three-dimensional communities, termed biofilms, 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 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.

Primary author: JIMENEZ SIEBERT, Eva (Biozentrum of the University of Basel)

Co-authors: Dr JECKEL, Hannah; STRENGER, Kerstin; DRESCHER, Knut (University Basel); NEUHAUS, Konstantin; BAYER, Miriam; NETTER, Niklas

Presenter: JIMENEZ SIEBERT, Eva (Biozentrum of the University of Basel)

Contribution ID: **71** Type: **Invited Talk (30 min)**

Active density patterns formation in bacterial binary mixtures

Wednesday 4 October 2023 14:00 (30 minutes)

Presenter: COLIN, Remy

Contribution ID: **72** Type: **Contributed talk (20 min)**

Optimal run-and-tumble in confinement

Wednesday 4 October 2023 14:30 (20 minutes)

Presenter: DETCHEVERRY, Francois

Contribution ID: **73** Type: **Contributed talk (20 min)**

Microfluidics to emulate the behavior of biological microswimmers using artificial alternatives

Wednesday 4 October 2023 14:50 (20 minutes)

Presenter: SHARAN, Priyanka

Contribution ID: **74** Type: **PHYMOT contributed talk (20 min)**

microArgos: a new tool for bacterial movement ecology

Wednesday 4 October 2023 15:10 (20 minutes)

Presenter: FOFFI, Riccardo

Contribution ID: **75** Type: **not specified**

Arrival - Registration - Lunch from 12.00

Wednesday 4 October 2023 11:30 (2h 20m)

Contribution ID: **76** Type: **Invited Talk (30 min)**

Elastic Bistability and the Geometry of Cellular Neighbourhoods in Choanoflagellates and Green Algae

Wednesday 4 October 2023 16:00 (30 minutes)

Presenter: GOLDSTEIN, Raymond

Contribution ID: **77** Type: **Contributed talk (20 min)**

Bacterial glass transition in Pseudomonas aeruginosa

Wednesday 4 October 2023 16:30 (20 minutes)

Presenter: MALIET, Martin

Contribution ID: **78** Type: **PHYMOT contributed talk (20 min)**

Effects of flagellar elasticity and cell body constraints on E.coli motility

Many motile bacteria, such as Escherichia coli, swim by rotating multiple flagella. These semi-flexible helical filaments are independently actuated by flagellar motors randomly distributed on the surface of the cell body. When all the motors rotate in the same direction, within a fraction of a second, this complex elastohydrodynamic system transforms into a straight swimmer in which all the flagella form a tight bundle propelling the cell forward.
Underlying this bundling phenomenon there are several physical factors, most of which have been analysed in isolation using theoretical or macroscopic models.

Here we report a direct study of bundling dynamics 1 in bacterial cells whose flagellar motors can be switched on and off by light, while fluorescently labelled flagella are observed. Using optical tweezers and microfabrication to constrain cell body kinematics, we found that although translations are not essential for bundling, wobbling plays an important role in achieving a stable configuration of the bundle and body complex. We find that the curved shape of the hook, a flexible joint that transmits motor torque to flagella, strongly affects the vectorial nature of the exchanged torques and must be taken into account to correctly reproduce experimental observations.

Primary author: BIANCHI, S (NANOTEC-CNR, Institute of Nanotechnology, Soft and Living Matter Laboratory, Rome, 00185 and Sapienza"University of Rome, Department of Physics, Rome, 00185)

Presenter: BIANCHI, S (NANOTEC-CNR, Institute of Nanotechnology, Soft and Living Matter Laboratory, Rome, 00185 and Sapienza"University of Rome, Department of Physics, Rome, 00185)

Contribution ID: **79** Type: **PHYMOT contributed talk (20 min)**

Effects of flagellar elasticity and cell body constraints on E.coli motility

Wednesday 4 October 2023 16:50 (20 minutes)

Presenter: BIANCHI, Silvio

Contribution ID: **80** Type: **PHYMOT contributed talk (20 min)**

Simultaneous spatiotemporal transcriptomics and microscopy of Bacillus subtilis swarm development reveal cooperation across generations

Wednesday 4 October 2023 17:10 (20 minutes)

Presenter: DRESCHER, Knut

Contribution ID: **81** Type: **Poster**

POSTER SESSION

Wednesday 4 October 2023 17:30 (2h 30m)

Contribution ID: **82** Type: **Invited Talk (30 min)**

Multicellular transitions in collective bacterial movements

Thursday 5 October 2023 09:00 (30 minutes)

Presenter: MIGNOT, Tam

Contribution ID: **83** Type: **Invited Talk (30 min)**

Signature of (anti)cooperativity in the stochastic fluctuations of small systems: application to the mechano-sensitive assembly of the bacterial flagellar motor

Thursday 5 October 2023 09:30 (20 minutes)

Presenter: WALLISER, Nils Ole

Contribution ID: **84** Type: **PHYMOT contributed talk (20 min)**

Control of bacteria turbulence through surfaces

Thursday 5 October 2023 09:50 (20 minutes)

Presenter: PEREZ, Benjamin

Contribution ID: **85** Type: **Contributed talk (20 min)**

Microfluidics Approaches for Selection and Enhancement of Sperm Motility for Improved Fertilization

Thursday 5 October 2023 10:10 (20 minutes)

Presenter: MISKO, Veaceslav

Contribution ID: **86** Type: **Invited Talk (30 min)**

The physics of bacterial transport in dilute and porous environments

Thursday 5 October 2023 11:00 (30 minutes)

Presenter: KURZTHALER, Christina

Contribution ID: **87** Type: **PHYMOT contributed talk (20 min)**

HoloV3C: unveiling eukaryotic flagella in 3D with holographic microscopy

Thursday 5 October 2023 11:30 (20 minutes)

Presenter: NIENAŁTOWSKI, Patryk

Contribution ID: **88** Type: **Contributed talk (20 min)**

Swimming vs gliding: Exploring the first steps of biofilm formation of motile microbes

Thursday 5 October 2023 11:50 (20 minutes)

Presenter: FRAGKOPOULOS, Alexandros

Contribution ID: **89** Type: **PHYMOT contributed talk (20 min)**

Sperm Navigation in Viscosity Gradients

Thursday 5 October 2023 12:10 (20 minutes)

Presenter: GOMPPER, Gerhard

Contribution ID: **90** Type: **Invited Talk (30 min)**

Bacterial Torpedoes Assaulting Biofilms

Thursday 5 October 2023 14:00 (30 minutes)

Presenter: BRIANDET, Romain

Contribution ID: **91** Type: **Contributed talk (20 min)**

Quantifying gliding forces of filamentous cyanobacteria

Thursday 5 October 2023 14:30 (20 minutes)

Presenter: KARPITSCHKA, Stefan

Contribution ID: **92** Type: **Contributed talk (20 min)**

Inadequate migration of Leishmania-infected macrophages –the driver of parasite dissemination?

Thursday 5 October 2023 14:50 (20 minutes)

Presenter: BENEKE, Tom

Contribution ID: **93** Type: **PHYMOT contributed talk (20 min)**

Evolution of micro-swimmer designs in distinct microenvironments

Thursday 5 October 2023 15:10 (20 minutes)

Presenter: JAMSHIDI, Narges

Contribution ID: **94** Type: **Invited Talk (30 min)**

The impact of elongation on transport in shear flow

Thursday 5 October 2023 16:00 (30 minutes)

Presenter: BEARON, Rachel

Contribution ID: **95** Type: **PHYMOT contributed talk (20 min)**

Functional morphologies and fluid dynamics of foraging in 'typical excavates'

Thursday 5 October 2023 16:30 (20 minutes)

Presenter: MIANO, Federica

Contribution ID: **96** Type: **Contributed talk (20 min)**

Colloidal transport by light-induced gradients of active pressure

Thursday 5 October 2023 17:10 (20 minutes)

Presenter: PELLICCIOTTA, Nicola

Contribution ID: **97** Type: **Invited Talk (30 min)**

Spectra of active turbulence

Friday 6 October 2023 09:00 (30 minutes)

Presenter: MOROZOV, Alexander

Contribution ID: **98** Type: **PHYMOT contributed talk (20 min)**

Multipad Agarose Plate (MAP): A Rapid and High-Throughput Approach for Anti-biotic Susceptibility Testing

Friday 6 October 2023 09:30 (20 minutes)

Presenter: KALS, Morten

Contribution ID: **99** Type: **Contributed talk (20 min)**

Hydrodynamic near field effects give rise to fast synchronisation in finite groups of cilia

Friday 6 October 2023 09:50 (20 minutes)

Presenter: VILFAN, Andrej

Contribution ID: **100** Type: **PHYMOT contributed talk (20 min)**

MECHANICAL COUPLING IS SUFFICIENT TO SYNCHRONIZE C. REINHARDTII FLAGELLA

Friday 6 October 2023 10:10 (20 minutes)

Presenter: ZORRILLA, Luc

Contribution ID: **101** Type: **Invited Talk (30 min)**

Swimming and Rheology of Active Suspensions in Viscoelastic Fluids

Friday 6 October 2023 11:00 (30 minutes)

Presenter: STARK, Holger

Contribution ID: **102** Type: **Contributed talk (20 min)**

Droplet and waving instabilities of an active fluid jet

Friday 6 October 2023 11:30 (20 minutes)

Presenter: EISENMANN, Isabelle

Contribution ID: **103** Type: **PHYMOT contributed talk (20 min)**

Dispersion of motile bacteria in confined and geometrically complex channels

Friday 6 October 2023 11:50 (20 minutes)

Presenter: CLÉMENT, Eric

Contribution ID: **104** Type: **Contributed talk (20 min)**

Utility of information in chemotaxis

Friday 6 October 2023 12:10 (20 minutes)

Presenter: DAS, Avishek

Contribution ID: **105** Type: **Invited Talk (30 min)**

SHOULD I STAY OR SHOULD I GO? THE ADHESION-MIGRATION TRADE-OFF OF PSEUDOMONAS AERUGINOSA

Friday 6 October 2023 14:00 (30 minutes)

Presenter: SABASS, Benedikt

Contribution ID: **106** Type: **PHYMOT contributed talk (20 min)**

Motile cilia induce Periciliary transport

Friday 6 October 2023 14:30 (20 minutes)

Presenter: CAUSA, Erika

Contribution ID: **107** Type: **Contributed talk (20 min)**

Transport of passive beads by random and directed motion of swimming micro-organisms

Friday 6 October 2023 14:50 (20 minutes)

Presenter: BOUVARD, Julien

Contribution ID: **108** Type: **PHYMOT contributed talk (20 min)**

Bacteria Propulsion and Interactions in Thin Biofilms

Friday 6 October 2023 15:10 (20 minutes)

Presenter: FEDOSOV, Dmitry

Contribution ID: **109** Type: **Contributed talk (20 min)**

Controlling bacterial swimming in wavy channels

Thursday 5 October 2023 16:50 (20 minutes)

Presenter: SCHMIDT, Winfried