Program of the SFP Physics & Life Days

2-3 October 2025

Institut Jacques Monod, Paris

Thursday, October 2nd

13.00 **Opening of the meeting** (badge & tea/coffee)
Buffon hall

14.00 **Opening remarks**
Buffon auditorium

Session 1

Buffon auditorium

14.15 **François Peaudecerf** - Institut de Physique (Rennes)
Environmental bacteria soft matter

15.00 **Aurore Woller** - Université Libre de Bruxelles (Bruxelles)
Immunity and competition between bacteria in the gut

15.15 **Nicolas Desprat** - Laboratoire de physique de l'ENS (Paris)
How Min oscillations drive polar localisation of an outer membrane protein in *E. coli*

15.30 **Julien Le Dreff** - Laboratoire d'Hydrodynamique (LadHyX, Palaiseau)
Swimming dynamics and efficiency in chain diatom colonies

15.45 **Frederic Català-Castro** - Impetux (sponsor)
SENSOCELL: Deciphering cell mechanobiology through optical tweezer force spectroscopy

16.00 **Coffee break**
Buffon hall

Session 2

Buffon auditorium

16.30 **Pauline Durand** - Laboratoire Matière et Systèmes Complexes (Paris)
Plant biomechanics

17.15 **Mathieu Rivière** - Institut universitaire des systèmes thermiques industriels (Marseille)
Fast movements of Mimosa pudica: an osmotic muscle?

17.30 **Camille Bagès** - Institut Jacques Monod (Paris)
Probing actin-tropomyosin interactions with drag force

17.45 **Julien Renaudeau** - Laboratoire du Futur (Bordeaux)
Study of sap transport in plants using microfluidics

18.00 **Poster session & Impetux optical tweezer demo**
IJM library

19.30 **Buffet dinner**
IJM library

Friday, October 3rd

Session 3
Buffon auditorium

09.00 **Laura Cantini** - Institut Pasteur (Paris)
Multi-modal learning for single-cell data integration

09.45 **Jami Ludovic** - Institut de Recherche sur les Phénomènes Hors Equilibre (Marseille)
Bioinspired Elasto-Active Fluidics

10.00 **Léa Rouquier** - Institut de biologie de l'ENS (Paris)
Junctured-DNA: a DNA scaffold enabling to study protein-protein interactions at single-molecule resolution

10.15 **Hadrien Boulay-Colonna** - Institut de Science des Matériau (Mulhouse)
Deciphering the R-body extension-retraction mechanism

10.30 **Serge Dmitrieff** - Institut Jacques Monod (Paris)
Does contractile actin behave as an active gel?

10.45 **Coffee break**
Buffon hall

Session 4
Buffon auditorium

11.15 **Barnabé Ledoux** - ESPCI (Paris)
Compositional memory matters for early molecular systems

11.30 **Simon Gsell** - Institut de Recherche sur les Phénomènes Hors Equilibre (Marseille)
Marangoni-like tissue flows enhance symmetry breaking of embryonic organoids

11.45 **Karine Guevorkian** - Institut Curie (Paris)
Spatio-temporal dynamics of mesoderm spreading during chicken embryo axis development

12.00 **Tree Frog Prize - Laurent Le, Istituto Italiano di Tecnologia (Genova, Italy)**
Developments for time-resolved and for single molecule localization microscopy

12.45 **Lunch & poster session**
Buffon hall & IJM library

Session 5

Buffon auditorium

14.15 **Sylvie Lorthois** - Institut de Mécanique des Fluides (Toulouse)
Brain microcirculation

15.00 **Delphine Debarre** - Laboratoire Interdisciplinaire de Physique (Grenoble)
Cell adhesion to the blood vessel wall: mechanical regulation of the adhesion cascade

15.15 **Simon Kouba** - Laboratoire Charles Fabry (Palaiseau)
Microrhéologie optique des caillots sanguin

15.30 **Yann Chalopin** - CentraleSupélec (Palaiseau)
Phonons, Localization, and Allosteric Communication in Proteins

15.45 **Arthur Genthon** - MPI-PKS (Dresden, Germany)
From noisy cell size control to population growth and back

16.00 **Closing remarks**

16.10 **Impetux optical tweezer demo**
Meet in Buffon Hall

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Posters

Two poster sessions are organized. Authors are invited to present their poster on either session depending on their poster number:

- **Even poster numbers: Thursday evening from 6pm**
- **Odd poster numbers: Friday after lunch.**

The poster room will be accessible during the entire meeting.

Presenting Author		**Poster Number**
MITRA	Suchetana	1
EL HAMOUI	Omar	2
D'ALESSANDRO	Joseph	3
ROBLES-AGUILAR	José Manuel	4
AKSIL	Matheo	5
SITOLEUX	Paul	6
PEREZ	Benjamin	7
LE GUEN	Alex	8
LACOSTE	David	9
CHEVALIER	Nicolas	10
DESTRIAN	Olivier	11
FIGÀ TALAMANCA	Elettra	12
MOSCIATTI JOFRÉ	Antonio Cosimo	13
KHOSRAVANIZADEH	Amir	14
LETROU	Mathieu	15
CATALÀ-CASTRO	Frederic	16
MOORE	Charles Paul	17
OUCHETTO	Wassim	18
JOUNEAU	Agathe	19
OUAZAN-REBOUL	Vincent	20
CHATURVEDI	Vaibhav	21
MOLNAR	Kelly	22
GARNIER	Bertrand	23
CHEN	Xiaohong	24

Abstracts

(by alphabetical order of first author's family name)

Oral Presentations

Probing actin-tropomyosin interactions with drag force

Camille Bagès*[1], Morgan Chabanon[2], Wouter Kools[1], Thomas Dos Santos[1], Rebecca Pagès[1], Maria Elena Sirkia[3], Cecile Leduc[1], Anne Houdusse[4], Antoine Jégou[1], Guillaume Romet-Lemonne[1], and Hugo Wioland†[1]

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[3]Compartimentation et dynamique cellulaires – CNRS : UMR144, Université Pierre et Marie Curie (UPMC) - Paris VI, Institut Curie – France

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Résumé

Tropomyosin are central regulators of the actin cytoskeleton. They form parallel dimeric coiled coils that bind cooperatively along actin filaments and control the binding and activity of the other cytoskeleton proteins. The interactions between tropomyosins and actin filaments are complex: single tropomyosin dimers bind weakly to actin subunits but get stabilised by end-to-end attachment with other tropomyosin dimers, forming clusters which wrap around the filament. Here, we use force spectroscopy to better understand tropomyosin-actin interactions.
Various approaches have been developed to apply controlled forces to protein-protein pairs. Each protein is typically anchored to a surface or bead. The proteins are then put in contact and pulled apart by diverse instruments such as optical traps or atomic force microscopy. But these methods are ill-suited for tropomyosins: a single tropomyosin dimer form a transient interaction with a filament, such that very weak forces would be required. Moreover, since tropomyosins form clusters, we must consider complexes with multiple interactions.

We propose a method in which a hydrodynamic drag force is applied directly to the protein of interest, by imposing a controlled fluid flow inside a microfluidic chamber. Tropomyosin clusters are assembled on actin filaments that are anchored by one end to the bottom glass coverslip. By changing the overall flow rate, we apply a controlled hydrodynamic drag force over the tropomyosin clusters and discovered that they spontaneously detach. By applying very low forces from 0.01 to 0.1 pN per Tpm dimer, we obtained key insights into Tpm-actin interaction and dynamics, for different Tpm isoforms.
This method is also well-suited for other actin binding proteins. As an example, we quantified the effect of a drag force on the movement of myosin motors. This approach bypasses the need for surface anchoring and widens the range of protein-protein interactions that can be studied by force spectroscopy.

*Intervenant

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Deciphering the R-body extension-retraction mechanism

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Résumé

R-bodies are giant proteins originally discovered in endosymbiotic bacteria residing within large eukaryotic cells called *Paramecia*. These molecular pistons can switch in a fraction of a second from self-rolling 500 nm ribbons to 20-micron membrane-piercing needles. The extension /retraction mechanism is triggered by pH variations. The acidification causes the extension of the protein and the retraction is observed when the pH returns to neutral. Operating without chemical energy such as ATP consumption, the cycle of extension and retraction can be repeated many times.
We combine approaches in biochemistry, imaging, and modelling to propose a model which may explain the specific behaviour of the R-body. Preliminary experiments of Phase-contrasts and confocal microscopy enabled us to observe its dynamics. Using a microfluidics setup to switch the buffer in the chamber from basic to acidic conditions, we have seen that the extension occurs in less than 1s and is faster than the retraction which can last a few seconds. We performed various complementary microscopic observations, AFM, conventional SEM, and cryo-SEM, providing high-resolution images of the protein, and allowing us to visualize the morphology of its two states. We show that the extension is accompanied by a change of the curvature of the ribbon along with the extension direction. In parallel we have measured the zeta potential of R bodies as a function of the pH.
We thus propose a preliminary model in which the mechanism can be decomposed in 2 parts: first, an electrostatic process driven by the interaction between the R-body and protons in solution, second, a geometric transformation resulting from proton–monomer interactions, which induce changes in curvature. A thorough understanding of the underlying mechanism will facilitate the design of organic actuators or micromotors.

Mots-Clés: molecular piston, micro biomechanics, self assembled protein based actuator

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Multi-modal learning for single-cell data integration

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Résumé

Single-cell RNA sequencing (scRNAseq) is revolutionizing biology and medicine. The possibility to assess cellular heterogeneity at a previously inaccessible resolution, has profoundly impacted our understanding of development, of the immune system functioning and of many diseases. While scRNAseq is now mature, the single-cell technological development has shifted to other large-scale quantitative measurements, a.k.a. 'omics', and even spatial positioning. Each single-cell omics presents intrinsic limitations and provides a different and complementary information on the same cell. The current main challenge in computational biology is to design appropriate methods to integrate this wealth of information and translate it into actionable biological knowledge. In this talk, I will discuss three main computational directions currently explored in my team: (i) dimensionality reduction to study cellular heterogeneity simultaneously from multiple omics; (ii) gene network inference to integrate a large range of interactions between the features of various omics and isolate the regulators underlying cellular heterogeneity and (iii) spatially-informed trajectory inference methods to reconstruct the spatiotemporal landscape underlying cell dynamics.

*Intervenant

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SENSOCELL: Deciphering cell mechanobiology through optical tweezer force spectroscopy

Frederic Català-Castro*†[1]

[1]Impetux Optics – Espagne

Résumé

Mechanical forces sculpt cells and tissues, modulate migration and intracellular transport, organize the scaffolding of different subcellular compartments and provide cues for mechanoresponsive and behavioral processes. At the same time, the specific fingerprint of mechanical and rheological properties of biological soft matter defines the range over which force and stress propagate and dissipate. Developing standardized tools is therefore essential in cell mechanobiology -not only to quantify material properties, but also to apply controlled forces in order to probe dynamic processes within cells. In this technical talk, we will present SENSOCELL, an optical tweezers platform specifically designed for biophysical studies in complex biological samples. SENSOCELL integrates two key technologies –the direct measurement of optical forces through light momentum detection and multiplexed trap generation through acousto-optic deflectors (AOD). Together, these allow manipulation and force measurements simultaneously at different sites of a cell without the need of *in situ* stiffness calibration of the optical trap, which allows us to analyze force propagation and material flow in different types of samples. We will showcase cutting-edge applications developed by some of our customers, which range from the biophysical properties of DNA or protein filaments and phase-separated protein condensates to the rheological spectrum of the cyto- and nucleoplasm. In addition, we will present studies on plasma membrane flow and tension propagation, followed by the mechanical gating of transmembrane ion channels, linking physical forces to biological responses.

Mots-Clés: Optical tweezers

*Intervenant

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Phonons, Localization, and Allosteric Communication in Proteins

Yann Chalopin*†[1]

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Résumé

Proteins are dynamic molecular machines whose function hinges on the intricate coupling between their three-dimensional structure and thermal vibrations. This talk explores the fundamental physical mechanisms governing protein dynamics at the interface of physics and biology, focusing on localized vibrations (phonons) and allosteric communication. We demonstrate that vibrational localization, encoded in the protein's folded structure, plays a critical role in enzymatic catalysis by modulating reaction coordinates and lowering energy barriers. Furthermore, allosteric communication relies on multi-scale dynamic networks, coupling fast vibrational modes (picoseconds) with slower conformational changes (nanoseconds). We also introduce the concept of energy bilocalization, revealing how structural irregularities partition vibrational energy into distinct molecular domains, enabling functional diversity. These insights, supported by theoretical models and experimental data across over 900 enzyme structures, highlight proteins as optimized mechanical transducers of vibrational energy. Our findings open new avenues for engineering catalytic activity and designing therapeutic strategies targeting allosteric networks.

Mots-Clés: phonons, vibrational localization, allosteric communication, protein dynamics, physics, biology interface

*Intervenant

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Cell adhesion to the blood vessel wall: mechanical regulation of the adhesion cascade

Heather Davies[1], Oksana Kirichuk[1], Natalia Baranova[2], Nouha El Amri[1], Liliane Coche-Guerente[2], Claude Verdier[1], Lionel Bureau[1], Ralf Richter[3], and Delphine Débarre*[1]

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Résumé

Blood cell - vessel wall interactions are critical both for the flow of red blood cells, and for the control of white blood cell adhesion to the walls (e.g. at a site of inflammation). However, the biochemical and mechanical cues governing their thigth regulation are still poorly understood, in particular because of the challenge of non-invasive investigation of cell-wall short-range interactions under flow in a complex environment. Using a home-built platform combining advanced biochemical surface functionalization, microfluidics and high-speed interferometric imaging, we have investigated experimentally the role of the softness of the vessel wall outer layer in the regulation of blood cell homing under flow. This brush, named glycocalyx and mainly composed of charged exopolysaccharides, is both thick (up to 1μm) and extremely soft (down to a few Pa in compression modulus). We have demonstrated that these peculiar mechanical properties induce a short-range repulsion of non-interacting cells, in good agreement with the theory of elastohydrodynamics that accounts for the effect of substrate deformation under hydrodynamic forces. We have thereby provided the first experimental evidence of this "soft biolubrication" effect at play at small scale. On the other hand, we have shown that these same mechanical properties are a critical factor that stabilizes the homing of cells bearing specific receptors (CD44) for one of the main compound of the glycocalyx, hyaluronan (HA). Furthermore, we have shown that the mechanical barrier created by the glycocalyx screens interactions with surface receptors involved in the adhesion cascade in a CD44-dependent manner. Our results thus highlight the role of the glycocalyx as a gatekeeper for the adhesion to the blood vessel wall.

Mots-Clés: Cell adhesion, in vitro model, glycocalyx, blood circulation

*Intervenant

How Min oscillations drive polar localisation of an outer membrane protein in E. coli

Nicolas Desprat*[1]

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Résumé

Protein localisation is essential for a wide range of biological functions. Understanding how certain proteins escape the pure laws of diffusion and do not distribute themselves homogeneously within cells is a central question in living systems. We report here that polar localisation of Ag43, an outer membrane adhesion protein, undergoes biased diffusion in the periplasm of E. Coli thanks to the oscillations of Min proteins in the cytoplasm. This discovery could reveal a new paradigm for the coupling of protein localisation across two distinct cellular compartments separated by a membrane.

Mots-Clés: Diffusion, microbiology, Dynamics, Microscopy

*Intervenant

Does contractile actin behave as an active gel ?

Serge Dmitrieff*[1]

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Résumé

In cells, complex networks of filaments, called the cytoskeleton allow the cell to interact mechanically with its environment. In particular, the actin cortex is a network of filaments connected by crosslinkers and molecular motors, that spans the periphery of animal cells. The networks are usually represented theoretically as active gels, i.e. continuous visco-elastic fluids with an additional active stress. However, because of the difference in scale between continuous models and microscopic components, there is little quantitative evidence that the correct continuous equations are used to model actin networks. Using a combination of theory and simulations, we find that some forms of active gel equations do accurately describe actin contraction. We will show that we can predict the contractile term from network architecture and motor properties - thus predicting how macroscopic mechanics emerge from microscopic elements.

Mots-Clés: mechanic, actin, cytoskeleton, active gel, theory

*Intervenant

Plant biomechanics

Pauline Durand-Smet*[1] and Cyril Grandjean[1]

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Résumé

Understanding how plants acquire their shape and integrate mechanical signals during development remains a central challenge in biology. Morphogenesis depends both on the mechanical properties of plant cells and on their ability to translate mechanical cues into biochemical responses. First, I will review how plant mechanics have been quantified over the past decades, emphasising experimental and modeling approaches that probe processes across scales-from cellular architecture to whole-organ mechanics. I will also highlight examples of how plant cells respond to mechanical stress, a process essential not only for morphogenesis but also for environmental adaptation. In the second part of the talk, I will focus on our recent work at the single-cell level. First, we quantified the mechanical properties of regenerating cell walls and demonstrated that synthetic walls provide a useful model system. Second, by confining individual plant cells in micro-wells of defined geometry, we explored how cell shape influences cytoskeletal organization.

Mots-Clés: plant, rheology, single cell, cytoskeleton, mechanobiology, mechanotransduction

*Intervenant

Spatio-temporal dynamics of mesoderm spreading during chicken embryo axis development

Pauline Gehan[1], Salomé Berland[1,2], Isabelle Bonnet[1], Carles Blanch-Mercader[1], and Karine Guevorkian[*†1]

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[2]Laboratoire de Physique des Solides - MMOI – Laboratoire de Physique des Solides – France

Résumé

Embryonic morphogenesis begins with a cluster of undifferentiated cells that gradually transform into specific tissues under the influence of biochemical and mechanical signals, determining the timing, location, and shape of emerging structures. In vertebrates, after gastrulation, the posterior mesoderm, known as the presomitic mesoderm (PSM), undergoes periodic segmentation to form compact multicellular units called somites, which give rise to musculoskeletal structures in later stages. This somitogenesis process coincides with the transition of the PSM from a mesenchymal to an epithelial state, leading to changes in tissue architecture and mechanics. The mechanical mechanisms underlying somite formation are not fully understood. In this study, we investigate the spatial and temporal mechanics of the PSM during the mesenchymal to epithelial transition under controlled ex vivo conditions. By conducting spreading assays and measuring traction stresses on PSM segments, we explore the occurrence of a wetting transition and identify cellular factors involved. Our results show distinct behaviors in mesenchymal and epithelial segments, highlighting the impact of epithelialization on spreading dynamics. We examine the roles of intercellular adhesion and actomyosin activity in these processes and discuss their implications.

Mots-Clés: Tissue Mechanics, Morphogenesis, Tissue Wetting, Tissue Stress

[*]Intervenant

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From noisy cell size control to population growth and back

Arthur Genthon*†[1,2]

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Résumé

To proliferate, cells must maintain a stable size. How cells regulate their cycles and control their sizes is an active field of research, which unexpectedly revealed that many organisms divide after growing by a constant increment of volume, obeying a mechanism called "adder".
When cells proliferate, the long term population growth rate is often used as a proxy of fitness, measuring the ability of a population to outcompete competitors and to adapt to changing environments.
In spite of their respective importances in cell biology and population dynamics, the interplay between cell size control, acting at the single cell level, and population growth has not received much attention.

In this talk, we bridge the gap between the scale of the single cell and that of the population and we demonstrate that

(i) Population growth depends on cell size control! We show that strong and weak mechanisms of size control do not confer the same fitness advantage. Moreover, in most cases the "adder" does not maximize population growth. This raises the question of the ubiquity of the adder: did it emerge because it represents an optimum to identify, or is it an evolutionary byproduct?

(ii) The experimental setup matters! Indeed, the mechanism of cell size control inferred from single lineages, grown in narrow micro channels called mother machines for example, is different from the mechanism of cell size control inferred from tree-structured data, obtained with freely-growing populations. This is because population data is biased towards cells with above-average reproductive success, and it raises the question of the natural scale to characterize cell size control.

In both points, we highlight the role of the different sources of noise acting on the cell cycle for the interplay.

Mots-Clés: cell size, population growth, poulation dynamics, fitness, evolution, adder, sizer, mother machine

*Intervenant
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Marangoni-like tissue flows enhance symmetry breaking of embryonic organoids

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Résumé

In multicellular animals, early development involves the self-organization of cells to establish body axes, such as the primary head-to-tail axis. While body axis formation is often attributed to specific signaling pathways, we show that tissue mechanics also play a pivotal role. Using spherical aggregates of mouse embryonic stem cells as a model system - mimicking early mouse embryo development - we observe that these aggregates break rotational symmetry by forming distinct domains of expression, for example of the transcription factor T/Bra and the adhesion molecule E-cadherin (1). Through quantitative microscopy and physical modeling, we uncover large-scale tissue flows with a recirculating component that significantly contribute to symmetry breaking. These recirculating flows, resembling Marangoni flows, are driven by differences in tissue surface tension, which we confirm through aggregate fusion experiments (2). Our findings reveal that body axis formation is not solely regulated by biochemical pathways but can be enhanced by mechanically driven tissue flows. This highlights a key role for physical forces in developmental processes and suggests that such amplification mechanisms may also be at play in other organoid systems and in vivo development.

(1) Hashmi et al., eLife, 2020. DOI: https://doi.org/10.7554/eLife.59371
(2) Gsell, Tlili et al., Nat. Phys., 2025. DOI: https://doi.org/10.1038/s41567-025-02802-2

Mots-Clés: Tissue morphogenesis, Organoids, Active matter

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Bioinspired Elasto-Active Fluidics

Ludovic Jami*†[1] and Martin Brandenbourger[1]

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Résumé

Biological vascular networks-such as those of the slime molds, the lymphatic system, or the intestine-can autonomously drive internal flows through spontaneous contractions of their channels. These flows emerge from local interactions involving fluid–structure coupling, mechanosensory feedback, and inter-channel fluid exchange. Inspired by these principles, we designed a controllable poroelastic network that incorporates pressure-based mechanosensory feedback. Such feedback emulates the core mechanisms of biological self-contracting networks. Varying the dynamics of the pressure feedback, we explore how flow patterns self-organize and further how active networks dynamically interact with external fields. These poroelastic, self-contracting networks provide both a basis for developing novel fluidic systems in soft robotics and a model system for uncovering the design principles underlying biological transport networks.

Mots-Clés: Vacular network flow, Mechanosensory feedback, Fluid transport, Contraction waves, Travelling instabilities

*Intervenant

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microrhéologie optique des caillots sanguin

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Résumé

Les événements thromboemboliques veineux se caractérisent par la formation de caillots sanguins dans les veines, et peuvent mener à des thromboses veineuses ou à des embolies pulmonaires. Cependant pour une grande partie des patients qui souffrent de ces événements à répétition, il n'est pas possible de poser un diagnostic. Des études génétiques, protéomiques et métaboliques sont en cours afin d'expliquer ces cas de récidive. Une autre approche consiste à examiner la microstructure des caillots, car les caillots pathologiques présentent des propriétés mécaniques différentes de celles des caillots sains. Nous présentons un dispositif de microrhéologie optique passif permettant d'évaluer localement les modules de stockage et de perte de caillots artificiels, en exploitant le mouvement brownien de microbilles de polystyrène intégrées au sein du caillot.
Le montage expérimental repose sur l'illumination d'une bille de 6 μm de diamètre par un laser dans le proche infrarouge (830 nm) focalisé via un objectif à immersion (100x, NA 1,3). Le mouvement brownien de la bille est suivi en mesurant la position de la lumière du laser réfléchie sur la bille à l'aide d'un photodétecteur à quatre quadrants. Il est ensuite analysé afin d'extraire les modules viscoélastiques locaux. Les mesures, réalisées sur des caillots synthétiques obtenus à partir de concentrations croissantes de fibrinogène (1,5 mg/mL, 2 mg/mL et 3 mg/mL), révèlent une augmentation systématique du module de stockage avec la concentration en fibrinogène, conformément aux observations rapportées dans la littérature. En effet, plus il y a de fibrinogène, plus le réseau de fibres sera dense, et plus le caillot sera rigide.

Ces résultats démontrent la pertinence de la microrhéologie optique pour étudier la mécanique des caillots sanguins.

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Compositional memory matters for early molecular systems

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Résumé

Transient compartmentalization is essential to avoid parasites (short non-functional RNA sequences) to invade a molecular replicating system, but how compartmentalization dynamics specifically affect the host-parasite dynamics is unclear. to address this issue, we use a combination of experiments and modeling, to show that compositional memory is present in this experiment and matters for early molecular systems.

The error catastrophe refers to the proliferation of non-functional molecules in conditions where molecular replication has low accuracy, which is likely to correspond to conditions present at the Origin of Life. This error catastrophe can be avoided thanks to transient compartmentalization, provided that the compartments are themselves functional. Usually, transient compartmentalization models assume that the content of the compartments is completely pooled at the end of a cycle, resulting in the complete loss of the compositional memory of the compartment. Here, we test this assumption by assessing the level of mixing in experiments with compartmentalized RNAs using a mixture of fluorescent dyes.
We find mixing to be incomplete, in other words, compartments do not completely lose their content despite the continuous stirring, and there is therefore a certain level of compositional memory. Then, we develop a specific framework to account for this compositional memory, and we explore its role in the emergence of complexity in early molecular systems.

Mots-Clés: Origin of Life, Compartments, Evolution, Hosts, Parasites, Stirring, Compositional memory

*Intervenant

Swimming dynamics and efficiency in chain diatom colonies

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Résumé

Diatom chains are cohesive assemblies of unicellular microorganisms typically found in still and freshwater environments. While some species are passively transported by ambient currents and settle due to the weight of their dense silica shells, others use various strategies to move or self-propel. One species in particular, *Bacillaria paxillifer*, forms colonies of stacked rectangular cells that slide along each other while remaining parallel. This unique collective motion leads to beautiful and nontrivial trajectories at the colony scale. Using a numerical method developed to simulate rigid bodies with kinematic constraints and hydrodynamic interactions in Stokes flows, we model a colony as an assembly of rigid rods constrained to remain parallel to one another. We impose periodic tangential sliding between neighboring cells, with a phase shift between the different rod pairs. This phase shift defines the number of oscillations of the deformation wave propagating along the colony. Unlike flagellated microorganisms, which swim in a constant direction regardless of the number of oscillations along the flagellum, we observe a reversal of swimming direction when the number of oscillations along the colony changes. We also identify a new optimal swimming gait that has not been observed previously in flagellar propulsion. This mechanism emerges from a coupling between the propulsion generated by the rotation of the colony and the wave propagation. In addition, the optimal cell aspect ratio for swimming found in our simulation corresponds to those observed in real diatoms.

Mots-Clés: Diatoms, Low Reynolds number swimming, Collective motion

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Modeling blood flow and mass transfers within the brain to highlight the vascular component of Alzheimer's Disease

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Résumé

Because the brain lacks any substantial energy reserves, the cerebral microvascular system is essential to a large variety of physiological processes in the brain, such as blood delivery and local blood flow regulation as a function of neuronal activity. It provides a unique window to observe the functioning brain using hemodynamically-based functional imaging techniques. It also plays a major role in disease (stroke, neurodegenerative diseases, ...). However, the functional consequences of vascular damage (including acute occlusions or long-term remodeling in ageing or disease) are poorly understood.

In this context, modeling approaches are increasingly important, and enable to integrate the specific multi-scale architecture of the brain microvascular network with the physics of blood flow in confined conditions. I will discuss how the resulting scaling-laws for blood flow and mass transport are mostly driven by the topology of the microvascular network and highlight how they help understand the vascular component of Alzheimer's Disease.

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Environmental Bacteria Soft Matter

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Résumé

Bacteria represent one of the dominant lifeforms on our planet, present in every ecosystem, appearing – sometimes by design, sometimes not – in countless industrial systems, and making up about half the cells inside a human body. As we continue to unravel the tapestry of their influence on our world, physicists can contribute novel perspectives, by studying bacteria as a physical system, but also by investigating how physico-chemical processes guide and constrain the reciprocal influences between bacteria and their environment.
In the first part of the talk, I will give a general overview of the diversity of approaches in which physics meets bacterial behavior – from the theory of an individual bacterium swimming, to the study of bacteria as a collective. I will identify key concepts in these approaches, such as chemotaxis or flow, which, together with a focus shifting back and forth between individual behavior and collective effects, provides a clearer picture of commonalities in this diversity.
In the second part of the talk, I will present some of our on-going work on bacterial behavior next to air-water interfaces. Bacteria in the environment encounter diverse air-water interfaces, be they around bubbles in waste water treatment plants, on top of the thin liquid film covering our lungs, or at the surface of the vast expanse of the oceans. Here I will present two examples of how air-water interfaces can shape bacterial dynamics in the environment. First, I will present how bacteria present in the sea surface microlayer - the thin layer of water separating the atmosphere from marine waters below - can successfully exploit the transient nutrient patches produced by surface-deposited aerosols, through a combination of active behavior and passive entrapment. Second, I will present our first steps investigating how soil bacteria behavior couples to the dynamics of evaporative air-water interfaces in soil, with potential impact on soil drying dynamics. Both studies highlight not only how interfaces in the environment modify the behavior of microorganisms, but also how these changes of behavior could in return impact larger scale transport processes.

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Study of sap transport in plants using microfluidics

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Résumé

Sap transport in vascular plants is ensured by a complex network of two "microfluidic channels", xylem and phloem, coupled by a biological membrane. Evapotranspiration drives a flow of almost pure water through the xylem, from the roots to the leaves. In parallel, the sugars produced in the leaves by photosynthesis are loaded into the phloem. The osmotic pressure in the phloem generates a large turgor pressure allowing the transport of sugars in the phloem towards the roots, shoots and fruits. The typical length scales in this system makes microfluidics a relevant field to study it in controlled synthetic environment. This work more precisely designs a microfluidic geometry to mimic the osmotic driven transport of sugars in the phloem, known as the Münch mechanism. A microfluidic chip was engineered, consisting of two parallel channels coupled by a hydrogel membrane permeable to water, with a molecular weight cutoff (MWCO) of around 1 kg/mol and able to resist up to 10 bar of hydrostatic pressures. The hydrogel was photo-crosslinked *in situ* using a maskless lithography device projecting collimated UV patterns. In contrast, transient flows are observed with solutes of smaller molecular weights because of their permeation through the membrane. We show that the dynamics of this transport can be described by a model coupling forward osmosis and solute permeation under dilute conditions, which was verified experimentally and allowed to estimate the membrane reflection and diffusion coefficients for a wide range of solutes. In the future, our objective is to expand this study to higher solute concentrations, as found in the phloem of plants, and couple the current device to an artificial xylem mimicking evapotranspiration, involving the integration of supplementary hydrogel membranes.

Mots-Clés: Microfluidics, Osmosis, Hydrogel, Membrane

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Fast movements of Mimosa pudica: an osmotic muscle?

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Résumé

Plant movements span timescales ranging from tenths of seconds to several hours, and rely on a rich variety of physical mechanisms. The “touch-me-not” plant, Mimosa pudica, folds its leaves in a couple of seconds in response to mechanical or electrical stimuli. This movement is reversible, and leaves reset within a few tens of minutes.

Purely osmotic water transport across the whole pulvinus—a flexible, hinge-like bulge at the base of each leaf—constitutes the textbook explanation of the motion. This scenario received only limited experimental evidence, however, and implies that pulvini operate near the physical limits of osmotic transport.

Here we experimentally characterize the kinematics of the movement and the mechanics of the pulvinus, and build the force-velocity law of this ”plant muscle”. This law can be modeled by a simple osmotic motor. However, we find that both the time scale of movement and the tissue permeability extracted from the model are

*Intervenant

too fast to be compatible with the time scale of water transport across the pulvinus, measured independently by osmotic swelling experiments.

To resolve this paradox, we note, following previous authors, that motion correlates with a change in the backscattered light from the pulvinus. This observation suggests that motion may not be due to long-distance water transport across the pulvinus, as classically thought, but rather to local water transfer between cells and adjacent gas channels surrounding the cells and forming a porous network extending throughout the whole pulvinus. This "air-buffering" mechanism would provide a unique means of generating rapid hydraulic movements in plants and non-muscular organisms that are not limited by long-distance water transport.

Mots-Clés: biomechanics, plants, osmosis, porous media, water transport

Junctured-DNA: a DNA scaffold enabling to study protein-protein interactions at single-molecule resolution

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Résumé

Our laboratory designed junctured-DNA (jDNA) tweezers, which are made of three long double-strands of DNA and on which pairs of proteins or oligonucleotides of interest can be engrafted and their interactions studied. One of the jDNA ends is fixed to a surface and the other is attached to a magnetic bead, allowing a precise control of the force applied to the complex thanks to a magnetic controller. This DNA scaffold thus allows real-time observation, at the single-molecule level, the measurement of the kinetic of dissociation involving biologically relevant partners.

First proof of concepts have already been established on the rapamycin-mediated association between FKBP12 and FRB (Kostrz 2019). Rapamycin is an immunosuppressive and antiproliferative drug modulating the mTOR signalling pathway. Our tool showed precise, accurate and model-independent measurements of the residence time of the drug, with error under 10 % and values corresponding those found in the literature (Banaszynski 2005). In addition, the amount of proteins reagents required is a hundred time lower than the ones used in other kinetic methods.

Forthcoming, the jDNA will be used as a tool to characterise a new nanoscale agent dedicated to cancer immunotherapy. The latter biologics is a hybrid platform combining two nanobodies (Muyldermans 2020) and a DNA origami. Its purpose is to direct immune cells to cancer cells with the two antibodies with specific of the respective cell surfaces, and the circular DNA-origami holding them in close proximity so as to favour the apparition of an immune synapse. The first step of the study will be to characterise the nanobodies-antigen pairs dissociation rate and its force-dependence as well as the stability of the origami under tension.

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Immunity and competition between bacteria in the gut

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Résumé

Antibiotic resistance is a major threat, motivating the development of new vaccination procedures to eliminate antibiotic resistant bacteria. Our collaborators (E. Slack's lab, ETH Zürich) have shown that intestinal antibodies, raised by oral vaccines, enforce the targeted bacterial strain to undergo "enchained growth", forming large clumps, which may be flushed out of the gut faster than free bacteria. They have developed a protocol combining vaccination with the introduction of a niche competitor to eliminate a pathogenic non-Typhoidal Salmonella from the gut lumen. As intestinal colonization is a highly dynamic process, we have built a simple mathematical model to generate predictions on the requirements for extinction of the pathogenic strain and the time-to-extinction. We have used trainining data to estimate key kinetic parameters such as growth rates of the pathogenic strain and the competitor, their loss rates, as well as the carrying capacity. We have then estimated the extinction probability and the extinction time distribution for different colonization strategies. Our model confirms that the preventive introduction of the competitor significantly reduces the extinction time of the pathogenic strain (1). (1) Lentsch, V et al. (2025). Vaccine-enhanced competition permits rational bacteria strain replacement in the gut. Science 388, 6742, pp. 74-81

Mots-Clés: infectious disease, within, host modeling, parameter estimation techniques

*Intervenant

Abstracts
(by poster number)

Posters

Poster number 01

Identifying rare cell types in the Arabidopsis Root fromscRNA-seq data.

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Résumé

The Arabidopsis Root is an ideal model to study cell fate determination in plants because it has stereotypical cell files in which cells divide along a single axis and undergo progressive differentiations. With the advent of high-quality single cell atlases of the Arabidopsis root transcriptome, there has been a lot of work on profiling these cell files and for inferring associated (continuous) changes to the cell transcriptomes. Unfortunately, these advances are inherently concentrated on the already partly differentiated cells of these cell files that express specific marker genes. In practice, it is much more difficult to profile the stem cells that give rise to these files because of their rarity and because they lack clear marker genes. However, anatomical studies show a clear spatial organisation of the different stem cells giving rise to these different cell files, along with the presence of cells forming the so called "quiescent center" that seem to control the stem cells without themselves undergoing divisions. I have been working on identifying the different transcriptomes of these multiple cell types that form the root stem cell niche. The specificities across these different cell types can shed light on the genes driving these different cell states,

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leading to candidate regulatory interactions between master transcription factors. My long term goal is to build a dynamical gene regulatory network model that can explain the different cell states and their differentiation steps.

Poster number 02

Actin filament assembly and disassembly regulation at the surface of a lipid bilayer: reconstituting the context of the cortex

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Résumé

The actin cortex is a 300-nm thick filamentous network located at the inner part of the plasma membrane that dynamically shapes the cell and maintains its physical integrity. This actin network is characterized by a turnover in the timescale of tens of seconds, being the result of a complex balance between actin assembly and disassembly. Furthermore, the actin cortex is attached to the plasma membrane thanks to the ERM (ezrin, radixin, moesin) protein family, making it a specific biological system with complex biochemical and physical characteristics. Moreover, we know that the actin elongators, formins, are sensitive to tension and geometrical restrictions, and that the severing activity of the actin disassembler, cofilin, also depends on mechanical constrains. All these constitute a challenge in the field of actin cortex-like network *in vitro* reconstitution with faithful dynamic properties. We investigated the activity of these two actin regulators, formin and cofilin, using purified, fluorescently labelled proteins, supported lipid bilayers (SLB) functionalized with ezrin, and TIRF microscopy. We show that the density of ezrin over the SLB influences their activity. The average formin-mediated elongation rate decreases as the filaments get more attached to the lipid bilayer. However, no sign of rate slowdown was detected during actin polymerization until the formin unbound, meaning that no matter the filament's length it is unlikely that it experiences any significant friction or geometrical constrains. Regarding cofilin, domain nucleation and filament severing rate decreases as well with higher density of ezrin. The magnitude of this trend is actin isoform-specific, certainly owing to the difference in ezrin affinity between alpha-skeletal and beta-cytoplasmic actin. These results contrast with the case of another way of anchoring, like biotin-neutravidin-based tethering, that increases the severing rate, suggesting an activity resting on a competition between ezrin and cofilin for actin binding, instead of purely mechanical constrains.

Mots-Clés: cytoskeleton, actin, cortex, microscopy, biochemistry, biophysics

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Poster number 03

Mechanical plasticity revealed by traction forces of migrating epithelial cell trains

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Résumé

To move, adherent cells generate active forces. In cell groups, forces distribute to cell-substrate and cell-cell adhesions so the stress increases towards the group centre, yet with large fluctuations. How do forces distribute and contribute to cell migration within a group of epithelial cells? To tackle this, we took a reductionist approach, by confining MDCK cells to linear fibronectin tracks.

We found that traction forces cluster into patches along the line, spanning subcellular to multicellular sizes. Thus, cell groups dynamically explore all the configurations from fully coupled "megacells" to fully independent, subcellular force dipoles. The number and location of such poles is predominantly controlled by the system's length. Average force-length relationships show that not only do cell-cell junctions act as mechanical linkers, but they also induce a collective increase of single cell contractility. We also studied the correlations between traction forces and cell motion. We found that those correlations rather lie in the spatial organization of traction forces than in their magnitude. In particular, the analysis of force pole dynamics in stick-slip motion suggests that the redistribution of substrate adhesion along the cell plays a key role.

Overall, our work sheds a new light on the dynamic regulation of force-transmitting modules in epithelial clusters, which impart them their ability to deform while keeping their cohesiveness.

Mots-Clés: Cell migration, cell mechanics, cell, cell junctions

*Intervenant

Poster number 04

AI-driven Prediction of Circular Dichroism Spectra of Proteins.

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Résumé

Circular Dichroism (CD) spectroscopy is a versatile and rapid method for characterizing the secondary structure, conformation, and folding of proteins under near-native conditions. While not a high-resolution technique, it is invaluable for analyzing protein-ligand interactions, assessing the effects of mutations, and validating computationally predicted structures. The ability to accurately predict CD spectra from high-resolution structural information is crucial for these applications.

The Knowledge-based Circular Dichroism (KCD) method has demonstrated superior accuracy in predicting far-UV CD spectra compared to other well-established approaches. It uses a model based on the classical theory of optical activity with a complex set of atomic polarizabilities derived from a database of SRCD spectra and PDB structures. However, its predictive power can be further enhanced by refining these polarizabilities.

In this work, we present a novel approach to enhance the accuracy of the KCD method. We have developed and implemented deep neural networks to optimize the weights of the complex polarizabilities used in the KCD algorithm. We will demonstrate how this data-driven approach significantly improves the accuracy of far-UV CD spectral predictions when compared to the original KCD method and other state-of-the-art prediction tools. This refined computational model offers a powerful new tool for the structural characterization of proteins.

Mots-Clés: Circular Dichroism, Deep Learning, Neural Networks, Protein Structure, Spectral Prediction

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Poster number 05

Statistical Field Theory for inference on a stochastic molecular circuit

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Résumé

Living systems functioning is intrisically stochastic at the molecular level, which has great consequences on gene expression. A key example is the role of microRNAs, which not only downregulate their target messenger-RNA, but also reshape protein distributions by decreasing their variance. We present a Statistical Field Theory framework to compute the first two moments of target mRNA distributions with high precision in the strong coupling, low-copy-number regime-where traditional "small noise" approaches fail. Our results capture the emergence of non-Gaussian fluctuations and enable robust and accurate estimates of kinetic parameters from synthetic data, using a moment-based inference procedure. This strategy will then be tested on fluorescence measurements derived from in vitro experiments.

Mots-Clés: Gene expression, Statistical field theory, noisy molecular circuits

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Poster number 06

Energy-based models for Gene-Regulatory Network inference from scRNA-seq data

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Résumé

Waddington's landscape picture depicts differentiating cells as marbles rolling down into valleys, analogously to landscapes where energy minima define states of a system. Recent progress in microfluidics and sequencing technologies allow to capture and sequence messenger RNAs at the single-cell resolution, offering a path to build a cell state landscape. We train a maximum entropy/energy based model to reproduce the marginals and covariances of a scRNA-seq dataset. Preliminary results show the model learns meaningful representations of the underlying data structure while preserving key distributional features
This task remain challenging and rests on the ability to efficiently sample from a high-dimensional and correlated multi-modal distribution. Future work will evaluate whether the model can generate biologically realistic cell profiles and identify which cell phenotypes can be reproduced by these kinds of models as we refine the sampling methodology and model architecture.

Mots-Clés: energy, based models, gene, regulatory networks, Waddington landscape, scRNAseq data

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Poster number 07

Bacteria collective motion is scale-free

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Abstract

Suspensions of swimming bacteria interact hydrodynamically over long ranges, organizing themselves into collective states that drive large-scale chaotic flows, often referred to as "bacterial turbulence". Despite extensive experimental and theoretical work, it remains unclear whether an intrinsic length scale underlies the observed patterns. To shed light on the mechanism driving active turbulence, we investigate the emergence of large-scale flows in E. coli suspensions confined within cylindrical chambers, systematically varying confinement height over more than two orders of magnitude. We first demonstrate that the critical density for the onset of collective motion scales inversely with this confinement height without saturation, even for the smallest densities observed. Near the onset, both the observed length and time scales increase sharply, with the length scale bounded only by the vertical confinement. Notably, both scales exhibit clear power-law dependence on the confinement height, demonstrating the absence of an intrinsic length scale in bacterial collective motion. This holds up to scales nearly 10,000 times the size of a single bacterium, as evidenced by transient coherent vortices spanning the full chamber width near the onset. Our experimental results, which demonstrate that bacterial turbulence is scale-free, provide essential constraints for theories aiming to capture the dynamics of wet active matter.

Keywords: wet active matter, collective motion, instability, vortices

*Speaker

Poster number 08

Chemotactic Drift and Surface-Borne Memory: A Lagrangian Perspective for Bacteria Exploring Confined Environments

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Abstract

Bacterial chemotaxis is driven by a temporal comparison of current and past environmental cues. This "memory effect" introduces variations of motion persistency in the direction of an increase or a decrease in ligand concentrations, reducing the impact of noise in chemical sensing and allowing adaptation of the response to a large range of chemical environments. We conducted systematic experiments with E. coli in confined environments under prescribed gradients of attractive chemicals. Using a Lagrangian tracking technique, we were able to monitor bacterial motion over long periods of time and relate the chemotactic responses to the actual chemical landscape experienced by individual bacteria. Recently using a similar technique, bacterial diffusivity for adapted E.coli was found to depend on the confinement height as well as the circular kinematics taking place at surfaces. Memory effects leading to large log-normal distributions of run-times, and consequently to large residence times at the surface, were attributed to the fluctuations of the CheY-P protein near the motor driving the tumbling process.

Similarly, our work shows that chemotactic flux depends on confinement. Since there is no net chemotactic flux at surfaces, chemotactic behavior is essentially driven by motion in the bulk. However, the impact of surfaces on chemotaxis extends beyond reducing the mean bacterial response. We found a correlation between bacterial memory time and surface residence time. When an E. coli bacterium swims toward a nutrient source and encounters a surface, it typically spends more time on the surface, effectively "remembering" that it was previously heading in the right direction. Conversely, when a bacterium moves down a gradient and encounters a surface, it rapidly tumbles and escapes. Direct comparisons between experimental results and a theory of stochastic chemotactic response, suggest that the duration of bacterial memory may vary depending on the nature of the chemical stimuli.

Keywords: chemotaxis, E.coli

*Speaker

Poster number 09

Inhibition of bacterial growth by antibiotics: a minimal model

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Résumé

Growth in bacterial populations generally depends on the environment (availability and quality of nutrients, presence of a toxic inhibitor, product inhibition..). Here, we build a minimal model to describe the action of a bacteriostatic antibiotic, assuming that this drug inhibits an essential autocatalytic cycle of the cell metabolism. The model recovers known growth laws, can describe various types of antibiotics and confirms the existence of two distinct regimes of growth-dependent susceptibility, previously identified only for ribosome targeting antibiotics. We introduce a proxy for cell risk, which proves useful to compare the effects of various types of antibiotics. We also develop extensions of our model to describe the effect of combining two antibiotics targeting two different autocatalytic cycles or a regime where cell growth is inhibited by a waste product.

Mots-Clés: cell growth, antibiotics, growth laws, metabolism

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Poster number 10

Neural crest cells are miniature bioelectric muscles that contract and crawl in response to vasoconstrictor peptides

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Résumé

Enteric neural crest cells (ENCCs) colonize the gut rostro-caudally in early embryogenesis and migration defects give rise to colonic aganglionosis, a pathology known as Hirschsprung disease (HD). Mutations in glial-derived neurotrophic factor / receptor tyrosine kinase (GDNF/RET) and the endothelin 3 / endothelin receptor B (EDN3/EDNRB) pathways are known to be causal in HD. Here, we show that migrating ENCCs exhibit endogenous calcium activity that is critically dependent on EDN3/EDNRB. We demonstrate that EDNRB activation opens chloride and CaV3.2 T-type Ca2+ channels to mediate oscillatory Ca2+ influx and release from inositol trisphosphate sensitive intracellular stores. We find that inhibiting Ca2+ activity by EDNRB, Cl- or CaV3.2 channel blockade results in an ENCC migration defect. We finally prove that the Ca2+ transients induced by EDN3 result in an increased traction force to the extracellular matrix, that drives ENCC migration. Our study demonstrates that embryonic endothelin-mediated neural crest migration and adult endothelin-mediated vasoconstriction is one and the same phenomenon, taking place in different cell types. Our results give a functional explanation of the link between rare mutations of *CACNA1H* (the gene encoding CaV3.2) and HD, and paves the way for a fundamental understanding of neurocristopathies in terms of neural crest cell bioelectric activity deficits.

Mots-Clés: cellules de la crête neurale, bioélectricité, imagerie calcique, contractilité, migration cellulaire, système nerveux entérique, neurocristopathie

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Poster number 11

Cytoplasmic crowding acts as a porous medium reducing macromolecule diffusion

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Résumé

Intracellular transport of macromolecules is crucial for the proper functioning of most cellular processes. Although intracellular crowding is known to strongly alter macromolecule mobility, how cytoplasmic structures physically modulate diffusion remains largely unexplored.
Here we investigated the mechanisms by which cytoplasmic crowding controls diffusivity using live-cell experiments and porous media modeling approaches. Confocal microscopy combined with fluorescence recovery after photobleaching (FRAP) and fluorescence correlation spectroscopy (FCS) measurements revealed an anti-correlation between free-GFP diffusivity and the heterogeneous cytoplasmic structure abundance in live mammalian cells.

This motivated the development of a multiscale model, where the cytoplasm is treated as a hierarchical porous medium with nanometric and micrometric obstacles. Numerically solving the model allowed us to predict the effective cytoplasmic diffusion coefficient for various obstacle volume fractions, and to identify tortuous and porous hydrodynamic hindrances as key diffusion reduction mechanisms. Comparison with our experimental results highlighted the importance of hydrodynamic interactions between diffusing molecules and nanometric obstacles. Importantly, we found that the effective cytoplasmic diffusivity was not dependent on specific intracellular regions but rather on the local intracellular obstacle volume fraction. Finally, the model was extended to predict the diffusivity of larger macromolecules, showing excellent agreement with literature data for several macromolecules and cell lines.
This study provides new insights into the physical mechanisms impeding intracellular diffusion, demonstrating the potential of porous media modeling approaches to predict transport mechanisms in dynamic or heterogeneous intracellular structures, as in cell motility, blebbing, and apoptosis.

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Poster number 12

Protists travelling in sea microdroplets

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Résumé

Marine seaspray are crucial to ocean/atmosphere exchanges; they are produced by the explosion of the many surface bubbles. Some of these micro-droplets travel long distances: their contents are distributed over a wide area. The ocean surface is covered with surfactants, biological matter and particles that are trapped and transported by these droplets. Particles attracted to liquid-gas interfaces are several orders of magnitude more concentrated in the droplet than in the bulk. Also, the presence of surfactants drastically influences the number, size, and velocity of drop ejection. How do these two aspects combine in the case of motile eukaryotic microorganisms? Are they captured and subsequently propagated over long distances? To address these questions, we design an experimental setup that allows us to study seaspray formation in a solution of micro-organisms. We decided to focus on microalgae, choosing *Chlamydomonas reinhardtii* as a model organism and *Ostreopsis Ovata* as a potential example in the context of harmful algae bloom. In the experiment, a millimeter-sized bubble is released into the algae solution, and the jet and droplet ejection are tracked using a high-speed camera. The first droplet is captured on a glass slide and then observed under a microscope. The aim of our study is to investigate the dynamic properties of the jet, as well as the concentration and the motility of microalgae in the droplet.

Mots-Clés: microdroplets, seaspray, microalgae, harmful algae bloom

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Poster number 13

Can Force Generation in Plant Cells be Predicted from Lockhart's Growth Law?

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Résumé

Through turgor pressure, plant cells generate incredible forces that exceed those attainable by muscle contraction in animals. The resulting forces drive the plants' growth, making it possible to pierce the soil and remain upright against the pull of gravity. Since turgor pressure is the main source of forces in plants, any behaviour that we observe must have an explanation at the level of water movements. Be it the fast, snapping-like motions of some carnivorous plants or the slower motion with which root hairs avoid hard obstacles, turgor pressure remains the core mechanism behind them. In our case, we have formulated an analytical description of plant cell twisting and elongation from Lockhart's growth law, which connects turgor pressure and growth. We focus on the case of axial compression of a cylindrical cell, using the algae *Chara corallina* as our model. To verify our hypothesis, an experimental setup has been made that allows us to monitor every quantity involved in Lockhart's growth law and their evolution throughout plant cell elongation: a pressure probe allows us to monitor turgor in real time, while a glass obstacle of known rigidity lets us measure the force exerted at the cell's apex. By coating the cell with fluorescent beads, we can track both elongation and twisting, allowing us to study a three-dimensional formulation of what originally is a one-dimensional phenomenological law.

Mots-Clés: Plant Cells, Pressure Probe, Lockhart's Law, Cell Growth, turgor pressure

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Poster number 14

Agent-based models of cytoplasm crowding and viscoelasticity

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Résumé

The cytoplasm is a complex medium crowded with diverse macromolecules, organelles, and entangled networks of cytoskeletal filaments. Many recent studies, based on active rheological measurements achieved with optical or magnetic tweezers, have shown that the cytoplasm exhibits size-dependent viscoelastic behavior. In general, however, how the density, dynamics or interaction of various components set the rich rheology of the cytoplasm remains poorly understood. We developed a numerical agent-based simulation for the cytoplasm using Cytosim. These consist of: (1) suspensions of spherical particles representing organelles such as yolk granules or mitochondria, and (2) elongated filaments interconnected by crosslinkers to mimic either a percolated cytoskeletal network or the endoplasmic reticulum. We performed numerical experiments of active rheology, by applying a direct force on probes of various sizes to compute simulated cytoplasm viscosity and elasticity, and compared our results with analogous experiments performed in sea urchin eggs and extracts. Our simulations allowed to recapitulate rheological signatures of the cytoplasm as in experiments, with a viscoelastic response at short time scales followed by a fluidization regime. In addition, the simulations allowed us to draw a phase portrait for how viscoelastic parameters depend on particle density, size, connectivity, as well as network percolation. Further, by simulating pulling on probes of various sizes, we also revealed that cytoplasm viscoelasticity increases nonlinearly with particle size, in agreement with experimental findings. These results suggest that size-dependent behavior may be governed by physical properties, such as crowding, confinement by cell boundaries and percolation, rather than biochemical reactions. Overall, this work represents the first agent-based framework to interpret active rheological measurements of the cytoplasm, and provide insights into the viscoelastic nature of the cytoplasm and its dependence on structural and physical factors, with implications for understanding intracellular transport and cellular mechanics.

Mots-Clés: cytoplasm viscoelasticity, agent, based simulation, Cytosim, magnetic tweezers simulation

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Poster number 15

Bacterial exploration on solid/liquid interfaces with complex topography

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Résumé

Motile bacteria can adhere to a solid/liquid interface and form biofilms that protect individual cells from external aggression. Although this behavior is common in nature, it poses a public health problem when these biofilms form on manmade surfaces, such as hospitals tools, leading to nosocomial diseases or antibiotic resistance. In this context, it has recently been demonstrated by several groups that the physical microenvironment could strongly influence the formation and structure of biofilms of the commensal human pathogen Pseudomonas Aeruginosa (PA). In particular, we have shown that the elasticity of the solid substrate influences the morphology of early colonies and the mixing of strains on the surface during co-colonization, through a modulation of the efficiency of surface motility ("twitching"). However, how the micron-size topology of surfaces modulates the surface motility of PA and the subsequent structure of biofilms has so far been little studied, mostly on surfaces with a high density of obstacles or a crystal-like organization topography. Here, we have developed surfaces with a homogeneous surface chemistry but present an adjustable density of randomly distributed obstacles in the μm size range. These surfaces are included in a microfluidic channel allowing precise control of the flow conditions (shear strain, nutrient renewal) and permit optical monitoring of surface colonization over several hours, from individual bacteria to microcolonies. We show how this platform paves the way towards the systematic study of the influence of micron-size roughness on the surface motility, microcolony morphology, strain mixing and phenotype of PA upon surface colonization.

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Poster number 16

SENSOCELL: Deciphering cell mechanobiology through optical tweezer force spectroscopy

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Résumé

Mechanical forces sculpt cells and tissues, modulate migration and intracellular transport, organize the scaffolding of different subcellular compartments and provide cues for mechanoresponsive and behavioral processes. At the same time, the specific fingerprint of mechanical and rheological properties of biological soft matter defines the range over which force and stress propagate and dissipate. Developing standardized tools is therefore essential in cell mechanobiology -not only to quantify material properties, but also to apply controlled forces in order to probe dynamic processes within cells. In this technical talk, we will present SENSOCELL, an optical tweezers platform specifically designed for biophysical studies in complex biological samples. SENSOCELL integrates two key technologies –the direct measurement of optical forces through light momentum detection and multiplexed trap generation through acousto-optic deflectors (AOD). Together, these allow manipulation and force measurements simultaneously at different sites of a cell without the need of *in situ* stiffness calibration of the optical trap, which allows us to analyze force propagation and material flow in different types of samples. We will showcase cutting-edge applications developed by some of our customers, which range from the biophysical properties of DNA or protein filaments and phase-separated protein condensates to the rheological spectrum of the cyto- and nucleoplasm. In addition, we will present studies on plasma membrane flow and tension propagation, followed by the mechanical gating of transmembrane ion channels, linking physical forces to biological responses.

Mots-Clés: Optical tweezers

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Poster number 17

Mucus pumping from artificial magnetic cilia in an open to air microfluidic channel

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Résumé

Pulmonary bronchi are lined with a thin layer of mucus, which protects the airways from foreign particulate. In order to remove this mucus from the lung, the epithelium of the lung is covered in ciliated cells, which beat, moving the mucus up and out of the bronchi to the throat. Dysfunction in this mucociliary clearance can result in impaired breathing, infection and an increase in mortality (1). One approach to studying mucociliary clearance has been using artificial cilia, and in particular microfabricated magnetic cilia (2).
Artificial cilia are actuated by placing the microchannel above a rotating set of permanent magnets, which actuate with a slow active stroke, and a rapid recovery stroke, caused by a magneto-elastic instability (3). The microchannel is filled with fluid which can be pumped by the cilia. In order to better mimic mucociliary clearance, we leave the top fluid surface open to air. To overcome surface tension effects, the microchannel is made hydrophilic by plasma activation, and surfactants are added to fluid solutions when necessary, resulting in a flat air-liquid interface.

Flow in our channel is measured using particle tracking velocimetry of suspended tracer particles. The flow profile in all fluids resembles that of fully developed flow with the maximum velocity achieved on the surface of the fluid. This flow is dependent upon the specifics of the cilia pathway, and proportional to their frequency. Flow generated is measured to decrease relative to viscosity in giant micelle solutions and in model snail slime mucus. Importantly, the comparison between mucus and micellar solutions reveals a greater decrease in flow for mucus, likely due to its particular rheology.
(1) Bustamante-Marin, and Ostrowski, (2017), Cold Spring Harb Perspect Biol, 9:a028241.
(2) ul Islam, *et al.* (2022), Lab Chip, 22.9:1650-1679.
(3) Moore *et al.* (2025), Lab Chip, 25.12:2949-2960.

Mots-Clés: cilia, microfluidic, fluid, structure interaction, mucus, biolocomotion, viscosity, magnetic, surface tension

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Poster number 18

Temperature scaling of gene regulatory networks for multicellular development.

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Résumé

Developmental rates of poikilothermic (warm-blooded) animals generally obey Arrhenius scaling, though scaling parameters are genus and even species dependent. Surprisingly, despite the myriads of diverse chemical reactions involved, this temperature scaling is uniform, leaving the relative timing of key developmental milestones unchanged. How this is achieved and, more generally, how individual molecular decisions or events that control developmental processes are buffered against temperature to maintain developmental precision is not well-understood.
Here, we address this question, using post-embryonic temporal cell-fate specification of C. elegans hypodermal stem cells as a model system. Specifically, we study the transcription factor (TF) LIN-14, a member of the developmental timing pathway, which mediates stem cell temporal identity progression. lin-14 has been shown to be expressed in a stereotypic dynamic fashion during larval development, offering convenient readout parameters to access temperature scaling. Timely downregulation of LIN-14 is critical for the correct fate transition of hypodermal stem cells in the first larval stage.

To measure lin-14 mRNA abundance and transcriptional kinetics as a function of developmental progression, we performed large-scale single-molecule fluorescent in-situ hybridization (smFISH) time course experiments at different temperatures. Using automated image analysis, we obtained per-cell cytoplasmic mRNA counts as well as a transcriptional-activity index by normalizing the nuclear active-transcription-site fluorescence to the intensity of single cytoplasmic mRNAs. Surprisingly, after aligning datasets by developmental stage across temperatures, our results show that cytoplasmic lin-14 mRNA counts are temperature-invariant and the dynamics of lin-14 mRNA counts exhibits near-perfect temperature scaling. In contrast, transcriptional metrics indicate shifts in expression rates, pointing towards a transcriptional strategy to maintain mRNA levels across conditions.
Overall, our results establish a novel system to quantitatively test how temperature rescales gene-expression and developmental timing and, more generally, to understand the molecular origin of developmental robustness in the face of environmental variation.

Mots-Clés: Developmental biology, transcription dynamics, temperature

*Intervenant

Poster number 19

Investigating the dynamics of cellular rearrangements in minimal four-cell clusters.

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Résumé

Animal cells assemble into tissues that exhibit diverse mechanical responses, from solid-like to liquid-like states. In solid-like states, tissues can withstand mechanical stress, whereas in liquid-like states, they release stress through cellular rearrangements. Recent evidence suggests that the transition between solid and liquid-like states is central to biological processes such as embryogenesis, wound healing and cancer metastasis. However, the way in which local interactions between the constituent cells control the tissue fluidity remains unclear. We study minimal cellular rearrangements involving four cells exchanging neighbors, also known as T1 transitions. Theoretical models have shown that the energy barrier associated with T1 transitions determines the fluidity of the tissue. In our work, we use time-lapse microscopy to image groups of four cells confined on an adhesive micropattern. We exploit the spontaneous rotation of the cells on elliptical micropatterns to induce effective deformation of the cell clusters. We record the dynamics of the resulting T1 transitions over time. In the future, we aim to use data-driven methods combined with vertex models to derive a physical description of the system, that could be used to calibrate numerical models. We also intend to use this platform to study the impact of perturbations of cell-cell adhesion proteins on the rearrangement dynamics.

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Poster number 20

Designing 3D particles for self-limiting self-assembly

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Résumé

Many proteins self-assemble into higher-order structures in a controlled manner, and can in particular form into aggregates with a large but finite size at equilibrium. Understanding how this self-limiting property generically emerges from the characteristics o individual components is an open problem, relevant to both the comprehension of biological self-assembly processes and the design of artificial particles. To uncover the broa design principles of objects which aggregate into finite-sized structures, we numerically study the self-assembly of three-dimensional lattice particles with simple geometries but complex interactions. We find that choosing particle interactions in a manner that introduces topological defects in the resulting aggregate is a novel and viable strategy for size control.

Mots-Clés: Self, assembly

*Intervenant

Poster number 21

Reinforcement learning for olfactory navigation in turbulent flows

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Résumé

Olfactory navigation is the process by which organisms use their sense of smell to navigate their environment and locate, for example, food or mates. In turbulent flows, odor-guided navigation is a formidable problem because odors are quickly dispersed by turbulence. The searcher must make decisions based on a highly intermittent odor signal, made of a few odor detections separated by long periods of voids. Yet numerous insects like moths or mosquitoes can locate odor sources from tens or even hundreds of meters away.
To elucidate possible solutions to odor-guided navigation, we propose a novel approach based on reinforcement learning. Reinforcement learning is a technique originating from artificial intelligence that allows approximating optimal strategies for game-like decision-making problems. We model a searcher by a deep neural network that, like an insect, must decide where to move simply based on odor detections, and we train it in a virtual environment that simulates odor transport by a turbulent flow. A particular point of attention is the modeling of the short-term memory of the searcher. We model memory as the hidden state of a recurrent network, which the agent learns to optimize during the training process, together with the navigation strategy.
We will present our first results obtained with this model in various simple 2D environments. We will show in particular that we can recover the performance of the best known strategies (e.g., infotaxis) based on perfect, infinite memory and that a low-dimensional memory is sufficient to ensure a high probability of finding the source within a relative short time.

Mots-Clés: Reinforcement learning, Olfactory navigation, Turbulence

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Poster number 22

CDC42 Regulates Golgi Mechanics and Cargo Transport Through Actin-Mediated Control of Organelle Stiffness

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Résumé

The Golgi apparatus functions as a central hub for protein processing and trafficking, yet the contribution of its mechanical properties to cargo transport remains poorly understood. Here, we investigate how the GTPase CDC42 regulates Golgi mechanics and transport dynamics through the actin cytoskeleton. Using fluorescence recovery after photobleaching (FRAP) of RAB6-GFP, we find that CDC42 overexpression slows recovery kinetics, whereas siRNA-mediated depletion accelerates recovery. Optical tweezer-based micromechanics measurements further demonstrate that CDC42 activity increases Golgi stiffness, while CDC42 depletion reduces stiffness. Furthermore, CDC42 impact the size and shape change of the Golgi over time. Together, these findings establish that CDC42 modulates Golgi transport by tuning the mechanical properties of the organelle through actin remodeling. This work identifies CDC42 as a regulator of Golgi mechanics and provides a mechanistic link between cytoskeletal control, organelle stiffness, and protein trafficking.

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Poster number 23

Thermal management of the hive: problematic, state of the art and a few solutions for temperature overshoot mitigation

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Résumé

It is well known that rapid variation and also excessive temperature in the hive have large impact on honey production and also in some cases can lead to the total destruction of the swarm. Bees have naturally developed skill in thermal management (water droplet introduction, ventilation ...) but especially nowadays these strategies are not sufficient. Temperature recordings shows various temperature profiles according to the location in the hive (wooden frame, brood, honey...) (Jahwar 2023, Beinat 2025). It has been shown that excessive temperature disorganizes the colony with bee activity reallocating. Indeed, bees are differently spread within the hive, some are going outside. After a return to normalcy, the usual activities resume without no apparent durable effect of the thermal stress. However, it is well known that repetitive and frequent expositions to thermal shock significantly result in a lower honey production and also with more diffuse brood, the explanation is linked to increased thermoregulation activity (Weinberg 2023). In addition, excessive temperature events even with short duration may affect brain development of young bees (learning capacity, memorization...) and finally may alter their behavior. Improved Heat management in the hive would help to limit the thermal stress applied to the honey bee colony. At that time, it is recommended to introduce insulation material (wood wool), to use radiative screen in order to protect the hives from solar radiation, to provide accessible water in the neighborhood... More could be done by using material with inertia judiciously located or a phase change material... and why not an also active cooling process especially designed as far as this does not affect the bee colony. Collaboration between Beekeepers, Biologists and Physicists with thermal science knowledge could be fruitful to find appropriate solutions in order to save or at least to help bees to store enough summer honey.

Mots-Clés: Bee, Hive, Thermal management, Therma shock, Temperature, Cooling

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Poster number 24

Questions sur l'oeil et la physique

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Résumé

Dans l'histoire, la lumière, l'objet, l'image, réelle et virtuelle, ces concepts de base en optique ont mis du temps à se construire. Ils ont permis à la compréhension des phénomènes de la vision par l'oeil humain. Aujourd'hui, avec le développement rapide des nouvelles technologies et de l'économie numérique, de nouveaux phénomènes en relation avec l'oeil humain ont été constatés. Ils ne sont pas tous compris. Ils sont parfois considérés comme phénomènes psychologiques. Dans cette présentation nous nous questionnons sur l'interaction entre les ondes physiques et l'oeil humain.

Mots-Clés: L'oeil, physique, technologie

*Intervenant

Poster number 25

Locomotion in Trichoplax, an animal without neurons or muscles

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Résumé

Locomotion in animals comes in many forms. In Trichoplax - a flat, early-divergent animal without neurons or muscles - thousands of epithelial cells in contact with the substrate bear motile cilia that enable crawling. Not only Trichoplax can navigate in a given direction, change direction in response to various gradients, and dramatically change its overall shape, we also found that it can redirect its movement in response to mechanical stimuli. How does ciliary beating align across the whole animal to achieve consistent directional movement ? How does coordinated redirection occur when the animal change direction ? We investigate the cellular determinants of Trichoplax movements, reorientation, and mechanosensation, from the ciliary structures to the locomotion behavior. https://www.biorxiv.org/content/10.1101/2025.08.22.671430v1

Mots-Clés: locomotion, cilia, basal bodies, mechanosensation

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