IntCha 2026

Institut d'études scientifiques Cargèse, Corsica
April 20th - April 24th 2026

Abstract booklet and timetable

We would like to thank our sponsors for their generous support

Table of contents

Monday, April 20, 2026

TIME	EVENT	(+)
12:00 - 13:45	Lunch	
13:45 - 14:00	Welcoming remarks	
14:00 - 15:30	Data driven modelling	(+)
14:00 - 14:30	› Characterizing the behavioral complexity of locomotion dynamics across scales - *Alasdair Hastewell, National Institute for Theory and Mathematics in Biology*	
14:30 - 15:00	› Geometric Perspectives on Structure in Complex Systems - *Alexandra Jurgens, Inria-Bordeaux*	
15:00 - 15:30	› Biophysical generative modeling of cell fate decision-making with single-cell omics - *Victor Chardès, Harvard University, Department of Molecular & Cellular Biology, Flatiron Institute*	
15:30 - 16:00	Coffee break	
16:00 - 18:00	Poster session	(+)
16:00 - 18:00	› Phase transition in statistical inference of spatial information from single-cell sequencing data - *Alican Saray, The Ohio State University [Columbus]*	
16:00 - 18:00	› Hydraulics, Flux and Microlumina in Active Multicellular Systems - *Jack Treado, Max Planck Institute for the Physics of Complex Systems, Technische Universität Dresden = Dresden University of Technology*	
16:00 - 18:00	› Applying Fluctuation Dissipation Relations to Active Systems - *Martin Johnsrud, Max Planck Institute of Dynamics and Self-organization*	
16:00 - 18:00	› Flow manipulation in mechanical ecology - *Hunter King, Rutgers University [Camden]*	
16:00 - 18:00	› Collective motion and ordering of polydisperse microswimmers - *Jakub Trzaska, Niels Bohr Institute [Copenhagen]*	
16:00 - 18:00	› Morpho flight study: wing kinematics and deformation - *Camille Aracheloff, Institut de Systématique, Evolution, Biodiversité*	
16:00 - 18:00	› 1st Year PhD on Modelling and Quantifying Parallelism in Community Evolution - *Tristan Barata, IBENS*	
16:00 - 18:00	› Emergence of inter-individual behavioral variability in unpredictable environment - *Rémi GAUTIER, Institut du Cerveau = Paris Brain Institute*	
16:00 - 18:00	› From order to topology - *Birte Geerds, Université de Genève = University of Geneva*	
16:00 - 18:00	› Anticipatory agents view their trajectories as polymers: a space-time analogy for decision-making - *Alexis Raulin-Foissac, Institut Lumière Matière [Villeurbanne]*	
16:00 - 18:00	› Control of contractile active materials using optically-induced force generation - *Sasha Toole, Brandeis University*	
16:00 - 18:00	› Equal Partitioning of the Min Proteins at Cell Division - *Natan Dominko Kobilica, Arnold Sommerfeld Center for Theoretical Physics [München]*	
16:00 - 18:00	› Modeling the dynamics of T lymphocytes performing reverse haptotaxis using data-driven methods - *Reya Negi, Aix-Marseille University*	
16:00 - 18:00	› How to escape the Red Queen? Towards nonlocal mutations in travelling wave descriptions of immune-viral coevolution - *Max Zayas Orihuela, Laboratoire de physique de l'ENS - ENS Paris*	
16:00 - 18:00	› Development of the human bronchial airway network - *Ivan Lobaskin, Department of Applied Mathematics and Theoretical Physics [Cambridge], Gurdon Institute*	
16:00 - 18:00	› Novel Phase Coexistence in a Multi-Species Vicsek Model - *Eloise Lardet, Imperial College London*	
16:00 - 18:00	› Super-resolved anomalous diffusion: deciphering the joint distribution of anomalous exponent and diffusion coefficient - *Yann Lanoiselée, Basque Center for Applied Mathematics*	
18:00 - 21:00	Welcome drinks	

Tuesday, April 21, 2026

TIME	EVENT	(+)
08:00 - 09:00	Breakfast	
09:00 - 10:30	Non-equilibrium systems	(+)
09:00 - 09:30	› Synchronisation and topological defects in 2D systems - *Ylann Rouzaire, University of Barcelona, UBICS (Uni. Barcelona Institute of Complex Systems)*	
09:30 - 10:00	› Information and chirality: emergent response from nonequilibrium bath - *Rémi Goerlich, Laboratoire de Physique de l'ENS Lyon*	
10:00 - 10:30	› Escaping Cahn-Hilliard: Active Model B- from Three-Component Reaction Diffusion - *Beatrice Nettuno, University of Munich (LMU)*	

TIME	EVENT	(+)
10:30 - 11:00	Coffee break	
11:00 - 12:00	Cells and tissues	(+)
11:00 - 11:30	› Morphogenesis across scales: the role of single-cell mechanics in regulating tissue fluidity during gastruloid development - *Marta Urbanska, University of Cambridge [Cambridge, UK]*	
11:30 - 12:00	› Shaping fate: geometric methods for cell fate transitions and tissue patterning in stem cells and organoids - *Dillon Cislo, Rockefeller University [New York]*	
12:00 - 14:00	Lunch	
14:00 - 15:30	Cells and tissues	(+)
14:00 - 14:30	› Self-assembly of three-dimensional particles with complex interactions - *Vincent Ouazan-Reboul, Laboratoire de Physique Théorique et Modèles Statistiques*	
14:30 - 15:30	› Cell shape-shifting across the tree of life - *Anđela Šarić, Institute of Science and Technology [Klosterneuburg, Austria]*	
15:30 - 16:00	Coffee break	
16:00 - 18:00	Poster session	(+)
16:00 - 18:00	› A Novel Perspective on Attention-Deficit/Hyperactivity Disorder: Analysing Behavioural and Neuronal Dynamics in Zebrafish Models - *Leonard Constien, Fondation ICM*	
16:00 - 18:00	› Inference from Biological Data: Undersampling and Multiple Scales - *Milo Repossi, Ecole Superieure de Physique et de Chimie Industrielles de la Ville de Paris*	
16:00 - 18:00	› Exploring collective cell dynamics in the subconfluent regime with asymmetric subcellular cues - *Clarisse Pierre, Laboratoire Physique des Cellules et Cancer UMR168, Institut Curie*	
16:00 - 18:00	› Learning the equations that govern collective motility in bacteria colonies - *Tanju Cakar, University of Sheffield [Sheffield]*	
16:00 - 18:00	› The spontaneous emergence of spatial structure in microbial communities - *Jan Kocka, Department of Physics and Astronomy, University College London*	
16:00 - 18:00	› Curvature and its effects on tissue morphology. - *Paula Belska, Paris-Lodron-Universität Salzburg = Paris-Lodron-University of Salzburg*	
16:00 - 18:00	› Exploring the Principles of Self-Assembly with Tunable and Flexible Colloidal Particles - *Lisa Shafroth, Laboratoire de Physique Théorique et Modèles Statistiques, Physique et mécanique des milieux hétérogènes*	
16:00 - 18:00	› Collective dynamics of active particles with memory - *Alexis Poncet, Laboratoire de Physique de l'ENS Lyon*	
16:00 - 18:00	› Modélisation empirique de systèmes complexes - *Nicolas Brodu, Centre Inria de l'Université de Bordeaux*	
16:00 - 18:00	› Information-optimal mixing at low Reynolds number - *Luca Cocconi, University of Cambridge [UK], Max Planck Institute for Dynamics and Self-Organization*	
16:00 - 18:00	› Density–Velocity Relation is Scale-Dependent in Epithelial Monolayers - *Hengdong Lu, Niels Bohr Institute [Copenhagen], EPFL*	
16:00 - 18:00	› Statistical Field Theory approach for inference on a stochastic molecular circuit - *Mathéo Aksil, Laboratoire Jean Perrin*	
16:00 - 18:00	› Cytoskeletal oscillations drive large-scale flows and nuclear organization in early embryonic systems. - *Lara Koehler, Physics of Life - TU Dresden*	
16:00 - 18:00	› Density mean back relaxation: Detecting activity from passive observations in many-particle systems - *Laila Henkes, University of Göttingen*	
16:00 - 18:00	› The 3-Components Problem - *Davide Toffenetti, Ludwig Maximilian University of Munich*	
16:00 - 18:00	› Nonreciprocal collective dynamics in a mixture of phoretic Janus colloids - *Gennaro Tucci, MPIDS*	
16:00 - 18:00	› Anisotropic hierarchy decides the fate of an amorphous droplet - *Pietro Caracciolo di Torella, Laboratoire de Physique Théorique et Modèles Statistiques*	
16:00 - 18:00	› Physics of morphogenesis via synthetic mechano-chemical couplings - *Nicolas LOBATO-DAUZIER, Laboratoire Jean Perrin*	
18:30 - 19:30	IL Y A DES TROUPEAUX DANS LE LABO ! Physique de la matière active - Alexandre Morin	

Wednesday, April 22, 2026

TIME	EVENT	(+)
08:00 - 09:00	Breakfast	
09:00 - 10:00	Non-equilibrium systems	(+)
09:00 - 10:00	› Learning and cognition in single cells - *David Jordan - University of Cambridge [Cambridge, UK], The living physics lab*	

TIME	EVENT	(+)
10:00 - 10:30	Coffee break	
10:30 - 12:00	Career session	(+)
10:30 - 11:00	› PhD: valuable skills, invisible value? - *Bastien Marguet, Université Claude Bernard Lyon 1, PhD outreach ambassador*	
11:00 - 11:30	› Publication in the Nature Portfolio - *Anjali Sharma, Nature publishing group*	
11:30 - 12:00	› Quantitative hedge funds, a (short) primer - *Riccardo Marcaccioli, Capital Fund Management*	
12:00 - 14:00	Lunch	
14:00 - 15:00	Career round table	
15:00 - 15:30	Coffee break	
15:30 - 19:00	Hike or beach time - For persons wishing to explore the area around Cargese, we will hike to Punta d'Omigna. Alternatively, conference members may wish to take advantage of the institute's beach.	

Thursday, April 23, 2026

TIME	EVENT	(+)
08:00 - 09:00	Breakfast	
09:00 - 10:00	Active matter	(+)
09:00 - 10:00	› Taming Collective Activity to Crystallize an Oscillator Gas - *Alexandre Morin, Leiden University*	
10:00 - 10:30	Coffee break	
10:30 - 12:00	Active matter	(+)
10:30 - 11:00	› The physical consequence of sperm gigantism - *Brato Chakrabarti, International Center for Theoretical Sciences*	
11:00 - 11:30	› Controlling microalgae populations by phototactic memory - *Gianni Jacucci, Physics Department, University of Calabria, Rende 87036, CS, Italy*	
11:30 - 12:00	› Can bacteria get tied up? Modelling microbial mechanics under large deformations - *Albane Théry, University of Warwick [Coventry]*	
12:00 - 14:00	Lunch	
14:00 - 15:30	Animal behaviour	(+)
14:00 - 14:30	› Whole-body flow sensing and center-of-mass referenced computations for motor control - *Lunsford Elias, Institut du Cerveau (ICM)*	
14:30 - 15:00	› From tower building to eco-evo dynamics: how tiny worms overcome physical constraints to disperse - *Siyu Serena Ding, Max Plank Institute of Animal Behavior*	
15:00 - 15:30	› Information-Theoretic Constraints on the Combinatorial Chemo-sensation of the Octopus - *Hugo Le Roy, Dipartimento di Ingegneria Civile, Chimica e Ambientale [Genova]*	
15:30 - 16:00	Coffee break	
16:00 - 18:00	Poster session	(+)
16:00 - 18:00	› ERK signaling waves encode a local-to-global transition in epithelial cell death patterns - *Maciej Dobrzynski, Institute of Cell Biology, University of Bern*	
16:00 - 18:00	› A new method for inverse problems at arbitrary densities - *Davide Paolino, Gulliver (UMR 7083)*	
16:00 - 18:00	› Run and chase dynamics in turbulent flows - *Mattia Scandolo, University of Chicago, Laboratoire de physique de l'ENS - ENS Paris*	
16:00 - 18:00	› Abundance Fluctuations in Metapopulations with Coloured Random Multiplicative Growth - *JAMES HENDERSON, University College London*	
16:00 - 18:00	› Joint evolution of hardware and artificial neural networks - *Sébastien Billès, Laboratoire Jean Perrin*	
16:00 - 18:00	› Non-Equilibrium Catalysis-Driven Phase Separation in Metabolic Pathways - *Varsha Traynor, Department of Physics and Astronomy [UCL London]*	
16:00 - 18:00	› Resource-mediated interactions shape diversity predictions and functional patterns in microbial communities - *Prajwal Padmanabha, Department of Fundamental Microbiology [Lausanne]*	
16:00 - 18:00	› The spontaneous patterning of feather arrays: a mechanical perspective - *Alessandro Chiappori, Institut de Biologie du Développement de Marseille*	
16:00 - 18:00	› Active nematics on complex curved substrates 9*Violeta Marcen, Matière et Systèmes Complexes*	

TIME	EVENT	(+)
16:00 - 18:00	› Mutual MultiLinearity of Network Currents - *Pedro Harunari, Aix Marseille Université*	
16:00 - 18:00	› 3D confinement reshapes RNA folding and enhances circularisation in the Zika virus - *Yavor Novev, Institute of Genetics and Cancer, University of Edinburgh*	
16:00 - 18:00	› Shape and consequent motion of topological defects in active nematics - *Giacomo Marco La Montagna, CY Cergy Paris Université*	
16:00 - 18:00	› Effective binary models of multicomponent phase separation - *Henri Schmidt, Max Planck Institute for Dynamics and Self-Organization*	
16:00 - 18:00	› Learning stochastic models from partially observed time series - *Joao Pedro Valeriano Miranda, Aix-Marseille Université*	
16:00 - 18:00	› Structural Investigation of Human Low Density Lipoprotein - *Madalena Branco, Université Grenoble Alpes - UFR Physique, Ingénierie, Terre, Environnement, Mécanique, Institut de biologie structurale*	
16:00 - 18:00	› Work minimizing closed-loop protocols for active Ornstein-Uhlenbeck particles with initial position measurements - *Lars Stutzer, Max Planck Institute for Dynamics and Self-Organization*	
16:00 - 18:00	› Maze-solving with density-driven swarms - *Esther María ZAMORA SÁNCHEZ, Laboratoire Jean Perrin*	
16:00 - 18:00	› Phototactic Decision making by micro algae - *Shantanu Raikwar, Laboratoire de physique de l'ENS - ENS Paris*	
18:00 - 21:00	Conference dinner and prize giving	

Friday, April 24, 2026

TIME	EVENT	(+)
08:00 - 09:00	Breakfast	
09:00 - 10:00	Transport across scales	(+)
09:00 - 09:30	› Biophysics of the environment regulates tube formation during vasculogenesis - *Lakshmi Balasubramaniam, University of Cambridge [Cambridge, UK]*	
09:30 - 10:00	› A modelling framework for non-Gaussian transport in complex media - *Vittoria Sposini, Università degli Studi di Padova = University of Padua*	
10:00 - 10:30	Coffee break	
10:30 - 12:30	Ecology & evolution	(+)
10:30 - 11:00	› From molecular interactions to emergent properties: quantifying the dynamics of multispecies biofilms - *Simon Van Vliet, Biozentrum, University of Basel*	
11:00 - 11:30	› Microbial communities in context: A stepwise approach to complexity - *Hannah Jeckel, California Institute of Technology*	
11:30 - 12:00	› When interactions change: Resolving temporal dynamics of bacterial interactions across metabolic conditions - *Anna Weiss, Swiss Federal Institute of Aquatic Science and Technology [Dübendorf], Department of Environmental Systems Science [ETH Zürich]*	
12:00 - 12:30	› Findability bias can strongly impact protein evolution - *Andrei Papkou, ALLOX Bio*	
12:30 - 14:00	Lunch	
14:00 - 15:30	AI and machine learning	(+)
14:00 - 14:30	› Emergent Adaptive Behavior from Simple Synaptic Learning Rules - *Chenguang Li, Sainsbury Wellcome Centre*	
14:30 - 15:00	› Normalizing Flows for Atomistic Simulations of Condensed Matter Systems - *Alessandro Coretti, Universität Wien = University of Vienna*	
15:00 - 15:30	› Where do the electrons go in atomistic ML? - *Jigyasa Nigam - Massachusetts Institute of Technology, MA, USA*	
15:30 - 16:00	Coffee break	
16:00 - 18:00	Q&A session	
18:00 - 21:00	End of conference drinks in Cargese village	

Statistical Field Theory approach for inference on a stochastic molecular circuit

Mathéo Aksil [*†] [1], Callum Britton [2], Carla Bosia [3,4], Gunnar Pruessner [2], Silvia Grigolon[‡] [1]

[1] Laboratoire Jean Perrin – Sorbonne Universite, Centre National de la Recherche Scientifique, Institut de Biologie Paris Seine – 4, place Jussieu, Tour 32-33, Case Courrier 114 75252 Paris Cedex 05, France
[2] Imperial College of Science, Technology and Medicine – United Kingdom
[3] Department of Applied Science and Technology [Politecnico di Torino] – Politecnico di Torino - Corso Duca degli Abruzzi, 24 - 10129 Torino, ITALY, Italy
[4] Italian Institute for Genomic Medicine – c/o IRCCS – SP142 km 3,95 – 10060 – Candiolo (TO), Italy

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.

*Speaker
†Corresponding author: matheo.aksil@sorbonne-universite.fr
‡Corresponding author: silvia.grigolon@gmail.com

Morpho flight study: wing kinematics and deformation

Camille Aracheloff *† [1], Vincent Debat [1], Florian Muijres [2]

[1] Institut de Systématique, Evolution, Biodiversité – Museum National d'Histoire Naturelle, Ecole Pratique des Hautes Etudes, Sorbonne Universite, Centre National de la Recherche Scientifique, Université des Antilles – 57 rue Cuvier - CP 50 - 75005 Paris, France
[2] Experimental Zoology Group, Wageningen University Research Center – the Netherlands – Netherlands

Morphos are one of the iconic groups of butterflies of South America. This genus comprises 30 species, half of which have large blue iridescent wings. All species are found in two micro-habitats within tropical forests: either in the undergrowth or in the canopy.
While all *Morpho* species have a flap-gliding flight, the ratio between these two phases varies significantly. Species with a higher gliding ratio are classified as gliders, whereas those with a lower gliding ratio are referred to as flappers.

In all case, flight performance results from complex fluid-structure interactions, where wing characteristics (morphology, mechanical properties, etc.) and kinematics, including deformation, play a prominent role.

We want to study the contribution of wing deformation to aerodynamic force production in the case of Morpho butterflies. We aim to determine if there is a difference in this contribution between flapping and gliding species.
We focus our study on the take-off phase of living butterflies. First, we analyze the fine wing kinematics. To do this, we track wing points using DeepLabCut, a deep learning-based toolbox, and FLiTrak3D to fit 3D skeletons both with and without deformation. The two sets of kinematic data will be used in Computational Fluid Dynamics (CFD) to compute aerodynamic forces and determine the differences.

*Speaker
†Corresponding author: camille.aracheloff@mnhn.fr

Biophysics of the environment regulates tube formation during vasculogenesis

Lakshmi Balasubramaniam *† [1]

[1] University of Cambridge [Cambridge, UK] – The Old Schools, Trinity Lane, Cambridge CB2 1TN, United Kingdom

Blood vessels are fundamental to morphogenesis, providing the essential pathways for nutrient transport and gas exchange that support developing tissues. In this talk, I will describe how the first signs of blood vessels arise during embryogenesis when mesenchymal cells initially characterized by low cell–cell adhesions, self-organize into multicellular aggregates referred to as blood islands. These aggregates subsequently fuse with neighbouring clusters forming an interconnected tubular structure composed of endothelial cells, which line the vessel, and blood cells on the inside.

The extracellular environment, particularly the extracellular matrix and hyaluronic acid, plays a critical role in shaping this process. These components influence cell morphology, promote cell–cell adhesion maturation, and regulate mechanical tension within and between cells. In doing so, they help guide cell fate decisions toward endothelial cells on the periphery and blood cells on the interior. Together, these biochemical and mechanical interactions drive the fusion of blood islands, into a functional vascular tube.

The direction of fusion is not random: it emerges from coordinated cellular motion coupled to active remodelling of the surrounding extracellular matrix, which creates physical pathways that guide vessel formation. By integrating experimental observations with mathematical modelling, I will show how this fusion process and the resulting vascular connectivity can be understood as a higher-order network problem. In this framework, elements such as matrix composition, architecture, remodelling, cell-adhesion dynamics, and evolving cell shapes act as key variables that collectively determine the structural order of the emergent vascular network.

*Speaker

†Corresponding author: lb935@cam.ac.uk

1st Year PhD on Modelling and Quantifying Parallelism in Community Evolution

Tristan Barata * [1], Silvia De Monte [2]

[1] IBENS – Institut de Biologie de l'École normale supérieure (IBENS), Département de Biologie, Ecole Normale Supérieure, CNRS, Inserm, PSL Research University, F-75005 Paris, France. – barata@bio.ens.psl.eu, France

[2] Institut de biologie de l'ENS Paris – Département de Biologie - ENS-PSL, Institut National de la Santé et de la Recherche Médicale, Centre National de la Recherche Scientifique – France

Ongoing global changes motivate increasing efforts towards understanding how natural communities are shaped by natural selection and respond to their environment. Microbial communities, such as marine plankton or the gut microbiome, are complex assemblages of a large number of species and strains, so that their ecological and evolutionary dynamics are difficult to grasp and model. Recently, assembling communities in the lab paved the way to exploring how their functions emerge and can be controlled. Of particular interest are collective functions that do not hinge on the presence of any particular species, but, like primary production, are distributed properties of the community. An increasing number of experiments and of numerical models are addressing the dynamics of communities that adapt simultaneously at the species and collective levels. Theoretical understanding of what should be the outcome of such multi-level selection processes, however, is still scant. In this project, we aim at providing null expectations about the species-level variability that is generated during community-level adaptation. In other words, how different are communities that have been selected in parallel to maximize a given collective function? We will use models for complex communities (generalized Lotka-Volterra and MacArthur equations) and methods from statistical physics for understanding: 1) how variable are communities that perform similar functions; 2) what functions can be attained (or not) by artificially selecting a microbial community; 3) what is repeatable and what is variable in communities evolved in parallel. This theoretical exploration bears implications for characterizing the resilience of natural communities and for designing protocols to efficiently engineer communities in the lab.

*Speaker

Curvature and its effects on tissue morphology.

Paula Belska * [1], Parvathy Anoop [1], Heidi Pertl-Obermeyer [1], John Dunlop [1], Andreas Roschger [1]

[1] Paris-Lodron-Universität Salzburg = Paris-Lodron-University of Salzburg – Austria

It has become increasingly evident that a substrate's surface curvature can have a significant impact on cell patterning and tissue growth. To explore how surface curvature influences tissue growth, we create polydimethylsiloxane (PDMS) scaffolds with a doubly curved surface. These surfaces are characterised by a negative Gaussian curvature. Murine pre-osteoblast cells (MC3T3-E1) are seeded onto these scaffolds and tissue growth is observed over time. The resulting tissue develops in a manner consistent with the geometry anticipated from a liquid. To put in other words, surface curvature and tissue area are minimised according to the Young-Laplace equation resulting in rotationally symmetric constant mean curvature surfaces of revolution. Moreover, fixed samples, stained for actin, are observed using Light Sheet (LS) microscopy. At shorter growth periods (day 7) the actin stress fibres are observed to align to the right direction, whereas later, at day 32 a left-handed alignment is observed. Interestingly, this alignment reverses again to a right-handed alignment at longer growth times (day 63), giving rise to a twisted multilayered tissue. Live cell imaging provides new insights into the formation of macroscopic multiscale tissues *in vivo* by revealing how cells orient themselves along different curvature directions.

*Speaker

Joint evolution of hardware and artificial neural networks

Sébastien Billès * [1], Nicolas Bredeche [2], Raphaël Candelier [3]

[1] Laboratoire Jean Perrin – Sorbonne Universite, Centre National de la Recherche Scientifique, Institut de Biologie Paris Seine – 4, place Jussieu, Tour 32-33, Case Courrier 114 75252 Paris Cedex 05, France
[2] Institut des Systèmes Intelligents et de Robotique – Sorbonne Universite, Centre National de la Recherche Scientifique – Sorbonne-Université, Boite courrier 173 4 Place JUSSIEU 75252 Paris cedex 05, France
[3] Laboratoire Jean Perrin – Sorbonne Universités, UPMC, CNRS – France

In the evolution of complex organisms, there is a dichotomy between the *body* and the *information* it processes: while the anatomy is governed by the rules of physics and chemistry, the information flows use abstract representation schemes, as exemplified by neuronal networks. The emergence of a new organ thus requires innovations in both realms, the embodiment and the control, each imposing constraints on the evolution of the other.

The aim of this project is to explore through simulations how a complex system is shaped by the simultaneous, joint evolution of its hardware and software in these very different spaces. We use the example of a multi-arm active pendulum, sometimes termed "acrobot", that requires the coordination of its different body parts to balance itself and reach an equilibrium position. We let the number of sensors and actuators evolve freely, as well as the architecture and connection weights of the controlling neural network, and characterized the homogeneity of the final solutions across multiple runs of evolution. We then compared the solutions to the control cases where only the hardware or the software can evolve, and found that the evolved structures are qualitatively different.

*Speaker

Structural Investigation of Human Low Density Lipoprotein

Madalena Branco * [1,2]

[1] Université Grenoble Alpes - UFR Physique, Ingénierie, Terre, Environnement, Mécanique – Université Grenoble Alpes – 230 rue de la physique - 38400 Saint-Martin-d'Hères, France
[2] Institut de biologie structurale – Centre National de la Recherche Scientifique, Institut de Recherche Interdisciplinaire de Grenoble, Université Grenoble Alpes – Institut de Biologie Structurale, 71 avenue des martyrs, CS 10090, 38044 Grenoble Cedex 9, France

Low-density lipoproteins (LDL) are vital for the transport of cholesterol in the blood. Malfunctions in this transport system are strongly associated with the development of atherosclerosis, a key factor in cardiovascular diseases. LDL particles, typically 17–28 nm in diameter, consist of a phospholipid membrane surface and a lipid core, wrapped around by a single large protein, apolipoprotein B-100 (500 kDa). Despite its critical biological role, due to its heterogeneous composition and flexibility, it has not yet been possible to resolve its structure at atomic resolution.
This study aims to bridge this gap in structural knowledge using an integrated approach that combines molecular dynamics simulations, cryo-electron microscopy (Cryo-EM), small-angle X-ray and neutron scattering (SAXS and SANS).

Cryo-EM experiments have successfully captured the overall shape and internal core organization of LDL. Efforts are ongoing to achieve higher-resolution 3D reconstruction maps. It is important to note that LDL undergoes a structural phase transition and due to the freezing process required for Cryo-EM imaging and the rapid nature of this transition, it has not been possible to capture the structures of LDL above the phase transition using this technique. In contrast, SAXS and SANS allow biomolecules to be studied in solution under near-native conditions, which facilitate the study of structural details of LDL across this transition.
Finally, these results can be compared with MD simulations, previously performed, that relies on AlphaFold protein structure predictive software and classical molecular dynamics at coarse-grain level.

*Speaker

Modélisation empirique de systèmes complexes

Nicolas Brodu * [1]

[1] Centre Inria de l'Université de Bordeaux – Institut National de Recherche en Informatique et en Automatique – 200, avenue de la Vieille Tour, 33405 Talence, France

Comment, à partir d'observations, reconstruire un modèle fiable de la dynamique d'un processus physique ? Existe-t'il des variables d'état, ou équivalents, qui portent l'information utile pour décrire l'évolution du système ? Lorsque différents processus interagissent, comment détecter leurs échelles caractéristiques ? Comment obtenir une modélisation significative à ces échelles ?

Ces travaux proposent des modèles statistiques qui mettent l'accent sur l'inférence de variable d'états, les propriétés Markoviennes qui en découlent comme pour la plupart des lois physiques, ainsi que sur l'usage de l'information en addition à l'énergie pour traiter des systèmes hors équilibre. Cette approche est différente des réseaux profonds. Ces derniers sont excellents concernant certains cas d'usage, mais souvent contre-productifs pour la modélisation des processus eux-mêmes.

Le poster explique la méthode et montre son usage sur des exemples concrets : reconstruction d'attracteurs, inférence de conformation en dynamique moléculaire, dynamique de taches solaires, dynamique El Niño, différenciation de cultures à partir de données de terrain.

*Speaker

Learning the equations that govern collective motility in bacteria colonies

Tanju Cakar * [1], Nigel Clarke [1], William Durham [1]

[1] University of Sheffield [Sheffield] – Western Bank Sheffield S10 2TN, United Kingdom

Bacterial suspensions, such as swarms of Pseudomonas aeruginosa, are capable of producing complex self-organising patterns reminiscent of classical turbulence through self-motility and steric interactions. Continuum models have proven fruitful in understanding the mechanisms underlying active turbulence. For instance, the phenomenological Toner-Tu-Swift-Hohenberg equation has been shown to effectively model active turbulence in bacterial monolayers in terms of flow velocity. A key challenge to furthering our understanding of active turbulence is mapping experimental data to continuum models. Recent advances in machine learning allow for the discovery of the structure and parameters of differential equations directly from data. In particular, sparse regression-based equation learning, such as SINDy (Sparse Identification of Nonlinear Dynamics) apply regularisation to select the optimal minimal model from a library of candidate terms. Phenomenological models for monolayers of wild-type and mutant (ΔpilH) Pseudomonas aeruginosa are selected using a machine learning pipeline tailored to experimental data of dense swarms of motile bacteria. The characteristic velocity and length scales of active turbulence for WT and ΔpilH strains can be inferred from the parameters of the learned model. The role of density fluctuations in collective motility are also considered within the context of equation learning outputs. If successful, regression-based equation learning could prove an useful tool for analysing more complex biological behaviours exhibited by collectives of bacteria, such as periodic reversals in the direction of bulk movement.

*Speaker

Anisotropic hierarchy decides the fate of an amorphous droplet

Pietro Caracciolo Di Torella * [1], Andrey Zelenskiy [1], Martin Lenz [1]

[1] Laboratoire de Physique Théorique et Modèles Statistiques – Centre National de la Recherche Scientifique – Bâtiment 100 Université Paris-Sud Centre Scientifique d'Orsay 15 rue Georges Clémenceau 91405 Orsay cedex, France

The classical description of ordering, from phase-transition theory to nucleation, usually depicts a direct change from disorder to order. Many real systems, however, do not follow such a simple route and instead go through disordered or partially ordered intermediates, the so-called amorphous precursors.
Here, we introduce a family of patchy-particle models in which interactions are organized through a simple hierarchy of geometric competitions. By tuning the anisotropy in this framework, the system can form a wide range of aggregates, including crystals, fibers, and gels. Yet, due to geometric frustration, these assemblies often arise through a dense amorphous stage where anisotropic interactions are effectively averaged out. This precursor appears both in the analytical solution of a one-dimensional version of the model and in numerical simulations on higher-dimensional lattices.
This framework offers a minimal view of non-classical assembly pathways and points to simple principles for designing complex structures.

*Speaker

The physical consequence of sperm gigantism

Brato Chakrabarti * [1]

[1] International Center for Theoretical Sciences – India

The male fruit fly produces $\sim$ 1.8 mm long sperm, thousands of which can be stored until mating in a $\sim$ 200 μm sac, the seminal vesicle. While the evolutionary pressures driving such extreme sperm (flagellar) lengths have long been investigated, the physical consequences of their gigantism are unstudied. Through high-resolution three-dimensional reconstructions of in vivo sperm morphologies and rapid live imaging, we discovered that stored sperm are organized into a dense and highly aligned state. The packed flagella exhibit system-wide collective 'material' flows, with persistent and slow-moving topological defects; individual sperm, despite their extraordinary lengths, propagate rapidly through the flagellar material, moving in either direction along material director lines. To understand how these collective behaviors arise from the constituents' nonequilibrium dynamics, we conceptualize the motion of individual sperm as topologically confined to a reptation-like tube formed by its neighbors. Therein, sperm propagate through observed amplitude-constrained and internally driven flagellar bending waves, pushing off counter-propagating neighbors. From this conception, we derive a continuum theory that produces an extensile material stress that can sustain an aligned flagellar material. Experimental perturbations and simulations of active elastic filaments verify our theoretical predictions. Our findings suggest that active stresses in the flagellar material maintain the sperm in an unentangled, hence functional state, in both sexes, and establish giant sperm in their native habitat as a novel and physiologically relevant active matter system.

*Speaker

Biophysical generative modeling of cell fate decision-making with single-cell omics

Victor Chardès *† [1,2]

[1] Harvard University, Department of Molecular Cellular Biology – Northwest Lab Building 469 52 Oxford Street Cambridge MA 02138, United States
[2] Flatiron Institute – 162 5th Avenue, New York, NY 10010, USA, United States

Single-cell omics methods provide high-throughput, molecular-scale measurements of cellular processes, offering insights into the machinery of cell fate decision-making. However, the high dimensionality, stochasticity, and cross-sectional nature of these measurements hinder their integration with biophysical models of gene regulation. My research aims to bridge this gap by combining generative AI with the biophysics of transcriptional regulation to infer actionable and interpretable models of cell fate decision-making from single-cell omics data. In this direction, I recently developed probability flow inference (PFI), a computational approach to infer models specified by arbitrary stochastic differential equations from time-resolved single-cell RNA-seq data. After presenting the mathematical underpinnings of the method, I will show that this versatile approach already enables the inference of models that naturally account for molecular noise in transcriptional regulation as well as for cellular proliferation. I will demonstrate that such biophysical models not only infer more accurate gene regulatory networks, but also generalize better to out-of-distribution data, outperforming state-of-the-art purely data-driven approaches. Finally, I will discuss how PFI offers an opportunity to test, at a genome-wide scale, biophysical hypotheses for transcriptional regulation, and in particular to probe its non-equilibrium nature.

*Speaker
†Corresponding author: vchardes@flatironinstitute.org

The spontaneous patterning of feather arrays: a mechanical perspective

Alessandro Chiappori * [1], Marie Manceau [2], Raphaël Clément [1], Pierre-François Lenne [1]

[1] Institut de Biologie du Développement de Marseille – Aix Marseille Université, Centre National de la Recherche Scientifique, CENTURI – Case 907 - Parc Scientifique de Luminy 13288 Marseille Cedex 9, France

[2] Centre interdisciplinaire de recherche en biologie – Collège de France, Institut National de la Santé et de la Recherche Médicale, Centre National de la Recherche Scientifique – 11 place Marcellin Berthelot 75005 Paris, France

Feathers are the specialized skin appendages that characterize the bird class. In some species, they are spatially distributed in a very regular manner, which reminds the periodic lattices of minerals. We have studied this process in embryos, where the skin transitions from homogeneous to clustered into regularly spaced cell aggregates, called feather primordia. This is a case of spontaneous symmetry breaking, made by cells that can migrate and interact. At this stage, the skin comprises two layers: an elastic sheet of cells tightly in contact with one another (epidermis) and a bulk of cells below, in a viscoelastic environment (dermis). We reasoned that, together with gene expression and cell differentiation, tensions in the tissue should play a crucial role in both the segregation into distinct cell clusters and their arrangement into a periodic lattice. We have thus estimated tensions in the tissues using several complementary approaches: (i) live imaging of actin and myosin, the proteins responsible for cell contractions; (ii) force inference in the epidermis; (iii) quantification of cell nematic order in the dermis; and (iv) laser tissue ablation. Additionally, we have built a model from first principles to reproduce the spontaneous aggregation from mechanical properties only. Using these methods, we could observe the setup of a tension field, with feather aggregates corresponding to areas of large-scale contraction and convergence. Despite these tension fields being correlated between both layers, the epidermis flows on the dermis during the process, except that it briefly anchors to the dermis during the aggregation of the feather primordia. Further investigation is required to get a more complete understanding of the process, but we suggest that the periodicity of the arrangement is attained through the progressive adjustment of tensions in between neighboring feather primordia.

*Speaker

Shaping fate: geometric methods for cell fate transitions and tissue patterning in stem cells and organoids

Dillon Cislo * [1]

[1] Rockefeller University [New York] – 1230 York Ave, New York, NY 10065, États-Unis, United States

Biology currently possesses unprecedented capabilities to generate genome-wide readouts of cells as they develop in embryos. It remains a challenge to parse this data into comprehensible models that can reveal the underlying principles of development and guide methods to engineer target cell and tissue fates. It has recently been demonstrated that Waddington's metaphor of development as downhill flow in an "epigenetic landscape" can be made mathematically rigorous using techniques from differential geometry and dynamical systems. I will discuss applications of these methods to lineage bifurcations in the early mouse embryo and *in vitro* recapitulations of floorplate induced dorsoventral patterning of the neural tube. In both cases, geometric reasoning simplifies complicated dynamic processes to enable testable predictions in terms of small sets of effective variables. I will show results, from both single-cell assays and whole-tissue live imaging, illustrating how cell signaling coordinates with biochemical and mechanical regulation at the scale of the embryo/organoid to dynamically organize developing tissues.

*Speaker

Information-optimal mixing at low Reynolds number

Luca Cocconi * [1,2]

[1] University of Cambridge [UK] – The Old Schools, Trinity Lane, Cambridge CB2 1TN, United Kingdom
[2] Max Planck Institute for Dynamics and Self-Organization – Am Faßberg 17, 37077 Göttingen, Germany

Mutual information between particle positions before and after mixing provides a universal assumption-free measure of mixing efficiency at low Reynolds number that accounts for the kinematic reversibility of the Stokes equation. For a generic planar shear flow with time-dependent shear rate, we derive a compact expression for the mutual information as a nonlinear functional of the shearing protocol and solve the associated extremization problem exactly to determine the optimal control under both linear and nonlinear constraints, specifically total shear and total dissipation per unit volume. Remarkably, optimal protocols turn out to be universal and time-reversal symmetric in both cases. Our results establish a minimum energetic cost of erasing information in a broad class of nonequilibrium drift-diffusive systems, with implications for life at low Reynolds numbers. Reference: LC et al. PRL 135 (3), 037101 (2025)

*Speaker

A Novel Perspective on Attention-Deficit/Hyperactivity Disorder: Analysing Behavioural and Neuronal Dynamics in Zebrafish Models

Leonard Constien * [1], Gautam Sridhar [2], Joao Marques , Drew Robson , Jennifer Li , Antonio Carlos Costa† , Claire Wyart‡ [3]

[1] Fondation ICM – Institut du Cerveau et de la Moelle épinière (ICM) – France
[2] Institut du cerveau – Institut du Cerveau et de la Moelle épinière (ICM) – France
[3] Institut du Cerveau (ICM) – Institut du Cerveau et de la Moelle épinière (ICM), Université Paris-Sorbonne - Paris IV – 47 Bd de l'Hôpital, 75013, France

With an estimated prevalence of 5.4% in children and 2.6% in adults, Attention-deficit/Hyperactivity disorder (ADHD) presents a significant global mental health concern. Despite that, the pathophysiology of ADHD is still largely unkown, although the improvement of core the symptoms inattention, hyperactivity and impulsivity by Dopamine and Norepinephrine reuptake inhibitors (DARIs and NERIs), as well as identified risk genes, strongly suggests a disruption in the monoaminergic system. However, the symptomatic heterogeneity and multitude of identified risk genes have complicated efforts to find a coherent mechanism behind the disorder. Animal models greatly increase experimental possibilities, and over the years multiple mice, rat and zebrafish models of ADHD have been suggested. Levaraging the genetic, optical and behavioural tractability of the larval zebrafish, this project aims to improve our understanding of ADHD on the behavioural and neuronal side. Going beyond traditional quantifications of ADHD-like behaviour we investigates ADHD from the perspective of behavioural dynamics across timescales. Using a Markov chain approach, we compare the stability of metastable states and transition statistics, in hour-timescale recordings of spontaneous hunting behaviour and sleep, between WT zebrafish, the previously studied ADHD zebrafihs model adgrl-/-, and the putative model cdh13-/-, at 6 days post fertilization. Later on, the analyis will be complemented by wide-field epifluorescence microscopy in freely moving fish to quantify whole-brain activity differences between the WT and mutant fish during behaviour and upon application of DARIs and NERIs. At this stage, I will present verifications of the knock-outs, their effect on GABA, dopamine and glutamate availability, and a first, comparative analysis of their behaviour.

*Speaker
†Corresponding author: antonio.costa@icm-institute.org
‡Corresponding author: claire.wyart@icm-institute.org

Normalizing Flows for Atomistic Simulations of Condensed Matter Systems

Alessandro Coretti * [1], Sebastian Falkner [2], Salvatore Romano [2], Nico Unglert [3], Livia Pàrtay [4], Georg Madsen [3], Phillip Geissler [5], Christoph Dellago [2]

[1] Universität Wien = University of Vienna – Universitätsring 1, 1010 Wien, Austria
[2] Universität Wien = University of Vienna – Universitätsring 1, 1010 Wien, Austria
[3] Vienna University of Technology = Technischen Universität Wien – Karlsplatz 13, 1040 Vienna, Austria
[4] University of Warwick [Coventry] – Coventry CV4 7AL, United Kingdom
[5] University of California [Berkeley] – Berkeley, CA, United States

Within the framework of deep learning, generative models are receiving increasing attention due to their ability to generate independent samples starting from a set of training examples. Their application to statistical mechanics is particularly promising, given the difficulty of generating decorrelated samples from physical distributions. This idea has recently given rise to a new line of research in which generative models, and in particular normalizing flows, are directly integrated into atomistic simulation workflows, yielding very encouraging results for biophysical and many-body systems. In this talk, I will present three novel approaches in which normalizing flows can be fruitfully applied to statistical mechanics: transition path sampling, equilibrium simulations of liquid systems, and nested sampling for materials. In the first case (1), we show how to condition a normalizing flow to generate shooting points at the top of an energy barrier. This not only improves the acceptance ratio of the transition path sampling algorithm, but also removes correlations between consecutively sampled paths, which are particularly problematic when multiple transition channels are present. In the second case (2), we explore different choices of source distributions that are closer, from a physical perspective, to the target distribution. This can lead, on the one hand, to efficient exploration of the space of thermodynamic variables for a given model and, on the other hand, to the possibility of transforming between configurations obtained using different representations of the same physical system. In the third case (3), we propose the use of a conditional normalizing flow to replace rejection Monte Carlo sampling in the nested sampling algorithm for condensed matter systems, where it often constitutes the main computational bottleneck.

(1) S. Falkner et al. MLST **4** (3), 035050 (2023).

(2) A. Coretti et al. J. Chem. Phys. **162**, 184102 (2025).
(3) A. Coretti et al. (in prep.) (2026).

*Speaker

From tower building to eco-evo dynamics: how tiny worms overcome physical constraints to disperse

Siyu Serena Ding * , Daniela Perez [1], Ryan Greenway [1]

[1] Max Plank Institute of Animal Behavior – Am Obstberg 1 D-78315 Radolfzell, Germany

Nematodes are tiny roundworms (_˜1 mm) that are ubiquitous and abundant. How such small animals colonize nearly every habitat on the planet is largely thanks to hitchhiking on larger vectors such as insects and isopods. Remarkably, nematodes can disperse on vectors not only as isolated individuals, but also collectively by building a tower together. How a group of limbless and soft-bodied animals build a living tower is still a mystery. Furthermore, nematode towers must sense and attach to passing vectors in order to move large distances; how physics constrains not only the form and also the function of such a collective structure has direct consequences on the ultimate dispersal success and the ensuing eco-evolutionary dynamics. In this talk, I will showcase behavioral observations and data we have recently collected on this experimental system and pose these questions for discussion.

*Speaker

ERK signaling waves encode a local-to-global transition in epithelial cell death patterns

Maciej Dobrzynski *† [1], Paolo Gagliardi‡

[1] Institute of Cell Biology, University of Bern – Baltzerstrasse 4, 3012 Bern, Switzerland

When a cell dies in an epithelium, its neighbours are temporarily protected from death. This protection propagates as a wave of ERK kinase activity, creating a survival zone spanning a few cell layers and lasting ¯2–4 hours around each dying cell. The way in which these microscale signalling events shape macroscale spatial organisation is still poorly understood.
We find that the answer lies in wave dynamics. Using live-cell imaging across three epithelial cell lines, we observe significantly different spatial distributions of apoptotic events, ranging from local depletion zones where deaths avoid each other, to spatially random patterns, to local clustering. These differences represent a local-to-global transition. As wave size and duration increases, spatial information about death locations is progressively averaged out, and the tissue shifts from local coordination to a spatially uniform response. When pro-survival waves are small, dying cells create depletion zones, protecting neighbouring cells and resulting in subsequent deaths occurring further away. When waves span the tissue, protection becomes spatially uniform as the memory of apoptosis timing and location is erased. Subsequently, death patterns become random or even clustered due to competing apoptosis-induced apoptosis signals.

Furthermore, using pharmacological perturbations, statistical modelling and agent-based simulations, we demonstrate that the spatio-temporal statistics of cell death reflect the strength of underlying cell-cell coupling. This creates an inverse problem, where macroscale pattern analysis can infer the signaling properties at a microscale, offering a non-invasive readout of the state of tissue communication.
This work reveals that, beyond epithelial homeostasis, frequency-encoded fate decisions and propagating activity waves (motifs common across excitable biological media) can generate emergent spatial organisation in living tissues. Understanding how tissues coordinate cell death at this collective level has implications for wound healing, tissue development, and diseases where cell death regulation fails, such as cancer and degenerative disorders.

*Speaker
†Corresponding author: maciej.dobrzynski@unibe.ch
‡Corresponding author: paolo.gagliardi@unito.it

Equal Partitioning of the Min Proteins at Cell Division

Natan Dominko Kobilica * [1], Nora Deiringer [2], Vitalii Grigorev [3], Antonia Winter [1], Robin Köhler [4], Sean Murray [5], Viktor Sourjik [3], Henrik Weyer [6], Erwin Frey [1]

[1] Arnold Sommerfeld Center for Theoretical Physics [München] – Ludwig-Maximilians Universität MünchenTheresienstr. 37, D-80333 München, Germany
[2] Technical University of Munich, Garching – Germany
[3] Max-Planck-Institute for Terrestrial Microbiology, Marburg – Germany
[4] Geomagic, Leipzig – Germany
[5] IMESO-IT, Giessen – Germany
[6] Kavli Institute for Theoretical Physics, University of California Santa Barbara, Santa Barbara – United States

The pole-to-pole oscillation of the Min proteins in Escherichia coli plays a crucial role in the process of cell division. The oscillation facilitates the formation of the FtsZ ring, which determines the division site. It is essential that the Min proteins are distributed equally between daughter cells to ensure precise determination of the division site in subsequent divisions. Previously, experiments and stochastic particle-based simulations have linked protein equipartition to the splitting of the pole-to-pole oscillation. Importantly, the splitting is already triggered before the division is fully completed. The goal of this study is to explain the mechanism underlying the splitting of oscillations using the well-known reaction-diffusion equations for the Min System. We model the constriction during cell division as a reduced diffusion rate between the two parts of the mother cell. This already captures the oscillation splitting and agrees well with realistic simulations of the constricting cell. Additionally, we conduct high-throughput microfluidic experiments which align well with the predicted protein dynamics.

*Speaker

Whole-body flow sensing and center-of-mass referenced computations for motor control

Lunsford Elias * [1]

[1] Institut du Cerveau (ICM) – Institut du Cerveau et de la Moelle épinière (ICM), Université Paris-Sorbonne - Paris IV – 47 Bd de l'Hôpital, 75013, France

From shifting visual scenes to tactile deformations and fluid motion, animals must interpret patterns of sensory flow around their body to construct stable internal models and produce adaptive behavior. Understanding of how such transformations are encoded within the brain remains incomplete. To tackle this question, we leverage the lateral line of larval zebrafish as a tractable sensory system sensitive to fluid motion that is used to steer navigation, feed, and avoid predators. By presenting directional stimuli to sensors along the body, we used high-resolution calcium imaging to map responses in the brain. Unexpectedly, our findings challenge the notion that central processing within the sensorimotor integration nuclei lacks topographic structure by revealing a simple yet powerful principle centered on a egocentric spatial framework: the direction and location of local flow motions are encoded in reference to the animal's center-of-mass. This simple representation enables the brain to register complex flow patterns and provides a robust basis for subsequent behavioral action selection. Neurons that encode flow toward the center-of-mass broadly project to form bilateral connections onto motor command neurons that coordinate forward locomotion while neurons that encode flow away from the center-of-mass displayed a more selective and unilateral projection profile to command neurons for turns. Our discovery represents a shift from purely somatotopic encoding toward an integrative representation of axial position and directionality combined, revealing a novel principle of encoding spatio-directional cues in the brain. This study advances our understanding of how complex mechanosensory inputs select appropriate motor outputs via simple egocentric neural maps in the hindbrain.

*Speaker

Emergence of inter-individual behavioral variability in unpredictable environment

Rémi Gautier * [1]

[1] Institut du Cerveau = Paris Brain Institute – Assistance publique - Hôpitaux de Paris (AP-HP), Institut National de la Santé et de la Recherche Médicale, CHU Pitié-Salpêtrière [AP-HP], Sorbonne Universite, Centre National de la Recherche Scientifique – 47-83 Boulevard de l'Hôpital 75651 Paris Cedex 13, France

/

*Speaker

From order to topology

Birte Geerds * [1], Daniel Pearce [1]

[1] Université de Genève = University of Geneva – 24 rue du Général-Dufour CH - 1211 Genève 4Suisse, Switzerland

The actin cortex of cell membranes consists of filaments that can exhibit long range order (director), which can be described as a liquid crystal. Additionally, consumption of energy by biomotors drive the system out of equilibrium leading to flow, stress, etc fields. The topology of the system imposes constraints that can lead to additional bend, splay and even topological defects. As cell membranes are hardly flat surfaces, studying the interplay between the curvature and topology of the surface and the (active) liquid crystal is important to understand fundamental processes in cell morphology. We use analytical as well as computational techniques to study this interplay on 2D manifolds embedded in 3D and work closely with experimentalists.

*Speaker

Information and chirality: emergent response from nonequilibrium bath

Rémi Goerlich * [1], Gilad Pollak , Eli Flaxer , Saar Rahav , Yael Roichman

[1] Laboratoire de Physique de l'ENS Lyon – Ecole Normale Supérieure de Lyon, Université de Lyon, Centre National de la Recherche Scientifique – 46 allée d'Italie 69007 Lyon, France

The ability to measure the stochastic degrees of freedom of a thermal system enables the extraction of energy from an equilibrium heat bath. This is the underlying principle of Maxwell's demon and subsequent information engines. This apparent thermodynamics paradox is resolved when accounting for the energetic cost of the associated information processing and these novel engines are consistently described by the framework of information thermodynamics. Information engines offer new possibilities to control fluctuations as well as energy and information flows through sub-parts of a system. For example, it is likely that biological processes at the microscopic scale, such as kinesin cargo-transport use information engine-like mechanism. In this work, we experimentally realize a microscopic information engine configured as a compressible piston containing a thermalized colloidal suspension. The particle positions are recorded to identify when a predefined region near the wall is empty, allowing the piston to compress the colloidal suspension without applying work on the system. We find that the stored compression energy is universally set by the probability of a positive measurement outcome, which in turn is controlled by parameters such as density and compression step size. We further demonstrate that mechanical work can be extracted during the decompression of the piston, thereby closing the engine's operating cycle.

*Speaker

Abundance Fluctuations in Metapopulations with Coloured Random Multiplicative Growth

James Henderson *† [1], Andreas Tiffeau-Mayer [2]

[1] University College London – University College London Gower Street London WC1E 6BT UK, United Kingdom
[2] University College, London – United Kingdom

In the adaptive immune system T cell clones exist as a metapopulation distributed across the body, enabling localized responses tailored to specific tissue contexts. Upon encounters with their cognate antigen, populations of specific T cells undergo rapid proliferation events known as clonal expansions. The timing and magnitude of these expansions are inherently random, with previous works successfully using stochastic differential equations with random multiplicative growth to model their dynamics. Recent studies suggest that many clones exhibit highly heterogeneous abundance distributions across anatomical sites. Here we ask how much of this spatial inequality can be explained as a consequence of non-equilibrated localized stochastic expansions. We study a minimal model in which a species migrates between two spatial sites while experiencing random multiplicative growth. We focus on a coordinate quantifying spatial inequality within the system which we take to be the log ratio of abundances between patches. We compare the steady-state behaviour of this coordinate under temporally uncorrelated (white) environmental fluctuations versus fluctuations with a finite correlation timescale (coloured noise). We show that coloured noise can induce bistability in the inequality coordinate, even when the deterministic and white-noise dynamics remain monostable, leading to switching between distinct typical levels of inequality. We characterise the transition to bistability via a phase diagram and discuss how this transition is influenced by non-reciprocal migration. Finally, using the resulting stationary distribution, we show that for a fixed environmental correlation time there exists an optimal migration rate that maximises the long-term growth rate of the metapopulation.

*Speaker
†Corresponding author: hendersonjfd@gmail.com

Mutual MultiLinearity of Network Currents

Pedro Harunari * [1]

[1] Aix Marseille Université – Aix Marseille Univ, CNRS, CINaM, Marseille, CENTURI – Aix Marseille Université, CNRS, CINAM, Turing Center for Living Systems, 13288 Marseille, France, France

Continuous-time Markov chains have been successful in modelling systems across numerous fields, with currents being fundamental entities that describe the flows of energy, particles, individuals, chemical species, information, or other quantities. They apply to systems described by agents transitioning between vertices along the edges of a network (at some rate in each direction). It has recently been shown that, at stationarity, a hidden linearity exists between currents that flow along edges: If one controls the current of a specific "input" edge (by tuning transition rates along it), any other current is a linear-affine function of the input current (Phys. Rev. Lett. 133, 047401 (2024)). This result was extended to the situation where one controls the currents of several edges, hence proving that any currents are in linear-affine relation with the input ones. It offers a generalization to Kirchhoff's current law, a tool for detecting violations of detailed balance, and uncovers insightful linear relations between visible and hidden currents in biophysical systems.

*Speaker

Characterizing the behavioral complexity of locomotion dynamics across scales

Alasdair Hastewell * [1]

[1] National Institute for Theory and Mathematics in Biology – 875 N Michigan Ave. Suite 3500 Chicago, IL, 60611, United States

From single-celled organisms to complex multi-limbed animals, the ability of living systems to precisely and robustly control their movement in ever-changing environments is essential for survival. Recent advances in experimental live imaging combined with machine learning-based algorithms enable us to track motion at unprecedented spatiotemporal resolutions. Here, we develop a computational framework that combines geometry-aware spectral mode representations with wavelet analysis and dynamical systems inference to translate these high-dimensional tracking data into interpretable low-dimensional representations and characterize the behavioral complexity of locomotion. I will demonstrate the flexibility of the framework, first, by applying it to cilia dynamics of a single-celled organism that exhibits a surprisingly rich locomotor repertoire. We reconstruct a low-dimensional embedded manifold in the behavioral space and derive a dispersion relation for the cilia oscillations, showing that despite the range and complexity of ciliary beating modes, the underlying behavior is intrinsically low-dimensional and physically constrained. Then, I will show how we can extend the framework to multi-limbed animals to study the jump takeoff kinematics of 14 genera of Amazonian jumping spiders with varied morphologies. Our results hint at conserved jumping strategies and decision-making across a wide range of evolutionary distance and morphology.

*Speaker

Density mean back relaxation: Detecting activity from passive observations in many-particle systems

Laila Henkes * [1], Matthias Krüger [1]

[1] University of Göttingen – Germany

Mean Back Relaxation (MBR) is a dimensionless quantity that correlates a scalar observable at three time points, relating the change of observable in a past time step to future displacement. It has been shown that deviation of the MBR long-term limit from 1/2 is a marker for broken detailed balance. This allows to detect activity from pure observation of trajectories. We specifically discuss a variant of MBR that uses the microscopic density as an input (dMBR), and which is especially useful for many-particle systems. We provide analytical expressions of dMBR for Gaussian example systems of both microscopic and macroscopic densities and find good agreement with results from simulations. Evaluating dMBR from experimental data, we demonstrate that dMBR can detect activity in biological cells from the observation of vesicle trajectories. We show how dMBR leads to a lower bound for entropy production of the system, which, for cell data, detects non-zero entropy production.

*Speaker

Controlling microalgae populations by phototactic memory

Gianni Jacucci * [1]

[1] Physics Department, University of Calabria, Rende 87036, CS, Italy – Italy

Understanding how microorganisms navigate in complex environments is a central question in active matter and biological physics. Phototaxis-the ability of motile cells to move in response to light-is a widespread strategy that enables microorganisms to optimise photosynthesis while avoiding light-induced stress. The green microalga *Chlamydomonas reinhardtii* is a key model for studying this behaviour, where navigation is classically attributed to a photosensitive organelle, the eyespot, that allows directional light sensing. Yet, how these cells respond to spatially varying light fields remains poorly understood.

Here, we design structured light landscapes to guide *Chlamydomonas* populations and localise them within well-defined spatial regions. By analysing single-cell trajectories, we show that cells actively steer relative to local light gradients. A comparison with a minimal theoretical model demonstrates that a short-term memory of light exposure is essential to reproduce the experimentally observed accumulation.

Our results reveal previously unexplored aspects of phototactic behaviour, identifying gradient-aligned steering and temporal integration as key mechanisms underpinning navigation in structured light environments. Beyond advancing the understanding of microbial motility, this approach provides a versatile framework for controlling active populations using light.

*Speaker

Microbial communities in context: A stepwise approach to complexity

Hannah Jeckel * [1], Reinaldo Alcade [1], Xiaoyu Shan [1], Inês Trindade [1], Dianne Newman [1]

[1] California Institute of Technology – 1200 East California Blvd, Pasadena, California 91125, United States

Microbial communities are ubiquitous on earth and play critical roles in many ecosystems, influencing the health of humans, animals and plants. They commonly consist of a variety of species, sometimes extending across kingdoms, with complex and context-dependent interactions. Predicting, understanding, or even observing these interactions and how they shape the development of a community can be a major challenge that requires simplified experimental setups and models which nevertheless capture the essential aspects of the system. But how do we know what is essential? Using rhizosphere communities as an example, I will discuss the tradeoff between simplicity and transferability of results inherent to any experimental platform mimicking a natural system and describe how a progression of experimental setups with increasing complexity can serve as a valuable tool to not only find balance but also identify key aspects of the environmental context that impact microbial interactions.

*Speaker

Applying Fluctuation Dissipation Relations to Active Systems

Martin Johnsrud * [1], Ramin Golestanian [1]

[1] Max Planck Institute of Dynamics and Self-organization – Germany

Active systems are not invariant under time-reversal, and therefore do not obey the Fluctuation Dissipation Theorem. Recent work, applying Martin-Siggia-Rose path integral methods, has shown that correlation functions and linear response functions of active systems obey a family of more general Fluctuation Dissipation Relations. This is, in the most general case, a formal relationship. However, in specific models we find directly applicable identities-exact or using systematic approximations schemes such as perturbative field theory. We therefore consider a range of models-for example the Noisy Complex Ginzburg-Landau equation, models of odd mobility, the Non-Reciprocal Cahn-Hilliard-and illustrate how to apply Fluctuation Dissipation Relations in models far from equilibrium.

*Speaker

Learning and cognition in single cells

David Jordan * [1,2]

[1] University of Cambridge [Cambridge, UK] – The Old Schools, Trinity Lane, Cambridge CB2 1TN, United Kingdom
[2] The living physics lab – Department of Biochemistry, University of Cambridge Sanger Building, Tennis Court Rd Cambridge, UK CB2 1GA, United Kingdom

Our current work explores how yeast cells adapt to "unforeseen" environmental challenges. Following the work of Erez Braun and colleagues, we have begun by recreating a yeast with a rewired genome where the essential HIS3 gene is controlled by the galactose regulatory system. When placed in glucose, which naturally suppresses the GAL promoter, a significant portion of the population achieves heritable adaptation through individual phenotypic switching rather than rare mutations and selection. This survival process involves global transcriptional reprogramming, where hundreds of genes across various metabolic pathways adjust their expression levels to meet new physiological demands. Evidence suggests this stochastic tuning is a universal feature of regulatory networks, allowing cells to navigate stressful and novel environments through epigenetic flexibility. While inherited mutations can eventually emerge to stabilize these states, the initial recovery relies on non-genetic mechanisms and individual cellular responses. This phenomena is an example of learning in single cells, and we would like to understand how to expand both traditional views of cognition and of evolution by demonstrating the inherent adaptive potential of complex gene regulatory and metabolic circuits.

*Speaker

Geometric Perspectives on Structure in Complex Systems

Alexandra Jurgens * [1]

[1] Inria-Bordeaux – L'Institut National de Recherche en Informatique et e n Automatique (INRIA) – 200 Av. de la Vieille Tour, 33405 Talence, France, France

The most basic task of science is the discovery of structure in the natural world. However, decades of work in nonlinear dynamics have shown that natural systems are typically both high dimensional and nonlinear, presenting a challenge to structure discovery. In modern scientific discourse, extant approaches to discovery of structure outside the constructionist paradigm-that is to say, data-driven model discovery-do not, in general, comprise a physics-informed theory about the nature and emergence of structure and complexity in the natural world. There has been a recent spate of work on both the theoretical and practical side of this question, including the development of multiple computational mechanics-influenced and information theory-based algorithms that aim to uncover the intrinsic geometric and/or topology of complex systems. This talk will review recent approaches and discuss the potential for a universal perspective on geometric and/or topological properties of complex systems.

*Speaker

Flow manipulation in mechanical ecology

Hunter King * [1]

[1] Rutgers University [Camden] – 303 Cooper Street, Camden, NJ 08102-1519, United States

Any organism's fitness depends on its ability to manage mechanical couplings and heat/mass exchanges with its surroundings. While humans may be masters of manipulating diverse environments, other species have evolved novel strategies that, if properly understood, can inspire zero-energy technologies. We present 3 short stories in which the evolutionary strategy, via niche construction and subtle biomechanics, involves manipulation of fluid flow: 1) a beetle manipulates flow physics with the shape of its body to separate fog droplets from the wind; 2) termites design hollow clay structures which harness thermal fluctuations to drive colonial respiration while conserving moisture; and 3) interplay between surface chemistry and softness mediate solid-solid contact formation under water, to counter-intuitive effect.

*Speaker

The spontaneous emergence of spatial structure in microbial communities

Jan Kocka * [1], Steven Redford [1,2], Wenying Shou [2], Jaime Agudo-Canalejo [1], Kabir Husain [1,3]

[1] Department of Physics and Astronomy, University College London – Gower Street, London WC1E 6BT, United Kingdom, United Kingdom
[2] Department of Genetics, Evolution and Environment, University College London – Darwin Building, 423 Gower St, London, WC1E 6BT, United Kingdom, United Kingdom
[3] Laboratory for Molecular Cell Biology, University College London – Gower St, London, WC1E 6BT, United Kingdom, United Kingdom

The stability, diversity, and function of a microbial community is shaped by the metabolic interactions between its constituent species. However, these interactions are often mediated by diffusible metabolites, whose efficacy depends on the spatial structure of the community. What determines this spatial structure remains broadly unknown. Here, we show that generic microbial communities spontaneously form spatial structure in resource-poor environments. The underlying Turing instability is driven by a feedback between metabolite diffusion and microbial growth arising from cross-feeding. From numerical solutions of the underlying partial differential equations, we find that the spatially-structured pattern often reflects the underlying metabolic logic of the community, and we determine regimes in which community diversity and biomass differ from the well-mixed state. Overall, our results argue for the inevitability of spatial structure, and delineate how spatial structure emerges from metabolic function in microbial consortia.

*Speaker

Cytoskeletal oscillations drive large-scale flows and nuclear organization in early embryonic systems.

Lara Koehler * [1]

[1] Physics of Life - TU Dresden – Germany

Synchronization drives early embryonic development, enabling simultaneous cell divisions and the spatial organization of nuclei within the embryo. In organisms such as Xenopus, Drosophila, and zebrafish, mitotic waves coordinate cell cycles across distances that exceed diffusion limits, guided by a chemical oscillator. At the same time, global cytoplasmic flows in these syncytial tissues contribute to the large-scale self-organization of nuclei, yet the coupling between biochemical signaling and cytoskeletal mechanics that underlies these directed flows remains poorly understood. Here, we relax the geometric constraints of the embryo and investigate nuclear dynamics in Xenopus egg extracts and complementary simulations. We show that the periodic polymerization and depolymerization of microtubule asters are sufficient to generate robust large-scale directed flows, even though the asters are intrinsically isotropic. Furthermore, we demonstrate that cell division stabilizes short-range order in a global synchronized system. Together, these findings reveal a minimal physical mechanism by which cytoskeletal dynamics and biochemical oscillations jointly organize flows and patterns, with implications for understanding the emergent principles that shape early development across species.

*Speaker

Physics of morphogenesis via synthetic mechano-chemical couplings

Nicolas Lobato-Dauzier *† [1], Romain Leroux [1], Anne-Lou Pinot [1], Ananyo Maitra [1,2], André Estevez-Torres [3,1], Raphaël Voituriez [1], Jean-Christophe Galas [1]

[1] Laboratoire Jean Perrin – Sorbonne Universite, Centre National de la Recherche Scientifique, Institut de Biologie Paris Seine – France
[2] Laboratoire de Physique Théorique et Modélisation – Centre National de la Recherche Scientifique, CY Cergy Paris Université – France
[3] Laboratoire Avancé de Spectroscopie pour les Intéractions la Réactivité et l'Environnement - UMR 8516 – Institut de Chimie - CNRS Chimie, Université de Lille, Centre National de la Recherche Scientifique – LASIRe, anciennement LASIR– Université de Lille - Bâtiment C5 (secrétariat), C8 et C4 - 59655 Villeneuve d'Ascq Cedex, France

Morphogenesis - the emergence of shape and organization in living systems - arises from a subtle interplay between chemical signaling and mechanical forces. Understanding how these processes couple across scales remains a central challenge in physics and biology.
My poster will present an in-vitro approach to study morphogenesis from the bottom up, using programmable synthetic systems where chemistry and mechanics can be independently designed and coupled. I will first introduce two powerful yet largely separate out-of-equilibrium systems: DNA-based reaction–diffusion systems, which enable programmable chemical patterning, and microtubule–kinesin active matter, which exhibit rich mechanical self-organization. Bringing these two worlds together opens the possibility to recreate, in the lab, the fundamental feedbacks that drive morphogenesis.

In this context, the poster focuses on our recent results on chemical transport (1) , where we coupled a DNA reaction–diffusion front to an active gel under confinement. This study demonstrates how mechanical activity reshapes chemical propagation, giving rise to reaction–diffusion–advection (RDA) dynamics - the first experimental realization of a synthetic mechano-chemical front.

Finally, I will introduce the next ongoing directions: the reciprocal coupling, where chemical reactions control mechanical activity, and the role of geometry in shaping mechanical organization, illustrated by active matter confined within droplets. Together, these studies outline a path toward synthetic cells and tissues capable of autonomous self-organization.
(1) N. Lobato-Dauzier, et al. "Confinement Determines Transport of a Reaction-Diffusion Active Matter Front", Physical Review X (2025)

*Speaker
†Corresponding author: nicolas.lobato-dauzier@sorbonne-universite.fr

Shape and consequent motion of topological defects in active nematics

Giacomo Marco La Montagna * [1], Cesare Nardini† [2,3], Ananyo Maitra [4,5], Sumeja Burekovic [2]

[1] CY Cergy Paris Université – Laboratoire de Physique Théorique et Modélisation – 33 boulevard du port, 95015 Cergy-Pontoise Cedex, France
[2] Service de physique de l'état condensé – Institut Rayonnement Matière de Saclay (DRF), Université Paris-Saclay, Centre National de la Recherche Scientifique – SPEC - UMR3680 CEA-CNRS(ex-URA 2464), CEA/Saclay, Orme des Merisiers, F-91191 GIF SUR YVETTE CEDEX, France
[3] Laboratoire de Physique Théorique de la Matière Condensée – Sorbonne Universite, Centre National de la Recherche Scientifique – LPTMC, Tour 24, Boîte 121, 4, Place Jussieu, 75252 Paris Cedex 05, France, France
[4] Laboratoire Jean Perrin – Sorbonne Universite, Centre National de la Recherche Scientifique, Institut de Biologie Paris Seine – France
[5] Laboratoire de Physique Théorique et Modélisation – Centre National de la Recherche Scientifique, CY Cergy Paris Université – France

Active systems continuously consume energy and self-organize into complex, dynamic states far from equilibrium; these properties make them a natural choice as models of living systems. Many of them display liquid crystalline order and, within these systems, topological defects act as key organising centers that control collective motion and pattern formation.
In my work, with Cesare Nardini and Ananyo Maitra, I revisit a common assumption in the theoretical description of these systems: that activity does not alter the form of the order parameter field in the presence of an isolated defect. I show that this simplification leads to inconsistent predictions. To address this, I develop an analytical framework that consistently accounts for active modification of defect shape in two-dimensional nematic systems. I present an analytical expression for the correction to the shape of a –1/2 defect both away from the core and near it, and demonstrate that, for +1/2 defects, the core field shape deformation is intimately connected to their self-propulsion speed. I confirm these analytical predictions through numerical simulations of a generic dry active nematic theory with a straightforward passive limit.
By revealing how activity modifies the geometry of topological defects, my work establishes a framework for understanding how local structure and dynamics are intertwined in active systems. This approach opens the way to extend the analysis to other kinds of liquid-crystalline order and to investigate how activity influences defect–defect interactions and collective behaviours. Beyond its immediate implications, this perspective provides a foundation for connecting the physics of topological defects to the organisation and transport processes observed in living systems, and for guiding the design of controllable, life-inspired active materials.

*Speaker
†Corresponding author: cesare.nardini@gmail.com

Super-resolved anomalous diffusion: deciphering the joint distribution of anomalous exponent and diffusion coefficient

Yann Lanoiselée *† [1]

[1] Basque Center for Applied Mathematics – Bizkaia Technology Park, Building 500 E-48160 Derio, Spain

The molecular motion in heterogeneous media displays anomalous diffusion by the mean-squared
displacement scaling as a power α of time. Motivated by experiments reporting populations of the anomalous
diffusion parameters α and D, we aim to disentangle their respective contributions to the observed
variability when this last is due to a true population of these parameters and when it arises due to finite-duration recordings. We introduce estimators of the anomalous diffusion parameters on the basis of the time-averaged mean-squared displacement and study their statistical properties. By using a copula approach, we derive a formula for the joint density function of their estimations
conditioned on their actual values. We also explain the experimentally reported relation D
exp(αc1 + c2) for which we provide the exact expression. Our approach (1) is general and it paves
the way to derive the PDF of any sufficiently smooth function of a quadratic form in Gaussian random variables. The practical aspect of this study is the development of universal estimators for
anomalous diffusion parameters, which provide a reliable way to separate true parameter variability
from measurement limitations in experiments. Thus, improving the analysis of molecular motion in heterogeneous media and enabling more accurate interpretations of data in biologically relevant
contexts. (1) Y. Lanoiselée, G. Pagnini, and A. Wylomańska, Super-resolved anomalous diffusion: Deciphering the joint distribution of anomalous exponent and diffusion coefficient, Phys. Rev. Lett. 135, 137101 (2025).

*Speaker
†Corresponding author: yann.lanoiselee@gmail.com

Novel Phase Coexistence in a Multi-Species Vicsek Model

Eloise Lardet [*†1], Letian Chen [1,2], Thibault Bertrand [1]

[1] Imperial College London – United Kingdom
[2] The University of Edinburgh – United Kingdom

A hallmark in natural systems, self-organization often stems from very simple interaction rules between individual agents. While single-species self-propelled particle (SPP) systems are well understood, the behavior of mixtures of self-propelled particles with general alignment interactions remains largely unexplored with a few scattered results hinting at the existence of a rich emergent phase behavior. Here, we first present a generalization of the two-species Vicsek model with reciprocal intra- and interspecies (anti-)alignment couplings, uncovering a rich phenomenology of emergent states. Notably, we show that rather than destroying polar order, anti-aligning interactions can promote phase separation and the emergence of global polar order. Secondly, we derive a kinetic theory for the system, finding good agreement between theoretical predictions and particle simulations. This includes a novel mechanism for microphase separation, as predicted by a Turing instability. We finally show that these coexistence patterns can be generalized to multi-species systems with cyclic alignment interactions.

*Speaker
†Corresponding author: el2021@ic.ac.uk

Information-Theoretic Constraints on the Combinatorial Chemo-sensation of the Octopus

Hugo Le Roy * [1]

[1] Dipartimento di Ingegneria Civile, Chimica e Ambientale [Genova] – Via Montallegro, 1 - 16145 Genova, Italy

Octopuses represent one of the most divergent lineages in the animal kingdom, characterized by a complex, decentralized nervous system that allows for unparalleled environmental adaptation. Central to this system are the arm suckers, a unique sensory organs capable of sophisticated chemotactile exploration. Unlike the olfactory systems of mammals and insects, which rely on hundreds or thousands of distinct genes to encode specific ligands, the octopus's chemotactile system is surprisingly compact, utilizing only 26 encoding genes. To bridge this gap between genetic scarcity and sensory complexity, the octopus assembles these proteins into pentameric ion channels. While the combinatorial generation of homo- and hetero-pentamers theoretically expands the receptor repertoire, these receptors are chemically coupled rather than independent, introducing significant constraints on encoding capacity.

In this work, we employ an information-theoretic framework combined with a biophysical model of ion channels to investigate the efficiency of this sensory architecture. We analyze the system's capacity to maximize mutual information between environmental ligands and receptor array signals. Specifically, we characterize the trade-offs required to optimize for distinct sensory objectives: distinguishing ligand concentration versus identity, and sensing a broad diversity of unknown ligands versus achieving high precision within a narrow range. Our results delineate the optimal chemical properties for such an array and provide critical insights into the biological function of the sucker's sensory organs, elucidating why the octopus maintains this specialized chemotactile system alongside a distinct, traditional olfactory system.

*Speaker

Emergent Adaptive Behavior from Simple Synaptic Learning Rules

Chenguang Li *† [1], Jeffrey Erlich [1]

[1] Sainsbury Wellcome Centre – 25 Howland St, Fitzrovia, London W1T 4JG, United Kingdom

Biologically plausible local learning rules can explain how neural circuits form sensory representations, including stimulus selectivity and predictive coding. However, it remains unclear whether these same rules can also generate reward-seeking behavior. While frameworks such as active inference have attempted to link representation-learning mechanisms to adaptive behavior, no fully emergent mechanistic model currently unifies both functions.
Here we propose that reward can be treated as a simple input signal, and that this representation is sufficient to generate reward-seeking behavior in an emergent manner. We show that by incorporating internal neuronal noise and by coupling slow neural activity updates with synaptic weight updates, minimal neural networks are sufficient to produce a variety of well-studied reward-guided behaviors.

We use this framework to test seven classic local learning rules across tasks spanning both representation learning and reward-based decision-making. After evaluating performance and analyzing network dynamics in minimal and larger architectures, we find that while all rules can generate some reward-seeking behavior, only a predictive coding-style rule performs robustly across all tasks. Moreover, we show that differences in performance between rules are explained by distinct attractor geometries that emerge from interactions between each rule and task environment, which is consistent with experimental observations in the literature.
Our results demonstrate that local rules traditionally associated with unsupervised learning can inherently support reward-driven actions. Treating reward as an input signal provides a mechanistically sufficient and generalizable framework for adaptive behavior, establishing a baseline for understanding how shared synaptic mechanisms may give rise to diverse and flexible neural functions, even including operations that have been traditionally challenging for machine learning systems (e.g. autonomous exploration and continual learning).

*Speaker
†Corresponding author: ccli.3896@gmail.com

Development of the human bronchial airway network

Ivan Lobaskin *† [1,2], Megumi Inoue [3], Ignacio Bordeu [4], Alain Chedotal [3], Benjamin Simons [1,2]

[1] Department of Applied Mathematics and Theoretical Physics [Cambridge] – DAMTP, Centre for Mathematical Sciences, Wilberforce Road, Cambridge CB3 0WA, United Kingdom
[2] Gurdon Institute – Henry Wellcome Building of Cancer and Developmental Biology, Tennis Court Road, Cambridge CB2 1QN, United Kingdom
[3] Institut de la Vision – Institut National de la Santé et de la Recherche Médicale, Sorbonne Universite, Centre National de la Recherche Scientifique – France
[4] Faculdad de Ciencias Físicas y Matemáticas, Universidad de Chile – Av. Beauchef 850, 851, 8370458 Santiago, Región Metropolitana, Chile, Chile

Branched networks abound in nature, fullfiling a great variety of functions. A fascinating question is to understand how biology regulates their growth to ensure that a specific final structure is achieved, especially in large networks that may involve the coordinated growth of thousands of branches. While in general, this may involve a highly complex interaction of genetic and physical factors, at a coarse scale, the growth of many branched structures can be understood using minimal models based on simple rules for branching, elongation and termination. Here, we study the development of the human bronchial airway in the embryonic and foetal stages. Advances in tissue clearing and image processing techniques have recently made it possible to produce whole-mount images with high resolution, resolving the full branched structure in 3D. We perform extensive computational network analysis of experimental images, which reveals that despite the complexity of the processes involved, many statistical properties are conserved throughout development, suggesting a stationary growth dynamic. Based on these findings, we propose a minimal model of network growth that can reproduce and predict numerous topological and morphometric features observed in the data. In particular, our model highlights a distinct role for tips growing on the surface and in the bulk of the organ, and surprisingly suggests that the basic branching dynamics are fundamentally asymmetric. Overall, our results support the view that human lung branching morphogenesis can be understood as a collective, self-organized process, where the growing tips coordinate to achieve a rapid and controlled invasion of an irregular volume, together with a dense and efficient packing of the available space.

*Speaker
†Corresponding author: il354@cam.ac.uk

Density–Velocity Relation is Scale-Dependent in Epithelial Monolayers

Hengdong Lu *† [1,2], Tianxiang Ma [1], Amin Doostmohammadi [1], Anne-Florence Bitbol [2], Aleksandra Ardaseva [1,2]

[1] Niels Bohr Institute [Copenhagen] – Denmark
[2] EPFL – Switzerland

The relationship between cell density and velocity is often assumed to be negative due to crowding. However, observations across systems reveal a more nuanced picture: while some emphasize contact inhibition of locomotion, others suggest that dense regions exhibit enhanced activity due to force generation.
Here we employ a minimal multiphase-field model incorporating activity-induced shape changes to simulate the two-dimensional confluent deformable cell collectives. By coarse-graining cell motion over multiple spatial windows, we find that cell velocity magnitude correlates positively with local density at small scales, but negatively at large scales. This scale-dependent relation arises from competition between active force generation and mechanical confinement. The same analysis applied to experimental data from MDCK epithelial monolayers corroborates our observations.
Our results reconcile conflicting views of density-regulated migration. Beyond this, our future efforts aim to extend the model by incorporating cellular adaptability, allowing mechanical parameters to evolve dynamically in response to local mechanical cues and environmental conditions. This extension will enable us to investigate how adaptive strategies influence collective dynamics and emergent behaviors in living active matter.

*Speaker
†Corresponding author: hengdong.lu@epfl.ch

Quantitative hedge funds, a (short) primer

Riccardo Marcaccioli *† [1]

[1] Capital Fund Management – Capital Fund Management, Capital Fund Management – 23/25, rue de l'Université 75007 Paris, France

In this talk I will try to give the audience a brief overview of what we do at CFM and the problems we face when building a quantitative investment strategy.

*Speaker
†Corresponding author: Riccardo.Marcaccioli@cfm.com

Active nematics on complex curved substrates

Violeta Marcen * [1], Andrew Callan-Jones [1], Raphaël Voituriez [2]

[1] Matière et Systèmes Complexes – Centre National de la Recherche Scientifique, Université Paris Cité – Université Paris Cité, Bât. Condorcet, case postale 7056, 10 rue Alice Domon et Léonie Duquet, 75205 PARIS Cedex 13, France

[2] Laboratoire Jean Perrin – Sorbonne Universite, Centre National de la Recherche Scientifique, Institut de Biologie Paris Seine – 4, place Jussieu, Tour 32-33, Case Courrier 114 75252 Paris Cedex 05, France

Topological defects have been shown to be relevant in different biological processes, such as morphogenesis or cell extrusion. While the dynamics of +/- 1/2 defects in nematic systems have been well-caracterised on flat surfaces, this is not the case for complex curved surfaces. This work uses analytical and computational methods to study how inhomogeneous extrinsic curvature affects the dynamics of these defects.
Future work will be focused on intrinsic or gaussian curvature effect on single defects. We then move into multidefect regime on curved substrates, which is highly relevant in the complex geometries found in the human body.

*Speaker

PhD: valuable skills, invisible value?

Bastien Marguet *† [1,2]

[1] Université Claude Bernard Lyon 1 – Université de Lyon – 43, boulevard du 11 novembre 1918, 69622 Villeurbanne cedex, France
[2] PhD outreach ambassador – Auvergne-Rhône-Alpes – France

A PhD builds rare skills that are often misunderstood.
Based on a survey conducted among participants, this talk aims to question their real value beyond academia. It offers a reading of doctoral skills, through concrete examples and their translation into other professional contexts.
The objective is to trigger a shift in awareness and initiate individual repositioning. One central question will guide this reflection: if you had to leave academia tomorrow, what would you be able to sell and how?

*Speaker
†Corresponding author: bastien.marguet@univ-lyon1.fr

Taming Collective Activity to Crystallize an Oscillator Gas

Alexandre Morin * [1]

[1] Leiden University – Leiden University — 2300 RA Leiden The Netherlands, Netherlands

Motility-induced phase separation occurs in assemblies of self-propelled units when activity is coupled negatively to density. By contrast, the consequences of a positive coupling between density and activity on the collective behaviour of active matter remain unexplored. Here we show that collective activity can emerge from such a positive coupling among non-motile building blocks. We perform experiments with self-sustained oscillators powered by contact-charge electrophoresis. Although the oscillators are non-motile by design, they spontaneously form an active gas when confined together. The super-elastic nature of collisions constitutes a positive density–activity coupling and underlies the active gas properties. Elucidating the origin of binary collisions allows us to precisely control the structure of the active gas and its eventual crystallization. Beyond considering the overlooked positive coupling between density and activity, our work suggests that rich collective properties can emerge not only from the symmetry of interactions between active building blocks but also from their adaptable and responsive behaviour.

*Speaker

Modeling the dynamics of T lymphocytes performing reverse haptotaxis using data-driven methods

Reya Negi *† [1], Ahmad Awada [2], Olivier Theodoly [2], Pierre Ronceray [3]

[1] Aix-Marseille University – Aix Marseille Univ, CNRS, CINaM, Marseille – 163 Avenue De Luminy, France
[2] Aix-Marseille University – Inserm U1067 CNRS – 163 Avenue De Luminy, France
[3] Aix-Marseille University – Aix Marseille Univ, CNRS, CINaM, Marseille – 163 Avenue De Luminy, France

T lymphocytes can exhibit *reverse haptotaxis* which is directed migration toward regions of lower adhesion density mediated by LFA-1 integrins. This counterintuitive guidance mechanism cannot be explained by classical models of mesenchymal haptotaxis and remains poorly understood at the level of underlying physical forces. Here, we combine high-resolution single-cell trajectories on controlled ICAM-1 adhesion landscapes with data-driven force inference based on underdamped Langevin modeling to reconstruct the effective drift and diffusion governing T-cell motion. Our approach quantifies how adhesion gradients reshape the local force field experienced by the cells and reveals a systematic active drift directed down the adhesion gradient, consistent with reverse haptotaxis. By modeling the full position-velocity dynamics, we identify which basis components contribute most strongly to gradient sensing, active propulsion, and directional bias. Together, this work provides a quantitative physical framework for understanding how T lymphocytes interpret adhesive cues and demonstrates the utility of stochastic force inference for dissecting complex migratory behaviors.

*Speaker
†Corresponding author: reya.negi@cnrs.fr

Escaping Cahn-Hilliard: Active Model B- from Three-Component Reaction Diffusion

Beatrice Nettuno *† [1]

[1] University of Munich (LMU) – Theresienstrasse 37, Germany

Reaction–diffusion models with mass conservation successfully describe intracellular protein patterns, yet analytical understanding remains limited. We show that the minimal tractable setting - two-component mass-conserving systems - is fundamentally insufficient, as they coarsen indefinitely, akin to the passive Cahn-Hilliard model. Three components are therefore the minimal requirement for genuine active patterning. We show that the three-component model maps onto a scalar active field theory for the conserved total mass, obtained via adiabatic elimination of fast degrees of freedom, which we term Active Model B- (AMB-). Activity enters through a density-dependent diffusion coefficient that can become negative at high densities, representing an alternative route to breaking the thermodynamic structure of passive systems, distinct from the ξ-term of Active Model B+, while retaining a well-defined notion of chemical potential. Numerical simulations confirm the predicted phase diagram, reproducing droplet, stripe, and foam-like patterns akin to those observed in the Min system.

*Speaker
†Corresponding author: beatrice.nettuno@lmu.de

Where do the electrons go in atomistic ML?

Jigyasa Nigam *† [1]

[1] Massachusetts Institute of Technology, MA, USA – United States

Machine learning (ML) has transformed our approach to modeling complex physical systems by not only enabling faster and more accurate simulations but also creating entirely new computational pathways for the atomic-scale discovery of compounds with distinct properties. Unlike many other domains, atomistic ML benefits from rich physical laws, as atomic structures transform predictably under rotations, translations, and inversions, and these symmetries can be embedded into models (1). Such physics-informed approaches have already advanced the prediction of critical material properties, bypassing the steep cost of ab-initio calculations for quantities ranging from potential energy surfaces to dipole moments and stress tensors. An alternative, and perhaps more powerful, use of ML is to move beyond accelerating single-property calculations. In this talk, I will present a framework that addresses this challenge by modeling intermediate quantities, such as effective single-particle Hamiltonians (2), underpinning the relationship between atomic structures and their macroscopic observables. Building on the interplay of ingredients that underlie the success of physics-aware atomistic ML surrogates, I will show how these methods can be extended to model elements of electronic structure (3).

(1) J. Nigam et al., *J. Chem. Phys.* 153, 121101, 2020

(2) J. Nigam, M. Willatt, M. Ceriotti, *J. Chem. Phys.* 156, 014115, 2022

(3) D. Suman, J.Nigam et al. , J . *Chem. Theory Comput.* 21 (13) 6505, 2025

*Speaker

†Corresponding author: jnigam@mit.edu

3D confinement reshapes RNA folding and enhances circularisation in the Zika virus

Yavor Novev *† [1], Davide Marenduzzo [2], Grzegorz Kudla [1]

[1] Institute of Genetics and Cancer, University of Edinburgh – United Kingdom
[2] School of Physics and Astronomy - University of Edinburgh – United Kingdom

The folding of RNA is essential to its function, but RNA's high flexibility makes it difficult to study with conventional experimental techniques. Proximity ligation assays such as COMRADES and SPLASH provide detailed information on contacts between RNA bases, but the full potential of such data has not been explored so far due to the lack of appropriate computational methods.

We use simulations to understand the spatial organization of the viral genome under in vivo and in virion conditions. Combining proximity ligation data with coarse-grained molecular dynamics simulations, we explore how distance-dependent contact probability differs between unconfined and virion-confined RNA. Our simulations recapitulate experimentally observed base-pairing and provide insight into the 3D structure of viral RNA in cells and virions. We construct a model that accounts for base stacking through incentivizing the formation of stems and prevents excessive bond stretching through an energy penalty for neighbouring bases paired to distant regions of the molecule. Our model predicts a pseudoknot genus consistent with expectations for RNAs of this size, links the experimental contact map to an ensemble of diverse RNA conformations and predicts that long double-stranded regions cause nematic ordering within the viral RNA. The simulations predict that confinement increases the propensity of the viral genome to circularize via base-pairing between its 3' and 5' ends, in line with experimental data. Genome circularization is a key mechanism for switching between translation and replication in flaviviruses.

Computational analysis of proximity ligation data can elucidate key aspects of the packaging and assembly of viral genomes, the conformation of non-coding RNAs, as well as for the optimization of drug delivery for RNA-based drugs such as mRNA vaccines, which typically requires nanoscale-particles. Our work fills a gap in understanding how confinement shapes RNA folding and function.

*Speaker
†Corresponding author: ynovev@ed.ac.uk

Self-assembly of three-dimensional particles with complex interactions

Vincent Ouazan-Reboul * [1]

[1] Laboratoire de Physique Théorique et Modèles Statistiques – Université Paris-Saclay, Centre National de la Recherche Scientifique – France

Proteins are biomolecules with an intricate structure that allows them to develop highly anisotropic interactions between each other. In many cases, these interactions have been fine-tuned by evolution in order to build functional assemblies. On the other hand, many proteins self-assemble when they are not supposed to and form into pathological aggregates. Strikingly, despite their constituent proteins having different structures and physico-chemical properties, many of these aggregates have a similar, fiber-like structure.

By performing lattice Monte-Carlo simulations of three-dimensional particles, I will show that complex anisotropic interactions lead to a great morphological diversity in the resulting assemblies. In particular, many choices of interactions lead to the formation of fibers, which are found to result from geometrical frustration. On the other hand, I will also demonstrate that anisotropy is a useful design tool for controlling the size and shape of equilibrium aggregates.

*Speaker

Resource-mediated interactions shape diversity predictions and functional patterns in microbial communities

Prajwal Padmanabha * [1]

[1] Department of Fundamental Microbiology [Lausanne] – Faculté de biologie et de médecine Biophore - CH-1015 Lausanne, Switzerland

Predicting microbial community diversity and function from species-level information remains an open problem. A central challenge is that species interactions depend strongly on environmental context, so interaction networks inferred in one setting often fail to predict community assembly in another. Community function presents an additional puzzle: single-species contributions show remarkable linearities across community compositions. Yet we lack frameworks explaining this regularity or its generalizability across environments. Underlying both is an incomplete understanding of how interactions are shaped by metabolic processes in different environments. Consumer-resource models offer a path forward to bridge this gap. We show that models with resource competition and crossfeeding generate a characteristic 'many weak, few strong' interaction distribution. Using these lognormal structures as informed priors in Lotka-Volterra models improves diversity predictions in experimental communities. On the functional side, we show that accounting for resource-mediated interactions predicts a) how the magnitude of a species' functional effect shifts across environments, and b) how strong facilitation through auxotrophy or detoxification generates observable non-linear patterns. Together, these projects identify statistical signatures from resource-mediated constraints in microbial communities, contributing to robust predictive frameworks grounded in ecological mechanisms.

*Speaker

A new method for inverse problems at arbitrary densities

Davide Paolino *† [1], Olivier Coquand [2], Ludovic Berthier [1]

[1] Gulliver (UMR 7083) – Ecole Supérieure de Physique et de Chimie Industrielles de la Ville de Paris, Centre National de la Recherche Scientifique – ESPCI, 10, rue Vauquelin, 75231 Paris cedex 05, France
[2] LAboratoire de Modélisation Pluridisciplinaire et Simulations – Université de Perpignan Via Domitia – 52, avenue Paul Alduy 66860 Perpignan cedex, France

Determining effective particle interactions from system trajectories or samples is a powerful tool for both experiment, where the true potential might be unknown, and theory, to simplify complex energy landscapes or to model out-of-equilibrium phenomena.
The Iterative Boltzmann Inversion algorithm remains the standard for these tasks due to its conceptual simplicity and minimal assumptions. However, its dependence on a full Molecular Dynamics or Monte Carlo simulation at every iteration creates a massive computational bottleneck, often prohibiting its use for large-scale or slowly relaxing systems.

In this work, we introduce a new algorithm that overcomes this limitation by exploiting an exact analytical relation that links the potential to the radial distribution function, eliminating the need for iterative simulations. This removes the central computational cost, allowing the inverse procedure to be applied to larger systems or to scenarios where simulations are difficult or unfeasible, such as out-of-equilibrium or glassy regimes. While recently a different analytical relation has been proposed to overcome the same limitations, our method is more general and maintains accuracy even at high densities.

We validate the algorithm against a dataset of numerical simulations, demonstrating accurate potential reconstruction for a range of different known potentials, such as the Lennard-Jones potential, Weeks-Chandler-Andersen potential, long-range dipole interactions and more exotic potentials.
Future work will focus on applying inverse methods to experimental colloidal systems and active matter simulations.

*Speaker
†Corresponding author: davide.paolino@espci.fr

Findability bias can strongly impact protein evolution

Andrei Papkou * [1], Andreas Wagner [2]

[1] ALLOX Bio – Barcelona, Spain
[2] University of Zurich – Zurich, Switzerland

Protein evolution occurs in a vast space of DNA sequences, in which some proteins can be easier to find than others, because they are encoded by more DNA sequences. As a result, evolution may be biased towards proteins that are easier to find. This findability bias has only been studied with computational models. We here provide empirical evidence from a recently mapped *E. coli* fitness landscape in which 14,853 DNA sequences (genotypes) encode 800 amino acid sequences (phenotypes) of the antibiotic resistance protein dihydrofolate reductase (DHFR). The fitness of nearly all synonymous DNA encoding each amino acid sequence has been measured experimentally. We computationally study the adaptive evolution of populations on this landscape and find that amino acid sequences encoded by more synonymous genotypes evolve up to 100 times more frequently than rare sequences. This holds even where rare sequences have a fitness advantage. Furthermore, the findability bias persists in very small and very large populations, at both low and high mutation rates, and whether synonymous mutations are neutral or not. The fundamental cause of this bias is the degeneracy of the genetic code, which suggests that it may universally impact protein evolution.

*Speaker

Exploring collective cell dynamics in the subconfluent regime with asymmetric subcellular cues

Clarisse Pierre * [1], Caroline Giuglaris [1], Pascal Silberzan† [1], Paule Dagenais‡ [1]

[1] Laboratoire Physique des Cellules et Cancer UMR168, Institut Curie – Université Paris sciences et lettres, Centre National de la Recherche Scientifique - CNRS, Equipe Labellisée Ligue Contre le Cancer, Sorbonne Université 75248 Paris – France

Collective behaviors of migrating cells are crucial in tissue homeostasis, morphogenesis and cancer invasion, and are largely controlled by their microenvironment. In the absence of biochemical gradients, subcellular mechanical cues can trigger the emergence of large-scale cellular flows by setting locally the direction of migration. In vivo, cells deposit fibrous ECM on surfaces which subsequently serve as guiding cues for neighboring cells. Such fibers can be mimicked in vitro with anisotropic "grooved" microfabricated substrates directing cell migration, both at the single cell and collective levels. Single cells migrate and elongate along the grooves in a process called "contact guidance". Confluent monolayers, on the other hand, form wide bidirectional lanes and migrate collectively. When the grooves cross-section is not symmetric (ratchet-like), we observe that cells migrate unidirectionally perpendicular to the grooves' direction in the regime of density preceding confluence. In contrast, at low or high density, cells do not respond to the asymmetry and migrate parallel to the rails. These asymmetric grooves impose a periodic asymmetric potential landscape for the cells, inducing a type of directed motion (ratchetaxis) by breaking the symmetry in the inherently out-of-equilibrium cellular system. We focus on characterizing the morphology and dynamics of the cells in this regime to better understand the underlying mechanism. This project delves into the impact of density, groove geometry, and cell type on this migration pattern, relying on innovative experimental techniques, data analysis, and theoretical modeling. It could provide the foundation for cell-sorting devices.

*Speaker
†Corresponding author: pascal.silberzan@curie.fr
‡Corresponding author: paule.dagenais@curie.fr

Collective dynamics of active particles with memory

Nikita Allaglo [1,2], Alexis Poncet *† [1]

[1] Laboratoire de Physique de l'ENS Lyon – Ecole Normale Supérieure de Lyon, Université de Lyon, Centre National de la Recherche Scientifique – 46 allée d'Italie 69007 Lyon, France
[2] Laboratoire de physique de l'ENS - ENS Paris – Sorbonne Universite, Centre National de la Recherche Scientifique, Université Paris Cité, Département de Physique de l'ENS-PSL – 24, rue Lhomond75005 Paris, France

Systems of interacting active particles have been the subject of extensive theoretical research, particularly to explore their phase diagrams and correlation functions. Recently, experimental studies have revealed strong memory effects when these active systems are immersed in a viscoelastic medium, leading to intriguing behaviors in both individual and collective dynamics. While memory effects have been well studied in equilibrium systems, their impact on out-of-equilibrium active phases remains a largely open topic.

In this poster, I will present a recent numerical and theoretical work investigating the dynamics of active particles embedded in a viscoelastic medium, modeled by a memory kernel acting on individual particles. The primary focus will be on how memory effects modify motility-induced phase separation (MIPS) at high density and activity. I will first analyze in details the trajectory of an individual particle in the system and explain how it can exhibit oscillatory behavior. I will then demonstrate that at the collective level memory hinders MIPS, resulting in a fluidized system even under high activity. In the full phase diagram, MIPS is shown to be reentrant both as a function of activity and memory strength. We believe that our findings pave the way to a better understanding of collective effects in the presence of memory. The numerical simulations have been performed by Nikita Allaglo, now PhD student at LPENS in Paris.

*Speaker
†Corresponding author: alexis.poncet@ens-lyon.fr

Phototactic Decision making by micro algae

Shantanu Raikwar * [1], Nir Gov [2], Adriana Pesci [3], Raphaël Jeanneret† [4], Raymond E. Goldstein [3]

[1] Laboratoire de physique de l'ENS - ENS Paris – Centre National de la Recherche Scientifique, Département de Physique de l'ENS-PSL – 24, rue Lhomond75005 Paris, France
[2] Weizmann Institute of Science [Rehovot, Israël] – 234 Herzl Street, Rehovot 7610001, Israel
[3] Department of Applied Mathematics and Theoretical Physics [Cambridge] – DAMTP, Centre for Mathematical Sciences, Wilberforce Road, Cambridge CB3 0WA, United Kingdom
[4] Laboratoire de physique de l'ENS - ENS Paris – Sorbonne Universite, Centre National de la Recherche Scientifique, Université Paris Cité, Département de Physique de l'ENS-PSL – 24, rue Lhomond75005 Paris, France

Chlamydomonas reinhardtii cells are able to orient themselves in light fields, a property called phototaxis. In Chlamydomonas, phototaxis is mediated by a specialized organelle called the eyespot, known to provide information about the direction of light propagation. However, very little is known about the swimming behavior of these algae when facing multiple competing light signals.
To gain insights on this question, we have designed a setup made of two collimated light beams whose propagation directions and intensities can be controlled precisely. For small enough angles between the lights ($<=140\circ$), we demonstrate that the algae swim along the direction given by the intensity-weighted average of the direction of lights (dubbed "tangent law"), which can be rationalized using a recently developed model of phototaxis. Increasing further the angle to almost $180\circ$, we observe a bifurcation transition in the behavior of the cells where they start following alternatively the direction of each light beam. Depending on the times spent in either state, different sub-populations emerge: i) cells that follow either light, ii) cells that switch quickly between the two lights and move on average along the tangent law, iii) cells with behavior intermediate between the two previous limits. We explain the emergence of these sub-populations by considering the cell-to-cell variability of the spatial location of the eyespot on the cell membrane.

These results bring strong insights onto the way these cells use light signals to navigate and allow us to better grasp the interactions taking place from shading effects in dense suspensions.

*Speaker
†Corresponding author: raphael.jeanneret@phys.ens.fr

Anticipatory agents view their trajectories as polymers: a space-time analogy for decision-making

Alexis Raulin-Foissac * [1], Alexandre Nicolas [1]

[1] Institut Lumière Matière [Villeurbanne] – Université Claude Bernard Lyon 1, Centre National de la Recherche Scientifique – UMR5306 CNRS Université Claude Bernard Lyon 1 Domaine Scientifique de La Doua Bâtiment Kastler, 10 rue Ada Byron 69622 Villeurbanne CEDEX, Franc, France

Pedestrians exhibit remarkable navigational abilities in crowded or cluttered environments. When individuals interact, complex collective behaviors emerge, such as lane formation and stop-and-go waves. Yet, few models account for their capacity to mutually anticipate non-linear motions over a finite time horizon. Here, we address this gap by introducing a new framework (briefly introduced in **(1)**) inspired by condensed-matter and statistical physics, exploiting an analogy between the space-time trajectories of pedestrians and polymers. Although focused on pedestrian dynamics, our approach can be extended to other intelligent active agents.

In our model, each pedestrian is represented as an intelligent agent that selects its trajectory by minimizing a cumulative cost over future time. The cost function accounts for multiple factors, including discomfort associated with occupying specific positions in space and time, the influence of nearby pedestrians, energy expenditure required for movement, and the desire to reach a target efficiently. Each agent anticipates the likely trajectories of neighboring agents and use these predictions into its cost function to adjust its own trajectory accordingly.

Fluctuations increasing with time are added onto the paths to capture the growing uncertainty in the anticipated trajectory as the prediction horizon extends. The minimization of these individual costs using gradient descent generates forces acting on the positions that we discretize to simplify the problem. Ultimately, the process by which a pedestrian chooses the optimal path, is analogous to the dynamic of polymers, representing the space-time trajectories, subjected to thermal fluctuations and interacting within each other to prevent collisions in the future. Insights and results from polymer dynamics can therefore be leveraged to refine the model and provide a deeper intuition about its outcomes.

(1) A. Raulin-Foissac, A. Nicolas, *EPJ Web Conf.* **334**, 04023 (2025).

*Speaker

Inference from Biological Data: Undersampling and Multiple Scales

Milo Repossi *† [1]

[1] Ecole Superieure de Physique et de Chimie Industrielles de la Ville de Paris – Université Paris sciences et lettres – 10 rue Vauquelin, 75231 Paris cedex 05, France

Machine learning models are increasingly used to extract functional and structural insights from protein sequence data. However, their predictive power is fundamentally constrained by undersampling: the number of available sequences is often small compared to the complexity of the models used to describe them. At the same time, proteins encode information across multiple, intertwined scales, from localized epistatic interactions between residue pairs to extended networks of collectively evolving sites. Previous studies have shown that in the undersampled regime, inference methods readily detect sparse, pairwise interactions (contacts), yet largely fail to capture broader, functionally relevant collective modes (sectors). This uneven sensitivity raises a fundamental question: how does data scarcity distort the representation of different scales in statistical models? In my project, I combine tools from Statistical Physics, Random Matrix Theory, and the theory of Disordered Systems to open the "black box" of protein inference models. Using a controlled teacher–student framework, I characterize how different structural scales are learned as a function of sampling depth. Building on this understanding, I propose strategies to mitigate scale-dependent biases, with the goal in mind of building more reliable inference machines for high-dimensional biological systems.

*Speaker

†Corresponding author: milo.repossi@espci.fr

Synchronisation and topological defects in 2D systems

Ylann Rouzaire *† [1,2], Demian Levis [1]

[1] University of Barcelona – Spain
[2] UBICS (Uni. Barcelona Institute of Complex Systems) – Spain

I will start by introducing two famous spins models: the XY model of topological phase transitions and the ***Kuramoto model*** of synchronisation. I will explain how those simple lattice models can model, to some extent, natural phenomena in the living world.
I will then introduce and focus on ***topological defects*** in such systems. First, I will show that defects generically unbind from each other, perturbing the system. Second, I will focus on their superdiffusive behaviour and explain how it is related to self-avoiding random walks. (1,2)

Finally, I will show that this simple, theoretical model actually shares common features with (very different) experimental systems. (3,4)

References:

1. Rouzaire and Levis, *Defect Superdiffusion and Unbinding in a 2D XY Model of Self-Driven Rotors,* Phys. Rev. Lett. (2021)

2. Rouzaire and Levis, *Dynamics of topological defects in the noisy Kuramoto model in two dimensions,* Front. Phys. (2022)

3. Kumar et al, *Catapulting of topological defects through elasticity bands in active nematics,* Soft Matter (2022)
4. Bililign et al, *Motile dislocations knead odd crystals into whorls,* Nature Physics (2022)

*Speaker
†Corresponding author: rouzaire.ylann@gmail.com

Phase transition in statistical inference of spatial information from single-cell sequencing data

Alican Saray * [1], Brian Skinner† [1], Calvin Pozderac‡

[1] The Ohio State University [Columbus] – 281 W Lane Ave, Columbus, OH 43210, United States

Abstract of the poster: A process of statistical inference can exhibit a phase transition as a function of the quantity or quality of the data used for the inference. In the "reconstructing" phase, the data is rich enough to enable the parameters to be inferred accurately, while in the "non-reconstructing" phase the data is sufficiently poor that errors in the inferred parameters grow extensively with the system size. Here we demonstrate this phase transition in a process of spatial genomics, in which the positions of cells in a biological tissue are reconstructed from single-cell sequencing data by examining correlations between the levels of DNA barcodes present within the cells. We provide analytical and numerical evidence for the transition and its critical properties using both simulated data and real experimental data collected by experiments at the Broad Institute. Personal Statement: I am interested in complex systems where collective behavior leads to sharp qualitative changes, particularly phase transitions that separate distinct macroscopic regimes. I enjoy uncovering the underlying physics through clear, qualitative arguments and identifying the nature of these transitions, such as percolation-like phenomena. I am especially motivated by biological systems, where spatial structure and randomness give rise to rich collective behavior, and I am eager to further explore this area using tools from statistical physics. My current project is a natural example of these interests, as it applies ideas from phase transitions and complex systems to a biologically motivated setting. Alongside theoretical understanding, I place strong emphasis on principled numerical methods to support and test physical intuition. I would be very happy to join IntCha26 and engage with the interdisciplinary community it brings together.

*Speaker
†Corresponding author:
‡Corresponding author:

Cell shape-shifting across the tree of life

Andela Saric * [1]

[1] Institute of Science and Technology [Klosterneuburg, Austria] – IST Austria Am Campus 1 3400 Klosterneuburg Austria, Austria

Cells are exquisite self-organised materials that shape-shift to fulfil many of their functions, such as moving, dividing, connecting with partners, or exchanging material. Today, I will discuss our research on the computational modelling of cell self-organisation and shape-shifting across the tree of life, carried out in close collaboration with living and synthetic cell experiments. I will first focus on cell division across different stages of evolution. I will then turn to cell reshaping driven by chemical exchanges with the environment, in the context of the evolution of complex cells. More broadly, I will show how modelling can help us understand the emergence of life from its building blocks and guide the design of artificial structures that mimic life at the nanoscale.

*Speaker

Run and chase dynamics in turbulent flows

Mattia Scandolo * [1,2]

[1] University of Chicago – Edward H. Levi Hall 5801 South Ellis Avenue Chicago, Illinois 60637, United States
[2] Laboratoire de physique de l'ENS - ENS Paris – Département de Physique de l'ENS-PSL – 24, rue Lhomond75005 Paris, France

Non-reciprocal interactions arise in a wide range of physical and biological systems, naturally lead to wave-like propagation mechanisms. A prototypical non-reciprocal setting is that of run-and-chase behavior, emerging whenever two (or more) species interact through non-symmetric attractive/repulsive forces, e.g. species A is attracted by B while species B is repelled by A. This behavior can be effectively captured by the presence of odd diffusion, with the scalar fields coupled through a non-Hermitian diffusion matrix.
In realistic settings, interacting species do not evolve in isolation but are embedded in complex environments, such as bacterial populations immersed in a fluid. Unfortunately, the interplay between non-reciprocal interactions and turbulent transport remains poorly understood. Here we investigate mixtures of non-reciprocally interacting scalar fields advected by strongly correlated velocity flows. As a reference framework, passive scalars transported by random velocities exhibit turbulence-like features, including an inertial range with diffusion-independent statistics, power-law structure functions, and anomalous scaling associated with intermittency.
We introduce a non-reciprocal generalization of the Kraichnan model, in which two scalar fields are coupled through odd diffusion. Owing to the analytical tractability of the model, we show that non-reciprocal couplings can profoundly modify the statistical properties of the mixture. For antisymmetric interactions of equal strength, the two-point correlation function remains unchanged, while higher-order structure functions display a distinct power-law behavior with a reduced level of intermittency. When the interaction strengths are strongly asymmetric, non-reciprocity affects even the two-point correlations, leading to a novel scaling regime for the strongly interacting field.

*Speaker

Effective binary models of multicomponent phase separation

Henri Schmidt * [1], David Zwicker [1]

[1] Max Planck Institute for Dynamics and Self-Organization – Am Faßberg 17, 37077 Göttingen, Germany

Biological cells rely on biomolecular condensates for spatiotemporal organization. Condensates consist of many differently interacting biomolecules, which leads to a rich and complex configuration space. Yet, only a few types of molecules can be measured in experiments, and the resulting phase behavior is typically explained using low-dimensional models. To understand the conditions under which such dimensionality reduction is feasible, we numerically explore multicomponent phase separation and ask when the behavior of a particular component can be explained by simple binary phase separation. This is surprisingly often the case, even when the unobserved components undergo phase separation on their own. However, the predicted interaction parameters and molecular volumes typically deviate from their true values, indicating that the reduction introduced systematic measurement errors. Understanding the details of the dimensionality reduction will allow us to better probe multicomponent phase separation by observing a few components in the future.

*Speaker

Exploring the Principles of Self-Assembly with Tunable and Flexible Colloidal Particles

Lisa Shafroth * [1,2], Dinesh Kumar Sahu [1,2], Jude Ann Vishnu [1], Martin Lenz [1,2], Olivia Du Roure [2], Julien Heuvingh [2]

[1] Laboratoire de Physique Théorique et Modèles Statistiques – Université Paris-Saclay, Centre National de la Recherche Scientifique – Bâtiment 100 Université Paris-Sud Centre Scientifique d'Orsay 15 rue Georges Clémenceau 91405 Orsay cedex, France

[2] Physique et mécanique des milieux hétérogènes – Ecole Supérieure de Physique et de Chimie Industrielles de la Ville de Paris, Sorbonne Universite, Centre National de la Recherche Scientifique, Université Paris Cité – ESPCI, 7 Quai Saint Bernard 75005 Paris, France

Self-assembly is a fundamental mechanism in biological systems. Beyond biological specificities, several observations suggest the existence of universal physical principles underlying self-assembly processes(1). These principles would govern how aggregates form, organize, and limit their size, independently of the biochemical nature of the building blocks. We aim to explore these general rules experimentally with microprinted colloids that can diffuse due to thermal agitation and aggregate via depletion interactions. Such an experimental approach was successfully implemented in our team, using a two-photon lithography technique(2). Both the particle shape and the strength of the interactions can be tuned, and we can selectively choose which facets of the colloids are attractive. In this context, we recently succeeded in introducing flexibility into our rigid colloids by designing particles composed of two mobile interconnected parts. We also succeeded in making frustrated particles in the sense that they cannot form large aggregates without accumulating strain. This is a promising first step toward developing flexible and more complex colloidal particles, paving the way for further studies on geometrical frustration in particle aggregates, where not all interactions between particles can be simultaneously satisfied. Our results suggest the presence of size self-limitation in the resulting aggregates, a key process in biological systems. Finally, our team implemented a molecular simulation that helps us identify the key ingredients governing the experimental system's behavior. Combined with theoretical calculations, this approach should allow us to gain deeper insight into the complex dynamics and equilibrium structures observed experimentally.

(1) L. Koehler, P. Ronceray and M. Lenz, *Phys. Rev. X*, 2024

(2) M. Mayarani, J. Laurent, M.Lenz, O. Du Roure and J.Heuvingh, *Soft Matter*, 2025

*Speaker

Publication in the Nature Portfolio

Anjali Sharma *† [1]

[1] Nature publishing group – United Kingdom

Anjali is an editor at Nature Communications, where she focuses on manuscripts related to soft matter physics. She will be discussing the publication process within the Nature Portfolio, emphasizing the following points:
(a) The key differences between Nature, Nature Research Journals, and Nature Communications.

(b) What editors look for in the papers they choose to publish.

(c) An insight into the editorial decision-making process.
(d) How early career researchers can get involved.

*Speaker
†Corresponding author: anjali.sharma@nature.com

Collective is different: Information exchange and speed-accuracy trade-offs in self-organized patterning

Ashutosh Tripathi , Jörn Dunkel , Dominic Skinner *† [1]

[1] Flatiron Institute – 162 5th Avenue, New York, NY 10010, USA, United States

During development, highly ordered structures emerge as cells collectively coordinate with each other. While recent advances have clarified how individual cells process and respond to external signals, understanding collective cellular decision making remains a major theoretical challenge. Here, we introduce a minimal, analytically tractable, model of cell patterning via local cell-cell communication. Using this framework, we prove that a trade-off between the speed and accuracy of collective pattern formation occurs and, by adapting techniques from stochastic chemical kinetics, quantify how information flows between cells during patterning. Our analysis reveals counterintuitive features of collective patterning: globally optimized solutions do not necessarily maximize intercellular information transfer and individual cells may appear suboptimal in isolation. Moreover, the model predicts that instantaneous information shared between cells can be non-monotonic in time as patterning occurs. An analysis of recent experimental data from lateral inhibition in Drosophila pupal abdomen finds a qualitatively similar effect.

*Speaker

†Corresponding author: dskinner@flatironinstitute.org

A modelling framework for non-Gaussian transport in complex media

Vittoria Sposini * [1]

[1] Università degli Studi di Padova = University of Padua – Via 8 Febbraio 2, 35122 Padova, Italy

Transport phenomena in soft matter systems play a fundamental role in a wide range of biological and industrial processes. Over the last decades, it has become clear that the motion of diffusive tracers in complex and disordered environments often deviates from classical Gaussian statistics described by standard Brownian motion, instead exhibiting (almost) universally non-Gaussian behaviour. Both analytical and numerical studies have linked non-Gaussian diffusion to sample-to-sample variability and/or spatio-temporal heterogeneity inherent to the system. My talk aims at exploring this phenomenon from two distinct yet complementary perspectives. In the first part, I will present a general theoretical framework based on the concept of subordination, which captures the emergence of non-Gaussian diffusion across a broad class of complex systems. In the second part I will focus on a specific case study, investigating how system heterogeneity influences the emergence of non-Gaussian diffusion in the transport of colloidal nanoparticles through a polymeric glassy matrix composed of star polymers. In particular, I will show that the emergence of arrested phase separation in this system interacts with the dynamics of the colloids in a non-trivial manner, leading to complex, multiscale phenomena. Overall, these two perspectives together highlight the importance of system heterogeneity in shaping transport behaviour in complex media.
References:

(1) V. Sposini, S. Nampoothiri, A. Chechkin, E. Orlandini, F. Seno, and F. Baldovin, Phys. Rev. Lett. 132, 117101 (2024).

(2) V. Sposini, S. Nampoothiri, A. Chechkin, E. Orlandini, F. Seno, and F. Baldovin, Phys. Rev. E 109, 034120 (2024).
(3) K. Moser, C.N. Likos, V. Sposini, arXiv:2601.07625 (2026).

*Speaker

Work minimizing closed-loop protocols for active Ornstein-Uhlenbeck particles with initial position measurements

Lars Stutzer * [1], Sarah Loos [2]

[1] Max Planck Institute for Dynamics and Self-Organization – Germany
[2] Max Planck Institute for Dynamics and Self-Organization – Germany

The seemingly simple problem of moving an optical trap containing an active particle with minimum work input in a finite time reveals rich and interesting features. Explicitly, the system connects active matter, optimal control, and information thermodynamic principles in an analytical tractable model to study how information can lead to work extraction through closed-loop (feedback) protocols. We extend the model of an active Ornstein-Uhlenbeck particle (AOUP) in an optical trap to include initial position measurements suitable for experiments. By analytically deriving the optimal closed-loop protocols and resulting minimum work, we are able to discern finite and asymptotic parameter regimes where adding activity yields a lower work input compared to the passive closed-loop problem. In contrast to the initial velocity closed-loop problem, performing an initial position measurement of an AOUP does not ensure a reduction of work compared to the passive case.

*Speaker

Can bacteria get tied up? Modelling microbial mechanics under large deformations

Albane Théry * [1], Zhi Ren [2], Edward Steager [2], Paulo Arratia [2], Kate Stebe [2], Hyun Koo [2], Rebecca Poon [1], Orkun Soyer [1]

[1] University of Warwick [Coventry] – Coventry CV4 7AL, United Kingdom
[2] University of Pennsylvania [Philadelphia] – 3451 Walnut Street, Philadelphia, PA 19104 — 215-898-5000, United States

Bacterial motility has a classical picture: bacteria swim by rotating helical flagella connected to their body by a flexible hook. However, as many biophysical models in biology, it derives from extensively studied model species like E. coli. In this talk, I will discuss how attempting to apply this framework to the motile oral pathogen *Selenonomas sputigena,* in collaboration with a dental lab, instead led us to new questions relating morphology and motility. "Why do these bacteria have a helical shape?" and "why are their flagella implanted to the side"? I will present the elasto-hydrodynamic model we are using to study the coupling between body shape and flagellar position, including regimes where buckling and large deformations of the flagellum occur. Large mechanical deformations-such as twisting and knot formation-also arise at the collective scale. I will show how similar modelling approaches can inform our understanding of filamentous cyanobacterial gliding motility at the colony scale. By highlighting the role of large deformations in bacterial behaviour, I hope to discuss the limitations of analytical approaches and large-scale simulations for microbial cell mechanics models.

*Speaker

The 3-Components Problem

Davide Toffenetti * [1], Beatrice Nettuno [1], Henrik Weyer [2], Erwin Frey† [1]

[1] Ludwig Maximilian University of Munich (LMU) – Germany
[2] KITP, Santa Barbara – United States

Our work develops a framework that connects reaction–diffusion systems with active-matter theories. Earlier studies showed that two-component mass-conserving reaction–diffusion (2cMcRD) systems can be mapped onto Model-B-type dynamics (1), which leads to the coarsening of patterns. We extend this idea by introducing a minimal three-component mass-conserving reaction–diffusion (3cMcRD) model. Using adiabatic elimination, we derive an effective active description for the total-mass dynamics, reminiscent of the well-known AMB+ theory. We validate the mapping through extensive numerical simulations. We find that the diffusive fluxes in the third component transport particles against gradients in the total mass and thus give rise to "anti-diffusive" behaviour in the effective active theory.
Only 3cMcRD systems and their associated effective active theory produce finite-wavelength patterns such as dots, stripes, and foam-like structures, in contrast to the coarsening dynamics of 2cMcRD models. Patterns with finite wavelengths are especially interesting, as they are realized in some biological systems, including the Min system (2). Employing a local quasi-steady-state approximation, we further determine the analytical thresholds separating distinct pattern-forming regimes. In particular, we analyze how a fingering instability emerges from an initially flat interface, marking the transition to foam-like patterns.
Our approach sheds light on the connection between reaction–diffusion and active systems. Moreover, as our analytical framework naturally generalizes to systems with more than three components, 3cMcRD serve as a minimal models for understanding certain pattern transitions in the Min system.

(1) Weyer, Brauns & Frey (2023). Phys. Rev. E 108, 064202.
(2) Glock et al., ACS SynBio 2018

*Speaker
†Corresponding author: frey@lmu.de

Control of contractile active materials using optically-induced force generation

Sasha Toole * [1], Guillaume Duclos† [1]

[1] Brandeis University – Brandeis University 415 South St. Waltham, MA 02453, United States

Biological systems exploit spatiotemporal control over force-generating molecular motors to orchestrate complex collective behaviors. Coordination of these cytoskeletal flows allows for vital cellular behaviors such as locomotion and replication. Contractile microtubule networks have been shown to form tunable asters under columns of light by engineering kinesin motors with optically-induced clustering. However, the ability to program active patterns into these contractile microtubule flows using feedback has not yet been explored. We plan to exploit an activation-inhibition relationship between projected light patterns and microtubule dynamics to externally control the spatial arrangement of microtubule bundles over time. Our aim is to develop a library of light projection programs that generate a variety of simple active microtubule patterns, which can be combined to create more complex patterns. These results will bring us closer to recreating the ability of cellular systems to exert spatiotemporal control over their bulk cytoskeletal flows

*Speaker
†Corresponding author: gduclos@brandeis.edu

Non-Equilibrium Catalysis-Driven Phase Separation in Metabolic Pathways

Varsha Traynor * [1]

[1] Department of Physics and Astronomy [UCL London] – Gower Street, London WC1E 6BT, UK, United Kingdom

Cells are fundamentally non-equilibrium, continuously consuming energy and matter to sustain the metabolic production of essential biomolecular components. Many metabolic processes are facilitated by *metabolons*, dynamic assemblies of enzymes that catalyse sequential reactions within metabolic pathways. These complexes can form in response to changing cellular demands and can channel substrates between enzymatic steps to regulate production rates. Although metabolons depend intrinsically on non-equilibrium activity, most theoretical descriptions until recently have relied on equilibrium Liquid–Liquid Phase Separation to account for their formation. Our work builds on Catalysis-Induced Phase Separation (CIPS), the first model in which phase separation arises solely from non-equilibrium catalytic activity. We extend single-enzyme CIPS to multi-enzyme metabolic network models within a thermodynamically consistent framework. The dynamics of clustering are explored using linear stability analysis to construct phase diagrams and spinodal boundaries, revealing regimes of distinct phase separation behaviours and their dependence on system parameters. Future work will use PDE simulations to study how channelling and production rates modify metabolic fluxes. Overall, this framework provides a foundation for understanding the relationship between metabolon function and form mediated by intrinsic autoregulation, and more generally contributes to a theoretical understanding of structure-function relationships in chemically-active mixtures.

*Speaker

Hydraulics, Flux and Microlumina in Active Multicellular Systems

Jack Treado *† [1,2]

[1] Max Planck Institute for the Physics of Complex Systems – Noethnitzer Str. 38, 01187 Dresden, Germany
[2] Technische Universität Dresden = Dresden University of Technology – TU Dresden 01062 Dresden, Germany

Multicellular systems contain rich physical phenomena due to cell deformability, activity, and interactions. However, many tissues, like wounded epithelia, developing blastocysts, and elongating embryos contain measurable quantities of interstitial fluid. The influence of interstitial fluid on tissue structure and dynamics has not been well characterized, as fluid transport and fluid-cell interactions pose experimental and theoretical challenges. In this work, we present a computational model of multicellular systems that contains both deformable cells and interstitial fluid transport. We consider densely-packed cells with permeable membranes that regulate volume through the balance of hydrostatic and osmotic pressure. We first demonstrate the physical effects of interstitial fluid flow in simulated tissues exposed to osmotic stress and external flow. We next investigate how tissue hydraulics respond to active noise. We find that, in the limit of low permeability, active noise is significantly less effective in fluidizing simulated tissues. These solid-like and impermeable states are shown to exhibit a curious structural feature: microlumina, or small pockets of extracellular fluid that grow from cellular interfaces. We show that this "microluminal" phase emerges due to an effective hydraulic ratchet that pumps fluid out of cells and into the interstitial space. We propose that the origin of this ratchet is the asymmetrical response of cell interfaces to changes in interfacial tension. Our work thus presents a novel perspective on the multifarious impacts of hydraulic forces in multicellular systems, and reveals both a possible origin for and the physical consequences of luminogenesis.

*Speaker
†Corresponding author: treado@pks.mpg.de

Collective motion and ordering of polydisperse microswimmers

Jakub Trzaska * [1], Timofey Kozhukhov [1], Michela Rocchetti [1], Kristian Thijssen [1]

[1] Niels Bohr Institute [Copenhagen] – Blegdamsvej 17, DK-2100 Copenhagen, Denmark

Microswimmers are found in a variety of natural environments, from soil and seawater to the human body. Through interactions with the surrounding fluid and with one another, they exhibit collective behaviour and organisation, including nematic orientational ordering observed in controlled experiments. In *in vitro* environments, however, heterogeneity in bacterial populations is expected, yet the role of size polydispersity has often been overlooked. In this work, we computationally investigate the effects of polydispersity in suspensions of self-propelled microswimmers. Using a Multi-Particle Collision Dynamics (MPCD) simulation framework, we analyse nematic ordering and flow characteristics for systems with varying packing fractions and swimmer length distributions. We compare the results obtained for different simulation parameters, to determine how polydispersity affects the dynamics of the system. We draw parallels between our results and experimental observations of swimming bacteria.

*Speaker

Nonreciprocal collective dynamics in a mixture of phoretic Janus colloids

Gennaro Tucci * [1]

[1] MPIDS – Germany

A multicomponent mixture of Janus colloids with distinct catalytic coats and phoretic mobilities is a promising theoretical system to explore the collective behavior arising from nonreciprocal interactions. An active colloid produces (or consumes) chemicals, self-propels, drifts along chemical gradients, and rotates its intrinsic polarity to align with a gradient. As a result, the connection from microscopics to continuum theories through coarse-graining couples densities and polarization fields in unique ways. Focusing on a binary mixture, we show that these couplings render the unpatterned reference state unstable to small perturbations through a variety of instabilities, including oscillatory ones that arise on crossing an exceptional point or through a Hopf bifurcation. To achieve rapid relaxation of the polar fields, they can be eliminated in favor of the density fields, yielding a microscopic realization of the Nonreciprocal Cahn–Hilliard model for two conserved species with two distinct sources of nonreciprocity, one in the interaction coefficient and the other in the interfacial tension. Our work establishes Janus colloids as a versatile model for a bottom-up approach to both scalar and polar active mixtures.

*Speaker

Morphogenesis across scales: the role of single-cell mechanics in regulating tissue fluidity during gastruloid development

Marta Urbanska *† [1], Wiktoria Brdej [1], Tianyin Hu [1], Ewa Paluch [1]

[1] University of Cambridge [Cambridge, UK] – The Old Schools, Trinity Lane, Cambridge CB2 1TN, United Kingdom

During early embryonic development, pluripotent cells differentiate, change shape, and rearrange spatially to form the blueprint of the adult body. While the molecular pathways controlling developmental morphogenesis have been studied extensively, the role of physical properties of cells and tissues in this inherently mechanical process has only recently been brought into focus. Gastruloids-three-dimensional aggregates of mouse embryonic stem cells-have emerged as a robust model system that recapitulates key features of early post-implantation development in mammals, including anterior-posterior patterning and body axis elongation. To address the mechanisms underlying gastruloid elongation, we examine the role of cell surface mechanics in this process. We show that gastruloid elongation is inhibited by maintaining high cellular plasma membrane tension through expression of constitutively active ezrin (ezrinCA), an actin-membrane linker protein. Interestingly, ezrinCA expression does not interfere with mesodermal lineage commitment, indicating that the morphogenetic defect is not the result of arrested developmental progression. Instead, ezrinCA-expressing gastruloids display impaired fusion dynamics in spheroid fusion assays, pointing to decreased tissue fluidity as a driver of the observed morphogenetic defect. Our work sheds light on the interplay between cell surface mechanics and morphogenetic movements in developing gastruloids, and more broadly on how mechanical properties of single cells regulate tissue fluidity.

*Speaker
†Corresponding author: mu272@cam.ac.uk

Learning stochastic models from partially observed time series

Joao Pedro Valeriano Miranda *† [1], Pierre Ronceray [2]

[1] Aix-Marseille Université – Aix Marseille Université – France
[2] Aix-Marseille Université – Aix Marseille Université – France

Studying the dynamics of biological systems often requires dealing with incomplete data: we can experimentally keep track of only a limited number of variables, while many others might go unobserved. To answer this challenge, we need inference methods that explicitly consider that we have an incomplete dataset that captures only a subset of the degrees of freedom in a system. The ability to infer models with hidden variables could significantly change how we look at data and would be a valuable contribution to the statistical tools used for studying complex systems. Here, I will present methods that provide parameter estimates while simultaneously reconstructing the trajectories of unobserved variables. I will present applications of such methods to simple systems such as small ecological communities, possibly with only relative abundance measurements. Going further, we also show how these methods can be easily extended to handle low sampling frequency during data collection. Our methods allow for a depth of analysis that otherwise would not be achievable by following an alternative inference route that ignores the presence of hidden variables. We hope these tools will be relevant to researchers working on data-driven investigations of dynamical systems.

*Speaker
†Corresponding author: joao-pedro.valeriano-miranda@univ-amu.fr

From molecular interactions to emergent properties: quantifying the dynamics of multispecies biofilms

Simon Van Vliet * [1]

[1] Biozentrum, University of Basel – Spitalstrasse 41, 4056 Basel, Switzerland

Microbes play a significant role in human and planetary health. Many of these microbes live in dense, spatially structured communities known as biofilms, where cells interact closely by exchanging diffusible molecules. To understand and manipulate the functions of these microbiomes, it is essential to uncover how community-level properties-such as composition, spatial arrangement, and growth rate-emerge from these molecular interactions. Here, I demonstrate how combining single-cell microscopy with mathematical modeling can provide quantitative insights into how these community properties develop from the underlying mechanisms of cell-cell interactions. This framework enables us to scale from molecular to community-level dynamics, laying the groundwork for a quantitative understanding of microbiome function.

*Speaker

When interactions change: Resolving temporal dynamics of bacterial interactions across metabolic conditions

Anna Weiss *† [1,2], Megan Lee [1,2], Giovanni Ugolini [3], Lukas Von Ziegler , Roman Stocker [3], Olga Schubert [1,2], Martin Ackermann [1,2,4]

[1] Swiss Federal Institute of Aquatic Science and Technology [Dübendorf] – Überlandstrasse 133Postfach 611CH-8600 Dübendorf, Switzerland
[2] Department of Environmental Systems Science [ETH Zürich] – Universitätstrasse 2, CH-8092 Zürich, Switzerland
[3] Department of Civil, Environmental and Geomatic Engineering [ETH Zürich] – Stefano-Franscini-Platz 5, Postfach 193, CH-8093 Zürich, Switzerland
[4] School of Architecture, Civil and Environmental Engineering [EPFL] – Switzerland

Within Earth's manifold microbiomes, microbial communities both shape and are shaped by their environment through the exchange of molecules. Individual bacterial cells interact via metabolites, signaling molecules, and other bioactive compounds that can impact growth. Through these interactions, microbes collectively modify their environment, altering nutrient availability, and local conditions. These environmental changes, in turn, can shift the nature of microbial interactions, creating a dynamic feedback between community activity and environmental state. Yet, we lack a mechanistic framework that links microbial growth, environmental modification, and the resulting shifts in interaction dynamics captured across diverse species and conditions. So far, most studies characterized interactions only from endpoint outcomes, overlooking how transient feedbacks accumulate over time.
To gain insights into these dynamic feedbacks, we implemented a high-throughput microdroplet platform that enables highly combinatorial and time-resolved phenotyping. This setup allows us to quantify how environmental modification and strain-specific interaction motifs feed back on interspecies outcomes across a panel of carbon sources and growth conditions. By tracking the dynamics of diverse bacterial co-cultures under differing metabolic conditions, we reveal how interactions change over time within and across environments.

We find that bacterial interactions are inherently dynamic, shifting between beneficial, competitive, and neutral over ecological timescales. These dynamic shifts follow distinct and quantifiable trajectories, exhibiting characteristic temporal patterns that differ across environmental contexts. Linking these data to a consumer–resource model uncovers systematic differences in the prevalence and temporal progression of interaction types on simple versus complex substrates.
Together, our findings highlight the importance of quantifying the temporal dynamics of interactions and disentangling how environmental modifications affect species relationships. Our work provides a foundation for the mechanistic dissection of interactions and a deeper understanding of how interaction dynamics in microbial communities scale up to community-level processes.

*Speaker
†Corresponding author: Anna.Weiss@eawag.ch

Maze-solving with density-driven swarms

Esther María Zamora SÁnchez * [1], Raphaël Candelier [1], Nicolas Bredeche [2], Sébastien Billès [1], Paul-Henry Glinel

[1] Laboratoire Jean Perrin – Sorbonne Universite, Centre National de la Recherche Scientifique, Institut de Biologie Paris Seine – 4, place Jussieu, Tour 32-33, Case Courrier 114 75252 Paris Cedex 05, France
[2] Institut des Systèmes Intelligents et de Robotique – Sorbonne Universite, Centre National de la Recherche Scientifique – Sorbonne-Université, Boite courrier 173 4 Place JUSSIEU 75252 Paris cedex 05, France

Many natural collective behaviors are 'smart,' meaning they allow a group to accomplish complex tasks that a single individual could not achieve (coordination, heavy load transport, long-range visibility, complex constructions, etc.). They currently find diverse applications, notably in swarm robotics or molecular programming, where many simple, inexpensive agents can be deployed to perform tasks that a single agent could not accomplish. This is the case, for example, when searching for a path or a target in a highly constrained environment.
We propose a new kind of collective motion where swarms of simple agents are able to find and fix the solution of two-dimensional mazes. The model consists of active, memoryless particles interacting exclusively via short-ranged perception of local density and orientations. This system generates traveling density waves when constrained in one dimension, and self-organized swarms exploring local branches in two-dimensional mazes. Depending on a single kinetic parameter, the swarms can develop large tails and further gain long-term persistence, which ultimately allows them to robustly solve mazes of virtually any kind and size. By systematic exploration of the parameter space, we show that there exists a fast solving regime where the resolution time is linear in the number of squares, hence making it an efficient maze-solving algorithm.
Our model represents a new class of active systems with unprecedented contrast between the minimality of the processed information and the complexity of the resolved task: this is, to our knowledge, the first time that such intelligent collective behavior has been observed with agents without memory or environmental markers ('stigmergy,' e.g., with pheromones), and with access only to local density information. This is of prime importance for the interpretation and modeling of collective intelligence in living systems as well as for the design of future swarms of active particles and robots.

*Speaker

How to escape the Red Queen? Towards nonlocal mutations in travelling wave descriptions of immune-viral coevolution

Max Zayas Orihuela * [1], Thierry Mora [1], Aleksandra M. Walczak [1]

[1] Laboratoire de physique de l'ENS - ENS Paris – Sorbonne Universite, Centre National de la Recherche Scientifique, Université Paris Cité, Département de Physique de l'ENS-PSL – 24, rue Lhomond75005 Paris, France

Viruses that infect a population and the hosts' adaptive immune response evolve together, as immunity chases viral mutations. The resulting coupled dynamics have been studied either in the infinite-dimensional gene space, with all mutations having the same effect, or in a low-dimensional antigenic space, assuming mutations to have a diffusive effect. In both cases, the virus-immune interaction gives rise to travelling evolutionary waves with constant speed. However, the recent pandemic has shown that viral evolution displays adaptive jumps, which cannot be recreated with current models. We hypothesise that these jumps are a result of rare mutations with large effects on viral fitness, and work in the antigenic space description, allowing for jumps that break the diffusive behaviour of the wave. We investigate different strategies that give rise to these adaptive sweeps through a combination of stochastic simulations and analytical tools, focusing on rare, long jumps that occur over a diffusive mutational background.

*Speaker

Università di Corsica Pasquale Paoli | Institut d'Études Scientifiques de Cargèse | Université Côte d'Azur | cnrs

Mardi
21 Avril
à 18h30

IL Y A DES TROUPEAUX DANS LE LABO !
Physique de la matière active

présentée par

Alexandre MORIN
Maître de conférence à l'Institut de physique
de l'Université de Leyde - Pays Bas

Des nuées d'oiseaux, aux bancs de poissons, aux colonies bactériennes, l'auto-organisation de grands groupes d'individus mobiles fascine.
Mais existe-t-il des points communs entre ces systèmes apparemment si différents ? C'est la question à laquelle tentent de répondre les physiciens qui étudient l'émergence de mouvements collectifs dans ces systèmes singuliers qu'ils nomment «matière active».
Nous verrons quelques exemples de matière active, de la morphogenèse cellulaire aux mouvements de foules humaines. Les difficultés inhérentes à l'étude de systèmes vivants nous mènerons à dresser un cahier des charges pour un système expérimental idéal adapté à l'étude des mouvements collectifs en laboratoire. Nous présenterons une telle expérience qui permet la formation sous un microscope de troupeaux pour le moins insolites : issus de l'auto-organisation de millions de micro-sphères synthétiques.