From Soft Matter to Biophysics 2025

French-German WE-Heraeus-Seminar

16 – 21 February 2025

at the École de Physique des Houches, France

WILHELM UND ELSE HERAEUS-STIFTUNG

Introduction

The Wilhelm und Else Heraeus-Stiftung is a private foundation that supports research and education in science with an emphasis on physics. It is recognized as Germany's most important private institution funding physics. Some of the activities of the foundation are carried out in close cooperation with the German Physical Society (Deutsche Physikalische Gesellschaft). For detailed information see https://www.we-heraeus-stiftung.de

Aims and scope of this French-German WE-Heraeus-Seminar:

Soft matter physics has historically contributed significantly to the emergence of the field of biological physics. But today, the two fields do not often have the opportunity to meet. This workshop therefore aims to bring the two communities together to discuss their latest advances and promote increased porosity in their respective methods and interests. The workshop will focus in particular on the hot topics of synthetic biology engineering and functional active materials.

Scientific Organizers:

Prof. Dr. Karen Alim	Technical University of Munich, Germany
Prof. Dr. Karin Jacobs	Saarland University, Germany
Prof. Dr. Martin Lenz	Université Paris-Saclay, France
Dr. Hervé Turlier	CNRS UMR7241 - Collège de France

Administrative Organization:

Dr. Stefan Jorda
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Venue:

Ecole de physique des Houches
149 Chemin de La Côte
74310 Les Houches, France

Program

Program

Sunday, 16 February 2025

from 15 :00	Registration	

Monday, 17 February 2025

07:45	*BREAKFAST*	
08:30 – 08:45	Organizers	**Opening Remarks**
08:45 – 09:00	Stefan Jorda	**About the Wilhelm and Else Heraeus Foundation**
09:00 – 09:40	Friedrich Simmel	**DNA origami super-assemblies**
09:40 – 10:20	Isabelle Eisenmann	**Drops, branches, pearls and waves in phototactic micro-algae**
10:20 – 11:00	*COFFEE BREAK*	
11:00 – 11:40	Franziska Lautenschläger	**The Cystoskeleton of Circulating Tumor Cells**
11:40 – 12:20	Heiko Rieger	**Centrosome positioning in cell migration and immune response**
12:30 – 14:00	*LUNCH*	
14:00 – 17:20	**Time for discussion – free afternoon**	
17:20 – 18:00	Paul Robin	**The coordinative role of cellular packing and osmosis in robustness of intestinal morphogenesis**
18:00 – 19:00	**Flash Talks (posters)**	
19:00 – 20:30	*WELCOME DRINKS and DINNER*	

Program

Tuesday, 18 February 2025

07:45	*BREAKFAST*	
09:00 – 09:40	Massimo Vergassola	**Cytoplasmic Mechanics during the Fly Embryonic Development**
09:40 – 10:20	Sebastian Fürthauer	**Synchronization driven flows in bulk and on surfaces**
10:20 – 11:00	*COFFEE BREAK*	
11:00 – 11:40	Sarah Köster	**High strains in biology: from single filaments to networks and cells**
11:40 – 12:20	Madan Rao	**Activating Epithelia**
12:30 – 14:00	*LUNCH*	
14:00 – 17:20	**Time for discussion – free afternoon**	
17:20 – 19:30	**Poster Session**	
19:30 – 20:30	*DINNER and free evening*	

Program

Wednesday, 19 February 2025

07:45	*BREAKFAST*	
09:00 – 09:40	Gasper Tkacik	**Crosstalk constraints on gene regulatory networks**
09:40 – 10:20	Iliya Stoev	**Microrheology of sequence-programmable and mechanically tunable DNA hydrogels**
10:20 – 11:00	*COFFEE BREAK*	
11:00 – 11:40	Chase Broedersz	**Learning the dynamics of collective cell migration**
11:40 – 12:20	Christina Kurzthaler	**Bacteria in motion: from run-and-tumble dynamics to surface interactions**
12:30 – 14:00	*LUNCH*	
14:00 – 17:20	**Time for discussion – free afternoon**	
17:20 – 18:00	Gaurau Gardi	**Perturbing Dynamics of Active Emulsions and Their Collectives**
18:00 – 18:40	Denis Bartolo	**Collective chiral oscillations in dense crowds**
18:40 – 19:20	Laura Heinen	**Synthetic Syntrophy between Metabolically Active Vesicles**
19:30 – 20:30	*DINNER and free evening*	

Program

Thursday, 20 February 2025

07:45	*BREAKFAST*	
09:00 – 09:40	Peter Sollich	**Intermittency, avalanches and aging in extremely persistent active matter**
09:40 – 10:20	Kim Lara Kreienkamp	**Symmetry breaking in active non-reciprocal systems**
10:20 – 11:00	*COFFEE BREAK*	
11:00 – 11:40	Andrea Liu	**Life with individually adjustable interactions**
11:40 – 12:20	Carl Goodrich	**The hidden architecture of self-assembly**
12:30 – 14:00	*LUNCH*	
14:00 – 17:20	**Time for discussion – free afternoon**	
17:20 – 18:00	Paul Baconnier	**Writing and erasing multiple mechanical memories**
18:00 – 18:40	Julien Tailleur	**Self-organization of motile active matter through mediated, random, and non-reciprocal interactions**
18:40 – 19:20	Andreas Ehrmann	**Controlled energy exchange in self-assembled nanomachines**
19:30 – 20:30	*DINNER and free evening*	

Program

Friday, 21 February 2025

07:45	*BREAKFAST*	
09:00 – 09:40	Virgile Viasnoff	**How do cells attach to one another?**
09:40 – 10:20	Yutin Irene Li	**Emergent dynamics of active elastic microbeams**
10:20 – 11:00	*COFFEE BREAK*	
11:00 – 11:40	Julien Heuvingh	**Wool-like Elasticity of Actin Filament Networks in Reconstituted Systems and Animal Cells**
11:40 – 12:20	Amelie Banc	**Soft matter approaches of a unique food protein network: gluten**
12:30 – 14:00	*LUNCH*	

End of the seminar and departure

Posters

Poster Session, Tuesday, 18 February, 17:20 h (CET)

Jan Albrecht	Likelihood-based inference for heterogeneous motile particle ensembles
Ricard Alert	Capillary interactions organize bacterial colonies
Carlos Arauz-Moreno	From Champagne to Glass: natural and artificial nucleation
Thorsten Auth	Adhesion-driven wrapping and pore translocation of elastic particles
Romane Braun	Self-Organization of Interacting Micromotors: From Synchronization to Phase Coherence
Claire Dessalles	Topological defects organize morphogenesis on closed curved surfaces
Alberto Dinelli	Quorum sensing and absorbing phase transitions in colloidal active matter
Anna Ermakova	Quantum sensing for soft matter study
Thomas Fai	Nuclear size control by osmotic forces in S. pombe
Isabelle Feller	Biohybrid microswimmer fabrication with controllable geometry using capillary-assisted endospore deposition
Nicola Galvanetto	Mesoscale properties of biomolecular condensates emerge from nanoscale dynamics
Juan Manuel Garcia Arcos	Actin dynamics sustains spatial gradients of membrane tension in adherent cells

Poster Session, Tuesday, 18 February, 17:20 h (CET)

Birte Christine Geerds	Twists, turns and surprising shapes: How a 2D liquid crystal influences geometry
Doron Grossman	Geometry and Mechanics of Living Materials
Lauritz Hahn	Streams of Janus Particle Dimers
Arsenii Hordeichyk	Reconstituted nascent adhesion condensates enable actin polymerisation on supported lipid bilayers.
Karin Jacobs	Are bacteria patchy colloids? Force spectroscopy on soft and biological matter
Manisha Jhajhria	Activity induced non-monotonic aggregation in a mixture of chemically active and passive particles
Camille Jorge	Active hydraulics
Leonie Karr	Quantifying flow induced remodeling on self organized vascular networks on a chip
Mukund Krishna Kothari	Bio-inspired self assembling active matter
Martin Lenz	Topological defect engineering enables size control in self-assembly
Romain Leroux	Microtubule-based active matter droplets: patterns of an extensile filament
Mathieu Le Verge-Serandour	Dynamical Network Remodeling of Slime Mold
Noemie Livne	Geometric theory of mechanical screening in 2D granular materials

Poster Session, Tuesday, 18 February, 17:20 h (CET)

Martin Maliet	Bacterial glass transition in Pseudomonas aeruginosa
Jakob Metson	Designing complex behaviours using transition-based allosteric self-assembly
Maitane Muñoz-Basagoiti	Shape through gradients: Deformations of chemically active membranes
Pietro Luigi Muzzeddu	Migration and separation of polymers in nonuniform active baths
Airi Nakamoto Kato	Active particle confined in a quasi-two-dimensional droplet
Vincent Ouazan-Reboul	Self-limiting self-assembly of particles with complex interactions
Alessandro Pasqui	VertAX: a novel framework for 2D vertex model inference through bilevel optimisation
Oliver Paulin	Active viscoelastic condensates provide controllable mechanical anchor points
Marc-Eric Perrin	Robust tree structure from stochastic branching processes: model and parameter inference from data.
Tuan Pham	Dynamical Theory for Adaptive Systems
Jared Popowski	From Brittle Fracture to Sticky Fluids: How Plant Trichomes Exploit Soft Matter Physics Against Insects
Sepideh Razavi	Probing the interfacial behavior of mucin solutions as model biofluidic drops

Poster Session, Tuesday, 18 February, 17:20 h (CET)

Pablo Saez	Electro-mechanical interactions in cellular systems
Noah Toyonaga	Hasamigami: The Art and Science of Scissored Surfaces
Michael Wang	Geometric frustration meets mechanical metamaterials: large-scale stress accumulation and enhanced size-selective assembly

Abstracts of Lectures

(in alphabetical order)

Writing and erasing multiple mechanical memories

P. Baconnier[1] and M. van Hecke[1,2]

[1]AMOLF, 1098 XG Amsterdam, The Netherlands.

[2]Huygens-Kamerlingh Onnes Laboratory, Leiden University, 2300 RA Leiden, The Netherlands.

We create building blocks for resettable metamaterials by embedding nitinol wires within silicone rubber springs (Fig. 1-a). Memory is encoded in the building block via plastic deformations of the wires, but can be erased, or reset, by heating the nitinol wire above the activation temperature through external electrical currents, triggering the shape memory effect. The ”nitinol springs” encode a memory of the largest drive amplitude, which can be selectively erased, providing ideal building blocks for meta-materials with on-demand, resettable memory content. Combining two nitinol springs into simple geometries and harnessing drive/reset protocols, we examine the effect of partial reset on the overall memory encoded in the system. For two nitinol springs in parallel (Fig. 1-b), we leverage partial reset to spatially distribute the memory of past drive, and show that the system can encode multiple memories. For serially-coupled nitinol springs (Fig. 1-c), we show that the memory of past drive is surprisingly robust to partial reset. Our findings pave the way for the development of resettable materials, where multi-dimensional inputs can be used to train and reprogram materials for diverse functionalities.

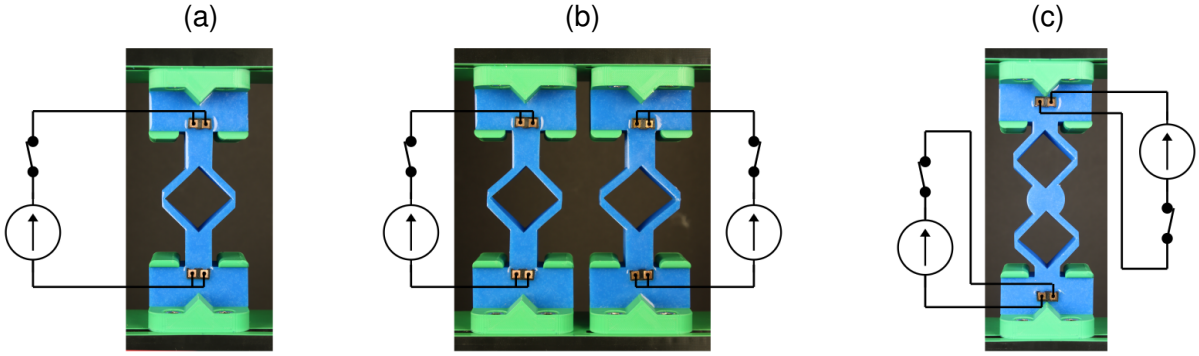


Figure 1: **Nitinol springs in different geometries.** (a) Single nitinol spring. (b) Two nitinol springs in parallel. (c) Two nitinol springs in series. The system is controlled in position, and we measure the force exerted on the system. The currents flowing through the circuits are controlled externally using switches.

Soft matter approaches of a unique food protein network: gluten

A. Louhichi[1], J-G. Pichon[1], L. Ramos[1], M-H. Morel[2] and A. Banc[1]

[1] Laboratoire Charles Coulomb, Université de Montpellier, France
[2] Laboratoire IATE, INRAE, Montpellier, France

Gluten is a complex protein network crucial for the breadmaking quality, and widely used in the food industry as a texturing agent. It forms a natural transient network including physical bonds (hydrogen bonds) and dynamic covalent bonds (disulfide bonds). To better understand the supramolecular structure of gluten and its link to its unique mechanical properties, we develop and characterize model gluten using a combination of rheology, biochemistry and scattering techniques.

We formulate model gluten samples with controlled protein compositions using a novel extraction protocol based on a liquid-liquid phase separation [1]. We show that gluten protein dispersions can be regarded as polymeric near critical gels [2] characterized by rheological parameters, elastic plateau, and characteristic relaxation time, which are related to one another, as a consequence of self-similarity, and span several orders of magnitude when changing the parameters such as protein concentration, ageing time [3] and solvent quality [4]. For its part, the protein composition controls both the distance to the gel point [5] and the critical exponent of the critical state.

To better understand the behaviour of gluten under large deformation we study samples stabilized at different distances from the gel point using cycles of start-up shear followed by stress relaxation after flow cessation. A double stress overshoot is observed during the first start-up shear of samples sufficiently close to the gel point, whereas a single stress overshoot is measured during the next cycles of start-up shear. Interestingly, the double overshoot can reappear after a long rest period, demonstrating the self-healing properties of the samples. In the single overshoot regime, we show that near-critical pre-gels exhibit self-similarities, and the parameters describing the characteristic linear features can be used to build master curves for the relevant parameters of the non-linear rheological responses. The scaling laws found in our work show intriguing similarities with those predicted and measured for systems close to the jamming and the glass transition, evidencing universalities in the mesoscopic dynamics involved in large strain experiments of arrested soft materials close to the glass transition or to the critical gel point [6].

References

[1] MH. Morel, J. Pincemaille, L. Lecacheux, P. Menut, L. Ramos, A. Banc *Food Hydrocolloids* 123 **2022** 107142.
[2] L. Ramos, A. Banc, A. Louhichi, J. Pincemaille, J. Jestin, Z. Fu, M. Appavou, P. Menut, MH. Morel. *J Physics: Condensed Matter***, 2021** 33, 144001.
[3] M. Dahesh, A. Banc, A. Duri, MH. Morel, L.Ramos *Food Hydrocolloids* **2016** *52*, 1.
[4] S.Costanzo, A. Banc, A. Louhichi, E.Chauveau, Wu, MH. Morel, l.Ramos*. Macromolecules* **2020** 53, 9470.
[5] A. Louhichi, MH. Morel, L. Ramos, A. Banc, *Phys. Fluids* **2022,** 34, 051906.
[6] A. Louhichi, MH. Morel, L. Ramos, A. Banc, *ACS MacroLetter* **2024** *13, 7, 826–831.*

Emergence of collective chiral oscillations in dense crowds
F. Gu, B. Guiselin, N. Bain, I. Zurigel and D. Bartolo

Building upon a combination of quantitative observations and theoretical insights, I will illustrate and elucidate the emergence of collective oscillations within densely packed pedestrian crowds. Our understanding of massive crowds has long been limited by the lack of quantitative measurements. I will demonstrate that the San Fermin Festival in the city of Pamplona, Spain, provides an opportunity to circumvent this limitation. For decades, every year, at the same day and exact hour, thousands of individuals gather in the same square to await the festival's opening within a secure environment, where crowd density can, nevertheless, exceed five people per square meter. Our data reveal that beyond a critical density, crowds of pedestrians waiting for the festival's opening undergo a dynamic transition from a quiesent to a dynamic state, in which the entire crowd oscillates with a period of approximately fifteen seconds. This emergent dynamics echoes the correlated motion of groups of hundreds of individuals along chiral trajectories. I will then explain how our observations constrain the description of dense crowds as active matter and show that dense crowds are odd frictional solids.

Learning the interactions and dynamics of collective cell migration

Chase Broedersz

Department of Physics and Astronomy, Vrije Universiteit Amsterdam, De Boelelaan 1105, 1081 HV Amsterdam, The Netherlands

Single and collective cell migration are fundamental processes critical for physiological phenomena ranging from embryonic development and immune response to wound healing and cancer metastasis. Yet, the underlying dynamics of how cells move and interact with each other, and their environment is still unclear. We employ a data-driven approach to infer the dynamics of cell movement, morphology and interactions of cells confined in artificial environments. By inferring a stochastic equation of motion directly from experimental data, we show that cells exhibit intricate non-linear deterministic dynamics that adapt to the geometry of confinement. We extend this approach to interacting systems, by tracking the repeated collisions of confined pairs and clusters of cells. This approach allows us to develop a phenomenological theory based on a large number of candidate contact-interaction mechanisms coupling cell position, protrusion, and polarity. Using high-throughput micropattern experiments, we detect which of these phenomenological contact-interactions captures the interaction behaviors of cells for a broad range of cell types. Finally, I will discuss how our approach can be used to identify the interction rules underlying the collective dynamics of large multicellular systems in 2D.

Controlled energy exchange in self-assembled nanomachines

A. Ehrmann[1] and C. P. Goodrich[1]

[1]Institute of Science and Technology Austria, 3400 Klosterneuburg, Austria

A hallmark of life is the precise control of energy dissipation - energetically charged molecules such as ATP efficiently deliver packets of energy where and when they are needed, powering a wide range of processes. For example, motor proteins like Myosin and Kinesin convert the chemical energy of ATP into mechanical work to generate forces and perform tasks such as muscle contraction and cargo transport. The past decades have seen increasingly rapid advances in the field of self-assembly, which offers a promising route towards biologically-inspired nanomachines, and enables the design of building blocks to assemble complex structures. However, very little is currently known about embedding these structures by functional behaviors. The ability to exchange and consume energy in a controlled manner is arguably an enabling mechanism for all kinds of nanomachines. In this talk, I will present a robust and transferable mechanism for how self-assembled nanomachines can exchange energy, roughly analogous to ATP hydrolysis, without any reliance on biochemistry. Instead, we consider two two-state structures modeled as dimers with binding sites at their ends. By manipulating energy profiles and interactions, we show how they can be coupled to reveal a hidden relaxation pathway that results in energy transfer from one to the other. The Source structure starts in a charged, high-energy state, whereas the Machine structure starts in an uncharged, low-energy state. The relaxation mechanism lowers the total free energy, has minimal free-energy barriers, and results in both structures switching their states. Therefore, the energy initially stored in the Source is partially transferred to the Machine, which can then use this energy to perform work. Furthermore, with a bath of charged Source structures, a single Machine can be systematically and repeatedly driven out of equilibrium to perform tasks. We use developed intuition and differentiable programming to find universal design principles and validate our theoretical predictions by molecular dynamics simulations. We show that performance, power, and occupation enhancement of the target state using the relaxation pathway outperforms the Machine alone. Our results present a baseline for nanomachine-design across a variety of experimental platforms.

References

[1] A. Ehrmann, C. P. Goodrich, in prep (2025)

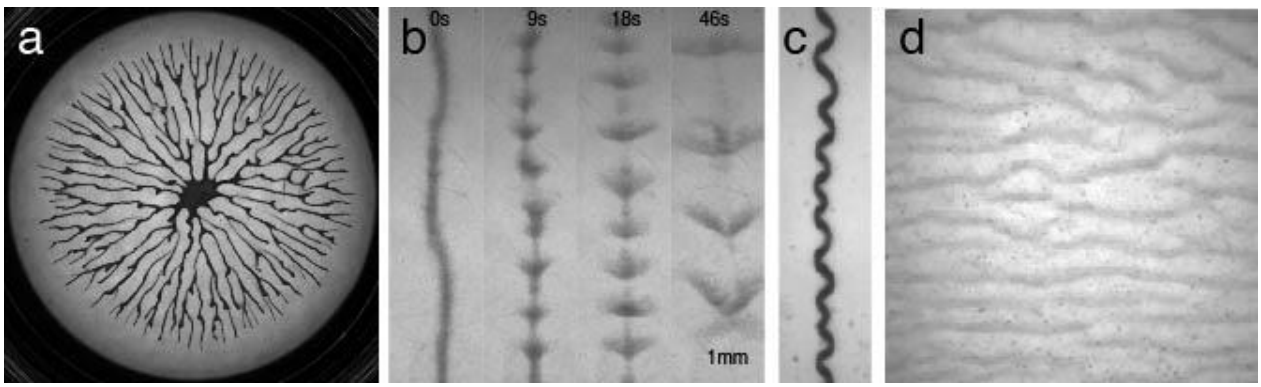
Drops, branches, pearls and waves in phototactic micro-algae

I.Eisenmann[1], M.Vona[2], A.Lhomme[3], A.Lahlou[4], S.Bujaldon[5], T.Le Saux[3], B.Bailleul[5], T.Ishikawa[6], N.Desprat[3], E.Lauga[2], R.Jeanneret[3]

[1]IOP, Amsterdam, The Netherlands, [2]DAMTP, Cambridge, UK, [3]LPENS, Paris, France, [4]PASTEUR, Paris, France, [5]IBPC, Paris, France, [6]DBE, Sendai, Japan

Motile micro-algae modify their environment by absorbing light, consuming and releasing chemical compounds and generating flows. Flows, light and chemicals in turn influence their motion. These complex interactions can drive the formation of patterns at macroscopic scales. In this talk I will explain how phototaxis can be harnessed to induce collective behaviors of these different nature in suspensions of *C.reinhardtii*. In each case I will aim to make a clear connection between the macroscopic observations and what happens at the micro-scale, and highlight the biological relevance of the phenomenon.

First, I will show how suspensions of photophobic cells can be unstable to density fluctuations, as a consequence of shading interactions mediated by light absorption. In a circular illumination geometry this mechanism leads to the complete phase separation of the system into transient branching patterns, providing the first experimental evidence of finite wavelength selection in an active phase-separating system without proliferation. I will then show how phototaxis can be harnessed to steer millions of swimming cells and realize hydrodynamic instabilities that had been predicted but never observed experimentally: the spontaneously breaking of a dense active jet into droplets, or its buckling into a zigzag structure, depending on the cells preferential orientation. These results are generic at low Reynolds number as shown by the extensive literature on band formation and destabilization in driven colloids. Our model, based on the symmetry of the flows, thus also encompasses this broad class of systems, and paves the way toward their fine experimental control.



Branching pattern (**a**), pearling (**b**) and buckling (**c**) instabilities, and travelling bands of density (**d**) in suspensions of *C.reinhardtii* driven by light

References

[1]: T.Ishikawa et al, Phys. Rev. Fluids **7**, 093102 (2022)
[2]: G.Junot et al, Phys. Rev. Lett. **131**, 068301 (2023)

Synchronization driven flows in bulk and on surfaces

Sebastian Fürthauer, Institute of Applied Physics, TU Wien, Wien, Austria

Abstract:
Many active biological particles, such as swimming microorganisms or motor-proteins, do work on their environment by going though a periodic sequence of shapes. Interactions between particles can lead to the phase-synchronization of their duty cycles. We consider collective dynamics in a suspension of such active particles coupled through hydrodynamics. We demonstrate that the emergent non-equilibrium states feature stationary patterned flows and robust unidirectional pumping states under confinement. Moreover the phase-synchronized state of the suspension exhibits spatially robust chimera patterns in which synchronized and phase-isotropic regions coexist within the same system. These findings demonstrate a new route to pattern formation and could guide the design of new active materials. An extension of the same theory for treating ciliated surfaces quantitatively captures the instabilities and flow pumping behaviour of ciliated carpets and metachronal waves.

#Abstract

Perturbing Dynamics of Active Emulsions and Their Collectives

M.T.A. Khan[1]*, **G. Gardi**[1]*, R. H. Soon[1], M. Zhang[1], M. Sitti[1,2]

1 Physical Intelligence Department, Max Planck Institute for Intelligent Systems, 70569 Stuttgart, Germany.

2 School of Medicine and College of Engineering, Koç University, 34450 Istanbul, Turkey.

Controlling fluidic flows in active droplets is crucial in developing intelligent models to understand and mimic single-celled microorganisms. Typically, these fluidic flows are affected by the interfacial dynamics of chemical agents. We found that these flows can be reconfigured by the mere presence of anisotropic solid boundary embedded within active droplets. Spontaneous fluidic flows dynamically orient an embedded magnetic cluster and the magnetic cluster, when realigned, causes these flows to reorient. Thus, providing an unprecedented control over the propulsion dynamics of chemotactic emulsions. When continuously perturbed, achiral emulsions exhibit emergent chiral motion with rotating fluidic flows. Such solid-fluid interactions removes barriers of specific emulsion chemistries and complements their inherent abilities thereby also enabling control over emergent collective behaviors of active droplets.

References

[1] M.T.A. Khan, et al., arXiv preprint arXiv:2405.05889 (2024).

The hidden architecture of self-assembly

Carl Goodrich

Institute of Science and Technology Austria (ISTA), Klosterneuburg, Austria

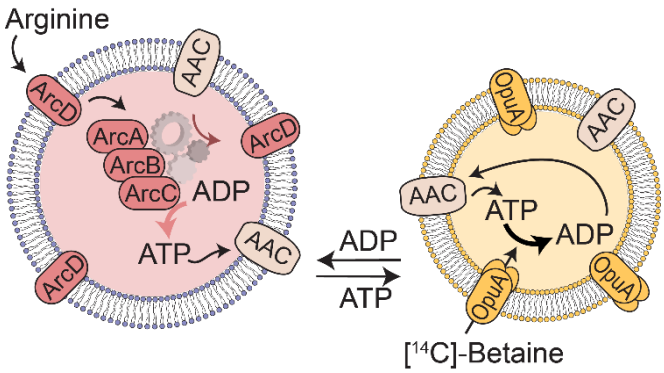
Experiments have reached a monumental capacity for designing, synthesizing, and controlling microscopic particles for self-assembly. However, our ability to take full-advantage of this vast design space to assemble nanomaterials with complex structure and function is hindered by the lack of inverse-design frameworks that connect the particle-level design attributes to the system-level assembly outcomes, like the yield of a user-specified target structure. I will show that equilibrium self-assembly is governed by an underlying mathematical architecture that robustly predicts which structures can be assembled at high yield, as well as how tuning the design-space parameters dictates the relative yields of competing structures. This framework leads to a series of quantitative predictions, such as the maximum possible yield that can be achieved for any target structure, which we verify through multifarious assembly experiments of nanoscale particles synthesized using DNA origami. Finally, I will discuss how this presents a practical and robust tool for the rational design of self-assembly, and speculate on its implications for biological systems.

Synthetic Syntrophy between Metabolically Active Vesicles

Laura Heinen[1]

[1]DWI – Leibniz-Institute for Interactive Materials, Aachen, Germany

Living systems depend on a continuous input of energy. The simplest form of life - a cell, for example, needs energy to grow, divide, process information and synthesize the basic building blocks. Intact biological cells usually absorb sugars or light, convert this energy, and store it in the form of adenosine triphosphate (ATP). However, certain pathogenic bacteria and organelles also rely on energy parasitism and cross-feeding from other organisms. This means that they take up energy from the environment to fuel their energy-demanding functions. We make use of this concept and developed synthetic vesicles that can shuttle ATP across their membrane by combining approaches from soft matter nanoscience and synthetic biology.[1] In my presentation I will demonstrate an example of ATP cross-feeding synthetic liposomes containing specific membrane proteins for this purpose.



One population of vesicles produces and exports ATP while a second population of vesicles takes up the ATP and uses this chemical energy to fuel ATP-consuming reactions. The hydrolyzed ATP feeds back into the first vesicle population where it will be recycled, and the interdependent metabolic cycle can start again. The vesicles represent a platform technology to fuel energy-dependent processes in a sustained fashion. By this we could demonstrate volume and energy homeostasis in synthetic vesicle systems. We foresee wide applications such as in synthetic cells, biological nanoreactors and life-like materials. Fundamentally, the vesicles allow us to study non-equilibrium processes in an energy-controlled environment and will promote our understanding of constructing life-like systems materials.

Reference:

(1) Heinen, L.*; van den Noort, M.; King, M. S.; Kunji, E. R. S.; Poolman, B.* Synthetic Syntrophy for Adenine Nucleotide Cross-Feeding between Metabolically Active Nanoreactors. *Nat. Nanotechnol.* **2024**. https://doi.org/10.1038/s41565-024-01811-1.

Wool-like Elasticity of Actin Filament Networks in Reconstituted Systems and Animal Cells

Julien Heuvingh

Physique et Mécanique des Milieux Hétérogènes, ESPCI, SU, UPC, Paris, France

Animal cells contain abundant actin filaments that form dynamic networks with specific localizations and biological functions. These networks generate most of the forces in animal cells through the nucleation and polymerization of new filaments or the movement of filaments driven by myosin motors. Similar to other biological fiber networks, actin networks exhibit strongly non-linear mechanical properties, such as stress-stiffening. These properties are typically attributed to the entropic stretching of filaments. However, this explanation falls short when applied to the weakly coordinated branched actin networks found at the leading edge of migrating cells.

Using experiments with controlled compression of reconstituted actin networks between cylindrical magnetic colloids, combined with theoretical modeling, we reveal that the elasticity of weakly coordinated actin networks is heavily influenced by reversible filament contacts. These interactions lead to a sharp increase in the network's apparent stiffness under applied stress, mimicking the mechanical behavior of sheep’s wool. Moreover, filament entanglements during network assembly can be adjusted to regulate the network’s final mechanical properties. Introducing a biologically relevant regulator of network dynamics demonstrated that these networks can sustain extensive deformations—compressing to a fraction of their original size—without experiencing significant structural failure.

The wool-like non-linear elasticity observed is not exclusive to the networks at the leading edge of migrating cells: We identified a similar behavior in the dense acto-myosin cortex beneath the membrane of animal cells. Mechanical properties of these networks were measured using magnetic colloids positioned on either side of the cell boundary. These networks displayed a combination of Hookean and wool-like behaviors, with the ability to transition between the two states. This behavior is highly dependent on myosin activity, as evidenced by experiments conducted across different cell lines, stages of the cell cycle, and optogenetic manipulations. These dynamic properties may be crucial for understanding how cells adapt their cytoskeleton to changing environmental conditions.

High strains in biology: from single filaments to networks and cells

Sarah Köster

When biological cells migrate or tissues develop, they experience high strains and stresses. The cytoskeleton, a composite biopolymer network composed of three filament systems - intermediate filaments, actin filaments and microtubules - ensures that the cell is not damaged as a result of these strong deformations. While actin filaments and microtubules break easily under stain, as do their networks, intermediate filaments such as vimentin and keratin have been shown to be remarkably energy dissipating and extensible, up to several times their original length. At the single filament level, this behavior can be precisely characterized by optical tweezer experiments and can be traced back to a very distinct hierarchical molecular architecture consisting of alpha-helical coils in a massively parallel arrangement. While these results suggest that intermediate filaments serve as "safety belts" and "shock absorbers" for the cell, it is not yet entirely clear whether the intriguing single filament behavior is relevant at the cellular level. Therefore, we complement our single filament measurements with active microrheology on filament networks and with cell stretching studies. Through this work we hope to elucidate the role of intermediate filaments within the composite cytoskeletal network and the complex environment of a biological cell.

Symmetry breaking in active non-reciprocal systems

Kim L. Kreienkamp[1] and Sabine H. L. Klapp[2]

[1]Institut für Theoretische Physik, Technische Universität Berlin, Berlin, Germany

Non-reciprocal couplings significantly impact the dynamical behavior in mixtures. A particularly striking consequence of such couplings is the spontaneous emergence of time-dependent phases that break parity-time symmetry [1-3]. Here, we study a paradigmatic model of a non-reciprocal polar active mixture with completely symmetric repulsion [3-6]. Using a combination of field theory and particle-based simulations, we identify two qualitatively distinct regimes of non-reciprocity-induced dynamics. In the regime of weak intra-species alignment, non-reciprocity leads to asymmetric clustering in which predominantly one of the two species forms clusters. Notably, the asymmetric density dynamics is driven alone by non-reciprocal orientational couplings [4,5]. In contrast, in the strongly coupled regime, the corresponding field theory exhibits exceptional points that have been associated with the emergence of chiral phases where the polarization direction rotates over time [2]. Our simulations confirm that spontaneous chirality arises at the particle level. In particular, we observe chimera-like states with coexisting locally synchronized and disordered regions and a peak of spontaneous chirality at coupling strengths associated with exceptional points [6]. Our results highlight the diverse effects of non-reciprocity across different scales.

References

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Bacteria in motion: from run-and-tumble dynamics to surface interactions

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Swimming microorganisms represent fascinating exemplars of non-equilibrium systems and their dynamics have been widely studied in the realm of fluid mechanics and statistical physics. Unraveling their motion in dilute and confined media is important for our understanding of both the molecular basis of their swim gait and their survival strategies in microbial habitats. In this talk, I will first show that by using renewal processes to analyze experimental measurements of wild-type *Escherichia Coli*, we can provide a quantitative spatiotemporal characterization of their run-and-tumble dynamics in bulk [1,2]. We further demonstrate quantitatively how the persistence length of an engineered strain can be controlled by a chemical inducer and characterize a transition from perpetual tumbling to smooth swimming.

Second, I will discuss the hydrodynamic interactions of microswimmers with a nearby deformable boundary. Employing a perturbation theory, valid for small deformations, and numerical simulations, we reveal that pusher-type microswimmers can both reorient away from the boundary, leading to overall hydroelastic scattering, or become trapped by the boundary. These findings demonstrate that the complex elastohydrodynamic coupling can generate behaviors that are fundamentally different to swimming near planar walls.

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The Cystoskeleton of Circulating Tumor Cells

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Living cells are typical soft matter objects with a clear biological functionality. Their mechanical properties are mainly determined by the cytoskeleton, of which actin and microtubules are prominent examples. We investigated how the interplay between the two is altered in circulating tumour cells (CTCs), which form so-called microtentacles: Microtubule-driven membrane protrusions that help CTCs attach to the vasculature of blood vessels, which is necessary for extravasation and metastasis formation. We have worked to understand the generation of these protrusions via cytoskeletal forces and cell mechanics. In my talk I will present experimental data as well as theoretical models to explain our understanding of microtentacle formation and its potential inhibition.

Emergent dynamics of active elastic microbeams

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In equilibrium, the physical properties of matter are set by the interactions between the constituents. In contrast, the energy input of the individual components controls the behavior of synthetic or living active matter. Great progress has been made in understanding the emergent phenomena in active fluids, though their inability to resist shear forces hinders their practical use. This motivates the exploration of active solids as shape-shifting materials, yet, we lack controlled synthetic systems to engineer active solids with unconventional properties, which could bridge the gap between macroscopic robotics and the complexity of biological materials. Here we build active elastic beams from dozens of active colloids and show they exhibit a variety of complex emergent behaviors such as self-oscillations or persistent rotations. Developing tensile tests at the microscale, we show that the active beams are ultra-soft materials, with large (non-equilibrium) fluctuations. Combining experiments, theory, and stochastic inference, we show that the dynamics of the active beams can be mapped on different phase transitions which are tuned by boundary conditions. More quantitatively, we assess all relevant parameters by independent measurements or first-principles calculations, and find that our theoretical description agrees with the experimental observations. Our results demonstrate that the simple addition of activity to an elastic beam unveils novel physics, which can inspire design strategies for active solids and functional microscopic machines.

Tunable Matter: Insights from Contrastive Local Learning Networks

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The relation between structure and function remains elusive despite thousands of studies across systems. For a broad class of tunable matter systems, ranging from physical networks that perform AI tasks to models of allosteric proteins, we have derived an equation specifying how much can be learned about small variations of function (phenotype) due to variations of structure. We apply the analysis to recently introduced electrical Contrastive Local Learning Networks that learn machine-learning tasks such as classification and regression without a processor or external memory. These networks have resistors that individually adjust their conductances to learn task and are constrained by physics to minimize electrical power. Here we show that this physical constraint yields powerful insight into how the networks perform tasks. Such insight is not available in digital neural networks because they live in the digital world—they are not physical objects. In particular, we identify the key resistors (structural features) responsible for the tasks, gaining microscopic physical insight into how collective function is achieved. These key resistors typically have higher resistances than their neighbors, acting as barriers to shape electrical current to produce desired output voltages in response to input voltages.

Our results represent a step toward understanding how desired functionality emerges as a collective phenomenon not only in contrastive local learning networks but also in mechanical metamaterials and many biological systems.

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Activating Epithelia

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Epithelial tissues, which are monolayers of confluent cells undergo a variety of shape deformations driven by cell autonomous active stresses arising from actomyosin. Recent experiments studying the early development of the *Drosophila* embryo, find a genetically induced tissue invagination that moves as a travelling pulse from the posterior to the anterior of the embryo. I will describe how an elastic epithelia, represented as a thick plate that maintains the integrity and impermeability of cells, can be driven by cell autonomous active stresses and inter-cell signalling, to exhibit travelling waves and pulses. Our work highlights the interplay between geometry, active mechanics, signalling and inherited initial and boundary conditions.

Centrosome positioning in cell migration and immune response

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Leukocytes are the key players of the immune system in eliminating pathogen-infected or tumorigenic cells. During these processes centrosome positioning plays a crucial role for establishing cell polarization and directed migration, targeted secretion of vesicles for T cell activation and cellular cytotoxicity as well as the maintenance of cell integrity. Here, we give an overview over microtubule organization and dynamics during immune processes and present models for centrosome repositioning during the formation of the immunological synapse and during cell migration. We focus particularly on actin-myosin crosstalk, which is involved in regulating the polarity and morphology of migrating cells and encompasses mechanical interactions, mediated by crosslinkers and molecular motors, as well as cytoskeletal regulators. Based on recent experimental results we develop a computational whole-cell model involving dynamical microtubules that interact not only mechanically but also via signaling with an active cell boundary. A rich self-organized dynamical behavior emerges, comprising varying positions of the microtubule organizing center relative to the nucleus in the migration direction, varying migration characteristics and cell shapes, and complex migratory behavior in obstacle parks and microfluidic setups. Specific dependencies of these behaviors from parameters like the average microtubule length or the cell-boundary stiffness are predicted and compared with experimental observations.

The coordinative role of cellular packing and osmosis in robustness of intestinal morphogenesis

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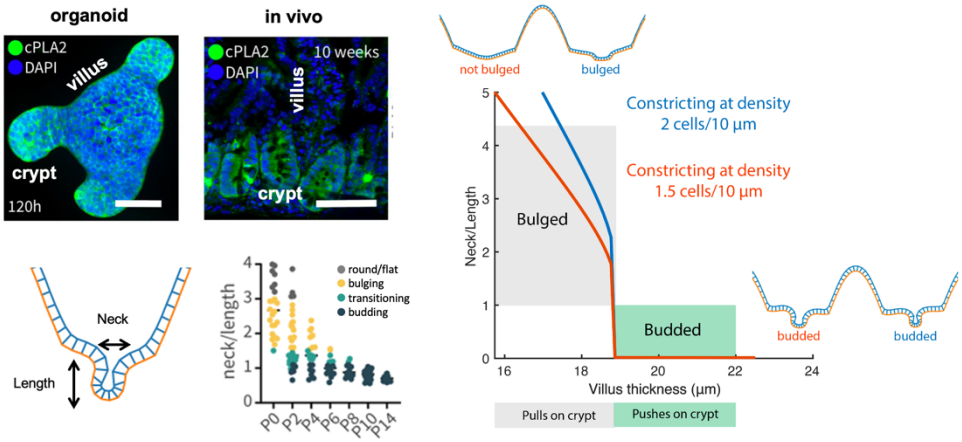

Figure 1. Intestinal crypt morphogenesis: Comparison between organoids, in vivo development and biophysical modelling. Crypt morphology (neck/length ratio) shows an abrupt reduction in variability due to packing-driven mechanosensation.

Embryo development is a fundamentally multiscale process requiring cellular self-organization into complex patterns of cell fates and tissue shapes. Recent progress has shown that, during intestinal morphogenesis, cytoskeletal forces coordinate with cell fate, osmotic and geometric changes to drive the emergence of intestinal crypts [1-2] - but how cells are able to individually adapt to such tissue-scale cues like curvature has yet to be understood. In this talk, I will present recent results combining biophysical modelling, in vivo and organoid light-sheet microscopy, shedding light on one such mechanism. We identified a mechanosensitive enzyme, cPLA2, that acts as an integrator of osmolarity changes and cell packing, governing an increase of actomyosin-driven apical contraction and crypt budding. Using vertex model theory and simulations, we find that packing-sensing plays a critical role in ensuring robust morphogenesis, as variations in cellular density effectively encode at the cellular level osmotic swelling and mechanical constraints of the entire tissue. I will show how this process can on its own regulate morphological parameters such as the number and size of crypts, and could also explain how multiple crypts can emerge with similar shapes and timings in vivo, despite a high initial variability. This work suggests general mechanisms behind tissue-scale coordination in cell fate and morphogenesis.

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DNA origami super-assemblies

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DNA origami allows the construction of almost arbitrarily shaped nanostructures with nanometer precision using around 100 individual oligonucleotides for objects around 100 nm in size, but this approach becomes impractical for much larger structures. Rather than making ever-larger origami objects, a more economoic strategy is to use DNA origami structures as programmable building blocks for the self-assembly of super-structures. Recent years have seen various approaches to create such super-assemblies, seeking control through the shape of building blocks, precisely defined interactions, nucleation kinetics, or the accumulation of mechanical strain. Here, we discuss the formation of large membran-like assemblies using radially symmetric DNA origami building blocks with programmable nearest-neighbor interactions. These programmable blocks can self-assemble into giant sheets, closed vesicle-like containers, cylindrical and finite assemblies, depending on the designed interactions.

Intermittent relaxation and avalanches in extremely persistent active matter

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Recent experiments and simulations have revealed glassy features in the cytoplasm, living tissues as well as dense assemblies of self propelled colloids. This leads to a fundamental question: how do these active amorphous materials differ from passive glasses, created either by lowering temperature or by increasing density?

To address this, we investigate dense systems of self-propelled particles, with an emphasis on the limit of large persistence times [1]. The system then evolves intermittently between mechanical equilibria where active forces balance interparticle interactions. We develop an efficient numerical strategy allowing us to resolve the statistical properties of elastic and plastic relaxation events caused by activity-driven fluctuations [2, 3]. We find a time evolution consisting of a succession of scale-free elastic events and broadly distributed plastic events, with both having properties that depend on the system size. Correlations between plastic events lead to emergent dynamic facilitation and heterogeneous relaxation dynamics. Our results show that the steady state dynamics of extremely persistent active systems is qualitatively similar to that of sheared amorphous solids, yet with some important differences. Time permitting, extensions to aging behaviour will be discussed.

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Microrheology of sequence-programmable and mechanically tunable DNA hydrogels

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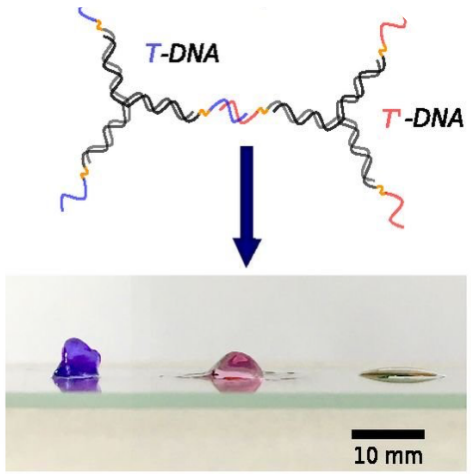
Many particles and polymers exhibit strong degree of swelling when dispersed in water. Local and directed attractive interactions between patchy colloids can then lead to the controlled formation of functional, soft and porous 3D networks called hydrogels. A central idea to the field of DNA nanotechnology is to use DNA as a 'smart glue' to construct highly programmable networks, where Watson-Crick base-pairing rules of complementarity govern the hierarchical step-by-step design of multivalent assemblies. Built on these concepts, DNA hydrogels represent transient self-healing materials that associate and disassociate reversibly when prompted by external factors, most often temperature changes. Falling into the class of physical hydrogels, these materials hold significant promise for applications in biosensing, artificial tissue engineering, and data processing, where precision in target identification and binding is key.

Together with members of University of Cambridge and Tsinghua University, we have initiated studies on the relationship between DNA oligonucleotide composition and bulk mechanical properties of DNA hydrogels. Our publications in *PNAS* [1] (Fig. 1) and *Soft Matter* [2] showed the effect of modifying the base composition of 'sticky ends' that linked DNA nanostars into a hydrogel. We found that reducing the number of bases connecting DNA nanostars lowered the sol-gel transition temperature. Additionally, adding inert, non-binding bases or introducing base mismatches further weakened the overall structure.



Machine learning tools could help us gain full predictive control over such structure-property relations, able to solve the inverse problem in DNA hydrogels (linking mechanics back to sequence). However, this requires generating large datasets (material libraries) that can be fed into ML algorithms. To this end, we focus now our efforts on systematic testing of how microstructure translates into macroproperties in DNA-based materials. We undertake a synergistic approach by combining coarse-grained simulations (oxDNA and LAMMPS) with cutting-edge microrheology experiments.

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Self-organization of motile active matter through mediated, random, and non-reciprocal interactions

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Mediated interactions like quorum-sensing or chemotaxis are ubiquitous in active matter. In this talk I will show how these interactions, which are typically non-reciprocal, lead to a wide variety of emergent phenomena that can be accounted for from first principles within a single theoretical framework. I will show how a large class of static patterns can be described by effective free energies, as opposed to the rich traveling patterns that emerge in the strongly non-reciprocal case. Finally, I will discuss the case of complex ecosystems, in which a large number of species interact via weak, random interactions, and show how these generically leads to the fragmentation the ecosystem into distinct communities.

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Crosstalk constraints on gene regulatory networks

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Biophysical constraints limit the specificity with which transcription factors (TFs) can target regulatory DNA. While individual nontarget binding events may be low affinity, the sheer number of such interactions could present a challenge for gene regulation by degrading its precision or possibly leading to an erroneous induction state. We first review our past work on how detrimental such nontarget binding ("crosstalk") is in the context of equilibrium gene regulatory schemes that have proven to be good models of regulation for prokaryotes [1]. We briefly review some suggestions for how non-equilibrium regulatory schemes could implement kinetic proofreading to circumvent the equilibrium constraints [2,3]. The focus of this presentation is our recent work [4] on how a particular non-equilibrium mechanism that involves chromatin remodeling can endow gene regulatory networks with precise regulation, despite nontarget binding.

Chromatin can prevent nontarget binding by rendering DNA physically inaccessible to TFs, at the cost of energy-consuming remodeling orchestrated by pioneer factors (PFs). Under what conditions and by how much can chromatin reduce regulatory errors on a global scale? We use a theoretical approach to compare two scenarios for gene regulation: one that relies on TF binding to free DNA alone, and one that uses a combination of TFs and chromatin-regulating PFs to achieve desired gene expression patterns. We find, first, that chromatin effectively silences groups of genes that should be simultaneously OFF, thereby allowing more accurate graded control of expression for the remaining ON genes. Second, chromatin buffers the deleterious consequences of nontarget binding as the number of OFF genes grows, permitting a substantial expansion in regulatory complexity. Third, chromatin-based regulation productively co-opts nontarget TF binding for ON genes in order to establish a "leaky" baseline expression level, which targeted activator or repressor binding subsequently up- or down-modulates. Thus, on a global scale, using chromatin simultaneously alleviates pressure for high specificity of regulatory interactions and enables an increase in genome size with minimal impact on global expression error.

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Cytoplasmic Mechanics during the Fly Embryonic Development

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The fruitfly Drosophila melanogaster is a classical model organism of embryonic development. The mechanisms that lead to an adult, fully-developed animal from an unstructured embryo involve a remarkable combination of chemical and mechanical regulatory processes that ensure proper spatial and temporal organization. We shall focus on the first couple of hours of embryonic development and present the various mechanisms and effects that have been unveiled in our recent and ongoing research.

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Title: **How do cells attach to one another?**

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We propose to challenge the conventional views on cell-cell adhesion stability, highlighting the importance of mechanical dissipation at the cellular level. We developed new microdevices to measure the energy needed to break junctions between cell-cell doublets. Using a synthetic cadherin approach, we separated the influence of cadherin binding energy from downstream cytoskeletal regulation. This revealed that the balance between cortical tension and cell shape recovery time determines a transition from ductile to brittle fracture in cell-cell contact. Similar to fracture in passive materials, our findings suggest that junction "toughness," defined as the energy required to disrupt the junction, offers a more accurate measure of junctional stability. We also show that cell cortical dissipation and hence contact stability is controlled by the E-cadherin dependent phosphorylation of Epithelial Growth Factor receptor (EGFR) in migrating cells. The modulation of the cortical viscosity leads to changes in the modes of collective migration of epithelial cells.
This challenges the current emphasis on bond energy and tension, highlighting the crucial role of energy dissipation in the cytoskeleton during junction deformation and its active regulation.

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Abstracts of Posters

(in alphabetical order)

Likelihood-based inference for heterogeneous motile particle ensembles

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The inherent complexity of biological agents often leads to motility behavior that appears to have random components. Robust stochastic inference methods are therefore required to understand and predict the motion patterns from time discrete trajectory data provided by experiments. In many cases second-order Langevin models are needed to adequately capture the motility. Additionally, population heterogeneity needs to be taken into account when analyzing data from multiple individual organisms. We present a maximum likelihood approach to infer dynamical, stochastic models and, simultaneously, estimate the heterogeneity in a population of motile active particles from discretely sampled, stochastic trajectories [1]. To this end we propose a new method to approximate the likelihood for nonlinear second order Langevin models. We demonstrate that the maximum likelihood ansatz outperforms alternative approaches for heterogeneity estimation, especially for short trajectories, while also providing a measure of uncertainty for the estimates. We use this likelihood approach to uncover time-dependent heterogeneity in an experimental cell-cargo system as well as to analyze motility data of developing ameboid cells.

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Capillary interactions organize bacterial colonies

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Many bacteria inhabit hydrated environments like soil, textiles and agar hydrogels in the lab. In these environments, cells are surrounded by a water meniscus, and they experience capillary forces. We found that capillary forces organize bacterial colonies, enabling cells to aggregate into densely packed nematic layers while still allowing them to slide past one another. We developed an experimental apparatus that allows us to control bacterial collective behaviors by varying the strength and range of capillary forces [1]. To explain the observations, we built a theory for the aggregation of self-propelled particles via capillary attraction [2]. Our results suggest that capillary forces may be a ubiquitous physical ingredient in shaping microbial communities in partially hydrated environments.

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From Champagne to Glass: natural and artificial nucleation

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Bubbles can dazzle the senses when pouring a Champagne glass, using either natural or artificial nucleation. Tartrate crystals from washing, cellulose fibers from cleaning or drying, or purposefully made crenels in a flute, can all be used to trigger bubble nucleation by lowering the energy barrier required to grow a bubble[1,2]. By using a model system of viscoelastic polyvinyl butyral (PVB)[3] confined in between two glass slides, we show that the concepts of natural and artificial nucleation from Champagne equally apply to safety glass and photovoltaic panels, both staples of modern life using viscoelastic polymers, and whose tendency to form bubbles may indicate early failure by water ingress (solar panels)[4] or may themselves constitute failure (architectural glass)[5]. Our experimental results show that water vapor, which tends to aggregate inside the polymer matrix in the form of clusters[6], escapes in copious amounts from the polymer bulk when the latter is heated and decompressed (e.g., at 140°C, dP=1bar). However, bubbles may only form at trapped fibers, dust speckles, or purposefully made crenels via laser patterning in the glass surface. The number of natural nuclei is apparently and counterintuitively inversely proportional to the applied temperature. In the artificial nucleation case, the growth or lack thereof of bubbles is linked to the morphology of the crenels. Finally, we also investigated how the growth rate of bubbles is impacted by whether nucleation is natural or artificial.

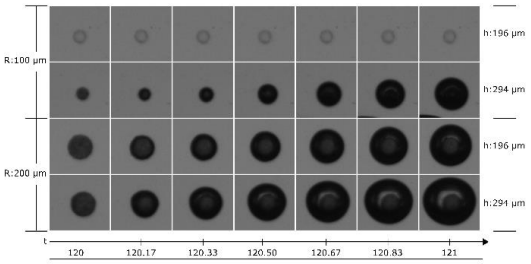

Fig.1: Artificial nucleation in model glass/pvb/glass system

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Adhesion-driven wrapping and pore translocation of elastic particles

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Membrane wrapping and endocytosis are involved in many signaling and transport processes, ranging from the uptake of synthetic drug-delivery vectors, vesicles, and viruses to parasite invasion. Wrapping of hard particles of various sizes and shapes has been studied extensively, both using theory and experiments [1]. Less is known for elastic particles—although they are abundant in vivo—for which the interplay of particle and membrane deformability determines membrane wrapping and cellular uptake [2].

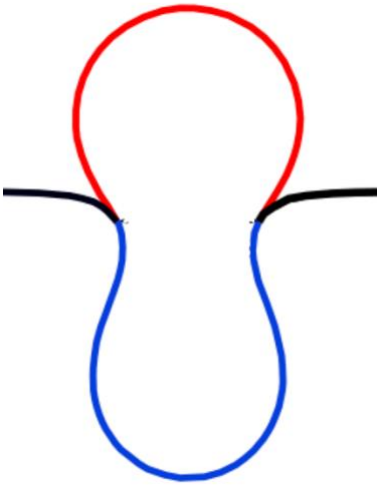

Figure 1: Translocation of an initially spherical vesicle through a membrane-covered pore.

Using numerical calculations, we study the interaction of both vesicles and microgels with lipid-bilayer membranes. We employ the Helfrich Hamiltonian and triangulated surfaces for the membranes and a mass-spring model for the microgels. This allows us to predict stable wrapping states and quantify energy barriers for the transitions. Furthermore, we characterize adhesion-driven vesicle translocation through membrane-covered pores [3], see Fig. 1. Strong vesicle deformation upon pore translocation is associated with a discontinuous transition between weak- and deep-translocated states. For prolate vesicles, the energy barrier can be significantly reduced compared to initially spherical vesicles, but the translocation can also be entirely suppressed if the vesicle membrane area is too small to enclose its volume at half-wrapping. Our wrapping diagrams for vesicle-pore translocation shed light on the role of the deformation of Toxoplasma parasites during host-cell invasion.

NB, AKD, and TA acknowledge support within the DFG SPP 2332.

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Self-Organization of Interacting Micromotors: From Synchronization to Phase Coherence

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Over the past two decades, a host of motorization techniques have been developed to motorize the fundamental building blocks of soft condensed matter, such as colloids, polymers, and droplets, thereby turning them into active matter. At the same time, advances in 3D printing technology now allow for the fabrication of complex but inert microscopic structures.

I will show how to combine 3D printing and colloidal motorization to self-organize collections of thousands of electric micromotors all driven independently. Through a combination of experiments, simulations, and theory, I will show and explain how transverse forces structure the spatial organization of the micro-motor dynamics: when sufficiently coupled, their rotation rates display a robust form of antiferromagnetic order. After having explained the ordering of the angular frequencies in rotor lattices, I will explain how to leverage electrostatic interactions and geometry to control their phase coherence, yielding to the spontaneous propagation of metachronal waves over system-spanning scale.

Topological defects organize morphogenesis on closed curved surfaces

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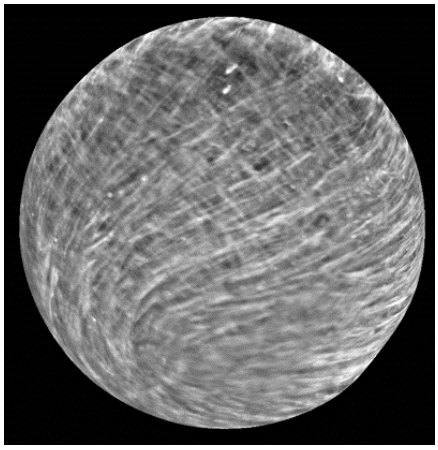
Morphogenesis, the process by which tissues acquire their shape, hinges on a finely orchestrated collective motion of cells. Accumulating evidence shows that many biological tissues behave as active nematics, both in vitro and in vivo. The collective motion of cells is controlled by the nematic order, and topological defects have been proposed as morphogenic organizers via active stresses. However, the generation and control of tissue-scale forces involved in morphogenesis remain poorly understood, in particular within 3D surfaces. To investigate how geometry and topology control morphogenesis, I grow myoblast cells on the surface of alginate microspheres and monitor the nematic field, cellular flows, and tissue growth. When the tissue reaches confluency, four equidistant +1/2 defects are observed in the actin network, consistent with the topological charge imposed by the sphere (see image below). Subsequent growth of the monolayer due to continuous proliferation shows the formation of multilayered tissue with two main orthogonal orientation. Upon further growth, the half defects fuse by pair, forming two +1 defects, and the thickness of the tissue becomes heterogeneous with the presence of two mounds co-localizing with the +1 defects. Together, the defect fusion and mound formation, form a first spontaneous symmetry breaking event. Finally, the two +1 defects migrate towards one another and form a +2, accompanied by the fusion of the two mounds into one main protrusions. In this synthetic model system, a complex and spontaneous morphogenesis emerges from the interplay between the topological defects and cellular flows, illustrating the role of physical principles in a fundamental biological process.



Quorum sensing and absorbing phase transitions in colloidal active matter

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Unlike biological active matter that constantly adapt to their environment, the motors of synthetic active particles are typically agnostic to their surroundings and merely operate at constant force. In this presentation, I show how one can design colloidal active rods capable of modulating their inner activity in response to crowding, thereby enforcing a primitive form of quorum sensing interactions. Through experiments, simulations and theory we elucidate the impact of these interactions on the phase behavior of isotropic active matter. I will show that, when conditioned to density, motility regulation can either lead to an absorbing phase transition, where all particles freeze their dynamics, or to atypical phase separation, where flat interfaces supporting a net pressure drop are in mechanical equilibrium. Fully active and fully arrested particles can then form heterogeneous patterns ruled by the competition between quorum sensing and mechanical interactions. Beyond the specifics of motile colloids, we expect our findings to apply broadly to adaptive active matter assembled from living or synthetic units.

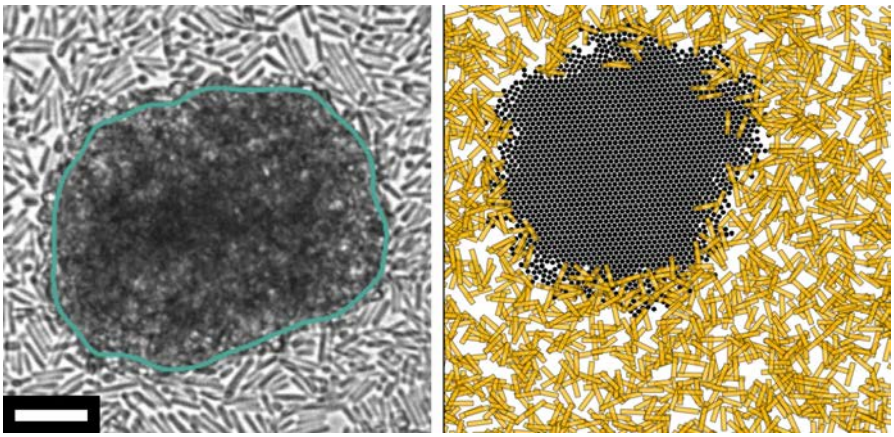

Figure 1: Phase separation of active rods: experiments vs numerics

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Quantum sensing for soft matter study

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Optically active crystal defects in diamonds can be used as highly sensitive sensors for observing magnetic and electric fields as well as temperature. Such quantum sensors are operated from cryogenic temperatures to room temperature and above. It allows them to be used for different applications, including navigation, space, medicine, etc. Color centers, especially in nanodiamonds, are extremely attractive for the investigation of biological systems and soft matter, where the nanoscale size of the sensors allows for their incorporation inside an investigated system. For example, Nitrogen-Vacancy centers were used to measure magnetic molecules and proteins [1]. Nitrogen-, Silicon- or Germanium-Vacancies were initialized as temperature sensors inside living cells [2].

Here, we discuss how diamond-based quantum sensors can help better understand processes in living cells and soft matter, including structure and defect transformation. We will focus on sample requirements and preparation. It is also important to remember the experimental limitations, which will also be addressed.

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Nuclear size control by osmotic forces in *S. pombe*

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The size of the nucleus scales robustly with cell size so that the nuclear-to-cell size—the N/C ratio—is maintained during growth in many cell types. To address the fundamental question of how cells maintain the size of their organelles despite the constant turnover of proteins and biomolecules, we consider a model based on osmotic force balance predicts a stable nuclear-to-cell size ratio, in good agreement with experiments on the fission yeast *Schizosaccharomyces pombe*. We model the synthesis of macromolecules during growth using chemical kinetics and demonstrate how the N/C ratio is maintained in homeostasis. We compare the variance in the N/C ratio predicted by the model to that observed experimentally.

Biohybrid microswimmer fabrication with controllable geometry using capillary-assisted endospore deposition

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Biohybrid microswimmers integrate the innate motility and sensing strategies of microorganisms with the properties of their variable artificial cargo. Thus, utilizing the natural ability of bacteria to swim towards attractants such as chemicals or light holds potential for targeted transport at the microscale. In order to attach functional cargo for delivery and control, we demonstrate the used of sequential capillarity-assisted particle assembly (sCAPA) to assemble biohybrid microswimmers, which allows to precisely control the geometry of the constructs and create them in a highly reproducible manner. By using *B. subtilis* endospores as biological starting material we introduce a novel cellular material into the field of research, which has not been previously used in the fabrication of comparable biohybrid constructs. Furthermore, we are able to harness the inherent resistivity of bacterial endospores towards unfavourable conditions such as heat and desiccation, by incorporating them into the colloidal approach of microswimmer fabrication, while retaining the advantages of the cellular actuation and sensing strategies of microorganisms.

By constructing biohybrid microswimmers with varying architectures, we aim at comparing the motility behaviour between different constructs in order to gain insight into the swimming mechanisms of the incorporated bacterial cells.

Mesoscale properties of biomolecular condensates emerge from nanoscale dynamics

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Biomolecular condensates are droplets-like structures originating from the phase-separation of biomolecules. The functions of condensates within living cells span many length scales: from the modulation of chemical reactions at the molecular scale to the compartmentalization of the cell at the mesoscale. We employ single-molecule fluorescence spectroscopy to study the conformations and dynamics of intrinsically disordered proteins within single droplets [1], combined with microrheology approaches to assess mesoscale properties. By tuning the strength of the interactions among the constituent proteins, we produced condensates spanning almost two orders of magnitude in viscosity. We find that the nanoscale chain dynamics on the nano- to microsecond timescale can be accurately related to both translational diffusion and mesoscale condensate viscosity by analytical relations from polymer physics [2]. Atomistic simulations reveal that the differences in friction — a key quantity underlying these relations — are caused by differences in inter-residue contact lifetimes, thereby leading to the vastly different dynamics among the condensates. The rapid exchange of inter-residue contacts we observe may be a general mechanism for preventing dynamic arrest in compartments densely packed with polyelectrolytes, such as the cell nucleus.

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Actin dynamics sustains spatial gradients of membrane tension in adherent cells.

Authors: Juan Manuel García-Arcos[1], Amine Mehidi[1], Julissa Sánchez Velázquez[2], Pau Guillamat[1], Caterina Tomba[1], Laura Houzet[1], Laura Capolupo[3], Giovanni D'Angelo[3], Adai Colom[4,5], Elizabeth Hinde[2,6], Charlotte Aumeier[1], Aurélien Roux[1].

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Tension propagates in lipid bilayers over hundreds of microns within milliseconds, precluding the formation of tension gradients. Nevertheless, plasma membrane tension gradients have been evidenced in migrating cells and along axons. Here, using a fluorescent membrane tension probe, we show that membrane tension gradients exist in all adherent cells, whether they migrate or not. Non-adhering cells do not display tension gradients. We further show that branched actin increases tension, while membrane-to-cortex attachments facilitate its propagation. Tension is the lowest at the edge of adhesion sites and highest at protrusions, setting the boundaries of the tension gradients. By providing a quantitative and mechanistic basis behind the organization of membrane tension gradients, our work explains how they are actively sustained in adherent cells.

Twists, turns and surprising shapes: How a 2D liquid crystal influences geometry

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Previous research considered a 2D passive nematic liquid crystal embedded in a surface. By minimizing the system's total energy subject to boundary conditions and bend, twist and splay in the system the final geometry of the embedded surface was established and quantified [1]. We extended this by asking, what shapes are formed, if instead of a disc-like shape, the surface is parametrized such that it allows for investigating more general surfaces, such as an annulus, a cylinder, a catenoid or a cone-like surface. This might be used as a model for wound healing or scission in biological systems.

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Geometry and Mechanics of Living Materials

D.Grossman[1]

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Living tissues may be viewed as active, viscoelastic(plastic) material that adapt to external stresses and actively generate stresses. Many of the properties and biological process occurring in tissues are related mechanical stresses: from cell division and differentiation to morphogenesis and organ shape control. A good mechanical model is therefore important in any successful description living material. Unfortunately, detailed cellular modelling is often to expensive computationally on one hand, and phenomenological continuous models may falter and are not easily relatable to the underlying detailed description. In this poster I will share my ideas and work on the subject, specifically how to derive geometrically exact – continuum description of tissues, within the formulation of “incompatible elasticity”, beginning from a detailed cell-scale (discrete) description, and finishing with a powerful continuum limit. Applying this approach both to animal tissues (which can be viewed as viscoelastic fluids) and plant tissues (viscoelastic solids) yields various interesting results that successfully describes the mechanical properties of living tissues (e.g – deriving the homeostatic pressure from first principle, and capturing complex rheology).

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Streams of Janus Particle Dimers

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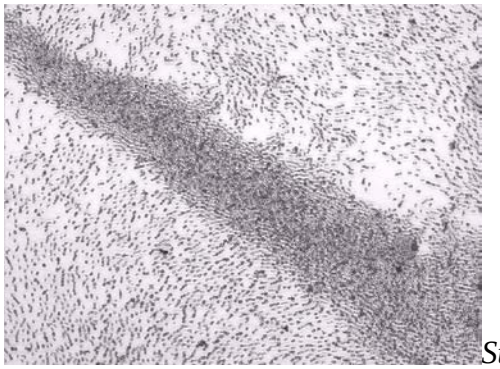
Interactions in active matter systems, both soft and biological, are generally non-reciprocal,[1] and can be tailored in colloidal systems to investigate the collective effects they induce. Here, we study self-propelling dimers of Janus particles that interact via non-reciprocal torques due to induced electrical dipoles, expanding previous work on non-reciprocal monomers.[2,3]

Experiments show these dimers forming polar streams or rivers, elongated regions with high particle density and orientational alignment along the extent of the stream. This distinguishes them from traveling bands observed in classical models of flocking, where particles are oriented perpendicularly to the band.



Stream observed in experiment

To analyze and understand the emergence of this phase, we perform Brownian dynamics simulations paired with analytical coarse-graining methods. With these analyses, we will test the hypothesis that polar streams emerge from the combination of two paradigmatic transitions in active matter: motility-induced phase separation and flocking.

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Reconstituted nascent adhesion condensates enable actin polymerisation on supported lipid bilayers

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Focal adhesions are membrane-associated protein complexes crucial for cell migration, adhesion, and signaling. Formation of focal adhesions requires the connection between the actin cytoskeleton and nascent adhesions, which cluster integrins and integrin-associated proteins on the membrane. While recent reconstitution assays suggest that nascent adhesions are formed by the liquid-liquid phase separation induced by protein interaction with charged lipid bilayers [1], how nascent adhesion protein phase separation organises and regulates actin polymerization within nascent adhesions remains an open question. To address this, we reconstituted protein condensates containing a minimal set of nascent adhesion proteins on solid-supported lipid bilayers. These membrane-associated assemblies localize G-actin and serve as nucleation sites for actin polymerisation. Our results demonstrate that zyxin or vinculin co-phase separate with VASP at the lipid bilayer. Phase separated nature of condensate is crucial for initiating actin polymerization from these condensates. While both zyxin-based and vinculin-based condensates can polymerise actin, the resulting actin network has different properties. This can be explained from the difference in condensates mechanical properties. These findings highlight the role of key nascent adhesion proteins in actin polymerisation and establish a model system for exploring how the actin cytoskeleton influences the dynamics of membrane-associated condensates.

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Are bacteria patchy colloids? Force spectroscopy on soft and biological matter

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Investigating bacterial adhesion at the single-cell level provides critical insights into biofilm formation and the influence of surface properties on microbial attachment. This study examines the adhesion behavior of *Staphylococcus aureus* on wrinkled polydimethylsiloxane (PDMS) surfaces using single cell force spectroscopy (SCFS) [1]. While conventional SCFS typically evaluates a single contact point, our approach—utilizing structured surfaces—enables mapping of adhesion across the lower portion of the bacterial cell envelope. This method reveals considerable variation in adhesion strength at different points on the cell surface, supporting the "patchy colloid" model originally proposed for *Escherichia coli*. Simulations, incorporating angle-dependent molecule-substrate interactions, suggest that localized adhesive “hotspots” on *S. aureus* may arise from surface roughness, chemical composition, and the clustering of specific adhesive proteins. These findings emphasize the significance of surface structuring in bacterial attachment and provide insights that inform the design of antimicrobial materials and enhanced models for bacterial surface interactions. By mapping adhesion across multiple contact points on individual cells, this work establishes a foundation for future research aimed at modulating bacterial adhesion on medical devices.

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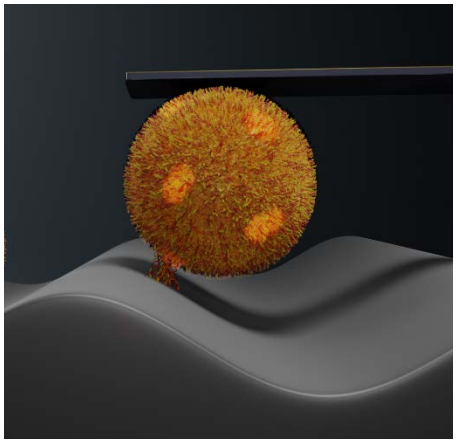

Model of the experimental setup for determining the adhesive force of a bacterium: The corrugated surface allows the lower part of the bacterium (diameter 1 µm) to be characterized using single-cell force spectroscopy. The results show that there are a few areas with high adhesive force on the surface of the bacterium.

Activity induced non-monotonic aggregation in a mixture of chemically active and passive particles

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Spontaneous symmetry breaking has been shown to be the genesis of self-assembly in a mixture of spherically symmetric chemically active and passive colloids, forming dense clusters [1, 2]. We study the kinetics of such self-assembly, driven by the phoretic motion of passive colloids following the chemical gradient generated by the active seeds (Fig. 1). A non-monotonic effect of activity on aggregation is the key observation in our work. We rationalize such non-monotonicity in the clustering by the hybrid coarse-grained simulations. The average cluster population and the variation of their size as a function of time, the stability of clusters, and their dynamics are the key quantifications that help us comprehend the aggregation. The model offers the additional advantage of including explicit hydrodynamic interaction among the colloids, which is often neglected in such simulations. And it turned out that hydrodynamics has a significant role in colloidal self-assembly and can not be overlooked in chemically active systems [3].

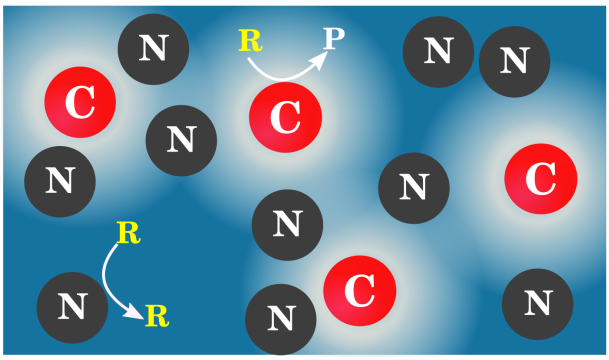

FIG. 1: Schematic illustration of catalytic C (red) and non-catalytic N (grey) colloids dispersed in a solvent. C takes part in a chemical reaction and converts the R solvent to P, thus creating a uniform distribution of P around it (white color), whose value is maximum near the catalytic sphere's surface and decays radially outwards. Non-catalytic colloids can react to the concentration gradient created by active particles due to diffusiophoresis, and give rise to self-assembled dynamic structures.

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Active hydraulics

Camille Jorge[1], Denis Bartolo[1]

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We explore the behavior of active fluids confined in microchannel networks, demonstrating how they deviate from the predictable laws of classical hydraulics, which govern viscous, laminar flows. While traditional systems like blood vessels and porous media are described by robust, linear laws, active fluids exhibit bistable and non-deterministic dynamics. Through a combination of experiments, simulations and theory I will show how to build a general framework for predicting the geometry of active-hydraulic flows in arbitrary networks.

First, focusing on square-grid networks, experiments with colloidal rollers reveal that the degenerate flows of active fluids correspond to configurations of the six-vertex model. This quantitative correspondence enables us to predict and control the Lagrangian trajectories of active particles, which form completely packed loops, as described by the Baxter-Kelland-Wu framework. This experiment teaches us how to map active-hydraulic flows on vertex physics and and how to lay out the first free rules obeyed by all active hydraulic flows. [1]

We then show that a crucial additional rule is required to account for geometry of active flows in network having an odd coordination number. We focus on trivalent networks and show show that active hydraulic flows act as dynamical spin-1 ices, resulting in degenerate streamline patterns. These patterns split into two geometric classes of self-similar loops, reflecting the fractionalization of topological defects at subchannel scales. From our observation we explain the interaction rules between the vertices that define active-hydraulic flows. [2]

Our findings offer new perspectives on active fluid dynamics and provide a foundation for the design of microfluidic devices and the study of biological transport in complex environments.

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Quantifying flow induced remodeling on self organized vascular networks on a chip

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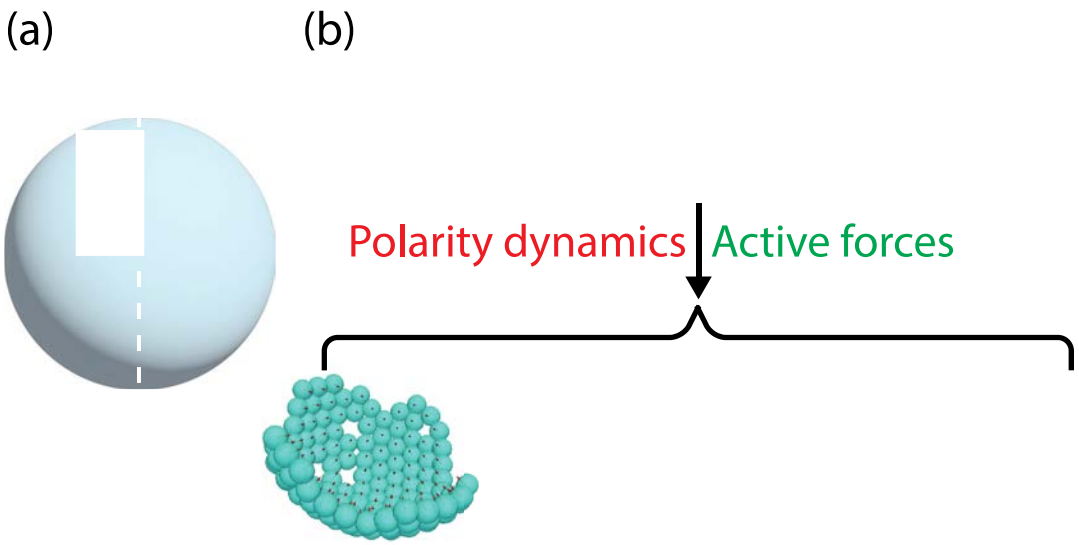
In the microvasculature, ensuring uniform nutrient transport while balancing energy dissipation and construction costs is critical for maintaining tissue health and function. The vasculature undergoes remodeling, characterized by the formation of new vessels, pruning of existing connections, and enlargement of specific branches. Our project leverages microfluidic technology to cultivate self-organized vascular networks on a chip, allowing us to perfuse these networks and observe their dynamic adaptation to varying flow conditions. By integrating microscopy data with numerical flow calculations, we analyze these complex networks to elucidate the interplay between network morphology and flow-driven feedback mechanisms.To further enhance the physiological relevance, contractile mural cells are integrated into the networks, providing a more realistic microenvironment and enabling the investigation of their role in vessel normalization.

Bio-inspired self-assembling active matter

Mukund Krishna Kothari[1], Guillaume Salbreux[1]

1 Department of Genetics and Evolution, Faculty of biology, University of Geneva

We present a minimal model of self-organization with cells described as polar active particles immersed in a three-dimensional medium[1]. The model is motivated by the self-organization of stem cells in the early stages of organoid development. In addition to friction and cell-cell adhesion, the system is made active through contact-based interaction forces between particles instead of more typical self-propulsion forces. The polarity dynamics of particles result from a response to the positions and polarities of neighbours. The feedback between polarity dynamics and mechanical forces leads to robust self-assembly of disordered aggregates into filaments, planes, curved surfaces, and hollow spheres. We develop order parameters to quantify spatial configurations and use these to identify parameter space regions for various assemblies in phase diagrams. The assemblies are robust to varying initial conditions and particle numbers. The linear stability of these assemblies is discussed through a continuum theory. We also compare our out-of-equilibrium simulations with simulations governed by free energy minimization and highlight the role of active forces in robust self-assembly. Our study aims to explain early stage development of organoids, embryos and several other self-assembly phenomena observed in biological systems



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Dynamical Network Remodeling of Slime Mold

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Remodeling of a network is one of the hallmarks of biological flow networks, ensuring their optimal morphology. Due to limited building costs, the removal of vessels allows these networks to reallocate matter to minimize dissipation, ensure maximum coverage, and even allow for migration.

Physarum polycephalum is a unicellular slime mold organized as a 2-dimensional tubular network that evolves drastically over a few hours, evacuating a large zone of a few millimeters squared [1]. Unfavorable competing parallel veins are first removed to form a tree-like structure, where veins prune sequentially until complete evacuation of the zone [2].

First, we use an analogy with power-grid networks to investigate the effect of sequential pruning based on the ratio of tube vs network resistance. We analytically show that regular graphs are pruning until the average node degree is smaller than four, a result robust with simulated random networks. Including mass redistribution with pruning leads to resistance homogenization.

Second, analyzing time-lapses of the slime mold, we find an exponential decrease in the number of tubes reproduced by a toy model based on the network structure. We show that the decay rate is controlled by the depth of the tree and the parallel branches' dynamics, which introduces a waiting time for pruning.

Our approach to flow networks may be generalized to pruning flow networks during embryonic development, stroke events, or evacuating networks for urban design.

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Topological defect engineering enables size control in self-assembly

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The self-assembly of complex structures from engineered subunits is a major goal of nanotechnology, but controlling their size becomes increasingly difficult in larger assemblies. Existing strategies present significant challenges, among which the use of multiple subunit types or the precise control of their shape and mechanics. Here we introduce an alternative approach based on identical subunits whose interactions promote crystals, but also favor crystalline defects. We theoretically show that topological restrictions on the scope of these defects in large assemblies imply that the assembly size is controlled by the magnitude of the defect-inducing interaction. Using DNA origami, we experimentally demonstrate both size and shape control in two-dimensional disk- and fiber-like assemblies. Our basic concept of defect engineering could be generalized well beyond these simple examples, and thus provide a broadly applicable scheme to control self-assembly.

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Microtubule-based active matter droplets: patterns of an extensile filament

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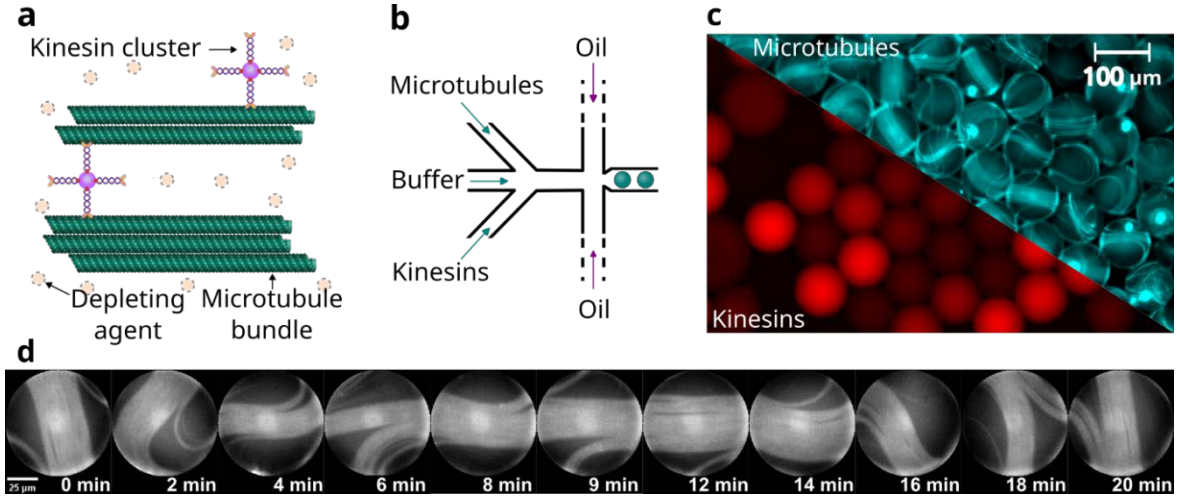
Known as the cytoskeleton, networks of active biopolymers dynamically shape the cell membrane. Described by active matter physics, the cytoskeleton has gained the attention of both theorists and experimentalists who developed filament-motor model systems that exhibit remarkable self-organizations [1].

Here, we encapsulate a microtubule-kinesin based active matter inside water-in-oil droplets. The microtubule packed in bundles spontaneously migrate to the oil-water interface and form an active filament. As the bundles slide along each other, the extensile filament confined on the surface of a sphere is folding and show a periodical pattern – related to similar models for DNA packing of viral capsids [2]. Repeated sequences of movements are revealed by studying hundreds of droplets layered in a two-dimensional tissue. In this work, we aim at studying this system to understand the dynamics of a growing filament confined into a sphere, the influence of varying parameters - such as confinement, amount of matter or energy, quantity of motors - on its movement and the robustness of this pattern.



(a) Scheme of the active matter formed by nongrowing microtubules bundled together by a depleting agent, and clusters of kinesin motors. (b) Scheme of the microfluidic device used to generate droplets. (c) Fluorescence two-color images of droplets showing microtubules (blue, upper right corner) and a reporter dye standing for the varying concentration of kinesin clusters (red, lower left corner). (d) Timelapse images showing a period of microtubule movement

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Geometric theory of mechanical screening in 2D granular materials

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Many materials have mechanisms for local stress relaxation, for example by local plastic rearrangements in granular solids, or cell neighbour-exchanges (T1 transformations) in cellular tissue. Such materials exhibit anomalous mechanical behaviour, qualitatively different from the predictions of classical mechanical theories of fluids and solids. Specifically, the local relaxation of stress screens the mechanical stress fields, reducing their magnitude in the material.

Due to geometric conservation laws, the non-elastic deformation mechanisms at the basis of this response are typically quadrupolar. However, when such deformations are abundant, they can collectively induce dipolar or monopolar defects, which also contribute to the screening of stress fields. By associating these deformation mechanisms with corresponding geometric quantities, we construct a theoretical framework for describing the mechanics of disordered materials. This framework allows us to derive a hierarchy of screening theories, analogous to electrostatic screening, which predict distinct mechanical behaviours depending on the dominant screening modes. These predictions are then compared with experimental observations in granular materials.

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Bacterial glass transition in *Pseudomonas aeruginosa*

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Motile bacteria self-organize in numerous collective phases, such as orientationally ordered phase or swarming state. These collective phases result from properties and activities at the single cell scale, such as growth rate, swimming speed and cell-cell interactions. Understanding how individual properties can trigger emergence of long range order is a crucial aspect of biological and physical studies on bacteria, and can lead to better understanding of the mechanisms of colonies and biofilms formation. Here we study the properties of the 2D swarming state of an elongated motile bacteria, *Pseudomonas aeruginosa*, in growing colonies. We are able to obtain large and dense bacterial monolayers at the edge of 3D colonies expanding on agar gels. We perform the detection of bacterial trajectories from high-speed movies through the use of DistNet2D, an innovative deep learning technique that compute segmentation and tracking altogether, taking advantage of temporal information. As density increases in bacterial monolayers, *P. aeruginosa* undergoes kinetic arrest, and collectively transitions from a liquid-like state to a glassy state. We show that this transition does not only affect the scales of the system's relaxation times, but also the very nature of the dynamics at play. We reproduce the analysis to several *P. aeruginosa* mutants of different shapes and single-cell motion properties, and show that all flagellated mutants exhibit a similar glass transition. The critical surface density to trigger the transition does not depend on single-cell motion properties, and seems to only depend on the aspect ratio of cells.

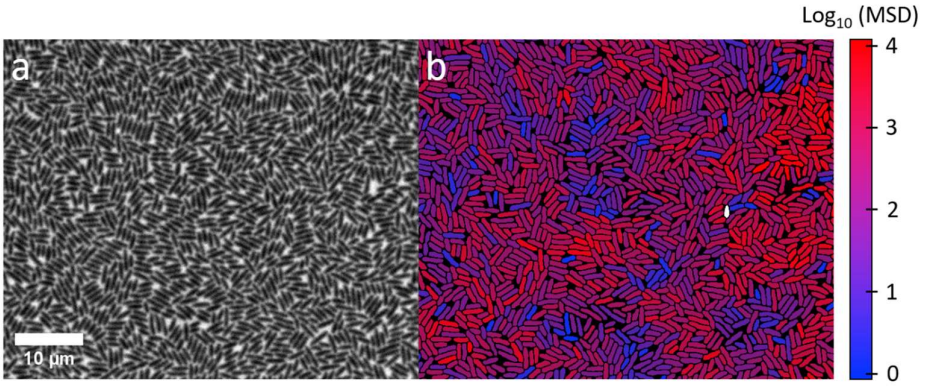

Fig. 1 : *a. Monolayer of P. aeruginosa displaying near-glass behavior; b. Coloring the bacteria by their mean squared displacement (MSD) brings into light the presence of dynamical heterogeneities (spatial segregation of bacteria by their motility), that are typical behavior in glassy systems; in white : tracking error*

Designing complex behaviours using transition-based allosteric self-assembly

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Allosteric interactions occur when binding at one part of a complex affects the interactions at another part. Allostery offers a high degree of control in multi-species processes, and these interactions play a crucial role in many biological and synthetic contexts. Leveraging allosteric principles in synthetic systems holds great potential for designing materials and systems that can autonomously adapt, reconfigure, or replicate. In this work we establish a basic allosteric model and develop an intuitive design process, which we demonstrate by constructing systems to exhibit four different complex behaviours: controlled fibre growth, shape-shifting, sorting, and self-replication. In order to verify that the systems evolve according to the pathways we have developed, we also calculate and measure key length and time scales. Our findings demonstrate that with minimal interaction rules, allosteric systems can be engineered to achieve sophisticated emergent behaviours, opening new avenues for the design of responsive and adaptive materials.

Shape through gradients: Deformations of chemically active membranes

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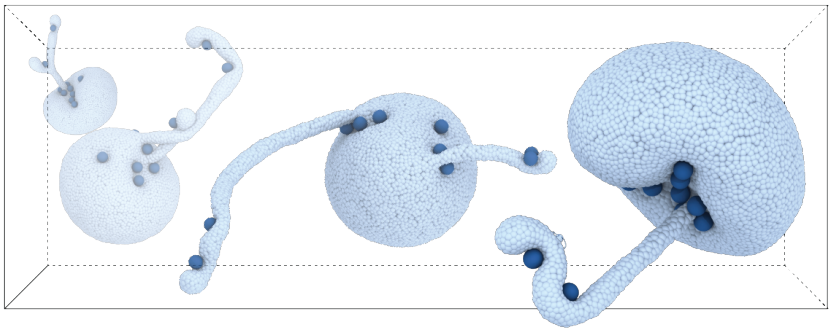
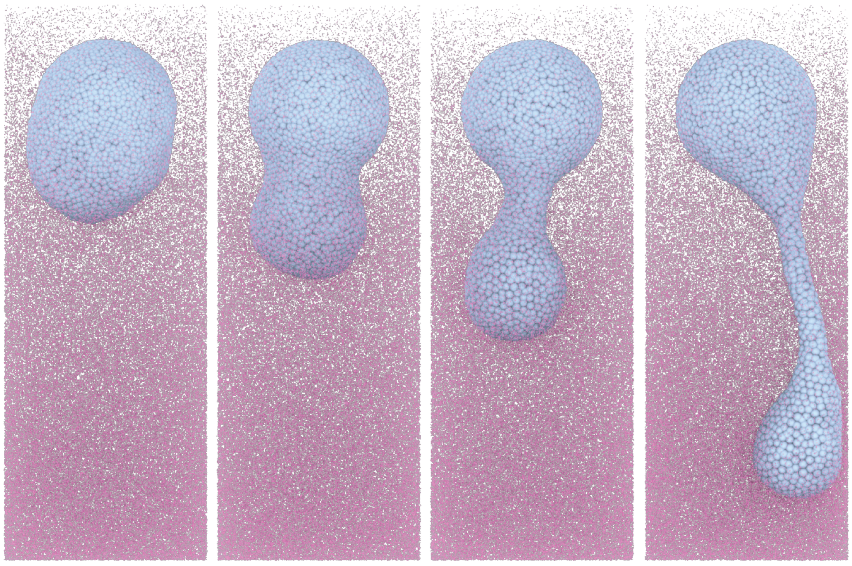
The plasma membrane plays a fundamental role in mediating the interaction between the cell and its environment. Beyond its function as the boundary between the cytoplasm and the cellular exterior, in reactant rich media the envelope of the cell acts as a semipermeable membrane that also hosts numerous chemical reactions. Can external chemical activity drive the emergence of morphologies that contribute to cellular function — even in the absence of cytoskeleton? Here we study the untapped potential of the plasma membrane to deform in gradients of reactive molecules using coarse-grained out-of-equilibrium simulations. Inspired by symbiotic associations in the micro-scale, we first introduce a minimal model that uses non-reciprocal pairwise interactions to encode an asymmetric exchange of chemicals between organisms, and classify the emergent membrane morphologies. We then show that explicit reactant gradients, modelled using discrete beads and consumed by our membrane model, can lead to membrane reshaping, from spheroidal vesicles to the extrusion of long protrusions. Understanding the plasma membrane's potential as a driver for cell deformations in complex chemical media may have fundamental implications in the context of ecology and evolution, which we can explore with our computer simulations.





Migration and separation of polymers in nonuniform active baths

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Polymer-like structures are ubiquitous in nature and synthetic materials. Their configurational and migration properties are often affected by crowded environments leading to non-thermal fluctuations. We study an ideal Rouse chain in contact with a non-homogeneous active bath, characterized by the presence of active self-propelled agents which exert time-correlated forces on the chain. By means of a coarse-graining procedure, we derive an effective evolution for the center of mass of the chain and show its tendency to migrate towards and preferentially localize in regions of high/low bath activity depending on the model parameters. In particular, we demonstrate that an active bath with non-uniform activity can be used to separate efficiently polymeric species with different lengths and/or connectivity.

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Active particle confined in a quasi-two-dimensional droplet

A. N. Kato[1], K. Xie[1,2], B. Gorin[1], J-M. Rampnaux[1], and H. Kellay[1]

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Soft boundaries, such as droplet interfaces are deformable confinements, where the deformation can occur and act on active particle dynamics through back action. However, the physical mechanisms underlying the interplay between activity and interfacial effects remain poorly understood, particularly in simpler quasi-two-dimensional systems. In this work, we focus on this point using a light-activated Janus particle [1] in a thin oil droplet at air—water interface (Figure 1). We found that the fast Janus particle motion exhibits diverse temporal features coupling with the interfacial profile. Despite the complex coupling with the particle motion, the temperature field, and hydrodynamic flow, we identified the capillarity due to the droplet geometry [2] as crucial for the periodicity of the motions.

Given the ubiquity of the particle-curved film interaction, the mechanism uncovered here is expected to be applicable in extending particle-containing soft matter systems to active counterparts.

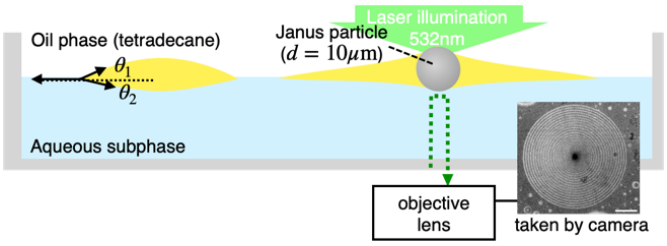

Figure 1 Experimental setup

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Self-limiting self-assembly of particles with complex interactions

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

VertAX: a novel framework for 2D vertex model inference through bilevel optimisation

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Confluent tissues are complex biological tissues whose macroscopic properties and behaviours are essential to understand for the advancement of knowledge in areas such as developmental biology, tissue engineering, and regenerative medicine. These tissues are commonly described as energy-based physical systems characterized by an internal energy optimization process, in which the energy function minimised by the system depends on microscopic parameters associated with each cell. It has been shown how appropriate choices of these microscopic parameters give rise to a wide and diverse expression of macroscopic behaviors, such as a rigidity transition between a liquid phase and a solid phase, or the formation of patterns in the tissue. To solve the inverse problem of obtaining specific material properties, these systems can be associated with an external loss function dependent on the microscopic parameters explicitly and implicitly through the minimum energy state. Here we present VertAX, an innovative framework, a fully differentiable vertex model written in Google Jax to quickly and easily address the inverse problem of learning these microscopic cellular parameters to achieve a given target behavior for confluent tissues. Our framework allows us to leverage bilevel optimization techniques to learn optimal parameters for these systems in order to achieve target macroscopic behaviours, such as specific patterns within the tissue, or specific system properties, such as liquid or solid phases, or even infer the optimal cellular parameters to match some real microscopic data. Implementing this framework in Jax allows the model to be fully differentiable, which gives us the freedom to automatically differentiate any energy or loss function with respect to any parameter of the system. Thus, our framework allows us to address inverse problems using techniques from machine learning, such as automatic differentiation, and even use GPUs to accelerate optimization processing time. Nevertheless, we also compare the performance of our novel variational formulation of mechanical inference using our framework with alternative optimization methods, such as classical implicit differentiation and equilibrium propagation, within this bilevel setting. In summary, we present a powerful, extensible approach for mechanical inference and cellular parameter identification in confluent tissues, providing a proof of concept for broader generalization across related scientific and engineering domains.

Active viscoelastic condensates provide controllable mechanical anchor points

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Many biological materials must couple mechanical strength with the ability to rapidly self-assemble at a specific location. In particular, biomolecular condensates readily self-assemble via phase separation, but may also need to anchor external forces to fulfil their function. Spatial localisation of condensate formation can be controlled by active cores that preferentially drive the production of condensate material at a particular point, while resistance to external forces can be facilitated by viscoelastic material properties. Here, we develop a continuum model of viscoelastic growth around an active core, and investigate the results in a spherically symmetric geometry. We find that viscoelastic stresses restrict condensate growth, but also impart resistance to deformation. We investigate the effect of varying different mechanical properties on condensate growth and strength, and also study how strain-dependent material incorporation may limit the maximum rate of growth. Finally, we compare the predictions of our model to experimental data from centrosomes in *C. elegans* embryos, identifying a parameter regime in which rapid growth can be combined with appropriate mechanical strength. Our results provide general design principles for other materials that must reconcile rapid, localised self-assembly with mechanical strength, such as focal adhesions.

Robust tree structure from stochastic branching processes: model and parameter inference from data.

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Dendritic morphology is crucial for defining a neuron's synaptic connections and function. To understand dendritic tree growth, we examine the stochastic branching dynamics, including side branching (new sprouts from existing branches), tip growth (branch tips growing and shrinking alternately), and contact-induced shrinkage (branches shrinking upon collision). Our research focuses on Drosophila sensory neurons, particularly class I and class IV neurons, which exhibit extreme morphological complexity. Class I neurons have a comb-like shape and occupy part of the hemisegment [1], while class IV neurons fill the entire segment. These neurons develop in a 2D space between the epidermis and muscles. We image them at high spatial and temporal resolution, enabling precise measurements of branching processes. The complex structure of neurons presents challenges in measurement: neurons undergo elastic deformations and rearrangements, and branches form loops when contacting pre-existing branches, complicating the reconstruction of branch hierarchies from single frames. We present several image analysis tools to overcome these challenges: 1. Deep learning-based detection of new branches, 2. Deep learning-based estimation of the age at each point of the neuron, trained on GAN-painted [2] simulations, and 3. Branch tracking using the structural information of the neuron. The fully automated analysis pipeline enables the testing of theoretical morphogenetic models and rapid iterations between perturbative biological experiments and dynamic measurements, allowing for the quantitative assessment of the role of different molecular mechanisms in the branching process. While new branches form stochastically, we observe an increasingly regular spacing between branches as development progresses. We relate this regularity to the onset of contact-induced shrinkage and propose an analytical model to explain its emergence.

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Dynamical Theory for Adaptive Systems

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Despite their differences in terms of dynamics and structures, genetic and neural networks are similar in the sense that they both are adaptive - their connections slowly change in response to the state of their constituting elements – the nodes, such as genes or neurons so as to make the collective states functionally robust under environmental stochasticity. To address this problem, we develop an exact analytical theory for multiple-time dynamical systems, where there exists a correspondence between global and local learning. As an illustration of our theory, we apply it to biological evolution, where phenotypes are shaped by gene-expression fast dynamics that are subjected to an external noise while genotypes are encoded by the configurations of a network of gene regulations. This network slowly evolves under natural selection with a mutation rate, depending on how adapted the shaped phenotypes are. Here we show how, high reciprocity of network interactions results in a trade-off between genotype and phenotype that, in turn, gives rise to a robust phase within an intermediate level of external noise.

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Probing the interfacial behavior of mucin solutions as model biofluidic drops

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The wetting behavior of simple fluids has been extensively studied; however, the concepts established for simple fluids do not apply to systems of practical interest such as salivary droplets, a complex biological fluid. Salivary droplets are composed of about 99% water and ions, and only 1% accounts for a mixture of biomolecules. The rheological and lubrication properties of saliva are attributed to the presence of mucin, a high molecular weight protein. The adsorption of a surface-active component such as mucin impacts the rheological properties of an interface, which could have implications for the wetting and spreading behavior of salivary droplets. Therefore, to create a fundamental understanding of the wetting and spreading behavior of this multicomponent fluidic system, the effects of mucin molecules near surfaces and interfaces needs to be studied. In this work, we aim to shed light on the role of mucin, as surface-active molecules, in the interfacial behavior of model respiratory droplets.

Electro-mechanical interactions in cellular systems

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Cell migration is essential for the most fundamental processes in life, such as embryonic development, wound healing, and tumor invasion. Active gel models have been very successful in describing the biophysical mechanisms that dictate cell migration [1]. The extracellular matrix is a fundamental regulator of cell function and it is well known that its viscoelastic properties determine cell function and cell migration in particular [2,3]. However, the cell is also an electric entity. Indeed, growing evidence shows that the external stimulation of cells by means of electric fields represents a precise and programmable method to control cell migration, with the potential to be integrated into cell synthetic biology. Here, we present a computational active gel model that explains and recapitulates electrotaxis across different cell types [4]. We identify membrane proteins directly related to the migration signaling pathways that polarize anodally and cathodally the cell. We show that the asymmetric distribution of charged membrane receptors towards the anode and the cathode establishes multiple cooperative and competing stimuli, which, eventually, dictates the directional migration of the cell. Our biophysical model rationalizes the mechanisms that determine electrotaxis across cell types. Our results open up new avenues not only to promote tissue regeneration or arrest tumor progression but also to engineer functional active materials.

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Hasamigami: The Art and Science of Scissored Surfaces

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We introduce an additive approach for the design of a class of transformable structures based on two-bar linkages (``scissor mechanisms'') joined at vertices to form a two dimensional lattice. Our discussion traces an underlying mathematical similarity between linkage mechanisms, origami, and kirigami and inspires our name for these structures: hasamigami. We show how to design hasamigami which unfold from a one dimensional collapsed state to two-dimensional surfaces of single and double curvature. Our algorithm for growing hasamigami structures is provably complete in providing the ability to explore the full space of possible mechanisms, and we use it to computationally design and physically realize a series of examples of varying complexity.

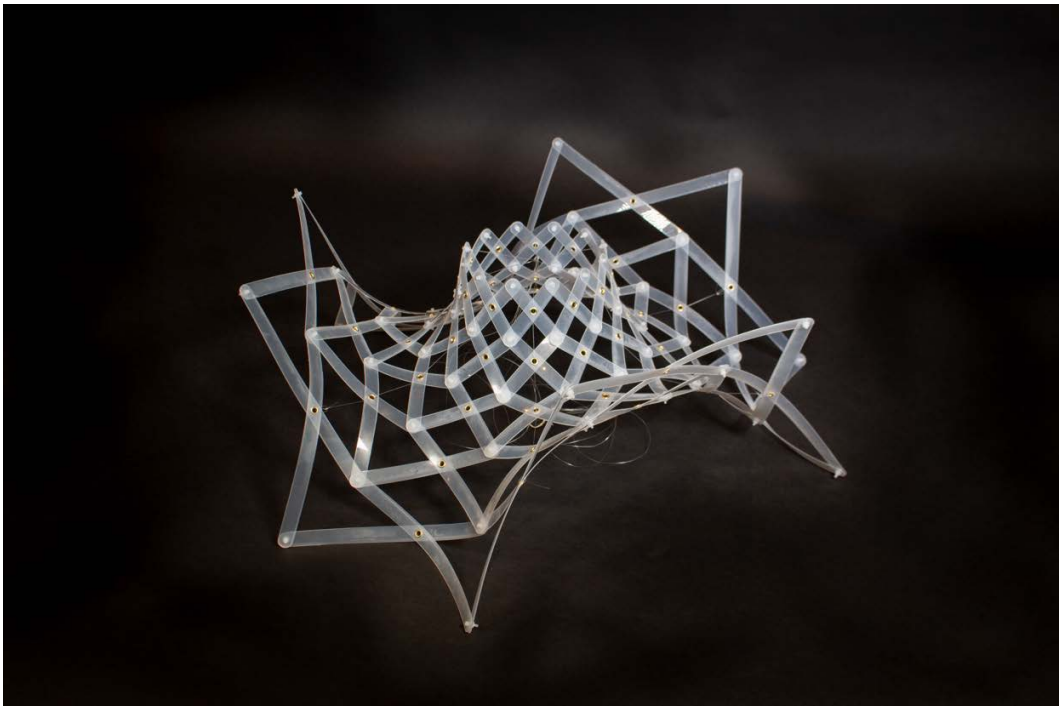

Figure 1. A hasamigami surace of constant negative gaussian curvature.

Geometric frustration meets mechanical metamaterials: large-scale stress accumulation and enhanced size-selective assembly

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Nature is replete with examples of assemblies with well-controlled sizes and structures, ranging from individual proteins to molecular motors and viral capsids all the way up to individual cells and entire organisms. A central goal of self-assembly is to build structures with functionalities inspired by nature. I here discuss the concept of geometric frustration which has recently emerged as a paradigm for controlling the shapes and sizes of self-assembled structures through the clever design of the shapes and interactions of the individual building blocks, much like how proteins come together to form complex structures in nature. In particular, I discuss how merging the two concepts of geometric frustration and mechanical metamaterials into so-called “metamembranes” (frustrated membranes with mechanical metamaterial behaviors) allows us to the have enhanced control over the structures and sizes of self-assembled materials [1]. I also briefly discuss how the inclusion of mechanical actuation into these metamembranes can imbue them with active shape-morphing properties.

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