

Alma Dal Co School 2025 on Collective Behaviour

BOOK OF ABSTRACTS

LECTURERS

Mon 29th Sept.

Collective behavior on the cellular scale

Thierry Emonet

Yale University, New Haven, USA

Cells live in communities where they interact with each other and their environment. By coordinating individuals, such interactions often result in collective behavior that emerge on scales larger than the individuals that are beneficial to the population. At the same time, populations of individuals display genotypic and phenotypic heterogeneity, which diversifies individual behavior, enables division of labor, and enhances the resilience of the population in unexpected or stressful situations. This presents a dilemma: while individuality confers advantages, it can undermine coordination, raising the question of how cell populations reconcile collective behavior with individuality. The first part of this talk will introduce some of the basic concepts that underly collective behavior on the cellular scale using examples from different systems. The second part will examine how populations of cells reconcile individuality with group behavior during collective migration, and how that leads to adaptation of phenotypic diversity without involving environment-dependent gene regulation or mutations.

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Multicellular collaboration: how do cells work together in the wild?

Allyson Sgro

Howard Hughes Medical Institute, Ashburn, USA

Cells of all kinds work together in multicellular behaviors ranging from collective migration to development. Simple laboratory assays have revealed a number of different behaviors cells engage in and how they're coordinated. However, natural environments are more spatially complex than these assays in ways that change both how cells can coordinate with one another and what behaviors they might need to perform. To understand how the complexity of natural environments shapes multicellular coordination and behaviors, we focus on how a soil-dwelling microbe communicates and behaves in a naturalistic soil model environment during starvation-induced aggregation. We find that to aggregate in synthetic soil, these cells engage in new behaviors such as bridge building and environmental remodeling that resemble how animals behave. These shared strategies for navigating complex spaces suggest there may also be shared coordination strategies that nature implements at both the cellular and organismal scales.

Tue 30th Sept.

Collective behaviour on the organismal scale

Matthieu Coppey

CNRS Paris, Paris, France

Multicellular organisms are composed of many distinct cell types that are tightly coordinated to support the functioning of the whole. The degree of collectiveness involved is extraordinarily high, so much so that the collective becomes an individual. This is most evident during development, where cascades of coordinated events unfold as cells work together to perform tasks no single cell could achieve alone. A hallmark of such collective behavior is the emergence of supracellular order. Whether observed in the system's dynamics or spatial organization, the ability of cellular collectives to self-organize into coherent entities that transcend individual cell boundaries is central to the makeup of an organism. Yet, to an external observer, these collective processes appear highly programmed. The reproducibility and robustness seen in development suggest a level of encoding, raising a provocative question: is all the complexity of multicellular coordination really encoded within the ~1 GB of our genome? If not, where does it come from? This raises a central tension: are emergent collective behaviors programmed, and if so, how? Or do they arise as spontaneous byproducts of collective dynamics with minimal constraint? I will begin with fundamentals of developmental biology to define the scale of the organism and revisit the historical debate between preformation and epigenesis. I will then focus on a specific process -collective cell migration- to highlight key features of biological collectiveness, particularly the concept of supracellularity. From there, I will turn to the concept of emergence, which underpins many forms of collective behavior. Drawing on physics, I will show how out-of-equilibrium systems can spontaneously organize, suggesting a physical route to complexity that does not rely on explicit genomic encoding. This view appears to resolve the paradox of limited genetic information giving rise to intricate organismal structures. But it also opens new questions. Can emergent behaviors be controlled to yield the reproducibility we observe in organisms? Is there a bijective mapping between cell states and whole-organism outcomes that allows collectivity to be encoded? If not, then what exactly is being selected through evolution to give rise to complex multicellular life?

Collective intelligence and collective adaptation

Mirta Galesic

*Santa Fe Institute, Santa Fe, USA
Complex Systems Hub, Vienna, Austria*

In this talk, I will first provide an overview of some of the most important findings in the field of collective intelligence and the related fields of social learning, wisdom of crowds, collective problem solving, group decision making, belief dynamics, and cultural evolution. I will then introduce the framework of collective adaptation and present ongoing empirical and modeling work on how collectives learn to adjust their cognitions and social networks in response to changing environments.

Tue 30th Sept

Collective migration in complex environments: the case of the trunk neural crest

Elena Scarpa

Cambridge University, Cambridge, UK

The neural crest is a highly invasive, multipotent embryonic cell population common to all vertebrates. Neural crest cells migrate all along the anteroposterior axis of the vertebrate embryos, crossing complex microenvironments during their journey and eventually halting their migration to give rise to a variety of derivatives. Considerable progress has been made in recent years in our understanding of the cell and mechanobiology-of-tissue-morphogenesis-and underlying collective cell migration of cranial neural crest cells. On the other hand, the extracellular environment trunk neural crest traverse in vivo is radically different from that experienced by cranial neural crest cells. I will present an overview of cranial and trunk neural crest collective cell migration under the lens of the complex interaction of this extraordinary cell population with its tissue environment.

Exploring the origin of multicellularity in real time: the MuLTEE

William Ratcliff

Georgia Tech, Atlanta, USA

The origin of multicellularity was one of the most significant innovations in the history of life. Our understanding of the evolutionary processes underlying this transition remains limited, however, mainly because extant multicellular lineages are ancient and most transitional forms have been lost to extinction. We bridge this knowledge gap by evolving novel multicellularity in the lab, using the 'snowflake yeast' model system. In this talk, I'll focus on our ongoing Multicellularity Long-Term Evolution Experiment (MuLTEE), in which we've put snowflake yeast through ~10,000 generations of selection for larger size and faster growth. We will examine key steps in the evolution of multicellularity, namely how multicellular traits arise and become heritable, how simple multicellular bodies evolve to become radically stronger and tougher, how cells divide labor through differentiation, and how groups overcome diffusion limitation by generating rapid hydrodynamic flows. Overall, our approach allows us to examine how simple groups of cells can evolve to become increasingly integrated and organismal, providing novel insight into this major evolutionary transition.

Wed 01st Oct.

Collective behavior in animal groups: from local interactions to global coordination

Irene Giardina

La Sapienza, Rome, Italy

Collective behavior is widespread in animal groups, ranging from the coordinated movements of flocks of birds and swarms of insects to the more complex structures of social species. In many cases, such behavior is self-organized, i.e., it is not driven by external factors or leaders, but it is uniquely determined by the mutual interactions between the individuals partaking in the group.

There are several aspects that have intrigued multidisciplinary interest in this phenomenon, from the sensory bases of fast responses and local interaction rules to the emergence—via the full interaction network—of global coordination on the large scales. In this section, we will explore several of these fascinating questions.

When groups are very large, hundreds to thousands of individuals, their collective properties obey well-defined statistical laws. The mechanistic process of group formation resembles, in this case, the physics of strongly interacting systems. A physics-based approach can therefore provide a powerful framework for data analysis and theoretical modelling. In the second part of my talk, I will discuss how we used such an approach to investigate natural flocks and swarms and how we developed experimentally based theories of their collective behavior. Finally, I will focus on the role of behavioral inertia and system size in determining different regimes of collective coordination and response.

Division of labour in clonal ant societies

Yuko Ulrich

Max Planck Institute for chemical ecology, Jena, Germany

Many groups rely on division of labour between group members to function. Division of labour, in turn, requires stable behavioural variation between group members. We investigated how behavioural variation is generated and modulated by the social environment in an experimentally accessible social insect, the clonal raider ant *Ooceraea biroi*. We find that increases in colony size can generate a rudimentary division of labour among otherwise identical workers. We then show how different sources of heterogeneity in group composition (e.g. genetic, demographic) have distinct effects on behaviour—ranging from behavioural convergence to behavioural divergence between behavioural types—and evaluate these results against the predictions of a widely used model for self-organised division of labour in social insects. Finally, we are collaborating with chemists to uncover some of the chemical bases of division of labour and cooperative behaviour in the clonal raider ant. I will highlight recent progress in identifying pheromones and characterising their social function, to shed light on the molecular mechanisms that regulate ant sociality.

Wed 01st Oct.

Collective adaptation in human and non-human animal groups

Ralf Kurvers

Max Planck Institute for Human Development, Berlin, Germany

In this talk, I will present recent work on how human and non-human collectives adapt to changing environments. In fish, I will present work in which we manipulate group composition and resource abundance of fish shoals in the wild, to study their causal role in shaping social network dynamics and foraging success. In humans, I will present work which integrates high-precision GPS tracking and video footage from large-scale foraging competitions with cognitive-computational modeling and agent-based simulations to uncover the decision-making mechanisms underlying human social foraging in the real world.

Thu 02nd Oct.

Scaling from individual physiology to collective metabolism in microbial communities

Matti Gralka

Vrije Universiteit Amsterdam, Amsterdam, Netherlands

Microbial communities underpin nearly every ecosystem on Earth, from the open ocean to the human gut. They drive key biogeochemical cycles and affect the health of hosts and environments alike. Understanding these communities is challenging because they are extraordinarily diverse and dynamic. In the first part of my talk, I will give a general introduction to microbial communities – why they matter and how we think they work. I will argue that a central challenge in microbial ecology is connecting two very different kinds of knowledge: the detailed mechanistic understanding we have of a few model species, and the large-scale, sequence-based descriptions we now have of natural communities that rarely contain those model species. In the second part, I will show how my own research addresses this challenge by identifying simplifying principles for marine bacteria and their communities. Focusing on the important polysaccharide chitin, we found that the bacterial members of polysaccharide-degrading communities can be described in three stably coexisting functional groups, which interact by dynamically exchanging metabolites. To dive deeper into these metabolic strategies, we used high-throughput metabolic profiling and comparative genomics to show that the vast diversity of heterotrophic bacteria can be captured by a simple dichotomy: a preference for consuming sugars versus amino and organic acids. This preference is encoded in their genomes, enabling us to make predictions about the metabolic strategies underpinning complex communities from sequencing data. Together, these results illustrate how trait-based frameworks can bridge scales and enable more predictive, theory-driven approaches to microbial community ecology.

Thu 02nd Oct.

Micro-crowdsourcing: how swarming bacteria integrate signals during collective migration

Karine Gibbs

UC Berkeley, Berkeley, USA

Collective behaviors, like those of ants, birds, and bacteria, inspire us with the promise of more immense achievements with fewer resources, and understanding these behaviors is vital in comprehending the world around us. Further, bacterial communities are dynamic societies where microbes communicate cooperatively and antagonistically with siblings and non-siblings. Individual bacteria must navigate the complexities of these interactions even as the whole population expands. In this seminar, I will discuss how bacteria use a local sense of identity to assemble and move as a community. Our model organism, *Proteus mirabilis*, lives in human and animal intestines and the environment and can cause disease after moving to the bladder. Individual cells move on the scale of micrometers per second; populations swarm on the order of millimeters per hour. Our data shows how *P. mirabilis* communicates identity between cells and how this identity-based signaling regulates cell development and population-wide swarming. Our research addresses how an organism's identity, communication, and local environment influence collective behaviors.

Ecological and Evolutionary consequences of emergent spatial structure in the gut microbiota

Markus Arnoldini

ETH Zürich, Zürich, Switzerland

The gut microbiota is an important host-associated microbial community, but what drives community assembly and dynamics in the gut is still not clear. We have analyzed the spatial distribution of bacteria in the gut of mice harboring a simplified microbiota, and found that bacteria preferentially cluster close to cells of the same species. We found that this is likely because microbial growth in the matrix of gut content leads to microcolony formation: due to its physical properties, gut content provides a stable matrix when undisturbed, but behaves more liquid-like when the gut walls apply force during a contraction. This spatial structure emerging from microbial activity can have important consequences. Depending on substrate availability and total microbial biomass, transient spatial structure can alter selection in such a system, which can change from favoring higher growth rate to a regime where metabolic efficiency is favored. Our findings offer insights into ecological and evolutionary forces at play in the gut, and enhance our understanding of how the host controls microbiota function through gut contractions and food intake.



Fri 03rd Oct.

The ecology of collective behavior

Deborah Gordon

Stanford University, Stanford, USA

Collective behavior operates as a distributed system without central control, using networks of interactions that in the aggregate allow the system to adjust to the current situation.. Collective behavior is extremely diverse. I will suggest hypotheses for how ecology shapes the evolution of collective behavior so that the dynamics of behavior, in rate, feedback regime and modularity of interaction networks, fits the dynamics of the environment. As examples I will discuss the regulation of foraging behavior in two ant species, harvester ants in the desert and turtle ants in the tropical forest. Harvester ant colonies in the desert, in a stable but harsh environment, regulate foraging activity slowly, using centralized information flow with low modularity, and feedback in which the default is not to forage so stimulation is needed to activate foraging. Turtle ants form trail networks in the canopy of the tropical forest. In an unstable but humid environment, where activity is easy, the trail is regulated locally depending on the physical configuration of each node in the vegetation, and the ants use highly modular search that fits the modular distribution of resources. The feedback regime is set with the default to go unless inhibited. The trail network can adjust to changing conditions and resources. These examples point to general trends in how collective behavior evolves in particular environments to respond to changing conditions.

Fri 03rd Oct.

Pan narrans | Collective narrative and cooperation

Chaitanya Gokhale

University of Würzburg, Würzburg, Germany

Human cooperation has always been underpinned by shared beliefs: mythologies, ideologies, and cultural narratives. These create a common ground among diverse individuals. While traditional views hold that these narratives must carry explicit moral imperatives to foster prosocial behaviour, we demonstrate that even arbitrary beliefs can effectively catalyse cooperation. Using evolutionary game dynamics, we reveal how these beliefs operate as coordination devices, fostering trust by aligning individual actions toward shared goals. Such narratives, even when morally neutral, transform self-interested actors into a cohesive group, suggesting that the power of collective imagination is rooted first in its ability to unite and, perhaps later, define morality. Socially structured communities with dense clusters only accelerate the spread of trust and collective action. These insights suggest that narrative and social connectivity are vital to sustaining cooperation, reflecting a deeply ingrained human tendency to seek common ground through shared stories.

Collective Behavior is not Collective Intelligence

Simon Garnier

NJ Institute of Technology, Rutgers, USA

The lecture will provide a general overview of collective behavior and collective intelligence in biological systems and the relationships between these concepts. It will discuss the mechanistic aspects of group living, in particular, those that lead to self-organization and the emergence of complex, large-scale collective behaviors. It will also review the conditions under which group behaviors can become intelligent, or lead to collective failure. The lecture will be accompanied by a discussion of two papers that both invite a reflection on the power and limitations of the reductionist approach in the field of collective behavior, and in science in general.

CONTRIBUTED TALKS

Tue 30th Sept.

A live-imaging system to study the spatiotemporal control of ovulation

Tabea Lillian Marx

Max Planck Institute for Multidisciplinary Sciences, Göttingen, Germany

During ovulation, an egg is released from an ovarian follicle, ready for fertilization. Ovulation occurs inside the body, making direct studies of its progression difficult. We developed live imaging methods to study the entire process in isolated mouse ovarian follicles. Our findings reveal that ovulation proceeds in three phases: follicle expansion (I), contraction (II), and rupture (III), leading to egg release. Follicle expansion is driven by hyaluronic acid secretion, creating an osmotic gradient that facilitates fluid influx into the follicle. Smooth muscle cells surrounding the follicle then drive contraction. Rupture begins with stigma formation, followed by the exit of follicular fluid and cumulus cells, and rapid egg release. These results provide a mechanistic framework for ovulation, a critical process in reproduction. Our study enhances understanding of the cellular and molecular dynamics behind ovulation, offering insights into this fundamental biological event.

Geometry, timescales and boundaries affect aggregation-based patterning in multicellular systems

Jan Rombouts

Université Libre de Bruxelles, Bruxelles, Belgium

Understanding how embryonic cells form structured patterns is an important goal of developmental biology. Here, I will discuss how we combined experimental and mathematical approaches to understand the effect of domain geometry on pattern formation. We used primary cells from mouse embryos that, after dissociation, are able to self-organize into spatial patterns. We show that there is a large role for cell movement in the formation of these patterns and corroborate this with a simple nonlocal continuum model. To study the effect of domain size on patterns, we developed analytical and numerical tools to extend our theory to short bounded domains. By pairing these theoretical results with experiments in which we manipulate the size of the cell seeding domains, we show how the patterns are controlled by domain size, timescales and boundary interactions.

Tue 30th Sept.

Repair condensates revealed by single molecule microscopy

Judith Mine-Hattab

Sorbonne University, Paris, France

The way proteins diffuse and collectively interact plays an essential role for the good functioning of the cell. Thanks to the recent progress in microscopy, it is now possible to measure the dynamics of individual proteins and explore how they change behavior in different contexts such as stress, mutations or treatments. Here, we focus on membrane-less assemblies known as bio-condensates, in particular condensates formed in response to DNA damage. By creating a micro-environment, condensates are hypothesized to help proteins coordinate themselves and collectively perform their function. An emerging hypothesis is that some condensates are formed via a phase transition inducing liquid-liquid phase separation. Using Single Particle tracking microscopy combined with micro UV-irradiation, we directly measure how proteins change diffusion in response to damage. Our results reveal the physical properties of p53 and FUS condensates in human cells, and how inhibitors can affect their formation or modulate their liquid-like properties.

Thu 02nd Oct. morning

Investigating the interactions between blacktip reef sharks and bait fish schools

Angela Albi

Max Planck Institute of Animal Behavior, Radolfzell, Germany

The interactions between predators and prey are crucial for maintaining ecosystem stability and are a significant driver of collective behaviour in animals. Despite the ecological importance of sharks, research on them is limited. Moreover, coral reefs have recently experienced significant declines in shark population. In our study, we combine drone technology and computer vision tools to analyze aggregations of fish and their interactions with predators in natural environments. We filmed blacktip reef sharks and other predatory species interacting with schools of silversides in different reef areas. We use a machine learning model to segment the outline of fish schools and track the posture of sharks and bait fish. With these measurements we analyze the behaviour of the fish in response to predation and quantify the physical properties of large swarms. Additionally, we can extract identity and kinematics of the sharks to probe whether the sharks are hunting collectively.

Movement behavior drives plastic decision-making of ant colonies during foraging

Pol Fernandez-Lopez

Centre d'Estudis Avançats de Blanes (CEAB-CSIC), Blanes, Spain

Liquid brains conceptualize living systems that operate without central control, where collective outcomes emerge from dynamic local interactions. Movement is therefore expected to play a key role in shaping these interactions, influencing how efficiently a system processes information. We empirically quantified ant movement across large spatiotemporal scales, reflecting the ecology of *Aphaenogaster senilis*. Integrating these patterns into a liquid brain framework, we replicated foraging efficiency and spatiotemporal dynamics. Our findings reveal a simple feedback mechanism governing foraging, regulated by two coexisting movement behaviors: recruits enhance information transfer and food exploitation by staying near the nest, while scouts may bypass this feedback to explore for alternative resources. This trade-off balances search efficiency with rapid information transfer. By linking empirical data with complex systems modeling, our studies underscore how movement-driven connectivity shapes collective intelligence. These insights advance our understanding of self-organization, decision-making, and emergent adaptive behavior in biological collectives.

Thu 02nd Oct. morning

Evaluating the effects of natural disasters on pathogenic resilience in a macaque population

Alba Motes Rodrigo

University of Lausanne, Lausanne, Switzerland

Climate change is intensifying extreme weather events, with severe implications for ecosystem dynamics. A key behavioural mechanism whereby animals may cope with such events is by altering their social structure, which in turn could influence epidemic risk. However, how and to what extent natural disasters affect disease risk via changes in sociality remains unexplored in animal populations. By simulating disease spread in free-living rhesus macaques (*Macaca mulatta*) before and after a hurricane, we demonstrate doubled pathogen transmission rates up to 5 years following the disaster, equivalent to an increase in pathogen infectivity from 10% to 20%. Moreover, the hurricane redistributed the risk of infection across the population by exacerbating sex-related differences. Overall, we demonstrate that natural disasters can amplify and redistribute epidemic risk in animals via changes in sociality. These observations provide unexpected further mechanisms by which extreme weather events can threaten wildlife health, population viability and spillover to humans.

Magnetic microrobot collective as model system for self-organisation

Gaurav Gardi

Max Planck Institute for Intelligent Systems, Stuttgart, Germany

Living beings often thrive in groups - from birds to bacteria. Ordered groups are formed when organisms interact locally with their neighbours, such as, force due to displacement of water by fish (hydrodynamics), chemical exchange between bacteria, and visual perception of neighbours by birds. But how do local interactions lead to the emergence of global order in self-organised groups, especially in microscopic systems? Here, we present a collective system made of magnetic microdisks. We design and control the balances of local interaction forces between the microdisks so that distinct globally ordered collective behaviours emerge. We study the effect of heterogeneity and non-reciprocal interactions on the collective behaviours of the disks. Some of the behaviours of the disks resemble crystals of starfish embryos. Overall, this talk highlights our system's capability to act as an adaptable and versatile model system for studying collective behaviours and for development of versatile microrobot collectives.

Thu 02nd Oct. afternoon

Topological defects drive self-sorting of mixed-activity microbial collectives

Oliver Meacock

University of Sheffield, Sheffield, UK

Many bacteria combine high-density lifestyles with motility, a combination of traits that is a rich source of collective behaviours. We study the pathogen *P. aeruginosa*, which moves around within biofilms using molecular grappling hooks known as type IV pili. By combining microscopic analyses with individual- and continuum-based modelling, we uncover the physical basis of this organism's collective movement and develop insights into the ecological relevance of such behaviours. Having previously shown the implications of collective motion for territorial expansion and intra-specific combat, in this talk I will discuss new data showing how it also drives segregation of mixed-activity populations. Topological defects, emergent structures where cells of differing orientations meet, are at the heart of this phenomenon: high-motility cells sort themselves into comet-like $+1/2$ defects, while lower-motility cells become enriched around trefoil-like $-1/2$ defects. This mechanism thus determines which partners motile microorganisms can associate with, with critical implications for their sociobiology.

Swimming behaviour of micro-algae in complex optical environments

Gianni Iacucci

Ecole Normale Supérieure de Paris, Paris, France

Chlamydomonas reinhardtii is a microalga equipped with an eyespot, a photosensitive organelle acting as a rudimentary light detector. It is generally thought that by aligning the eyespot with the light's direction, microalgae adjust their motion in response to light (phototaxis). However, this mechanism alone would fail to navigate diffuse, spatially complex illuminations typical of natural environments. This raises the question: can microalgae sense only light direction, or can they also respond to other illumination properties? Using tailored illuminations and single-cell tracking, we demonstrate that microalgae can detect light gradients and that their phototaxis exhibits memory, meaning their motion is influenced by the history of light intensity along their trajectory. These findings provide new insights into how *Chlamydomonas* motility is modulated and suggest innovative strategies for controlling and redirecting their movement.

Thu 02nd Oct. afternoon

Do higher-order interactions promote coexistence in diverse ecological communities?

Theo Gibbs

Princeton University, Princeton, USA

From the human microbiome to the Amazon rainforest, diverse ecological communities are widespread in the natural world, but we do not know how this diversity is maintained by the interactions between species. A central assumption in most ecological models is that the interactions in a community operate only between pairs of species. However, two species may interactively affect the growth of a third species. Although interactions among three or more species, called higher-order interactions, have the potential to modify our theoretical understanding of coexistence, ecologists lack clear expectations for how these interactions shape community structure.

In this talk, I will show that randomly-sampled higher-order interactions are unlikely to generate widespread coexistence. By contrast, higher-order interactions that have specific relationships with the underlying pairwise interactions can stabilize coexistence in diverse communities. Last, I will present ongoing experimental work that demonstrates higher-order interactions likely structure the dynamics of annual plant communities.

POSTERS

Wed 01st Oct.

1

Harnessing work production of synchronized active particles under confinement

Francesco Arceri

University of Padua, Padua, Italy

Active agents convert internal energy into motion, enabling coordinated responses to their environment. When confined, these self-propelled objects transfer finite translational and angular momentum to their boundaries. We investigate the minimal ingredients required for work production in a two-dimensional system of active particles governed by Langevin dynamics and a Kuramoto synchronization term, which promotes velocity alignment among neighbors. We first focus on reflective boundaries, identifying distinct phases-gaseous, flocking, and clustered-emerging from the interplay of alignment strength, white noise, inertia, and friction. We then extend the model to include mechanical coupling between the particles and the boundary, modeled as a ring polymer of rotating and deforming due to particle interactions.

This study offers a theoretical framework for understanding energy transfer in active systems and has a wide range of applications from the design of self-powered bio-robotic systems to the control of collective dynamics in crowded environments.

3

Deliberation during online bargaining reveals strategic information

Miruna Cotet

Complexity Science Hub, Vienna, Austria

Individual decisions often involve weighing the evidence for different options, with people exhibiting longer response times (RT) when choosing between more similarly appealing options. Thus, RT might reveal private information about the decision-maker. However, in strategic situations people are thought to have prepared plans, which would make RT uninformative. Here, we examined bargaining behavior to determine whether RT reveals information. Using pre-existing and experimental data from eBay, we show that both buyers and sellers take hours longer to accept bad offers and to reject good offers. We also show that a drift diffusion model, traditionally limited to decisions on the order of seconds, can account for eBay decisions on the order of hours, sometimes days. In summary, strategic decisions are consistent with on-the-spot evaluation. This underscores the need for game theory to incorporate RT as a strategic variable and broadens the applicability of sequential-sampling models to longer decisions.

5

How do short-range interactions affect the diversity of a microbial community?

Alessia Del Panta

University of Lausanne, Lausanne, Switzerland

Inter-species interactions shape bacterial community diversity, yet their spatial context is often overlooked. In space, interactions are typically short-range, which limits the number of interactions taking place to the ones between cells that are sufficiently close to each other. We expect the network of potential inter-species interactions (fundamental network) to be different from the network of interactions that do take place in space (realized network).

We perform simulations to understand which types of interaction networks allow for higher diversity in the spatial context. Our results suggest that negative short-range interactions play a role in maintaining diversity. We next aim at understanding how the realized network differs from the fundamental network, and how this influences the spatial patterns that emerge in space. Preliminary results suggest that the fundamental network breaks down into sub-networks containing only positive interactions, and that species involved in different sub-networks occupy distinct regions of space (domains).

7

Diverse Nitrogen Utilization Strategies Among Marine Heterotrophic Bacteria

Sarah Flickinger

Vrije Universiteit Amsterdam, Amsterdam, Netherlands

Marine heterotrophic bacteria are central to the marine nitrogen cycle. They remineralize organic nitrogen, fueling primary productivity through rapid recycling, and assimilate inorganic nitrogen, accounting for up to 55% of uptake in pelagic environments. By competing with phytoplankton for inorganic nitrogen, they impact nutrient dynamics, and potentially community composition and ecosystem function. Their broad metabolic diversity and access to diverse nitrogen compounds make understanding nitrogen preferences among bacterial species essential for predicting ecological and biogeochemical roles. While genomic data highlight the extensive diversity of marine heterotrophs, nitrogen utilization traits remain difficult to infer from genomes alone. To address this gap, we screened 186 marine heterotrophic strains for growth on 32 nitrogen sources, including inorganic compounds, amino acids, amines, amides, and nucleotides. We found that amino acids were the preferred nitrogen source across taxonomic orders and observed putative evidence of sustained growth in the absence of an added nitrogen source. These findings provide a framework for linking bacterial taxonomy and genomes with nitrogen metabolism, advancing our understanding of heterotrophs in marine nitrogen cycling.

9

Nesting architecture in social wasps

Shivani Krishna

Ashoka University, Sonapat, India

Social insects have evolved a variety of architectural formations. Bees and wasps are well known for their ability to achieve compact structures by building hexagonal cells. *Polistes wattii*, an open nesting paper wasp species, builds planar hexagonal structures. Here, using the pair correlation function approach, we show that their nests exhibit short-range hexagonal order (no long-range order) akin to amorphous materials. Hexagonal orientational order was well preserved globally. We also show the presence of topological defects such as dislocations (pentagon-heptagon disclination pairs) and Stone-Wales quadrupoles, and discuss how these defects were organised in the nest, thereby restoring order. Furthermore, we suggest the possible role of such defects in shaping nesting architectures of other social insect species.

Cooperative virulence and leaf tissue properties drive the outcome of plant-microbiota-pathogen interactions.

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Cooperative virulence and leaf tissue properties drive the outcome of plant-microbiota-pathogen interactions

Julien Luneau

University of Lausanne, Lausanne, Switzerland

Crop pathogens significantly reduce agricultural production. Early interactions between the pathogen and its environment in the host (plant immunity, microbiota, abiotic factors, etc.) are crucial because they determine whether the pathogen can establish and cause disease. However, disentangling the complexity of microscale plant-microbiota-pathogen interactions is experimentally challenging. Therefore, we developed computational simulations of plant infection and asked how plant and microbial traits contribute to pathogen exclusion. We found that initial spatial arrangement, microbiota abundance, and plant tissue bottlenecks decrease pathogen colonization. On the other hand, phenotypic heterogeneity in virulence functions promotes pathogen success through division of labor for immunosuppression. This collective behavior also led to the emergence of spatial patterns in our simulations. Plant infection experiments with pathogens carrying fluorescent reporters also uncovered the emergence of spatial and temporal patterns in bacterial virulence functions. Altogether, these results will help elucidate the mechanisms driving colonization resistance in the plant microbiome.

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Towards unifying principles of fish schooling dynamics

Arshed Nabeel

Indian Institute of Science, Bengaluru, India

Collective movement is ubiquitous in biology, across scales from cells to organisms, where individuals interact and move together with striking synchronous patterns. Importantly, the group-level order is a self-organized outcome of simple, local interactions, with little global coordination. Here, we analyse the schooling dynamics of many different species of schooling fish to identify unifying principles. Using both data-driven model discovery techniques, agent-based modelling and analytical theory, we build a unifying framework to understand the schooling dynamics of small (mesoscale) groups. Under this framework, we characterize the dynamics of fish schools into distinct classes, based on the emergent states and the role of noise fluctuations in the group synchrony. We use computational and theoretical modelling to understand simple mechanisms that leads to these different classes of order. Taken together, we aim to provide a comprehensive understanding of the dynamics of order and the role of stochasticity in fish schools and beyond.

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The role of geometry in cytoplasmic streaming

Jain Olenka

Princeton University/Flatiron Institute, Princeton, USA

This work probes the role of cell geometry in orienting self-organized fluid flows in the late stage *Drosophila* oocyte. Recent theoretical work has shown that a model, which relies only on hydrodynamic interactions of flexible, cortically anchored microtubules (MTs) and the mechanical loads from molecular motors moving upon them, is sufficient to generate observed flows. While the emergence of flows has been studied in spheres, oocytes change shape during streaming and it was unclear how robust these flows are to the geometry of the cell.

Here we use biophysical theory and computational analysis to investigate the role of geometry and find that the axis of rotation is set by the shape of the domain and that the flow is robust to biologically relevant perturbations of the domain shape. Using live imaging and 3D flow reconstruction, we test the predictions of the theory/simulation, finding consistency between the model and live experiments, further demonstrating a geometric dependence on flow direction in late-stage *Drosophila* oocytes.

Stochastic modeling of functional patterns in phytoplankton communities

Emanuele Pigani

International Centre for Theoretical Physics, Trieste, Italy

Phytoplankton communities are increasingly recognized as being shaped by functional traits, particularly gene expression, rather than taxonomic composition alone. While meta-omics technologies provide access to both taxonomic and functional information, theoretical models that link molecular-level processes to emergent community-scale patterns remain scarce. In this work, we develop a stochastic framework that integrates population-level gene abundance with transcriptional activity, capturing the joint dynamics of gene presence and expression. Applying our model to phytoplankton communities from the Tara Oceans dataset, we show that it accurately reproduces observed abundance distributions and reveals a strong temperature dependence of transcription efficiency. Our results suggest that large-scale functional patterns in microbial communities can emerge from minimal stochastic assumptions. This framework provides a quantitative baseline for understanding functional dynamics in phytoplankton and can be extended to other microbiomes and transcriptomic datasets.

From diversity to uniformity: the evolutionary impact of population mixing on bacterial predator-prey dynamics

Shaeli Saha

Indian Institute of Science, Bengaluru, India

Population mixing plays a crucial role in microbial predator-prey evolution, yet its impact remains underexplored. We evolved *Myxococcus xanthus* (predator) and *Escherichia coli* (prey) under two regimens: repeated mixing (horizontal transfer) and no mixing (vertical transfer). In the vertical regimen, prey evolved diverse resistance strategies, including generalists with high fitness in both predator presence and absence, and variants sensitive to predation but still competitively superior to ancestors. This suggests that both interspecies (predator-prey) and intraspecies (prey-prey) competition shaped evolution. Some sensitive isolates outcompeted ancestors, indicating success driven by intraspecies competition rather than resistance. In contrast, the horizontal regimen selected for a single, uniformly resistant strategy, with prey outcompeting ancestors across conditions, suggesting an arms-race-like response. Our findings demonstrate that population mixing shapes coevolutionary trajectories, shifting predator-prey dynamics between Red Queen-like diversity, where multiple resistance strategies coexist, and an arms-race-driven response favouring uniform resistance.

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Pathways for overturning consensus in human collective decision-making

Andrei Sontag

University College London, London, UK

Political decisions are the epitome of how many aspects of our lives are determined by collective decision-making. However, active participation in collective decision-making is often highly variable, with many individuals temporarily abstaining from voting in the face of uncertainty. Whilst memory and noise have been found to aid consensus formation, the role of neutrality in collective decision-making is not well understood, and the level of individual behavioural complexity required for the emergence of group consensus is not well-characterised. In this talk, I will show that symmetric autonomous systems with neutral intermediate states, such as voters of a two-party system who can abstain, present only two possible dynamical pathways for consensus switching. I will also show how experiments with human participants helped us verify our predictions. The typical pathway observed in our experimental data corresponds to an increase in the number of abstentions as the system transitions from one state of consensus to the other, suggesting that they play a critical role in facilitating consensus change by reducing the effective population size, making it more susceptible to fluctuations, as opposed to what has been previously believed. Our findings provide a parsimonious explanation of consensus formation and change, giving insight into distributed decision-making protocols in animal and human collectives and suggesting efficient solutions to automated collective decision-making problems.

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A modular, low-cost co-culture plate for studying microbial community and environmental interactions

Carles Tardio Pi

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Microbial interactions within a community, as well as between the community and its environment, are central to its dynamics, influencing microbial diversity, abundance and function. To deepen our understanding of intra-community interactions, we use co-culture chambers that position individual species on opposite sides of a permeable vertical membrane, facilitating controlled exchange of diffusible molecules. Analogously, to explore community-environment interactions, we integrate a horizontal membrane, inspired by isolation chip designs, which enables bidirectional diffusible exchange with the surroundings.

We present a low-cost, modular co-culture device for standardized optical density measurements of different community permutations across various spatial arrangements. We demonstrate its application in a seven-species rhizosphere isolate community and assess its versatility across in vitro, in vivo, and in situ experimental setups. By adapting this system to diverse contexts—from synthetic industrial consortia to biodiversity monitoring in synthetic ecology—we highlight its potential as a scalable, tool for investigating microbial interactions.

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Species-specific collective behaviours shape their interactions in soil-like environments

Andrea Zanon*EMBL, Heidelberg, Germany*

Microbes within soil communities exhibit diverse collective phenotypes that shape their ecological interactions. My research focuses on the interplay between the Gram-positive bacterium *Bacillus subtilis* and the amoebal predator *Dictyostelium discoideum*. *B. subtilis* expresses many collective phenotypes, including biofilm formation, whereas *D. discoideum* cells can aggregate into fruiting bodies in response to starvation. However, how these collective phenotypes influence each other remains largely unexplored. To address this, I developed a synthetic-soil assay to investigate these interactions in real-time and high-throughput. My findings reveal that different collective strategies confer distinct survival advantages to *B. subtilis* and uniquely impact *D. discoideum* multicellular development. This approach highlights the importance of studying microbial collectives in their ecological context to better understand predatory dynamics in soil ecosystems.

Fri 03rd Oct.

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Communication-driven geometric bias enhances multi-agent olfactory search efficiency

Francesco Boccardo*Università di Genova - Machine Learning Genoa Center, Genoa, Italy*

A vital problem for many living organisms is to find the source of an odor carried by a turbulent flow, e.g., to find food or to escape from a predator. When multiple individuals search simultaneously, communication can enhance group performance. We study the dynamics of multi-agent olfactory search using a swarm model inspired by moth behavior, where agents process two types of information: private (olfactory cues, perceived individually) and public (visual cues from neighbors). These are weighted by a "trust parameter" that regulates communication. When the olfactory signal is sparse or absent, agents mainly explore space with a casting behaviour biased toward the opposite direction of the turbulent flow. Our numerical and analytical results show that increasing communication amplifies this bias, affecting the swarm's overall efficiency. This highlights how the success of collective olfactory search depends on both the degree of communication and the geometric constraints of the environment.

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Learning from Evolution to reorganise groups to find better solutions
Joshua Cox*Complexity Science Hub, Vienna, Austria*

Evolution can be considered a combinatorial search problem for genetically fit sequences. Groups solving their own combinatorial search problems can learn from the successful strategies of evolution. One such insight is that evolution has mechanisms to maintain diversity. In contrast, group leaders can homogenise search efforts given the best current solution, reducing diversity and harming performance. This harm is magnified in the face of changing environments, paralleling the tension between evolving specialist or generalist phenotypes. The interplay between search strategy (e.g. copying best or majority conforming) and network structure (e.g. degree of centralisation) complicate the best way for groups to organise themselves to find the best solutions. Combining computational biology and social science, we present simulation findings on how groups should reorganise themselves to find solutions in changing problem landscapes. We contribute new methodological approaches to facilitate the use of combinatorial search landscape in future behavioural experiments.

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**Bridge over troubled soil: learning how groups of cells
navigate voids in their environment****John Durel***Janelia Research Campus, Ashburn, USA*

Cell signaling and collective migration in the social amoeba *Dictyostelium* have been studied for well over half a century, but nearly all of this work has relied on 2D substrates. These traditional experimental conditions are convenient for imaging but do not necessarily yield results representative of the amoeba's behavior when confronted with the wild environments in which they evolved. For example, a continuous planar environment cannot give insight into how starving cells migrate up to the soil surface as part of their developmental cycle—a traversal which must overcome topological irregularities in often ephemeral substrates. By investigating these processes in engineered 3D soil microcosms coupled with high-speed fluorescence microscopy, we are able to see intriguing modes of migratory behavior that shed light on the means by which cellular aggregates form bridges to cross physical discontinuities that would be otherwise insurmountable for single cells.

Building a biophysical model of insulin-secreting organoids to design optimal tissue architectures

Ilaria Iuliani

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Type 1 diabetes is characterised by the autoimmune destruction of pancreatic β -cells, the only source of endogenous insulin. Transplantation of islet cells offers a therapeutic solution, but its success is often limited by immune rejection and poor cell viability. To address these challenges, we aim to engineer a functional, immunoprotected bioartificial endocrine pancreas by combining dissociated pancreatic islet cells (ICs), extravillous cytotrophoblasts (evCTBs), and a human amniotic membrane-derived hydrogel (amniogel). Using computational models, we investigate how organoid size, cellular composition, and hydrogel-mediated nutrient and oxygen diffusion affect oxygen availability and cell viability. A central objective is to define a radius range that ensures both physiological allometric scaling and sufficient oxygenation at the spheroid core. To this end, we developed a biophysical model of oxygen dynamics informed by experimental data. Brightfield and confocal imaging quantified cell size and spatial organisation, while profilometry and scanning electron microscopy (SEM) were used to characterise microwell geometry. Basal respiration was measured using the Seahorse Mito Stress Test. These data were integrated into a framework coupling a steady-state reaction-diffusion equation with Michaelis-Menten kinetics, and finite element simulations were performed in COMSOL Multiphysics. This framework enabled us to predict oxygen distribution and consumption within organoids of varying sizes and cellular compositions. These results contribute to the design of optimal tissue architectures for functional and immunoprotected insulin-secreting organoids.

Cilia synchronization and emergence of directional flow in a closed confinement

Jingyi Liu

University of Southern California, Los Angeles, USA

In vertebrate embryogenesis, coordinated ciliary beating within the confined embryonic node generates flow patterns that is crucial for left-right asymmetric development, so as proper organ development. This flow-mediated transport of morphogens is an example of how biological systems utilize hydrodynamic coupling to self-organize and regulate cellular processes. Inspired by this mechanism, we develop a minimal model of distributed hydrodynamically coupled rotors confined to an inner spherical surface in a Stokes flow regime. Through numerical analysis of their phase dynamics, we identify directional flow formation accompanying the emergent synchronization and traveling wave patterns of rotor phases. Our findings establish a connection between directional flow formation and cilia synchronization driven by hydrodynamic interactions. This work provides a physical framework that helps explain self-organized intracellular transport.

Prediction of minimal metabolic exchanges for microbial communities in a chemostat at steady state

Alix Moawad

ETH Zürich, Zürich, Switzerland

Microorganisms growing together within a community can either cooperate by exchanging nutrients or compete for the same nutrients. The resulting complex network of interactions leads to the emergence of various community functions. However, metabolic interactions are difficult to identify experimentally, and current computational predictions assume a community objective. Here, we propose a community objective-free computational method using a constraint-based metabolic model for predicting the minimal exchanges of nutrients between species coexisting in a chemostat at steady state. For a toy model, we showed that the species can be involved in different metabolic strategies, depending on the scarcity of resources and on their biomasses, as well as the existence of alternate steady states. We then analysed all possible pairs of amino acid auxotrophic *E. coli* strains and compared the predicted minimal interactions with experimental data. Overall, our approach proves promising for better identifying community interactions, for example, in the gut microbiome.

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The role of behavioural individuality in the collective behaviour of vertebrates

Marina Papadopolou

Tuscia University, Viterbo, Italy

Animals on the move fascinate us with the diverse spatiotemporal patterns of their collectives. Identifying unique and common traits across species is necessary to understand the ecological and evolutionary processes that shape this diversity. However, species-specific characteristics, such as individual heterogeneity, are often overlooked in theoretical studies of collective behaviour. In this talk, I will present ongoing projects on several species, such as schools of genetically-identical Amazon mollies, flocks of homing pigeons, and troops of chacma baboons, focusing on identifying inter- and intra-specific variation in collective motion and decision-making, and understanding the individual rules that underlie their collective dynamics while moving or escaping predators. We approach these through the remote sensing and tracking of the animals' movement in the laboratory and the field, the use of robotic conspecifics and predators, and the development of data-inspired agent-based models, with future applications in the field of swarm robotics and wildlife conservation.

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The mechanisms of microbial cooperation: role of diverse nutrient environments and metabolic trade-offs in shaping crossfeeding

Anjana Prasad

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Microorganisms exist in communities and exchange metabolites to sustain growth. Such interactions shape the structure and function of these communities. While metabolic cross-feeding offers evolutionary and ecological advantages, the underlying mechanisms remain poorly understood. This study establishes the existence of metabolic trade-offs, arising from inherent metabolic architecture of bacteria within communities, and whether cross-feeding can break these trade-offs providing growth advantages. Coexisting bacterial species may have different resource preferences which influences metabolic costs and flux distributions. In the first phase, we characterized the carbon utilization profiles of various bacterial strains. Our experiments suggest that carbon source preferences impact cellular resource allocation and trade-offs in amino acid production. Pairwise and community-level co-culture experiments will reveal how trade-offs resulting from diverse carbon source preferences influence cross-feeding interactions and strain fitness. This work aims to provide insights into drivers of metabolic division of labor, offering a framework for designing microbial consortia for biotechnological applications.

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Improving community breeding strategies through evolutionary individuality first

Afra Salazar

University of Lausanne, Lausanne, Switzerland

Microbial communities play crucial roles in ecosystem functioning, driving an interest in designing and controlling microbial communities towards optimised or novel functions. However, promising strategies such as community breeding have shown limited success. That is because microbial communities in the laboratory are not evolutionary individuals. Here, we built a consumer-resource model to simulate the ecology and evolution of microbial communities subjected to breeding. We simulate hundreds of communities, measuring properties that constitute a measurement of their evolutionary individuality. We hypothesise that the response to selection should correlate positively with the average degree of individuality. Further, we hypothesise that communities whose transition is irreversible will outcompete those in which within-community competition reemerges. Overall, our work is intended to provide a novel perspective to community breeding discussions, helping experimentalists design more effective breeding strategies. It remains to be seen whether our hypotheses hold. We hope to gather enough data to provide answers on time for the school.

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Uncovering predictive rules for phage community assembly across scales

Rachel Szabo

ETH Zürich & Eawag, Zürich, Switzerland

In microbiomes – the microbial collectives that sustain ecosystems across our planet – there is a constant contest between communities of bacteria and their viruses, known as phages. We remain unable to predict how phages shape microbiomes. This is, in part, because our primary framework for interpreting phage communities is taxonomic, but phage taxonomy is uncorrelated with their traits underlying their propagation and survival. Therefore, I am developing a quantitative, trait-based framework for predicting the assembly of phage communities within microbiomes. I am using this approach to address questions about phages across scales of complexity: Do trade-offs in phage traits define distinct ecological strategies? How do host physiology and environmental factors tune phage-host interactions? Which phage and host traits are predictive of their collective dynamics? To this end, I am combining systematic phenotyping of diverse *E. coli* phages with mathematical modeling to test the predictability of phage infection outcomes in synthetic communities.

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Coordinated expansion and virulence during collective migration

Lam Vo*Yale University, New Haven, USA*

During collective migration, bacterial cells spatially organize along the attractant gradient they generate. Faster gradient climbers lead at the front, where the attractant signal is weaker, while worse climbers follow at the back, where the signal is stronger, but eventually fall behind. Often in pathogens, chemotaxis and motility are co-regulated with virulence factors through signaling by the secondary messenger cyclic-di-GMP (cdG). This raises the question: could virulence traits be spatially sorted during migration? Using the sensor cdGreen2.1, we found that cdG levels are spatially sorted in migrating populations of *Pseudomonas aeruginosa*, but not in other species. We also observed spatial organization of virulence traits, such as *cdsA* (a biofilm matrix component) and *exoT* (a type-3 secreted effector), in migrating *P. aeruginosa* populations. These findings suggest that spatial sorting of cdG levels may drive the co-organization of chemotaxis and virulence traits, allowing bacterial pathogens to migrate and perform virulence simultaneously.

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Task allocation and collective defences in clonal ants

Li Zimai*Max Planck Institute for Chemical Ecology, Jena, Germany*

Social organisms thrive through cooperation but simultaneously face heightened risks, such as disease transmission. Social insect colonies deploy sophisticated responses to these challenges, integrating individual and collective behavioural and immune defences. Using the clonal raider ant (*Ooceraea biroi*)—a queenless, asexually-reproducing species offering unparalleled experimental control over group composition—we investigate how colony organisation, infection risk, and collective defence interact. By integrating automated behavioural tracking, molecular tools, and controlled exposure to threats in ant colonies composed of genetically identical, age-matched individuals, we address three interconnected questions: (1) how does division of labour and infection risk shape one another? (2) does individual immune investment mediate these dynamics? and (3) what are the social drivers of specialisation in defence? This work sheds light on the coordination of behavioural individuality and colony-level defences in social systems.

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