MATTER TO LIFE CONFERENCE

June 9 - 11, 2026

Forum of Bildungscampus
Bildungscampus 1, 74076

Sloan Foundation and Max Planck School Matter to Life

ALFRED P. SLOAN
FOUNDATION

MAX PLANCK SCHOOL
matter to life

Welcome to the Joint Matter to Life Conference 2026!

We are delighted to welcome you to Heilbronn for the second edition of the joint Matter to Life Conference between the Alfred P. Sloan Foundation and the Max Planck School Matter to Life.
Two years ago, the Sloan Foundation brought us together for the first time in New York – this year, we are proud to be your hosts at the Bildungscampus Heilbronn. Over three days, PhD candidates, scholars, and researchers from both programs will come together for a rich scientific exchange spanning origins of life, synthetic cells, biophysics, and the chemistry of living systems, with ample time for discussion, collaboration, and networking.
We hope the conference will inspire new ideas and new connections along with strengthening existing collaborations – and that you will also enjoy a little taste of Heilbronn along the way.
We are thrilled to have you here!

If you have any questions, please don't hesitate to reach out to the organizing team:
Julia Ricken, Scientific Coordinator
Phone: 0049 160 99444284
Email: mattertolife@maxplanckschools.de

Sincerely,
Joachim Spatz, Max Planck School Matter to Life and on behalf of Ernie Glover, Director of the Alfred P. Sloan Foundation's Matter-to-Life Program

CONTENTS

Matter-to-Life Conference 2026 - Program Overview

Tuesday, 09 June 2026

09:00 – 09:15	**Petra Schwille & Ernie Glover – Opening Remarks**
09:15 – 10:15	**Frank Jülicher; Kerstin Göpfrich; Thomas Scheibel** *Chair: Petra Schwille*
10:15 – 11:00	**Coffee Break**
11:00 – 12:20	**Petra Schwille; Dieter Braun; Karin Jacobs; Thomas Preston** *Chair: Jennifer Ross*
13:00 – 14:00	**Lunch & Poster Session**
14:00 – 15:20	**Philip Kurian; Nicholas Hud; Neal Devaraj; Pablo Sartori** *Chair: Thomas Scheibel*
15:30 – 16:00	**Coffee Break**
16:00 – 17:20	**Sam Peng; Job Boekhoven; Markus Covert; Wilhelm Huck** *Chair: Ido Golding*
19:00	**Conference Dinner – Alte Reederei**

Wednesday, 10 June 2026

09:00 – 10:20	**Erwin Frey; Rebecca Schulman; Patrick Oakes; Zhiyue Lu** *Chair: David Baum*
10:20 – 10:30	**Group Photo**
10:30 – 11:00	**Coffee Break & Poster Session**
11:00 – 12:40	**Cecilia Garraffo; Jennifer Ross; Charlie Carter; Srigokul Upadhyayula; Michael Murell** *Chair: Erwin Frey*
13:00 – 14:00	**Lunch & Poster Session**
14:00 – 15:00	**Kai Johnsson; Dimitris Missirlis/Peer Fischer; Roseanna Zia** *Chair: Sam Peng*
15:00 – 15:30	**Coffee Break & Poster Session**
15:30 – 18:00	**Experimenta Visit**

Thursday, 11 June 2026

09:00 – 10:20	**Anton Jackson-Smith / Richard Murray; Milo Lin; Ido Golding; Andrew Spakowitz** *Chair: Andrea Musacchio*
10:20 – 11:20	**Coffee Break & Poster Session**

11:00 – 12:40	**Laura Heinen, Joachim P. Spatz; Seraphine Wegner; Andrea Musacchio; Kate Adamala** *Chair: Zhiyue Lu*
13:00 – 14:00	**Lunch & Poster Session**
14:00 – 15:15	**David Baum; Ayusman Sen; Rein Ulijn** *Chair: Job Boekhoven*
15:00 – 15:15	**Closing Remarks**
15:15 – 16:00	**Coffee Break**

Speaker Abstracts

9 June
9:15 am

Emergent crystalline order in a developing epithelium – Frank Jülicher

Max Planck Institute for the Physics of Complex Systems

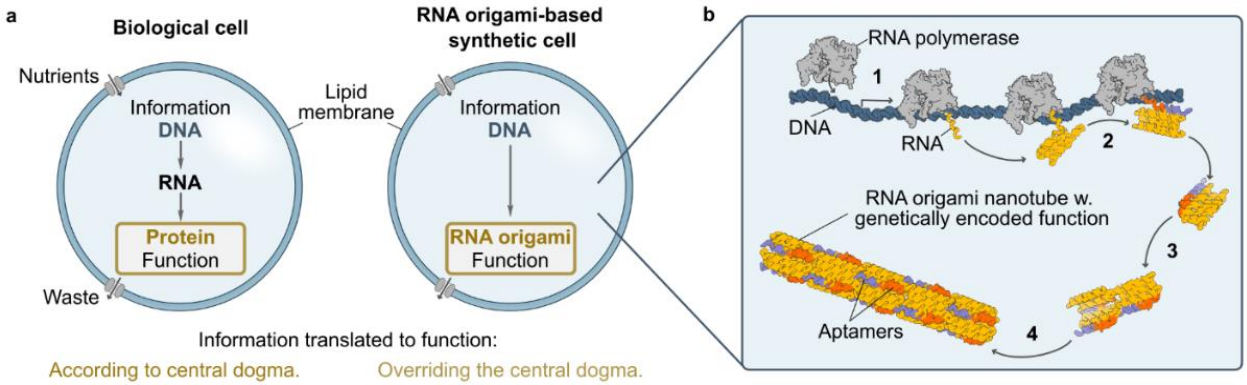
A fundamental question in Biology is to understand how patterns and shapes emerge from the collective interplay of large numbers of cells. Cells forming two-dimensional epithelial tissues behave as active materials that can undergo remodelling and spontaneous shape changes. Focussing on the fly wing as a model system, I will discuss the physics underlying the emergence of crystalline order in the wing epithelium during the pupal phase of morphogenesis. Using a vertex model of epithelial tissue, we demonstrate that when cell size heterogeneity exceeds a critical value, cellular packing remains disordered, whereas reducing heterogeneity below this value induces a phase transition to crystalline packing. This order to disorder transition extends a known phase transition in colloidal systems to out-of-equilibrium ordering. Combining these results with analysis of experimental data reveals that cell size heterogeneity controls crystallization in the developing fly wing during pupal development. Shear flows facilitate this process but are not the main driver of the disorder-to-order transition. Our work reveals how order can emerge during morphogenesis by the dynamic remodelling of tissues.

9 June
9:35 am

RNA Design for Synthetic Immunology – Kerstin Göpfrich

Center for Molecular Biology of Heidelberg University, Heidelberg University, Berliner Str. 45, 69120 Heidelberg, Germany; k.goepfrich@zmbh.uni-heidelberg.de

RNA design is still in its infancy compared to protein folding and DNA nanotechnology. Nonetheless, fundamental questions on the origins of life in an RNA world as well as the rise of RNA therapeutics make RNA design a highly exciting upcoming field. The vision of our group is to create a lipid vesicle as a simple model of a cell, capable of self-replication and evolution, that operates based on custom-engineered molecular hardware made from highly functional and folded RNA. We have recently developed an open-source software platform for RNA design, pyFuRNAce [1], which enabled us to realize the first RNA origami to reach the 20kb scale – limited only by current gene synthesis capabilities (unpublished). Our RNA origami is an order of magnitude larger than previous co-transcriptional RNA structures, exceeding the theoretical size limit postulated for RNA origami (at 8.5kb). It is larger than DNA origami monomers, and larger than the entire human ribosome. This leap was made possible by (i) a dedicated inverse folding algorithm and (ii) a co-transcriptional folding pathway that bypasses previous theoretical size limits (unpublished). We also demonstrate programmable assembly through multimeric puzzles in a “multi-gene” one-pot transcription reaction. By integrating specific membrane aptamers, RNA sequences which target lipid membranes, into cytoskeleton-like RNA nanostructures [2], we control membrane mechanics and pore formation in giant unilamellar lipid vesicles. We further show that mutagenesis can lead to emergent phenotypes and functions even in relatively simple systems [3]. Since all our RNA nanostructures are produced by transcription from a synthetic gene, they can, in principle, transfected and expressed in cells. Due to their compatibility with directed evolution pipelines [4], and the possibility to integrate target aptamers and ribozymes [5], we envision that they contribute to the development of evolvable synthetic cells as well as RNA-based vaccines and therapeutics.



Co-transcriptional folding of RNA origami-based hardware for synthetic cells [2].

References:

[1] Monari, Luca, […], Göpfrich, K. "PyFuRNAce: an integrated design engine for RNA origami." *Nature Communications* 16.1 (2025): 10815.

[2] Tran, Mai P., […], Göpfrich, K. "Genetic encoding and expression of RNA origami cytoskeletons in synthetic cells." *Nature Nanotechnology* 20.5 (2025): 664-671.

[3] Verstraeten, William, […], Göpfrich, K. "Genetic encoding and mutagenesis of RNA droplet phenotypes.", *ChemRxiv* (2025). In revision in *Nature Chemical Engineering*.

[4] Maurer, Stefan J., […], Göpfrich, K. "Automated Image-Based Cell Sorting by Targeted Photopolymerization." *bioRxiv* (2025): 2025-12. In revision in *Nature Communications*.

[5] Giessler, Franziska, […], Göpfrich, K. "Growth, dissolution and segregation of genetically encoded rna droplets by ribozyme catalysis." *Angewandte Chemie International Edition* 65.7 (2026): e19002.

9 June
9:55 am

Biofabrication using spider silk proteins – Thomas Scheibel

University of Bayreuth

Spider silk is a protein fiber with excellent mechanical properties such as strength and toughness. We have developed biotechnological methods to obtain structural proteins mimicking natural ones, as well as spinning techniques to produce protein threads closely resembling natural silk fibers. In addition, we employ silk proteins in other application forms such as hydrogels or coatingss with tailored properties, e.g. we designed spider silk-based sheets and scaffolds that prevent adherence of microbes. Without microbe adherence, biofilm formation cannot occur, which lowers the frequency of infections in surgical patients. The designed spider silk scaffolds are even bioselective, while repelling microbes they allow for human cell attachment. Exemplarily, 3D-printed spider silk scaffolds can be used for the growth of heart muscle patches.

9 June
11:00 am

Designing Key Functions for Minimal Cells – Petra Schwille

MPI of Biochemistry, Martinsried

Bottom-up synthetic biology aims to construct cell-like systems from minimal, well-characterized components, building complex biological functions through controlled assembly rather than the modification of existing organisms. A central challenge in this approach is that natural proteins, having evolved for specific intracellular environments, often behave unexpectedly when reconstituted in synthetic cells, and tend to lose or modify their desired function when combined with other modules. I will present experimental work from our group addressing these challenges, and suggest that de novo protein design offers a fundamental shift in how synthetic cells may be constructed in the future. Rather than searching for natural proteins that approximate a desired function, computational design tools now allow the generation of entirely new proteins tailored to the environment and functional requirements of a synthetic cell.

9 June
11:20 am

Homing in on the Origin of Life in the Lab – Dieter Braun

LMU Munich

We are pursuing lab experiments to assemble a hypothesis for the emergence of Life. We will review the lessons we have learned in recent years. These experiments challenged preconceptions often taken for granted in the field, such as: Life emerged in the liquid state • Activation is at the 5' end of RNA • Life emerged at pH 7 • RNA is unstable and does not hybridize at high pH • Amino acids to not play an early role • RNA is only catalytic in the form of Ribozymes • Chirality has to be solved at the nucleotide level • Activated molecules are sufficient to drive early evolution • Early life needs cells • Early life required constant molecule synthesis • Origin of Life is slow.

The hypothesis that emerged from these lab experiments is as follows: Polymerising molecules, in our case RNA, are exponentially amplified from mixtures by geological flow non-equilibria in microscale porous rock matrices. We focus on 2',3'-cyclic phosphate activated nucleotides which are found to polymerize to RNA efficiently in the dry state at the pH of 9–10. This pH is found on volcanic islands even today. Templated ligation in liquid state at the same pH is efficient and precise and will create Darwinian evolution through autocatalytic replication networks. The characteristics of RNA polymerization and templated ligation will self-select left- or right-handed RNA strands, thus not requiring an initial homochiral pool of RNA monomers for Darwinian evolution.

While wet-dry cycles can grow these networks, the dynamics of replication is significantly enhanced when the RNA oligomers are pinned, fed, and self-selected for replication speed and increasing length by local geological flows. Modern biochemistry in the form of the PURE system is accumulated and fed by the same geological flow settings inside pores of rock, demonstrating a geological setting for long-term evolution without the need for protocells. In the present of lipids, these pinned molecule distributions are shown to autonomously encapsulate and accumulated into giant vesicles, creating a bridge towards lateral gene transfer and the evolution of modern cells.

9 June
11:40 am

Proteins, Vesicles, Bacteria: New Insights From Physics – Karin Jacobs

Saarland University

Karin Jacobs, Hannah Heintz, Samer Alokaidi, Jens Uwe Neurohr and Frank Müller
Experimental Physics and Center for Biophysics, Saarland University, Saarbrücken, Germany

Biological function often begins at interfaces. Proteins adsorb, vesicles assemble, and bacteria attach to surfaces before developing into biofilms. In this talk, I will focus on one example where physics provides particularly direct insight: the initial adhesion of *Staphylococcus aureus* to abiotic surfaces.

Using atomic force microscopy-based single-cell force spectroscopy, we study how a living bacterial cell interacts with materials of defined chemistry and topography. These measurements reveal that bacterial adhesion is governed not only by molecular biology, but also by physical parameters such as hydrophobicity, nanoscale roughness, contact geometry, and the thermal motion of cell-wall macromolecules [1-3]. Recent results further show that *S. aureus* should not be treated as a uniformly adhesive sphere. Instead, adhesion appears to be heterogeneously distributed over the bacterial surface, with localized adhesive patches contributing strongly to cell-surface interactions [1].

Together, these findings illustrate how physics can uncover hidden structure in biological adhesion: from molecular interactions to whole-cell mechanics and early biofilm formation. The talk will highlight how such approaches may help us understand why bacteria attach so efficiently to some materials, and how this knowledge could guide the design of anti-adhesive surfaces.

[1] C. Spengler et al., Soft Matter 20 (2024) 484.
[2] E. Maikranz et al., Nanoscale 12 (2020) 19267.
[3] F. Nolle et al., ACS Omega 10 (2025).

9 June
12:00 pm

Single-Particle Studies of Prebiotic Photochemistry in Aerosol Microdroplets – Thomas Preston

McGill University

Single-particle studies provide a direct route to probing prebiotic photochemistry in aerosol microdroplets under controlled environmental conditions. In this work, we use levitated droplets as model atmospheric microreactors to examine how confinement, composition, relative humidity, and irradiation influence chemical transformation pathways relevant to early Earth environments. By combining optical trapping or electrodynamic balance methods with Raman spectroscopy and mass spectrometry, we track size-dependent changes in individual particles without ensemble averaging. These measurements help reveal how aerosol microdroplets concentrate reactants, alter reaction kinetics, and promote photochemical processes that could have contributed to molecular complexity in prebiotic atmospheres.

9 June
14:00 pm

Morphological Computational Capacity and Nonequilibrium Problem-Solving of the Aneural Slime Mold Physarum Polycephalum – Philip Kurian

Howard University

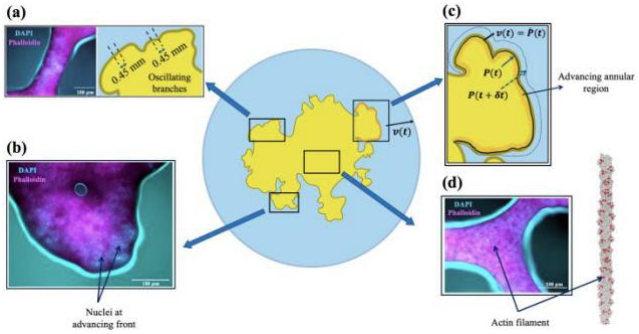


Fig. 1: **Distinct physical degrees of freedom equip the slime mold amoeba with unique morphological capabilities, which determine respective upper bounds on biocomputing speeds—a first-ever quantification in an aneural organism.** The figure illustrates with histological stains (DAPI for DNA, phalloidin for actin filaments) the biophysical processes that confer on *Physarum* distinct zones of computational power: (a) Oscillating branches act as individual hydrodynamic oscillators. (b) Dividing nuclei and mitochondria localized at the advancing front mirror the spatial distribution of ATP. (c) The rate of perimeter expansion characterizes the kinetic growth of the organism's advancing front (d) Actin filament bundles with organized tryptophan networks (shown in red) are predicted to maintain photoexcited superradiant states for ultrafast information processing [1, 6].

As physical systems, all life in the universe processes information according to physical laws. Estimates for the computational capacity of living systems generally assume that the fundamental information-processing unit is the Hodgkin-Huxley neuron. However, Physarum polycephalum, a unicellular, multinucleated amoeba, is capable of complex problem-solving despite lacking neurons [1, 2]. By analyzing growth dynamics in two distinct Physarum strains under diverse biological conditions, we map morphological evolution to information processing (Fig. 1). As the Margolus-Levitin theorem constrains maximum computation rates by accessible energies for unitarily evolving (closed) systems, we analyze high-throughput time-series data of Physarum's morphology—quantified through area, perimeter, circularity, and fractal dimension—to determine upper bounds on the logical operations achievable through hydromechanical, chemical, kinetic, and quantum-optical degrees of freedom [3-6]. Treating the slime mold as a driven-dissipative system of coupled oscillators, we prove that the bound for the corresponding open quantum system is higher than the Margolus–Levitin bound by at least a factor of $\pi/\_\sqrt{2}\_$. The resulting enhancement in computational rate is largely robust to the choice of cutoff energy and the system size. Notably, a crossover in the computational enhancement is observed in the moderate-coupling regime at drive and dissipative strengths consistent with the Markovian approximation. Fourier and power spectral density analyses of Physarum while solving the traveling salesman problem (TSP) also reveal signatures of Fröhlich condensation in the optically pumped, non-equilibrium steady state [2]. The optical drive, based on a modified Hopfield network, induces a defining, predictable bifurcation in the synchronization dynamics between solution and non-solution branches, consistently observed across 41 trials with robust statistics and spanning multiple TSP sizes from four to eight cities. Suggesting more efficient search algorithms and improved slime-machine computing interfaces, our results also motivated a revisiting of the computing limits of cytoskeletal architectures [3], where superradiant states in proteinaceous tryptophan lattices allow information-processing pulses at orders of magnitude faster speeds than conventional Hodgkin-Huxley chemical potential spikes, at significantly lower power consumptions, by operating within two orders of magnitude of the quantum speed limit for ultraviolet-excited states. The robustness of superradiant states (~picoseconds) complemented by subradiant states (~seconds to minutes) in these protein architectures thus offers a novel paradigm for understanding the role of large collectives of quantum emitters in warm, wet, and wiggly

environments, and it may illuminate the vast computational capacities of both neural and aneural organisms [1-3] in the search for life on other habitable planets.

ACKNOWLEDGEMENTS: This work was supported in parts by the Alfred P. Sloan Foundation Matter-to-Life program; the Howard University Graduate School; and the Guy, Chaikin-Wile, and National Science Foundations. HPC resources are provided by the Leadership Computing Facilities at Argonne and Oak Ridge National Laboratories. Portions of this work were discussed during PK's residencies as a Fellow of the Kavli Institute for Theoretical Physics and as a Simons Scholar at the UCLA Institute for Pure and Applied Mathematics.

REFERENCES: [1] S. Bajpai, A. Lucas-DeMott, N.J. Murugan, M. Levin, & PK. Morphological computational capacity of Physarum polycephalum. arXiv:2510.19976 [quant-ph] (2025). [2] S. Bajpai, M. Aono, & PK. Tracking and distinguishing slime mold solutions to traveling salesman problems through synchronized amplification in the non-equilibrium steady state. arXiv:2504.03492 [physics.bio-ph] (2025). [3] PK. Computational capacity of life in relation to the universe. Science Advances 11, eadt4623 (2025). [4] H. Patwa & PK. Single-photon superradiance and subradiance in helical collectives of quantum emitters. Physical Review A 113, 043708 (2026). [5] N.S. Babcock, G.M.-Cabrera, K.E. Oberhofer, M. Chergui, G.L. Celardo, & PK. Ultraviolet superradiance from mega-networks of tryptophan in biological architectures. Journal of Physical Chemistry B 128, 4035 (2024). [6] H. Patwa, N.S. Babcock, & PK. Quantum-enhanced photoprotection in neuroprotein architectures emerges from collective light-matter interactions. Frontiers in Physics 12, 1387271 (2024).

9 June
14:20 pm

A Robust Reaction for Prebiotic Peptide Bond Formation – Nicholas Hud

Georgia Institute of Technology

We have discovered a simple yet robust reaction that may solve the long-standing problem of how amino acids became peptides on the prebiotic Earth, a transition that is considered central in the matter-to-life transition that ultimately gave rise to extant life. The conversion of amino acids to peptides requires the formation of amide bonds. Although there are numerous ways that these bonds can be formed, none of the established methods proved adequate for our work on the development of a molecular system with the ability to replicate and exhibit open-ended sequence/functional evolution, a system that is dependent on amide bond formation. The most widely used methods for amide bond formation in water use carbodiimides that produce side products, waste molecules and monomer modifications that severely limit their utility. These issues are especially severe for systems designed to alternatively promote polymerization and sequence/functional selection as a means toward chemical evolution. We sought to develop a new reagent that provides a simple, robust abiotic route from amino acids to polypeptides in good yield during heating-drying reactions that mimic the conditions on the early Earth. We discovered that a solution comprised of ammonia and hydrogen sulfide – two compounds that are present in the atmosphere of other planets in our solar system and are believed to have been plentiful in the atmosphere of the early Earth – cleanly form the necessary amide bonds between amino acids under mild conditions. Moreover, the volatile nature of these reagents allows solutions to be readily cycled between conditions that promote peptide bond formation and pristine solutions of the newly formed peptides. These features make this surprisingly simple reagent mixture of great potential utility for the development of artificial self-replicating systems, which we consider key to demonstrating a matter-to-life transition and could prove relevant to understanding how polypeptides first emerged on the prebiotic Earth.

9 June
14:40 pm

RNA Driven Formation of Synthetic Compartments – Neal Devaraj

University of California at San Diego

The emergence of living systems required mechanisms that transformed simple molecular mixtures into organized, functional compartments capable of concentrating and activating informational polymers. We have discovered a synthetic chemical system in which RNA actively drives the spontaneous formation of membrane-bound compartments from dilute molecular precursors. The process proceeds through transient phase-separated intermediates that are chemically converted into stable vesicular compartments, enabling dramatic concentration of RNA and selective retention of longer polymers while excluding shorter species. Spatial chemical gradients further generate distinct compartment populations with different molecular compositions, revealing how simple environmental cues can drive molecular differentiation. The resulting concentration of RNA is sufficient to activate catalytic function from otherwise inactive dilute solutions. These findings suggest a plausible physicochemical route by which chemical reactivity, compartment formation, and molecular function could become coupled during the transition from non-living matter to organized living systems.

9 June
15:00 pm

Quantifying the energy content of the biosphere – Pablo Sartori

Gulbenkian Science Institute

Abstract: All organisms continuously import energy and matter from the environment to sustain their living state. Despite the enormous diversity of environmental substrates and metabolic pathways across the tree of life, metabolism ultimately converts external resources into biomass, which serves as the primary biological reservoir of stored chemical energy. A fundamental question is therefore: what is the energy content of biomass across different organisms? In this talk, I will show how the energy content of biomass varies across the kingdoms of life, and how this variation can be related to the molecular composition of different organisms. To do so, I will discuss our analysis of a newly compiled dataset that includes approximately 2,000 biomass combustion measurements reported in the literature. We believe this work is key for the fields of bioenergetics, ecology, and Earth sciences, as it can help infer the energetic cost of biomass production and the energy fluxes that mediate ecological interactions.

9 June
16:00 pm

ErbB Family Receptor Dimerization Dynamics and Dysregulation Via Long-Term Single-Molecule Imaging – Sam Peng

Broad Institute of MIT and Harvard

Abstract: Single-particle tracking (SPT) is a powerful tool to unveil crucial molecular behaviors, but it is limited by probe photostability and spectral orthogonality. We develop upconverting nanoparticles (UCNPs), which are photostable over several hours, enabling long-term multicolor SPT. The ErbB family of receptors plays a critical role in cell signaling, with dysregulation frequently linked to oncogenesis. We perform long-term, multicolor SPT of EGFR/HER2/HER3 in living cells, revealing their detailed dimerization dynamics. EGFR mutations promote stable dimerization.
Unexpectedly, we also observe homodimerization of HER2 and HER3, prompting a revised activation model. These findings provide a comprehensive view of the ErbB receptor interaction network and the diverse dimerization mechanisms.

9 June
16:20 pm

Genotype-Phenotype Coupling in Synthetic Cells – Job Boekhoven

Technical University of Munich

I'll be discussing our efforts to transition from Matter to Life. As evolution is a clear hallmark of life, we aim to establish genotype–phenotype coupling in synthetic cells by combining fuel-dependent synthetic cells that decay under starvation periods with self-replicating molecules. By coupling information-bearing molecules that can replicate as a genotype to the physical properties of the synthetic cells as their phenotype, we aim to show evolution in non-biological systems.

9 June
16:40 pm

The Transcriptional "Dark Matter" in Bacterial Cells is Characterized by Heterogeneous Gene Expression, Not Low Expression – Markus Covert

Stanford University

Roughly 30% of genes in *Escherichia coli* remain functionally uncharacterized despite decades of research. A large fraction of these "dark matter" genes appear at the very lowest levels of expression in transcriptomic and proteomic assays. A whole-cell computational model of *E. coli* developed in our lab has predicted a number of surprising behaviors, including that a majority of its genes are transcribed at a rate of less than once per cell cycle – a phenomenon we call "sub-generational gene expression". Interestingly, the low-expression "dark matter" genes are almost entirely expressed sub-generationally in our simulations, which enables a population of cells to hedge against unpredictable environmental challenges while respecting the resource and space constraints of individual cells. Using time-lapse microscopy, we are able to observe individual burst events, and single-cell RNA-sequencing confirms genome-wide heterogeneity patterns. The detailed experimental validation of these predictions has significant ramifications, in terms of fundamental biological understanding as well as demonstrating the capacity of whole-cell modeling to generate novel, systems-level insights.

9 June
17:00 pm

Exploring prebiotic reaction space using high throughput methods and active learning – Wilhelm Huck

Radboud University

Anika du Plessis, Amit Kahana, Thijs de Jong, Wilhelm T. S. Huck

Life as we know it is the product of evolution. This evolutionary process of 'trial and error' is very different from hypothesis-driven scientific research. However, we need new approaches as in a prebiotic context, as we lack a hypothesis of how evolution could have worked in a prebiotic context.
In this talk, I will show our first steps towards machine-learning driven automated experimental workflow that captures the key aspects of natural evolution (variation, inheritance, selection, adaptation). This artificial version of evolution is designed to discover how changes in the environment nudge complex systems and how functions arise within a certain chemical space.

10 June
9:00 am

Emergence and Self-organisation in Biological Systems – Erwin Frey

LMU Munich

Living cells achieve their remarkable functions through the spatiotemporal organization of proteins on deformable membranes. In this talk I will present our understanding of how protein patterns self-organize, what governs their dynamics, and how they couple to the geometry and elasticity of the membrane. Using examples such as Min protein oscillations, cortical polarity, and curvature-sensitive protein assemblies, I will show how the interplay between protein patterning and membrane shape gives rise to cell-like behaviors including polarization, division, and shape change. These results provide physical design principles for the rational engineering of synthetic cells with life-like functionality.

10 June
9:20 am

Active Control of Biomolecular Condensates with Coupled Chemical Reactions – Rebecca Schulman

Johns Hopkins University

Chemical reaction networks are often introduced through a minimal set of ingredients: molecular species, stoichiometric reactions, and rules that assign rates to those reactions. Even in well-mixed systems, these simple ingredients can generate rich dynamical behavior, including multistability, oscillations, hysteresis, bifurcations, robustness, ultrasensitivity, and adaptation. But living matter is not well mixed. Biomolecular condensates offer a powerful example of this principle. Through phase separation, condensates partition molecules into distinct environments. When this partitioning is coupled to chemical reactions, reaction rates become local, substrates and products become heterogeneously distributed, and reaction pathways can acquire spatial structure. These heterogeneous distributions can alter exchange times, tune selectivity, and change robustness to perturbations. The ability of biomolecules to phase separate thus expands the design space available to reaction networks. In bulk, control over the reaction graph is exerted mainly by changing effective rates. In condensates, spatial organization can also change the graph itself: reactions can be localized to particular phases, transport can be enabled or restricted by phase adjacency, and network connectivity can become a property of material design.

In this talk, I will describe our efforts to use biomolecular condensates as spatially structured multicomponent chemical reaction networks. We show that multiple reactions can be directed into distinct microenvironments within the same system, and that these local reaction environments can influence downstream chemical propagation. We demonstrate how partitioning and competition can be used to control reaction order and selectivity, and how localized chemical reactions create microenvironments with distinct reaction propensities. Finally, we show that chemical processes can feed back onto the geometry and structure of phase separation itself, making the reaction medium not just a passive container, but a chemically responsive material.

Together, these results suggest a way to think about condensates as more than compartments: they are reaction-network architectures. By coupling chemical transformations to spatial partitioning, condensates may allow functional pathways to emerge from chemically promiscuous components, provide routes to controlling pathway flux without directly programming every microscopic rate, and accelerate distinct reactions in different regions of the same system.

10 June
9:40 am

Crosstalk Between Mechanics and Metabolism – Patrick Oakes

Loyola University Chicago

Mechanical interactions allow cells to move, proliferate, change their shape, and build multicellular organisms. Like their biochemical counterparts, these mechanical interactions require energy. Living systems, however, are also inherently non-equilibrium, meaning that their energy usage must be actively managed for them to maintain their shape and structure. Here we show that cellular contractility is directly proportional to the global level of ATP availability. Increasing ATP production leads to increased contractility, while decreased ATP production slows cytoskeletal dynamics and reduces contractility. Our data suggests a fundamental connection between cellular metabolism and cytoskeletal activity.

10 June
10:00 am

A Trajectory-Based Response Theory for Systems Far from Equilibrium – Zhiyue Lu

University of North Carolina at Chapel Hill

How do living systems sense and respond to external signals? Such questions require a response theory arbitrarily far from equilibrium. I will present a trajectory-based response theory that addresses this gap. Expressing response functions as correlations over trajectory ensembles, the framework systematically decomposes linear and nonlinear responses in terms of dynamical observables such as entropy production and activity, exposing universal constraints linking sensitivity, dissipation, and information extraction. I will then translate these results into design principles for living and synthetic systems, building a quantitative bridge between physical response, information processing, and biological function.

10 June
11:00 am

Finding Life in the Universe with AI – Cecilia Garraffo

Harvard-Smithsonian Center for Astrophysics

For centuries, humanity has wondered whether life exists beyond Earth. Until recently, this question belonged largely to philosophy and science fiction. Today, a new generation of telescopes, including the James Webb Space Telescope and upcoming missions such as Ariel, is transforming that dream into a scientific possibility by allowing us to probe the atmospheres of distant worlds.
But a major challenge remains: the data we receive from these planets are extremely sparse, noisy, and low resolution. From tiny variations in starlight filtered through alien atmospheres, we must solve a difficult inverse problem: determining which molecules, temperatures, clouds, and physical conditions produced the observed signal. Traditional atmospheric retrieval methods can typically explore only a small number of molecules at a time, leading to strong degeneracies and increasing the risk of false positives when searching for biosignatures.
In this talk, I will discuss how recent advances in artificial intelligence are beginning to change this landscape. I will present work from AstroAI on AI-driven atmospheric retrieval models that combine physical simulations, probabilistic inference, and generative machine learning to characterize exoplanet atmospheres at unprecedented scale. These methods were first demonstrated in the international Ariel Data Challenge, where our team developed AI models capable of robustly retrieving multiple atmospheric species simultaneously.
Building on this foundation, we are now developing approaches that move beyond the traditional search for a handful of predefined "Earth-like" biosignatures. Instead, we aim to explore thousands of known and unknown molecular combinations simultaneously, enabling a broader and less anthropocentric search for life. This work illustrates how physically grounded AI can help science tackle inverse problems that were previously computationally intractable, opening new pathways for discovery at the intersection of astronomy, chemistry, and the origins of life.

10 June
11:20 am

Sculpting Energy and Entropy Landscapes in Biological Systems – Jennifer Ross

Syracuse University

Biological systems appear to be able to rectify active processes into productive work using enzymes, assemblies of enzymes, and larger-scale machines made of those assemblies. We seek to recapitulate and understand the phenomena of biological self-organization from the molecular to the cellular scale in the hopes of someday recreating synthetic systems with the same astonishing properties. We discuss our recent work on how molecular condensates are affected by a background activity of weakly-interacting catalytic proteins, specifically those that can perform enhanced diffusion. We carefully control the environment with a chemostatic chamber and perform controls to demonstrate that the physical activity of enzymes may be able to alter the amount of protein condensing – shifting the phase diagram. Our carefully controlled in vitro reconstitution experiments provide evidence that these enzymes may be acting as an active bath creating an effective temperature, as previously proposed inside living cells

10 June
11:40 am

Toward a Reflexive Set of Ancestral Aminoacyl-tRNA Synthtetase Genes Whose Translated Products Can Interpret Their Own Genes – Charlie Carter

University of North Carolina at Chapel Hill

Charles W. Carter, Jr[1], Guo Qing Tang[1], Sourav Kumar Patra[1], Laurie Betts[1], Mark Ditzler[2], Milena Popovic[3], Peter R. Wills[4,5], and Jordan Douglas[4,5]

[1]Department of Biochemistry and Biophysics, University of North Carolina at Chapel Hill Chapel Hill, NC; [2] Center for the Emergence of Life, Space Science & Astrobiology Division, NASA Ames Research Center, Moffett Field, CA; [3]Blue Marble Space Institute of Science, Moffat Field, CA; [4]Department of Physics, University of Auckland; [5]Centre for Computational Evolution, University of Auckland

The reflexive nature of aminoacyl-tRNA synthetase genes is a subtle puzzle. Their translated products must enforce the coding rules by which they, themselves were assembled. Aminoacyl-tRNA synthetases (synthetases) are enzymes that translate the code by forming a covalent bond between specific amino acids and RNA substrates carrying anticodons. We try to unravel how nature first found out how to do that and thus invented genetic coding. There are two distinct synthetase superfamilies. Each Class manages about ten of the twenty amino acids. There is mounting evidence that at one time they were encoded on opposite strands of the same ancestral gene(s). Class 1 and 2 synthetase ancestries may thus be coupled. Their sequences are a rich source of relevant data, as are inferences based in structural alignments. Neither kind of inference has been sufficient, as yet, to enable us to reconstruct their ancestry. In order to go beyond those inferences, we created ways to express and assay two different ancestral synthetase models. Protozymes have ~50 amino acids. They retain binding sites for amino acids and ATPand accelerate amino acid activation by a million-fold. Urzymes have 80-130 amino acids. They can both activate amino acids and transfer them to cognate tRNA minihelices. These experiments furnish rates and specificities for the ancestral models. Recently, we also have seen that E. coli produces related constructsin vivo from full-length plasmids. We seek to compare of sequences reconstructed from phylogenetic trees with those arising from our in vitro designs. We hope to define a set of complementary urzyme gene libraries whose translated products form a self-consistent reflexive set. In such a reflexive set, purified synthetase urzyme quasispecies would be capable of translating the combinatorial libraries of their genes. Our latest models open a wide range of new possibilities that bring our goal into view.

10 June
12:00 pm

AI-Driven Cell Observatory to Explore the Dynamic Machinery Governing Life From Molecules to Organisms – Srigokul Upadhyayula

University of California, Berkeley

Life is inherently four-dimensional. While reductionism identifies molecular components, emergent physiology requires direct in vivo observation. Modern microscopy captures these dynamics, but petabyte-scale data exceeds human analytical capacity and current AI lacks annotated datasets to interpret it. I'll describe the Cell Observatory: a platform combining industrial-scale in vivo microscopy, custom reagents, and 5D dynamic atlases to train a spatiotemporal vision model of life. To break the annotation bottleneck, we are creating ~500 transgenic lines with combinatorial tags and biosensors encoding ground truth, enabling self-supervised pretraining across labs and modalities, paired with an LLM layer for reasoning over living systems.

10 June
12:20 pm

Optimization Principles in Living Systems – Michael Murell

Yale University

Self-organized criticality produces intermittent, scale-free energy release in systems like earthquakes and cells. In the actin cytoskeleton, molecular motors generate stresses that drive large dissipative events, but the origin of this behavior is unclear. Here we show it arises from coupling between actin organization and active stress. Using a minimal in vitro actomyosin system, we vary network connectivity and order. Ordered, sparse networks show exponential stress release, while disordered, highly connected networks exhibit heavy-tailed dynamics and 1/f noise. Disorder localizes stress into stiffer modes, akin to Anderson localization. Overall, cytoskeletal architecture sets the pathway and statistics of energy dissipation, providing a physical basis for cellular criticality.

10 June
14:00 pm

Recording the Physiological History of Cells With Chemical Labeling – Kai Johnsson

Max Planck Institute for Medical Research, Heidelberg & EPFL Lausanne

Recordings of the physiology of cells provide insights into biological processes, yet obtaining such recordings is a challenge. To address this challenge, I will discuss a conceptually new approach to record transient cellular events for later analysis, including imaging and/or transcriptomics. The approach is based on designed proteins that become labeled in the presence of both a specific physiological activity and a fluorescent substrate. The recording period is set by the presence of the substrate, whereas the physiological activity controls the degree of the labeling. The use of substrates of different colors enables the recording of successive periods of activity, either in cell culture experiments or in vivo. Applications include the recording of protein-protein interactions, receptor activation and elevations in intracellular calcium as well as the recording of kinase activities. The recording of physiological activities can be used, among other things, for the sorting of cells from heterogenous populations for transcriptomic analysis, or for the tracking of neuronal activities in vivo.

10 June
14:20 pm

Physical Tools to Interact With Living Systems – Dimitris Missirlis; Peer Fischer

Heidelberg University & Max Planck Institute for Medical Research

We are exploring ways that permit the controlled interaction with living systems and cells. Magnetic fields and ultrasound offer the possibility to reach deep inside the body and there is evidence that both interact with cells. In particular, ultrasound enables the non-invasive stimulation of cells and tissues for therapeutic purposes. However, despite evidence of the action of ultrasound, including in clinical settings and indications of neuromodulation, it remains an open question how high-frequency ultrasound precisely interacts with cells and elicits a biological response. We describe how we have explored ways to shape and control ultrasound to investigate the biophysical mechanisms that underlie ultrasound-cell interactions.

10 June
14:40 pm

Finding Life in the Universe with AI – Ribogenesis in Minimal Cells: Using AI to accelerate near-atomistic modeling – Roseanna Zia

University of Missouri

R. N. Zia, V. Sivasankar, H. Sachar, and J. G. Wang
Zia Lab

A major challenge in synthetic biology is constructing cells that autonomously grow, divide and adapt. Ribogenesis and nucleoid physical architecture are critical for this goal: together, they coordinate spatial organization and self-assembly of molecules in crowded cytoplasm, enabling complexification of matter into life. Synthetic systems lack this cytoplasmic spatial architecture, suggesting that sustained growth requires specific physical architecture. Here we identify specific physical conditions in cells that are essential to ribogenesis. To do so, we will use AI-enhanced multi-scale pipelines to expand our whole-cell models. We will use the resulting framework to achieve autonomous self-assembly of the ribosome's 30S subunit and the principles learned to improve autonomous growth outcomes for synthetic cells.

11 June
9:00 am

Developer Cells: A Modular, Extensible Chassis for Building Synthetic Cells – Anton Jackson-Smith/ Richard Murray

California Institute of Technology

Synthetic cells constructed using compositional biology provide a means to engineer biology at scale for applications and research. Building these cells requires integration, collaboration and coordination between tools, techniques, people, and biology itself. Over the past two years, we have developed Nucleus, an open-source community and technology platform to enable this work; manufacturing for critical research reagents needed to perform it; and synthetic cells, cell modules, and cell engineering tools. We demonstrate this combined platform through with the Developer Cell. The Developer Cell combines integrated energy, control, and membrane-translation modules to provide an improved chassis for research, demonstrates the potential of new modules and module integration, and provides a new baseline for cell-module development and synthetic cell applications.

11 June
9:20 am

Thermodynamic Limits of Biomolecular Computation – Milo Lin

University of Texas Southwestern Southwestern Medical Center

Electrical circuits have long served as a metaphor for intracellular systems, yet the quantitative power of circuit analysis has been inaccessible for biomolecular systems, whose nonequilibrium behavior is challenging to predict. We establish a mathematical mapping between the Markov chain of any nonequilibrium system and an Ohm's law circuit, generalizing the Boltzmann distribution to nonequilibrium conditions. Transitions in the Markov chain that are decoupled from the chemical driving force map to resistors, enabling systematic coarse-graining and modular design. This framework reinterprets classical circuit theorems as general nonequilibrium statistical mechanical relationships, which we apply to derive performance limits for biomolecular computation and guide the evolution of scalable molecular logic gates.

11 June
9:40 am

Spatiality in the bacterial cell: updates and open questions – Ido Golding

University of Illinois at Urbana Champaign

We use phage infection as both motivation and a tool to study the role of spatiality in the bacterial cell. Our starting point is the observation that viral genomes coinhabiting the same cell maintain a degree of individuality in their developmental choices, despite sharing a small, well-mixed cytoplasm. I will briefly describe two ongoing efforts to address this mystery: (i) Introducing single-phage profiling to determine the transcriptional activity of coinfecting phages during determination of host fate. (ii) Utilizing MINFLUX microscopy to characterize the spatial statistics of phage and host gene expression machinery and infer their molecular organization during transcription, translation, and regulation by transcription factors.

11 June
10:00 am

Physical Mechanisms Underlying the Programming and Reprogramming of Cell Behavior – Andrew Spakowitz

Department of Chemical Engineering at Stanford University

Gene expression that establishes cell identity within eukaryotic cells is governed by segregation of chromosomal DNA into active euchromatin and inactive heterochromatin. This control mechanism is dubbed epigenetics, as it operates above the genetic instructions written in the DNA. Our research leverages theoretical and computational approaches to establish physical understanding of the mechanisms that control chromosomal segregation and the maintenance of the chemical modifications that comprise an epigenetic code that orchestrates gene expression. In this talk, we discuss how the cell utilizes weak, multivalent interactions between reader proteins to control segregation and to maintain the epigenetic code over multiple cell generations.

11 June
11:00 am

Energizing Synthetic Cells – Laura Heinen

DWI – Leibniz Institute for Interactive Materials, Aachen

A continuous flux of energy and information is essential to life-like behaviors and complex, autonomous functions in synthetic cells. Following the bottom-up approach i.e., assembling synthetic cells from scratch using well-defined synthetic and biologically isolated building blocks, it remains a major challenge to energize these synthetic cell-like entities in a sustained fashion and maintain out of equilibrium. In my group we approach this by exploring the construction of synthetic cellular compartments that are able to build-up and maintain the necessary concentration gradients, but likewise allow for the selective transport of energy and matter. To this end, we incorporate membrane proteins into our vesicular structures that enable the construction of selectively open, active compartments that serve as chassis for synthetic cells. Further, we embed chemical reaction networks for the guided flow and transduction of molecular energy. By energizing these synthetic cell constructs, more complex and autonomous functions are envisioned. I will follow these principles to demonstrate metabolically active vesicles that act as self-sustaining nanoreactors, artificial mitochondria, and interdependent cross-feeding organelles.

11 June
11:20 am

Bottom-Up Assembly of Synthetic Cells – Joachim P. Spatz

Max Planck Institute for Medical Research

The evolution of cellular compartments for spatially and temporally controlled assembly of biological processes was an essential step in developing life by evolution. Synthetic approaches to cellular-like compartments are still lacking well-controlled functionalities, as would be needed for more complex synthetic cells. With the ultimate aim to construct life-like materials such as a living cell, matter-to-life strives to reconstitute cellular phenomena *in vitro* – disentangled from the complex environment of a cell. In recent years, working towards this ambitious goal gave new insights into the mechanisms governing life. With the fast-growing library of functional modules assembled for synthetic cells, their classification and integration become increasingly important. We will discuss strategies to reverse-engineer and recombine functional parts for synthetic eukaryotes, mimicking the characteristics of nature's own prototype. Particularly, we will focus on large outer compartments, complex endomembrane systems with organelles and versatile cytoskeletons as hallmarks of eukaryotic life. Moreover, we identify microfluidics and DNA nanotechnology as two highly promising technologies which can achieve the integration of these functional modules into sophisticated multifunctional synthetic cells.

11 June
11:40 am

Light Based Communication in Synthetic And Living Cells – Seraphine Wegner

University of Münster

A central challenge in synthetic biology is to identify the minimal components required to realize cellular functions and to harness these principles for the rational engineering of living systems. In natural cells, complex behaviors emerge from the precise spatial and temporal control of processes such as protein localization, adhesion, and signaling. Here, I present a bottom-up approach using synthetic and living cells to reconstruct and control these processes with light. By employing photoswitchable proteins and optogenetic tools responsive to visible light, we achieve dynamic spatiotemporal regulation at cellular and multicellular scales. This enables light-controlled adhesion, guiding cells of different types to migrate, self-assemble, and self-sort into programmable multicellular architectures. The spatial organization within these assemblies governs intercellular communication and gives rise to collective behaviors, underscoring the link between structure and function. Beyond classical signaling via diffusible molecules, we establish a non-chemical mode of cell-to-cell communication based on light. Here, the light-based signals propagate rapidly, bypass diffusion and membrane transport, and provide a modular strategy to program communication within diverse communities of synthetic and living cells. In this research program, simplified, cell-mimetic systems allow us to quantitatively link molecular design to emergent behavior and to derive general principles. By transferring these modules into bacterial and mammalian cells and integrating synthetic with living systems, we create hybrid platforms that bridge biological complexity. Together, this work establishes light as a powerful tool to control and connect cells, advancing both our understanding of fundamental design principles and the engineering of cellular systems with programmable functions beyond those observed in nature.

11 June
12:00 pm

Chromosome segregation at the nanoscale – Andrea Musacchio

Max Planck Institute of Molecular Physiology, Dortmund (Germany) & University of Duisburg Essen, Essen (Germany)
musacchio@mpi-dortmund.mpg.de

Kinetochores are complex protein scaffolds comprising ~30 core subunits in two subcomplexes, the CCAN and the KMN. They provide chromosomes with points of attachment to spindle microtubules during cell division. In addition to binding microtubules, the kinetochore "hardware" controls an "operating system" of proteins involved in mitotic surveillance, and promoting chromosome bi-orientation (error correction mechanism) as well as preventing premature mitotic exit in presence of incomplete or incorrect microtubule attachments (spindle assembly checkpoint, SAC). To dissect kinetochore function, our laboratory combines cell biology with holistic biophysical investigations of in vitro-reconstituted human kinetochores.

11 June
12:20 pm

Synthetic Minimal Cells that Pretend to be Real – Kate Adamala

University of Minnesota

11 June
14:00 pm

Multilevel Selection and the Emergence of Ecosystems of Cooperating Genetic Polymers – David Baum

University of Wisconsin–Madison

The evolution of cooperation among catalytic polymers requires a balance between selection acting on individual replicators and on ensembles of interacting molecules. Using simulations, we show that multilevel selection promotes the persistence of template-replicating polymers that perform diverse cooperative functions, including ligation, monomer synthesis, and mutation inhibition. Guided by these results, we are developing experiments in which droplets are selected based on ensemble-level traits to test whether this favors the emergence of cooperation among nucleic acid variants. We find, unexpectedly, that recursive wet–dry cycling of nucleotides can drive substantial accumulation of nucleic acids, and that this effect is amplified when we select for the most productive ensembles. Together, these results will help clarify the role of multilevel selection in the origins of the cooperative genetic systems found in cellular life.

11 June
14:20 pm

Harnessing Amino Acid Chirality to Control Biomacromolecular Structure and Function – Ayusman Sen

Departments of Chemistry, Chemical Engineering, Materials Science & Engineering
The Pennsylvania State University, University Park, PA16802 (USA)
Contact: asen@psu.edu

In nature, almost all amino acids are found in the L-form, while sugars are predominantly in the D-form, creating the phenomenon of biological homochirality. This exclusive use of a single enantiomer gives biomacromolecules a remarkable level of specificity, controlling which molecules they bind and how efficiently they catalyze reactions. Despite its importance, how and why this chiral preference arose remains a central scientific question. We will discuss how the chirality of amino acid additives profoundly influences biomolecular structure and function.

11 June
14:40 pm

Learning and Memory based on Assembly Code of Supramolecular Peptide Systems – Rein Ulijn

Nanoscience Initiative at the Advanced Science Research Center (ASRC), New York

Peptides are promising building blocks for designer materials with functions beyond those explored by biology. Our work develops bottom-up approaches for the discovery and evolution of adaptive peptide materials based on an assembly code linking sequence, conformation, interaction dynamics, and environmental context to emergent function. Using integrated computational and experimental approaches, we explore short peptide systems that dynamically reorganize in response to water content, ionic composition, and guest molecules. We demonstrate adaptive supramolecular dispersions, dynamic peptide exchange, and ongoing work showing how peptide networks can learn and memorize new functions through repeated drying-rehydration cycles, enabling information accumulation, adaptive aggregation, and emergent behavior.

Poster Abstracts

9 June
13:00 – 14:00 pm: Lunch/Poster Session
10 June
10:30 – 11:00 am: Coffee Break/Poster Session
13:00 – 14:00 pm: Lunch/Poster Session
11 June
10:20 – 11:00 am: Coffee Break/Poster Session
13:00 – 14:00 pm: Lunch/Poster Session

Poster #1: Nonchemical Communication Using Luminescent Hydrogel Synthetic Cells – Matthew Allen

University of Münster

Synthetic cells are biomimetic constructs that aim to reproduce biological form and functionality to improve our understanding of cellular biology. Of these biological functionalities, inter and intracellular communication are essential biological functionalities that synthetic cells aim to replicate. However, a communication approach in synthetic cells is not yet developed that can be used in different physiological environments, and with a variety of cells. Consequently, we have manufactured, using microfluidics, a suite of bioluminescent organelle containing hydrogel synthetic cells. Through using the microfluidic platform, we can customise the architecture of the hydrogel synthetic cells, allowing the bioluminescence intensity to be adjusted and a variety of different organelles and cells to be inserted within the hydrogel chassis. We then show that the internal bioluminescent signal from the hydrogel synthetic cells can communicate with light responsive proteins, other synthetic cells and biological cells, both within the hydrogel synthetic cell (intracellular) and the surrounding environment (intercellular), through the activation of a variety of functionalities, including adhesion and gene expression. Our developed hydrogel synthetic cells will provide access to new biomimetic behaviours and supply a scaffold for light dependent microdevices for biotechnological utilisation.

Poster #2: Solving the Traveling Salesperson Problem with Slime Mold-Inspired Algorithms – Margie Christ, Suyash Bajpai, Philip Kurian

Quantum Biology Laboratory, Howard University

NP-hard combinatorial optimization problems like the travelling salesperson problem (TSP) are a rich source of discovery and frustration, as exact solutions elude researchers due to resource constraints. Can the slime mold Physarum polycephalum serve as biological inspiration to improve upon existing TSP solution methods? In their 2018 work, Zhu et al. [1] experimentally monitored P. polycephalum's high-quality solutions to the TSP, generated in response to optical feedback controlled by a modified Hopfield neural network, and wrote a computer program to mimic the results. Subsequently, Miyajima et al. [2] proposed performance-enhancing modifications, relaxing certain assumptions to reduce the number of iterations needed to find a high-quality solution. Both codes require a small amount of computational noise for success, added as a uniform random number distribution [1] or a Gaussian distribution [2]. To minimize the performance metrics of solution length and iteration count, we varied the noise's magnitude and profile. Overall, [1] with uniform noise minimizes solution length, while [2] with Gaussian noise minimizes iteration count. However, the modifications from [2] reduce the iteration count by an order of magnitude, while differences in solution length are typically within one standard deviation.

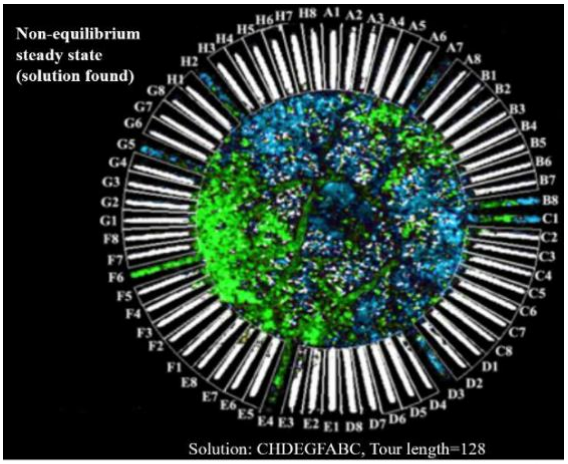


Fig. 1: *P. polycephalum* solution to an 8-city TSP. The amoeba rests on a nutrient-rich agar plate and a 64-lane container chip for the eight-city TSP. Green (blue) indicates an increase (decrease) in out-of-plane thickness. Through its photophobic response to optical feedback control, *Physarum* adapts its oscillatory dynamics, optimizing its growth to solve the TSP. Adapted from [3].

Comparing the logarithmic product of the performance metrics, [2] presents the most computationally efficient method, without compromising solution quality. We then change the code parameters to better mimic P. polycephalum's behavior. Small influx/outflux fluctuations are expressed through two variables, one for expansion and one for contraction; we examine the effect of changing the ratio of these quantities. Solution length does not vary significantly, but the iteration count for both codes is minimized when the ratio of expansion to contraction is less than 0.5. We finally propose a future improvement: changing the noise profile from white (constant power spectral density or PSD) to pink (PSD of 1/f), as pink noise is commonly found in biological systems and may provide a better computational approximation of P. polycephalum's behavior.

Methods such as the Lin-Kernighan-Helsgaun (LKH) algorithm (our best TSP heuristic) provide high-quality solutions, often within less than 1% of the optimal tour length. However, while the computational time of the LKH algorithm scales quadratically, the experimentally observed amoeba solutions of the TSP exhibit near-linear time scaling for small N, while the improved code from [2] exhibits iteration count scaling with $\sqrt{N}$ [3]. Another potential solution method for the TSP is an unstructured database search, such as the quantum Grover's algorithm, which also scales with $\sqrt{N}$. This milestone algorithm can be implemented upon any system that supports superposition (such as a system of coupled harmonic oscillators [4]).

Fig. 1: P. polycephalum solution to an 8-city TSP.

References: [1] Zhu et al., R. Soc. Open Sci. 5(12): 180396 (2018). [2] Miyajima & Mochizuki, Nonlinear Theory and Its Applications, IEICE 15(4), 824–837 (2024). [3] Bajpai et al., arXiv:2504.03492 (2025). [4] Grover & Sengupta, Phys. Rev. A 65, 032319 (2002). [5] Patel, Pramana – J Phys 56, 367–381 (2001). [6] Kurian et al., J. Theor. Biol. 391, 102–112 (2016).

Poster #3: From Bits to Qubits: Scaling Alzheimer's Research with Quantum Fourier Transforms – Rania Jones, Mohsen Izadyari, James Murray, Philip Kurian

Quantum Biology Laboratory, Howard University

The study and practice of magnetic resonance imaging (MRI) have long served researchers and healthcare professionals in advancing the understanding of Alzheimer's disease (AD), offering the ability to capture extremely detailed brain images without the need for invasive procedures. Much of the traditional research that utilizes MRI—such as voxel-based morphometry and region-specific segmentation—focuses on identifying volumetric reductions in key areas like the hippocampus, entorhinal cortex, and posterior cingulate [1]. These regions are strongly associated with early symptoms of memory loss and cognitive decline. However, it is crucial to note that these traditional methods may present challenges when it comes to subtle microstructural changes, especially in areas found across varied spatial scales. These limitations may trigger classical pipelines to overlook early biomarkers embedded in complex tissue textures [2].

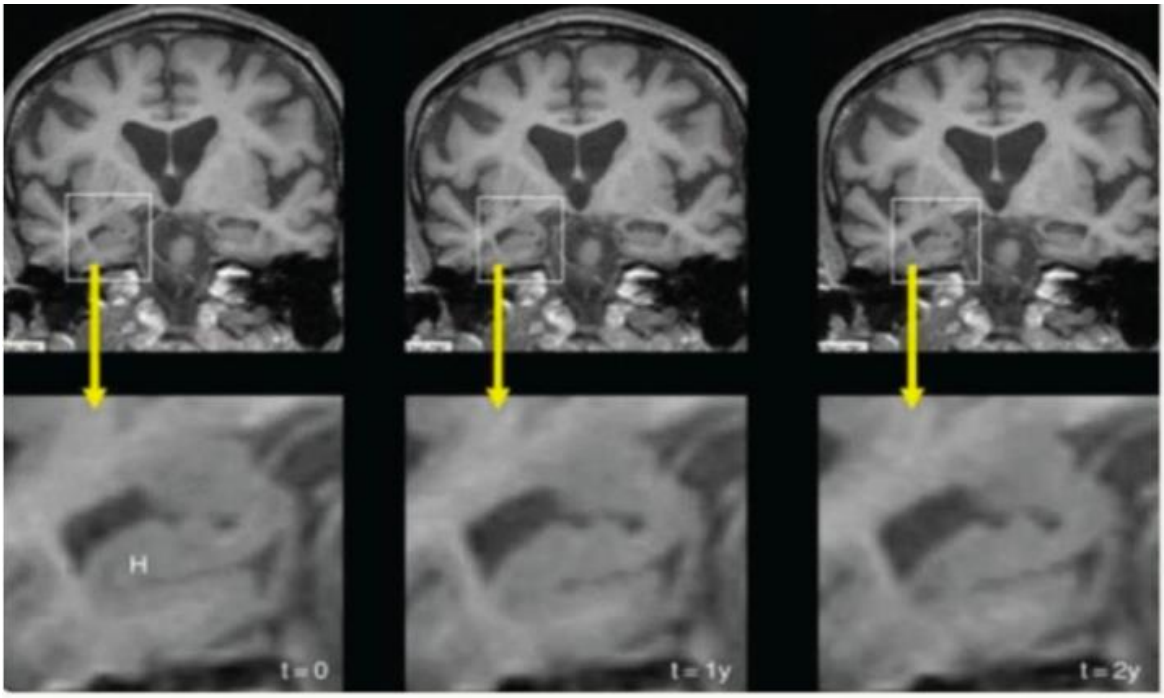


Figure 1. Hippocampal volume loss indicates areas of early neurodegeneration. Series of three coronal T1-weighted studies of patient with autopsy-proven Alzheimer's disease (AD), exposing progressive hippocampal atrophy [7]. Similar localization is utilized when overlaying Quantum Fourier Transform (QFT)- derived frequency features to determine how well QFT report subtle structural changes.

Recent research and developments in quantum computing have introduced promising tools to extend this line of work—most notably through the application of Quantum Fourier Transforms (QFTs) to MRI data. QFT, the quantum analogue of the classical discrete Fourier transform, employs quantum superposition to decompose data retrieved into frequency components with exponential efficiency [3]. QFTs allow for the encoding of spatially distributed MRI signals into quantum amplitudes, allowing for the opportunity to seize fine-grained structural variations that retain in the frequency domain. QFTs can be used to trigger the detection of higher-order features such as localized textural or morphological shifts that regular MRI methods frequently cannot detect [4, 5]. A promising QFT-based application lies in region of interest (ROI) analysis, specifically relating to the hippocampus region, as studies have shown it is a critically affected area in the earliest stages of AD [1]. By integrating QFT-derived imaging with ADNI's unique data types, improvements in diagnostic sensitivity and comprehension regarding disease evolution can be realized through various biological and spatial domains.

References: [1] Jack et al., Lancet Neurology 9(1), 119–128 (2010). [2] Briegel et al., Nat. Commun. 16, 1281 (2025). [3] Toussi Kiani et al., arXiv:2004.02036 (2020). [4] Li et al., Optica 9(8), 959–964 (2022). [5] Nielsen & Chuang, Cambridge University Press (2000). [6] Petersen et al., Neurology 74(3), 201–209 (2010). [7] Johnson et al., Cold Spring Harb. Perspect. Med. 2(4), a006213 (2012).

Poster #4: Exploring Quantum Life: Three Years of Tailored Research Experiences for Trainees at the Quantum Biology Laboratory – James Murray and Philip Kurian

Quantum Biology Laboratory, Howard University

With support from the Alfred P. Sloan Foundation's Matter-to-Life program and the Howard University Graduate School, we have built a stipend-based internship program at the Quantum Biology Laboratory (QBL) that creates tailored, collaborative research experiences for undergraduate and graduate student trainees, with travel within the greater Washington area, domestically, and abroad to engage the global network of QBL collaborators. Leveraging the Sloan Matter-to-Life project and the IBM-HBCU Quantum Center at Howard, we expose a broad range of science majors to the physical and quantum sciences and their applications to quantum biology.

Fig. 1: Year 1 (2024) and Years 2–3 (2025–2026) milestones of the Sloan-supported QBL internship program.

Across the first three years of Sloan support, the program has mentored twelve trainees and expanded its postdoctoral capacity with a new scholar in open quantum systems and quantum thermodynamics. Notable year-three publications include a first-author paper by a trainee alumnus in Physical Review A on single-photon superradiance and subradiance in helical collectives of quantum emitters [3], and a paper in Quantum Information Processing developing natural language processing on quantum computers [5]. One undergraduate trainee received the 2025 UT-Austin College of Natural Sciences Research Distinction Award for QBL work on quantum algorithms and neuroproteins. Quantum Math Camps deliver a developing grades 1–7 Quantum Biology curriculum through inquiry-based learning, aligned with Next Generation Science Standards and Common Core State Standards.

References: [1] Bajpai et al., arXiv:2510.19976 (2025). [2] Bajpai et al., arXiv:2504.03492 (2025). [3] Patwa & Kurian, Phys. Rev. A 113, 043708 (2026). [4] Patwa et al., Frontiers in Physics 12, 1387271 (2024). [5] Abbaszadeh et al., Quantum Inf. Process. 25, 49 (2026).

Poster #5: Thermal Non-Equilibrium Processes to Drive Prebiotic Chemistry – Christof Mast

Faculty of Physics, LMU Munich

The question of the essential physical and chemical conditions that drove early molecular evolution lies at the heart of the way to understand life's origin on Earth, yet remains highly challenging to probe. Early Earth must have hosted environments capable of sustaining complex, multistep prebiotic chemistries—environments that could generate chemical gradients, maintain suitable solution compositions, and provide protection from damaging factors such as UV radiation, extreme pH or saline conditions.

We show that simple, ubiquitous heat flows through networks of thin rock fractures, combining thermal convection and thermophoresis, create sustained chemical gradients in pH, salinity, and molecular composition. This selective thermophoretic enrichment promotes amino acid dimerization through localization of trimetaphosphate (TMP). It also generates local pH gradients from geologically plausible rock leachates, acting as a physical buffer-mechanism for spatially confined RNA ligation reactions. Selective accumulation of phosphates over calcium by thermophoresis likewise enables the solubilization of apatite-derived leachates even under neutral conditions, offering a potential pathway to address the long-standing phosphate problem in prebiotic chemistry.

UV irradiation of oligonucleotides introduces an additional selection pressure in such settings. Using UV-quenched high-throughput sequencing, we quantified UV-induced damage in early model genomes of proto-organisms and compared the patterns with amino acid-associated codon chronologies. These analyses indicate that prevailing consensus models for the emergence of amino acids remain compatible with UV-stable proto-genomes.

Poster #6: Integrating Geodesic Actin Dome into Viscoelastic Nematodynamics during Epithelial-Mesenchymal Transition – Chin-Yao Chang

University of Göttingen

Epithelial–mesenchymal transition (EMT) is a fundamental biological process in which epithelial cells progressively lose their junctional organization and polarity while acquiring mesenchymal features such as elongation, increased motility, enhanced contractility, and altered mechanical properties. In this research, TGF-β1-induced EMT in NMuMG epithelial cells was used as a model system to investigate how biochemical EMT progression is coupled to changes in collective cell alignment, cytoskeletal architecture, and cellular mechanics. With nematic order analysis applied to time-resolved images over 48 hours, control cells maintained low and stable orientational order, whereas TGF-β1-treated cells showed a progressive increase in alignment during EMT. Interestingly, topological defects occur within mesenchymal samples, suggesting that EMT progression generates not only global alignment but also local orientational disorder.
Further examination of regions with topological defects revealed a special actin-based structure known as the geodesic actin dome (GAD). Although GAD-like structures have been reported previously, their biological function and formation mechanism remain poorly understood, particularly in the context of EMT. In this work, GADs were analyzed through fixed-cell imaging, live-cell actin staining, unroofing experiments, atomic force microscopy, and geometric modeling. Live imaging showed that GADs can form reversibly under multidirectional stretching forces from neighboring cells. Mechanical measurements further showed that TGF-β1-treated cells became stiffer as EMT progressed. GAD regions displayed distinct local mechanical properties, suggesting that they may function as transient force-bearing structures during cytoskeletal remodeling. Finally, the geometry of GADs was described using Delaunay triangulation, and simulations supported the idea that increased actin-network connectivity enhances stiffness. Together, these findings suggest that EMT is not only a molecular transition but also a physical reorganization of tissue alignment, actin architecture, and cellular mechanics.

Poster #7: Dynamically Induced Spatial Segregation in Multi-Species Bacterial Bioconvection – Mingqi Yan

Department of Physics, Ludwig-Maximilians-Universität München;
Max Planck School Matter to Life

Bacterial bioconvection is a classic example of collective behavior in active matter, where upward-swimming bacteria create density instabilities leading to large-scale fluid flows. While this phenomenon is well-studied in single-species suspensions, natural environments are typically inhabited by diverse microbial communities. Here, we investigate the collective dynamics of multi-species bacterial suspensions. Combining experiments with a continuum model, we show that different bacterial species can spontaneously segregate into stable, spatially interlocked domains. Our theoretical analysis reveals that this segregation is not driven by biochemical antagonism but rather by the interplay between species-specific motility characteristics and the self-generated hydrodynamic flows. This work provides new insights into how physical interactions alone can drive the spatial organization of complex microbial communities.

Poster #8: Engineering Red Blood Cell–Derived Nanoghosts for Biomedical Applications – Sunnatullo Fazliev

Sunnatullo Fazliev
Max Planck Institute for Medical Research

The central promise of targeted drug delivery is enhancing local therapeutic efficiency while reducing off-target effects. Natural-derived drug delivery systems such as extracellular vesicles, viruses, and whole cells have been extensively tested to deliver drugs in vivo. However, several challenges related to large-scale production, batch-to-batch variability, and laborious sample preparation continue to impede their clinical translation. Here, we present a comprehensive and systematic study on the production of red blood cell (RBC)-derived nanovesicles, termed nanoghosts, as a potential drug delivery platform. We investigate how different fabrication methods—including extrusion, sonication, and freeze-thaw cycles—affect yield, size distribution, structural morphology, surface properties (zeta potential and membrane topology), and biological composition (membrane proteins and carbohydrates) of the resulting nanoghosts. Furthermore, using primary human macrophages, we assess their immune evasion and biocompatibility. Our results highlight the potential of natural cell-derived drug delivery systems and establish key design principles for engineering nanoscale membranous delivery systems derived from RBC membranes.

Poster #9: Investigating the Impact of Hydrotrope-Driven Solvent Structuring on Reaction Kinetics and Selectivity in Water – Rayan Bhattacharya

PhD Candidate, Zarzar Lab, Department of Chemistry, Penn State, USA

Hydrotropes are small amphiphilic molecules forming transient nanostructures which have been found to affect reactivity in water. Incidentally, hydrotropes have a chemical structure analogous to early protocell-forming fatty acids, making their study relevant from a prebiotic chemistry perspective. This work utilizes hydrotropes with different apolar moieties to create varying structure-dependent chemical environments and study their effect on reaction kinetics and selectivity in water.

Poster #10: A Minimal Synthetic Cell Platform for Genotype–Phenotype Coupling via DNA-Based Replication and RNA Nanostructure Expression – Nicolas Glück

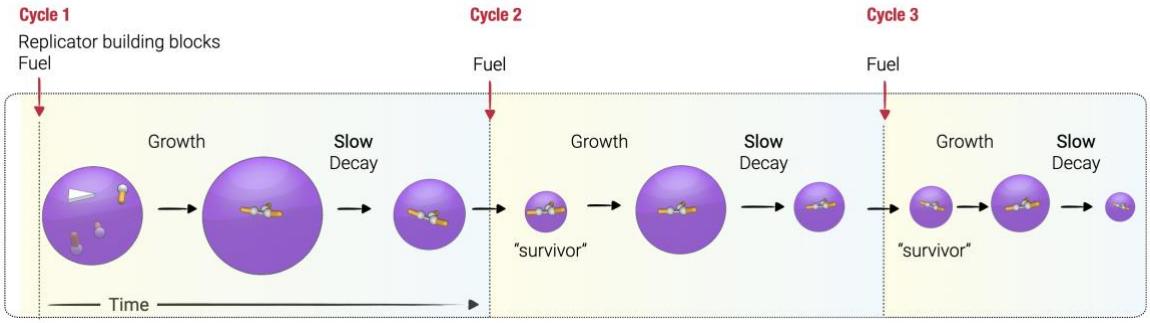
Technical University of Munich

Establishing robust genotype–phenotype coupling in synthetic cells remains a central requirement for achieving open-ended evolution. Here, we demonstrate primitive genotype–phenotype coupling in DOPC vesicles using DNA-based replicator systems that regulate and induce the transcription of functional RNA nanostructures upon successful replication. An isothermal ligation-based method was used to construct a network of self-replicating, short, variable DNA oligonucleotides, characterized by HPLC and PAGE. RNA transcription was achieved by designing inducible short synthetic transcriptional templates (genelets), in which a fluorescent RNA aptamer is transcribed only when a self-replicating DNA sequence binds to an incomplete T7 RNAP promoter. Subpopulations of synthetic cells exhibiting distinct fluorescent readouts were sorted and further analyzed by FACS. By introducing resource-sharing replicators, we show that these replicating "genes" can compete with one another, demonstrating a pivotal hallmark of Darwinian evolution. This bottom-up approach establishes a minimal synthetic cell platform achieving genotype–phenotype coupling with only two proteins, laying the foundation for increasingly complex synthetic systems capable of Darwinian evolution.

Poster #11: Genotype-Phenotype Coupling in Fuel-Dependent Synthetic Cells with an Autocatalyst – H. Soria-Carrera, L. Kauling & J. Boekhoven

Department of Bioscience, School of Natural Sciences, Technical University of Munich

The central dogma of molecular biology describes how a genotype influences a phenotype by transferring genetic information from DNA to RNA to proteins, thereby shaping the cell's traits. Reciprocally, the phenotype affects the success of the genotype by determining the organism's ability to survive, reproduce, and thereby pass on its genetic material. This reciprocal genotype-phenotype relationship is crucial for Darwinian evolution. Creating de novo life from scratch faces the challenge of establishing a similar coupling between genotype and phenotype. This study uses fuel-dependent synthetic cells to explore genotype-phenotype coupling. We endowed these synthetic cells with a genotype in the form of a replicator. The droplets selectively filter building blocks, decreasing the replication error rate. Reciprocally, the replicator prolongs the droplet's lifespan but only when produced in the droplets. Under fuel-starvation conditions, the prolonged lifetime results in increased replicator fidelity, demonstrating that the genotype helps the phenotype, which in the end helps the genotype again—genotype-phenotype coupling in a synthetic system. Future research aims to achieve autonomous division of these compartments for generational transfer of the replicator.



References: [1] Kriebisch et al., Chem 2025, 102399. [2] Soria-Carrera et al., Chem. 2025, 102816.

Poster #12: Bio-Interfaces Engineering Using Recombinant Spider Silk Proteins on Homologous and Heterologous Biomaterials – M. Humenik, N. Best, M. Prinzler, T. Schiller

Department of Biomaterials, Faculty of Engineering Science, University of Bayreuth, Germany

Recombinant spider silk proteins allow scalable production of biomaterials tailored for both biomedical and technical applications [1]. The underlying processing strategy for the recombinant variant eADF4(C16) is based on the self-assembly into insoluble, β-sheet-rich fibrils—a process involving the protein structural transformation and nucleation under mild aqueous conditions [2]. This mechanism can be employed on different surfaces to form several hundred nanometre-thick fibrillar networks, known as nanohydrogels.

The chemically modified nanohydrogels with aptamers can be used as selective biomolecule depots [3], or to recognize specific cellular markers for targeted immobilization of diverse cell types [4, 5]. Importantly, the self-assembly on homologous, spider silk-based surfaces can be integrated into lithographic processes to create patterned cellular microarrays [4, 5, 6]. Furthermore, the distinct surface properties of various biomaterials, such as the high surface energy of gold, the hydrophobicity of polycaprolactone (PCL), or the positive charge of chitosan, can be used to trigger interactions with the amphiphilic, negatively charged spider silk protein [7]. The formation of nanohydrogels on the homologous and heterologous scaffolds, in combination with established enzymatic and aptameric modifications, enables a variety of applications, including biosensing, tissue engineering and micro-tissue engineering.

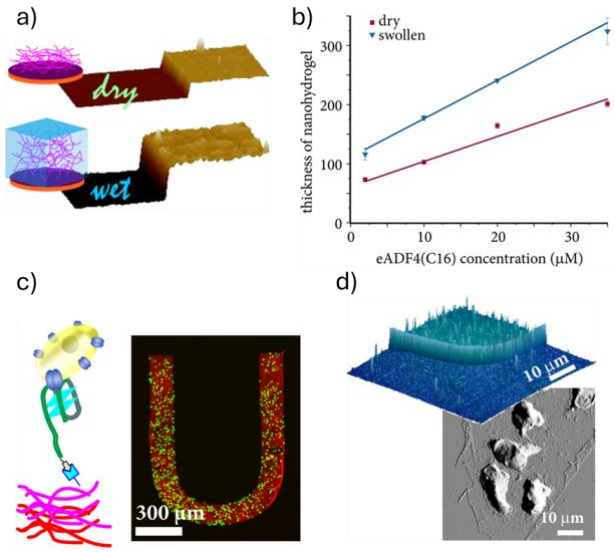


Figure 1. a) Schematic representation of nanohydrogels assembled on a spider silk nanofilm in a dry (above) and a swollen state (below), as analysed by atomic force microscopy (AFM). b) Comprehensive analysis of nanohydrogel thickness in a dry and a swollen state after assembly at different protein concentrations. c) Representation of aptamer-modified nanohydrogel allowing the specific immobilisation of cells, as visualised by a microscopy image on a U-shaped nanohydrogel pattern. d) AFM detail of a nanohydrogel micropattern without cells (above) and with cells (below).

References: [1] Humenik & Scheibel, Adv. Mater. 2025, e08959. [2] Hovanová et al., Protein Sci. 2023, 32, e4722. [3] Humenik et al., Mater. Today Bio 2020, 6, 100045. [4] Heinritz et al., ACS Nano 2022, 16, 7626. [5] Lamberger et al., Adv. Funct. Mater. 2022, 32, 2207270. [6] Molina et al., Biomacromolecules 2019, 20, 347. [7] Best et al., Submitted 2026.

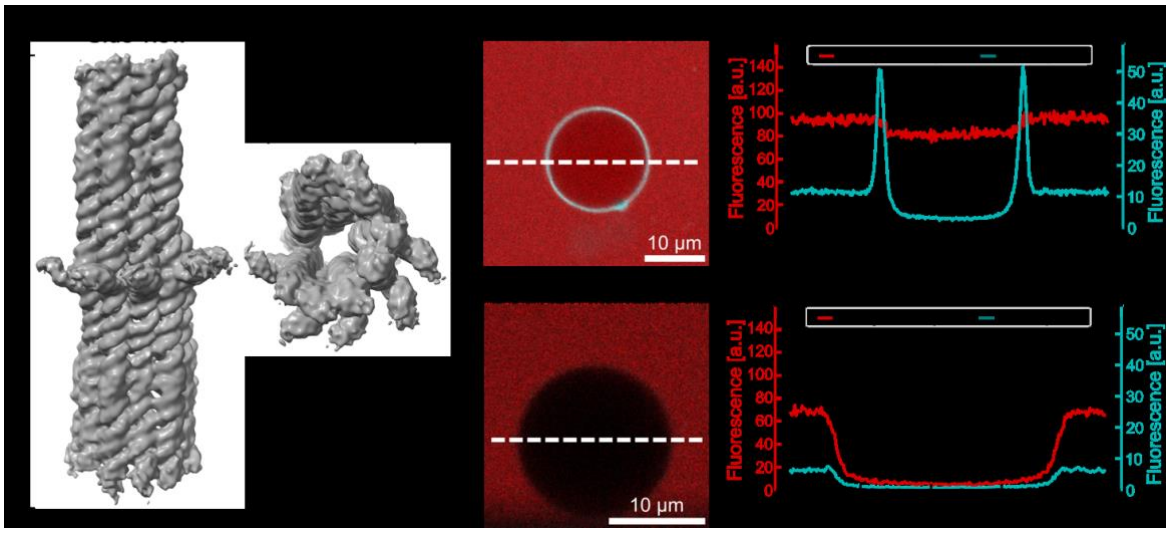
Poster #13: RNA Origami Transmembrane Pores Inside Synthetic Cells –

Tim Karrasch, Luca Monari, Erik Poppleton, Fenja Murken, Sebastian Eustermann, Kerstin Göpfrich

ZMBH Heidelberg University; Max Planck School Matter to Life; MPI for Polymer Research; EMBL

Spatial compartmentalization is a fundamental property of life, enabling the formation of concentration gradients, facilitating biochemical reactions, and shielding internal processes from environmental fluctuations and harmful agents. Maintaining such out-of-equilibrium systems, however, requires the continuous uptake of nutrients and the removal of waste products. Essential molecules, including ions and metabolites, often diffuse poorly through biological barriers such as phospholipid bilayers. To permit their transport, living cells predominantly rely on transmembrane proteins that form selective pores. Here we present a genetically encodable RNA origami pore designed to mediate molecular transport across lipid membranes.

In our effort to construct a protein-free synthetic cell from the bottom up, we aim to replace these protein pores with engineered molecular hardware. To this end, we designed a ~2.4-kb DNA template that, upon transcription, folds into a hollow eight-helix RNA bundle, an RNA origami transmembrane pore with a ~5-nm cavity. Seven biotin aptamers are positioned around the central plane of the pore to enable binding to biotinylated membranes. Correct folding of the RNA origami nanopore into the target 3D structure was confirmed by cryo-electron microscopy. Binding and insertion into lipid bilayers were validated using fluorescence confocal microscopy in dye-influx assays and by negative-stain electron microscopy. We further demonstrate that the pore can be produced by in vitro transcription (IVT) inside giant unilamellar vesicles (GUVs).



RNA origami transmembrane pore: A 3D structure of the RNA origami nanopore visualized by cryo-electron microscopy (6.7 Å resolution). The left panel shows a side view, revealing the finger-like protrusions at the midplane of the structure that incorporate biotin aptamers enabling membrane binding. The right panel presents a top view, highlighting the hollow central cavity of the pore. **B** Confocal microscopy images (left) show fluorescently labeled RNA nanopores (cyan), produced by in-vitro transcription with fluorescent nucleotides, binding to giant unilamellar vesicles (GUVs) with biotinylated membranes (top) but not to PEGylated membranes (bottom). A fluorescent dye (red) diffuses into biotinylated GUVs where pores can insert, but not into PEGylated GUVs, where binding is prevented by the absence of biotin. Fluorescence intensity profiles (right) confirm specific membrane binding and dye influx exclusively in biotinylated GUVs.

Poster #14: Application of the Kohlrausch Function to Ultrafast Transient Absorption Spectral Kinetics – Abdul-Malik Saiid, Philip Kurian

Quantum Biology Laboratory, Howard University

The Kohlrausch (stretched exponential) function, I(t) = exp(−(t/τ)^β), is widely used in luminescence decay analysis and is associated with an underlying distribution of decay rates [1]. We investigate its role in ultrafast transient absorption spectral kinetics by examining whether such relaxation behavior can emerge directly from the intrinsic decay-rate spectrum of microtubule architectures, which are found in all eukaryotic organisms. Using the 1JFF Protein Data Bank structure, we construct a non-Hermitian effective Hamiltonian for microtubules composed of 1, 4, 10, and 100 spirals [2]. Diagonalization yields complex eigenvalues whose imaginary parts define the decay-rate spectrum, spanning both superradiant and subradiant modes [3].

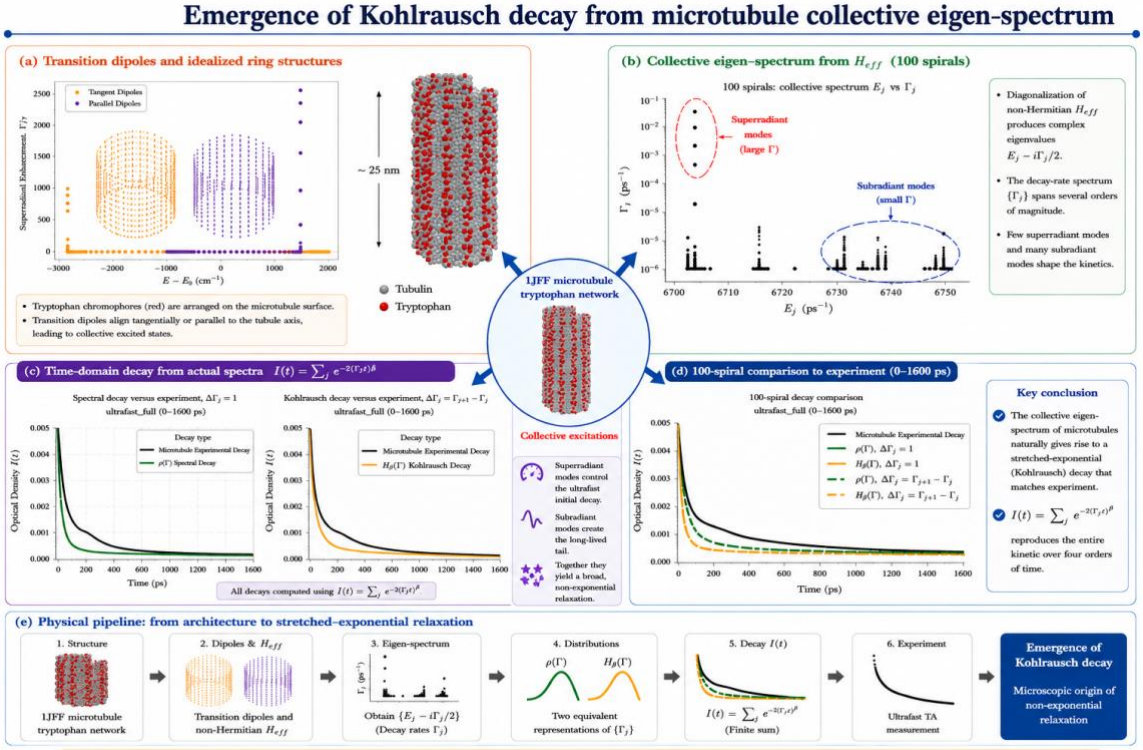


Fig. 1: Microtubule architecture, collective eigen-spectrum, transient spectral kinetics, and emergence of Kohlrausch relaxation.

The comparison yields consistently small error values across all investigated microtubule architectures, with MSE values reaching the order of 10^{-9}–10^{-7} and log MSE values remaining below approximately 8.4×10^{-2}, indicating strong agreement between the constructed decay-rate representations and the observed experimental transient absorption decay. Superradiant modes govern the short-time dynamics, while subradiant modes control the long-time behavior, together producing a broad, stretched-exponential decay profile. This demonstrates that the observed ultrafast relaxation in microtubules can be traced directly to collective excitonic interactions, providing a clear link between microscopic architecture and macroscopic decay behavior.

References: [1] Berberan-Santos et al., Chem. Phys. 315, 171–182 (2005). [2] Patwa et al., Frontiers in Physics 12, 1387271 (2024). [3] Babcock et al., J. Phys. Chem. B 128, 4035–4046 (2024). [4] Patwa & Kurian, Phys. Rev. A 113, 043708 (2026).

Poster #15: Codispersal and the Origin of Cells – Nicole Anderson, David Baum

Nicole Anderson[1],[2] and David Baum[1],[2]
[1]Wisconsin Institute for Discovery
[2]Department of Botany, University of Wisconsin-Madison

The cells on Earth today are too complex to have arisen spontaneously. Biological individuality must therefore have developed from a more amorphous pre-cellular and perhaps pre-genetic state in which evolution was still possible. Pre-genetic evolution could have occurred through drift or selection on networks of autocatalytic cycles (ACs), series of reactions whose member species self-propagate by increasing their own population sizes (Baum et al., 2023). The ability of ACs to interact in manners reminiscent of biological ecology is well-known and could result in ecosystem-level selection between spatially clustered groups of ACs (Plum et al., 2025).
We speculate that the problem of the emergence of individuality might be viewed partly as a problem of the emergence of chemical codispersal. Here, codispersal is the tendency for multiple particles to move through space together. Forms of association that could produce this effect include particles reversibly bonding into new molecules or being held together by non-covalent forces in micelles, coacervates, or vesicles. We hypothesized that propagule formation will be advantageous when 1) catalytic mineral surfaces necessary for autocatalysis are distantly spaced and 2) the environment undergoes periodic disturbances in which a mineral surface is cleared of all its adsorbed autocatalytic species. We tested this by analyzing computational reaction-diffusion models of surface-catalyzed ACs, some of which are able to form molecular propagules containing all their member species. Our results show that propagules tend not to be useful in well-mixed environments or environments where catalytic surfaces are close enough together to be reliably seeded through singlespecies dispersal. However, propagule formation is advantageous to a cycle when environmental disturbances are frequent and/or long stretches of empty space must be crossed to reach new resources. These findings suggest spatial structure can selectively favor reliable forms of codispersal. Evolution in response to this mechanism could lead to the emergence of vesicles that transport many member species of ACs and may become independent protocells.

References:
Baum, D. A., Peng, Z., Dolson, E., et al. 2023, Journal of The Royal Society Interface, 20, 20230346, doi: 10.1098/rsif.2023.0346. Plum, A. M., Kempes, C. P., Peng, Z., & Baum, D. A. 2025, npj Complexity, 2, 21, doi: 10.1038/s44260-025-00045-z