**Bio-inspired Soft Matter 2025 (4-6 June 2025)**

**Abstracts**

**Invited talks**

**Dwaipayan Chakrabarti** (University of Birmingham) - Colloidal Advanced Materials: Building Them Like Biology

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Biology provides fascinating examples of functional architectures, often involving a structural hierarchy, built from the bottom up via self-assembly of diverse building blocks [1,2]. Photonic structures in the realm of biology provide great inspiration for developing advanced materials [3]. In particular, the single network gyroids are known as biophotonic nanostructures, imparting vivid structural colour to the wing scales of certain butterflies [4]. In this presentation, I will talk about a series of computational studies on programming facile self-assembly pathways for rationally designed patchy particles to yield colloidal advanced materials, especially those much sought-after as photonic crystals. I will illustrate how, following biomimicry [5], hierarchical self-assembly pathways can be programmed and medium-range order can be encoded along crystallisation pathways to push the frontiers of colloidal self-assembly for advanced materials [6-10]. Finally, I will discuss how our design rules have wider implications for developing biomaterials.

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**Erica Del Grosso** (University of Rome Tor Vergata) - Responsive DNA supramolecular structures

The interdisciplinary research area of Supramolecular Chemistry, that spans the fields of chemistry, biology, nanotechnology and materials science, focuses on the development of molecular assemblies and complex materials that play an important role in various applications. Recently, synthetic DNA has emerged as a particularly suitable biomaterial for engineering supramolecular devices with predefined geometries and functions, at the nanoscale. Many efforts have been dedicated to create artificial materials that exhibit unprecedented properties similar to their natural counterparts, such as the ability to adapt, reorganize and move in response to different molecular cues.

In the last years, we have re-engineered supramolecular DNA-based structures to respond to various biochemical inputs, and we have demonstrated several kinetically-controlled strategies to reconfigure their spatial reorganization.1 In addition, thanking advantage of the precise spatial addressability of synthetic DNA, we have also decorated our supramolecular DNA structures with different ligands and responsive elements to endow them with a variety of functions that could have potential applications in sensing, bioimaging and drug delivery.2,3

Our approaches to engineer responsive supramolecular DNA structures offer incredible opportunities to develop functional biomaterials with improved adaptability, precision and sensing capabilities.

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**Lorenzo Di Michele** (University of Cambridge) - Genetically encoded designer RNA condensates and organelles

Condensation of RNA and proteins leads to the formation of functional membrane-less organelles, which are central to cellular functions. The ability to program biomolecular condensation and build “designer” membrane-less organelles is considered highly valuable for metabolic engineering of living cells and for creating ever more complex synthetic cells. I will introduce a modular platform for engineering de novo synthetic RNA condensates from tailor-made, branched RNA nanostructures that fold and assemble co-transcriptionally. Up to three orthogonal condensates can form simultaneously and selectively accumulate fluorophores through embedded fluorescent light-up aptamers. The RNA condensates are genetically encoded in DNA templates, which can be expressed within synthetic cells to produce membrane-less organelles with a controlled number and relative size, and which show the ability to capture proteins. The affinity between otherwise orthogonal nanostructures can be modulated by introducing dedicated linker constructs, enabling the production of bi-phasic RNA condensates with a prescribed degree of interphase mixing and diverse morphologies. Sequestering enzymes within the condensates and tuning their localization in co-existing RNA sub-phases enables modulation of the activity of individual enzymes and model cascades, exemplifying the applicability of the designer RNA condensates to metabolic engineering.

**Yair Fosado** (University of Edinburgh) - Topological viscoelasticity: when DNA nanostars and amorphous materials form loopy networks

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Understanding how microscopic structure and topology shape macroscopic properties is a central challenge across many fields [1-3]. In this talk, we explore the viscoelasticity of DNA nanostar hydrogels, a model system to study limited-valence networks, where nodes are constrained to have a restricted number of connections [4]. Using rheology, confocal imaging, and molecular dynamics simulations, we find that these networks form highly interpenetrated, loop-rich structures, where loops are topologically linked. At low concentrations, elasticity is governed by branching and pore size, but at higher concentrations, it is related to abundant topological links. These results reveal *topological viscoelasticity* as a key, previously overlooked mechanism in soft and amorphous materials, with implications for designing materials with controllable mechanical properties.

A picture containing art, child art, drawing, graphics

Description automatically generatedI will also discuss our current efforts to understand the role of similar topological features in other disordered systems such as amorphous ice [5], silica, colloidal gels and Olympic gels [6].

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**Elisha Krieg** (Leibniz Institute for Polymer Research Dresden) - Assembling a true Olympic Gel from >16,000 combinatorial DNA rings

An Olympic Gel comprises a three-dimensional network of molecules, but instead of distinct crosslinks, the network is held together purely by mechanically interlocked molecular rings. Polymer physicists have theorized that such a material would exhibit highly unusual mechanical properties. Yet, Olympic Gels have remained a notoriously challenging target that defies traditional synthesis approaches. In this talk I present a scalable and versatile approach towards true Olympic Gels by employing concepts of DNA nanotechnology, synthetic biology, and combinatorial supramolecular chemistry. A key innovation is the use of large combinatorial libraries of DNA plasmid rings that contain thousands of chemically distinct molecules. The rings exhibit enzymatically activated lock & key domains that allow reversible mechanical interlocking. Their large constitutional diversity and exceptional binding selectivity avoids non-specific cross reactions. The Olympic gels exhibit swelling and concentration-dependent scaling properties that are fundamentally different from traditional molecular networks. Our approach provides access to a new class of soft, biologically inspired materials that can have unusual stretchability, toughness, and swelling behavior. This work demonstrates that exotic material properties can emerge in systems with a high compositional complexity that is more reminiscent of biological than synthetic matter.

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**Michael Lang** (Leibniz Institute of Polymer Research in Dresden) - Olympic gels: a model system for understanding permanent entanglements

Olympic gels are macroscopic gels made of concatenated cyclic polymers that resemble microscopically the structure of the Olympic rings. Starting from a brief review of entangled polymers and theoretical works about Olympic gels, I will discuss first different pathways of how to generate Olympic gels. The concatenations of the rings is analyzed in simulations using knot theory. For Olympic gels made of monodisperse rings, it turns out that the network topology is fully described by the average number of concatenations per ring. I will introduce a very simplistic model to understand the scaling of concatenations and to predict the sol-gel transition of these materials both as a function of concentration and the molar mass of the rings. Next, I will sketch how the structure of Olympic gels can be modeled and which expectations we have for the elastic properties of Olympic gels. Finally, I will discuss which different regimes for the equilibrium swelling of Olympic gels are possible. All steps of my discussion will be compared with computer simulations and experimental data, if available.

**Maitane Muñoz-Basagoiti** (ISTA, Austria) - Bottom-up design of artificial machines with programmable matter: Catalysis and Treadmilling

Living and non-living matter are constituted of the same fundamental building blocks. And yet, while inanimate matter is functionally-rigid, living matter is remarkably versatile and adaptable. These properties stem from the concerted action of an ensemble of key molecular players: Proteins. From catalysing chemical reactions to self-organising into force-generating complexes, what are the minimal design principles that govern protein function? More importantly, how can we realise these principles in the lab with programmable building blocks? By combining theoretical toy models and coarse-grained computer simulations, in this talk I will present the design of two artificial machines: a mechanical catalyst that cleaves bonds, and a self-fitting monomer that polymerises with treadmilling dynamics. I will discuss the physical and geometrical constraints that give rise to each functionality, emphasising the maximal efficiency that can be obtained from the catalytic design on the one hand, and the treadmilling kinetics that result from a bistable monomer, on the other. These designs contribute to the future realisation of self-regulated artificial systems with bio-inspired functionalities using designer building blocks such as DNA-coated colloids.

**Susana Rocha** (KU Leuven) - Seeing is believing: microscopic techniques to uncover cell-matrix interactions in biomimetic hydrogels

Understanding the complex interplay between cells and their surrounding matrix is paramount for advancing biomimetic scaffold design. By pushing and pulling on the extracellular matrix (ECM), cells continuously sense the dynamic mechanical cues from their environment and generate mechanical feedback. Mechanical characterization of the matrix surrounding the cells has shown that contractile cells can generate a stiffness gradient in biological gels. Such cell-generated forces can reorganize and deform the natural ECM fibers, causing fiber densification and alignment. Traditional methods like electron microscopy and scanning probe microscopy provide high spatial resolution but fall short in capturing these dynamic processes in situ. This talk highlights the use of fluorescence microscopy to characterize the structure of biomimetic hydrogels and quantify the traction forces generated by the cells.

We use confocal imaging and bead-free traction force microscopy (TFM) to demonstrate how a fully synthetic biomimetic hydrogel can be used as a platform for exploring the influence of biochemical and mechanical factors on cell-matrix interactions.. This biomimetic hydrogel, formed from oligo(ethyleneglycol)-functionalized polyisocyanate (PIC) polymers, is formed by non-covalent interactions and exhibits a nonlinear mechanical response at low stresses.

We further investigate the forces that cells apply at a molecular scale using FRET-based tension sensors. These sensors allow us to measure the molecular-scale forces exerted by the cells, providing insights into how cells interact with and remodel their microenvironment. Our fluorescence microscopy-based approach sheds light on how physical cues regulate cell-matrix interactions, offering insights for the rational design of improved biomimetic materials.

**Omar Saleh** (UC Santa Barbara) - Diverse and entangled DNA droplets

We seek to create novel biomaterials platforms through mesoscopic assemblies of droplets of DNA. The droplets are self-assembled biomolecular liquids, formed from ~10 nm, branched DNA particles termed 'nanostars'.  With appropriate materials processing, nanostars condense into micron-scale droplets that act as rough mimics of biological condensates. I will briefly review certain aspects of this materials platform, but primarily focus on two recent projects: First ,we have explored interfacing the DNA droplets with actin gels, finding, somewhat surprisingly, that the droplets can entangle with the actin, and cause huge changes to the gel modulus. This has some promise as a general means to control hydrogel elasticity. Second, we have developed a highly diverse platform of multi-phase DNA droplets, in which the diversity permits the droplets to take relatively stable 2-D 'proto-tissue' structures with interesting physical dynamics.

**Fredrik Schaufelberger** (KTH Royal institute of Technology) - Metal Chelate Rotaxanes for Biosensing and Therapeutics

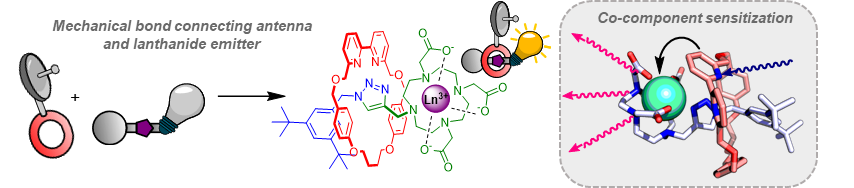
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Luminescent emitters based on lanthanide ions are of ubiquitous importance in the biological sciences, but typically need sensitization from a covalently attached adjacent chromophore – an “antenna” – to have suitable emission intensities.1 There is a constant requirement for improved methods of combining antennas and emitters, especially to construct dynamic and (bio)responsive systems. In this work I will first show that the ***mechanical bond*** can be used to connect the antenna to the emitter, providing unique dynamic features and stimuli-responsiveness to the resulting assemblies.2-4 We have developed a strategy to synthesize [2]rotaxanes capped with strong chelating groups, and also established that post-functionalization of these interlocked scaffold by metal ion insertion is modular, high-yielding and straightforward.5 The Eu-capped rotaxane was shown to have unique selectivity towards Cu(II) ions, acting as an efficient turn-off sensor.

Recently, we have also used Ga- and Tb-capped rotaxanes as novel radioimaging agents, demonstrating how the mechanical bond can be used to alter biodistribution and metabolic lifetime in mice models. These studies demonstrate that the mechanical bond can be useful to fine-tune pharmacokinetics of bioimaging agents, and constitute a valuable conjugation method for attaching antennas to emitters, while also providing otherwise hard-to-access and beneficial stimuli-responsive features to the resulting molecular systems.



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**Rebecca Schulman** (Johns Hopkins University) - Biomolecular Fields

Biological development shows how reaction-diffusion processes serve as crucial forms of organization at micron to millimeter scale. Biomolecular reactions produce concentration fields that, for example, serve as maps to pattern fly compound eyes, weave nerves into brain circuitry, and organize microbial communities. While pattern formation through reaction-diffusion has been studied as far back as Turing in the 1950s, we still do not have clear principles by which the kinds of patterns seen in development might emerge through reaction-diffusion processes involving chemical reactions such those that underlie genetic regulation or cell-celI communication. I will describe a structured approach for designing biochemical reaction-diffusion processes forms by sources, or "monopoles," that generate signals that, because they are degraded throughout a vessel, form concentration fields that have well-defined structure and size. These concentration fields form independently of container size and shape and can be designed so that their shape is purely a function of different reaction rates in the system. I will show how then chemical reactions can "transform" these patterns to produce more intricately patterned output fields, or transmit information digitally by design. In such systems, we also observe new phenomena such as oscillations by reactions that do not oscillate in a test tube. Finally, biomolecular fields are stable energy sources and can drive processes at non-equilibrium steady state. I will describe some simple examples of how fields can direct materials assembly, order chemical reactions, and control flow.



**Contributed Talks**

**Kasturi Barkataki** (Arizona State University) - Novel topological measures of multi-chain complexity in biopolymers

Biopolymers live in crowded environments where they attain complex 3 dimensional conformations that are related to their sequence and function. To characterize the multi-component structure of biopolymers we employ methods from topology. A new framework in knot theory was introduced recently that enables one to characterize the complexity of collections of open curves in 3-space using the theory of knotoids and linkoids, which are equivalence classes of diagrams with open arcs. This gives rise to a collection of novel measures of entanglement of open curves in 3-space, which are continuous functions of the curve coordinates and tend to their corresponding classical invariants when the endpoints of the curves tend to coincide. We will show how knot theoretic measures, such as the Jones polynomial can be used to distinguish between systems of biopolymers and quantify the net entanglement present in such systems that is relevant to their function.

**Jordi Faraudo** (ICMAB-CSIC) - Engineered hydrogels for cancer immunotherapy: a theoretical/computational perspective

Immunotherapies (therapies based on expanding and enhancing our own immune system cells “in vitro” to be injected again to the patient) have shown unprecedented results in clinical practice to fight cancer, including long term complete responses. The main challenge of these therapies is to optimize “in vitro” immune T cell production. Current “in vitro” practice overlooks the importance of the complex environment in which T cells activate and proliferate in vivo (the lymph nodes). Hydrogels are an ideal soft matter candidate for mimicking the natural environment of T cells and hence greatly optimize immunotherapy, as we have recently shown (ACS Appl. Mater. Interfaces 2025, 17, 16548−16560). Here I will present an overview of the theoretical concepts (based on different molecular modelling techniques) that are beyond the successful use of Lymph-Node inspired hydrogels in immunotherapy.

**Tom Girard** (Laboratoire Charles Coulombs (L2C, Université de Montpellier)) - Stress localization in biomimetic prototissues

Tom Girard, Remi Merindol, Laura Casanellas  
Understanding the way tissues respond to mechanical forces is crucial in complex biological processes such as embryogenesis or tumor growth. The development of biomimetic model tissues with simplified biochemical complexity, but capable of reproducing essential mechanical features of living tissues, can help in achieving this major goal. In this work, we  
design artificial prototissue which are obtained by the controlled assembly of Giant Unilamellar Vesicles. Vesicle-vesicle adhesion is mediated by the incorporation of complementarity DNA strands on vesicle membranes, which enables to program their interactions. We implement novel prototissues which can exhibit a mechano-fluorescence  
response. This is achieved by using mechano-fluorescent probes that consist of DNA strands functionalized with a FRET pair, which becomes fluorescent under load. At rest the probe is non fluorescent, and the fluorescence is activated only under the application of a force that  
overcomes the hybridization energy of the DNA duplex (which is set by the length of the complementary DNA strand). Therefore, mechano-fluorescent probes report the association/dissociation of the DNA duplex with time, and we use them as local force sensors, sensitive to weak forces to follow local stresses in biomimetic tissues with good spatial resolution. Experimentally, the external load is applied locally to the prototissue making use of a nano-indentation technique. The applied force can be tuned based on the size and stiffness of the probe. Simultaneous confocal microscopy imaging is achieved in order to correlate the mechanical signature to the fluorescence response of the prototissue, and eventually, to evaluate the force transmission within the vesicle network.

**Oliver Henrich** (Department of Physics, University of Strathclyde, Glasgow) - oxDNA3 – Introducing Sequence-Specific Curvature and Elasticity into a Coarse-Grained DNA Model

Coarse-grained modelling of DNA [1] is not only an efficient alternative to atomistic approaches. It is indispensable for the modelling of DNA on timescales in the millisecond range and beyond, or when long DNA strands of tens of thousands of base pairs or more must be considered, for instance to study the dynamics of DNA supercoiling, which is important for gene regulation and expression.  
  
In this regard the oxDNA2 model [2] is one of the most successful coarse-grained models of DNA to date. While it features the correct thermodynamic behaviour of duplex formation as well as a good average representation of both single and double stranded DNA, it lacks crucial aspects such as sequence-specific curvature and elasticity.  
  
To address this shortcoming, we recently developed the third-generation oxDNA3 model, whose design and properties we will present.  
  
oxDNA3 has been trained on state-of-the-art atomistic DNA simulations [3] and has the correct local and global sequence-dependent geometry. In terms of sequence-dependent elasticity oxDNA3 combines the best of both, the nano- and mesoscopic world. While it retains the variations of elasticity with sequence from all-atom simulations, oxDNA3 mitigates the tendency of current atomistic models to exhibit longitudinal and torsional persistence lengths that are too large.  
  
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**Manish S Kushwah** (Aston Institute for Membrane Excellence) - Deciphering Dynamin Polymerisation Mechanism and Regulation using Mass Photometry enabled Single-Molecule-Counting and Particle-Tracking

Membrane binding proteins (MBPs) such as Dynamin1 (Dyn1) serve a critical function of remodelling membranes to catalyse membrane fission in endocytosis. Loss or perturbation of Dyn1, and its homologs, function leads to perturbation of neuronal transduction and disease such as Charcot-Marrie-Tooth syndrome. Dyn1 is a prototypical member of Dynamin superfamily of proteins which are involved in regulating cell function both at plasma membranes and various cell organelles. Dyn1 function is critically linked to its ability to polymerise only on membranes to catalyse membrane fission. Despite the extensive studies using biochemical, microscopy and structural methods, the precise mechanism of Dyn1 polymerisation and regulation to inhibit polymerisation remains obscure.   
  
To elucidate the Dyn1 polymerisation, we use mass photometry (MP), a label-free single-molecule microscopy technique, that estimates molecular weight and abundance of the species, enabling affinity estimation and the determination of assembly mechanisms. MP also has high mass determination accuracy and dynamic range, making it extremely suitable to study protein polymerisation mechanism.  
  
Our findings reveal that Dyn1 polymerization occurs in two distinct phases: a rate-limiting step followed by a spontaneous step. The rate-limiting step is regulated by a two-tiered autoinhibitory mechanism in solution. Additionally, using MP enabled, label-free, single-particle tracking (dynamic MP), we demonstrate that membrane binding provides the energy needed to overcome this two-tiered autoinhibition at the rate-limiting step, thereby promoting Dyn1 polymerization. Furthermore, we show that this polymerization mechanism is conserved across dynamin isoforms and explain how aberrant Dyn2 polymerization in solution contributes to the Charcot-Marie-Tooth disease.   
Taken together, our findings establish a framework to quantitatively understand polymerisation of MBPs and discover specific avenues to target their dysfunction in various diseases including cancers.

**Diego Lopez Barreiro** (University College London) - Bio-inspired materials based on chimeric structural proteins

Nature leverages the self-assembly propensity of structural proteins like elastin, resilin, collagen, or silk to generate sustainable functional materials with remarkable performance and that span a wide range of mechanical and structural properties: from soft to stiff, from porous to densely packed, from static to dynamic... This is inspiring scientists and engineers to use structural proteins as a sustainable replacement for fossil-based polymers in the manufacture of synthetic functional materials with applications in food, healthcare, adhesives, energy, textiles, or membrane technology, to name a few.   
  
Structural proteins are normally harvested from animal sources (e.g., silkworm cocoons, animal tissue), but these suffer from batch-to-batch variability, presence of contaminants, and cultural or religious concerns that limit their commercial use. Fortunately, developments in engineering biology allow us to overcome these issues and biofabricate non-animal-derived recombinant structural proteins. Furthermore, by carefully engineering their amino acid sequence, we can design entirely new structural proteins with properties inspired by natural structural proteins, but that do not exist in Nature, and use them to develop materials with e.g., adjustable mechanical properties, programmed functionalities, or the ability to adapt or respond to the environment.  
  
However, a complete framework that connects amino acid sequence to material properties is unavailable. Thus, de novo recombinant structural proteins are normally developed through low-throughput trial-and-error experimentation, which impedes rapid prototyping. In this talk, we will showcase our work on combining computational and experimental tools to accelerate the exploration of the design space of structural proteins. Specifically, we will present examples of how this approach has aided us in the design of new protein-based materials including flexible conductive films, biomineralizing films, or injectable stimuli-responsive hydrogels.

**Thomas Williamson** (School of Engineering, University of Edinburgh) - Quantifying the Mechanical Properties of Biomolecular Condensates

Biomolecular condensates are viscoelastic droplets, rich in specific biomolecules, which play many important roles in sub-cellular organisation such as regulating stress response [1]. There is growing recognition that the mechanical properties of condensates govern their macroscopic behaviour, which is often substantially different from that of purely viscous droplets. However, until recently, it has been difficult to measure these properties at scale. We demonstrate a non-invasive flicker spectroscopy method for measuring two key mechanical properties of thousands of condensates in live cells [2], and present FlickerPrint, an open-source Python package for handling the computational requirements of the method [3]. We find that the fluctuation spectra of stress granules (a type of condensate) in live cells cannot be adequately fitted with an interfacial tension-only model, as expected for simple Newtonian liquids. Instead, the measured fluctuation spectra require an additional contribution, which we attribute to an elastic bending deformation. We then show that at the population level, interfacial tension and bending rigidity span several orders of magnitude so cannot be accurately determined by observing only a small number of condensates. However, the mean behaviour of these properties across a population of stress granules can be used to distinguish between granules containing different ratios of constituent proteins. In addition, we have preliminary results which suggest that stress granules display broken detailed balance in the amplitudes of the fluctuation modes, which we believe is a signature of the liquid-to-solid ageing transition which many condensates undergo.

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**Posters**

**Filippo Conforto** (University of Edinburgh) - Optimised Assemble Pathways for Olympic Gels

Olympic gels are an extremely promising form of soft matter and, because of their unique topological properties, they have significative different material properties compared to classic cross-link gels. Stimulated by the current challenges in finding a reliable and efficient way to assemble these materials, we simulated two different pathways for generating percolating networks of cyclic polymers. Firstly we discussed the "progressive construction", where gels are formed by ligating linear polymers at low density within a high-density solution of circular polymers. We found that the average valence of links and the mass of the the linked network is highly dependent on the length of both polymer populations. Second, we explored the "Pickett" construction where linear polymers belong to separate families and can only ligate within the same family. Interestingly, we discovered that the degree of linking of the gel can be optimised choosing a suitable number of families. Finally, we analysed the viscoelastic properties of the gels, connecting them with total linking number, valence, and gel mass. Our results provide insight on how olympic gels can be assembled through different frameworks, and will assist the creation of novel sustainable material with tuneable properties based on network linking.

**Ruiyan Gao** (University College London) - Improving the performance and sustainability of biosensing platforms by using recombinant structural proteins

With the rapid advancement of point-of-care (PoC) technologies and increasing use of disposable medical diagnostics, there is a growing concern regarding the environmental impact of electronic waste. This research investigates the development of sustainable, flexible, and biodegradable conductive films for electrochemical biosensors using bio-inspired silk-elastin-like proteins (SELPs) and biomass-derived carbon materials (BCMs). SELPs are recombinantly produced proteins that combine the mechanical robustness of silk-like blocks (with amino acid sequence GAGAGS) with the thermal responsiveness of elastin-like blocks (e.g., IPAVG or VPGXG, being X any amino acid except proline). By varying the amino acid sequence and/or post-treatment film manufacturing methods (e.g., water annealing or ethanol annealing), SELPs enable precise control over mechanical properties of the resulting films. Additionally, biomass-derived carbon materials (BCMs) produced via hydrothermal carbonisation and physical activation are integrated into SELPs to provide them with electrical conductivity. These carbon fillers are naturally doped with nitrogen and oxygen, which facilitates their dispersion within protein matrix materials while enabling conjugation with biomolecules for biosensing purposes. In this work, we showcase preliminary results demonstrating the successful SELP expression and composite film fabrication. Overall, this study presents a proof-of-concept for SELP/BCM composites as sustainable biosensing platforms.

**Zoubeir Saraw** (EPFL) - Mussel byssus-inspired spinning of ionically crosslinked fibers

Sustainable, bio-derived materials such as cellulose have attracted significant interest for applications ranging from food packaging to textiles. Most notably, high-aspect-ratio cellulose nanocrystals and nanofibers show promise in wet spinning processes, enabling the fabrication of fibers with high stiffness and strength—ideal candidates for advanced engineering applications. However, these fibers often suffer from poor elongation and toughness, limiting their widespread use in high-impact scenarios. Furthermore, achieving the necessary mechanical performance typically requires extensive post-processing to improve alignment. In nature, marine mussels produce tough, extensible byssal threads via a highly efficient, microfluidic-like process. These threads are composed of well-aligned, ionically crosslinked proteins which allow them to withstand repeated wave impacts. Inspired by the mussel, I will employ a microfluidic system to spin tempo-oxidized cellulose nanofibrils (TO-CNFs)—which feature abundant carboxylic side groups—into aligned fibers. By introducing multivalent metallic ions and polycations, I will induce ionic crosslinking between TO-CNFs to enhance the alignment and mechanical performance. Such fibers have the potential to be applied as sustainable textile linings in shock-absorbing applications such as helmets and grips.

**Ebony Shire** (University College London) - Influence of sequence arrangement on self-assembly of thermoresponsive silk-elastin-like polypeptides

Structural proteins such as silk, elastin, resilin and collagen represent some of the most varied and impressive mechanical and structural properties of the natural world. Thanks to recombinant DNA technology, we can merge building blocks (and associated mechanical structural properties) of multiple structural proteins in a single protein biopolymer, with the aim of new developing multifunctional materials. An example of this is silk-elastin-like polypeptides (SELPs), which combine the strength and toughness of silk (via GAGAGS building blocks) with the elasticity and thermoresponsiveness of elastin (via IPAVG or VPGXG building blocks) [1]. These biopolymers can be used to manufacture protein-based materials with potential applications in areas such as soft robotics and biomedical applications [2-4].   
  
To make functional biomaterials from SELPs, it is important that these materials are stable across a range of temperatures, and understanding the self-assembly of SELPs is a key factor in determining this. These aspects can be carefully controlled through sequence design, but there is currently a gap in our understanding of how the sequence of SELPs relates to their self-assembly, and subsequently how this impacts the macroscopic behaviour and mechanical properties of the materials derived from them – the sequence-property relationships.   
  
Our work aims to unveil these relationships, with the purpose of designing novel SELPs that can be used as functional biomaterials. To that end, a library of SELPs with a range of silk-like (GAGAGS) and elastin-like (IPAVG, VPGVG, VPGEG, VPGIG and VPGKG) building blocks were designed and synthesised using microbial fermentation. These proteins also featured different net charges (positive, neutral or negative). We purified them using an inverse temperature cycling method that leveraged their thermoresponsiveness to avoid chromatography purification methods.  
  
Subsequently, the viscoelastic and structural properties of these proteins were characterised across multiple scales (e.g., molecular, condensate and macroscopic level) to understand their self-assembly, and how this defines their ability to form thermoresponsive hydrogels. This work contributes to a fundamental understanding of self-assembly in SELPs, providing further rationale for sequence design of high-performance protein-based materials.   
  
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