Poster Presentations
Monday 24 March, Poster Session 1, Drinks Reception and Exhibition Commences

Poster No.	First Name	Last Name	Organisation	Paper Title	Topic
33	Peter	Adams	University of Leeds	Exploring the “concentration quenching” effect of small-molecule fluorophores and fluorescent proteins by using lipid membranes and electrophoresis	Imaging and single molecule biology
91	Caranfil	Anca	Université Paris-Saclay	Towards the modelling of chromosome movements during meiotic prophase I in Arabidopsis thaliana	Physics of the nucleus
34	Claudia	Andrews		Detergent-Induced Membrane Solubilization Monitored with Fluorescence De-Quenching	Imaging and single molecule biology
23	Matthew	Asker	University of Leeds	Fixation and extinction in fluctuating metapopulations subject to bottlenecks and migration	Evolution ecology and epidemiology
24	Rafael	Ayala Lara	Aalto University	Noise and global warming effects on the swimming dynamics of copepods.	Evolution ecology and epidemiology
35	Lu	Bai		Adaptive 3D Multiphoton Microscopy for Deeper and Higher Spatial Resolution Imaging	Imaging and single molecule biology
25	Alexander	Baker	University of Cambridge	Long term evolution of spatially structured microbial communities in controlled environments	Evolution ecology and epidemiology
62	Oleksandr	Baziei	The Universtiry of Edinburgh	Hybrid Computational Framework for Active Polar Fluids	Patterns, waves, transport, collective phenomena, and microswimmers
63	Francesco	Boccardo	University of Genoa	Communication-driven geometric bias enhances multi-agent olfactory search efficiency	Patterns, waves, transport, collective phenomena, and microswimmers
92	Andrea	Bonato	University of Strathclyde	Spontaneous unidirectional loop extrusion by SMC proteins	Physics of the nucleus
98	Ahmad	Boroumand		Scaling Behaviour of the Mechanics and Mesoscale Structure of Folded Protein Hydrogels	Protein structure, dynamics and interactions
54	Federico	Bosetto		In vitro expression and characterization of the heme binding domain of HasR from Pseudomonas aeruginosa	Immunity, resistance and host/pathogen dynamics
99	Victoria	Byelova	University of Leeds	From worm-like to blobby: coarse-graining protein unfolding in hydrogel networks	Protein structure, dynamics and interactions
36	Colleen	Caldwell	Vrije Universiteit Amsterdam	Untangling chromatin loops: uncovering biophysical characteristics of CCCTC-binding factor (CTCF)	Imaging and single molecule biology
64	Sam	Cameron	The Open University	Entropy production in spatially diffuse division-death dynamics.	Patterns, waves, transport, collective phenomena, and microswimmers
65	Jan	Cammann	Loughborough University	Active Spaghetti: Collective Organization in Filamentous Cyanobacteria	Patterns, waves, transport, collective phenomena, and microswimmers
1	Maria Cristina	Cannarsa	Sapienza University of Rome	Light-driven synchronization of optogenetic clocks	Clocks, timers and cell cycle dynamics
66	Jared	Carpenter	John Innes Centre	A mathematical investigation into how surfactants influence nanobubble stability in the plant xylem	Patterns, waves, transport, collective phenomena, and microswimmers
37	Thomas	Catley	University of Sheffield	Understanding the Mechanism of Novel Anticancer Drugs with Atomic Force Microscopy	Imaging and single molecule biology
67	Tristan	Cerdin	Sorbonne Université	Counting Active Particles in Boxes to Quantify their Dynamics	Patterns, waves, transport, collective phenomena, and microswimmers
100	Yean Ming	Chew	The University of Warwick	The subtle allostery of kinesin and tubulin	Protein structure, dynamics and interactions
93	Michael	Chiang	University of Edinburgh	Bridging-Induced Phase Separation and Loop Extrusion Drive Noise in Chromatin Transcription	Physics of the nucleus

5	Luca	Cocconi	Max Planck Institute For Dynamics And Self-organisation	Formation and decoding of morphogen gradients in developmental space-time	Differentiation and development
101	Noor	Daudi		Rab11-FIP1 interacts with Rab11-FIP5 in p53 mutant cancer cells.	Protein structure, dynamics and interactions
68	François	De Tournemire	University of Edinburgh	Role of Length Scales in Bacterial Swarming	Patterns, waves, transport, collective phenomena, and microswimmers
69	William	Durham	University of Sheffield	Twitching bacteria actively reverse direction to travel with their neighbours	Patterns, waves, transport, collective phenomena, and microswimmers
102	Timea	Feller		High extensibility of fibrin is supported by unstructured side region, while general mechanical behaviour may arise from random backbone structure	Protein structure, dynamics and interactions
6	Elisa	Floris	University of Graz	Uncoupling jamming- and adhesion-induced phase transition in embryonic tissues	Differentiation and development
70	Tonmoy	Gogoi	Tezpur University	Spontaneous Vortex Dynamics in Active Apolar Rods	Patterns, waves, transport, collective phenomena, and microswimmers
38	Sarah	Graham	University of York	Exploring the Frameshifting Element in SARS-CoV-2 Using smFRET	Imaging and single molecule biology
7	Philip	Greulich	University of Southampton	Emergent order in epithelial sheets by interplay of cell divisions and cell fate regulation	Differentiation and development
71	Simon	Hanna	University of Bristol	Optical trapping of active particles	Patterns, waves, transport, collective phenomena, and microswimmers
39	Tess	Harrison	Cardiff University	Correlative light electron microscopy of individual receptor trafficking in neurons enabled by background-free four-wave mixing imaging	Imaging and single molecule biology
72	Benedikt	Hartl	Tu Wien and Allen Discovery Center at Tufts University	Neuroevolution of Decentralized Decision-Making in N-Bead Swimmers leads to Scalable and Robust Collective Locomotion	Patterns, waves, transport, collective phenomena, and microswimmers
94	Oliver	Henrich	University of Strathclyde	oxDNA3 – Introducing Sequence-Specific Curvature and Elasticity into a Coarse-Grained DNA Model	Physics of the nucleus
27	Lluís	Hernández-Navarro	University of Leeds	Eco-evolutionary dynamics of cooperative antimicrobial resistance in time-varying environments with spatial structure	Evolution ecology and epidemiology
103	Katy	Hollands	University of York	Modelling DNA in Complex Topologies: The Role of Gyrase	Protein structure, dynamics and interactions
40	Libby	Holmes		UNTANGLING HOW THE SHELTERIN COMPLEX TANGLES DNA USING ATOMIC FORCE MICROSCOPY	Imaging and single molecule biology
41	Jamieson	Howard	University of York	Towards Unraveling Nucleoprotein interactions in Supercoiled DNA: Structural Dynamics of Model Catenanes	Imaging and single molecule biology
28	Kabir	Husain	University College London	The Noise is the Signal: Luria-Delbruck in High Resolution	Evolution ecology and epidemiology
73	Shunsuke	Ichii	The University of Tokyo	Enhanced Enzyme Diffusion as Maxwell's Demon: Selective Increase of Exothermal Reaction	Patterns, waves, transport, collective phenomena, and microswimmers
29	Claudia	Igler	University of Manchester	The biophysics of transcription factor binding shapes gene regulation	Evolution ecology and epidemiology
95	Antonio	Iorio	University of Dundee	Tension-dependent kinetochore-microtubule interactions	Physics of the nucleus
74	Purnima	Jain	Tata Institute of Fundamental Research	Inertial swimmer suspensions : Instability and turbulence	Patterns, waves, transport, collective phenomena, and microswimmers
75	Purnima	Jain	Tata Institute of Fundamental Research	Inertial swimmer suspensions : Instability and turbulence	Patterns, waves, transport, collective phenomena, and microswimmers
8	Mahendra Kumar	Jothi Letchumy	School of Physics And Astronomy	Fluorescence microscopy approaches to monitor cell-to-cell heterogeneity in the regulation of cardiomyocyte contractility	Differentiation and development
42	Aneeth	Kakkanattu Arunkumar	University of Exeter	Optoplasmonic single-molecule Whispering Gallery Mode (WGM) sensing platform for probing neurotransmitter-lipid membrane interactions	Imaging and single molecule biology

43	Praveen	Kalarickel Ramakrishnan	University College London	Towards accurate and efficient simulations of multiphoton fluorescence microscopy in mouse brain tissue using the beam propagation method	Imaging and single molecule biology
105	Dimitra	Katrantzi		Unveiling the structure of protein-based hydrogels by overcoming cryo-SEM sample preparation challenges	Protein structure, dynamics and interactions
106	Emma	Kerklingh		Advancing Biophysical Research with the C-Trap: Unveiling Molecular Mechanisms at the Single-Molecule Level	Protein structure, dynamics and interactions
2	Jan	Kocka	UCL	Topological States in Out-of-Equilibrium Allosteric Molecular Assemblies	Clocks, timers and cell cycle dynamics
44	Abhinav Paul	Kongari	The Francis Crick Institute	Optimisation of Electromagnetic Tweezers for Intracellular Force Application	Imaging and single molecule biology
45	Wolfgang	Langbein	Cardiff University	Interferometric Gated Off-Axis Reflectometry (iGOR) - ultrasensitive label-free tracking of nanoparticles and suspended membranes in three dimensions	Imaging and single molecule biology
9	Crisandro Allen	Lazo	University of The Philippines Manila	Thermodynamic Consequences of Bursty Gene Expression on the Mesoscopic Dynamics of Two-Node Gene Networks in Response to an External Forcing	Differentiation and development
76	Anna S.	Leathard	The University of Sheffield	Oscillations and collective behaviour in compartmentalised enzymatic reactions: Insights from numerical models	Patterns, waves, transport, collective phenomena, and microswimmers
55	Yael	Lebel		Excitable systems as a design principle of the immune system	Immunity, resistance and host/pathogen dynamics
56	Yael	Lebel		Excitable dynamics of flares and relapses in autoimmune diseases	Immunity, resistance and host/pathogen dynamics
46	Zekai	Li	Imperial College London	Identifying Molecular Interactions through Stochastic Modelling and Optimisation	Imaging and single molecule biology
57	Ruizhe	Li	University of Cambridge	Host cell cycle and ribosomal resources drive phage infection outcomes	Immunity, resistance and host/pathogen dynamics
10	Yi Ting	Loo	University of Warwick	Modelling pattern formation and self-organisation during neuruloid development	Differentiation and development
58	Carol	Lu	Arizona State University	Quantitative Modeling of Bacterial Population Kinetics in the Gut Microbiome of Individual C. elegans	Immunity, resistance and host/pathogen dynamics
11	Aileen	Magilin	John Innes Centre	Unlocking early flowering: The role of microRNAs in accelerating flowering time through small RNA transcriptomics	Differentiation and development
107	Vuk	Malis	University of York	Molecular Simulations of the Pyrenoid	Protein structure, dynamics and interactions
30	Daniel	Malumphy Montesdeoca	The University of Manchester	Expanding the P. bursaria-algal model for endosymbiosis	Evolution ecology and epidemiology
3	Smitha	Maretvadakethope	Imperial College London	Guidelines for the development of genetic AC-DC circuits	Clocks, timers and cell cycle dynamics
47	Eva	Martin-Cuevas	University of Sheffield	AFM-based approaches for RNA structure characterization	Imaging and single molecule biology
108	Giorgia	Marucci	HORIBA UK	Pioneering a New Era in Live Tissue Imaging with Fluorescence Lifetime Microscopy (FLIM)	Protein structure, dynamics and interactions
77	Sam	Matthews	University of York	Translational impact of rapid digital holographic microscopy.	Patterns, waves, transport, collective phenomena, and microswimmers
59	Conrad	McDonnell	University of Sheffield	Mechanically killing bacterial pathogens on nanostructured surfaces	Immunity, resistance and host/pathogen dynamics
78	Laura	Meissner	Uniwersytet Warszawski	Odd viscous Stokes flow around a single sphere	Patterns, waves, transport, collective phenomena, and microswimmers
96	Akinori	Miyamoto	Tokyo University of Agriculture and Technology	Physical property of the nucleoplasm revealed by creep-relaxation dynamics	Physics of the nucleus
12	Lewis	Mosby	The Francis Crick Institute and University College London	Evolving Tissue Pattern Scaling and Robustness Through Spatially Heterogeneous Feedback	Differentiation and development
13	Ander	Movilla Miangolarra	John Innes Centre	Epigenetic variability in induced pluripotency – How much does it contribute?	Differentiation and development

79	Daniel	Muzatko	University of Aberdeen	Fundamental limits on pattern formation in Turing-like reaction-diffusion systems	Patterns, waves, transport, collective phenomena, and microswimmers
80	Sharadhi	Nagaraja	Aalto University	Direct force measurement on swimming meso-organisms	Patterns, waves, transport, collective phenomena, and microswimmers
17	Tasmin	Nahar	Keele University	Development of magnetic force biotechnology for neural regeneration	Engineering tissues, organoids and biohybrids
81	Cara	Neal	University College London	A computational approach to simulating a three-sphere swimmer in a viscoelastic fluid modelled via the Giesekus constitutive law	Patterns, waves, transport, collective phenomena, and microswimmers
117	Isaac	Noble	University of Leeds	Gallium ions can target chronic Pseudomonas aeruginosa biofilm infections by hijacking its ferric PQS transport system	Physics of Disease
82	Devi Prasad	Panigrahi	University College London	Intermittent cell-cell attachments generate emergent fluid-like properties in migrating cell aggregates	Patterns, waves, transport, collective phenomena, and microswimmers
109	Auro	Patnaik	University of Edinburgh	Zero-shot Adaptation of Drug Diffusion Model for Fragment Elaboration.	Protein structure, dynamics and interactions
83	Luca	Pellegrino	Humanitas University	Reduction of bacterial adhesion on wrinkled surfaces under fluid shear	Patterns, waves, transport, collective phenomena, and microswimmers
14	Ella	Penny	John Innes Centre	Modelling The Meristem Transitions Underlying Development of Wheat Inflorescence Architecture	Differentiation and development
15	Julia	Pfanzelter	MPI-CBG Dresden	Mechanical coupling of tissue layers facilitates avian left-right symmetry breaking	Differentiation and development
84	Diogo	Pinto	University of Oxford	Spontaneous flows in confined epithelial cell sheets	Patterns, waves, transport, collective phenomena, and microswimmers
85	Praneet	Prakash	University of Cambridge	Dynamics of an Algae-Bacteria Inhomogeneous Active Suspension	Patterns, waves, transport, collective phenomena, and microswimmers
110	Chloe	Randall	University of Leeds	Using molecular dynamics simulations to understand PIEZO1 mechanosensitive ion channel in red blood cells	Protein structure, dynamics and interactions
60	Ankita	Ray	University of Sheffield	Feeling piconewton forces in single-molecule biology	Immunity, resistance and host/pathogen dynamics
18	Natalie	Richards	Durham University	pH-taxis Biohybrid Lipid Vesicles	Engineering tissues, organoids and biohybrids
97	Rodrigo	Rivas-Barbosa	University of Edinburgh	A Numerical Study of the Role of Hijacked Enhancers in B-Cell Cancers	Physics of the nucleus
48	Christian	Rodriguez-camargo	University College London	The role of vibrational molecular structure in entangled two photon absorption in biomolecules	Imaging and single molecule biology
61	Jordan	Romeyer Dherbey	University of Cambridge	Phage T7-E. coli AR3110 long-term coevolution experiment in a spatially structured environment	Immunity, resistance and host/pathogen dynamics
19	Kenza	Sackho	University of Surrey	Multimodal characterisation of an epicardial spheroid model	Engineering tissues, organoids and biohybrids
4	Jhonatan	Salgado	Qmul	Bacterial super-exponential growth and cell wall dynamics	Clocks, timers and cell cycle dynamics
111	Mona	Sarter	Isis Neutron And Muon Source	Probing Drug Pharmacokinetics - Can the impact of Cisplatin-like Anticancer Drugs on Protein Dynamics explain the difference in toxicity	Protein structure, dynamics and interactions
112	Sagar	Satpathi	University of Leeds	Understanding the Roles of Carotenoids in the Photophysics of Bacterial Light-Harvesting Protein Complexes	Protein structure, dynamics and interactions
31	Luca	Sesta	University of Basel	Detecting epistasis from SARS-CoV-2 genomic data	Evolution ecology and epidemiology
20	Jack	Shepherd		Understanding algal pyrenoid dynamics with coarse grained molecular dynamics	Engineering tissues, organoids and biohybrids
16	Gurpinder Singh	Sidhu	John Innes Centre	From model to crops: Determining the regulatory control of floral transition	Differentiation and development
49	Emma	Silvester	University of Oxford	DNA nanostructure tags for electron cryotomography	Imaging and single molecule biology

86	Gianmarco	Spera	University of Oxford	Nematic Torques in Scalar Active Matter	Patterns, waves, transport, collective phenomena, and microswimmers
21	Raveen	Tank	University of Manchester	Advancing Gynaecological Disease Research: A Fallopian Tube-on-a-Chip Model for STIC Progression and High-Grade Serous Ovarian Cancer Development	Engineering tissues, organoids and biohybrids
32	Anna	Tarodi		Modelling spatial competition in toxin-antitoxin producing bacterial populations	Evolution ecology and epidemiology
87	Mykola	Tasinkevych	Nottingham Trent University	How to steer catalytic nanoswimmers?	Patterns, waves, transport, collective phenomena, and microswimmers
113	Matthew	Thomas	University of Edinburgh	Investigating the Effects of Nucleosome Positional Irregularity on Chromatin using a Nucleosome-Scale Computational Model	Protein structure, dynamics and interactions
22	Conor	Treacy	King's College London	Multiphoton line-scanning FLIM for fast, dynamic 3D imaging of breast cancer spheroids.	Engineering tissues, organoids and biohybrids
88	Mehmet Can	Ucar	University of Sheffield	Self-organized guidance of mixed cell populations	Patterns, waves, transport, collective phenomena, and microswimmers
89	Rahil	Valani	University of Oxford	Nonlinear and chaotic dynamics of a microswimmer in confined flows	Patterns, waves, transport, collective phenomena, and microswimmers
50	Mo	Vali	University of Cambridge	Signalling Molecule Detection in Liquid Cultures Using Surface-Enhanced Raman Spectroscopy	Imaging and single molecule biology
114	Sam	Von Der Dunk	University of Oxford	Proteins evolve structural robustness to cope with locally chaotic folding landscape as predicted by ESMfold	Protein structure, dynamics and interactions
51	Jingyu	Wang	University of Oxford	OPTIMISED ADAPTIVE OPTICS ILLUMINATION STRATEGIES FOR THREE-PHOTON MICROSCOPY IN DEEP NEUROIMAGING	Imaging and single molecule biology
115	George	Weston	Durham University	A Machine Learning Approach to Identify Carbon Dioxide Binding Proteins for Sustainability and Health	Protein structure, dynamics and interactions
52	Sylvia	Whittle	University of Sheffield	Quantifying the Role of DNA Topology in Cas9 Activity using Atomic Force Microscopy	Imaging and single molecule biology
116	Maria	Zacharopoulou	University of Cambridge	Design of DNA-peptide nanostructures against intracellular targets in cancer	Protein structure, dynamics and interactions
90	Qi	Zhou	University of Edinburgh	Transport Dynamics of Red Blood Cells in the Microcirculation	Patterns, waves, transport, collective phenomena, and microswimmers

Poster Presentations
Tuesday 25 March, Poster Session 2, Drinks Reception and Exhibition

Poster No.	First Name	Last Name	Organisation	Paper Title	Topic
90	Dorothy	Aboagye-Mensah	University College London	Unravelling the effect of divalent salt on the structure of negatively supercoiled DNA	Physics of Disease
2	Jaime	Agudo-canalejo	UCL	Biomolecular condensates mediate bending and scission of endosome membranes	Biomolecular assemblies and condensates
57	Hadi	Al-Sagur	University of Hull	Complementary insights into Silicosis gained with revisit of Cytotoxic Effects of Silica	Emerging Areas in the Physics of Life
3	Henry	Alston	Laboratoire de Physique de l'Ecole Normale Supérieure (LPENS)	Making fast decisions with phase separation	Biomolecular assemblies and condensates
30	Henry	Andralojc	University of Bristol	Dynamics of Wound Closure in Active Nematic Epithelia	Cell architecture and forces
98	Shohreh	Askari	Aalto University	Soft matter physics of immune cell aggregates	Tissue growth, mechanics and mechanosensing
4	Roi	Asor	The University of Oxford	Cooperativity and induced oligomerization control the interaction of SARS-CoV-2 with its cellular receptor and patient-derived antibodies	Biomolecular assemblies and condensates
58	Prasoon	Awasthi	University of Southern Denmark	Tuning the collective cell behavior by surface functionalization	Emerging Areas in the Physics of Life
31	Filip	Ayazi	University of Cambridge	Automated High-Throughput Flickering Spectroscopy for Measurements of Red Blood Cell Membrane Properties	Cell architecture and forces
32	Innes	Bakkali	University of St Andrews	A Platform for Studying Cellular Responses to Mechanical Cues	Cell architecture and forces
33	Matthew	Barker		The Biophysics of the Main Synthase During Gram-Positive Bacterial Cell Division Using AFM	Cell architecture and forces
34	Charlotte	Benney	University of Bristol	Stress patterns in a model of epithelial cell sheets.	Cell architecture and forces
5	Stefano	Bo	King's College London	Single-molecule trajectories of reactants in chemically active condensates	Biomolecular assemblies and condensates
99	Douglas	Brown	Oxford University	Friction controls spatial patterning in active fluids	Tissue growth, mechanics and mechanosensing
100	Luisa	Bruno	Institut Cochin, Cnrs	Lymph node mechanics and its impact on immune cells	Tissue growth, mechanics and mechanosensing
6	Antonio	Calabrese	University of Leeds	Uncovering protein conformational dynamics within two-component viral biomolecular condensates	Biomolecular assemblies and condensates
59	Zoya	Cassidy	University of Cambridge	Functionalising DNA Nanostructures for Lysosomal Escape and Tankyrase Inhibition	Emerging Areas in the Physics of Life
7	Rosa	Catania	University of Leeds	Optimising hybrid vesicles for membrane protein reconstitution: applications and insights	Biomolecular assemblies and condensates
101	KVS	Chaithanya		Homeostasis in confined environments	Tissue growth, mechanics and mechanosensing
76	Jinju	Chen	Loughborough University	The Physics of Bacterial Survival: A Mechanical Mystery	Microbes across length scales
8	Nga Man	Cheng	University of Nottingham	Impact of mRNA structures on the interaction with lipids and nanoparticle formulation properties	Biomolecular assemblies and condensates

102	Michael	Chiang	University of Edinburgh	Intercellular Friction and Motility Drive Orientational Order in Cell Monolayers	Tissue growth, mechanics and mechanosensing
35	Lee-Ya	Chu	The Francis Crick Institute	Microtubule Tip-Generated Forces Drive Bipolar Spindle Organization and Chromosome Segregation	Cell architecture and forces
77	Cameron	Colclough	University of Sheffield	Uncovering the Fungal Cell Wall at the Nanoscale	Microbes across length scales
60	Fabian	Coupette		Optimising fixational eye movements	Emerging Areas in the Physics of Life
61	Jiahe	Cui	University of Oxford	A multi-functional AOSLO for high-resolution imaging and stimulation in the living human retina	Emerging Areas in the Physics of Life
103	Isabella	Davis	University of Sheffield	How does chemoresistance emerge as a product of matrix stiffness in pancreatic cancer?	Tissue growth, mechanics and mechanosensing
36	Oleg	Dobrokhotov	Francis Crick Institute	Structural integration of integrins and cadherins at cell-cell junction sites	Cell architecture and forces
37	Franziska	Dorn	University of Rostock	The influence of electrostimulation and conductive surfaces on the membrane fluctuation of osteoblast-like cells with a scanning ion conductance microscope	Cell architecture and forces
78	Yulin	Du	University of Cambridge	Spatio-Temporal Dynamics of Gene Expression in Biofilm under Varying Environments	Microbes across length scales
38	Jocelyn	Etienne	Univ Grenoble Alpes–cnrs	Surfing one's own wave: Initiation of motility on a compliant substrate	Cell architecture and forces
9	Catherine	Fan	University of Cambridge	Protein Capture using Synthetic Co-Transcriptionally Folded RNA Condensates in Mammalian cells	Biomolecular assemblies and condensates
104	Jonathan	Fouchard	Sorbonne Université	Active and passive response of soft fibrous tissue in compression	Tissue growth, mechanics and mechanosensing
10	Lewis	Frame	University of York	Biophysics of liquid-phase bacterial Protein-RNA droplets	Biomolecular assemblies and condensates
62	Polina	Gaindrik	Albert Ludwig University of Freiburg	Multi-Source Data Fusion and Dimensionality Reduction Predictive Microbial Modeling	Emerging Areas in the Physics of Life
11	Subhadip	Ghosh	University College London	Molecular mechanisms of condensate membrane interaction and mutual reshaping	Biomolecular assemblies and condensates
39	Rini	Ghosh	University of Cambridge	Exploring Dynamic Cellular Response of Erythrocytes to Rapid Deformations	Cell architecture and forces
122	Gabriela	Gomes	University of Strathclyde	The effects of individual nonheritable variation on fitness estimation and coexistence	Evolution ecology and epidemiology
91	Yaniv	Grosskopf	Weizmann Institute of Science	PTSD as a Bias Toward Perceiving a Dangerous World: An Evolutionary and Mathematical Perspective	Physics of Disease
105	Valeriia	Grudtsyna	Niels Bohr Institute, University of Copenhagen	Local Density as a Determinant of YAP Mechanotransduction in Multicellular Assemblies	Tissue growth, mechanics and mechanosensing
87	Jeremy	Guntoro		The Interplay of Heterogeneity and Product Detachment in Templated Polymer Copying	Natural and synthetic molecular machines
106	Himadri Shikhar	Gupta	Queen Mary, University of London	Uncovering the coordinated nanoscale fibrillar mechanical response in the bone-cartilage unit during physiological loading	Tissue growth, mechanics and mechanosensing
12	Ehud	Haimov	Imperial College London	Homology recognition through intrinsic interactions - kinetics, equilibrium and stability properties	Biomolecular assemblies and condensates
13	Ellie	Hansen	University of York	The roles of Ribosomal Proteins L2 and L15 in regulating Bacterial Aggresomes	Biomolecular assemblies and condensates

79	Richard	Henshaw	ETH Zurich	How small is too small: a spatio-temporal spectroscopic quantification of single-cell exchange between marine microbes	Microbes across length scales
63	Alexander	Houston	University of Glasgow	Seeing through the noise: how fixational eye movements can aid the acquisition of visual information	Emerging Areas in the Physics of Life
14	Matt	Hughes	Univeristy of Leeds	Capturing Dynamic Assembly of Protein Network Formation	Biomolecular assemblies and condensates
80	Rita	Invernizzi	Humanitas University	Spatiotemporal Dynamics of Bacterial Growth in Non-Well-Mixed Environments	Microbes across length scales
54	Panayiotis	Ioannou	University of Cambridge	HyperGenie: A new method for predicting enzymatic gene essentiality using Hypergraph neural networks and Genome-scale metabolic models	Cell metabolism and growth
15	Pranay	Jaiswal	University Ausgburg	Theory of spatial aggregation and shell formation	Biomolecular assemblies and condensates
74	Aparna	Kaaraal Mohan	University of Cambridge	Single-cell analysis of the effects of cellular dormancy on the efficacy of bacteriophages	Imaging and single molecule biology
40	Yohalie	Kalukula		The actin cortex acts as a mechanical memory of morphology in confined migrating cells	Cell architecture and forces
88	Thomas	Kolbe	Ulb- Universite Libre De Bruxelles	Influenza A Virion Dynamics at the Cell Surface	Natural and synthetic molecular machines
16	Gaurav	Kumar	University of York	The stickers and spacers of Rubisco condensation in CO2-fixing organelles	Biomolecular assemblies and condensates
64	Oliver	Kurilov	University of Cambridge	Collective molecular dynamics behind biofilm dynamics: using anisotropic to model mixed bacterial interfaces	Emerging Areas in the Physics of Life
17	Alvaro	Lanza	King's College London	Measuring Entropy from Coarse-grained Single-molecule Statistics in Langevin Systems	Biomolecular assemblies and condensates
107	Francesca Cecilia	Lauta	Humanitas University	Macrophage behavior in 3D biomaterial microenvironments	Tissue growth, mechanics and mechanosensing
108	Rachel	Lawson	University of Sheffield	Investigating the mechanical and adhesive properties of mitosis within a tissue, and the role of oncogenic Ras in regulating these	Tissue growth, mechanics and mechanosensing
109	Mathieu	Le Verge-serandour	Technical University of Munich	Dynamical Network Remodeling of Slime Mold	Tissue growth, mechanics and mechanosensing
110	Jiayu	Li	Queen Mary University of London	A computational model for deformation of cancer cells in microchannels	Tissue growth, mechanics and mechanosensing
111	Sulaimaan	Lim	Imperial College London, Francis Crick Institute	Heartbeat driven self organisation of the Endocardium during Zebrafish heart morphogenesis	Tissue growth, mechanics and mechanosensing
41	Calum	Lloyd	University of Sheffield	Exploring Bacterial Resistance: Mechanisms of Reduced Susceptibility in Staphylococcus aureus During Stationary Phase	Cell architecture and forces
112	Ivan	Lobaskin	University of Cambridge	A statistical theory of human lung branching morphogenesis from organ-scale imaging	Tissue growth, mechanics and mechanosensing
42	Euan	Mackay	University of Dundee	Modelling Actomyosin Oscillations in Morphogenetic Dynamics Using an Active Elastomer Framework	Cell architecture and forces
43	Bhagyashri	Mahajan	Ncbs, Bangalore, India And Cmcb, University of Warwick	Exploring the role of class I myosins in plasma membrane organization using an in vitro reconstitution approach	Cell architecture and forces
44	Bhagyashri	Mahajan	Ncbs, Bangalore, India And Cmcb, University of Warwick	The role of class I myosins in plasma membrane organization	Cell architecture and forces
18	Najet	Mahmoudi	Rutherford Appleton Laboratory	Structure and stability of self-assembled multidomain peptide fibres	Biomolecular assemblies and condensates
65	Francesco	Marcolli	University of Genova	Evidence of Stochastic Resonance in Multi-Sensor Odor Source Localisation	Emerging Areas in the Physics of Life

66	Tom	Mason	Loughborough University	Active particles in nematic fluids	Emerging Areas in the Physics of Life
113	Khushboo	Matwani	University of Cambridge	Mechanical force measurements of tandem-repeat proteins	Tissue growth, mechanics and mechanosensing
45	Waleed Ahmad	Mirza	European Molecular Biology Laboratory	Active self-organization of focal adhesions driving cell shape changes	Cell architecture and forces
46	Benjamin	Mitchell	Univeristy of Strathclyde	Simulation of Monoglyceride-Induced Bilayer Deformation in Model Membrane Systems	Cell architecture and forces
114	Elise	Muller	Cnrs	Dual role of the FERONIA cell wall sensor in the regulation of plant mechanical properties and growth	Tissue growth, mechanics and mechanosensing
67	Amritpal Singh	Nafria	Lovely Professional University	Astrobiological Adaptation: Biophysical Dynamics of Life Migration in a Evolving Solar System.	Emerging Areas in the Physics of Life
89	Brian	Ng	University of Cambridge	Co-transcriptional assembly and dissolution of computational RNA condensates	Natural and synthetic molecular machines
68	Katharine	Ninham	University of Cambridge	Probing hydrodynamics of early development in C. elegans using diamond quantum sensors	Emerging Areas in the Physics of Life
47	Ryota	Orii		Structural response of microtubule and actin cytoskeletons to direct intracellular loads	Cell architecture and forces
19	Miguel	Paez Perez		Benchmarking viscosity-sensitive optical probes to quantify the structural architecture of lipid interfaces	Biomolecular assemblies and condensates
48	Eleni	Papafilippou	University of Cambridge	Characterising the rupture, fatigue and recovery of intercellular junctions using a stochastic bond model	Cell architecture and forces
49	Laia	Pasquina-Lemonche	University of Sheffield	Quantitative imaging of bacterial cell wall with AFM : function of PBP1a synthase	Cell architecture and forces
20	Alex	Payne-Dwyer	University of York	The single-molecule biophysics of turbocharged, carbon-fixing condensates	Biomolecular assemblies and condensates
81	Joe	Pollacco	University of Oxford	RecA filament kinetics explain heterogenous SOS response induction and cell death	Microbes across length scales
82	Rebecca	Poon		Multiscale dynamics in filamentous cyanobacteria: from filament to aggregate motility	Microbes across length scales
1	Anna	Radjenovic	University of Bristol	Electroreceptive Sensitivity Analysis of Mechanosensory Hair Arrays	Bioelectricity across scales
93	Callum	Rafferty	The University of Edinburgh	Identifying biophysical mechanisms in health-to-disease (MASLD-MASH) transition of human HepaRG cells	Physics of Disease
21	Saminathan	Ramakrishnan	University of Edinburgh	Investigating IHF-DNA Interactions at Biofilm pH Using Single-Molecule Techniques	Biomolecular assemblies and condensates
75	Ankita	Ray	University of Sheffield	The curious case of alternative mode of cell division in Staphylococcus aureus	Imaging and single molecule biology
115	Avishuman	Ray	University of Southern California	Mechanics of force sensing in Piezo ion channels	Tissue growth, mechanics and mechanosensing
55	James	Rayner	Queen Mary University of London	Modelling the role of the SOS response on bacterial filamentation and survival under antibiotic stress	Cell metabolism and growth
83	Steven	Redford	University College London	Investigating the physical underpinnings of collective function in synthetic microbial communities	Microbes across length scales

22	David	Regan	Cardiff University	Supported lipid bilayer tubular network dynamics measured by quantitative differential interference contrast microscopy	Biomolecular assemblies and condensates
116	Leon	Rembotte	IOGS	Deformation cytometry for high-throughput rheological analysis of 3D multicellular systems	Tissue growth, mechanics and mechanosensing
84	Abigail	Roberts	University of Sheffield	AFM to probe structural changes involved in Clostridium sporogenes germination	Microbes across length scales
23	James Aaron	Robins	University of Nottingham	Molecular Dynamics Simulations to Investigate Interactions Between Polymers and RNA in Polymer Nanoparticles	Biomolecular assemblies and condensates
117	Jan	Rozman	University of Oxford	Dissipation, Flows, and Sorting in an Active Nematic Vertex Model	Tissue growth, mechanics and mechanosensing
69	Riddhima	Sadhu	Birla Institute of Technology,mesra	Optical Coherence Tomography:An Emerging Modality in Deep Tissue Imaging	Emerging Areas in the Physics of Life
24	Ignacio	Sanchez Burgos	University of Cambridge	Charged peptides enriched in aromatic residues can decelerate condensate ageing	Biomolecular assemblies and condensates
94	Jenna	Schafers	University of Edinburgh	Turning up the heat; mechanistic insights from thermal inactivation of influenza A virus	Physics of Disease
118	Aakanksha	Shetty		Fluorescence spectroscopy of cell membranes under dynamic mechanical perturbation: investigating modulations to cell signalling	Tissue growth, mechanics and mechanosensing
95	Zhiyuan	Song	University of Cambridge	AI-Driven Temporal Feature Analysis for Forecasting of Alzheimer's Disease Progression	Physics of Disease
25	Alisdair	Stevenson	Eth Zürich	Synchronisation of chemical reactions in a population of condensates	Biomolecular assemblies and condensates
50	Jess	Stone		Exploring the Impact of Tumour Mechanics on Immunological Synapse Formation	Cell architecture and forces
70	Yuening	Su	Sidney Sussex College	DNA nanostructures targeting activated platelets	Emerging Areas in the Physics of Life
71	Zachary	Sun	Yale University	Feedback between F-actin organization and active stress govern criticality and energy localization in the cell cytoskeleton	Emerging Areas in the Physics of Life
26	Bidisha	Tah Roy	university of Leeds	Crowding and Its Role in Calcium Carbonate Crystallization Processes	Biomolecular assemblies and condensates
27	Andres R.	Tejedor	University of Cambridge	Optimized residue-resolution coarse-grained model for electrostatic-driven biomolecular condensates	Biomolecular assemblies and condensates
28	Damien	Thompson	University of Limerick	Modelling-guided engineering and rerouting of biomolecular assemblies	Biomolecular assemblies and condensates
56	Keshav	Todi	University of Edinburgh	Is the energetics of E.coli influenced by the nature of stress that stops it from growing?	Cell metabolism and growth
51	Ayama	Tokuyasu	Yokohama City University	Force propagation inside a living cell	Cell architecture and forces
85	William	Trewby	University College London	Direct, nanoscale mapping of molecular organisation and biogenesis in the Escherichia coli outer membrane	Microbes across length scales
119	Rahil	Valani	University of Oxford	Intermittent migration of a cell cluster in a confluent tissue	Tissue growth, mechanics and mechanosensing
96	Mo	Vali	University of Cambridge	Characterising the microbial composition of follicular fluid using 16srRNA sequencing and its importance for IVF outcomes	Physics of Disease
72	Mengxin	Wang	University of Oxford	From physics to vision: using ISETBio to predict visual performance from physical information	Emerging Areas in the Physics of Life

73	Celeste	Watson		Developing a modular platform of DNA-protein nanostructures for targeted protein degradation	Emerging Areas in the Physics of Life
52	Andreas	Weber	University College London	Molecular determinants of mechanics and shape changes during cell division	Cell architecture and forces
97	Peter	Weightman	University of Liverpool	Can AI classification of cancerous tissue yield chemical insight and prognosis?	Physics of Disease
86	Anne	Williams	University of Sheffield	Spore germination: what can we learn from live spore imaging?	Microbes across length scales
29	Thomas	Williamson	University of Edinburgh	Quantifying the Mechanical Properties of Stress Granules in Live Cells	Biomolecular assemblies and condensates
53	Rebecca	Wurr	King's College London	Extracellular matrix alignment regulates cellular mechanotransduction	Cell architecture and forces
120	Richa	Yeshvekar	University of Leeds	Mechanobiology of Tomato Fruit Cell Walls During Ripening: Insights into Callose and Cellulose Dynamics	Tissue growth, mechanics and mechanosensing
121	Dražen	Zanchi	Msc, Université Paris Cité	Bionics of Plant Tendrils	Tissue growth, mechanics and mechanosensing

Plenary Speakers

A Statistical Physics Approach to Bacteria under Strong Perturbations

Nathalie Balaban[1]
[1]*The Hebrew University of Jerusalem, Israel*

Keynote Speaker: Nathalie Balaban, March 25, 2025, 16:45-17:30

Statistical physics successfully accounts for phenomena involving a large number of components using a probabilistic approach with predictions for collective properties of the system. While biological cells contain a very large number of interacting components, (proteins, RNA molecules, metabolites, etc.), the cellular network is understood as a particular, highly specific, choice of interactions shaped by evolution, and therefore difficultly amenable to a statistical physics description. Here we show that when a cell encounters an acute but non-lethal stress, its perturbed state can be modelled as random network dynamics. Strong perturbations may therefore reveal the dynamics of the underlying network that are amenable to a statistical physics description.

We show that our experimental measurements of the recovery dynamics of bacteria from a strong perturbation can be described in the framework of physical aging in disordered systems (Kaplan Y. et al, Nature 2021). Further experiments on gene expression confirm predictions of the model. The predictive description of cells under and after strong perturbations may lead to new ways to fight bacterial infections, as well as the relapse of cancer after treatment.

Sculpting life through rigidity transitions

Otger Campas[1]
[1]*TU-Dresden, Germany*

Keynote Speaker: Otger Campàs, March 26, 2025, 17:45-18:30

During embryonic development, cells self-organize to build functional structures, like tissues and organs, and progressively shape the organism. While many key molecular players that orchestrate embryonic development are known, the physical mechanisms underlying embryonic morphogenesis remain unclear. Performing direct measurements of the tissue physical state in situ and in vivo using microdroplet techniques, I will show that embryonic tissues undergo fluid-to-solid (rigidity) transitions that are controlled in space and time to guide morphogenesis.

First, I will discuss body axis elongation in vertebrates and show that posterior tissues are fluid-like at their elongating end and become solid-like as they mature anteriorly through a jamming transition of the cell collective. Beyond axis elongation, I will discuss a new nuclear jamming transition that controls tissue architecture during vertebrate eye and brain organogenesis.

Hierarchical biomechanics: understanding and exploiting the physics of protein networks

Lorna Dougan[1]
[1]*University of Leeds, United Kingdom*

Keynote Speaker: Lorna Dougan, March 24, 2025, 14:15-15:00

Hierarchical assemblies are ubiquitous to all living systems, demonstrating remarkable mechanical properties and the ability to adapt to their environment. Proteins are the building blocks of these assemblies, performing their function through structural and mechanical changes. However, a major challenge is to understand how the mechanical properties of an individual protein translates to the collective response of a protein network. This is limiting our ability to understand the hierarchical biomechanics of living systems and our potential to exploit biomolecules as building blocks in functional biomaterials. An interdisciplinary, collaborative approach provides an opportunity to tackle this complex and interesting problem.

In this talk, I will share our recent progress in understanding the cross length-scale behaviour of folded protein networks, how this helps us to understand more complex networks in living systems, and how it is supporting the development of engineered living matrices with applications in medicine and healthcare.

Mechanical Information Processing in Adherent Cells

Margaret Gardel[1]
[1]*University of Chicago, USA*

Keynote Speaker: Margaret Gardel, March 27, 2025, 11:30-12:15

My lab studies how the movement and shape of living cells is controlled by living materials constructed by protein assemblies within the cell interior. In this talk, I will describe our recent efforts to understand the design principles of the active, soft materials that drive morphogenesis of multicellular tissue.

In particular, I will discuss design principles by which the cellular cytoskeleton senses, generates, and adapts to mechanical forces and couples to biochemical and transcriptional pathways. Such mechanical information processing controls diverse processes including cell proliferation, barrier function and cell fate determination.

Evolutionary tales of biological shape: bodies, guts and beaks

L Mahadevan[1]
[1]*Harvard University, USA*

Keynote Speaker: L Mahadevan, March 25, 2025, 09:00-09:45

Using the chick as a model, I will explore key aspects of morphogenesis, from gastrulation to organogenesis, linking molecular and cellular processes to tissue shaping. I will discuss experimental manipulations that alter chick gastrulation to resemble other organisms and propose a mathematical framework for an evo-devo phase diagram.

Next, I will present a minimal theory for somitogenesis, connecting cellular oscillations to tissue elongation. For organ development, I will introduce a predictive model for gut looping and villi patterning, generating morphospace diagrams. Finally, I will examine finch beak morphogenesis, integrating morphometry with a biophysical framework to define a beak-space diagram. diagram.

The membrane of a living cell: an ATP fuelled fabric

Satyajit Mayor[1]
[1]*University of Warwick, United Kingdom*

Keynote Speaker: Satyajit Mayor, March 26, 2025, 09:00-09:45

A eukaryotic cell interfaces with the external milieu constantly, decoding signals in the form of chemical and mechanical inputs and responding to it almost instantly. These cues are interpreted by membrane receptors embedded in the plasma membrane. One such membrane receptor, the integrin receptor, receives chemical inputs in the form of cues from the extracellular matrix and mechanical signals from the external environment. Chemical cues activate Rho A-dependent signalling cascades generating actomyosin stresses in the cell whereas mechanical cues activate mechano-transducers.

By studying the impact of the integrin receptor activation on membrane organization we find that the activation of these two pathways result in the creation of localized mesoscale liquid-ordered (lo) membrane domains consisting of nanoclusters of GPI-anchored proteins and lipids (termed active emulsions)1, necessary for this response. These membrane domains encode information about the chemical and mechanical nature of the substrate, regulating crucial aspects of integrin receptor function including cell spreading and migration. This level of regulated organization in a fluid membrane bilayer is only possible due to its engagement with an energy consuming medley of myosin proteins at or near the plasma membrane, draped over a cortical actin meshwork. This active actin-membrane composite behaves as a mechano-responsive medium, serving to integrate chemical and physical cues presented at the cell periphery for the regulation of cell physiology.

1) S. Saha, et al. Active emulsions in living cell membranes driven by contractile stresses and transbilayer coupling, Proc. Natl. Acad. Sci. U.S.A. 119 (30) e2123056119, (2022).
*Online from National Centre for Biological Science- TIFR, Bangalore, India

How personalised is your immune repertoire?

Aleksandra Walczak[1]
[1]*Ecole Normale Supérieure, France*

Keynote Speaker: Aleksandra Walczak, March 25, 2025, 13:15-14:00

Immune lymphocyte repertoires provide a unique fingerprint reflecting the immune history of individuals, with potential applications in precision medicine. Can this information be used to identify a person uniquely?

I will describe how these diverse repertoires are generated. I will then discuss current ideas and evidence for how self-reactive T cells are eliminated leading to naive repertoires.

Invited Speakers

Modelling bacterial colonisation of a urinary catheter: different factors control long-term versus short-term clinical outcomes

Prof. Rosalind Allen[1]
[1]*University of Jena, Germany*

Microbes Across Length Scales, March 26, 2025, 10:15-12:15

Urinary catheters are used extensively in hospitals and long-term care and they are highly prone to infection. Understanding the pathways by which bacteria colonise a urinary catheter could guide strategies to mitigate infection, but quantitative models for this colonisation process are lacking. This is a classic example of "microbes across scales" since a bacterial cells is of micron scale but a urinary catheter is tens of centimetres in dimension.

We have developed a mathematical model for bacterial colonisation of a urinary catheter, that integrates population dynamics and fluid dynamics. The model describes bacteria migrating up the outside surface of the catheter, spreading into the bladder and being swept through the catheter lumen. The model exhibits a phase transitions between states corresponding to bacteriuria (bacteria in the urine) vs no bacteriuria. Computer simulations of the model reveal that clinical outcomes for long-term versus short-term catheterisation are controlled by different factors, that could be targeted by different interventions in catheter design and management protocols.

Time-resolved measurement of phage infection cycles in individual cells

Somenath Bakshi[1]
[1]*University of Cambridge, United Kingdom*

Immunity, Resistance and Host/Pathogen Dynamics, March 26, 2025, 15:30-17:30

Bacteriophages rely on their bacterial hosts for replication, making their infection dynamics inherently dependent on the host's physiological state. However, even genetically identical bacterial cells exhibit significant physiological heterogeneity, raising fundamental questions about how this variability shapes the phage infection cycle and their effectiveness in eliminating bacterial populations.

We introduce a high-throughput microfluidic imaging assay that tracks phage infection in real time at single-phage single-cell resolution, capturing individual infection steps—including adsorption, replication, and lysis—across thousands of cells simultaneously. This approach not only quantifies the extent of heterogeneity in infection kinetics but also links infection variability to the physiological state of host cells, allowing us to identify the sources of heterogeneity. By dissecting how cell-to-cell differences in physiology influence infection progression, we uncover key determinants that govern phage-host interactions. Our computational models suggest that this heterogeneity significantly impacts the effectiveness and fitness of phage populations.

This detailed characterization of infection dynamics provides critical insights into the mechanisms driving variability in phage infection outcomes, with implications for understanding resistance, optimizing phage therapy, and advancing biotechnological applications.

Deciphering the mechanical code of DNA and its impact on DNA:protein interactions

Dr Aakash Basu[1]
[1]Durham University, United Kingdom

Emerging Areas in the Physics of Life, March 26, 2025, 10:15-12:15

Mechanical deformations of DNA are ubiquitous in Biology and occurs as part of critical processes involved in the reading, repair, copying, and packaging of genetic information. Therefore, such processes may be regulated by the local mechanical pliability of DNA to accommodate physical deformations.

We have developed high-throughput technology to measure how local sequence impacts local DNA bendability via a “mechanical code”. We show that via the mechanical code, genomes encoded regulatory information impacting diverse processes such as gene expression, nucleosome organization and remodelling, transcription factor binding, and DNA supercoiling by topoisomerases. We are currently exploring how chemical alterations to DNA such as via epigenetic modifications or DNA damage may alter the mechanical code, resulting in downstream functional consequences. Overall, we advance our understanding of how physical forces have impacted the evolution of genomes.

Physicochemical regulation of chromatin phase transitions

Professor Rosana Collepardo Guevara[1]
[1]*University of Cambridge, United Kingdom*

Physics of the Nucleus, March 25, 2025, 14:15-16:15

The internal organisation of the cell nucleus is one of the great marvels of physical chemistry. Besides housing a giant DNA-based polymer named chromatin, our nucleus is filled with thousands of proteins, RNAs, and metabolites.

Transformative experiments in the past decade have proposed that chromatin and its associated biomolecules exploit the physical chemistry of phase transitions to form multi-component chromatin-rich nano-droplets inside the nucleus—termed condensates. This new paradigm conceives the nucleus as an emulsion of functionally diverse condensates: each containing a distinct chromatin region and microenvironment—a unique collection of biomolecules, metabolites, and thermodynamic parameters— to favour precise chemical reactions on the chromatin. Controlling the formation and physical properties of these condensates is hypothesized to contribute to the tight regulation of gene function in the nucleus. The question is: how?

In this talk, I will present our multiscale modelling techniques for investigating the liquid-like structure of chromatin, its phase transitions, and their regulation by different types of chromatin-binding proteins.

References:
https://www.nature.com/articles/s41467-021-23090-3
https://www.biorxiv.org/content/10.1101/2024.12.23.627571v1

Nanoscale viscoelasticity of living tissues with AFM: physics of biological growth and shape across temporal and spatial scales

Prof. Sonia Contera[1]
[1]*University of Oxford, United Kingdom*

Tissue Growth, Mechanics and Mechanosensing, March 26, 2025, 15:30-17:30

The dynamic shapes of biological tissues result from a complex interplay of physics, chemistry and genetics that determines, at each temporal and spatial scale, the mechanical properties that ultimately shape the adaptive structures of living organisms. The shape and mechanical stability of living organisms depend on precise temporal and spatial control of growth, which is achieved by dynamically tuning the mechanical (viscous and elastic) properties of their hierarchically built structures at the nanometre scale. It is now well established that cellular behaviour (including stem cell differentiation) is critically dependent on the mechanical properties of the cells' environment. The importance of the stiffness of the matrices in which cells grow has been highlighted, either to understand mechanotransduction or to control cell behaviour in tissue engineering. While stiffness (i.e. the ability of a material to elastically store mechanical energy) has been the focus of most experimental research, neither cells nor matrices are elastic.

Biological systems dissipate energy (i.e. they are viscous) and therefore do not respond instantaneously to mechanical deformations (like an ideal Hooke's spring), but exhibit different temporal responses at different spatial scales that characterise their responses to external stimuli. Measuring viscoelasticity (especially at the nanoscale) has remained experimentally challenging. I will present atomic force microscopy (AFM)-based techniques developed in my laboratory to measure and map the nanoviscoelasticity of growing plant cells, allowing us to generate maps of elastic, viscous and mechanical properties, including local time responses and maps of viscoelastic gradients.

We have shown how nanoscale viscoelasticity correlates with growth rate and how stomata can adapt to environmental changes by controlling their temporal responses. We have also been able to use non-equilibrium thermodynamics (Onsager principle) to obtain key thermodynamic parameters related to plant growth dynamics and how they can be extracted from AFM experiments.

Seeing double: using integrative structural methods to understand dsRNA recognition by nuclear factor proteins

Sophie Winterbourne[1], Uma Jayachandran[1], Juan Zou[2], Prof. Atlanta Cook[1], Juri Rappsilber[2,3], Sander Granneman[1,4]

[1]Institute of Quantitative Biology, University of Edinburgh, United Kingdom, [2]Institute of Cell Biology, University of Edinburgh, United Kingdom, [3]Institute of Biotechnology, Technische Universität Berlin, Germany, [4]Centre for Engineering Biology, University of Edinburgh, United Kingdom

Natural and Synthetic Molecular Machines, March 27, 2025, 09:00-11:00

The DZF (domain associated with zinc fingers) family of RNA binding proteins regulate RNA splicing events in mammalian cells. Two DZF family members, known as nuclear factors 45 and 90 (NF45 and NF90) recognise stretches of dsRNA greater than 18 bp and, in human cells, primarily interact with inverted repeats derived from Alu transposable elements (AluIRs) that are commonly inserted into introns. Intronic AluIRs of ~300 bp can regulate splicing outcomes, such as generation of circRNAs. How NF45-NF90 complexes recognise long stretches of dsRNA is poorly understood but is likely to be important for their ability to regulate splicing outcomes. To address this, we have used an integrative structural biology approach to examine how the multi-domain structure of NF45-NF90 complexes is reorganised on binding to dsRNAs exceeding 50 bp. We use solution methods such as small angle X-ray scattering and quantitative cross-linking mass spectrometry to define dsRNA occupancy and domain rearrangements.

By combining these methods with structural modelling, negative stain electron microscopy and a machine learning method for predicting RNA binding sites, we find that NF45-NF90 complexes can coat long stretches of dsRNA. This property of the NF45-NF90 complex is likely to stabilize bound dsRNA structures and suggests a model of how these proteins might promote specific alternative splicing events.

Laws for cellular growth, and models to frame them

Marco Cosentino-Lagomarsino[1]
[1]*IFOM, and University of Milan, Italy*

Cell Metabolism and Growth, March 27, 2025, 09:00-11:00

Proliferating cells organize their resources in order to harness nutrients from the environment and grow. Work in bacteria has highlighted how this behavior leads to striking emergent "growth laws" linking growth to cellular composition. However, beyond bacteria, we still have limited insight on the generality of such laws and even in bacteria some of the key mechanistic aspects underlying them are unclear.

I will present our efforts towards a flexible and predictive modeling framework integrating different aspects of biosynthesis and its regulation, with applications in bacteria, budding yeast and mammalian cells.

High-speed and high-content 3D light-sheet fluorescence microscopy

Chris Dunsby[1]
[1]*Imperial College London, United Kingdom*

Imaging and Single Molecule Biology, March 25, 2025, 10:15-12:15

Light-sheet fluorescence microscopy (LSFM) provides low out-of-plane photobleaching and phototoxicity and is therefore well suited to high-speed optically-sectioned imaging of biological specimens in 2D or 3D. Conventional LSFM configuration employs two microscope objective lenses orientated at 90° to one another; the first is used to generate an illumination light sheet and the second is used to collect fluorescence from the illuminated plane. However, in order to be able to scan the detection plane through the sample rapidly, some form of optical remote-refocusing is required.

My lab has explored a number of approaches for video-rate 3D LSFM. One approach is the use of adaptive-optics by employing a deformable mirror (DM). This allows the collected fluorescence to be refocused very efficiently, but is technically challenging to implement. An alternative approach is the refocusing approach of Botcherby et al. in the detection path of LSFM. This approach allows a larger field of view compared to the DM-based approach, but the emitted fluorescence is only partly collected due to a polarisation beam splitter in the emission path. A third approach is oblique plane microscopy (OPM), which uses a single high numerical aperture microscope objective to provide both fluorescence excitation and detection whilst maintaining the advantages of LSFM, enabling it to provide high-speed 3D imaging for a range of applications on a conventional fluorescence microscope frame. The speed of OPM imaging can also be applied to image samples arrayed in multiwell plates in 3D over time with 10s of volumes imaged in multiple colour channels on a timescale of 10 minutes. This talk will review these different approaches and give examples of their application in biology.

Lipid composition defines Endoplasmic Reticulum morphology and function

Riki Eggert[1]
[1]*King's College London, United Kingdom*

Cell Metabolism and Growth, March 27, 2025, 09:00-11:00

Although lipids are essential contributors to numerous cellular functions, they are understudied relative to other biological molecules like proteins. While lipids have been connected to many diseases, their therapeutic potential has not yet been realised, in part due to our poor understanding of their metabolism and functions. Lipids are fundamentally small molecules and as such chemical biology approaches are essential to investigate their roles. A primary interest of my laboratory is to understand the cell biology of lipids. We are investigating the roles of lipids in a range of biological processes, including cell division, cell-cell interactions and organelle structure, using lipidomics, imaging, cell biology and chemical biology.

The complex network of the endoplasmic reticulum (ER) is responsible for the synthesis, folding and secretion of many membrane proteins, and is recognised as the main site of calcium storage, lipid synthesis and the ER's contact with other organelles. We have shown that the cellular and organelle lipid compositions are crucial to maintain ER morphology and function. We conducted a phenotypic siRNA screen in which HeLa cells were treated with 258 different siRNAs targeting lipid-metabolising enzymes. Removal of several enzymes, and therefore perturbation of the lipids they metabolize, resulted in dramatic changes to the ER. We developed a protocol to rapidly isolate ER lipids and identified which lipids change in organelles and cells with morphological alterations. Double knock down of enzymes with opposing phenotypes restored near wild type morphology and lipid composition, providing evidence for lipid involvement. In parallel, we analysed the impact of these lipidomic changes in functional assays, systematically linking lipid composition to ER structure and function.

Engineering symbiosis between living cells and synthetic cell compartments

Yuval Elani[1]
[1]*Imperial College London, United Kingdom*

Engineering Tissues and Organoids and Biohybrids, March 25, 2025, 14:15-16:15

Synthetic cells are bioinspired micromachines constructed from biomolecular building blocks. They are increasingly used as both simplified cell models and engineered microdevices, offering broad applications in industrial and clinical biotechnology. We have been working on such systems for many years now, aiming to recapitulate the architectures, processes, and behaviours that are the hallmarks of life. However, we have an inconvenient truth is increasingly apparent: synthetic cells lack the biomolecular complexity of living cells, leading to a disparity between the sophisticated functionalities of living systems and their synthetic counterparts.

To address this, we have conducted a series of studies exploring different modes of hybridization between living and synthetic cells: (i) Population Hybridization, where living and synthetic cell populations communicate with one another; (ii) Embedded Hybridization, where living cells are encapsulated within synthetic cells or vice versa; and (iii) Network Hybridization, where synthetic compartments are attached to the surface of living cells, functioning as artificial organelles to enhance functionality.

By engineering a symbiosis between the living and synthetic modules in these hybrid systems, we aim to harness the strengths of both. This presentation will detail our efforts to create “cellular bionic” systems that blend the best of living and synthetic cells.

Modelling how lamellipodia-driven cells maintain persistent migration and interact with external barriers

Nir Gov
[1]*Weizmann Institute of Science, Israel*

Patterns, Waves, Transport, Collective Phenomena and Microswimmers, March 25, 2025, 10:15-12:15

Cell motility is fundamental to many biological processes, and cells exhibit a variety of migration patterns. Many motile cell types follow a universal law that connects their speed and persistency, a property that can originate from the intracellular transport of polarity cues due to the global actin retrograde flow. This mechanism was termed the “Universal Coupling between cell Speed and Persistency”(UCSP). Here we implemented a simplified version of the UCSP mechanism in a coarse-grained “minimal-cell” model, which is composed of a three-dimensional vesicle that contains curved active proteins.

This model spontaneously forms a lamellipodia-like motile cell shape, which is however sensitive and can depolarize into a non-motile form due to random fluctuations or when interacting with external obstacles. The UCSP implementation introduces long-range inhibition, which stabilizes the motile phenotype. This allows our model to describe the robust polarity observed in cells and explain a large variety of cellular dynamics, such as the relation between cell speed and aspect ratio, cell-barrier scattering, and cellular oscillations in different types of geometric confinements.

Chance and constraints in the evolution of GRN-driven developmental patterning

Zena Hadjivasiliou[1]
[1]*The Francis Crick Institute, United Kingdom*

Evolution, Ecology and Epidemiology, March 24, 2025, 15:30-17:30

Much of the striking diversity of life on earth arises from mutations in conserved regulatory elements that govern reduced modules of Gene Regulatory Networks (GRNs). Although the mechanistic basis by which GRNs orchestrate cellular responses and tissue patterning during development is well understood, their evolutionary dynamics remain less clear. In this talk, I will discuss ongoing efforts in my lab to explore how conserved GRNs can give rise to diverse patterning forms. I will first present data across species that highlight how the same regulatory interactions underly early forebrain development in species that have very diverse adult brain morphologies.

I will then present a theoretical framework that we have developed to address how key evolutionary forces such as mutation, selection and historical contingency interact with GRN architecture to drive the diversification of developmental mechanisms and patterns.

Progress Towards Programmable Biological Matter

Professor Jonathan Heddle[1]
[1]*Durham University, United Kingdom*

Natural and Synthetic Molecular Machines, March 27, 2025, 09:00-11:00

Computational, machine learning and AI tools are now making it easier to design nanoscale 3D shapes from biological materials, notably proteins and nucleic acids which have numerous advantages, particularly in a biomedical setting. However, animating these objects is a major challenge particularly when complex movements and activities are required. When achieved, such “biological nanomachines” can have a major impact as designed drugs, effective vaccines and smart drug-delivery systems. The newly established Centre for Programmable Biological Matter aims to understand, design and build natural and artificial nanomachines using nucleic acid, lipid and protein building blocks with the hope of instigating major advances in all of these areas.

Here we will give a brief overview of our recent work in understanding a fascinating biological nanomachine (DNA gyrase) and in building systems such as responsive, dynamic protein cages and DNA/lipid constructs.

•Show Reversible, pH-Dependent Assembly." Macromolecular Rapid Communications (2024): 2400712.
•Michalczyk, Elizabeth, et al. "Structural basis of chiral wrap and T-segment capture by Escherichia coli DNA gyrase." Proceedings of the National Academy of Sciences 121.49 (2024): e2407398121.
•Michalczyk, Elizabeth, et al. "Molecular mechanism of topoisomerase poisoning by the peptide antibiotic albicidin." Nature catalysis 6.1 (2023): 52-67.
•Stępień, Piotr, et al. "CRAFTing Delivery of Membrane Proteins into Protocells using Nanodiscs." ACS Applied Materials & Interfaces 15.49 (2023): 56689-56701.
•Stupka, Izabela, et al. "Chemically induced protein cage assembly with programmable opening and cargo release." Science Advances 8.1 (2022): eabj9424.
•Malay, Ali D., et al. "An ultra-stable gold-coordinated protein cage displaying reversible assembly." Nature 569.7756 (2019): 438-442.

Optimality for developmental robustness

Takashi Hiiragi[1]
[1]*Hubrecht Institute, Netherlands*

Differentiation and Development, March 24, 2025, 15:30-17:30

Tissue patterning depends on the coordination between cellular dynamics, fate specification and tissue morphogenesis. Understanding how precision in patterning is robustly achieved despite the inherent developmental variability remains a challenge. Our group aims to understand the design principle of multi-cellular organisms using early mammalian embryos as a model system.

Our studies showed that feedbacks between cell fate, polarity and cell/tissue mechanics underlie the robust formation of early mouse embryos. I will discuss our recent work that presents yet another mechanism that ensures robustness in development.

Engineering the folding and function of tandem-repeat proteins: Teaching old proteins new tricks

Laura Itzhaki[1]
[1]*University of Cambridge, United Kingdom*

Protein Structure, Dynamics and Interactions, March 24, 2025, 15:30-17:30

In recent years, a major focus of my group has been the tandem-repeat protein class (e.g., tetratricopeptide repeats and ankyrin repeats). Their simple, modular, and quasi-linear architectures have allowed us to resolve their folding and functional energy landscapes in unprecedented detail and to engineer them in a strikingly predictable way. These proteins also provide us with exceptionally versatile scaffolds for designing new functions in a precise and predictable manner.

I will discuss our work on designed single- and multi-valent repeat proteins and how we are exploiting these types of scaffolds for targeted protein degradation. Lastly, we are using natural, as well as nanomaterial-inspired strategies to accelerate targeted protein degradation for therapeutic benefit.

Organising bacterial transcription via liquid-liquid phase separation of transcription factors

Mr Jacob Wright, Dr Hafez El Sayyed, Mr Pratip Mukherjee, Dr Abhishek Mazumder, Professor Achillefs Kapanidis[1]
[1]*University of Oxford, United Kingdom*

Microbes Across Length Scales, March 26, 2025, 10:15-12:15

Transcription is a key process that allows bacteria to respond to their environment and tune their growth rate. Transcription is often highly organised, as exemplified by the formation of large RNA polymerase (RNAP) clusters during fast growth in E. coli and B. subtilis; previous work suggested that such structures are phase-separated condensates which maximise ribosomal RNA (rRNA) transcription. We recently showed that these structures contain clusters of universal transcription factor NusG. However, the mechanisms by which these clusters enable cells to modulate transcription remain unclear.

To understand the organisation and physical nature of bacterial transcriptional clusters, we performed in vivo time-lapse imaging of clusters (via NusG) in different growth conditions. Tracking clusters using a machine-learning pixel classification workflow revealed that NusG clusters have similar mobilities to DNA, suggesting they are chromosome-anchored.

Surprisingly, substantial NusG clustering persisted even during slow growth; this was in contrast to the loss of RNAP clustering during slow growth. The persistence of NusG clustering could be due to its re-allocation to other processes and may indicate that NusG facilitates the weak protein-protein interactions that form phase-separated condensates. Consistent with the latter proposal, we showed that NusG forms phase-separated condensates in vitro, raising the possibility that NusG is the key host protein in these transcription condensates. In ongoing work, we use novel chromosomal labelling approaches to reveal the chromosome organisation relative to the NusG condensates. Our work advances our understanding of how phase separation can tune transcription and bacterial physiology.

A deep dive into the material world of the human body

Prof. Dr. Gijsje Koenderink[1]
[1]*Delft University of Technology, Netherlands*

Cell Architecture and Forces, March 26, 2025, 10:15-12:15

Our bodies are built up of cells and tissues with unique physical properties. Cells and tissues are living materials that combine high mechanical stability with active reshaping. This paradoxical mechanical behavior is governed by fibrous protein scaffolds known as the cytoskeleton and the extracellular matrix. Fibrous networks have many advantageous mechanical properties: fibers can form space-filling elastic networks at low volume fractions and they reversibly stress-stiffen, which provides protection from damage. However, it is still poorly understood how biopolymer networks can combine these features with the ability to dynamically adapt their structure and mechanics.

I will summarize recent insights in this question obtained via quantitative measurements on cells and tissues and on simplified reconstituted model systems. Along the way I will mention connections to applications in bottom-up synthetic biology and in tissue (re)generation.

Designing synthetic biomolecular condensates for specific client protein recruitment to facilitate protein degradation

Janet Kumita[1]
[1]*University of Cambridge, United Kingdom*

Biomolecular Assemblies and Condensates, March 25, 2025, 10:15-12:15

The ability of the cell to rapidly partition biomolecules into membraneless organelles, or biomolecular condensates, has been linked to a diverse range of cellular functions. To understand how the dynamics and physical attributes of these biomolecular condensates are linked with their biological roles, it is necessary to explore the design of synthetic systems that allow systematic tuning of the physico-chemical properties of the condensates. This includes rational designs to alter the condensate's material properties and methods to introduce specific recruitment of different client proteins to the condensate dense phase. Here we describe the design and characterisation of a phase-separating, consensus-designed tetratricopeptide repeat (CTPR) protein system that allows us to make precise and predictable changes to the CTPR domain that tune the condensates in these ways.

This system allows us to explore the condensates, at a mechanistic level, using in silico modelling, in vitro experiments and cell-based models. The ability to incorporate peptide motifs to specifically recruit different client proteins, including LC3, a key protein involved in the autophagy-lysosome degradation pathway may allow us to define a structure-function relationship between the physicochemical properties of these biomolecular condensates and their ability to target degradation via autophagy in the complex cellular environment.

Biomolecular Condensates and Surface Tension Phenomena

Prof. Halim Kusumaatmaja[1]
[1]*University of Edinburgh, United Kingdom*

Biomolecular Assemblies and Condensates, March 25, 2025, 10:15-12:15

Many biomolecular condensates are liquid-like droplets composed of proteins and/or RNAs, and a key mechanical property for any liquid droplet is its surface tension. Here, I will discuss two surface tension phenomena involving biomolecular condensates. First, there is now increasing evidence that biomolecular condensates interact with other cellular components, such as lipid membranes, for important biological functions [1]. For example, during seed development of the plant Arabidopsis thaliana, micrometer-sized condensates form within the vacuolar lumen and wet the tonoplast. Distinct tonoplast shapes arise in response to membrane wetting by condensates, including membrane budding and membrane nanotubes [2]. Another example is the formation of capillary bridges between lipid vesicles by protein condensates, as recently observed, for example, in damaged mitochondria of HeLa cells [3]. Studying the morphology of the capillary bridges, we find three distinct morphologies (bridging, enclosing and zipping), each with distinct mechanical responses. Second, given the relevance of surface tension for wide-ranging cellular processes, there is a need to measure its value in living cells.

Correspondingly, we have recently developed a high-throughput flicker spectroscopy approach to calculate the surface tension of thousands of condensates [4]. Demonstrating this approach on stress granules, we discovered that a surface tension-only model is inadequate for describing stress granules in live cells. We find that the measured fluctuation spectra require an additional bending rigidity parameter, which supports the view that stress granules are viscoelastic droplets with a structured interface. Moreover, we observe that the measured interfacial tensions and bending rigidities span a range of several orders of magnitude. Hence, different types of stress granules (and more generally, other biomolecular condensates) can only be differentiated via large-scale surveys.

References:
[1] H. Kusumaatmaja et al., Journal of Cell Biology 220, e202103175 (2021).
[2] H. Kusumaatmaja et al., Proceedings of the National Academy of Sciences 118, e2024109118 (2021).
[3] Y. Wong and E. Holzbaur, Proceedings of the National Academy of Sciences 111, E4439 (2014).
[4] J. Law et al., Science Advances 9, eadg0432 (2023).

Alternative intrinsic properties of single molecule emission for enhanced super-resolution microscopy

Sandrine Leveque-Fort[1]
[1]*ISMO, Université Paris Saclay, France*

Imaging and Single Molecule Biology, March 25, 2025, 10:15-12:15

Single-molecule localisation microscopy makes it possible to bypass the diffraction limit and thus to reach observation scales previously inaccessible in biological samples. However, to understand subcellular organisation at the nanometric scale, a number of developments are still needed, in particular to image complex samples (embryos, spheroids, tissues) in 3D and in depth, and also to reveal several proteins simultaneously.

We have proposed various alternatives for improving the localisation of single molecules, in particular by taking advantage of the intrinsic information when a fluorophore emits in the regime of the single molecule. For multi-target imaging, the single molecule allows spectrally close dyes to be imaged simultaneously using ratiometric measurements. I will show that not only can spectral information be used, but that brightness is a robust signature at the single-molecule level.

To improve axial resolution, we have proposed two complementary strategies that offer major advantages over the usual strategies based on engineering the point spread function. In particular, I will show that the intrinsic near-field emission (supercritical angle fluorescence - SAF) of any fluorophore can be used to position its absolute elevation relative to the coverslip, allowing ideal imaging of various adhesion processes. For more in-depth observation of complex samples such as spheroids or tissues, we introduce time-modulated illumination to achieve uniform axial precision. This approach, called ModLoc, allows us to image at depth (~40 µm) and is compatible with multi-target imaging.

Finally, I will discuss the challenges of extending single molecule imaging to live cell imaging.

Coevolution of diplopterol and asymmetric acyl tails enables eukaryotic survival in oxygen-deprived niches through metabolic adaptation

Maria Makarova[1]
[1]*University of Birmingham, United Kingdom*

Cell Metabolism and Growth, March 27, 2025, 09:00-11:00

Cell membranes are pivotal to cell physiology, not only serving as structural barriers but also regulating essential biological processes through their physical state. This physical state is primarily defined by lipids, with sterols and phosphoglycerolipids playing a central role in shaping membrane biophysics. In eukaryotes, sterols and the saturation level of phospholipid acyl tails require oxygen for synthesis. This raises a key question: how do eukaryotic organisms adapt to oxygen deprivation?

Here, we examine how the single-celled eukaryote Schizosaccharomyces. japonicus has evolved two distinct strategies to overcome this challenge: replacing conventional phospholipids with asymmetric saturated acyl tails and substituting sterols with the sterol-like molecule diplopterol. These two lipid bilayer components co-evolve to maintain membrane physical properties and functionality under low-oxygen conditions. Furthermore, we present evidence of metabolic adaptations that support survival in oxygen-limited environments.

HiP-HoP: predictive polymer modelling of 3D structure and transcription in human chromatin

Prof. Davide Marenduzzo
[1]*University of Edinburgh, United Kingdom*

Physics of the Nucleus, March 25, 2025, 14:15-16:15

I will present results from HiP-HoP, a predictive polymer model which we have used to predict 3D structure and transcription in human chromatin genome-wide (see https://3dgene.igc.ed.ac.uk). HiP-HoP simulations show that transcription is linked to the formation of microphase separated clusters of chromatin-binding proteins, reminiscent of transcription factories observed by microscopy. By combining modelling and super-resolution microscopy, we further show these transcriptionally active clusters are associated with a self-organised interconnected microgels made of RNA, chromatin and RNA-binding proteins.

Predicting future biological forms through mechano-eco-evo-devo

Naomi Nakayama[1,2]
[1]Okinawa Institute of Science and Technology, Japan, [2]Imperial College London, United Kingdom

Tissue Growth, Mechanics and Mechanosensing, March 26, 2025, 15:30-17:30

From hairs to worm-like bodies, slender body structures are ubiquitous throughout the Tree of Life, from hairs to worm-like bodies. This prevalence may be because such structures can confer various fitness-enhancing functions by interacting with the physical factors in the environment. Small changes in their forms may shift their functions and vice versa; these functional structures are anticipated to evolve in the changing climate. A likely example is the environmentally sensitive flight of the common dandelion – one of Nature's most iconic flyers.

The dandelion pappus increases air drag, although the parachute-like structure contains >90% empty space. Through a fluid dynamical characterization, we revealed a previously unseen flow behaviour likely aiding flight. The pappus is sensitive to the moisture level in the air and closes when wet; this morphing tunes the flight capacity. Through an imaging-based deformation analysis, material characterisation, and finite element method mechanical modelling, we gain insights into the mechanisms of the pappus actuator. The dandelion is a pioneer and foundation-building species of an ecosystem that feeds numerous bees and birds. Its dispersal dynamics have deep impacts on ecological geography and agriculture. A future direction will be discussed as to how we could predict and engineer climate-resilient plant forms.

Mutation, purifying selection, and adaptive evolution of SARS-CoV-2

Richard Neher[1]
[1]*University of Basel, Switzerland*

Evolution, Ecology and Epidemiology, March 24, 2025, 15:30-17:30

The unprecedented efforts to track SARS-CoV-2 during the pandemic generated millions of consensus viral genomes. I will discuss how these millions of genomes can be used to infer detailed models of the neutral mutations rates that account for sequence context, RNA secondary structure, and other genomic features.

Furthermore, I will show how one can estimate the fitness cost of almost all amino acid substitutions across the viral genome.

Finally, I will discuss how the cumulative divergence of SARS-CoV-2 can be decomposed into neutral, deleterious, and adaptive components.

Probing spatiotemportal electrochemical dynamics on single bacterial cells

Ashley Nord[1]
[1]*CBS, France*

Bioelectricity Across Scales, March 26, 2025, 15:30-17:30

Electrochemical gradients across biological membranes are fundamental to cellular bioenergetics. In bacteria, the proton motive force (PMF) drives critical functions such as ATP synthesis and motility. Although historically regarded as temporally and spatially stable, recent studies have revealed dynamic PMF behaviors at single-cell and community levels, which are implicated in processes like intracellular communication and coordination. The bacterial flagellar motor, a rotary nanomachine directly powered by the PMF, provides a unique and sensitive tool for probing these dynamics. By employing light-activated proton pumps and monitoring changes in flagellar motor activity, we perturb and investigate the PMF at the single-cell level.

This approach reveals millisecond-scale temporal fluctuations and rapid lateral homogenization of the PMF, reminiscent of the electrotonic potential spread observed in passive neurons.

Timers, clocks and echoes in embryonic development

Andrew Charles Oates[1]
[1]*EPFL, Switzerland*

Clocks, Timers and Cell Cycle Dynamics, March 25, 2025, 14:15-16:15

For the last 20 years, the segmentation clock has been the dominant paradigm to explain the rhythmic and sequential segmentation of the vertebrate body plan during embryogenesis – and justly so. Yet this model does not account for a fascinating classical result: the heat-shock echo, in which periodic segment defects recur, like an echo, along the axis. The interval separating the defects ranges from 5-7 segments depending on the species, but - critically - there are no known multiple-segment periodicities in the segmentation clocks of any vertebrates. Our current inability to explain this echo suggests that something fundamental is still missing from our overall picture of segmentation.

I will present our recent studies on this phenomenon using modern tools, which reveal a set of characteristic defects associated with the first defect, and which hint at the echo mechanism.

Cross-talk between cell mechanics, cell shape and cell state

Ewa Paluch[1]
[1]*University of Cambridge, United Kingdom*

Differentiation and Development, March 24, 2025, 15:30-17:30

Precise control of cell morphology is key for cell physiology, and cell shape deregulation is at the heart of many pathological disorders. Furthermore, transitions in cellular fate and state are often associated with changes in cell shape, and strong evidence points to the existence of feedbacks between mechanics, morphology and fate decisions. Cell morphology is intrinsically controlled by mechanical forces acting on the cell surface, to understand shape it is thus essential to investigate the regulation of cellular mechanics.

I will discuss how cellular mechanical properties drive cellular shape changes, and the cross-talk between mechanics and state in cellular transitions.

NGN3 oscillatory expression controls the timing of human pancreatic endocrine differentiation

Prof. Nancy Papalopulu[1]
[1]*University of Manchester, United Kingdom*

Clocks, Timers and Cell Cycle Dynamics, March 25, 2025, 14:15-16:15

In recent years, our understanding of how cells make timed cell state transitions has been transformed by the discovery of short-time scale (ultradian) oscillatory dynamics for many key proteins in differentiation. Here, I will describe our recent insights on the role of ultradian oscillations of Neurogenin 3 (NGN3) in developmental timing, during human pancreatic development [1]. By using a knock-in endogenous reporter we showed that NGN3 protein oscillates with a 13-hour periodicity in human iPS-derived endocrine progenitors and is switched off as cells differentiate to β-like and pre-alpha cells. Experimentally Increasing NGN3 protein stability changes these dynamics, resulting in one broad peak of expression instead of oscillations, with a larger peak to trough fold-change.

This leads to precocious endocrine differentiation and earlier expression of key NGN3 target genes. Single-cell analysis of dynamics, mathematical modelling and experimental validation suggest that NGN3 oscillations are decoded by fold-change detection (FCD) rather than the level of expression via an incoherent feedforward loop motif (IFFL), that explains both normal and precocious differentiation.

Our findings suggest that oscillatory NGN3 dynamics control the timing of differentiation, and such timer is likely to be imprecise; this may be advantageous for spreading out in time the process of differentiation.

[1] https://www.biorxiv.org/content/10.1101/2024.01.10.574974v1

Dismantling the fibrotic fortress: modelling the biophysical barriers to drug delivery in Pancreatic Cancer

Dr Sally Peyman
[1]*Heriot Watt University, United Kingdom*

Physics of Disease, March 27, 2025, 09:00-11:00

Pancreatic cancer, the most common of which is Pancreatic Ductal Adenocarcinoma (PDAC), has one of the worst prognoses of all solid tumours with 10-year survival rates of < 10%, and 5-year survival rates of < 1%, with no improvement in clinical outcomes for nearly 50 years. This is in part due to late detection, as the cancer is often asymptomatic until later stages when the tumour is already too advanced to be surgically removed. But in addition to this, the PDAC tumour surrounds itself with a dense, rigid extracellular matrix (ECM) that is similar in rigidity to scar tissue. This fibrotic fortress impedes drug delivery, by collapsing vasculature and restricting flow into the tumour core, resulting in dismal clinical outcomes.[1] However, current *in vitro* models of PDAC for drug discovery rarely recapitulate these mechanical features, and so new drugs and interventions are often tested against models that do not mimic these major contributors to drug resistance, leading to failure to improve patient outcomes.
Here, we show our approaches to understanding the mechanical development of *in vitro* PDAC models with a combination of rheology and AFM. With this understanding, we have developed a microfluidic, organ-on-chip platform that mimics the biophysical drug resistance observed *in vivo*.[2] We then show how this technology can be used to test new intervention strategies that specifically target PDAC's fibrotic defences.

1. Myo Min *et al*. 2023. Cancers, 15 (8) 2354
2. Kpeglo *et al*. 2024. Lab Chip, 24 (4) 854

Water movements in and out of the cell nucleus

Matthieu Piel[1]
[1]*Institut Curie, France*

Cell Architecture and Forces, March 26, 2025, 10:15-12:15

The cell and its compartments are delineated by semi-permeable membranes with high permeation, meaning that their water content adjusts rapidly to balance osmotic and hydrostatic pressures. The consequence of these water movements, that can happen at a variety of timescales, from milliseconds to days, is primarily to change the concentration of the macromolecules trapped in the cell and its compartments. This can have multiple effects, from reaction rates, to condensate formation and changes in the mobility of a variety of intracellular objects depending on their size. In this talk I will focus on the case of the nucleus to describe how it differs from the cell - although the physical principles remain the same, the precise quantities matter and determine various regimes. The nucleus is more compressible than the cell due to a lower osmotic modulus, and water movements in and out of the nucleus are slower because of bulk friction on chromatin.

I will discuss the consequences of these differences on the response of the cell and nucleus to confinement in terms of mechanics, formation of protein condensates and molecular crowding.

Structural biology of the Virosphere

Ehmke Pohl[1]
[1]Durham University, United Kingdom[1]

Protein Structure, Dynamics and Interactions, March 24, 2025, 15:30-17:30

Viruses are the most diverse and most abundant life-form on the planet. They hence represent the largest natural reservoir of genetic diversity only accessible by metagenomics sequencing efforts including the Virus-X consortium focussed on extreme environment such as Icelandic hot lakes and the deep-sea smoker in the Mid-Atlantic Ocean[1]. Here we will present the structural and functional diversity of viral proteins and explore current and future application in the bio-economy[2].

References
1. Aevarsson A., *et al.* (2021) "Going to extremes – a metagenomic journey into the dark matter of life" *FEMS Microbiology letters.* 368.
2. Jasilionis, A*., et al*. "AmiP from hyperthermophilic *Thermus parvatiensis* prophage is a thermoactive and ultrathermostable peptidoglycan lytic amidase" (2023) *Protein Science* 32:e4585.

Bladder battleground: probing host/pathogen interactions in advanced human cell-based urothelial microtissue models

Prof. Jennifer Rohn[1]
[1]*University College London, United Kingdom*

Immunity, Resistance and Host/Pathogen Dynamics, March 26, 2025, 15:30-17:30

Diseases of the bladder impose an enormous economic and healthcare burden to society, but are highly understudied. Urinary tract infections (UTI) are among the most common in the world. Given their sheer prevalence alongside their tendency to recur, UTI treatment is a critical exacerbating factor in the global antimicrobial resistance crisis. Crucially, a full century after Alexander Fleming discovered antibiotics, we still don't have a better first-line treatment. Therapeutic innovation has lagged in part due to the reliance on mouse models; although these have yielded great insights, there are nevertheless key species differences in urinary tract structure, function, biomarkers and immunity whose consequences to disease relevance are not fully understood.

In recent years, we and others have developed in vitro human cell-based urothelial microtissue models as a complement to mice. Our most recent iteration, 3D-UHU, is planar, three-dimensional and fully stratified to human thickness (up to seven layers, as opposed to the mouse urothelium, which only expresses three); is terminally differentiated with correct biomarkers; has robust barrier function; and is fully urine-tolerant, allowing the exposure of bacteria or drugs in their native environment: 100% human urine. 3D-UHU also elaborates a glycosaminoglycan layer on the luminal side, secretes key cytokines in response to bacterial infection, and undergoes physiological cell shedding. We have been using this model to understand bacterial/host interactions at the human cell interface and to trial novel antimicrobial therapies; moreover, we have been improving the model further to understand the role of flow and mechanical stretch on the infection process. These approaches illustrate the power of human cell-based microtissue platforms to complement in vivo studies in animal models.

Engineered viscoelasticity in cell microenvironments

Prof. Manuel Salmeron-Sanchez[1]
[1]*University of Glasgow, United Kingdom*

Engineering Tissues and Organoids and Biohybrids, March 25, 2025, 14:15-16:15

The physical properties of the extracellular matrix (ECM) and the use of growth factors are powerful tools to control cell behaviour, including fundamental processes such as cell migration and (stem) cell differentiation. Integrins are mechanotransductors that feel and respond towards the mechanical properties of the ECM. We have developed material systems that allow simultaneous stimulation of integrins and growth factors receptors. We have engineered polymers and 3D hydrogels that unfold and assemble proteins to allow exposure of the integrin and growth factor binding regions. For example, we show the use of BMP-2 in synergy with □5□1 integrins to promote osteogenesis and regeneration of critical-sized defects. Further, we have developed interfaces that bind latent proteins that induce integrin-mediated mechanical activation of growth factors. We will demonstrate the use of TGF-□1 that is released and activated by using engineered surfaces that organise fibrinectin to promote binding of LTBP1 and enable integrin B1 to pull on active TGFB1.

In the second part of the talk, we will use surfaces of controlled viscosity in our pathway to engineer and understand the viscoelastic properties of the ECM. We use supported lipid bilayers that are functionalised with either RGD (integrin binding) or HAVDI (cadherin binding) to demonstrate the molecular clutch is engaged on surfaces of high enough viscosity and, importantly, that it is weaken upon N-cadherin binding, controlled by the competition between vinculin and □-catenin for actin filaments. We then introduced substrates of controlled elasticity and viscosity, first in 2D using polyacrylamide hydrogels that were further patterned using fibronecin and then in 3D using PEG-hydrogels functionalised with fibronectin. We will discuss the unexpected interplay between viscoelasticity, cell adhesion and molecular clutch engagement. We introduce Brillouin microscopy as a way to follow the evolution of the viscoelastic properties of cells and the engineered hydrogels in 3D in a non-invasive way and in real time.

The physics of small-scale eye movements

Hannah Smithson[1]
[1]*University of Oxford, UK*

Emerging Areas in the Physics of Life, March 26, 2025, 10:15-12:15

Human vision depends on absorption of light by the rod and cone photoreceptors of the eye. However, if an optical image is stabilised on the retina, it perceptually fades to a featureless grey within a few hundred milliseconds. This is a consequence of the biphasic temporal response of neurons in the visual processing pathway, giving zero integrated response to prolonged stimulation. Counteracting perceptual fading, continual small movements of the eyes, once thought to be only a nuisance, are vital in translating the optical image across the retina and refreshing the visual percept. In this project we ask what are the optimal movements of the eyes to support efficient information transmission through the human visual system? The answer depends on the nature of the optical input; on what needs to be estimated; and on the nature of processing by visual neurons. We take an integrated, interdisciplinary approach, developing instrumentation to non-invasively track the retina and deliver visual stimulation at the required micron-scale; building computational models of the known physiological components early stages of the visual system; and formulation of an information-theoretic framework to explore and generate testable hypotheses. We consider detection, discrimination, localisation or identification of visual stimuli designed to reveal performance differences that depend on the eye-movement paths. The project provides new insights into the nature of human visual processing; and a new framework for calculating with respect to these questions.

Pattern formation and wave propagation in ciliated organisms

Kirsty Wan[1]
[1]*University of Exeter, United Kingdom*

Patterns, Waves, Transport, Collective Phenomena and Microswimmers, March 25, 2025, 10:15-12:15

Active hair-like protrusions called cilia are found in many eukaryotes where they produce physiological flows for a variety of functions. Dysfunction of motile cilia is implicated in a variety of human diseases. Ciliated structures assume a myriad of configurations, depending on the topology and geometry of the organism. Groups of cilia enable feeding or swimming motility when attached to a cell body, while mucociliary clearance arises from the coordinated activity of multiciliated epithelia.

In all these cases, multiple cilia interact to produce different types of local and global coordination patterns, including robust metachronal waves. Do these dynamic states of coordination arise spontaneously, or do they require some form of internal control? How do metachronal waves emerge in different systems, and how is the wave direction selected? Do ciliary metachronal waves transmit across physical gaps? We propose new and emerging model organisms to address these questions.

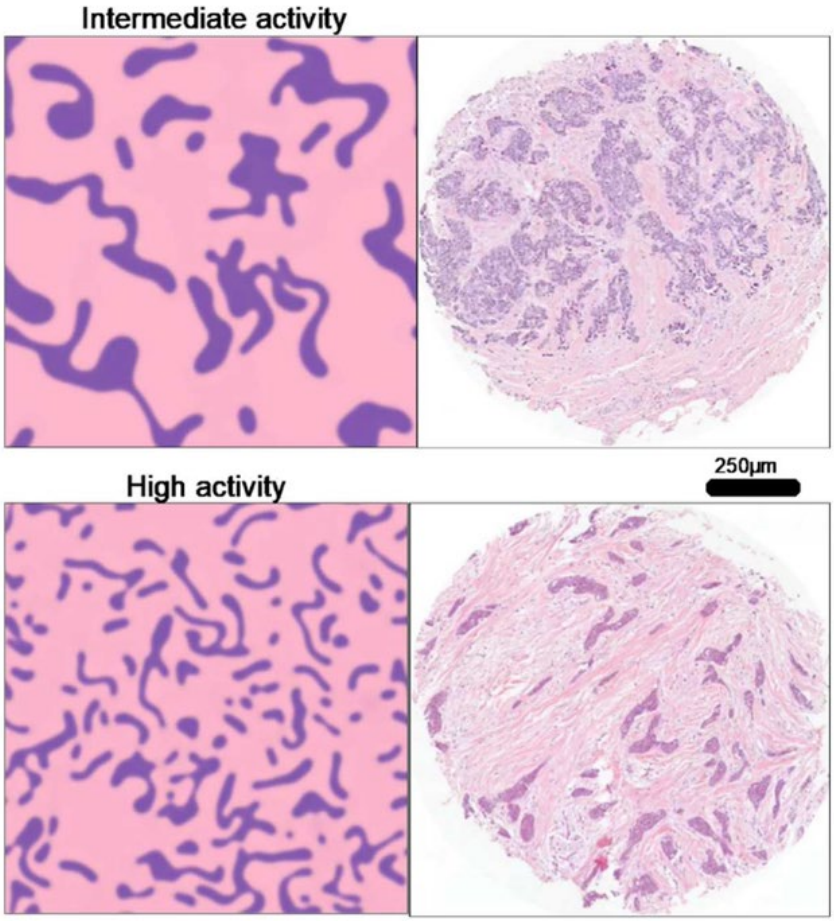
Self organisation of invasive breast cancer driven by the interplay of active and passive nematic dynamics

Professor Julia Yeomans[1], Dr Saraswat Bhattacharyya[1], Dr Pablo Gottheil[2], Professor Josef Kas[2]
[1]University of Oxford, United Kingdom, [2]University of Leipzig, Germany

Physics of Disease, March 27, 2025, 09:00-11:00

In invasive breast cancer, cell clusters of varying sizes are embedded in the fibrous extracellular matrix (ECM). Contrary to the current view that this structure arises from increasing disorder, our findings suggest that it results from active self-organization triggered by cancer cell motility.

Simulations and histological analyses of tumours from over 2,000 breast cancer patients reveal that motile, aligned cancer cells within clusters move as active nematic aggregates through the surrounding highly aligned ECM fibres, which form a confining, passive nematic phase. Cellular motion leads to cluster splitting and coalescence. The degree of cluster activity, combined with heterogeneity in cell motility, is reflected in specific scaling behaviours for cluster shape, size distribution, and the distance between cluster boundaries and nematic defects in ECM alignment. Increased activity estimates correlate with tumour progression and are associated with a poorer prognosis for patients.



Malignant cancer clusters embedded in ECM. Dynamical simulations (left) are compared to examples from histological images (right).

Photosynthesis on an electrode

Jenny Zhang[1]
[1]*University of Cambridge, United Kingdom*

Bioelectricity Across Scales, March 26, 2025, 15:30-17:30

The harnessing of solar energy to perform complex chemistries sustainably and on a global scale has been mastered by nature over 3 billion years ago with the emergence of photosynthesis. The ability to wire photosynthetic machineries to electrodes for performing photo-electrochemistry is a relatively new approach for studying photosynthesis and generating bioelectricity. We are now developing this as a way to re-wire photosynthesis to create novel pathways for performing solar-energy conversion.(1-3)

Here, I will give an overview of efforts in my lab to wire into a range of photosynthetic model systems. These range from more simple model in vitro systems, to membrane bound electron transport chains, to complex living organisms.

References:
1.J. Z. Zhang, E. Reisner, Advancing photosystem II photoelectrochemistry for semi-artificial photosynthesis. Nature Rev. Chem. 4, 6 (2020).
2.J. M. Lawrence, J. Z. Zhang et al., Rewiring photosynthetic electron transport chains for solar energy conversion. Nature Reviews Bioengineering, 1, 887 (2023).
3.T. Baikie et al., Photosynthesis re-wired on the pico-second timescale. Nature, in press (2023).

ECR Session Talks

Quantum Spin Resonance in Engineered Magneto-Sensitive Fluorescent Proteins Enables Multi-Modal Sensing in Living Cells

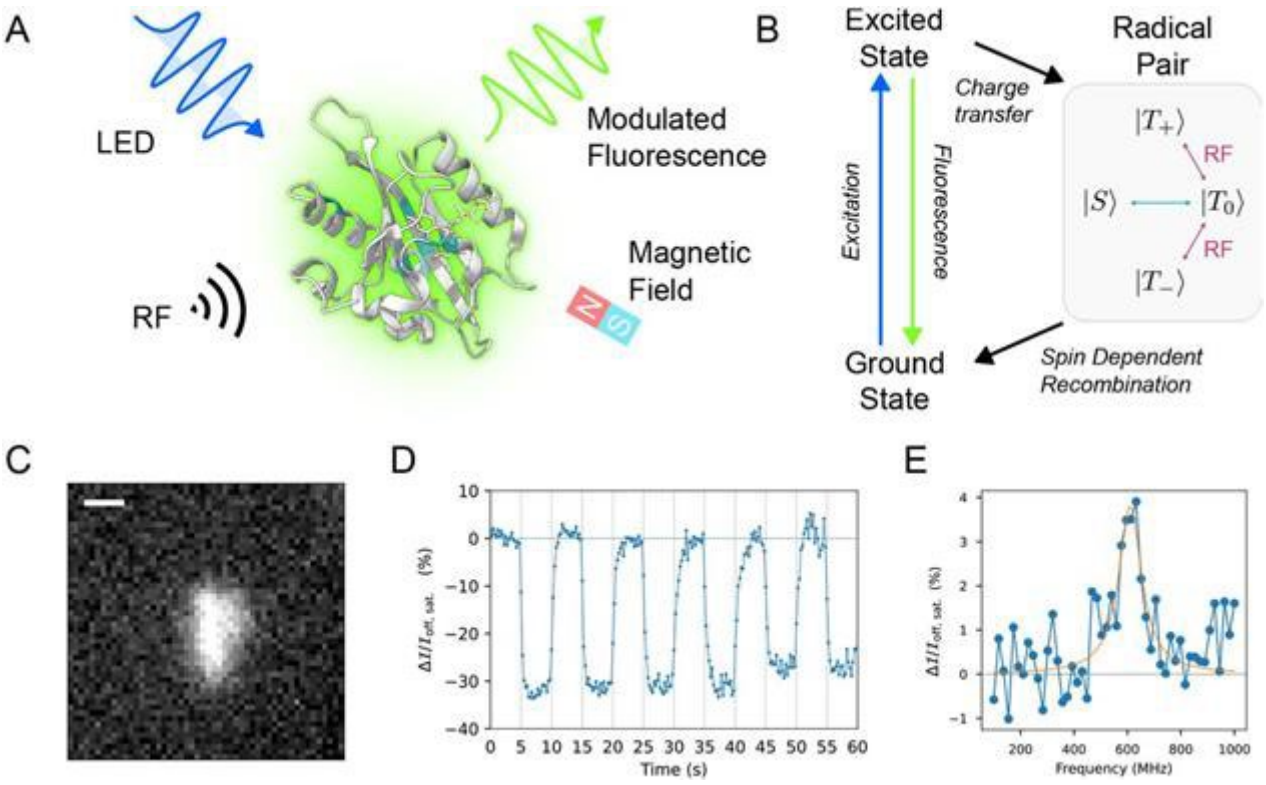
Gabriel Abrahams[1], Vincent Spreng[1,2], Ana Stuhec[1], Dr Idris Kempf[1], Jessica James[1], Kirill Sechkar[1], Scott Stacey[1], Vicente Trelles-Fernandez[1], Dr Lewis Antill[1,3], Prof. Christiane Timmel[1], Maria Ingaramo[4], Andrew York[4], Dr Jean-Philippe Tetienne[5], Prof. Harrison Steel[1]
[1]University of Oxford, United Kingdom, [2]Heidelberg University, Germany, [3]Sungkyunkwan University, Republic of Korea, [4]Calico Life Sciences, USA, [5]Royal Melbourne Institute of Technology, Australia

Early Career Satellite Event - Session 1 Full Oral Talks, March 24, 2025, 09:15-10:15

Quantum phenomena have been identified as fundamentally significant to an increasing number of biological processes. However, biological based candidates for quantum-sensors have thus far been limited to in vitro systems, are prone to light induced degradation, and require sophisticated experimental setups. We recently created a new class of magneto-sensitive fluorescent proteins (MFPs), which we now show overcome these challenges and represent the first biological quantum-based sensor that functions at physiological conditions and in living cells. Through directed evolution, we demonstrate the possibility of engineering these proteins to alter properties of their response to magnetic fields and radio frequencies, effects explained in terms of the spin correlated radical pair mechanism.

Using this engineered system we demonstrate the first observation of a fluorescent protein exhibiting Optically Detected Magnetic Resonance (ODMR) in living bacterial cells at room temperature, at sufficiently high signal-to-noise to be detected in a single cell, paving the way for development of a new class of in vivo biosensors. Magnetic resonance measurements using fluorescent proteins enable unprecedented technologies, for instance 3D spatial localisation of the fluorescence using gradient fields (i.e. Magnetic Resonance Imaging but using an endogenous probe).

We further demonstrate the use of multiple variants of MFPs for multiplexing or lock-in amplification of fluorescence signals, opening a new approach to combining or extracting multiple signals from a biological measurement. Taken together, our results represent a new intersection of imaging and perhaps actuation modalities for engineered biological systems, based on and designed around understanding the quantum mechanical properties of MFPs.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Using Whispering Gallery Modes to Monitor Single-Enzyme turnover events of NanoLuc

Alice Attenborough[1], Professor Frank Vollmer[1]
[1]*University of Exeter, United Kingdom*

Early Career Satellite Event - Session 2 Flash Talks, March 24, 2025, 10:15-10:35

Whispering Gallery Mode (WGM) sensing is an optoplasmonic technique capable of detecting the binding and movement of single molecules with Angstrom-scale precision and millisecond time resolution, without requiring fluorescent tags [1]. This universal, label-free platform provides a powerful alternative to fluorescence-based methods, enabling the direct study of enzyme kinetics and molecular interactions in real-time [2]. However, a key challenge in enzymology is the ability to directly monitor enzymatic turnover at the single-molecule level on such platforms while simultaneously verifying the production of reaction products.
This study addresses this challenge by integrating WGM sensing with a bioluminescent enzyme, NanoLuc (NLuc), whose turnover produces detectable photons as reaction products.

Using Furimazine as a substrate, we demonstrate that WGM sensing can detect both single-enzyme binding events to plasmonic gold nanorods and real-time enzyme turnover. Moreover, these results produced a unique signal pattern, contributing to a new area of investigation which will provide new insights into NLuc kinetics. These WGM single molecule results provide a first step in developing a photosensitive WGM hybrid sensor, which will establish a framework to correlate enzymatic activity with product formation, providing conclusive insights into reaction mechanisms.

This approach represents a significant start toward the direct, label-free monitoring of enzymatic turnover events, opening new avenues for studying single-molecule biological systems and advancing the understanding of widely used enzymes like NanoLuc, which have numerous industrial applications.

[1] M.D. Baaske, et. al. Nature Photonics 10, 733-739 (2016).
[2] M.C. Houghton, et. al. Advanced Science 11(35) (2024).

Friction controls spatial patterning in active fluids

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Early Career Satellite Event - Session 4 Flash Talks, March 24, 2025, 12:15-12:35

Mechanical stresses are known play a crucial role in a wide range of developmental processes, including cell division, gastrulation and symmetry breaking. Increasing experimental evidence suggests in addition that complex properties of the surrounding material are responsible for guiding morphogenetic processes – a feature often overlooked in theoretical models.

We consider a minimal hydrodynamic model of an active fluid in which chemically organised isotropic stresses are generated. Previous work has shown that active stresses promote the spontaneous formation of non-trivial concentration patterning [1].

To account for inhomogeneous mechanical properties of the surrounding material, we allow spatially varying patterns of external friction. We study this system by analysing non-linear mode couplings which appear as a result of inhomogeneous friction. We identify basic principles that determine how spontaneously emerging internal stress distributions orient themselves with respect to friction patterns. Numerical analysis confirms these results and reveals a rich phenomenology of non-linear steady states when inhomogeneous friction is present.

This work provides new insights into how mechanical interactions with the surrounding can guide the self-organisation of active fluids with potential applications in developmental symmetry-breaking processes and the design of synthetic active materials.

[1] Bois, et al. PRL 106, no. 2 (2011).

Optimising hybrid vesicles for membrane protein reconstitution: applications and insights

Dr Rosa Catania[1,5], Prof Michael Rappolt[2], Prof Stephen Muench[3,5], Prof Lars Jeuken[4], Prof Paul Beales[1,5]

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Early Career Satellite Event - Session 1 Full Oral Talks, March 24, 2025, 09:15-10:15

Hybrid vesicles (HVs), composed of diblock copolymers like poly(butadiene-b-ethylene oxide) and phospholipids, provide a versatile platform for membrane protein (MP) reconstitution, effectively overcoming the stability challenges of liposomes. Our recent work has focused on enhancing the usability and optimisation of HVs for this purpose. We developed a detergent-free method that allows for the direct incorporation of MPs from styrene-maleic acid lipid particles (SMALPs) into HVs, significantly improving both efficiency and ease of use. Specifically, we successfully reconstituted the multi-subunit cytochrome bo3 (cyt bo3), a terminal oxidase from Escherichia coli, without the need for detergents. We also demonstrated that this method is applicable to complex membrane protein mixtures. In contrast, reconstitution from SMALPs into liposomes was unsuccessful.

Notably, HVs retained cyt bo3 bioelectrocatalytic activity even after being stored for over a year, as assessed by the formation of solid-supported hybrid membranes (SSHMs) that were comparable to freshly prepared samples, with cyt bo3 maintaining over 50% of its original activity. This finding confirms the longevity and stability of HV systems that we previously established.

To further understand how polymer structures influence MP reconstitution, we systematically screened various copolymer architectures, varying headgroup-to-tail ratios and polymer chain lengths. We observed significant effects on reconstitution efficiency, orientation and activity of cyt bo3. Our findings highlight the versatility of HVs as a biomimetic platform for MP, paving the way for advancements in artificial cell development and other applications.

Microtubule Tip-Generated Forces Drive Bipolar Spindle Organization and Chromosome Segregation

Dr. Lee-Ya Chu[1], Dr. Daniel Stedman[3], Dr. Julian Gannon[1], Dr. Susan Cox[3], Dr. Georgii Pobegalov[2], Dr. Maxim Molodtsov[2]
[1]The Francis Crick Institute, United Kingdom, [2]University College London, United Kingdom, [3]King's College London, United Kingdom

Early Career Satellite Event - Session 3 Full Oral Talks, March 24, 2025, 11:15-12:15

The mitotic spindle is a bipolar structure essential for accurate chromosome segregation during cell division. Its size and organization are regulated by mechanical forces from molecular motors and non-motor proteins to spindle b-orientation remain unclear.
To investigate this, we developed methods using dual-beam optical trapping system to measure molecular forces in an artificially reconstituted bi-polar spindle. Oure study identifies a new mechanism where microtubule tip-trackers work synergistically with minus-end-directed motors to generate both pushing and pulling forces. Unlike the force generators that act withing antiparallel microtubule overlaps, this system operates at growing microtubule tips, harnessing the forces generated from microtubule polymerization. These tip-generated forces scale differently with spindle size, providing a distinct contribution to force balance.

We demonstrated that this mechanism can independently establish and stabilize a bipolar spindle, both in vitro and in mammalian cells, demonstrating the system's role in organizing spindles during mitosis. These findings offer a new perspective on spindle mechanics, highlighting the importance of tip-generated forces in regulating spindle organization and chromosome segregation.

Protein Capture using Synthetic Co-Transcriptionally Folded RNA Condensates in Mammalian cells

Dr Catherine Fan[1], Professor Lorenzo Di Michele[1]
[1]*University of Cambridge, United Kingdom*

Poster Session 2, Drinks Reception and Exhibition, March 25, 2025, 17:30-19:30

The ability to capture, transport and manipulate protein and enzymatic machinery within living cells is a critical challenge in cell biology and biotechnology. By designing and producing co-transcriptionally assembled RNA nanostructures that form condensates through liquid-liquid phase-separation (LLPS), we are able to recruit and concentrate targeted proteins to bespoke subcellular compartments in mammalian cells. Our system is underpinned by RNA transcripts that fold into discrete nanostar geometries, which contain a Pepper aptamer to bind fluorogenic HBC620 ligands and the AP3 aptamer to capture GFP protein (PeA_AP3 in the figure).

Through Kissing Loop (KL) interactions, these nanostars are able to co-transcriptionally self-assemble from transfected plasmids into addressable condensates. With our Pe_AP3 nanostar system we have demonstrated the binding of the condensates to free cytosolic GFP protein (FigureA-ii) as well as to GFP-tagged laminA localised to the nuclear membrane (FigureB-ii) in HeLa cells. Additionally, through our system, we investigate the dynamics of condensate formation and protein association, providing insights into the fundamental principles of phase separation in the cellular environment. Beyond protein isolation, our synthetic RNA condensate platform can be modified to bind any protein of interest opening new avenues for protein engineering, drug discovery, and the development of synthetic biology tools for cellular manipulation.

Exploring the Frameshifting Element in SARS-CoV-2 Using smFRET

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[1]University of York, United Kingdom

Early Career Satellite Event - Session 2 Flash Talks, March 24, 2025, 10:15-10:35

A key feature of SARS-CoV-2 and many other viruses is programmed ribosomal frameshifting, which is essential for replication. This process relies on the presence of a slippery sequence and a stimulatory RNA secondary structure, in this case, a psuedoknot. While the secondary structure of this RNA fragment has previously been evaluated, several different conformations have been proposed.

We present here the first single-molecule Förster resonance energy transfer (smFRET) characterization of the pseudoknot structure labelled with donor (Cy3) and acceptor (Cy5) dyes, and using fluorescence burst analysis, we investigate the conformational landscape of the structure across a range of physiological environmental conditions. In contrast to static Cryo-EM and X-ray crystallographic predictions, the smFRET population distributions unveil heterogeneity within the pseudoknot, indicative of a range of structures and dynamics that may be correlated with function. By revealing the structural heterogeneity of this pseudoknot we demonstrate the feasibility of smFRET studies for studying otherwise inaccessible pseudoknot interactions, and we provide a platform for obtaining further insights into the vital process of frameshifting and viral replication.

How small is too small: a spatio-temporal spectroscopic quantification of single-cell exchange between marine microbes

Dr Richard Henshaw[1], Dr Kang Soo Lee[2], Professor Roman Stocker
[1]ETH Zürich, Switzerland, [2]Department of Mechanical Engineering, UNIST, Republic of Korea

Early Career Satellite Event - Session 1 Full Oral Talks, March 24, 2025, 09:15-10:15

Chemical cues dominate marine microbial interactions, with the repercussions of these microscale interactions reverberating up through the ecosystem, ultimately dictating global-scale processes such as carbon fixation and nutrient recycling. Prominent amongst the marine primary producers are picocyanobacteria such as Synechococcus and Prochlorococcus, who contribute approximately one quarter of global oceanic primary production. Whilst previously considered effectively invisible to nearby heterotrophic bacteria, recent experimental work [1] has shown that chemotaxis does significantly increase reciprocal exchange between heterotrophic bacteria and cyanobacteria at the bulk scale, and that chemotaxis can be enhanced through the viral infection of cyanobacteria [2].

However, direct experimental measurements of single cell exchange have proven elusive to date. Here, we combine Raman spectroscopy with microfluidics to quantify for the first time the spatio-temporal flux between a single heterotrophic bacteria and an individual cyanobacteria. By measuring the exchange of heavy carbon isotopes from the marine bacteria Vibrio alginolyticus to the cyanobacteria Synechococcus, we provide the first direct quantification of the spatiotemporal extent of bacteria-cyanobacteria interactions at the single-cell scale. These results signify a substantial step forward in our understanding of marine microbial interactions, with significant implications for both experimental and modelling-driven efforts to elucidate these key microscale interactions which underpin the critical ecosystem-scale processes driving life on our planet.

[1] Raina, et al. Nature Microbiology, 2023.
[2] Henshaw, et al. Nature Microbiology, 2024.

Enhanced Enzyme Diffusion as Maxwell’s Demon: Selective Increase of Exothermal Reaction

Shunsuke Ichii[1,2], Tetsuhiro Hatakeyama[2], Kunihiko Kaneko[4]
[1]The University of Tokyo, Japan, [2]RIKEN, Japan, [3]Institute of Science Tokyo, Japan, [4]Copenhagen University, Denmark

Early Career Satellite Event - Session 3 Full Oral Talks, March 24, 2025, 11:15-12:15

In recent years, a phenomenon known as enhanced enzyme diffusion (EED), in which the diffusion rate of enzymes increases as a result of enzymatic reactions, has been reported. Using particle simulations that incorporate this microscopic effect, we discovered that EED can alter macroscopic concentrations in the equilibrium state even in the absence of spatial organization. Furthermore, theoretical model analyses revealed that this effect allows enzymes to act as Maxwell's demons, carrying information about the type of particles they interact with and using that information to shift the balance of reactions. Additionally, we demonstrated that the conditions under which this effect operates can be derived from the relationship between the reaction rate constants, the dissipation rate of enzyme motility, and the system’s viscosity coefficient.

These findings suggest that the spatial effects of EED can influence macroscopic concentrations, potentially challenging the conventional assumptions about enzyme behavior. Specifically, we revealed the possibility that enzymatic reactions, previously thought only to accelerate reactions without altering equilibrium distributions, can have macroscopic effects on the balance of those distributions. Moreover, this study highlights the potential of enzymatic reaction systems to serve as a new subject for exploring Maxwell's demon-like phenomena.

Topological States in Out-of-Equilibrium Allosteric Molecular Assemblies

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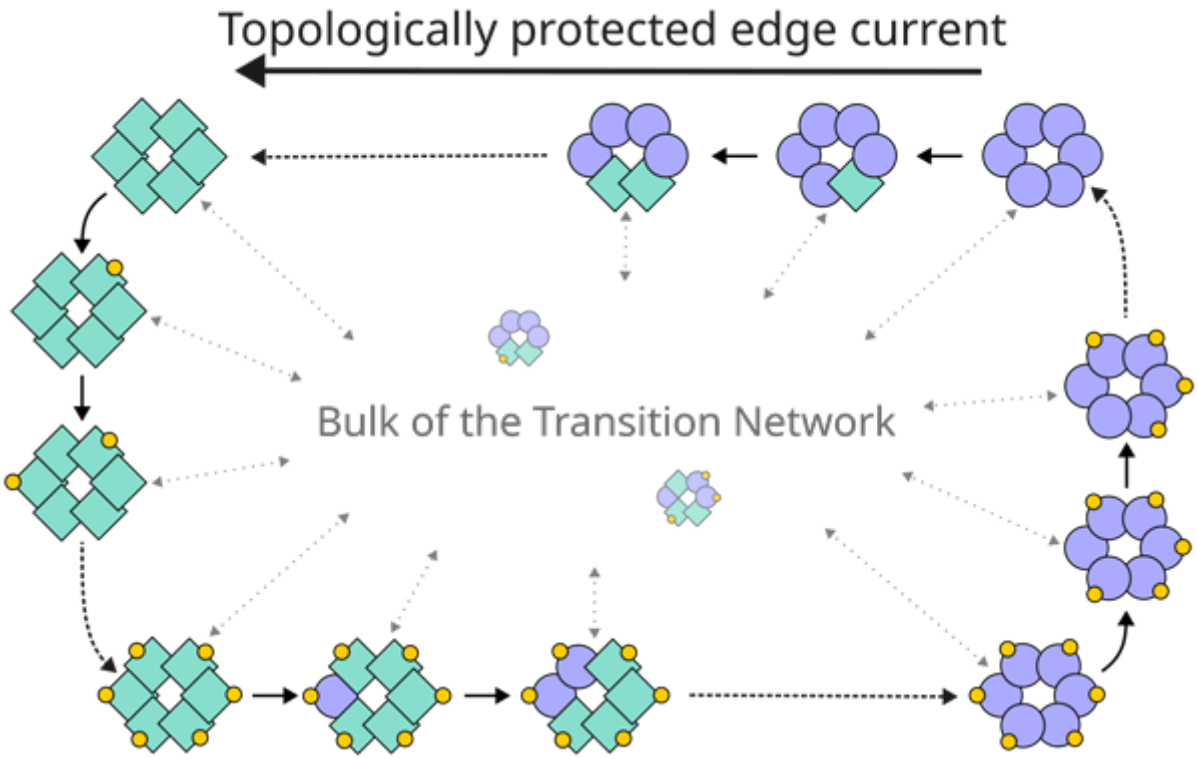
Early Career Satellite Event - Session 4 Flash Talks, March 24, 2025, 12:15-12:35

Despite noisiness in the cellular environment, molecular systems show a high degree of robustness. A recent new direction in understanding this apparent paradox is the study of topologically protected states in stochastic systems, which robustly confine the dynamics of the system to a lower-dimensional space. However, it is unclear what the minimal biochemical ingredients are for such states to occur. Here, we study topological features in a non-equilibrium, thermodynamically-consistent model of a molecular assembly, made of subunits that undergo futile cycles of conformational change and phosphorylation. When the subunits interact allosterically with each other, we find global, concerted cycles that emerge at the scale of the whole assembly. These involve only a small subset of all possible conformations, analogous to topological edge currents in quantum systems.

We map out the kinetics, energetics, and biochemical interactions necessary to obtain distinct classes of topological behaviour. Our results suggest that topological states can provide a minimal description of molecular coordination in protein complexes, such as circadian oscillators (e.g., KaiABC) or polymer assembly and disassembly (e.g., microtubules). More broadly, our results demonstrate that stereotyped dynamics can arise purely from non-equilibrium kinetic effects, without the need for an underlying energy landscape to channel them.



Structural response of microtubule and actin cytoskeletons to direct intracellular loads

Ryota Orii[1], Hirokazu Tanimoto[1]
[1]*Yokohama City University, Japan*

Early Career Satellite Event - Session 4 Flash Talks, March 24, 2025, 12:15-12:35

Microtubule and actin are the two major cytoskeletal polymers physically driving fundamental biological processes in the cell interior in eucaryotes. How microtubule and actin cytoskeletons respond to the loads is poorly understood. In this study, we directly applied perturbing intracellular forces to microtubule and actin cytoskeletons and quantitatively evaluated how these cytoskeletons structurally respond to the loads [1]. We established a new ferrofluid-based intracellular magnetic tweezers and observed that in a creep experiment, ~10 nN loads displaced the microtubule-nucleus complex several micrometers away from the stationary position over 10-20 seconds and revealed that rheological properties of the microtubule complex primarily determined by filamentous actin. The deformation of the microtubules was largest at the load position and decayed toward the cell periphery.

We found that the deformations of actin meshwork follow the same scaling of microtubules. This result suggests that the two cytoskeletal systems behave as an integrated elastic body. We then investigated shape dynamics of a single microtubule under the perturbing loads. The microtubules exhibited non-Euler buckling in response to compressed loads, suggesting that microtubules are enclosed within actin meshwork at the polymer scale.

Lastly, we demonstrated that a point force localized in the cytoplasm propagates in actin meshwork and deforms a microtubule at a distance. Taken together, our results suggest that microtubule and actin cytoskeletons act as an integrated continuum in the cytoplasm in response to intracellular loads.

[1] Orii, Ryota, and Hirokazu Tanimoto. Journal of Cell Biology 224.2 (2025).

Mechanics of force sensing in Piezo ion channels

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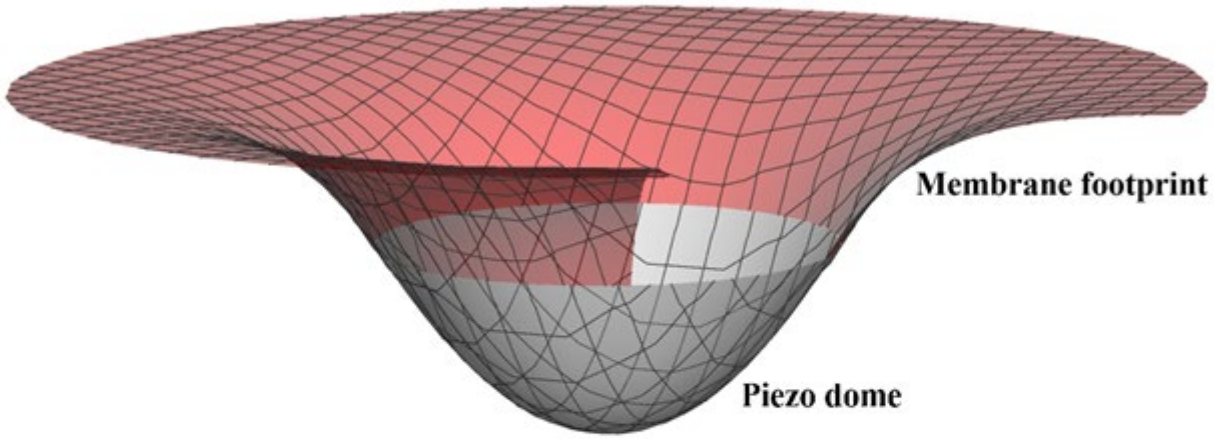
Early Career Satellite Event - Session 4 Flash Talks, March 24, 2025, 12:15-12:35

Since their discovery in 2010, Piezo proteins have been found to provide the molecular basis for many different forms of mechanosensation, including the sensation of touch in humans. Piezo proteins are mechanosensitive ion channels that locally bend the membrane into the shape of a spherical cap that can, in turn, produce a large membrane footprint. Previous work has shown that the shape of Piezo's membrane footprint can be predicted quantitatively through membrane elasticity theory, that Piezo ion channels are similarly flexible as a typical lipid bilayer membrane, and that Piezo's gating properties emerge from the interplay of Piezo structure, membrane shape, and the mechanics of the Piezo-membrane system [1]. Building on this previous work, we develop a simple analytic model of Piezo gating, which we test against fully nonlinear, numerical solutions.

This analytic model provides us with straightforward mathematical expressions describing the dominant physics of Piezo's response to lateral membrane tension. We then extend the theory of Piezo gating to account for vertical forces exerted onto the cell membrane by, for instance, the cytoskeleton. We employ this generalized theory to systematically explore the modulation of Piezo's gating response by such vertical forces. The results of this study shed light on how Piezo can be gated by a combination of vertical forces onto the membrane and membrane tension.

1. C. A. Haselwandter, Y. R. Guo, Z. Fu, R. MacKinnon. Proc. Natl. Acad. Sci. U.S.A. 119 (40) e2208034119 (2022).



Synchronisation of chemical reactions in a population of condensates

Alisdair Stevenson[1]
[1]*ETH Zürich, Switzerland*

Early Career Satellite Event - Session 2 Flash Talks, March 24, 2025, 10:15-10:35

Collective behaviour refers to the actions and interactions of a group of individuals, which results in emergent patterns and behaviour that cannot be explained by individual actions alone. Examples of this emergent behaviour from complex systems are widespread in physics, ecology and biology and include phase transitions in materials and ant or bee colonies displaying swarm intelligence. How is this possible? A method of communication is universally required for a complex system to exhibit collective behaviour. In this project, we explore whether biomolecular condensates formed via liquid-liquid phase separation could act as a means for collective behaviour to emerge within a cellular environment to enable population-level control of chemical reactions relevant to complex biological processes.

If such processes are regulated at the cellular scale by condensates, how is communication possible between spatially distinct condensates? How does this coordinate the behaviour of multiple droplets, resulting in a more predictable and stable outcome of chemical reactions, with specific functions, at the population level? As the mechanisms by which communication and population-level regulation may be possible for in vitro/vivo systems that form droplets have not been explored, this is an exciting opportunity to generate a novel understanding of how complex processes are regulated at the cellular scale. Here we have demonstrated that communication via the dynamic exchange of materials to maintain partition concentrations between the dense phases of individual droplets and the surrounding dilute phase is able to efficiently synchronise chemical clock reactions occurring within the droplets.

Feedback between F-actin organization and active stress govern criticality and energy localization in the cell cytoskeleton

Zachary Sun[1], Nathan Zimmerberg[2], Patrick Kelly[2], Carlos Floyd[3], Garegin Papoian[2], Michael Murrell[1]
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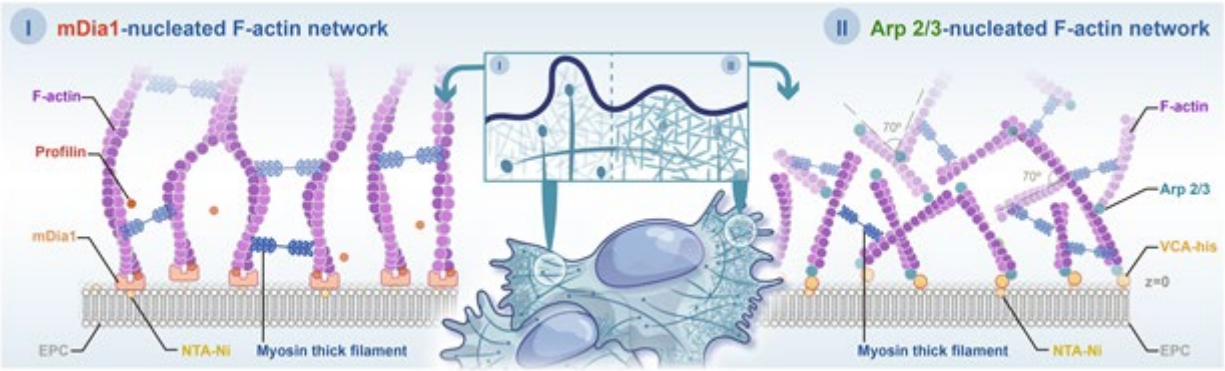
Early Career Satellite Event - Session 2 Flash Talks, March 24, 2025, 10:15-10:35

Self-Organized criticality (SOC) is characterized by cascading dissipative events observed across diverse natural phenomena, including earthquakes, avalanches, and landslides. During complex physical behaviors of the cell such as migration and division, the F-actin cytoskeleton undergoes dramatic changes in structure, organization, and dynamics, suggestive of large dissipative events. To drive these changes, non-equilibrium activities of molecular motors impart mechanical stresses upon the cytoskeleton. To explore criticality in the dynamics of the cytoskeleton, we reconstruct an experimental model of the cytoskeleton in vitro, composed of purified protein polymers (F-actin), motors (myosin II), and nucleating promoting factors (NPFs).

We alter the connectivity and nematic order of F-actin networks through varying NPF concentrations. In ordered (nematic) and poorly percolated networks, dissipative events are exponentially distributed. By contrast, in disordered (branched) and highly percolated networks, dissipative events are Levy-a distributed and exhibit 1/f noise, characteristic to SOC. The increased disorder attenuates the propagation of stress, distributes it amongst stiffer eigenmodes, and localizes it spatially, reminiscent of strong localization of electromagnetic waves in disordered lattices. Finally, the extent of disorder determines the magnitude of mechanical stress applied, as it influences the size and activity of myosin II filaments, demonstrating that SOC is regulated by chemical-mechanical feedback.



Designing modular DNA-protein nanostructures against hard-to-treat cancer targets

Dr Maria Zacharopoulou[1], Ms Zoya Cassidy, Ms Celeste Watson, Dr Joseph Chambers, Prof Laura Itzhaki, Dr Ioanna Mela
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Early Career Satellite Event - Session 3 Full Oral Talks, March 24, 2025, 11:15-12:15

We are building a modular platform of DNA nanostructures functionalised with peptide therapeutics to inhibit or degrade protein targets upregulated in cancer. A principal target for inhibition is the intracellular tankyrase protein (TNKS), a key player in the Wnt signalling pathway, whose dysregulation leads to carcinogenesis. In parallel, we target the extracellular protein EGFR (epidermal growth factor receptor), commonly overexpressed in solid cancers, for targeted degradation. EGFR degradation has been shown to slow down or stop cell division in cancer cells. DNA nanostructures act as a drug delivery vehicle for the active peptides. DNA nanostructures are easily synthesised by predictably folding a long single-stranded DNA scaffold with shorter complementary DNA strands (staples), and they are designable and biocompatible. They are also easily functionalised with fluorophores and active molecules (e.g., inhibitor peptides) to high degree of multivalency. We have successfully loaded DNA nanostructures of two different geometries with peptides using azide-DBCO click chemistry.

We show that HeLa cells and the Wnt-active cell line SW480 readily uptake non-functionalised DNA nanostructures, as well as DNA nanostructures that carry the tankyrase binding peptide. Using super-resolution microscopy, we show that the DNA nanostructures are primarily localised within the lysosomes, indicating that they are entering the cells through the endolysosomal pathway. Our current strategies are focused on functionalising the nanostructures with lysosomal escape peptides, to direct them to the desired site of action. We also show that the nanostructures carrying the EGFR-binding peptide, can bind and internalise the protein target for degradation in the endolysosomal system.

Transport Dynamics of Red Blood Cells in the Microcirculation

Dr. Qi Zhou[1], Prof. Miguel O. Bernabeu[2], Prof. Timm Krüger[3]
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Early Career Satellite Event - Session 4 Flash Talks, March 24, 2025, 12:15-12:35

Red blood cells (RBCs) are essential in delivering oxygen to tissues and organs across intricate networks of small vessels or narrow passages. Notwithstanding decades-long research, it remains elusive until recently how the transport dynamics of RBCs can mechanistically contribute to the pathophysiology of microcirculatory disorders, either through modulating the haematocrit distribution or wall shear stress patterning.

This talk will introduce the key findings of our recent modelling works based on hamster capillaries [1], mouse retina [2] and human placenta [3], respectively. Through combining cell-resolved mesoscopic simulations with imaging data of animal models or biological tissues, we have qualitatively and quantitatively investigated the RBC behaviour in a range of vascular/extravascular environments including capillary-level bifurcations, microvascular networks and porous media. Our studies provide potential mechanisms for hindered microcirculatory blood flow under pathological conditions where the RBC stiffness or vascular morphology have markedly altered.

[1] Rashidi, Simionato, Zhou et al. Biophysical Journal 122: 2561-2573, 2023.
[2] Zhou et al. Journal of the Royal Society Interface 18: 20210113, 2021.
[3] Zhou et al. Interface Focus 12:20220037, 2022.