SUN1: Keynote Session including guitar and music songs show

Time: Sunday, 20:00–21:30 Location: Auditorium

Keynote SUN1.1 20:00 Auditorium
Evolutionary tradeoffs and the geometry of biological design space — •Uri Alon — The Weizmann Institute of science Rehovot, Israel
Organisms, tissues and molecules that perform multiple tasks face a tradeoff: no design can be optimal at all tasks at once. We show that this fundamental tradeoff leads to simplex-like patterns in data on biological traits. The evolutionary tasks can be inferred based on the vertices of these simplexes.

MON1a: Session 1

Time: Monday, 8:45–10:30 Location: Auditorium

Welcome Address by Felix Ritort

Invited MON1a.1 9:00 Auditorium
Physical Biology or Biological Physics? — •Carlos Bustamante — University of California at Berkeley, CA, USA
In this presentation I will discuss what makes living matter unique and special. How its emergence through spontaneous and random self-assembly and organization, and its ability to evolve, determines its uniqueness; what Jacques Monod called 'Chance and Necessity.'

Invited MON1a.2 9:30 Auditorium
There is New Many-Body Physics in Neurobiology — •Theo Geisel — Max Planck Institute for Dynamics and Self-Organization — Bernstein Center for Computational Neuroscience Göttingen
The collective dynamics of cortical networks exhibits features that elude conventional many-body approaches: e.g. they interact at discrete times with significant interaction delays and not continuously in time. We devise new methods and address the question whether in biophysical models their dynamics is chaotic and whether this is compatible with reliable information processing.

Invited MON1a.3 10:00 Auditorium
Collective motion: New physics, inspired by animal groups, realized at cellular and subcellular level — •Hugues Chaté — CEA - Saclay, France, & Beijing Computational Science Research Center, China
The birth of active matter physics can be traced back to 1995 when Vicsek et al. proposed a minimal model for collective motion. Such models are not realistic but they reveal qualitatively new physics. In principle, their emergent properties are generic and should thus be observed in real situations. In practice, this is often a different, richer story...

10:30–11:00: Coffee Break

MON1b: Session 1 continued

Time: Monday, 11:00–12:30 Location: Auditorium

Invited MON1b.1 11:00 Auditorium
Emergent, self-assembled structures and pattern formation in synthetic and biological colonies — •Ignacio Pagonabarraga — Department of Condensed Matter Physics, University of Barcelona, Barcelona, Spain
This presentation will address the potential that generic, mechanical models offer to address the generic mechanisms underlying analyze the development of emergent, self-assembled structures in intrinsically non-equilibrium systems. I will describe the impact that self-propulsion, chemical interactions and reproduction have in the collective behavior of cellular tissues, microorganism colonies and self-propelling colloidal suspensions.

Oral MON1b.2 11:30 Auditorium
Taming active materials: New insights into cell Physics? — Pau Guillamat, Jordi Ignés-Mullol, and •Francesc Sagués — Departament de Ciència de Materials i Química Física, and Institute of Nanoscience and Nanotechnology, Universitat de Barcelona
Living cells sense the mechanical features of their environment and adapt to it by actively remodeling their peripheral network of filamentary proteins known as cortical cytoskeleton. By mimicking this principle, we demonstrate an effective control strategy for a microtubule-based active nematic material in contact with a passive thermotropic liquid crystal.

Oral MON1b.3 11:50 Auditorium
Still and rotating myosin clusters determine cytokinetic ring constriction — Viktoria Wollrab[1,2,3,4,5,6], Raghavan Thiagarajan[1,2,3,4,5], Anne Wald[6], •Karsten Kruse[6], and Daniel Riveline[1,2,3,4,5] — [1]Laboratory of Cell Physics ISIS/IGBMC, CNRS and University of Strasbourg, Strasbourg, France — [2]Institut de Génétique et de Biologie Moléculaire et Cellulaire, Illkirch, France — [3]Centre National de la Recherche Scientifique, UMR7104, Illkirch, France — [4]Institut National de la Santé et de la Recherche Médicale, U964, Illkirch, France — [5]Université de Strasbourg, Illkirch, France — [6]Theoretical Physics, Saarland University, Saarbrücken, Germany
We observed cytokinetic rings in a single focal plane during complete constriction. Myosin formed clusters that were still in mammalian cells, but rotated in fission yeast. We propose a common mechanism for self-organization of these patterns. Our analysis suggests different roles for cytokinetic rings in mammalian and yeast cells.

Oral MON1b.4 12:10 Auditorium
A complex interaction between actin and microtubules regulate cellular self-organization — Maik Drechsler and •Isabel M Palacios — University of Cambridge, Cambridge, UK
Little is known about how actin and microtubules cooperate to regulate cellular organization at the mesoscale level. We study the physical properties of this cytoskeletal interplay in oocytes, a powerful biophysical system, where a novel cytoplasmic F-actin mesh regulates the biophysical properties of microtubule-dependent ooplasmic flows, which impact on self-organization.

MON2a: Session 2

Time: Monday, 14:00–15:30 Location: Auditorium

Invited MON2a.1 14:00 Auditorium
From pattern formation of cell-division proteins in shaped bacteria towards bottom up assembly of a synthetic divisome — •Cees Dekker — Kavli Institute of Nanoscience, Delft University of Technology, The Netherlands
no abstract

Invited MON2a.2 14:30 Auditorium
Evolution of genomes and gene regulation: Looking for natural selection between the laws of physics and biological data — •Erik van Nimwegen — University of Basel, Switzerland
In this talk I want to discuss my views on the reasons for this disconnect between physics, evolutionary theory, and experimental observations, the challenges in addressing this disconnect, and some of the simple phenomenological approaches that mine and other groups are taking in trying to address these challenges.

Invited MON2a.3 15:00 Auditorium
New physics from evolution ? — •Olivier Rivoire — CIRB, Collège de France, Paris, France
Living matter evolves by natural selection. Does it imply specific physical properties? I'll present a general mathematical framework to study the implications of evolution by natural selection independently of any physical implementation and then discuss the case of one of the most elementary forms of living matter, proteins.

15:30–16:00: Coffee Break

MON2b: Session 2 continued

Time: Monday, 16:00–17:10 Location: Auditorium

Invited MON2b.1 16:00 Auditorium
What biology, more particularly evolution, has to say about the physics of DNA? — •Ivan Junier — TIMC-IMAG, Grenoble, France
Can evolutionary studies of transcriptional regulation unravel novel, unexploited aspects of the physics of DNA? With this question in mind, I will discuss the unsolved problem of the engineering of transcriptional regulatory networks, which was raised more than 50 years ago by François Jacob and Jacques Monod.

Oral MON2b.2 16:30 Auditorium
Physical model of the genotype-to-phenotype map of proteins: Mechanical origins of dimensional reduction and spectrum of evolution — •Tsvi Tlusty[1,2,3], Albert Libchaber[4], and Jean-Pierre Eckmann[5,6] — [1]Center for Soft and Living Matter, Institute for Basic Science, Korea. — [2]Department of Physics, UNIST, Ulsan, Korea. — [3]Institute for Advanced Study, Princeton, NJ. — [4]Center for Physics and Biology, Rockefeller University, New York. — [5]Départ. Physique Théorique, Université de Genève, Switzerland. — [6]Section de Mathématiques, Université de Genève, Switzerland.
We report on a physical model of the genotype-to-phenotype map. By treating protein as learning amorphous matter, the model reveals hallmarks of protein evolution: projection of the high-dimensional sequence space onto a low-dimensional space of mechanical modes and spectral correspondence between floppy mechanical modes and sequence correlation ripples.

Oral MON2b.3 16:50 Auditorium
Information Management in DNA replication — •J. Ricardo Arias-Gonzalez — Instituto Madrileño de Estudios Avanzados en Nanociencia, C/Faraday 9, Cantoblanco, 28049 Madrid, Spain
We develop an information theory framework to describe fidelity in DNA replication. We ab initio derive measured error rates in the real, non-equilibrium process and explain how proofreading increases fidelity by a typical 100-fold. We reveal that the energy required to increase fidelity is ≈1 kT/nucleotide per order of magnitude.

17:15–19:15: Monday Poster Session

20:00–22:00: Conference Dinner

TUE1a: Session 3

Time: Tuesday, 9:00–10:30 Location: Auditorium

Invited TUE1a.1 9:00 Auditorium
Phase transitions and the principle of detailed balance in living systems — •Fred MacKintosh — Departments of Chemical & Biomolecular Engineering, Chemistry, Physics & Astronomy, and Center for Theoretical Biophysics, Rice University, Houston, TX USA
The mechanics of cells and tissues are largely governed by scaffolds of filamentous proteins that make up the cytoskeleton, as well as extracellular matrices. We will present recent theoretical predictions and experimental evidence for mechanical phase transitions in in both synthetic and biopolymer networks. We will also discuss violations of detailed balance at the meso-scale of whole cells.

Invited TUE1a.2 9:30 Auditorium
Self-driven phase transitions in living matter — •Joshua Shaevitz — Departments of Physics and Genomics, Princeton University, Princeton, NJ, USA
Moving bacteria can collectively form spatial patterns to gain specific benefits in different environments. While this can often involve complex signaling chemistry, I will discuss how the soil-dwelling bacterium Myxococcus xanthus takes advantage of the physics of active matter to form complex patterns without the need for signaling between cells.

Invited TUE1a.3 10:00 Auditorium
Chaperones turn the energy of ATP into an enhanced non-equilibrium stability of native proteins. — •Paolo De Los Rios[1], Pierre Goloubinoff[2], Alberto Sassi[1], and Alessandro Barducci[3] — [1]Institute of Physics, School of Basic Sciences and Institute of Bioengineering, School of Life Sciences, EPFL, Lausanne, Switzerland — [2]Department of Plant Physiology and Pathology, Université de Lausanne, Lausanne, Switzerland — [3]Centre de Biochimie Structurale, Montpellier, France
Chaperones assist the correct folding of other proteins in the cell. They depend on ATP hydrolysis for their function and here we show, through experiments and theory, that energy consumption drives the system in a non-equilibrium steady-state where the folded state of proteins is more populated than it would be at thermodynamic equilibrium.

10:30–11:00: Coffee Break

TUE1b: Session 3 continued

Time: Tuesday, 11:00–12:30 Location: Auditorium

Invited TUE1b.1 11:00 Auditorium
Thermodynamic uncertainty relation for biomolecular processes — •Udo Seifert — University Stuttgart, Stuttgart, Germany
Essentially all biomolecular processes require the input of free energy. Thermal fluctuations necessarily imply that the outcome of such a process comes with some dispersion, i.e. uncertainty. Using the tools of stochastic thermodynamics, we have recently derived a universal relation showing that the product of thermodynamic cost and uncertainty is bounded by 2 k_B T.

Discussion

TUE2a: Session 4

Time: Tuesday, 14:00–15:40 Location: Auditorium

Invited TUE2a.1 14:00 Auditorium
The neuro-neuronal synapse a strange biological object for physicists — •Antoine Triller — IBENS Institut de Biologie de l'École Normale Supérieure, Paris, France
abstract missing

Invited TUE2a.2 14:30 Auditorium
Do Quantum Phenomena Play a Role in Photosynthesis ? Tracking Light-Harvesting on the nm and fs Scale — •Niek F. van Hulst — ICFO – the Institute of Photonic Sciences, Castelldefels, Barcelona; ICREA – Institució Catalana de Recerca i Estudis Avançats, Barcelona
Quantum coherences are observed in energy transfer of photosynthetic complexes, hinting to a role of deep physics in light harvesting. Does nature exploit quantum concepts? Do coherences help to find an optimal path for efficient transfer What is the spatial extent in a real network? Advances and ideas will be discussed.

Oral TUE2a.3 15:00 Auditorium
Conversion of an Ultrafast Downhill Folding Protein into a Slow Two-State Folder by Mechanical Force — Jörg Schönfelder[1], Victor Muñoz [2], and •Raul Perez Jimenez[1,3] — [1]CIC nanoGUNE, Av. Tolosa Hiribidea 76 , E-20018 San Sebastián, Spain — [2]University of California, Merced, California 95343, USA — [3]IKERBASQUE, Basque Foundation for Science, 48013, Bilbao, Spain
This investigation shows that a protein can switch its unfolding behaviour from a downhill to a two state scenario by using mechanical force. Our findings reveal the slowing down of the folding rate of a fast folding protein as theoretically predicted by using the Bell Model as a first approach.

Oral TUE2a.4 15:20 Auditorium
Intrinsically disordered proteins. Function out of chaos? — •Miquel Pons, Miguel Arbesú, and Anabel-Lise Le Roux — Biomolecular NMR group. Department of Inorganic and Organic Chemistry. University of Barcelona. Spain
Two thirds of the eukaryotic proteins have long disordered regions. Disordered proteins challenge the classical structure-function paradigm similarly as software-based access systems changed the classical lock and key. How function-enabling information is encoded in the sequence of unstructured proteins is still an open question in the physics-biology interface.

15:40–16:00: Coffee Break

TUE2b: Session 4 continued

Time: Tuesday, 16:00–17:20 Location: Auditorium

Invited TUE2b.1 16:00 Auditorium
A single-molecule view on intracellular transport in C. elegans chemosensory cilia — •Erwin Peterman — Department of Physics and Astronomy, and LaserLaB Amsterdam, Vrije Universiteit Amsterdam, Amsterdam, The Netherlands
In my contribution, I will discuss how we use single-molecule fluorescence microscopy to unravel the dynamics and cooperation of motor proteins in intracellular transport in living, multicellular organisms.

Invited TUE2b.2 16:30 Auditorium
The role of spatiotemporal compartmentalization on integrin activation and cell migration in the immune system — Alberto Sosa-Costa[1], Izabela Piechocka[1], Carlo Manzo[1], and •Maria Garcia-Parajo[1,2] — [1]ICFO- Institute of Photonic Sciences, The Barcelona Institute of Science and Technology, 08860 Castelldefels (Barcelona), Spain — [2]ICREA, Pg. Lluís Companys 23, 08010 Barcelona, Spain
Combining a palette of biophysical tools we investigate the role of spatiotemporal organization on integrin activation and immune-cell migration. We find that tight regulation of integrin mobility and spatial surface arrangement brought about by biochemical and/or mechanical stimuli is crucial to modulate integrin adhesiveness in cells of the immune system.

Oral TUE2b.3 17:00 Auditorium
Nonergodic subdiffusion and heterogeneous interactions in living cell membranes — •Carlo Manzo — ICFO-Institut de Ciències Fotòniques, The Barcelona Institute of Science and Technology, E-08860 Castelldefels (Barcelona), Spain — Universitat de Vic, Universitat Central de Catalunya (UVic-UCC), E-08500 Vic, Spain
We describe single particle tracking experiments showing anomalous nonergodic diffusion occurring for receptor motion in living cell membranes. We discuss the biological implications of this exotic behavior as well as how it can be described through microscopic models of disordered transport, arising from heterogeneous interactions among diffusing partners.

17:25–19:25: Tuesday Poster Session

WED1a: Session 5

Time: Wednesday, 9:00–10:30 Location: Auditorium

Invited WED1a.1 9:00 Auditorium
Physics for Biology or Biology for Physicists? — •Jacques Prost — Institut Curie, Paris, France
I will give a few examples of physical constructions useful to Cell and Tissue Biology, yielding new physical concepts, such as anomalous density fluctuations, low Reynolds number turbulence, homeostatic pressure, or soft condensed matter without compression modulus.

Invited WED1a.2 9:30 Auditorium
Physics of Actomyosin-based Morphogenetic Processes — •Stephan W. Grill — Biotechnology Center, Technical University of Dresden, Germany
I will discuss physical activities of the actomyosin cytoskeleton that emerge on the mesoscale and that drive cell-scale morphogenetic processes, for example the generation of active tension and active torque. A particular focus will be the coupling of biochemical regulation with active mechanical processes for generating spatiotemporal patterns and form.

Invited WED1a.3 10:00 Auditorium
The physical basis of coordinated tissue spreading in zebrafish gastrulation — Hitoshi Morita and •Carl-Philipp Heisenberg — Institute of Science and Technology Austria, Klosterneuburg, Austria
abstract missing

10:30–11:00: Coffee Break

WED1b: Session 5 continued

Time: Wednesday, 11:00–12:10 Location: Auditorium

Invited WED1b.1 11:00 Auditorium
Mechanical guidance of collective cell migration and invasion — •Xavier Trepat — ICREA - Institute for Bioengineering of Catalonia (IBEC), Barcelona, Spain
no abstract

Oral WED1b.2 11:30 Auditorium
Multicellular regulation of entropy, spatial order, and information — •Hyun Youk — Kavli Institute of Nanoscience, Delft University of Technology, Delft, the Netherlands
Understanding multicellular behaviours emerging from myriad cellular interactions is challenging because we lack proper quantitative metrics. To address this, we engineered yeasts that secrete molecules to extracellularly store and collectively remember information and developed a theoretical framework that introduces cellular entropy and Hamiltonian to understand these cells forming spatial patterns.

Oral WED1b.3 11:50 Auditorium
Physical principles of spindle self-organization — Franziska Decker[1,2], David Oriola[1,2], Elisa Rieckhoff [1,2], and •Jan Brugues[1,2] — [1]Max Planck Institute for the Physics of Complex Systems, Dresden, Germany — [2]Max Planck Institute of the Molecular Cell Biology and Genetics, Dresden, Germany
The cytoskeleton forms subcellular structures that are maintained by continuous fluxes of molecules and energy. These systems are active materials that behave drastically differently from matter at equilibrium. We combine theory and experiments to construct an active liquid-crystal theory for spindles—the cytoskeletal structure that segregates chromosomes during cell division

12:10–12:30: Poster Prize Event

WED2: Second Keynote Talk

Time: Wednesday, 12:30–13:30 Location: Auditorium

Keynote Talk

P: Poster Session

Time: Monday and Tuesday, 17:15–19:15 Location: Auditorium foyer

Poster P.1 17:15 Auditorium foyer
Dynamical compensation in physiological circuits — •Omer Karin[1], Avital Swisa[2], Benjamin Glaser[3], Yuval Dor[2], and Uri Alon[1] — [1]Department of Molecular Cell Biology, Weizmann Institute of Science, Rehovot, Israel — [2]Department of Developmental Biology and Cancer Research and Molecular Biology, The Institute for Medical Research Israel-Canada, The Hebrew University-Hadassah Medical School, Jerusalem, Israel. — [3]Endocrinology and Metabolism Service, Department of Internal Medicine, Hadassah-Hebrew University Medical Center, Jerusalem, Israel
Physiological circuits must keep their output dynamics precise despite wide variation in circuit parameters. We present a design principle for this robustness, find that it explains experimental observations on glucose homeostasis, and show that it may apply to other physiological circuits.

Poster P.2 17:15 Auditorium foyer
Co-replicational organization of single-stranded DNA by the human mitochondrial SSB proteins — •Fernando Cerrón[1,2], José A. Morín[3], Javier Jarillo[2], Elena Beltrán[2], Grzegorz L. Cieselki[4], Francisco J. Cao[2], Laurie S. Kaguni[4], and Borja Ibarra[1] — [1]Imdea Nanociencia, Faraday 9, Ciudad Universitaria de Cantoblanco, 28049, Madrid, Spain. — [2]Departamento de Física Atómica, Molecular y Nuclear, Universidad Complutense, 28040, Madrid, Spain — [3]Max Planck Institute of Molecular Cell Biology and Genetics, Pfotenhauerstrasse 108, 01307, Dresden, Germany. — [4]Department of Biochemistry and Molecular Biology and Center for Mitochondrial Science and Medicine, Michigan State University, East Lansing, MI, USA
The human mitochondrial single-stranded DNA binding protein binds single-stranded DNA with high affinity and defines the nucleoprotein substrate upon which DNA replication and repair processes must act. We used optical tweezers to measure the binding properties of the HmtSSB proteins to long ssDNA molecules and their elastic and energetic properties.

Poster P.3 17:15 Auditorium foyer

A force toolkit for topographical and mechanical characterization of soft biological samples — Tanja Neumann, Torsten Müller, •Benjamin L. Holmes, and Torsten Jähnke — JPK Instruments AG, Berlin, Germany

Cells represent highly complex biological systems operating and reacting not only by biochemical cues, but in many different ways, such as varying their physical properties. We present an enhancement of the atomic force microscopy technique in order to characterize the topography and mechanical properties of soft biological samples conveniently and to obtain high quality results.

Poster P.4 17:15 Auditorium foyer

Modelling random crawling, membrane deformation and biochemical patterns in amoeba — •Sergio Alonso[1] and Carsten Beta[2] — [1]Department of Physics, Universitat Politècnica de Catalunya, Barcelona, Spain — [2]Institute of Physics and Astronomy, University of Potsdam, Potsdam, Germany

We construct a mathematical model to study the interplay between spontaneous cell polarization and cellular locomotion. In particular we consider the motion of the amoeba Dictyostelium discoideum, which under starvation randomly moves seeking for food. We compare and fit the model to experimental data to obtain realistic deformations and velocities.

Poster P.5 17:15 Auditorium foyer

Probing the molecular origin of liquid properties in protein systems. A single molecule force spectroscopy approach. — •Jose A. Morin[1,2], Enrico D. Perini[2], Roman Renger[2], Avinash Patel[3], Anthony A. Hyman[3], and Stephan W. Grill[2,3] — [1]Max Plank Institute for the Physics of Complex Systems, Dresden, Germany — [2]Biotechnology Center (BIOTEC), Dresden Technical University, Dresden, Germany — [3]Max Plank Institute for Molecular Cell Biology and Genetics, Dresden, Germany

Liquid state in the cytosol provides the separation of matter in time and space required by cells. Using Optical Tweezers we measured the properties of a reduced and size-controlled droplet system. Preliminary results hints the effect of individual FUS monomers to the global state of a fiber-like state.

Poster P.6 17:15 Auditorium foyer

Double-stranded DNA and RNA under constant stretching forces: insights from molecular dynamics — •Alberto Marín-González[1], J. G. Vilhena[1,2], Rubén Pérez[2,3], and Fernando Moreno-Herrero[1] — [1]Department of Macromolecular Structures, Centro Nacional de Biotecnología, CSIC — [2]Departamento de Física Teórica de la Materia Condensada, Universidad Autónoma de Madrid — [3]IFIMAC-Condensed Matter Physics Center, Universidad Autónoma de Madrid

We use all-atom microsecond-long molecular dynamics to simulate the mechanical response of dsDNA and dsRNA subjected to stretching forces up to 20 pN. We determine all the elastic constants and explain three striking differences: the three-fold softer dsRNA stretching constant, the opposite twist-stretch coupling and its non-trivial force dependence.

Poster P.7 17:15 Auditorium foyer

Mechanics, thermodynamics, and kinetics of ligand binding to biopolymers — Javier Jarillo[1], Elena Beltrán-Heredia[1], José Morín[2], Juan P.G. Villaluenga[3], Borja Ibarra[2], and •Francisco J. Cao[1] — [1]Departamento de Física Atómica, Molecular y Nuclear, Facultad de Ciencias Físicas, Universidad Complutense de Madrid, Pza. de las Ciencias, 1, 28040 Madrid, Spain — [2]Instituto Madrileño de Estudios Avanzados en Nanociencia, 28049 Madrid, Spain — [3]Departamento de Física Aplicada I, Facultad de Ciencias Físicas, Universidad Complutense de Madrid, Pza. de las Ciencias, 1, 28040 Madrid, Spain

We propose a model to explain the mechanical, thermodynamic, and kinetic properties of the process of binding of small ligands to long biopolymers. This model provides a new method to estimate ligand coverage and ligand binding mode from experimental force extension curves of the ligand-polymer system.

Poster P.8 17:15 Auditorium foyer

The multi-scale importance of hubs in protein-protein interactions — •Gustavo R. Ferreira and Luciano da F. Costa — São Carlos Physics Institute of the University of São Paulo, São Carlos, Brazil

It has been observed in PPI networks that hubs tend to be essential to the organism. While Barabasi-Albert networks are indeed susceptible to hub-targeted attacks, in biological networks the importance of a node is related to other properties. Here, we investigate the essentiality of hubs across local and global scales.

Poster P.9 17:15 Auditorium foyer

A hybrid framework for simulating the dynamics of epithelial monolayers — Ismael Gonzalez-Valverde and •Jose Manuel García-Aznar — Aragón Institute of Engineering Research (I3A), Universidad de Zaragoza, Zaragoza, Spain

We present a hybrid computational framework to simulate the dynamics of epithelial monolayers. The cells are modelled using an off-lattice agent-based method that keeps the information of each cell. Otherwise, we model the passive mechanical behavior of the tissue using a continuum material model, which approximates its mechanical properties.

Poster P.10 17:15 Auditorium foyer

Fluidization and active thinning by molecular kinetics in active gels — •Ricard Alert, David Oriola, and Jaume Casademunt — Departament de Física de la Matèria Condensada, Universitat de Barcelona, Barcelona, Spain

We derive the constitutive equations of an active polar gel from a model for the stochastic dynamics of elastic molecules that link polar elements. We thus give explicit expressions for the transport coefficients of active gels in terms of molecular properties, including nonlinear contributions on the departure from detailed balance.

Poster P.11 17:15 Auditorium foyer

Single-molecule level study of the mechanism of human mitochondrial DNA replication — •Kateryna Lemishko[1,2], Borja Ibarra[1], and Laurie Kaguni[3] — [1]IMDEA-Nanoscience, Madrid, Spain — [2]Spanish National Center for Biotechnology (CSIC), Madrid, Spain — [3]3. Department of Biochemistry and Molecular Biology, Michigan State University, East Lansing, Michigan

In this work, we aimed to develop hairpin-based DNA systems that would allow us to detect and characterize at the single-molecule level activities of the proteins participating in human mitochondrial DNA replication.

Poster P.12 17:15 Auditorium foyer

Actively driven acto-myosin networks and their effect on the organization of multi-component lipid membranes — •Darius V. Köster[1], Jonathon Ditlev[2], Xiaolei Su[3], Anthony Vega[2], Amit Das[1], Kabir Husain[1], Khaloud Jaqaman[2], Michael Rosen[2], Ron Vale[3], Madan Rao[1], and Satyajit Mayor[1,4] — [1]National Centre for Biological Sciences, Bangalore, India — [2]University of Texas Southwestern Medical Centre, Dallas, USA — [3]University of California San Francisco, San Francisco, USA — [4]Institute for Stem Cell Biology and Regenerative Medicine, Bangalore, India

At the surface of a living cell, the plasma membrane and the cell cortex are highly intertwined. Using simplified in vitro reconstitutions of acto-myosin networks linked to multi-component lipid membranes and comparison with Monte Carlo simulations, we aim to understand experimentally and theoretically the special dynamics of this active composite.

Poster P.13 17:15 Auditorium foyer

A phase diagram of cell-like particles with contact inhibition of locomotion — •Bart Smeets[1], Ricard Alert[2], Jiří Pešek[1], Ignacio Pagonabarraga[2], Herman Ramon[1], and Romaric Vincent[3] — [1]Division of Mechatronics, Biostatistics and Sensors (MeBioS) Kasteelpark Arenberg 30 - box 2456 3001 Leuven, Belgium — [2]Departament de Fisica de la Materia Condensada, Facultat de Fiusica, Universitat de Barcelona, 08028 Barcelona, Spain — [3]CEA, LETI, MINATEC, 17 rue des Martyrs, 38054 Grenoble cedex 9, France

By modeling cells as 2D self-propelled particles governed by cell-cell adhesion and contact inhibition of locomotion, we built a phase diagram which captures several multicellular organizations, including self-organized collective migration, cell extrusion and cell dispersion. Based on experimental observations, we link these phases to mesenchymal, epithelial and 3D tissue phenotypes.

Poster P.14 17:15 Auditorium foyer

Towards Rolling Circle Replication at the Single-Molecule Level — •Cesar L. Pastrana[1], Carolina Carrasco[1], Parvez Akhtar[2], Sanford H. Leuba [3], Saleem A. Khan[2], and Fernando Moreno-Herrero[1] — [1]Department of Macromolecular Structures, Centro Nacional de Biotecnología, CSIC, Darwin 3, 28049 Cantoblanco, Madrid, Spain. — [2]Department of Microbiology and Molecular Genetics, University of Pittsburgh School of Medicine, Pittsburgh, PA 15219, USA — [3]Department of Cell Biology, University of Pittsburgh School of Medicine, Pittsburgh, PA 15213, USA.

We have measured the nicking activity of the replicator-initiator protein RepC, finding it force- and twist-dependent and relying on the extrusion of a cruciform structure. Furthermore, we have characterized the unwinding rate of PcrA, a helicase loaded by RepC to the nicking site.

Poster P.15 17:15 Auditorium foyer

Computational simulation of mesenchymal cell migration in 3D — •Clara Valero and José Manuel García-Aznar — M2BE (I3A), University of Zaragoza, Spain

Mesenchymal cell migration is a process guided by cell protrusions. They exert traction forces on the surrounding matrix depending on the physical and chemical microenvironmental conditions. In this work we study computationally the effect of the substrate mechanical properties and chemotactic factors during migration.

Poster P.16 17:15 Auditorium foyer

Non-aggregated cells can favor the persistence of multicellular fruiting bodies against destructive social cheaters in Dictyostelium discoideum. — •Ricardo Martinez-Garcia and Corina E. Tarnita — Department of Ecology and Evolutionary Biology, Princeton University. 08544 Princeton NJ, USA.

In *D. discoideum* starvation triggers population partitioning between non-aggregators and aggregators, which form possibly non-clonal fruiting bodies with division of labor between reproductive spores and dead stalk cells. Selection should favor parasites that only produce spores. Non-aggregators, however, can stabilize the multicellular complex against free-riders due to cooperative strains diversity.

Poster P.17 17:15 Auditorium foyer

Single Molecule Localisation and Discrimination of DNA-Protein Complexes with a Nanocapillary — •Sebastian Davis — EPFL, Lausanne, Switzerland

We localise DNA-bound proteins as well discriminate them through controlled translocations through a nanocapillary using optical tweezers. Localisation is based on peak detection. Discrimination is obtained through two separate methods. The first uses conductance drops to compare protein size, while the second uses the Jarzynski equality to compare effective charge.

Poster P.18 17:15 Auditorium foyer

Simulations of thin semi-flexible polymers — •Jiří Pešek[1], Pieter Baerts[2], Bart Smeets[1], Christian Maes[2], and Herman Ramon[1] — [1]Division of Mechatronics, Biostatistics and Sensors (MeBioS), KU Leuven, Leuven, Belgium — [2]Institute for Theoretical Physics, KU Leuven, Leuven, Belgium

We present an alternative approach for simulations of thin semi-flexible polymers. In contrast with the usual approaches, we use deformable cylindrical segments as basic units of the polymer. The model allows the simulation of tension propagation and elasticity properties. We describe a new cooperative regime in the relaxation of the polymer from its fully elongated configuration.

Poster P.19 17:15 Auditorium foyer

Membrane crowding and complexity: interplay between protein-lipid interactions, clustering and diffusion. — •Anna Duncan[1], Heidi Kolds$\emptyset$[1,2], Matthieu Chavent[1], Tyler Reddy[1], Jean Hélie[1], and Mark Sansom[1] — [1]Department of Biochemistry, University of Oxford, United Kingdom — [2]D. E. Shaw Research, 120 W45th Street, New York, NY 10036

To investigate the molecular mechanisms underlying the effect of protein crowding and lipid complexity in biomembranes, large-scale coarse-grained molecular dynamics simulations are performed of potassium channels embedded in a mammalian cell membrane. Thus, we explore the use of molecular dynamics simulations as a computational microscope to complement other techniques.

Poster P.20 17:15 Auditorium foyer

Nanomechanical phenotypes in hypertrophic cardiomyopathy caused by missense mutations in cardiac myosin-binding protein C — •Carmen Suay-Corredera[1], Elías Herrero-Galán[1], Diana Velázquez-Carreras[1], Iñigo Urrutia-Irazabal[1], Diego García-Giustiniani[2], Javier Delgado[3], Luis Serrano[3], Pablo García-Pavía[4], Lorenzo Monserrat[2], and Jorge Alegre-Cebollada[1] — [1]Spanish National Centre for Cardiovascular Research Carlos III (CNIC), Madrid, Spain — [2]Health in Code, A Coruña, Spain — [3]EMBL/CRG Systems Biology Research Unit, Centre for Genomic Regulation (CRG), Barcelona, Spain — [4]Puerta de Hierro Hospital, Majadahonda (Madrid), Spain

Hypertrophic Cardiomyopathy (HCM) is the most common inherited cardiac muscle disease and mutations in cardiac myosin-binding protein C, cMyBP-C, account for nearly 50% of its genetic basis. We support the idea that single-amino-acid changes in cMyBP-C could affect its mechanical properties, impairing its braking function and thus triggering HCM.

Poster P.21 17:15 Auditorium foyer

From shape behavior of vesicles to plausible mechanism for the origin of life: on the development of concepts — •Saša Svetina — Institute of Biophysics, Faculty of Medicine, University of Ljubljana, and Jožef Stefan Institute, Ljubljana, Slovenia

On the basis of existing knowledge about vesicle shape behavior we studied vesicle self-reproduction and have shown that it can occur under the condition that relates vesicle structural parameters and the parameters of the environment. By thus involving growth, division and selectivity, this process can be considered as a possible origin of cellular life.

Poster P.22 17:15 Auditorium foyer

Sample heating in optical tweezers — •Frederic Català[1], Ferran Marsà[2], Mario Montes-Usategui[1], Arnau Farré[2], and Estela Martín-Badosa[1] — [1]Optical Trapping Lab – Grup de Biofotònica, Departament de Física Aplicada i Òptica, Universitat de Barcelona, Martí i Franquès 1, Barcelona 08028, Spain — [2]Impetux Optics S. L., Trias i Giró 15 1-5, Barcelona 08034, Spain

The high concentration of laser light necessary to create an optical trap produces notable heating due to IR absorption. From direct measurements of water viscosity through Stokes drag experiments, we determine the local temperature rise in different experimental conditions and find that, in some cases, it can reach 4ºC in a 100mW trap.

Poster P.23 17:15 Auditorium foyer

Protein-based biomaterials mimicking the passive elastic properties of striated muscle tissue — •Carla Huerta-López, Diana Velázquez-Carreras, Elías Herrero-Galán, and Jorge Alegre-Cebollada — Spanish National Centre for Cardiovascular Research (CNIC). Madrid. Spain

Striated muscle function depends on its single-molecule level properties. There are no models that predict macroscopic muscle behaviour from single-molecule behaviour. Via a photocatalytic reaction that links together titin polyproteins we want to produce hydrogels that recapitulate muscle properties. This allows the examination of correlations between single-molecule and mesoscopic level.

Poster P.24 17:15 Auditorium foyer

An Adaptive Gravity Model for Interactions in Insect Swarms — •Dan Gorbonos[1], Reuven Ianconescu[1,2], James G. Puckett[3], Rui Ni[4], Nicholas T. Ouellette[5], and Nir Gov[1] — [1]Dept. of Chemical Physics, Weizmann Institute of Science, Rehovot, Israel — [2]Shenkar College of Engineering and Design, Ramat-Gan, Israel — [3]Department of Physics, Gettysburg College, USA — [4]Department of Mechanical and Nuclear Engineering, The Pennsylvania State University, USA — [5]Department of Civil and Environmental Engineering, Stanford University, Stanford,, USA

We consider mating swarms of midges, which are thought to interact primarily via long-range acoustic stimuli. We exploit the similarity between the decay of acoustic and gravitational sources and the adaptive nature of the midges' acoustic sensing to build a model for swarm behavior.

Poster P.25 17:15 Auditorium foyer

Self-assembly of protocells in a temperature gradient — Juan Iglesias-Artola, Dora Tang, and •Moritz Kreysing — Max Planck Institute of Molecular Cell Biology and Genetics

Threatened by the 2nd law, it remains unclear how the first living cells assembled and became sustainable. Open out-of-equlibrium sys-

tems offer a feasible solution: we experimentally show driven protocell assembly based on the co-accumulation of RNA and peptides in temperature gradients. We theoretically discuss their chances to start life again.

Poster P.26 17:15 Auditorium foyer

Understanding the light harvesting process in plants: good vibrations in photosynthesis — •Juan Manuel Artes Vivancos, Yusaku Hontani, John Kennis, and Rienk van Grondelle — Vrije Universiteit Amsterdam, Amsterdam, Netherlands

Understanding the mechanisms that modulate photosynthesis is a challenge in biophysics, and obtaining that knowledge could help for the design of highly-efficient light-conversion devices. We used fs-Raman spectroscopy to study trimeric Light-Harvesting Complexes from higher plants, obtaining the dynamics of the vibrations of the pigments with femtoseconds temporal resolution.

Poster P.27 17:15 Auditorium foyer

Coevolutionary Analysis of the Hsp70 chaperone machinery — •Duccio Malinverni[1], Alessandro Barducci[2,3], Alfredo Jost-Lopez[4], Gerhard Hummer[4], and Paolo De Los Rios[1,5] — [1]Laboratoire de Biophysique Statistique, Faculté de Sciences de Base, École Polytechnique Fédérale de Lausanne - EPFL, 1015 Lausanne, Switzerland — [2]Inserm, U1054, Montpellier, France — [3]Université de Montpellier, CNRS, UMR 5048, Centre de Biochimie Structurale, Montpellier, France — [4]Institut für Biophysik, Johan Wolfgang Goethe Universität Frankfurt, 60438 Frankfurt am Main, Germany — [5]Institute of Bioengineering, School of Life Sciences, École Polytechnique Fédérale de Lausanne - EPFL, 1015 Lausanne, Switzerland

Coevolutionary analysis of the Hsp70 chaperone machinery reveals the existence of an evolutionary conserved homo-dimeric arrangement. Extending the analysis to protein complex predictions, we show how combining coevolutionary analysis with simulations can be used to build a structural model of the complex formed by Hsp70 with its cochaperone Hsp40.

Poster P.28 17:15 Auditorium foyer

Molecular Chaperones as Non-equilibrium Machines — •Alberto Sassi[1], Paolo De Los Rios[1], and Alessandro Barducci[2] — [1]École Polytechnique Fédérale de Lausanne, Lausanne, Switzerland — [2]Centre de Biochimie Structurale CNRS UMR5048 - INSERM U1054 Montpellier

We implemented a kinetic model for the description of a system with substrate proteins and chaperones Hsp70. In particular, we studied the role of the energy consumption in the determination of the binding affinity between the chaperones and the client protein.

Poster P.29 17:15 Auditorium foyer

A Surface to Twist the FtsZ Filament: A Good Strategy to Generate Force — Ileana Marquez[1], Paulino Gomez-Puertas[2], Pedro Tarazona[3], and •Marisela Velez[1] — [1]Instituto de Catálisis y Petroleoquímica, CSIC — [2]Centro de Biología Molecular Severo Ochoa (CSIC-UAM), C/ Nicolás Cabrera, 1, Cantoblanco, 28049 Madrid, Spain — [3]Dpto. Física Teórica de la Materia Condensada. Universidad Autónoma de Madrid. Cantoblanco. Madrid 28049, Spain

Single molecule analysis of the dynamics and structure of FtsZ filaments on lipid surfaces with different attachments, combined with theoretical simulations, highlight the overlooked importance of monomer flexibility and filament twist. Orientation and flexibility of monomers and their attachment to the surface can modulate the force exerted on the membrane.

Poster P.30 17:15 Auditorium foyer

Filament flexibility enhances power transduction of F-actin bundles — Alessia Perilli[1], Carlo Pierleoni[2], Giovanni Ciccotti[1,3], and •Jean Paul Ryckaert[4] — [1]Physics Department, Sapienza University of Rome, P. A. Moro 5, 00185 Rome, Italy — [2]Department of Physical and Chemical Sciences, University of L'Aquila, and CNISM UdR L'Aquila, Via Vetoio 10, 67100 L'Aquila, Italy — [3]School of Physics, University College Dublin (UCD), Belfield, Dublin 4, Ireland — [4]Physics Dept., Université Libre de Bruxelles (ULB), Campus Plaine, CP 223, B-1050 Brussels, Belgium

With a stochastic dynamical model of a living WLC we determine the force-velocity relation of a bundle of active actin filaments. The transduction power (chemical into mechanical) increases (in a suitable range) with bundle length thanks to the improved load sharing capacities of flexible filaments touching the wall.

Poster P.31 17:15 Auditorium foyer

Stability analysis of a simple Ca^{2+} regulation model in muscle cells — Ricardo T. Paéz-Hernández[1], •Norma Sánchez-Salas[2], and Moisés Santillán[3] — [1]Área de Física de Procesos Irreversibles, Departamento de Ciencias Básicas, Universidad Autónoma Metropolitana Azcapotzalco, Ciudad de México, México — [2]Escuela Superior de Física y Matemáticas, Instituto Politécnico Nacional, Ciudad de México, México — [3]Unidad Monterrey, Centro de Investigación y de Estudios Avanzados del IPN, Apodaca NL, México

This work presents a local stability analysis for a simplified flow of calcium between the cytoplasm and the sarcoplasmic reticulum in a smooth muscle cell model. Two schemes, the so called SK and KonD schemes are analyzed. Using experimental data to estimate some of the parameters involved in the model.

Poster P.32 17:15 Auditorium foyer

New insight into the role of C–terminal tails in intracellular transport along microtubules — •Dalibor Sekulic, Natasa Samardzic, Ana Joza, and Miljko Sataric — University of Novi Sad, Faculty of Technical Sciences

We have established a nonlinear biophysical model which offers a new insight into the mechano–electrical kink–wave propagation mediated by C–terminal tails. This original idea offers the plausible way to feel the gap in understanding the signalling mechanism responsible for the tuning of cellular traffic performed by motor proteins.

Poster P.33 17:15 Auditorium foyer

Modelling enzymatic reaction-diffusion processes in in vivo-like systems — •Pablo M. Blanco[1], Sergio Madurga[1], Josep Lluís Garcés[2], Marta Cascante[3], and Francesc Mas[1] — [1]Department of Material Science and Physical Chemistry and Research Institute of Theoretical and Computational Chemistry (IQTCUB) of the Barcelona University, Barcelona, Spain — [2]Department of Chemistry, University of Lleida (UdL), Lleida, Spain — [3]Department of Biochemistry and Molecular Biomedicine and Research Institute of Biomedicine (IBUB) of the Barcelona University, Barcelona, Spain

Biological media is a complex solution with a high concentration of macromolecules (macromolecular crowding) which have a large effect on reaction-diffusion biological processes. In this study, a new model for Dextran macromolecules is proposed to model computationally experimental studies of diffusion of proteins in crowded media. Furthermore, Hydrodynamic Interaction and excluded volume effects are studied in diffusion-controlled enzyme kinetics.

Poster P.34 17:15 Auditorium foyer

Mechanochemical modelling as an explorative tool to study dorsal closure — •Francesco Atzeni[1,2], Christof M. Aegerter[1,2], and Damian Brunner[2] — [1]Physics Institute, University of Zurich, Zurich, Switzerland — [2]Institute of Molecular Life Sciences, University of Zurich, Zurich, Switzerland

We present a computational model to explore dorsal closure. Therefore, we couple actomyosin network formation, active force generation, and shape change, building on the frameworks of continuum mechanics and reaction-diffusion equations. Our simulations reproduce dorsal closure and predict emergent behaviour that was previously thought to require control by signalling networks.

Poster P.35 17:15 Auditorium foyer

Active wetting of epithelial tissues — •Ricard Alert[1], Carlos Pérez-González[2], Carles Blanch-Mercader[3], Xavier Trepat[2], and Jaume Casademunt[1] — [1]Universitat de Barcelona, Barcelona, Spain — [2]Institute for Bioengineering of Catalonia, Barcelona, Spain — [3]Institut Curie, Paris, France

We study the transition between a cell monolayer and a spheroidal cell aggregate, which is analogous to the wetting transition of fluids. We develop and active polar fluid model of the monolayer that predicts a critical size for the tissue wetting transition, which is verified in experiments.

Poster P.36 17:15 Auditorium foyer

Gluten: a fluid or a solid? Insights from coarse-grained molecular dynamics simulations — •Łukasz Mioduszewski and Marek Cieplak — Institute of Physics, Polish Academy of Sciences, Al. Lotników 32/46, PL-02-668 Warsaw, Poland

Gluten is a protein component of wheat dough, responsible for its elasticity. It has both liquid and solid properties. Existing theories explain them by the role of hydrogen bonds and disulfide bridges. We use them in a novel coarse-grained model of gluten to recreate its viscoelasticity in computer simulations.

Poster P.37 17:15 Auditorium foyer

Single Molecule Force Spectroscopy Reveals Hidden Complexity in the Protein Unfolding Process for a Prototypical Two-State Folding Protein. — •Jörg Schönfelder[1], Raúl Pérez-Jiménez[1,2], and Victor Muñoz[3] — [1]CIC nanoGUNE, Av. Tolosa Hiribidea 76 , E-20018 San Sebastián, Spain — [2]IKERBASQUE, Basque Foundation for Science, 48013, Bilbao, Spain — [3]University of California, Merced, California 95343, USA

In this work we demonstrate that the small cold shock protein Csp unfolds via clearly distinguishable intermediates when pulling it from both ends by the application of a mechanical force. This finding is in stark contrast to the determined 2-state unfolding for Csp when using a chemical denaturant.

Poster P.38 17:15 Auditorium foyer

Pili-mediated dynamics of *Neisseria gonorrhoeae* microcolonies — •Wolfram Pönisch[1], Christoph A. Weber[2], Nicolas Biais[3], and Vasily Zaburdaev[1] — [1]Max Planck Institute for the Physics of Complex Systems, 01187 Dresden, Germany — [2]Paulson School of Engineering and Applied Sciences, Harvard University, Cambridge, MA 02138, USA — [3]Department of Biology, Brooklyn College, City University of New York, Brooklyn, New York 11210, USA

A crucial step of many bacterial infections is the pili-mediated formation of microcolonies. Type IV pili are thin and long polymers that grow out of the cells and generate attractive cell-cell forces. We present experimental and numerical data showing how pili-mediated forces shape the dynamics of *N. gonorrhoeae* microcolonies.

Poster P.39 17:15 Auditorium foyer

Structural changes of LTP1 isoforms at air-water interface — •Yani Zhao and Marek Cieplak — Institute of Physics, Polish Academy of Sciences, Al. Lotnikow 32/46, 02-668 Warsaw, Poland

LTP1 isoforms promote formation of foam in beer. A coarse-grained model is employed to understand what happens to the conformations of those proteins at air-water interface of a foam. The interface is represent by a phenomenologically added force that couples to the hydropathy indices of residues.

Poster P.40 17:15 Auditorium foyer

Development of a computational model of calcium signaling in cardiac cells at the submicron scale — •Miquel Marchena — Physics Department, Universitat Politècnica de Catalunya, Barcelona, Spain

We have developed a bidomain model of subcellular calcium concentration, in which the complex sarcoplasmic reticulum (SR) structure is considered through effective diffusion resulting from homogeneization. We have used this model to study the effect of heterogeneities in ryanodine receptor (RyR) distribution on the appearance of calcium waves and sparks.

Poster P.41 17:15 Auditorium foyer

Probing the torsional stiffness of dsDNA with magnetic torque tweezers — •Franziska Kriegel and Jan Lipfert — Department of Physics, Nanosystems Initiative Munich, and Center of NanoScience, LMU Munich, Amalienstr. 54, 80799 Munich

Mechanical properties play a crucial role for the genetic read-out or the processing of nucleic acids. Small deformations from the nucleic's equilibrium, can be described by the isotropic elastic rod model, including bending, stretching and twisting. We use multiplexed magnetic torque tweezers (mMTT) to study the torsional stiffness (Ceff) of dsDNA under varying forces, salt conditions and temperatures.

Poster P.42 17:15 Auditorium foyer

Self organization of ciliary activity and mucus transport in reconstituted human bronchial epithelium — •Annie Viallat[1], Kamel Khelloufi[1], Delphine Gras[2], and Pascal Chanez[2] — [1]Aix Marseille Univ, CNRS UMR 7325 — [2]Aix Marseille Univ, CNRS UMR 7333 Inserm UMR1067

Mucus is propelled along bronchial airways by the continuous coordinated beating of microscopic cilia located on ciliated epithelial cells. We find that ciliary activity self-organizes to generate local flow patterns at the epithelium surface. We relate mucus transport to hydrodynamic interactions and cilia beats and reveal active mechano-transductional effects.

Poster P.43 17:15 Auditorium foyer

Macroscale Brownian motion in chaotic flows — •Hua Xia, Nicolas Francois, Horst Punzmann, and Michael Shats — Research School of Physics and Engineering, The Australian National University

Particle motions in chaotic flows exhibit macroscopic Brownian walk. As found in the cellular molecular sub-micron bio-systems, Brownian motion can assist directed motion of particles. I will show that in macroscopic flows turbulent Brownian motion can help to control motion of floating objects, and possibly convert wave energy into currents.

Poster P.44 17:15 Auditorium foyer

Assembly and aggregation of thermally denaturated protein complexes in coarse-grained models — •Karol Wołek and Marek Cieplak — Institute of Physics, Polish Academy of Science, al. Lotników 32/46, PL-02-668 Warsaw, Poland

In our studies, we focused on the thermostability and self-organization phenomena of virus capsides as well as the aggregation ability of capsid proteins. We will present results from our simulation using structure-based coarse-grained model of virus capsides.

Poster P.45 17:15 Auditorium foyer

Environment-dependent conductance of solid-state hemoglobin networks — •Anastasia Holovchenko and Herre S.J. van der Zant — Technical University of Delft, Delft, The Netherlands

We report on environment-dependent charge transport properties of hemoglobin networks, trapped in between platinum nanogaps with 100-nm separation. The electrical measurements were performed while the environment parameters were varied. The current flowing through the hemoglobin network is higher at ambient, suppressed in nitrogen gas atmosphere and not detectable in vacuum.

Poster P.46 17:15 Auditorium foyer

Single molecule measurement of thermodynamic information in heterogeneous DNA ensembles — •Alvaro Martinez-Monge[1], Anna Alemany[2], Marco Ribezzi-Crivellari[3,4], and Felix Ritort[1,4] — [1]Departament de Física de la Matèria Condensada (Universitat de Barcelona), Barcelona, Spain — [2]Hubrecht Institute-KNAW (Royal Netherlands Academy of Arts and Sciences), Utrecht, the Netherlands — [3]École Supérieure de Physique et de Chimie Industrielles de la Ville de Paris (ESPCI ParisTech), Paris, France — [4]Centro de Investigacion Biomedica en Red-Bioingeneria, Biomateriales y Nanomedicina (CIBER-BBN) Instituto de Salud Carlos III, Madrid, Spain

Building on recent work on thermodynamic inference in stochastic thermodynamics we have developed a theoretical framework that allows us to extract the intrinsic thermodynamic information of a disordered ensemble of DNA hairpins using single-molecule force spectroscopy.

Poster P.47 17:15 Auditorium foyer

Single-Molecule Imaging of Electroporated Dye-Labelled Chemotaxis Proteins in Live Bacteria — •Diana Di Paolo[1,3], Oshri Afanzar[2], Richard Berry[1], and Judith Armiatge[3] — [1]Biological Physics Research Group, Clarendon Laboratory, Department of Physics, University of Oxford, Oxford, OX1 3PU, U.K — [2]Department of Biological Chemistry, The Weizmann Institute of Science, 7610001 Rehovot, Israel — [3]Department of Biochemistry, University of Oxford, Oxford OX1 3QU, U.K.

A novel application of electroporation allows to overcome the limitations of fluorescent protein fusions and to internalize proteins labelled with organic dyes into bacterial cells in controllable concentrations. Single molecules can be imaged with video fluorescence microscopy while diffusing within cells and interacting with biologically relevant loci in real time.

Poster P.48 17:15 Auditorium foyer

Heat capacity change directly measured in single molecule experiments — •Marc Rico-Pasto[1], Marco Ribezzi-Crivellar[2,3], and Felix Ritort[1,3] — [1]Departament de Física de la Materia Condensada, Universitat de Barcelona, C/ Martí i Franques 1, 08028, Barcelona, Spain — [2]École Supérieure de Physique et de Chimie Industrielles de la Ville de Paris, 10 rue Vauquelin, F-75231 Paris Cedex 05, France — [3]CIBER_BNN, Instituto de Salud Carlos III, 28029 Madrid, Spain

In this work, we propose a novel method to determine the enthalpy, the entropy and the heat capacity change from the force dependence kinetic rates at one unique salt concentration using SME, in contrast with the traditional bulk experiments, where the melting temperature is changed by tunning the salt concentration.

Poster P.49 17:15 Auditorium foyer

Viscoelastic properties of Red Blood Cells — •Marta Gironella-Torrent[1], Marco Ribezzi-Crivellari[2], and Felix Ritort[1,3] — [1]Small Biosystems Lab, Universitat de Barcelona, C/ Martí i Franquès 1, 08028 Barcelona, Spain — [2] École Supérieure de Physique et de Chimie Industrielles de la Ville de Paris , 10 rue Vauquelin, F-75231 Paris Cedex 05, France — [3] CIBER-BBN, Instituto de Salud Carlos III, 28029 Madrid, Spain

By using two different experimental procedures: 1) Applying a flow to a trapped bead attached to the Red Blood Cells (RBC) membrane. 2) Measuring the force signal fluctuations of the attached bead, we are able to measure the global and local membrane deformability of RBC.

Poster P.50 17:15 Auditorium foyer

STUDY OF THE INTERACTION OF SMALL MOLECULES WITH DNA USING SINGLE MOLECULE FOOTPRINTING — •Isabel Pastor[1,2], Joan Camunas-Soler[2,3], and Felix Ritort[1,2] — [1]Small Biosystems Lab, Universitat de Barcelona, C/ Marti i Franquès 1, 08028 Barcelona , Spain — [2]CIBER-BBN, Instituto de Salud Carlos III, 28029 Madrid, Spain — [3] Stanford University, Clark Center E300, 318 Campus Drive, Stanford, CA 94305, USA

Recently, in our Lab, a new single molecule footprinting technique using optical tweezers have been developed. Here, this technique had been used to study the interaction of Netropsin to oligonucleotides. Our results suggest an overall increase in the stability of the oligonucleotides studied in the presence of this small molecule.

Poster P.51 17:15 Auditorium foyer

Length-dependence of the elastic response and secondary structure of single-stranded DNA — •Xavier Viader-Godoy[1], Joan Camunas-Soler[1], and Felix Ritort[1,2] — [1]Departament de Física de la Matèria Condensada, Universitat de Barcelona, C/Martí i Franquès 1, 08028, Barcelona, Spain — [2]Ciber-BBN, Instituto de Salud Carlos III, 28029 Madrid, Spain

Single-stranded DNA plays a major role in several biological processes, such as replication or transcription. In this work, we study the elastic properties and secondary structures of different molecules of ssDNA (between 60-14kbases) to give some insight on how these depend on parameters such as their extension or GC-content.

Poster P.52 17:15 Auditorium foyer

Control of active gels with addressable soft interfaces — •Pau Guillamat, Jordi Ignés-Mullol, and Francesc Sagués — Department of Materials Science and Physical Chemistry and Institute of Nanoscience and Nanotechnology (IN2UB), University of Barcelona, Catalonia

Active systems often exhibit turbulent flows that span a wide range of lengthscales. Here, we prepare a two-dimensional active gel in contact with a lamellar liquid crystal, whose rheological anisotropy allows controlling the active flows to follow preassigned directions by aligning the passive fluid with an external magnetic field.

Poster P.53 17:15 Auditorium foyer

Models of brain design: is physics more important than evolutionary optimization? — •Jan Karbowski — Institute of Applied Mathematics and Mechanics, University of Warsaw, Warsaw, Poland

Brains of different mammalian species share a common architecture despite 4 orders of magnitude span in brain sizes. This conservation in structure is amazing, and suggests a design principle that is robust and optimal in some sense. What are the candidates for such a principle, and what is their relation to physical laws and evolutionary optimization?

Poster P.54 17:15 Auditorium foyer

Kinetically Constrained Evolution Under Horizontal Gene Transfer — •Masahiko Ueda, Nobuto Takeuchi, and Kunihiko Kaneko — The University of Tokyo, Tokyo, Japan

Evolution by horizontal gene transfer with migration is numerically studied. A phenomenon similar to negative differential resistance is observed, where the growth rate of fitness becomes smaller by increasing selection pressure.

Poster P.55 17:15 Auditorium foyer

Brownian pump powered by colored noise in bacterial channels under acidic stress — Lidón Lopez[1], María Queralt-Martin[2], Vicente Aguilella[1], and •Antonio Alcaraz[1] — [1]Laboratory of Molecular Biophysics, Department of Physics, Universitat Jaume I, Av. Vicent Sos Baynat s/n 12071 Castellón, Spain — [2]Program in Physical Biology, Eunice Kennedy Shriver NICHD, National Institutes of Health, Bethesda, Maryland 20892, USA

Fluctuation-driven ion transport can be obtained in bacterial channels with the aid of different types of noise including biologically relevant Lorentzian one. Using the electrochemical rectification of the channel current as ratchet mechanism we observe transport of ions up their concentration gradient in conditions similar to that met in vivo.

Poster P.56 17:15 Auditorium foyer

Molecular force loading explains cell sensing of extracellular ligand density and distribution — •Roger Oria[1,2], Tina Wiegand[3,4], Jorge Escribano[5], Alberto Elosegui-Artola[1], Juan Jose Uriarte[2], Cristian Moreno-Pulido[2], Jose Manuel Garcia-Aznar[5], Daniel Navajas[1,2], Xavier Trepat[6], Ada Cavalcanti-Adam[3,4], and Pere Roca-Cusachs[1,2] — [1]Institute for Bioengineering of Catalonia, Barcelona, Spain — [2]University of Barcelona, Spain — [3]Max-Planck Institute for Medical Research, Heidelberg, Germany — [4]University of Heidelberg, Germany — [5]Aragon Institute of Engineering Research (I3A), University of Zaragoza, Zaragoza, Spain — [6]Institució Catalana de Recerca i Estudis Avançats, Barcelona, Spain

Integrin-mediated adhesions between cells and the extracellular matrix (ECM) are crucial in many cellular processes. Here, we show that molecular force loading drives focal adhesion formation and collapse in response to ligand density and distribution. Combination of biophysical techniques and an expanded computational molecular clutch model validate our results

Poster P.57 17:15 Auditorium foyer

Graphene devices for probing biomolecules and cells — •Wayne Yang, Jakub Wiktor, Thomas van der Sijs, Daniel Verschueren, Sergii Pud, and Cees Dekker — Bionanoscience Department, Kavli Institute of Nanoscience, Delft University of Technology, Delft, Netherlands

We study graphene devices for biophysics applications – nanopore sequencing and cell imaging. First, plasmonics antenna fabricated near a graphene nanopore induces a trapping force on DNA allowing for longer readtimes. Second, graphene liquid cells allow for high-resolution dynamic imaging of biological cells in high vacuum electron microscopy.

Poster P.58 17:15 Auditorium foyer

Stochastic resonance in a proton pumping Complex-I of mitochondria membranes — •Lev Mourokh — Queens College, The City University of New York, Flushing, USA

We address the proton-pumping in the Complex-I within mitochondria membranes. Conformation changes are represented by a charged piston facilitating the indirect electron-proton coupling. We demonstrate that only the joint action of the periodic energy modulations and thermal noise leads to efficient uphill proton transfer, being a manifestation of stochastic resonance.

Poster P.59 17:15 Auditorium foyer

Quantitative Measurement of Tight Junction Morphology of a Single Cyst and the Implication in Apical Constriction — Ivan Alex Priela Lazarte[1], Wan-jung Lin[1], Ching-chung Hsueh[2], and •Keng-hui Lin[1] — [1]Institute of Physics, Academia Sinica, Taipei, Taiwan — [2]Dept. of Physics, National Taiwan University, Taipei, Taiwan

Apical constriction is important process in embryogenesis and tissue morphology but difficult to measure. Based on theoretical simulation, we found that tight junction morphology depends on apical tension and cell-cell interactions. We explained the reported tortuous tight junction morphology is due to high apical tension.

Poster P.60 17:15 Auditorium foyer

Crooks fluctuation theorem applied to controlled force measurements — •Ainara Morera — Departament de Física de la Matèria Condensada (Universitat de Barcelona), Barcelona, Spain

Magnetic tweezers is a single molecule technique that have been used for the measurement of mechanical work in small DNA hairpins. Using Crooks fluctuation theorem we can relate that work with the free energy of the process.

Poster P.61 17:15 Auditorium foyer

Stimulated emission depletion microscopy — •Sujitha Puthukodan[1], Richard Wollhofen[1], Jaroslaw Jacak[1,2], and Thomas Klar[1] — [1]Institute of Applied Physics, Johannes Kepler University, Altenberger Straße 69, 4040 Linz, Austria — [2]University of Applied Sciences Upper Austria, Garnisonstraße 21, 4020, Linz, Austria

Using a gated continuous wave stimulated emission depletion microscope, a lateral resolution of 80 nm and axial resolution of 200 nm was achieved. This is being used to study the role of proteins in migration of cells, colocalization of proteins and cytoskeleton etc.

Poster P.62 17:15 Auditorium foyer

A mechanochemical network regulating the form and function of the Golgi membranes — •Felix Campelo[1], Josse van Galen[2,3], Maria F. Garcia-Parajo[1,4], and Vivek Malhotra[2,3,4] — [1]ICFO-Institut de Ciencies Fotoniques, The Barcelona Institute of Science and Technology, 08860 Castelldefels (Barcelona), Spain — [2]Cell and Developmental Biology Programme, Centre for Genomic Regulation (CRG), The Barcelona Institute of Science and Technology, Dr. Aiguader 88, 08003 Barcelona, Spain — [3]Universitat Pompeu Fabra (UPF), Barcelona, Spain — [4]Institució Catalana de Recerca i Estudis Avançats (ICREA), Pg. Lluís Companys 23, 08010 Barcelona, Spain

I will describe the mechanochemical network by which sphingomyelin metabolism at the Golgi complex regulates the mechanical properties of these membranes to control the shape and the functions of this organelle.

Poster P.63 17:15 Auditorium foyer

A Novel Method to Distinguish and Quantify Intercellular Shear and Normal Tractions within Cell Aggregates — •Bugra Kaytanli[1], Aimal H. Khankhel[2], Avik Mondal[3], and Megan T. Valentine[1] — [1]Department of Mechanical Engineering, University of California, Santa Barbara, California, USA — [2]Biomolecular Science and Engineering Program, University of California, Santa Barbara, California, USA — [3]Department of Physics, University of California, Santa Barbara, California, USA

Quantitative measurements of cell-generated shear and normal forces in tissues have proven challenging. We present a new method to quantify three-dimensional full traction fields generated within cell aggregates, using cell-sized spherical hydrogels with well-defined elastic properties. Using this approach, we investigate the interactive mechanical behavior of several mammalian cell types.

Poster P.64 17:15 Auditorium foyer

Stochastic continuum mechanics for interacting biomolecules: New methods and software implementation — •Albert Solernou[1], Daniel J Read[2], Oliver H Harlen[2], and Sarah A Harris[1] — [1]School of Physics and Astronomy, University of Leeds, LS2 9JT Leeds, United Kingdom — [2]School of Mathematics, University of Leeds, LS2 9JT Leeds, United Kingdom

I will introduce Fluctuating Finite Element Analysis (FFEA), a new methodology that models globular biomolecules and their interactions using stochastic continuum mechanics, thus covering the existing gap between atomistic and macroscopic simulations. Furthermore, I will illustrate its capabilities on biologically relevant systems presenting a free software package that implements FFEA.

Poster P.65 17:15 Auditorium foyer

Unbinding properties of syndecan-1 in human bladder cancer cells — •Joanna Danilkiewicz[1], Joanna Pabijan[1], Arkadiusz Ptak[2], and Małgorzata Lekka[1] — [1]Institute of Nuclear Physics, PAS Radzikowskiego 152, Krakow Poland. — [2]2 Institute of Physics, Poznan University of Technology, Piotrowo 3, 60-965 Poznań, Poland.

The unbinding properties of syndecan-1, ECM protein receptor, were examined using dynamic force spectroscopy between a monoclonal antibody against SDC-1 and syndecan-1 in plasma membrane of living human bladder cell lines both non-malignant and malignant. The energy landscapes of the interaction were calculated using two theoretical models to prove the difference between different malignancy levels.

Poster P.66 17:15 Auditorium foyer

Dissecting the roles of the aberrant collagen mechanobiology in lung fibrosis and cancer — Rafael Ikemori[1], Marta Gabasa[1], Marta Puig[1], Alicia Giménez[1], Roland Galgoczy[1], Anna Labernardie[2], Xavier Trepat[2], and •Jordi Alcaraz[1] — [1]Unit of Biophysics and Bioengineering, Dept of Biomedicine, School of Medicine and Health Sciences, University of Barcelona (UB), Barcelona 08036, Spain — [2]Institute for Bioengineering of Catalonia (IBEC), Barcelona 08028, Spain,

Collagen-I is a key regulator of tissue architecture and function, and is dysregulated in fibrosis and cancer. We have analyzed how is collagen deposition regulated, how its accumulation elicits a vicious feedforward mechanism that increases fibroblast population, and how such accumulation hinders the diffusion of small molecules used in therapy.

Poster P.67 17:15 Auditorium foyer

Linear irreversible thermodynamics and Onsager reciprocity for information-driven engines — •Shumpei Yamamoto, Sosuke Ito, Naoto Shiraishi, and Takahiro Sagawa — The University of Tokyo, Tokyo, Japan

In the recent progress in stochastic thermodynamics, information has been recognized as a kind of thermodynamic resource. We establish the framework of the linear irreversible thermodynamics for a broad class of autonomous information processing and prove that the Onsager reciprocity holds with the information affinity.

Poster P.68 17:15 Auditorium foyer

Evolving quantum superposition states: A new physical phenomenon in biology — •Ian Mercer — UCD Dublin, Dublin, Ireland

Quantum superposition states underpin phenomena ranging from chemical bonding to entanglement. Can the state-energies of a quantum superposition state evolve in time, and if so, is this exploited by nature? We explore this idea, and what we believe to be its first observation, made recently in a protein under physiological conditions.

Poster P.69 17:15 Auditorium foyer

Sub-diffractional laser induced molecular patterning — •Eljesa Murtezi[1], Richard Wollhofen[1], Jaroslaw Jacak[1,2], and Thomas Klar[1] — [1]Institute of Applied Physics, Johannes Kepler University Linz, 4040 Linz, Austria — [2]Department of Medical Engineering, Upper Austria University of Applied Sciences, 4020 Linz, Austria

LAPAP (Laser-Assisted Protein Adsorption by Photobleaching) represents an innovative way to fabricate protein patterns relying on photobleaching of the fluorophores to bind proteins on a cell culture substrate. LAPAP can as well be combined with STED (STimulated Emission Depletion) in order to confine the volume of patterning into nanometer range.

Poster P.70 17:15 Auditorium foyer

Top-down (i.e. based on extant biology) inference of some of the disequilibrium-converting engines involved in driving the emergence of the dissipative structure "Life" fuelled from electrochemical gradients — •Wolfgang Nitschke[1], Frauke Baymann[1], Barbara Schoepp-Cothenet[1], and Michael J. Russell[2] — [1]BIP/CNRS, Aix-Marseille University, Marseille, France — [2]Jet Propulsion Laboratory, California Institute of Technology, Pasadena, California, USA

The inventory of energy conversion in extant biology indicates that the dissipative structure life is invariably maintained by electrochemical gradients suggesting that its emergence also was driven by redox energy. We discuss potential dissipative engines fuelling life's order from the electrochemically low-entropy bath, i.e. redox bifurcations and feedbacking redox cascades.

Poster P.71 17:15 Auditorium foyer

Intracellular medium of living cells - a viscoelastic liquid or a gel? — •Jean-François Berret — Université Paris-Diderot/CNRS

We address the question of the rheological nature of the cytoplasm. Internalized micron-size wires are actuated by the application of a rotating magnetic field. In contrast to earlier studies it is concluded that the living cell interior can be described as a viscoelastic liquid, and not as an elastic gel.

Poster P.72 17:15 Auditorium foyer

Impact of the Cytoskeleton Architecture on Intracellular Transport Efficiency to Specific Membranous Targets — •Anne E. Hafner and Heiko Rieger — Theoretical Physics, Saarland University, Saarbrücken, Germany

To investigate the efficiency of search strategies established by a cell's spatial organization of the cytoskeleton we formulate a random-velocity-model with intermittent arrest states. We analyze the dependence of the mean-first-passage-time to specific membrane targets on the cytoskeleton structure, motor properties and fraction of time spent in each motility state.

Poster P.73 17:15 Auditorium foyer

Reciprocity between Robustness and Plasticity in the Biological clock and in the Reaction-diffusion System — •Tetsuhiro S. Hatakeyama and Kunihiko Kaneko — The University of Tokyo, Tokyo, Japan

Robustness and plasticity are important characteristics common to a variety of biological systems. How these two properties are compatible with each other is an important question to be addressed. Here, we uncover universal reciprocity relationship between robustness and plasticity in the biological clock and in the spatial pattern.

Poster P.74 17:15 Auditorium foyer

Ezrin membrane recruitment is facilitated by I-BAR domains irrespective of membrane curvature — •Feng-Ching Tsai[1], Aurélie Bertin[1], Stéphanie Miserey-Lenkei[2], Hugo Bousquet[2], Laura Picas[3], Bruno Goud[2], Evelyne Coudrier[2], and Patricia Bassereau[1] — [1]Institut Curie, PSL Research University and C.N.R.S. UMR 168, 26 rue d'Ulm, Paris, France — [2]Institut Curie, PSL Research University and C.N.R.S. UMR 144, 26 rue d'Ulm, Paris, France — [3]Centre de Biochimie Structurale, C.N.R.S. UMR 5048, INSERM U1054, Université de Montpellier, Montpellier, France

The ezrin-radixin-moesin (ERM) proteins are key membrane organizers. We assess how ezrin interacts with and is recruited to membranes of biologically relevant curvatures. We observe that the recruitment of ezrin to negatively curved membranes is facilitated by IRSp53 I-BAR domains. We demonstrate that ezrin can sense positive membrane curvature.

Poster P.75 17:15 Auditorium foyer

Type IV pili mediated mechanical interactions across bacterial genera — •Nicolas Biais — Brooklyn Colleg of CUNY, Brooklyn, U.S.A.

Type IV pili are ubiquitous nanomachines among prokaryotes. In particular, they enable bacteria to create a network of dynamical polymers that can exert forces on their surroundings. We are interested in what commonality in the biophysics of these appendages has been retained across evolutionary time scales.

Poster P.76 17:15 Auditorium foyer

Engineered swift equilibration to separate time scales in biology. — •Ignacio A. Martínez — Departamento de Fisica Atómica, Molecular y Nuclear, Universidad Complutense Madrid, 28040 Madrid, Spain

A new approach to travel between equilibrium state as fast as needed is presented: engineered swift equilibration. The contribution is divided between the presentation of the proof of principle experiment, done with optical trapping and AFM, and a possible immediate application in the study of single biopolymers.

Poster P.77 17:15 Auditorium foyer

Physical basis of magneto-sensing by live cells — •Sufi Raja[2], Avik Mukherjee[1], Akash Gulyani[2], and Sufi Raja[3] — [1]Department of Genetics University of Cambridge, Downing Street, Cambridge CB2 3EH, United Kingdom — [2]Institute for Stem Cell Biology and Regenerative medicine, Bengaluru-560065, India — [3]Department of Biochemistry, University of Calcutta, 35 Ballygunge Circular Road, 700019 Kolkata, India

We report emergence of magnetic memory of living cells and the consequent field dependent modulation of sub-cellular streaming. This is validated by enhanced rate of fluorescence recovery after photobleaching. This cellular attribute can be traced back to field altered hydrodynamics of proteins.

Poster P.78 17:15 Auditorium foyer

Discrete model for the dynamics of neurotransmitters and receptors of the pre and post-synaptic neuron region — Jorge A. Herrera-Magaña[1], Juan C. Chimal-Eguía[1], and •Norma Sánchez-Salas[2] — [1]Centro de Investigación en Computación, Instituto Politécnico Nacional, Ciudad de México, México — [2]Escuela Superior de Física y Matemáticas, Instituto Politécnico Nacional, Ciudad de México, México

This work propose a model for dynamics of neurotransmitters by means of random walks, it is possible to affirm that there is a relation of the distance between neurons and the amount of neurotransmitters that reach the receptors of the post-synaptic neuron, the former to understand how neural connections work.

Poster P.79 17:15 Auditorium foyer

Non-Elastic Mechanical Remodeling of the 3D Extracellular Matrix by Cell-Generated Forces — •Andrea Malandrino[1,2], Michael Mak[1,3,4], and Roger D Kamm[1,5] — [1]Department of Mechanical Engineering,Massachusetts Institute of Technology, Cambridge, MA, USA — [2]Institute for Bioengineering of Catalonia, Barcelona, Spain — [3]Boston University Biomedical Engineering, Boston, MA, USA — [4]Yale Biomedical Engineering, New Haven, CT, USA — [5]Department of Biological Engineering,Massachusetts Institute of Technology, Cambridge, MA, USA

Cells propagate inside an evolving 3D extracellular matrix (ECM). ECM remodelling of physical cues in physiological and pathological processes is not well understood. Here, integrated computational-experimental approaches assess remodeling through cell-generated forces. Non-elastic mechanical remodeling of diverse 3D cell culture systems is correlated to 3D simulations of filament-crosslinker dynamics.

Poster P.80 17:15 Auditorium foyer

Physical picture for mechanical dissociation of biological complexes. — Rafael Tapia-Rojo[1], Carlos Marcuello[2], Anabel Lostao[3], Carlos Gómez-Moreno[4], Juan José Mazo[5], and •Fernando Falo[6] — [1]Department of Biological Sciences, Columbia University, New York 10027, USA — [2]Departamento de Física, Universidade de Lisboa, 1749-016 Lisboa, Portugal — [3]Fundación ARAID and Instituto de Nanociencia de Aragón, Universidad de Zaragoza, 50018 Zaragoza, Spain — [4]Biochemistry Department and Instituto de Nanociencia de Aragón, Universidad de Zaragoza, 50018 Zaragoza, Spain — [5]Instituto de Ciencia de Materiales de Aragón and Departamento de Física de la Materia Condensada, CSIC-Universidad de Zaragoza, E-50009 Zaragoza, Spain — [6]Instituto de Biocomputación y Física de Sistemas Complejos and Departamento de Física de la Materia Condensada, Universidad de Zaragoza, E-50009 Zaragoza, Spain

We present a careful analysis of AFM rupture experiments for two protein-protein complexes -FNR-Ferredoxin and FNR-Flavodoxin. We propose a free energy profile for this process with two magnitudes to determine, a free energy barrier $\Delta G+$, controlling the kinetic behaviour, and the dissociation free energy $\Delta G0$, controlling the equilibrium behaviour.

Poster P.81 17:15 Auditorium foyer

Kinetics of surface-tethered antigen-antibodies bonds — •Laurent Limozin[1], Cristina Gonzalez Gutierrez[1], Patrick Chames[2], and Philippe Robert[1,3] — [1]Laboratoire Adhésion et Inflammation – AMU/CNRS/INSERM, 163 av. de Luminy, F-13288 Marseille, France — [2] Centre de Recherche en Cancérologie de Marseille – AMU/CNRS/INSERM/IPC, 163 av. de Luminy, F-13288 Marseille, France — [3]Laboratoire d'Immunologie – Hôpital La Conception, 147 bd. Baille, F-13385 Marseille, France

Using a laminar flow chamber, we measure association and dissociation of antigen-antibody trans-bonds when reactants are tethered to opposite surfaces (2D). We estimate the roughness of the putative energy landscape for bond association. We also compare 2D and 3D (in solution) affinities of a panel of single domain antibodies.

Poster P.82 17:15 Auditorium foyer

Scaling and universality in soft biological membranes — •Horia I. Petrache[1] and Michael F. Brown[2] — [1]Department of Physics, Indiana University Purdue University Indianapolis, Indianapolis, IN 46202, USA — [2]Department of Chemistry and Biochemistry, University of Arizona, Tucson, AZ 85721, USA

We show that lipid bilayers are discrete realizations of a universal, continuum profile for acyl chains that emerges from the forces involving the lipid polar headgroups and acyl chains. We discuss short and infinitely long chains and we show how various lipids correspond to different segments of the universal profile.

Poster P.83 17:15 Auditorium foyer

Min protein patterns in fully confined fluidic chambers — •Yaron Caspi[1,2] and Cees Dekker[1] — [1]Department of Bionanoscience, Kavli Institute of Nanoscience, Delft University of Technology, Van der Maasweg 9, 2629 HZ Delft, The Netherlands — [2]Current Address: Brain Center Rudolf Magnus, University of Utrecht medical center, Universiteitsweg 100, 3584 CG Utrecht, The Netherlands

We determine the geometry selection rules of the dynamic Min protein

patterns in fully confined fluidic chambers, showing that both oscillations and running waves are derivatives of spiral rotations that are established as the majority pattern over a wide range of the geometric phase diagram.

Poster P.84 17:15 Auditorium foyer

Thermal versus Mechanical Unfolding of a Model Protein: Free Energy Profiles, Configurational Networks and Folding Pathways — Rafael Tapia-Rojo[1], •Juan José Mazo[2], and Fernando Falo[3] — [1]Department of Biological Sciences, Columbia University, New York 10027, USA — [2]Departamento de Física de la Materia Condensada and Instituto de Ciencia de Materiales de Aragón, CSIC-Universidad de Zaragoza, E-50009 Zaragoza, Spain — [3]Departamento de Física de la Materia Condensada and Instituto de Biocomputación y Física de Sistemas Complejos, Universidad de Zaragoza, E-50009 Zaragoza, Spain

We study the thermal and the mechanical unfolding of a simple model protein. The Langevin dynamics results are analyzed using Markov-model methods that allow describing completely the configurational space of the system. Using transition-path theory we also provide a quantitative description of the unfolding pathways followed by the system.

Poster P.85 17:15 Auditorium foyer

Cellular and Biomechanical Mechanisms of Liver Morphogenesis — •Aliaksandr Dzementsei[1], Younes Farhangibarooj[2], Gopal Karemore[3], Lene Oddershede[2], and Elke Ober[1] — [1]Danish Stem Cell Center (DanStem), University of Copenhagen, Copenhagen, Denmark — [2]Niels Bohr Institute, University of Copenhagen, Copenhagen, Denmark — [3]Novo Nordisk Foundation Center for Protein Research & Danish Stem Cell Center, University of Copenhagen, Copenhagen, Denmark

Combining developmental biology and biophysics approaches, we investigate how liver progenitors interact with their environment during organ formation in zebrafish. We develop non-invasive in vivo assays to study biomechanical properties of deep internal tissues and aim to understand whether liver progenitors actively migrate or are pushed by the surrounding tissue.

Poster P.86 17:15 Auditorium foyer

Actin networks' mechanics and growth assessed by a new magnetic colloids technique — •Olivia du Roure[1], Pierre Bauër[1], Jessica Planade[1], Audrey Guillotin[2], Alphée Michelot[2], and Julien Heuvingh[1] — [1]PMMH, CNRS ESPCI Paris PSL research University, Sorbonne University, Univ. Paris Diderot, 10 rue Vauuqelin 75005 Paris, France — [2]Aix Marseille Univ., CNRS, Institute of Developmental Biology of Marseille (IBDM), case 907, 13288 Marseille cedex 09, France.

Actin cytoskeleton bestows the cell its ability to deform, migrate and organize its inner life. We show here some features of the mechanics of actin networks obtained by a new technique that allows elasticity and plasticity to be measured and assembly when facing an opposing force to be followed.

Poster P.87 17:15 Auditorium foyer

Efficient leucocyte migration by tuning biochemical feedback loops and temperature — •Stefan Wieser[1], Verena Ruprecht[2], Monika Ritsch-Marte[3], Carl-Philipp Heisenberg[4], Matthieu Piel[5], Raphael Voituriez[6], and Michael Sixt[4] — [1]ICFO, The Institute of Photonic Sciences, 08860 Castelldefels (Barcelona), Spain — [2]Center of Genomic Regulation (CRG), Dr. Aiguader 88, 08003 Barcelona, Spain — [3]Division of Biomedical Physics, Innsbruck Medical University, 6020 Innsbruck, Austria — [4]Institue of Science and Technology Austria, 3400 Klosterneuburg, Austria — [5]Institut Curie, CNRS UMR 144, 75005Paris, France — [6]Laboratoire de Physique Theorique de la Matiere Condensée, 75255 Paris Cedex, France

Cell movement requires the establishment of an axis of polarity. Here we describe a feedback mechanism coupling the retrograde flowing actin cytoskeleton in migrating cells to cell polarity. We further show that the efficiency of immune cell migration depends on intrinsic migration persistence tunable via chemotactic cues and temperature modulations.

Poster P.88 17:15 Auditorium foyer

Neutral theory of scale-invariant outbursts of neural activity — •Miguel A Muñoz — Instituto Carlos 1 de Física Teórica y Computacional, Universidad de Granada

Computational modeling allows us to show that the dynamics of perturbations in neural networks is neutral with respect to the endogenous background activity. Causal avalanches turn out to be scale-invariant even if they are not necessarily poised at criticality. The origin, relevance, and consequences of such a dynamics are scrutinized.

Poster P.89 17:15 Auditorium foyer

Shape Transformation of Model Vesicles in the Presence of Adsorbing Particles: A Dissipative Particle Dynamics Simulation Study — •Rikhia Ghosh and Reinhard Lipowsky — Max Planck Institute of Colloids and Interfaces, Potsdam, Germany

Biomimetic membranes are popularly known to have simpler compositions but possess one crucial physical property, namely their fluidity, which enables them to undergo remodelling processes. We explore the prospect of shape transformation of a model vesicle in presence of the adsorbing particles that preferentially induce spontaneous curvature.

Poster P.90 17:15 Auditorium foyer

Single Molecule Study of an RNA Thermosensor — •Laura Asensio Puig[1], Aurelien Severino[1], and Felix Ritort Farran[1,2] — [1]Small Biosystems Lab, Facultat de Física, Universitat de Barcelona, diagonal 647, 08028, Barcelona, Spain — [2]CIBER BBN, Networking Centre of Bioengineering, Biomaterials and Nanomedicine, ISCIII, Madrid, Spain

CssA is an mRNA thermosensor (RNAT) found in Neisseria meningiditis which is expected to exhibit temperature-dependent properties. Its kinetics, states, and free energy landscape were investigated as a function of temperature using optical tweezers, in what is known from the authors as the first single-molecule study an RNAT.

Poster P.91 17:15 Auditorium foyer

Inflexible search statistics in C. elegans — •Alfonso Pérez-Escudero and Jeff Gore — Massachusetts Institute of Technology

Theory predicts that animals should adapt their search strategy to the estimated distance to the target, searching more locally when the target is nearby. We tested this hypothesis in C. elegans, using salt concentration as a proxy of distance to the target. Contrary to the prediction, the statistics of search behavior are independent of salt concentration.

Poster P.92 17:15 Auditorium foyer

Repetitive unwinding of the BLM helicase investigated by combined fluorescence and force spectroscopy — •Felix E. Kemmerich, Jonas Reinboth, and Ralf Seidel — Institute for Experimental Physics I, Universität Leipzig, Linnéstr. 5, 04103 Leipzig, Germany

Single-molecule analysis techniques can expose the highly-dynamic nature of enzymatic activities. Studying DNA unwinding of RecQ-helicases using magnetic tweezers, reveals repetitive-shuttling events. By combining this technique with fluorescence-spectroscopy, we show that repetitive unwinding of the BLM-helicase is carried out by monomers, and plan to further decipher the molecular mechanisms.

Poster P.93 17:15 Auditorium foyer

withdrawn

Poster P.94 17:15 Auditorium foyer

Mechanisms of substrate stress relaxation in supported lipid bilayers — •Liam Stubbington and Margarita Staykova — Durham University Physics Department, South Road, Durham, DH1 3LE, UK

Soft lipid membranes provide nature with the unique capacity of robust compartmentalisation together with the unrivalled response to mechanical deformation. We report of a model lipid-polymer interface, which displays a substrate stress – lipid strain response that can be easily controlled in the laboratory.

Poster P.95 17:15 Auditorium foyer

The puzzling folding behavior of protein gankyrin. — Richard Hutton[1], James Wilkinson[1], Mauro Faccin[2], Elin Sivertsson[3], Alessandro Pelizzola[4], Alan Lowe[5], •Pierpaolo Bruscolini[6], and Laura Itzhaki[3] — [1]Hutchison/MRC Research Centre, Cambridge, UK — [2]Université Catholique de Lovain, Louvain-la-Neuve, Belgium — [3]University of Cambridge, Cambridge, UK — [4]Politecnico di Torino, Torino, Italy — [5]University College and Birkbeck College, London, UK — [6]Universidad de Zaragoza, Zaragoza, Spain

Gankyrin is a tandem-repeat protein, formed by seven ankyrin repeats, presenting intriguing equilibrium and kinetics behavior, including an apparent paradox between them. Here we address the theoretical modeling of such behavior using a simple native-centric model, capable of reproducing the main features of the experimental findings.

Poster P.96 17:15 Auditorium foyer

investigating the binding between 3WJ RNA and S15 protein with force spectroscopy experiments at singe molecule level — •carmina verdiá-báguena[1], joan camuñas[2], álvaro martínez[1], and felix ritort[1] — [1]small biosystems lab, faculty of physics – department of condensed matter physics, university of barcelona — [2]stanford bio-x james h. clark center 318 campus drive west, university of stanford

the 16S/3-way-junction is a ribosomal RNA molecule that participates in ribosome assembly by binding protein S15. in this poster we investigated the binding between these two molecules by means of optical tweezers measurements.

Poster P.97 17:15 Auditorium foyer

Universal bound on the efficiency of molecular motors — •Patrick Pietzonka[1], Andre C. Barato[2], and Udo Seifert[1] — [1]II. Institut für Theoretische Physik, Universität Stuttgart, Germany — [2]Max Planck Institute for the Physics of Complex Systems, Dresden, Germany

The thermodynamic uncertainty relation provides an inequality relating any mean current, the associated dispersion and the entropy production rate for non-equilibrium steady states. Applying it to a general model of molecular motors, we show that the thermodynamic efficiency is universally bounded by an expression involving only experimentally accessible quantities.

Poster P.98 17:15 Auditorium foyer

Rheology of the active cell cortex in mitosis — •Elisabeth Fischer-Friedrich[1,2], Yusuke Toyoda[1,3], Cedric Cattin[4], Daniel Müller[4], Anthony Hyman[1], and Frank Jülicher[2] — [1]Max Planck Institute of Molecular Cell Biology and Genetics, Dresden, Germany — [2]Max Planck Institute for the Physics of Complex Systems, Dresden, Germany — [3]Institute of Life Science, Kurume University, Kurume, Japan — [4]Departement of Biosystems Science and Engineering, Eidgenössische Technische Hochschule Zürich, Basel, Switzerland

To study the time-dependent rheological response of the cortex, we probed mitotic HeLa cells in a parallel plate compression assay. We find that cortex rheology exhibits a new type of rheological response with characteristic time scale of approximately 10 s. This time scale is adjusted by actin cross-linkers.

Poster P.99 17:15 Auditorium foyer

Experimental validation of direct uphill and downhill translocation time equivalence — •Jannes Gladrow and Ulrich F Keyser — Cavendish Laboratory, University of Cambridge, JJ Thomson Ave Cambridge CB3 0HE, United Kingdom

Diffusion in a force field is ubiquitous in nature. Unituitively, bias forces affect passage times in both directions equally. In fact, uphill and downhill passage times are predicted to be identically distributed. We here validate this prediction by measuring passage times of diffusing colloids biased by optical forces and flows.

Poster P.100 17:15 Auditorium foyer

Evolutionary dynamics in the polarity network in budding yeast. — Werner Daalman[1], Marit Smeets[1], Fridtjof Brauns[2], Eveline Diepeveen[1], Erwin Frey[2], and •Liedewij Laan[1] — [1]Bionanoscience Department, Kavli Institute for Nanoscience, TU Delft, Delft, Netherlands — [2]Arnold Sommerfeld Center for Theoretical Physics (ASC) and Center for NanoScience (CeNS), Department of Physics, Ludwig-Maximilians-Universität München, München, Germany

How do self-organisational properties of proteins affect the evolutionary dynamics of a biochemical network? We address this question by focussing on the polarity establishment network in budding yeast. We combine experimental evolution, reaction-diffusion models and quantitative cell biology to obtain a biophysical understanding of the evolutionary reorganization of this network.

Poster P.101 17:15 Auditorium foyer

A Novel Way To Trap DNA In A Nanopore — •Sergii Pud[1], Shu-Han Chao[2], Maxim Belkin[2], Daniel Verschueren[1], Teun Huijben[1], Casper van Engelenburg[1], Cees Dekker[1], and Alek-sei Aksimentiev[2] — [1]Department of Bionanoscience, Kavli Institute of Nanoscience, Delft University of Technology, Van der Maasweg 9, 2629 HZ Delft, The Netherlands — [2]Department of Physics, University of Illinois at Urbana—Champaign, Urbana, Illinois 61801, United States

We present a double-pore system where two nanopores are drilled in parallel within the same solid-state membrane. Simultaneous electrophoretic capture of a DNA molecule by the two nanopores mechanically traps the molecule, increasing its residence time within the nanopores by orders of magnitude.

Poster P.102 17:15 Auditorium foyer

Large fluctuations and dynamic phase transition in self-propelled particles systems — •Francesco Cagnetta[1], Federico Corberi[2], Giuseppe Gonnella[3], and Antonio Suma[4] — [1]School of Physics and Astronomy, University of Edinburgh, Edinburgh, United Kingdom — [2]Dipartimento di Fisica E. R. Caianiello and INFN, Gruppo Collegato di Salerno, Università di Salerno, Fisciano (SA), Italy — [3]Dipartimento di Fisica M. Merlin and INFN, sezione di Bari, Università di Bari, Bari, Italy — [4]SISSA Scuola Internazionale Superiore di Studi Avanzati, Trieste, Italy

The Large Deviations of the work done by the active force are studied in several models of interacting self-propelled particles. Remarkably, the corresponding rate function displays a parabolic and an anomalously-scaling linear branch joined together by a singularity, resulting in a non-equilibrium phase transition undetectable by more conventional tools.

Poster P.103 17:15 Auditorium foyer

Modelling growth-induced wrinkling of elastic biofilms — •Horst-Holger Boltz and Stefan Klumpp — Institute for nonlinear dynamics, Georg-August-University Göttingen, Friedrich-Hund-Platz 1, D-37077 Göttingen, Germany

Biofilms are large multicellular structures of microorganisms adherent to a substrate. An elastic film is created whose growth leads to residual and dynamic stresses that are relieved by a non-planar patternformation (wrinkling). We present a reductionist model highlighting the physical origin of the different morphotypes observed.

Poster P.104 17:15 Auditorium foyer

A high throughput approach to helicase biophysics — •Marco RIBEZZI — ESPCI Paris-Tech

We combine droplet-microfluidics and next-generation sequencing to test large (millions of elements) libraries of helicase mutants for both helicase and ATPase activity. The aim is to identify all single-point mutants with ATPase but not helicase activity providing insight into the structural origin of the chemo-mechanical coupling.

Poster P.105 17:15 Auditorium foyer

Unveiling the role of TKTL1 in metabolic reprogramming of hematological malignancies through GSMMs — •Effrosyni Karalitsou[1,2], Ines Baptista[1,2], Carles Foguet[1,2], Pedro Atauri[1,2], and Marta Cascante[1,2] — [1]Department of Biochemistry and Molecular Biomedicine, Faculty of Biology, Universitat de Barcelona, Av Diagonal 643, 08028, Barcelona, Spain — [2]Institute of Biomedicine of University of Barcelona (IBUB) and Associated unit to CSIC, Av Diagonal 643, 08028, Barcelona, Spain

Development of a new integrative systems biology approach to decipher the metabolic reprogramming of cells that occurs in hematological malignancies. 13C flux balance analysis and constraint-based modeling of genome-scale metabolic networks will be employed to explore the role of TKTL-1 in cancer metabolism and determine therapeutic strategies.

Poster P.106 17:15 Auditorium foyer

Statistical mechanics approaches to protein sequence evolution improve phylogenetic inference and contact prediction — •Ugo Bastolla — Centro de Biologia Molecular Severo Ochoa (CSIC-UAM), Madrid, Spain

We model the sequence-space distribution of protein families through the Boltzmann principle that these distributions have minimal Kullback-Leibler divergence from a mutational distribution and given average folding free energy of the native state. Site-specific distributions obtained from this principle improve phylogenetic inference, while pairwise distributions are useful for contact prediction.

Poster P.107 17:15 Auditorium foyer

Collective motion and avalanche behavior in animal groups — •Javier Cristín[1], María Carmen Miguel[1], and Romualdo Pastor-Satorras[2] — [1]Universitat de Barcelona, Av. Diagonal 645, 08028 Barcelona, Spain — [2]Universitat Politecnica de Catalunya, Campus Nord B4, 08034 Barcelona, Spain

We analyze animal collective motion with the basis of the Vicsek model when there is a hierarchical organization (leadership). Furthermore, we provide evidence of avalanche processes characterizing the rearrangements of the system after a perturbation, and we find the system shows a scale-free avalanche behavior.

Poster P.108 17:15 Auditorium foyer

Mechanical folding and unfolding of protein Flavodoxin — •Annamaria Zaltron[1], Enric Sanmartí[2], Anna Alemany[2], and Felix Ritort[2,3] — [1]Physics and Astronomy Department, University of Padua, via Marzolo 8, 35131, Padova, Italy — [2]Small Biosystems Lab, Faculty of Physics, University of Barcelona, Diagonal 647, 08028, Barcelona, Spain — [3]CIBER BBN, Networking Centre of Bioengineering, Biomaterials and Nanomedicine, ISCIII, Madrid, Spain

Flavodoxin is a protein with electron transfer functions which plays a key role in redox reactions. New insights on its biological activity can be gained by Optical Tweezers technique, thanks to its capability to perform single-molecule experiments, which provide valuable information on the free energy landscape of this fascinating protein.

Poster P.109 17:15 Auditorium foyer

Pathogenic protein aggregation in confined space — •Jacek Siódmiak — Institute of Mathematics and Physics, UTP University of Science and Technology, Bydgoszcz, Poland

The results of studies on the influence of boundary conditions on protein aggregation are presented. In an open environment proteins form branched aggregates. Their secondary structure is mostly preserved. In confined environment proteins form dense spherical aggregates. All molecules lose their characteristic secondary structure and as a consequence their functionality.

Poster P.110 17:15 Auditorium foyer

Cooperative phenomena in the mechanical behaviour of filamentous materials with molecular motors — Agustín Sánchez-Cobos and •M. Carmen Miguel — Department de Física de la Matèria Condensada, University of Barcelona, Barcelona, Spain

Mechanical force acting on actin networks is shared between molecular motors like myosins and actin crosslinkers. Motors transport various cargoes in cells under mechanical load and often work more efficiently in small teams. We determine the effects of elastic interaction in the cooperative dynamics of motor complexes under controlled deformation.

Poster P.111 17:15 Auditorium foyer

Characterization of ligand-receptor interactions measured by an optical biosensor based on photonic crystal surface waves — •Ekaterina Rostova, Carine Ben Adiba, Giovanni Dietler, and Sergey K. Sekatskii — École Polytechnique Fédérale de Lausanne (EPFL), Laboratoire de physique de la matière vivante Rte de la Sorge , 1015 Lausanne, Switzerland

Unique qualitative information on drug binding can be revealed from real time measurements of binding kinetics measured by biosensors based on photonic crystal surface waves. Using this biosensor, we measured binding of antibodies against lipopolysaccharides to living bacteria Escherichia coli and determined a dissociation constant KD = 6.23.4 nM.

Poster P.112 17:15 Auditorium foyer

Self-organizing amyloid in bacteria — •Daniel Otzen[1], Brian Vad[1], Morten Dueholm[2], Per Halkjaer Nielsen[2], Sarah Rouse[3], and Steve Matthews[3] — [1]iNANO, Aarhus University, Aarhus, Denmark — [2]Aalborg University, 9000 Aalborg, Denmark — [3]Imperial College, London SW72AZ, UK.

Bacteria producing functional amyloid harness a potentially destructive protein fold into a powerfully stable structure. They achieve this using evolutionarily optimized imperfect sequence repeats combined with a highly sculpted energy funnel that directs metastable random coiled polypeptides into a highly organized assembly. Recent structures shed more light on this.

Poster P.113 17:15 Auditorium foyer

Automatic staging system for E7.5-E8.5 mouse embryos — •Isaac Esteban and Miguel Torres — Spanish National Centre for Cardiovascular Research Carlos III (CNIC), Madrid, Spain

We are developing an automatic staging system, based on objective morphometry, to precisely stage mouse embryos between day 7.5 and day 8.5. This tool, will allow to properly compare 3D data from different specimens and experiments, where stage determination is crucial. The approach is based in transformation-invariant spherical harmonic representation.

Poster P.114 17:15 Auditorium foyer

Aβ amyloid folding and interactions investigated by Small Angle X-ray Scattering — •Caterina Ricci — Polytechnic University of Marche - DiSVA, Ancona, Italy

The study of Aβ interaction with other protein systems can unveil the mechanism of amyloid fibril formation and therefore allow to suggest a methodology to prevent non-specific aggregation, related to Alzheimer's disease. A SAXS study, mainly focused on Aβ interaction with human chaperones, and its perspectives will be presented.

Poster P.115 17:15 Auditorium foyer

Stochastic terminal dynamics: Characterizing the behavior of terminal biological systems — •Nicolas Lenner, Stephan Eule, and Fred Wolf — MPI for Dynamics and Self-Organization

We present a new meaningful way to analyze the behavior of biological systems close to a terminal point by aligning the measured noisy timetraces to this specific point. We derive a rigorous mathematical description for the resulting time-reversed ensemble and provide analytic expressions for its mean, variance and covariance.

Poster P.116 17:15 Auditorium foyer

Experimental measurement of binding energy, selectivity and allostery using fluctuation theorems — •Anna Alemany — Hubrecht Institute, Utrecht, Netherlands

We introduce a fluctuation theorem for ligand binding and an experimental approach using single-molecule force-spectroscopy to determine binding energies, selectivity and allostery of nucleic acids, proteins and peptides in a model-independent fashion. This work extends the use of fluctuation theorems beyond folding reactions, bridging thermodynamics of small systems and laws of chemical equilibrium.

Poster P.117 17:15 Auditorium foyer

Single molecule pulling experiments under feedback — •Regina K. Schmitt[1], Jonas Johansson[1], Marc R. Pasto[2], and Felix Ritort[2,3] — [1]Solid State Physics and NanoLund,LundUniversity, PO Box 118, SE-22100Lund, Sweden — [2]Departament de Física Fonamental, Universitat de Barcelona, Diagonal 647, 08028 Barcelona, Spain — [3]CIBER de Bioingeniería, Biomateriales y Nanomedicina, Instituto de Salud Carlos III, 28029 Madrid, Spain

Fluctuation theorems such as the Jarzynsk's equality (JE) and Crooks fluctuation theorem (CFT) show impressingly the connection between non-equilibrium and equilibrium quantities. Experimentally single molecule pulling experiments have been used to validate these theorems. We apply feedback to single molecule pulling experiments continiously and at discrete times and compare with CFT and a generalized JE.

Poster P.118 17:15 Auditorium foyer

Role of the Central Ion in the Telomeric G-quadrulplex: Simulations at Micro and Mesoscopic Level — •Alessandro Fiasconaro[1], Ana Elisa Bergues-Pupo[1], and Fernando Falo[1,2] — [1]Departamento de Física dela Materia Condensada, Universidad de Zaragoza, Zaragoza, Spain — [2]Instituto de Biocomputación y Física de Sistemas Complejos (BIFI), Universidad de Zaragoza, Zaragoza, Spain

We present a theoretical unfolding analysis of the G-quadruplex structure of a Telomeric DNA segment subject to a stretching force. The simulations, in both the two levels, classic microscopic, and mesoscopic, reveal the importance of the ion present in between the guanine planes to maintain the stability of the structure.