SUN-1: Keynote Talk 1

Time: Sunday, 19:00–20:00 Location: Auditorium

Keynote SUN-1.1 19:00 Auditorium
A brief overview on the search for life beyond Earth — •Roberto Orosei — INAF-IRA, Bologna, Italy
In the Solar System, both Mars and Venus have been inhabitable in the past but are now nearly sterile. Several moons harbour liquid water beneath their surface, and they might constitute the most common type of habitat in the Universe. Our galaxy alone could host perhaps a billion Earth-like worlds.

MON: Welcome

Time: Monday, 8:50–9:00 Location: Auditorium

Welcome by Felix Ritort

MON-1: Session 1

Time: Monday, 9:00–10:40 Location: Auditorium

Invited MON-1.1 9:00 Auditorium
Why is there so much fine-scale microbial diversity? — •Daniel S Fisher — Stanford University, Stanford, CA, USA
A fundamental question, motivated by findings of extensive strain-level bacterial diversity competing and coexisting, is addressed via simple models. In a constant uniform environment, in the absence of any niche structure, can populations sustain and evolve extensive diversity? A scenario with spatiotemporal ecological chaos and continual diversification is developed.

Invited MON-1.2 9:30 Auditorium
Incongruent Evolution of Sequences and Structure in RNA and Proteins — •Peter F. Stadler — Leipzig University, Leipzig, Germany
Evolutionary pressures may lead to discrepancies between the conservation of sequence and structure. In both proteins and RNA this may lead to an apparent shift between sequence and structural features. Conventional alignment-based methods fail to identify consensus structure in this case. Bi-alignments represent sequence alignment, structure alignments, and their relationship explicitly and serve as suitable formal framework to describe incongruent evolution.

Oral MON-1.3 10:00 Auditorium
Fitness landscape analysis of a tRNA gene reveals that the wild type allele is sub-optimal, yet mutationally robust — Tzahi Gabzi[1], Yitzhak Pilpel[1], and •Tamar Friedlander[2] — [1]Weizmann Institute of Science, Rehovot, Israel — [2]Hebrew University of Jerusalem, Rehovot, Israel
We analyzed fitness data of 23,284 tRNA gene variants. We found that the wild-type is suboptimal and ruled out the possibilities that it is the fittest on average on multiple conditions or a local fitness maximum. Instead, the wildtype is amongst the least mutationally fragile genotypes in the dataset.

Oral MON-1.4 10:20 Auditorium
Quantifying the interplay between transcription, DNA supercoiling and topoisomerase activity in vivo — •Ivan Junier — TIMC, Grenoble, France
I will present a first-principle biophysical model of transcription allowing to rationalize the behavior of a wide range of gene promoters in various topological contexts and to highlights the specific implication of topoisomerases in vivo.

10:40–11:15: Coffee Break

MON-2: Session 2

Time: Monday, 11:15–12:55 Location: Auditorium

Invited MON-2.1 11:15 Auditorium
Compensatory epistasis maintains ACE2 affinity in SARS-CoV-2 Omicron BA.1 — •Michael Desai — Harvard University, Cambridge, USA
Relative to the ancestral Wuhan Hu-1 strain and other pre-Omicron SARS-CoV-2 variants, Omicron BA.1 has many mutations, a number of which are known to enable antibody escape. I will describe our work to map the epistatic interactions that allow BA.1 to tolerate these antibody escape mutations while maintaining ACE2 affinity.

Invited MON-2.2 11:45 Auditorium
Adaptive ratchets and the evolution of molecular complexity — Tom Röschinger[1], Roberto Moran-Tovar[2], Simone Pompei[2,3], and •Michael Lässig[2] — [1]California Institute of Technology, Pasadena, USA — [2]University of Cologne, Cologne, Germany — [3]FIRC Institute for Molecular Oncology, Milan, Italy
We study the evolution of complexity in a minimal biophysical model for molecular recognition sites in the cell. We show that long and fuzzy sites can evolve by continuous adaptation to moving recognition targets. Our results suggest a link between two fundamental aspects of evolution, non-equilibrium and molecular complexity.

Oral MON-2.3 12:15 Auditorium
Antibody sequence-affinity landscapes reveal evolutionary constraints of affinity maturation — •Angela Phillips[1], Daniel Maurer[2,3], Aaron Schmidt[2,3], and Michael Desai[1] — [1]Harvard University, Cambridge, USA — [2]Ragon Institute, Cambridge, USA — [3]Harvard Medical School, Boston, USA
Our understanding of the evolutionary pathways leading to broadly neutralizing antibodies (bnAbs) remains limited. We measure equilibrium dissociation constants of combinatorially complete mutational libraries (~100k variants) for human bnAbs, reconstructing all possible evolutionary intermediates. We find that epistasis between mutations critically defines the mapping between antibody sequence, affinity, and breadth.

Oral MON-2.4 12:35 Auditorium
Playing it safe: information constrains collective betting strategies — •Philipp Fleig[1,2] and Vijay Balasubramanian[2] — [1]Max Planck Institute for Medical Research, Heidelberg, Germany — [2]Department of Physics & Astronomy, University of Pennsylvania, Philadelphia, USA
Biological functions are partly shaped by the need to reduce risk arising from stochastic interactions with the environment. However, an organism can typically only gather limited information to guide such adaptation. We develop a theoretical principle where information geometric model complexity guides stochastic biological functions towards optimal, less risky strategies.

12:55–14:30: Lunch Break

MON-3: Session 3

Time: Monday, 14:30–15:50 Location: Auditorium

Invited MON-3.1 14:30 Auditorium
Identifying molecules as products of evolution with assembly theory — •Leroy Cronin — University of Glasgow, Glasgow, United Kingdom
I will show why complex molecules found in high abundance are products of evolution and demonstrate the first intrinsic experimentally tractable measure of molecular complexity: molecular assembly index and explain the theory, Assembly Theory(AT), outlining why the theory might be useful to explore the emergence of selection and evolution.

Invited MON-3.2 15:00 Auditorium
Microfluidic Island Biogeography — •Oskar Hallatschek — University of California, Berkeley, USA — University Leipzig, Leipzig, Germany
Bacteria colonize a wide range of spatial scales. Yet, the scale-dependence of microbial evolution is poorly understood. Using a microfluidic device to systematically vary incubation scales, we uncover sharp transitions between different colonization states with different evolutionary properties. Our findings highlight a tight feedback between spatial structure and evolution.

Oral MON-3.3 15:30 Auditorium
Multigenerational memory in bacterial size control — •Motasem ElGamel, Harsh Vashistha, Hanna Salman, and Andrew Mugler — Department of Physics and Astronomy, University of Pittsburgh, Pittsburgh, USA
Cells maintain a stable size as they grow and divide. Most experiments suggest that deviations from the stable size last for a generation or two. Recent evidence from comparing sister lineages suggests that deviations can persist for many generations. We develop a minimal model that explains these seemingly contradictory results.

15:50–16:15: Coffee Break

MON-4: Session 4

Time: Monday, 16:15–17:25 Location: Auditorium

Invited MON-4.1 16:15 Auditorium
Learning how to find an odor source with minimal memory — •Antonio Celani, Emanuele Panizon, and Kyrell Vann B. Verano — ICTP, Trieste, Italy
Many organisms, from insects to mammals, have developed exquisite skills in searching for sources of odor from huge distances in turbulent atmospheric conditions. How are these sequences of very sparse detections translated into effective strategies to reach the source in the shortest time? Here we present a Reinforcement Learning algorithm that discovers such strategies with minimal memory requirements.

Oral MON-4.2 16:45 Auditorium
Elongation enhances encounter rates between phytoplankton in turbulence — José-Agustín Arguedas-Leiva[1], •Jonasz Slomka[2], Cristian Lalescu[3], Roman Stocker[2], and Michael Wilczek[1,4] — [1]Max Planck Institute for Dynamics and Self-Organization, Göttingen, Germany — [2]Institute of Environmental Engineering, Department of Civil, Environmental and Geomatic Engineering, ETH Zurich, Zurich, Switzerland — [3]Max Planck Computing and Data Facility, Garching, Germany — [4]Theoretical Physics I, University of Bayreuth, Bayreuth, Germany
Phytoplankton cells are often highly elongated, yet how elongation affects encounter rates and thus marine snow formation by phytoplankton in turbulence has remained unknown. Here, we present simulations of encounters among elongated phytoplankton in turbulence, showing that encounter rates between cells are up to ten-fold higher than for spherical cells.

Oral MON-4.3 17:05 Auditorium
Marginal model reconciles long-range correlation and speed control in collective behaviour — Andrea Cavagna[1,2,3], •Antonio Culla[1,2], Xiao Feng[1,2], Irene Giardina[1,2,3], Tomas S. Grigera[1,4,5,6], Willow Kion-Crosby[1,2], Stefania Melillo[1,2], Giulia Pisegna[1,2], Lorena Postiglione[1,2], and Pablo Villegas[7,8] — [1]Institute for Complex Systems, CNR, Rome, Italy — [2]Sapienza University, Rome, Italy — [3]INFN, Rome, Italy — [4]Instituto de Física de Líquidos y Sistemas Biológicos CONICET - Universidad Nacional de La Plata, La Plata, Argentina — [5]CCT CONICET La Plata, Consejo Nacional de Investigaciones Científicas y Técnicas, Buenos Aires, Argentina — [6]Departamento de Física, Facultad de Ciencias Exactas, Universidad Nacional de La Plata, La Plata, Argentina — [7]IMT Institute for Advanced Studies, Lucca, Italy — [8]Enrico Fermi Research Center (CREF), Rome, Italy
Empirical data show that bird's speed fluctuations within starling flocks are correlated over large distances. Long-range correlations, though, coexist with strong biomechanical constraints, as birds' speed must remain close to a natural reference value. We propose a new control mechanism that explains how these two phenomena can coexist.

MON-P: Monday Poster Session

Time: Monday, 17:30–19:00 Location: Foyer

Poster MON-P.1 17:30 Foyer
ABC Transporters are billion-year-old Maxwell Demons — •Solange M. Flatt[1], Daniel M. Busiello[1], Stefano Zamuner[1], and Paolo De Los Rios[1,2] — [1]Institute of Physics, School of Basic Sciences, École Polytechnique Fédérale de Lausanne, Lausanne, Switzerland — [2]Institute of Bioengineering, School of Life Sciences, École Polytechnique Fédérale de Lausanne, Lausanne, Switzerland
In our work, we build a thermodynamically consistent model of ATP-Binding Cassette (ABC) transporters which is able to qualitatively reproduce their entire phenomenology. We show that a description in terms of information theory arises naturally from structural and biochemical considerations, revealing that ABC transporters are exactly autonomous Maxwell's Demons.

Poster MON-P.2 17:30 Foyer
Stochastic modelling of agent based populations — •Francesco Puccioni and Philipp Thomas — Imperial College of London, London, United Kingdom
I present a stochastic model to address the role of cell heterogeneity on population dynamics. We show that the population structure can be characterized by a functional master equation that can be manipulated to obtain a novel integral renewal equation that encodes the stochastic description of the cell population dynamics.

Poster MON-P.3 17:30 Foyer
Directed Evolution of DNA Polymerases and the Thermodynamics of Activity – Fidelity Trade-Offs — •Viktor Wendelin Zahoransky, Marco Ribezzi Crivellari, and Andrew Griffiths — École supérieure de physique et de chimie industrielles de la ville de Paris, Paris, France
Directed evolution of DNA-Polymerases: Exploring the tradeoffs between activity and fidelity by combining massively parallel activity screens based on microdroplets, the synthesis of large gene libraries and high-throughput sequencing. Investigation of the kinetics of Phi29 polymerase variants based on Michaelis-Menten theory.

Poster MON-P.4 17:30 Foyer
Hydrodynamic Interactions Can Induce Jamming in Flow-Driven Systems — Eric Cereceda López[1], Antonio Ortiz Ambriz[1], Dominik Lips[2], Artem Ryabov[3], Philipp Maass[2], and •Pietro Tierno[1] — [1]University of Barcelona, Barcelona, Spain — [2]Universität Osnabrück, Osnabrück, Germany — [3]Charles University, Praha, Czech Republic
Hydrodynamic interactions between fluid-dispersed particles are ubiquitous in biological systems. Here we combine experiments and theory to show that such interactions hinder the transport across energetic barriers. Our colloidal model system is based on driven particles within rotating optical traps that create a vor-

tex flow in the corotating reference frame.

Poster MON-P.5 17:30 Foyer

Heteroclinic units acting as pacemakers for information transfer in cognitive processes — •Bhumika Thakur and Hildegard Meyer-Ortmanns — Jacobs University Bremen, Bremen, Germany

Heteroclinic dynamics is a suitable framework for describing reproducible transient dynamics such as cognitive processes. Heteroclinic units acting as pacemakers are shown to entrain larger sets of units from a resting state to hierarchical heteroclinic motion describing fast oscillations modulated by slow oscillations, features which are observed in brain dynamics.

Poster MON-P.6 17:30 Foyer

Methodological notes on pandemic virus SARS-CoV-2 research — •Gianluigi Zangari del Balzo — Sapienza University, Rome, Italy

Given the global relevance of the topics related to the COVID-19 pandemic, we would like to present the work published on 8 September 2021 by the Nature Public Health Emergency Collection and by the World Health Organization (covidwho-1397057), containing an energy landscape statistical theory of the new quasi-species and variants of the pandemic SARS-CoV-2 virus in its environment.

Poster MON-P.7 17:30 Foyer

An active wetting transition enables optimal collective durotaxis — Macià-Esteve Pallarès[1], Irina Pi-Jaumà[2,3], Isabela Corina Fortunato[1], Valeria Grazu[4,5,6], Manuel Gómez-González[1], Pere Roca-Cusachs[1,7], Jesus M de la Fuente[4,5,6], Ricard Alert Alert[8,9], •Raimon Sunyer[1,7,10], Jaume Casademunt[2,3], and Xavier Trepat[1,6,7,11] — [1]Institute for Bioengineering of Catalonia (IBEC), The Barcelona Institute for Science and Technology (BIST) , Barcelona, Spain — [2]Departament de Física de la Matèria Condensada, Universitat de Barcelona, Barcelona, Spain — [3]Universitat de Barcelona Institute of Complex Systems (UBICS), Barcelona, Spain — [4]Instituto de Nanociencia y Materiales de Aragón (INMA), CSIC-Universidad de Zaragoza, Zaragoza, Spain — [5]Consejo Superior de Investigaciones Científicas, Zaragoza, Spain — [6]Centro de Investigación Biomédica en Red de Bioingeniería (CIBER-BBN), Barcelona, Spain — [7]Departament de Biomedicina, Universitat de Barcelona, Barcelona, Spain — [8]Max Planck Institute for the Physics of Complex Systems, Dresden, Germany — [9]Center for Systems Biology Dresden, Dresden, Germany — [10]Institute of Nanoscience and Nanotechnology (IN2UB), Barcelona, Spain — [11]Institució Catalana de Recerca i Estudis Avançats (ICREA), Barcelona, Spain

The directed migration of cellular clusters enables morphogenesis, wound healing, and cancer invasion. Gradients of substrate stiffness are known to direct cluster migration in a process called collective durotaxis. Here we identify and model a new mode of collective durotaxis that emerges at the proximity of an active wetting transition.

Poster MON-P.8 17:30 Foyer

The minimal chemotactic cell — •Barbara B. Fernandes[1,2], Azzurra Apriceno [1], Safa Almadhi[3], Ian Williams[1,6], and Giuseppe Battaglia[1,3,4,5] — [1]Institute for Bioengineering of Catalonia (IBEC), The Barcelona Institute of Science and Technology (BIST), Barcelona, Spain — [2]Department of Physics, University of Barcelona, Barcelona, Spain — [3]Department of Chemistry, University College London, London, United Kingdom — [4]University College London, Institute for the Physics of Living Systems, London, United Kingdom — [5]Catalan Institution for Research and Advanced Studies (ICREA), Barcelona, Spain — [6]Department of Physics, University of Surrey, Guildford, United Kingdom

Porated liposomes with encapsulated glucose oxidase were developed to move in response to glucose concentration gradients. The experiment in a microfluidic device highlights the contribution of diffusioosmophoresis and chemotaxis. The liposome's movement direction could be controlled according to the presence/absence of pores in its membrane.

Poster MON-P.9 17:30 Foyer

withdrawn

Poster MON-P.10 17:30 Foyer

Phenotypic targeting of different macrophages states — •Lara Victoria Aiassa[1,5], Claudia Di Guglielmo[1], Silvia Acosta-Gutiérrez[1,2,3], Diana Matias[2,3], Loris Rizzello[1,4,5], and Giuseppe Battaglia[1,2,3,6] — [1]Institute for Bioengineering of Catalunya (IBEC), Barcelona, Spain — [2]Department of Chemistry, University College London, London, United Kingdom — [3]Institute for the Physics of Living Systems, University College London, London, United Kingdom — [4]Department of Pharmaceutical Sciences, University of Milan, Milan, Italy — [5]Istituto Nazionale di Genetica Molecolare (INGM), Milan, Italy — [6]Catalan Institution for Research and Advanced Studies (ICREA), Barcelona, Spain

Scaffolds functionalized with multiple ligands display peculiar binding properties that arise from multivalent effects. Using statistical modelling, we describe the particle-cell interaction and demonstrated how multivalency can be exploited to achieve specific cell-phenotype selectivity. To further validate our phenotypic targeting strategy and refine our in-silico model, we propose the design of super-selective nanoparticles for specific macrophage phenotypes.

Poster MON-P.11 17:30 Foyer

A spin-glass approach to spatial distributions in biology — •Javier Cristin[1], Vicenc Mendez[2], and Daniel Campos[2] — [1]Institute for Complex Systems, Rome, Italy — [2]Universitat Autònoma de Barcelona, Barcelona, Spain

We propose a data-driven method, based on the framework of spin-glasses (SG), to interpret the evolutionary collective dynamics of biological populations.

Poster MON-P.12 17:30 Foyer

Geometry-based decomposition of forces and currents in complex reaction networks — •Sara Dal Cengio[1], Matteo Polettini[2], and Vivien Lecomte[1] — [1]LiPHY (Université Grenoble Alpes), Grenoble, France — [2]University of Luxembourg, Luxembourg, Luxembourg

Combining tools from graph theory and linear algebra, we propose a framework to identify the thermodynamical observables in complex reaction networks. We apply the formalism to study the linear response, unveiling the Onsager symmetries between response and relaxation in arbitrarily complex networks.

Poster MON-P.13 17:30 Foyer

The effect of glycans steric potentials on virus infectivity: the SARS-CoV-2 case — •Silvia Acosta-Gutierrez[1,2,3,4], Joseph Buckley[1,2,3], and Giuseppe Battaglia[1,2,3,4,5,6] — [1]Institute for Bioengineering of Catalonia, Barcelona, Spain — [2]Physical Chemistry Chemical Physics Division, Department of Chemistry, University College London, London, United Kingdom — [3]Institute of Structural and Molecular Biology, University College London, London, United Kingdom — [4]Institute for the Physics of Living Systems, University College London, London, United Kingdom — [5]EPSRC/JEOL Centre for Liquid Phase Electron Microscopy, University College London, London, United Kingdom — [6]Catalan Institution for Research and Advanced Studies (ICREA), Barcelona, Spain

Glycans are sugars coating both the cell and the protein surfaces. This sugar cushion, the glycocalyx, modulates specific interactions and protects the cell. Here we show how glycans expressed on the surface of both the host and virus proteins have a critical role in modulating viral attachment to the cell.

Poster MON-P.14 17:30 Foyer

First-passage statistics of movement models with home-ranging behavior — •Benjamin Garcia de Figueiredo[1,2] and Ricardo Martinez-Garcia[1,2] — [1]Instituto de Física Teórica - Universidade Estadual Paulista, São Paulo, Brazil — [2]International Center for Theoretical Physics - South American Institute for Fundamental Research, São Paulo, Brazil

We study the probabilistic interaction between a range-resident animal and traffic by studying analytically the first-passage properties of Ornstein-Uhlenbeck processes. OU first encounter times are both higher and lower than in well-mixed scenarios depending on model parameterization, which indicates the importance of considering realistic movement to develop realistic ecosystem-level models.

Poster MON-P.15 17:30 Foyer

Bifurcations in droplet collisions — •Anshuman Dubey[1], Kristian Gustavsson[1], Gregory Bewley[2], and Bernhard Mehlig[1] — [1]University of Gothenburg, Gothenburg, Sweden — [2]Cornell University, Ithaca, USA

The effects of charges, continuum breakdown, and hydrodynamic interactions on collisions of droplets is a critical problem in various fields. However, how the collision mechanism is determined by various effects is not understood. We use dynamical-systems theory to explain the mechanisms governing collisions of water droplets settling in still air.

Poster MON-P.16 17:30 Foyer

Vaccination Shapes Evolutionary Trajectories of SARS-CoV-2 — •Matthijs Meijers, Denis Ruchnewitz, and Michael Laessig — Institute of Biological Physics, University of Cologne, Cologne, Germany

Vaccine-induced antigenicity shapes the evolution of SARS-CoV-2, accelerating the turnover to clades with increased distance to the wild type strain used for vaccination. Our results explain the observed dynamics of the frequency data of major variants, and stresses the effect of population immunity of the selection of novel variants.

Poster MON-P.17 17:30 Foyer

Understanding the genetic determinants in antibiotic resistance evolution — •Gabriela Petrungaro and Tobias Bollenbach — Institute for Biological Physics, University of Cologne, Köln, Germany

We explore how the genetic background of a founding population affects its dynamics towards evolution of resistance to several antibiotics. By comparing between parallel evolution experiments under controlled selection, we identified specific genes whose deletion on the founding genome has a strong effect on the rate of resistance evolution.

Poster MON-P.18 17:30 Foyer

Epidemiological control shapes the evolution of emerging pathogens towards endemicity — •Denny Trimcev and Michael Lässig — Institute for Biological Physics, Cologne, Germany

An emerging epidemic creates complex eco-evolutionary dynamics, in which antigenic differentiation may lead to an endemic state. Human interventions play a fate deciding role in this transition. We find that strong interventions increase time for vaccine developement, increasing expected vaccine efficacy by limiting antigenic advance of the escape mutant.

Poster MON-P.19 17:30 Foyer

Quantification of flow-driven microbial encounters to better characterize bacterial gene exchange by conjugation — •Matti Zbinden, Roman Stocker, and Jonasz Slomka — ETH Zurich, Zurich, Switzerland

Conjugation, a key example of horizontal gene transfer between bacteria, requires cell-cell encounters, yet how physical encounters impact conjugation remains largely unexplored. Here, we present an experimental set up to better characterize bacterial conjugation by controlling cell-cell encounters in a liquid suspension.

Poster MON-P.20 17:30 Foyer

Experimental Measurement of Information-Content in Mutational Ensembles — •F. Ritort, A.M. Monge, M. Manosas, D. Incarnato, A. Alemany, and M. Ribezzi-Crivellari — Small Biosystems Lab, Facultat de Física, Departament de Física de la Matèria Condensada, Universitat de Barcelona, Diagonal 647, 08028, Barcelona, Spain

Biology is noisy at all levels, from molecules to cells, tissues, organs, communities and ecosystems [1]. While thermodynamic processes in ordinary matter are driven by free- energy minimization, living matter and biology delineate a fascinating evolutionary state governed by information flows across all organizational levels [2].

Poster MON-P.21 17:30 Foyer

Modeling drug resistance: Evolutionary dynamics that shape fitness landscapes of human cancers — •Nicola Dick and Donate Weghorn — Centre for Genomic Regulation, Barcelona, Spain

In population genetics, the therapeutic pressure on a cancer cell population represents a shift in its fitness landscape. Therefore, tumors with higher variability in cellular fitness should recover from the attack more quickly. We study this by modelling different modes of tumor drug response in numerical simulations.

MON-5: Keynote Talk 2

Time: Monday, 19:00–20:00 Location: Auditorium

Keynote MON-5.1 19:00 Auditorium

Genotype to phenotype from natural and experimental evolution — •Chris Sander — Harvard Medical School, Boston, MA, USA

The author will discuss about genotype to phenotype from natural and experimental evolution

TUE-1: Session 1

Time: Tuesday, 9:00–10:40 Location: Auditorium

Invited TUE-1.1 9:00 Auditorium

How the topology of genotype spaces shapes evolutionary dynamics — •Susanna Manrubia — National Biotechnology Centre, Madrid, Spain — Grupo Interdisciplinar de Sistemas Complejos, Madrid, Spain

Genotype-phenotype maps break genotype spaces into a large number of highly intermingled networks of uneven size. Understanding this network-of-networks structure is essential to update evolutionary theory, since, contrary to more gradualistic descriptions, the evolutionary dynamics of molecular populations becomes intrinsically non-uniform and displays nonlinear responses analogous to critical transitions.

Invited TUE-1.2 9:30 Auditorium

Attempting to understand fitness landscapes in the context of protein physics — •Fyodor Kondrashov — Evolutionary and Synthetic Biology Unit, Okinawa Institute of Science and Technology Graduate University, Okinawa, Japan

Understanding how the phenotype is formed by the underlying genotype is one of the most important questions in biology. I will talk about our recent work characterizing the fitness landscapes of four orthologous proteins with a broad range of sequence divergence.

Oral TUE-1.3 10:00 Auditorium

Contingency and Entrenchment in Molecular Evolution: a Fitness Landscape Perspective — •Lucy Lansch-Justen[1] and Joachim Krug[2] — [1]Institute of Evolution and Ecology, University of Edinburgh, Edinburgh, United Kingdom — [2]Institute for Biological Physics, University of Cologne, Cologne, Germany

Epistasis can contribute to irreversibility in molecular evolution for example because substitutions are contingent on previous/get entrenched by subsequent substitutions. We use random fitness landscapes to show that contingency and entrenchment arise in rugged landscapes and under dynamics which are manifestly reversible, and that they are robust but not universal.

Oral TUE-1.4 10:20 Auditorium

Variational bias in the genotype-phenotype map of Richard Dawkins' biomorphs — •Nora S. Martin[1], Chico Q. Camargo[2], and Ard A. Louis[1] — [1]Department of Physics, University of Oxford, Oxford, United Kingdom — [2]Department of Computer Science, University of Exeter, Exeter, United Kingdom

Genotype-phenotype maps provide information on the phenotypic effect of mutations and thus on variation in evolutionary processes. However, most existing work focuses on the molecular scale, such as RNA or protein structures. To go beyond this scale, we analyse Richard Dawkins' biomorphs, a toy model of a developmental process.

10:40–11:15: Coffee Break

TUE-2: Session 2

Time: Tuesday, 11:15–12:55 Location: Auditorium

Invited TUE-2.1 11:15 Auditorium
A Statistical Mechanics for Living Chemistries — •Sara WALKER — Arizona State University, Tempe, AZ, USA
In this talk I discuss new approaches to understanding what universal principles might explain the nature of life and elucidate the mechanisms of its origins, focusing on recent work elucidating regularities and law-like behavior of living chemistries on Earth and how the molecules of life are assembled.

Oral TUE-2.2 11:45 Auditorium
Synthetic evolution of DNA oligomers — Luca Casiraghi[1], Elvezia Paraboschi[2], Francesco Mambretti[3], Samir Suweis[3], and •Tommaso Bellini[1] — [1]University of Milano, Milano, Italy — [2]Humanitas University, Pieve Emanuele (Milano), Italy — [3]University of Padova, Padova, Italy
We introduce a synthetic evolution platform based on SELEX that enables following an ecosystem formed by DNA 50mers across generations. In a single niche-type condition, the population of DNA oligomers evolves from random to dominated by a few coexisting species. A fitness based on DNA-DNA interactions enables quantifying the process.

Oral TUE-2.3 12:15 Auditorium
Robustness of Compositional Heredity to the Growth and Division Dynamics of Prebiotic Compartments — •Yoshiya J. Matsubara[1], Sandeep Ameta[1], Shashi Thutupalli[1,2], Philippe Nghe[3], and Sandeep Krishna[1] — [1]National Centre for Biological Sciences, TIFR, Bangalore, India — [2]International Centre for Theoretical Sciences, TIFR, Bangalore, India — [3]ESPCI Paris, PSL University, Paris, France
How did self-reproducing entities capable of inheriting compositional information emerge? Using a bistable autocatalytic chemical system, we investigate conditions for heredity under the growth and division of compartments. We find the serial dilution protocol rigorously bounds such conditions, allowing laboratory tests for the ability of chemical systems to evolve.

Oral TUE-2.4 12:35 Auditorium
Generative power of a protein language model trained on MSAs — •Damiano Sgarbossa, Umberto Lupo, and Anne-Florence Bitbol — Institute of Bioengineering, School of Life Sciences, École Polytechnique Fédérale de Lausanne (EPFL), Lausanne, Switzerland
We propose a method to generate novel protein sequences using MSA Transformer, a protein language model trained on multiple sequence alignments. Our method uses masked language modeling iteratively. The resulting sequences score better than those generated by Potts models, and even than natural sequences, for homology, coevolution and structure-based measures.

12:55–14:30: Lunch Break

TUE-3: Session 3

Time: Tuesday, 14:30–15:50 Location: Auditorium

Invited TUE-3.1 14:30 Auditorium
The coevolved web of life — •Jordi Bascompte — University of Zurich, Zurich, Switzerland
The mutualistic interactions between plants and their pollinators or seed dispersers form complex networks of mutual dependencies. Coevolution within such networks is driven by non-interacting species as much as by directly interacting species. Indirect effects result in a continuous reorganization of the adaptive landscape and a highly unpredictable coevolutionary process.

Invited TUE-3.2 15:00 Auditorium
Symmetry and simplicity spontaneously emerge from the algorithmic nature of evolution — •Iain Johnston[1,2,3,4], Kamaludin Dingle[5], Sam Greenbury[6,7], Chico Camargo[8], Jonathan Doye[9], Sebastian Ahnert[4,6,10], and Ard Louis[3] — [1]Department of Mathematics, University of Bergen, Bergen, Norway — [2]Computational Biology Unit, University of Bergen, Bergen, Norway — [3]Rudolf Peierls Centre for Theoretical Physics, University of Oxford, Oxford, United Kingdom — [4]The Alan Turing Institute, London, United Kingdom — [5]Centre for Applied Mathematics and Bioinformatics, Department of Mathematics and Natural Sciences, Gulf University for Science and Technology, Hallwaly, Kuwait — [6]Theory of Condensed Matter Group, Cavendish Laboratory, University of Cambridge, Cambridge, United Kingdom — [7]Department of Metabolism, Digestion and Reproduction, Imperial College London, London, United Kingdom — [8]Department of Computer Science, University of Exeter, Exeter, United Kingdom — [9]Physical and Theoretical Chemistry Laboratory, Department of Chemistry, University of Oxford, Oxford, United Kingdom — [10]Department of Chemical Engineering and Biotechnology, University of Cambridge, Cambridge, United Kingdom
Symmetry appears everywhere in biology, from body plans to molecular machines. But why? Combining evolutionary and physical models with computer science, we argue that evolution has a "built-in" preference for symmetry: symmetric and simple structures require less complex algorithms to produce, which are discovered more easily through evolutionary search.

Oral TUE-3.3 15:30 Auditorium
Synchronous behavior of crops: Alternate bearing strategies of adaptation — •Clara Salueña[1] and Sergei Esipov[2] — [1]Universitat Rovira i Virgili, Tarragona, Spain — [2]Quant Isle Ltd., New York, USA
WWe present the statistical analysis of fifteen years of experimental data on the collective growth of Olea europaea in an experimental grove. Fluctuations quickly synchronize forming two groups; one with biennial bearing in even years and another in odd years. Intensive pruning leads to intensified overall oscillations. The collective behavior of the grove may represent a resistance strategy.

15:50–16:15: Coffee Break

TUE-4: Session 4

Time: Tuesday, 16:15–17:25 Location: Auditorium

Invited TUE-4.1 16:15 Auditorium

Protein sequence coevolution, energy landscapes and their connections to structural maintenance of chromosomes (SMC) proteins — •Jose Onuchic — CTBP - Rice University , Houston, Texas , USA

Energy landscape theory is combined with protein sequence co-evolution to explore the three-dimensional and the sequence space landscapes for protein folding. The synergy between these landscapes is a powerful tool to help to determine protein structure but also helps with a quantitative understanding of the mechanisms governing folding and function.

Oral TUE-4.2 16:45 Auditorium

Regulation of stem cell dynamics through volume exclusion — •Roddrigo García-Tejera, Linus Schumacher, and Ramon Grima — University of Edinburgh, Edinburgh, United Kingdom

We propose the stochastic birth-death process with volume exclusion (vBD), an extension of the critical birth-death process that considers crowding effects in stem cell populations, such as may arise due to limited space in a stem cell niche. We show that volume exclusion acts as a feedback regulator.

Oral TUE-4.3 17:05 Auditorium

Shaping the embyo: blastoderm stress maps reveal early mechanical symmetry breaking — •Alejandro Jurado[1,2], Leon Lettermann[1], Bernhard Wallmeyer[2], and Timo Betz[1] — [1]Drittes Physikalisches Institut, Georg-August-Universität Göttingen, Göttingen, Germany — [2]Institute of Cell Biology, ZMBE, Westfälische Wilhelms-Universität Münster, Münster, Germany

A combination of Light-Sheet microscopy and in-vivo force measurements in Zebrafish embryos at very early developmental stages allows a full mechanical characterization of the system. Supported by a Neuronal-Netword model based on the blastocyte velocity fields, our analysis predicts the first mechanical symmetry breaking in the embryo.

TUE-P: Tuesday Poster Session

Time: Tuesday, 17:30–19:00 Location: Foyer

Poster TUE-P.1 17:30 Foyer

Understanding the Role of Hydration Water in the Self-Replication of Prebiotic Amyloid-Entities: A Comparative Thermodynamic Study using Dielectric Relaxation Spectroscopy — •Izabela Stroe[1] and Najma Bibi[2] — [1]Worcester Polytechnic Institute, WORCESTER, USA — [2]Brandeis University, Waltham, USA

Recent hypothesis of the origin of life suggests amyloids as the self-replicating and evolving prebiotic informational entities. Self-replication is dictated by thermodynamic laws and should occur with an increase in entropy. This thermodynamic study aims at deciphering the role of hydration water in the self-replication and stability of the amyloids.

Poster TUE-P.2 17:30 Foyer

Protocells and Surface-adhered Biomembrane Networks — •Ruslan Ryskulov[1], Esteban Pedrueza[1], Lin Xue[2], Elif Köksal[2], Karolina Spustova[2], Aldo Jesorka[1], and Irep Gözen[2] — [1]Chalmers University of Technology, Gothenburg, Sweden — [2]University of Oslo, Oslo, Norway

We study surface driven transformation of multilayered vesicles with further formation of protocells colonies interconnected by lipid nanotubes network. Further research aims to implement chemical/enzymatic reactions within such networks in order to gain new insights into possible protocell development scenarios in the context of the origins of life.

Poster TUE-P.3 17:30 Foyer

Driven disordered systems and antibiotic resistance evolution — •Suman Das[1], Joachim Krug[1], and Muhittin Mungan[2] — [1]Institute for Biological Physics, University of Cologne, Cologne, Germany — [2]Institut für Angewandte Mathematik, Universiät Bonn, Bonn, Germany

We introduce an empirically-based framework for the modeling of environment-dependent fitness landscapes, and use it to study bacterial evolution under changing antibiotic concentration. We use a formalism familiar from driven disordered systems to quantify effects such as hysteresis and memory formation in these models.

Poster TUE-P.4 17:30 Foyer

Migration of active fluid droplets through interstices — •Adriano Tiribocchi[1], Mihir Durve[2], Marco Lauricella[1], Andrea Montessori[3], and Sauro Succi[1,2,4] — [1]Istituto per le Applicazioni del Calcolo CNR, Via dei Taurini 19, 00185, Rome, Italy — [2]Center for Life Nano Science@La Sapienza, Viale Regina Elena, 291, 00161 Roma, Italy — [3]Department of Engineering, Roma Tre University, Via Vito Volterra 62, 00146 Rome, Italy, Italy — [4]Department of Physics, Harvard University, Cambridge, MA, 02138, USA

We numerically study the physics of a droplet of active polar fluid migrating through an interstice with adhesive properties, and report evidence of a striking variety of dynamic regimes and morphological features, whose properties depend upon droplet speed and elasticity, degree of confinement and adhesiveness to the pore.

Poster TUE-P.5 17:30 Foyer

Translocation, Rejection and Trapping of Polyampholytes — •Yeong-Beom Kim[1], Min-Kyung Chae[1], Jeong-Man Park[2], Albert Johner[3], and Nam-Kyung Lee[1] — [1]Department of Physics and Astronomy, Sejong university, Seoul 05006, South Korea — [2]Department of Physics, The Catholic University of Korea, Bucheon 14662, South Korea — [3]Institut Charles Sadron (ICS), CNRS-Unistra, Université de Strasbourg, F-67000 Strasbourg, France

We investigate the role of the charge-sequence on the translocation behavior of polyampholyte chains by means of Monte Carlo simulations that incorporates a realistic translocation potential profile. Translocation and rejection are escape out of traps built up along the random sequences, and trapped sequences relax logarithmically over time.

Poster TUE-P.6 17:30 Foyer

Simple reaction-diffusion modelling predicts inconspicuous neighbourhood-dependent colour sub-clustering of lizard scales — •Szabolcs Zakany and Michel Milinkovitch — Laboratory of Artificial & Natural Evolution (LANE), Dept. of Genetics & Evolution, University of Geneva, Geneva, Switzerland

Scale-by-scale colour patterning of adult ocellated lizards is effectively well modelled by a reaction-diffusion (RD) system. We show that unsuspected model-predicted skin scale neighbourhood dependence of RD reactants in the final pattern is actually present in both hyperspectral colour measurements and chromatophore distribution within skin scales.

Poster TUE-P.7 17:30 Foyer

Fire Ants as Active Matter – Motility Induced Attraction, Activity Cycles, and Travelling Waves — •Caleb Anderson[1,2] and Alberto Fernandez-Nieves[1,2,3,4] — [1]Georgia Institute of Technology, Atlanta, USA — [2]University of Barcelona, Barcelona, Spain — [3]Institucio Catalana de Recerca i Estudis Avancats, Barcelona, Spain — [4]Institute for Complex Systems, Barcelona, Spain

Collectives of Solenopsis Invicta, fire ants, can be viewed as a special type of out-of-equilibrium matter called active matter. We show that several of their surprising group behaviors can be understood within the framework of active matter by studying how pairs of ants interact.

Poster TUE-P.8 17:30 Foyer

Ligand Discrimination in the Notch Signaling Pathway — •Sergio Casajus and Marta Ibañes — Universitat de Barcelona, Barcelona, Spain

We propose a set of models that, making use of observed processes, are able to describe the different dynamics present in the Notch Signaling Pathway, not considered in previous theoretical descriptions.

Poster TUE-P.9 17:30 Foyer

Physical models for viral RNA resistance to in vivo degradation — Matteo Becchi[1], •Pietro Chiarantoni[1], Antonio Suma[2], and Cristian Micheletti[1] — [1]Physics Area, Scuola Internazionale Superiore di Studi Avanzati (SISSA), Trieste, Italy — [2]Dipartimento di Fisica, Università di Bari and Sezione INFN di Bari, Bari, Italy

We used MD simulations of nanopore translocation to investigate how the Zika xrRNA responds to enzymes' processing. We found that the translocation is highly sensitive to the pulling direction, with the largest hindrance observed for the 5' end, the one resistant to degradation by exonucleases. A mechanistic inter-

pretation is given in terms of the molecule's secondary and tertiary organization.

Poster TUE-P.10 17:30 Foyer

Dynamics of HIV Infection: an entropic-energetic view — •Ramón Enrique Ramayo González[1], Pedro Hugo de Figueirêdo[1], and Sergio Coutinho[2] — [1]Departamento de Física, Universidade Federal Rural de Pernambuco, Recife, Brazil — [2]Departamento de Física, Universidade Federal de Pernambuco, Recife, Brazil

We present an analogy between HIV infection with a 3-level energy system. The instants associated with particular time intervals of the evolution of internal energy and entropy are obtained. The maximum entropy point corresponds to the onset of the immune system's exhaustion and the concomitant and inexorable progression to AIDS.

Poster TUE-P.11 17:30 Foyer

How the Immune System chills — •Roberto Morán-Tovar and Michael Lässig — Institute for Biological Physics, University of Cologne, Zülpicherstr. 77, 50937, Köln, Germany

We propose a non-equilibrium model where exponential growth of the antigen, coupled to a kinetic proof-reading mechanism, drives the B cell recognition process. We predict observed clone size distributions and a novel relation between the clone size and affinity. We show how kinetic proofreading generates a higly specific response.

Poster TUE-P.12 17:30 Foyer

Information encoded in sizes of synapses is nearly maximal across the brains of mammals — •Jan Karbowski[1] and Paulina Urban[2] — [1]Institute of Applied Mathematics and Mechanics, University of Warsaw, Warszawa, Poland — [2]College of Inter-Faculty Studies in Math and Natural Sciences, University of Warsaw, Warszawa, Poland

Long-term information associated with neuronal memory resides in synapses. It is shown using empirical data for several mammalian brains that synapses nearly maximize entropy contained in their sizes for a given mean size. Depending on a species and brain region, a synapse can encode 2-6 bits of information. This suggests universality of entropy maximization in synapses, which can be a new principle of brain organization.

Poster TUE-P.13 17:30 Foyer

Narrowing of the drople size distribution funcion in active emulsions — •Jacqueline Janssen[1], Frank Jülicher[1], and Christoph A. Weber[2] — [1]Max Planck Institute for the Physics of Complex Systems, Dresden, Germany — [2]Universität Augsburg, Theoretische Physik I, Augsburg, Germany

Emulsions with maintained concentration levels of the dilute phase exhibit fast growth. Surprisingly the droplet size distribution function narrows in time in contrary to emulsions coarsening via Ostwald ripening or fusion. The discussed physical principles could be relevant for the size control of biomolecular condensates in living cells.

Poster TUE-P.14 17:30 Foyer

Scaling properties of range Expansions — •Meesoon Ha — Chosun University, Gwangju, South Korea

In this presentation, we discuss scaling properties of range expansions in ecological processes, which are compared to the surface roughness and dynamic scaling in growing surfaces and fluctuation interfaces. Our numerical results and analytic conjecture have potentially interesting and important implications for describing and predicting evolutionary trajectories of ecological processes and microbial temporal community networks.

Poster TUE-P.15 17:30 Foyer

Transport in complex intracellular environments — •Mohammad Amin Eskandari, Bart Vos, Mattias Luber, and Timo Betz — Third Institute of Physics – Biophysics, Georg-August-Universität Göttingen, Göttingen, Germany

Active transport is vital for delivery of biological material in cells and defects in active transport are linked to different diseases. Since the cytoplasm is highly crowded, one might ask how associated motor proteins bypass possible intracellular obstacles. We aim to study possible mechanisms that motors use to overcome the obstacles.

Poster TUE-P.16 17:30 Foyer

Cancer tissue dynamics as active liquids — •Mahboubeh Farajian[1], Swetha Raghuraman[2], Alejandro Jurado Jimenez[1], Fatemeh Abbasi Abbasi[1], and Timo Betz[1] — [1]Third Institute of Physics – Biophysics, Georg August University Göttingen, Göttingen, Germany — [2]Institute of Cell Biology, ZMBE, Münster, Germany

In this project we address the question: "Can statistical mechanics explain the local and global characteristics of cell migration in cancer tumors?" Doing so we will change the physical parameters of the environment and look at a statistical mechanics type of analysis of the cells' migration inside a model tumor.

Poster TUE-P.17 17:30 Foyer

A model for bipartite gene-sharing networks — •José A. Cuesta[1,2,3], Pedro J. Jódar[1,2], Jaime Iranzo[3,4], Eugene V. Koonin[5], and Susanna Manrubia[1,6] — [1]Grupo Interdisciplinar de Sistemas Complejos (GISC), Madrid, Spain — [2]Departamento de Matemáticas, Universidad Carlos III de Madrid, Leganés, Spain — [3]Institute for Biocomputation and Physics of Complex Systems (BIFI), University of Zaragoza, Zaragoza, Spain — [4]Centro de Biotecnología y Genómica de Plantas, Universidad Politécnica de Madrid (UPM) - Instituto Nacional de Investigación y Tecnología Agraria y Alimentaria (INIA), Madrid, Spain — [5]National Center for Biotechnology Information, National Library of Medicine, National Institutes of Health, Bethesda MD, USA — [6]Department of Systems Biology, Centro Nacional de Biotecnología (CSIC), Madrid, Spain

Viral evolution can be described with bipartite networks of genes and genomes, with links connecting genes with the genomes they belong to. Gene's degree distributions are power law, whereas those of genomes are flatter. We propose a model that captures these distributions for viruses with double-stranded DNA and RNA genomes.

Poster TUE-P.18 17:30 Foyer

Fuel-driven processes in DNA-biosensors investigated by optical tweezers — •Xavier Viader[1], Leonard Prins[2], and Annamaria Zaltron[1] — [1]Via Francesco Marzolo, 8, Dipartimento di Fisica e Astronomia Galileo Galilei, Università degli Studi di Padova, Padova, Italy — [2]Via Francesco Marzolo, 1, Dipartimento di Scienze Chimiche, Università degli Studi di Padova, Padova, Italy

Over the past decades, synthetic DNA have emerged as ideal components for self-assembly processes. Here, we use Optical Tweezers to fully-characterize the kinetics and thermodynamics of the energy storage and dissipative mechanisms of a complex energy-dissipating biochemical system consisting of a cargo(DNA)+fuel(oligo)+fuel-consuming-unit(Nuclease).

Poster TUE-P.19 17:30 Foyer

On the interplay between phase separation and reversible aggregation — •Giacomo Bartolucci[1], Thomas Michaels[2], and Christoph Weber[3] — [1]Max Planck Institute PKS, Dresden, Germany — [2]University of Cambridge, Cambridge, United Kingdom — [3]University of Augsburg, Augsburg, Germany

In cells, protein interactions can lead to both coexisting phases as well as aggregates of different sizes. Here, we investigate how phase coexistence influences aggregation equilibrium finding that the size distributions of aggregates can significantly differ in the two phases. We then characterize the aggregation kinetics.

Poster TUE-P.20 17:30 Foyer

RNA Cold Misfolding in Mechanical Unzipping of Short Duplexes — •Paolo Rissone, Aurelien Severino, Isabel Pastor, and Felix Ritort — Universitat de Barcelona, Barcelona, Spain

Biological systems evolve under the rules of Darwinian selection led by the survival of the fittest to environmental pressure. Varying the environmental conditions changes the free energy governing the spontaneous evolution of all thermodynamic transformations. We investigate the misfolded state of short RNA duplexes with pulling experiments at low temperatures.

Poster TUE-P.21 17:30 Foyer

Optimal spatial allocation of enzymes as an investment problem — •Giovanni Giunta[1], Filipe Tostevin[1], Sorin Tanase-Nicola[2], and Ulrich Gerland[1] — [1]Physics Department, Technische Universität München, München, Germany — [2]Department of Cell and Molecular Biology, Uppsala University, Uppsala, Sweden

Cells spatially arrange their enzymes to optimize chemical reactions. Inspired by this, we derive a spatial allocation strategy to arrange enzymes so as to maximize their reaction flux for a wide class of reaction-diffusion systems.

TUE-5: Clarinett and Piano Recital

Time: Tuesday, 19:00–20:00 Location: Auditorium

Recital kindly interpreted by Patrizia Marcatello (Piano), Antonio Amanti and Simona Mariani (Clarinets). The following musical masterpieces will be played: 1) Felix Mendelssohn: Konzertstück nr. 1 op. 113 2) Felix Mendelssohn: Konzertstück nr. 2 op. 114 3) John Williams: Viktor's Tale 4) Béla Kovacs: Sholem-alekhem, rov Feidman! 5) Claude Debussy: Valse Romantique.

TUE-6: Conference Reception

Time: Tuesday, 20:30–22:30 Location: Arenal

Conference Dinner to take place on the terrace of the Arenal restaurant, Paseo Maritimo de la Barceloneta s/n, Barcelona (on the beach, 5 minutes away South from PRBB).

WED-1: Session 1

Time: Wednesday, 9:00–10:40 Location: Auditorium

Invited WED-1.1 9:00 Auditorium

How personalised is our immune repertoire? — •Aleksandra Walczak — CNRS ENS, Paris, France

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

Invited WED-1.2 9:30 Auditorium

The Unreasonable Effectiveness of Reaction-Diffusion in Vertebrate Skin Colour Patterning — •Michel Milinkovitch — Laboratory of Artificial & Natural Evolution (LANE), Dept. of Genetics & Evolution, University of Geneva, Geneva, Switzerland — SIB Swiss Institute of Bioinformatics, Geneva, Switzerland

Using our recent research results in non-model species, I will discuss how deterministic reaction-diffusion models quantitatively predict the dynamics of scale-by-scale ontogenic colour change in multiple species of lizards as well as individual patterns and real-life features at a much finer level of analysis.

Oral WED-1.3 10:00 Auditorium

Simple Reaction-Diffusion Modelling Produces High Predictability of Convergent Skin Colour Patterning in Multiple Species of Lizards — •Ebrahim Jahanbakhsh and Michel Milinkovitch — Laboratory of Artificial & Natural Evolution (LANE), Dept. of Genetics & Evolution, University of Geneva, Geneva, Switzerland

Taking advantage of the convergent mesoscopic scale-by-scale skin-colour patterning dynamics in divergent species of lizards, we quantify the respective efficiencies of stochastic and RD models to predict individual patterns and their statistical attributes. We also identify and quantify the sources of residual unpredictability of adult individual patterns.

Oral WED-1.4 10:20 Auditorium

Adapt to survive: proteome allocation affects coexistence in models of competitive microbial communities — •Samir Suweis[1], Leonardo Pacciani Mori[2], Andrea Giometto[3], and Amos Maritan[1] — [1]University of Padova, Padova, Italy — [2]University of California, San Diego, USA — [3]Cornell University, Ithaca, USA

We present a theoretical framework for population dynamics in competitive ecosystems, at an intermediate level of complexity between classical consumer-resource models and biochemical models of microbial metabolism. The model naturally accounts for temporally varying proteome allocation subject to constraints, in agreement with experimental evidences. We found that metabolic adaptation promotes biodiversity

10:40–11:15: Coffee Break

WED-2: Session 2

Time: Wednesday, 11:15–12:55 Location: Auditorium

Invited WED-2.1 11:15 Auditorium

Fluctuation Relations and Fitness in Cell Populations — •Luca Peliti — Santa Marinella Research Institute, Roma, Italy

Recent advances in single-cell lapse microscopy allow to monitor the division dynamics and the phenotypic state in growing cell populations. The resulting data allow to infer the fitness of a phenotype in constant and varying environments, by exploiting fluctuation relations similar to those of stochastic thermodynamics. I shall provide a short summary of these techniques.

Oral WED-2.2 11:45 Auditorium

The theory of phenotypic association — •Giuseppe Battaglia — Catalan Institution for Research and Advanced Studies (ICREA),, Barcelona, Spain — Institute for Bioengineering of Catalonia - Barcelona Institute of Science and Technology, Barcelona, Spain — Department of Chemistry & Institute for the Physics of Living Systems -University College London, London, United Kingdom

One of the most difficult challenges in medicine is to target specific cells. Here I present a theory that rationalises cells regarding their internal state energetic configurations or phenotypes. I demonstrate that selective association can be obtained by matching the cell phenotype with complementary multivalent units based on multiple bonds

Oral WED-2.3 12:15 Auditorium

Arrays of noisy, coupled circadian clocks in a multicellular cyanobacterial organism; experiment and stochastic model — Rinat Arbel-Goren[1], Ana Valladares[2], Sergio Camargo[1], Antonia Herrero[2], Enrique Flores[2], Francesca Di Patti[3], Valentina Buonfiglio[3], Duccio Fanelli[3], and •Joel Stavans[1] — [1]Department of Physics of Complex Systems, Weizmann Institute of Science, Rehovot, Israel — [2]Instituto de Bioquímica Vegetal y Fotosíntesis, CSIC and Universidad de Sevilla, Sevilla, Spain — [3]Dipartimento di Fisica e Astronomia, Universita' di Firenze, Sesto Fiorentino, Italy

We study one-dimensional arrays of coupled circadian clocks in Anabaena, a multicellular cyanobacterium. Arrays display high spatiotemporal coherence at filament scales due to clock coupling by cell-cell communication, despite significant demographic noise. A stochastic model shows that noise can seed oscillations in a broad range of parameters resulting in robustness.

Oral WED-2.4 12:35 Auditorium

Circadian clocks control gene expression and gate cell division via an oscillatory master regulator in multicellular Anabaena — •Rinat Arbel-Goren[1], Ana Valladares[2], Sergio Camargo[1], Antonia Herrero[2], Enrique Flores[2], and Joel Stavans[1] — [1]Department of Physics of Complex Systems, Weizmann Institute of Science, Rehovot, Israel — [2]Instituto de Bioquímica Vegetal y Fotosíntesis, CSIC and Universidad de Sevilla, Seville, Spain

Little is known about circadian clock regulation by cell-cell communication in Anabaena, a multicellular filamentous cyanobacterium. We have demonstrated gating of the cell cycle via high-amplitude transcriptional oscillations of the master regulator RpaA, which transduces the core clock output, suggesting an additional level of regulation in contrast to Synechococcus.

12:55–14:30: Lunch Break

WED-3: Session 3

Time: Wednesday, 14:30–15:50 Location: Auditorium

Invited WED-3.1 14:30 Auditorium
Spatial evolution of a solid tumour — Arman Angaji[1], Christoph Velling[1], Nicola Dick[1], Michel Owuso[2], Donate Weghorn[2], and •Johannes Berg[1] — [1]Institute of Biological Physiscs, University of Cologne, Cologne, Germany — [2]Centre for Genomic Regulation, Barcelona, Spain
What can we learn from the genomic data of a tumour on the evolutionary forces that shaped it? In this talk I discuss how genomic tumour data at high spatial resolution can be used as a window on the early evolution of a solid tumour, with a particular focus on spatial constraints and tissue dynamics.

Invited WED-3.2 15:00 Auditorium
How rates of evolution is affected by mutation rate and sexual mating — •Yitzhak Pilpel — Weizmann Institute of Science, Department of Molecular Geneticsl, Rehovot, Israel
I will discuss how rates of evolution is affected by mutation rate and sexual mating.

Oral WED-3.3 15:30 Auditorium
Nonequilibrium Selection of Chemical States: a Possible Solution to the Furanose Conundrum — •Daniel Maria Busiello[1,2], Shiling Liang[1], Francesco Piazza[3], and Paolo De Los Rios[1,4] — [1]Institute of Physics, Ecole Polytechnique Federale de Lausanne, Lausanne, Switzerland — [2]Max Planck Institute for the Physics of Complex Systems, Dresden, Germany — [3]Department of Physics and Astronomy, University of Florence, Florence, Italy — [4]Institute of Bioengineering, Ecole Polytechnique Federale de Lausanne, Lausanne, Switzerland
Life has most likely originated under strong nonequilibrium constraints, e.g., deep-sea vents and thermal gradients. In similar conditions, chemical states can be selected according to their dissipation rate, favouring molecules that would be unfavourable at equilibrium. This result provides a possible explanation for the exclusive presence of furanose in RNA.

15:50–16:15: Coffee Break

WED-4: Session 4 and Keynote Talk 3

Time: Wednesday, 16:15–18:15 Location: Auditorium

Invited WED-4.1 16:15 Auditorium
The biophysical basis for the origin of complex life: the evolution of multicellularity — •Peter Yunker — Georgia Inst of Tech, Atlanta, USA
The evolution of multicellularity was transformative, lifting limits on organismal complexity. Multicellular groups are mechanically, topologically, geometrically, and functionally constrained by physical interactions, all of which is filtered and amplified by Darwinian evolution. We combine physical and evolutionary insight to understand how clumps of cells evolve into integrated organisms.

Invited WED-4.2 16:45 Auditorium
How on Earth can Aliens Survive: Concept and Case Study — •Aviv BERGMAN — Albert Einstein College of Medicine, New York, NY, USA
Understanding the evolutionary causes and consequences of robustness and its breakdown, will result with a deeper understanding of the mechanism behind the loss of phenotypic fidelity. Such understanding may lead to a more parsimonious explanation of the emergence and progression of complex diseases such as the transition of cancer to metastatic stage.

Keynote WED-4.3 17:15 Auditorium
Topological scaling laws and the statistical mechanics of evolution — •Nigel Goldenfeld — University of California San Diego, San Diego, USA — University of Illinois at Urbana-Champaign, Urbana, USA
I describe scaling in the large-scale structure of phylogenetic trees. I show they can arise from niche construction, where the critical behavior reflects the indelible imprint of ecological processes. I describe two unsolved evolutionary questions: the origin of open-ended growth of complexity, and the response of evolving systems to perturbations.

THU-1: Session 1

Time: Thursday, 9:00–10:40 Location: Auditorium

Invited THU-1.1 9:00 Auditorium
Mechanics of Morphogenesis – Out-of-plane stresses in dynamic cell sheets — •Stephanie Höhn[1] and Pierre Haas[2] — [1]DAMTP, University of Cambrige, Cambridge, United Kingdom — [2]MPI Complex Systems, Dresden, Germany
Mechanical forces crucially impact embryonic development. In spherical Volvox embryos waves of cell shape changes drive invagination, resembling gastrulation [https://doi.org/10.1186/1741-7007-9-89]. Light sheet imaging and computational modelling revealed concerted tissue bending, contraction and expansion [https://doi.org/10.1103/PhysRevLett.114.178101, https://doi.org/10.1371/journal.pbio.2005536]. Microsurgery reveals residual torques affecting the mechanics of invagination and possibly driving elastic tissue movements.

Invited THU-1.2 9:30 Auditorium
Universal Biology in Adaptation and Evolution: Dimensional Reduction and Fluctuation-Response Relationship — •Kunihiko Kaneko — Niels Bohr Institute, Copenhague, Denmark
A macroscopic theory for adaptive changes of cells is presented, based on consistency between cellular growth and molecular replication, as well as robustness of fitted phenotypes against perturbations. Adaptive changes in high-dimensional phenotypes are shown to be restricted within a low-dimensional slow manifold, from which a macroscopic law for cellular states is derived, as is confirmed by adaptation experiments of bacteria under stress.

Oral THU-1.3 10:00 Auditorium
Active inference in biological systems — •Chang-Sub Kim — Chonnam National University, Gwangju, South Korea
At the core of evolution is to understand the driving mechanisms of natural selection or autopoiesis. The recent efforts in neurosciences suggest a universal biological principle that accounts for the autopoiesis of living organisms as minimizing informational free energy. We treat how to make the theory more physically grounded.

Oral THU-1.4 10:20 Auditorium
Multifunctionality and pattern formation in a reversible mixed feedback loop — •Josep Mercadal — Universitat de Barcelona, Barcelona, Spain
We study mathematically a simple genetic circuit capable of displaying multiple dynamical behaviours, including monostability, bistability, and oscillations. When coupled diffusively, the circuit can exhibit distinct types of patterns. Our study sheds light on the principles by which organisms use genetic circuits to perform different tasks.

10:40–11:15: Coffee Break

THU-2: Session 2

Time: Thursday, 11:15–11:45 Location: Auditorium

Oral THU-2.1 11:15 Auditorium

On the Irreversible Nature of Evolution — •Matteo Sireci and Miguel Ángel Muñoz — Departamento de Electromagnetismo y Física de la Materia e Instituto Carlos I de Física Teórica y Computacional, Universidad de Granada, Granada, Spain

In microbial evolution, ecological and evolutionary processes coexist in the same timescales. A general quantitative theory allows us to show that non-equilibrium stationary states emerge as a balance between selection and mutational fluxes in the population. Their intrinsic irreversibility quantifies the constant transformation of information

THU-3: Poster Prize Event

Time: Thursday, 11:45–12:00 Location: Auditorium

Poster Prize Event

THU-4: EPS Young Minds

Time: Thursday, 12:00–12:15 Location: Auditorium

EPS Young Minds

THU-5: Keynote Talk 4

Time: Thursday, 12:15–13:15 Location: Auditorium

Keynote THU-5.1 12:15 Auditorium

Evolutionary innovations as phase transitions: the synthetic path — •Ricard Sole — UNIVERSITAT POMPEU FABRA, Barcelona, Spain

Major evolutionary transitions have marked the evolution of life in our biosphere, from the origin of life to multicellularity, language or cognition. Synthetic biology, evolutionary robotics or artificial life open the possibility of exploring these innovations,theoretically described within the context of phase transitions. Several examples and open questions will be discussed.

THU-6: Conference Closure and Farewell

Time: Thursday, 13:15–13:25 Location: Auditorium

Conference Closure