POSTDOC DAY

WELCOME TO THE 4th UNIGE

Thursday 27th May 2021
From 9am onwards on ZOOM

Organized by the UNIGE PostDoc Association - APDU

POSTDOC DAY

CONFERENCE BOOKLET

PROGRAM

9h00 - 9h15	*Opening Remarks* **Prof. Yves Flückiger - Rector of the University of Geneva**
	Part I - Who are our colleagues?
9h15 – 10h	*Postdoc scientific talks*
9h15-9h30	***Dr. Liam Scarrat (Dept. of Inorganic and Analytical Chemistry)*** *Structural and Double Layer Forces between Silica Surfaces in Suspensions of Negatively Charged Nanoparticles*
9h30-9h45	***Dr. Luca Barberi (Depts. of Biochemistry and Theoretical Physics)*** *Mechanochemical pattern formation in cells*
9h45-10h	***Dr. Sofia Barbieri (Dept. of cell physiology and metabolism)*** *PLK-1 and MEX-5 gradient formation in C. elegans embryos: interpreting the dynamic partnered dance with computational modelling*
10h – 10h45	**Keynote speaker BIOLOGY – Prof. Gilles Mithieux** **Laboratory INSERM U1213, University Claude Bernard Lyon 1** *Intestinal gluconeogenesis: what could be the purpose?*
10h45 – 10h55	*Short break*
10h55 – 11h40	*Postdoc scientific talks*
10h55- 11h10	***Dr. Olivier Mercey (Dept. of Cell Biology)*** *The connecting cilium inner scaffold provides the structural foundation protecting against retinal degeneration*
11h10- 11h25	***Dr. Raquel Rouco (Dept. of Genetics Medicine and Development)*** *Cell-specific alterations in Pitx1 regulatory landscape activation caused by the loss of a single enhancer*
11h25- 11h40	***Dr. Nicolas Ubrig (Dept. of Quantum Matter Physics)*** *Tunable interlayer transitions in Van der Waals heterostructures*

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11h40 – 12h25	**Keynote speaker PHYSICS – Prof. Nicola Spaldin** **Department of Materials at ETH Zürich** *Finding happiness and Saving the World through Materials Science*
12h30 – 13h30	*Lunch*
13h30 – 14h00 *13h30- 13h45*	*Postdoc scientific talks* ***Dr. Paola Ruggiero (Dept. of Quantum Matter Physics)*** *Quantum dynamics of coupled Luttinger liquids*
13h45- 14h00	***Dr. Cédric Castrogiovanni (Dep. of cell physiology and metabolism)*** *Revealing the third microtubule state: the mixed-nucleotide zone*
14h05 – 14h15	**APDU committee - PostDoc Day 2022 organizers** **Dr. Nirvana Caballero** (President)**, Dr. Manuela Leonardinelli** (Vice President)**,** **Dr. Julie Savarin** (Secretary)**, Dr. Monika Gjorgjieva**
14h15 – 15h00	**Keynote speaker – CHEMISTRY – Prof. Cornelia Palivan** **Department of Chemistry, University of Basel** *Bio-hybrid multicompartments for advanced medical applications*
15h00 – 15h15	*Short break*
15h15 – 15h25	***Part II - Focus on your career:*** *Jessica Plucain - LS2 "Presentation of the PI's of tomorrow competition and other LS2 activities for postdocs"*
15h30 – 17h30	***Open Discussion – round table*** ***Zena Hadjivasiliou*** *(PhD UCL, PostDoc UNIGE - incoming Group Leader at The Crick Institute/UCL)* ***Kelvin Lau*** *(PhD UBC, PostDoc UNIGE - now Scientist at Protein Production and Structure Core facility, EPFL)* ***Rebekka Wild*** *(PhD UNIGE, Postdoc ETH - now CNRS researcher, Grenoble)* ***Jared Fudge*** *(PhD UNIGE - Commissioning editor at Frontiers - now assistant editor at Current Biology, London)*

Jill Guyonnet *(Phd UNIGE, Postdoc UCD - now Senior Software Engineer at Zendesk)*

Shan Yao *(PhD ETH, Data Scientist Swisscom - now Scientific mediator, EPFL)*
Filippo Passardi *(PhD UNIGE - now Senior Sale Representative Thermo Fisher Scientific)*
Joël Busse*t (CTO of Distran -spin-off from the Autonomous System Lab, ETH Zurich)*

17h30 *Final remarks and talk - scientific image prize*

LINKS

ZOOM link for the day

https://unige.zoom.us/j/5351263551?pwd=WGhtdFcvT3ZKRWtnb1BrSERDcWw1UT09

Meeting ID: 535 126 3551

Passcode: PDD2021

Vote for your favorite talk here:

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For any information regarding the Postdoc Day or technical difficulties please contact us at: association-postdoc-sciences@unige.ch

LIST OF POSTDOC TALKS

Structural and Double Layer Forces between Silica Surfaces in Suspensions of Negatively Charged Nanoparticles

Liam R. J. Scarratt[1], Katarzyna Kubiak[1], Plinio Maroni[1], Gregor Trefalt[1], Michal Borkovec[1]
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Concentrated suspensions of charged nanoparticles are relevant in numerous applications, such as papermaking, ceramic processing, and food technology. One of their unique properties is the liquid-like structuring of nanoparticles, which has been shown to originate from the double layer repulsion between them. This property has been heavily explored in the last 10 years, predominately by colloidal probe atomic force microscopy (AFM) using like charged confining surfaces. Here, the resulting force profiles show an oscillatory behaviour with wavelengths of several nanometres as nanoparticle layers are squeezed out. However, despite the wealth of knowledge of these oscillatory structural forces, less information is available on the double layer forces acting in these systems at confining surfaces which dominate at smaller separations resulting in a particle-free layer. Here, we present direct force measurements between negatively charged silica microparticles carried out in suspensions of like-charged nanoparticles with colloidal probe AFM. At smaller distances, soft and strongly repulsive forces are present due to double layer repulsion between the like-charged surfaces, which is quantitatively interpreted with the Poisson–Boltzmann (PB) model adapted to a strongly asymmetric electrolyte to capture the nonexponential nature of these forces. By modelling the nanoparticles as highly charged co-ions, while the counter ions are monovalent, this model permits extraction of the effective charge of the nanoparticles and helps further understanding of the particle-free layer at confining surfaces.

Mechanochemical pattern formation in cells

Luca Barberi [1, 2], Karsten Kruse [1, 2, 3]
(*1) Department of Biochemistry, University of Geneva, Geneva, Switzerland*
(2) Department of Theoretical Physics, University of Geneva, Geneva, Switzerland
(3) NCCR Chemical Biology, University of Geneva, Geneva, Switzerland

The cortex is a thin network of filamentous proteins lying on the inner face of animal cell membranes, which crucially contributes to controlling cell shape. It exhibits a rich spatiotemporal dynamics, which emerges from mechanical and chemical contributions of various origin. Mechanical contributions come, for instance, from the molecular motors that cross-link cortical filaments, which produce local stresses thanks to different means of energy consumption. Chemical contributions come from signaling cascades, which consist of complicated chemical reactions often initiated by environmental stimuli. In biology, the interpretation of pattern formation events in the cortex is historically based on the assumption that chemistry (signaling) governs mechanics, for instance by recruiting cortical components or by activating molecular motors, without being affected by it. However, mechanics can feed back into chemistry, for instance because molecular motors produce advective cortical flows able to spatially redistribute signaling molecules. The spatiotemporal dynamics resulting from such mechanochemical coupling is largely unexplored. We investigate it by developing a hydrodynamic theory which accounts for experimentally relevant mechanochemical feedbacks. We find that mechanics and chemistry reinforce each other's nonlinear dynamics, producing patterns of exquisitely mechanochemical origin. Interestingly, we predict mechanochemical patterns that are qualitatively similar to self-organized patterns of either purely mechanical or chemical origin, produced in absence of coupling. Overall, our findings pose an interpretive challenge for pattern formation experiments in cell biology, where the qualitative consistency between the observed patterns and purely mechanical or chemical ones is used to neglect the role of mechanochemical coupling in cells.


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PLK-1 and MEX-5 gradient formation in C. elegans embryos: interpreting the dynamic partnered dance with computational modelling

Sofia Barbieri[1, 2], Monica Gotta [1, 2]

(1) Department of Cell Physiology and Metabolism, University of Geneva, Switzerland

(2) CMU, University of Geneva, Switzerland

In C. elegans embryos, PLK-1 and MEX-5 are pivotal for cell division and polarity establishment. To achieve this, their localization must be precisely regulated. MEX-5 enrichment at the anterior cytoplasm results from a change in its diffusivity along the embryo axis. We know PLK-1 relocalization to the anterior depends on MEX-5. However, the biological/physical mechanisms behind the dynamics of this protein are still poorly described.PLK-1 and MEX-5 gradient formation was measured in two CRISPR strains and significant discrepancies were revealed between the two proteins in terms of: 1) gradient steepness, as PLK-1 forms a less steep gradient compared to MEX-5; 2) dynamics, with PLK-1 gradient establishment delayed and slower; 3) diffusivity, as PLK-1 diffusion coefficient does not correspond to MEX-5's one from anterior to posterior. To shed light on PLK-1 dynamics, we developed a novel Monte Carlo simulation framework able to recreate the protein motions in the C. elegans one-cell embryo. Thanks to our computational approach, we were able to postulate on the biological mechanisms behind MEX-5 and PLK-1 dynamics during the whole cell division. The simulations succeed in reproducing PLK-1 gradient formation, in agreement with experimental measurements, if: 1) PLK-1 binds to phosphorylated MEX-5; 2) the binding is triggered after a defined time-delay; 3) PLK-1 dynamically interacts with MEX-5, leading to a continuous replenishment of a pool of unbound PLK-1. The Monte Carlo framework we propose can be applied to other polarity-related factors or mutants in which polarization is perturbed, to understand if it can be traced back to a failure in PLK-1 localization.

The connecting cilium inner scaffold provides the structural foundation protecting against retinal degeneration

Mercey Olivier [1], Kostic C[2], Arsenijevic Y[2], Guichard P[1], Hamel V[1]
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(2) Hôpital ophtalmique Jules-Gonin, Lausanne, Switzerland

The retina is a thin tissue lining the back of the eyeball, crucial for visual stimuli interpretation by converting light inputs into electrical signals. This complex process starts with the capture of photons by photoreceptors cells. These highly specialized ciliated cells are partitioned in two main regions: a photosensitive cilium (the outer segment) and a cell body, connected via a thin bridging region called the connecting cilium. Despite the number of retinal pathologies associated with structural defects at the level of the connecting cilium, its molecular architecture, assembly and function are barely known. Here, combining Ultrastructure Expansion Microscopy (U-ExM) and electron microscopy, we performed a nanoscale molecular mapping of the connecting cilium in mouse photoreceptors. We notably demonstrated the presence of an inner scaffold decorating the inner microtubule wall of the connecting cilium, reminiscent of the structure granting microtubule cohesion in the centriole. Furthermore, we found that this structure is composed of the same molecular components, namely Centrin-2, FAM161A and POC5 proteins, and that its appearance coincides with the bundling of the connecting cilium axoneme during the assembly of the outer segment. Finally, we showed that deficiency of the inner scaffold protein FAM161A, causing retinitis pigmentosa in human, induces a progressive loss of the inner scaffold accompanied by a loss of structural cohesion of the connecting cilium and outer segment axoneme, leading to photoreceptor degeneration. Our results suggest that the inner scaffold act as a molecular zipper to maintain microtubule cohesion within the connecting cilium to preserve outer segment integrity

Cell-specific alterations in Pitx1 regulatory landscape activation caused by the loss of a single enhancer

Raquel Rouco [1,2,*], Olimpia Bompadre[1,2,*], Antonella Rauseo[1,2], Olivier Fazio[3], Rodrigue Peraldi[1,2], Fabrizio Thorel[3], Guillaume Andrey[1,2]

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3. Transgenesis Core Facility, Faculty of Medicine, University of Geneva, Geneva, Switzerland

**Authors contributed equally*

Most developmental genes rely on multiple transcriptional enhancers for their accurate expression during embryogenesis. Because enhancers may have partially redundant activities, the loss of one of them often leads to a partial loss of gene expression and concurrent moderate phenotypic outcome, if any. While such a phenomenon has been observed in many instances, the nature of the underlying mechanisms remains elusive. We used the Pitx1 testbed locus to characterize in detail the regulatory and cellular identity alterations following the deletion in vivo of one of its enhancers (Pen), which normally accounts for 30 percent of Pitx1 expression in hindlimb buds. By combining single cell transcriptomics and a novel in embryo cell tracing approach, we observed that this global decrease in Pitx1 expression results from both an increase in the number of non- or low-expressing cells, and a decrease in the number of high-expressing cells. We found that the over-representation of Pitx1 non/low-expressing cells originates from a failure of the Pitx1 locus to coordinate enhancer activities and 3D chromatin changes. The resulting increase in Pitx1 non/low-expressing cells eventually affects the proximal limb more severely than the distal limb, leading to a clubfoot phenotype likely produced through a localized heterochrony and concurrent loss of irregular connective tissue. This data suggests that, in some cases, redundant enhancers may be used to locally enforce a robust activation of their host regulatory landscapes.

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Tunable interlayer transitions in van der Waals heterostructures

Nicolas Ubrig
Department of Quantum Matter Physics, University of Geneva, Switzerland

Van der Waals (vdW) interfaces based on 2D materials are promising for optoelectronics, as interlayer transitions between different compounds allow tailoring of the spectral response over a broad range. However, issues such as lattice mismatch or a small misalignment of the constituent layers can drastically suppress electron-photon coupling for these interlayer transitions. Here, we engineered type-II interfaces by assembling atomically thin crystals that have the bottom of the conduction band and the top of the valence band at the Γ point, and thus avoid any momentum mismatch. We found that these van der Waals interfaces exhibit radiative optical transitions irrspective of the lattice constant, the rotational and/or translational alignment of the two layers or whether the constituent materials are direct or indirect gap semiconductors. Being robust and of general validity, our results broaden the scope of future optoelectronics device applications based on two-dimensional materials.

Quantum dynamics of coupled Luttinger Liquids

Paola Ruggiero [1], Laura Foini[2], Pasquale Calabrese[3], Thierry Giamarchi[1]
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(2) CEA, University Paris Saclay, France
(3) SISSA, Trieste, Italy

Quantum systems in low-dimensions are special in that the effects of strong correlations and interactions are enhanced and lead to dramatic effects A celebrated example from condensed matter physics is the breakdown of Landau's Fermi liquid theory in 1D, which is replaced by the Luttinger liquid (LL) paradigm. The latter has being largely employed to study both equilibrium and out-of-equilibrium problems, with particular reference in more recent times to the dynamics generated after a ``quantum quench'' protocol. In this last case, while a lot is known for a single LL, less is known when two (or more) of them are coupled: this situation is relevant, for example, for the quench dynamics in the Hubbard model, or in tunnel-coupled tubes in cold atoms experiments.
This problem was initially studied under the assumption for the two LLs to be identical, which leads to major simplifications. Recently, instead, a couple of works considered the quench dynamics of two different LL, aiming at understanding the effect of the "imbalance" between them. In our contributions, the problem was solved at first relying semiclassical approximation [1]. This approximation gives access already to a very rich phenomenology, with (i) the emergence of multiple lightcones, separating different decaying regimes; (ii) a prethermal regime eventually decaying into a quasi-thermal one; (iii) non-trivial effects of a non-zero temperature in the initial state. We then extended such results to more general situations relying on Conformal Field Theory methods [2].

[1] P. Ruggiero, L. Foini, T. Giamarchi, Phys. Rev. Research 3, 013048 (2021)
[2] P. Ruggiero, P. Calabrese, L. Foini, T. Giamarchi, arXiv:2103.08927.

Revealing the third microtubule state: the mixed-nucleotide zone

Cédric Castrogiovanni[1,*], Alessio Inchingolo[2,*], Jonathan Harrison[3], Damian Dudka[4], Nigel Burroughs[3], Andrew McAinsh[2,§] and Patrick Meraldi[1,§]

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(4) Department of Biology, School of Arts and Sciences, University of Pennsylvania, Philadelphia, PA.

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§ These authors contributed equally.

Microtubules are dynamic polymers that form the basis of the mitotic spindle. They grow by adding GTP-bound tubulin dimers that hydrolyze GTP to GDP once incorporated into the microtubule lattice. This process results in a GTP-tubulin cap at microtubule ends. If this cap is converted to GDP-tubulin faster than the addition of new GTP-tubulin dimers, microtubules will depolymerize. Current theoretical models predict the existence of a mixed-nucleotide zone between the GTP-tubulin cap and the GDP-tubulin lattice, but such a zone has never been experimentally validated. Here, we uncover a mixed-nucleotide zone within kinetochore-fibres, the microtubule bundles that connect mitotic chromosomes to the mitotic spindle. This zone can be visualized using cells expressing fluorescent EB3, a known GTP-tubulin marker, and endogenously tagged HURP, a protein which we show to specifically bind to GDP-bound microtubule lattices. Live cell experiments with non-hydrolysable tubulin-mutants and in vitro microtubule binding assays with recombinant proteins, demonstrate that HURP preferentially binds to microtubules in the GDP-bound form and is displaced by GTP-tubulin. Live cell imaging of the mitotic spindle in metaphase reveals the presence of three distinct regions on growing kinetochore-fibres: a EB3-positive/HURP-negative GTP-cap, followed by an EB3/HURP-negative zone that can reach up to 2 microns, and a HURP-positive GDP-bound lattice. We postulate that EB3/HURP-negative zone, which appears specifically on kinetochore-fibres represents the mixed-nucleotide zone.

Career session

Zena Hadjivasiliou (PhD UCL, PostDoc UNIGE - incoming Group Leader at The Crick Institute/UCL)

Kelvin Lau (PhD UBC, PostDoc UNIGE - now Scientist at Protein Production and Structure Core facility, EPFL)

Rebekka Wild (PhD UNIGE, Postdoc ETH - now CNRS researcher, Grenoble)

Jared Fudge (PhD UNIGE - Commissioning editor at Frontiers - now assistant editor at Current Biology, London)

Jill Guyonnet (Phd UNIGE, Postdoc UCD - now Senior Software Engineer at Zendesk)

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Filippo Passardi (PhD UNIGE - now Senior Sale Representative Thermo Fisher Scientific)

Joël Busset (CTO of Distran -spin-off from the Autonomous System Lab, ETH Zurich)

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