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A vote of thanks. A lot of things have happened since the last activity report. A “no-brainer” to mention is the COVID crisis, which has challenged us all. But positive developments have clearly prevailed, as this report bears witness to. It’s a pleasure to see how active, dynamic and successful our department is. But rather than reviewing all (mostly very positive!) that has happened over the past two years (e.g., a new organizational structure, new hires, a new building, new MSc programs, and so forth), I would like to thank all of you for helping to make this department “work” on a daily basis, both in happy times but especially in the face of challenges. I am especially grateful to everyone serving in our working groups, committees and the “collège” – as the word “collège” implies, the well-being of our department is a community effort. But several members of our department deserve our very special gratitude: Philippe Baumann, Evelyn Boll, Boris Egger, Jean-Claude Jaquier, Sabrina Lutz, Jean-Daniel Niederhäuser, Julien Comelli, Eirini Maikanti, Felix Meyenhofer, Laura Morello, Alessandro Puoti, Michael Stumpe, and Alain Werro. Without you, nothing would work. It is because of your dedicated work and because of the collegial collaboration amongst all of us – students, staff and researchers – that our department is fit for the future!

Sincerely,

Prof. Thomas Flatt
President of the Department of Biology
BBP

The Bioinformatics & Biostatistics Core Facility (established in 2013) is a joint platform between the Department of Biology and the section of Medicine. It is managed by Dr. Laurent Falquet and Dr. Rudolf Rohr. The expertise of the platform is primarily the analysis of Next Generation Sequencing data and Biostatistics analysis, with emphasis on genome assembly and metagenomics, as well as DNA methylation. We also perform other analyses, such as ANOVA, mixed effect models, RNAseq, ChIPseq, and any large scale data analysis upon request.

For Bioinformatics matter please contact
Dr. Laurent Falquet: bugfri@unifr.ch
For Biostatistics matter please contact
Dr. Rudolf Rohr: rudolf.rohr@unifr.ch

MAPP

The Metabolomics and Proteomics Platform (MAPP) is a service of the Department of Biology of the University of Fribourg. The mission of the platform is to provide expertise, instrumentation, and manpower to enable state-of-the-art implementation of metabolomic and proteomic analyses. To this end, the MAPP offers support in the planning and execution of experiments, including custom-tailored method development, sample preparation, data acquisition and analysis, and researcher training. Since its official start in January 2017, the MAPP has provided its services to many research groups of the Department of Biology as well as to some external customers.

Metabolomics Unit
The Metabolomics Unit offers services ranging from sample preparation to data acquisition and data interpretation. The analytical platform allows for Gas Chromatography (GC) based profiling with a GC-FID (Agilent 7890) and a high-resolution Time of Flight mass spectrometer GC-QTOF (Agilent 7200) and for Liquid Chromatography (LC) profiling on a UHPLC-HRMS Orbitrap (Vanquish Fusion + Q Exactive Plus). In addition to data acquisition, state-of-the-art computational solutions and biostatistics are proposed for the analysis of untargeted metabolomics datasets.
In the last year, 7 research groups of the Department of Biology, as well as three external customers have utilized the services of the Metabolomics Unit.

Proteomics Unit
The Proteomics Unit mainly offers diverse mass spectrometric (MS) analyses of protein samples. The Proteomics Unit is in the fortunate situation to have access to three high-end nanoLC-ESI-MS/MS instruments, the newly purchased Orbitrap Exploris 480 (2022), a Q Exactive HF-X (2018, financed in part by a R’Equip grant), and a Q Exactive Plus (2016, mainly used by the Metabolomics Unit).
In the last two years, 14 research groups of the Department of Biology, as well as ten external customers (including six research groups of the Section of Medicine), have utilized the services of the Proteomics Unit.

Selected publications
42 Nationalities

268 peer-reviewed publications in 2021 and 2022

142 courses and 188 exams during the academic year 21/22

61 completed MSc and PhD theses with graduations

31 research groups

260 people worked at the Department of Biology in 2021 and 2022
Circadian clock and light

How light affects the clock and mental health

The earth’s rotation around its axis causes periodic exposure of half of its surface to sunlight. This daily recurring event has been internalized in most organisms in the form of cellular circadian clock mechanisms. These cellular clocks are synchronized with each other in various ways to establish circadian networks that build the circadian program in tissues and organs, coordinating physiology and behavior in the entire organism.

In the mammalian brain, the suprachiasmatic nucleus (SCN) receive light information via the retina and synchronize their own neuronal clocks to the light signal. Subsequently, the SCN transmits this information to the network of clocks in tissues and organs, thereby synchronizing body physiology and behavior. Disruption of cellular clocks and/or destruction of the synchronization between the clocks, as experienced for instance in jet-lag and shift work conditions, affects normal brain function and can lead to metabolic problems, sleep disturbance, and accelerated neurological decline. We aim to decipher the ways through which light affects the circadian system and thus influences normal brain function. Disturbance of the clock by nocturnal light will lead to sleep problems and age-related cognitive decline, which are on the rise in modern societies. We are using normal and genetically modified mice in order to study causal relationships between light, the circadian clock and neurological disorders. We aim to decipher the ways through which light affects the circadian system and thus influences normal brain function. Disturbance of the clock by nocturnal light will lead to sleep problems and age-related cognitive decline, which are on the rise in modern societies. We are using normal and genetically modified mice in order to study causal relationships between light, the circadian clock and neurological disorders.

Light and the circadian clock are important factors impinging on health and well-being.

Group members

Stéphanie Aebischer, Lab technician
Antoinette Hayoz, Lab technician
Tomaz Martini, PhD student
Kathrin Wendrich, PhD student
Yankey Yungdun, PhD student
Dr. Jürgen Ripperger, Maitre Assistant
Maude Marmy, animal caretaker
Mariana Gutiérrez Pérez, exchange student

Selected publications


Molecules in Context

**Linked Open Data to explore Life’s chemistry**

Metabolism embodies the dynamic nature of living processes. The constant interconversion of molecules provides energy and generates the chemical bricks of life. The natural products assembled from these building blocks radiate from a central metabolome, shared by all organisms and consisting of fundamental polymers such as nucleic acids or proteins, to a specialized metabolome consisting of an infinitely more diverse set of molecules shaped by evolutionary processes and which are specific in terms of occurrences in the tree of life, chemical structures and biological functions. Characterization of natural products and elucidation of the roles of specialized metabolites are essential for the fundamental understanding of chemical evolution and ecological interactions, as well as for more applied topics such as drug discovery.

In the **COMMONS Lab**, we explore and develop knowledge management solutions for the study of the chemistry of life. These solutions are aimed to support the stages of knowledge acquisition, knowledge organization and knowledge dissemination.

【Knowledge acquisition】We use mass spectrometry (because of its unrivalled sensitivity and structural determination potential) to profile biological matrices and we develop computational tools to organize, annotate and visualize the obtained spectral data.

【Knowledge organization】We employ **Linked Open Data** principles to organize and connect mass spectrometry experimental results with publicly available and relevant datasets. The gathered information is organized as hybrid and cross-domain knowledge graphs. These graphs allow to better capture the complexity of the ecological, biological, and chemical context in which the analytes are originally found in, but isolated from, when using powerful hyper-reductionist approaches such as untargeted fragmentation mass spectrometry.

【Knowledge dissemination】We finally explore solutions to share the acquired knowledge inside and outside of academia (e.g. the ongoing LOTUS initiative).

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**Group members**

Emmanuel Defossez, Postdoc

**Selected publications**


Humans change the planet faster than ever before in history. These changes create challenges for science and society, but also opportunities to create better futures. Our research contributes to understanding the mechanisms and consequences of these changes, developing strategies how we can prevent harmful impacts and how we can use this knowledge to enhance ecosystem services we receive from nature. We collaborate with researchers all over the world and advise organizations such as the International Union for Conservation of Nature (IUCN), the Intergovernmental Science-Policy Platform on Biodiversity and Ecosystem Services (IPBES), and the European Commission (EC).

Which are the worst invasive alien species? The number of alien species is increasing exponentially worldwide and there are many more species than can be managed. There are more than 14,000 alien species in Europe, but not all of them cause problems to the environment or human well-being. The seemingly simple and straightforward question «which are the worst invaders?» is difficult to answer because the impacts of alien species can be manifold and comparisons need to work for species as different as for example snails, insects, mammals and plants. We developed methods that allow classifying alien species according to the magnitude of their environmental and socio-economic impacts (S/EICAT), which are now adopted as international standards by the IUCN.

Are all alien species bad? Not all alien species are harmful, some can even be beneficial for native species or humans. Current research incorporates beneficial impacts into S/EICAT for a more comprehensive understanding of how alien species change local ecosystems and human well-being.

Improving biological control In collaboration with the Swiss Federal Research station Agroscope we are improving biocontrol of important insect pests such as pollen beetles (Brassicanegethes spp.) and spotted wing fruitfly (Drosophila suzukii). Can we improve wine quality with biodiversity? In the European project PromESSinG (www.promessing.eu) we investigate how we can use biodiversity-friendly agricultural management techniques to improve grape quality.

Selected publications

Forgione, L. et al. (2022). Are species more harmful in their native, neonative or alien range? Insights from a global analysis of bark beetles. Diversity and Distributions, 28(9), 1832-1849.


Community ecology

Community structure and functioning

Natural communities are composed of numerous species that interact between themselves and with their environment. Communities deliver essential “services” like food provisioning or carbon sequestration. Understanding how communities are organised and how they function is thus a primary task. The inherent complexity and variability of natural communities makes this undertaking conceptually and methodologically challenging. Microbial systems inhabiting the pitcher-shaped leaves of Sarracenia purpurea are a perfect system, being amenable to replicated experiments.

We conducted an experiment in the field, manipulating the amount of resource, the temperature and the dispersal between local communities. We found that resource and temperature had the strongest impact on diversity. However, by combining all possible treatments, we found a hidden effect of dispersal: it preserves diversity when resource and temperature had negative impacts.

“Dispersal between communities saves biodiversity”

Temperature performance curves (TPCs) describe the response of vital parameters to temperature and are a key tool to understand the effects of global warming. We analysed TPCs for six protist species in our system. This undertaking was much more complex than expected, leading to the development of new TPC models.

Dr. Sarah Gray formed a Sarracenia purpurea International Network (SPIN) with scientists to conduct research on this system. It resulted in the hosting of two US PhD students, Alicia McGrew and Jessica Bernardin. We also hosted a visiting professor, Dr. Thomas Miller, funded through the SNSF. Sarah Gray is also a collaborator on an USA NSF-funded Rules of Life grant, with the overarching objective of using the Sarracenia system to define general rules for how microbiome composition and function change during succession.

Group members

Sarah M. Gray, junior group leader
Reham F. El-Barougy, Postdoc
Samantha Coinus, PhD student
Rachel Korn, PhD student
Thomas E. Miller, visiting professor
Nilgün Sailer, technical assistant

Selected publications

Bittleston L, Freedman Z, Bernardin J, Jacob JG, Young EB, Record S, Baiser BH, Gray SM (2021) Exploring microbiome functional dynamics through space and time with trait-based theory. mSystems 6: e00530-21

Chordate regeneration

Investigating the extreme regenerative capacity of colonial tunicates

Tunicates are marine invertebrates that belong to the Tunicata subphylum. Together with the more basal Cephalochordata (i.e. the lancelets) and the Vertebrata (i.e. us), they compose the Chordata phylum. Tunicates are estimated to have separated from the vertebrates 500 million years ago, which thus makes them our closest invertebrate relatives! In addition to this unique taxonomic position, tunicates display a variety of physiological and morphological traits that are truly fascinating.

There are currently over 3'000 different species of tunicates identified. Tunicates have a tissue complexity reminiscent of vertebrates, and a morphology organized around a barrel-shaped body with two siphons to filter water. Tunicates are named after the structuring semi-rigid layer of cellulose-based extracellular matrix that encompasses their body.

The diversity of adult forms ranges from from the 15 cm-long Korean delicacy Halocynthia to the developmental model organism Ciona, from the solitary carnivorous abyssal Dicopia to the colonial invasive subtidal Botrylloides and from the 1 mm-long dioecious Oikopleura that builds extra-corporeal houses for funneling its food to the bioluminescent Pyrosoma that assembles into up to 18 m-long tube-shaped pelagic colonies.

In our lab, we are particularly interested in the powerful regenerative capacity of Botrylloides. Extraordinarily, these animals can regenerate a fully functional adult from a minute fragment of its vascular system in just 10 days. In this species, one tissue has thus the stem-like capacity to recreate all other tissues of an animal! In addition to this dramatic process, we are investigating other fascinating facets of these animals, including asexual reproduction, locomotion, taxonomy and genomics.

Our group works at the interface between engineering and biology, innovating solutions to dissect the unusual scientific questions brought to us by these tunicates.

Group members
Marta Wawrzyniak, lab manager
Nathalie Weber, animal caretaker

Selected publications
Domart-Coulon I & Blanchoud S (2022) From Primary Cell and Tissue Cultures to Aquatic Invertebrate Cell Lines: An Updated Overview. MDPI. Advances in aquatic invertebrate stem cell research: 1-64
Cellular Recycling

Stay healthy, recycle your proteome

We study the regulation of protein homeostasis focusing on protein degradation by autophagy, which is an evolutionary conserved, cytoprotective, lysosomal degradation pathway. Autophagy initiation is mainly regulated on a posttranslational level; hence, we study posttranslational protein modifications with the use of quantitative mass spectrometry-based proteomics to characterize mechanisms driving autophagy and regulating protein turnover.

One subtype of autophagy is macroautophagy (hereafter referred to as autophagy), in which new double membrane vesicles are formed, autophagosomes, which enwrap cellular cargo for lysosomal targeting. Initially, autophagy was regarded as non-specific lysosomal degradation pathway; however, it is now clear that autophagy can be very specific leading to the degradation of defined subsets of organelles and/or proteins, especially under stress conditions. Dysregulation of autophagy has been linked to ageing as well as to many human diseases, most notably to neurodegeneration and cancer. We aim to characterize new proteins being crucial for functional autophagy, or being specifically degraded by autophagy, presumably to ensure cell survival under stress conditions. In parallel, we study proteins known to be involved in autophagy regulation, specifically kinases and phosphatases, to better understand their function and to be able to better assess their potential to be used in therapy. A special focus is the crosstalk between the cellular microenvironment, i.e. extracellular matrix and soluble proteins, and autophagy regulators. Here, we use skin as a model system to study the role of autophagy in wound healing employing primary skin fibroblasts and keratinocytes in 3D cell culture systems.

“Constant turnover is the goal”

Prof. Jörn Dengjel
Cellular signaling events regulating proteome homeostasis

Group members
Melanie Brunner, PhD student
Zehan Hu, Postdoc
Stéphanie Kaeser-Pebernard, Lab Manager
Esther Martinez-Martinez, Postdoc
Alexandre Leytens, PhD student
Alessandra Louison, PhD student
Carole Roubaud, Lab technician
Donarayanan Sivasankar, PhD student
Christine Vionnet, Lab technician
Bich Vu, PhD student
Jianwen Zhou, Postdoc

Selected publications


Fluorescent micrographs of MCF7 cells expressing WT (upper panel) or mutant (lower panel) version of the scaffold protein SCYL1. RAB5 (red) and RAB7 (green) localization changes SCYL1-dependent.
All living cells can exit the normal cell cycle and enter into a resting state termed quiescence or G0. Interestingly, most eukaryotic cells, whether they exist as single cells or as part of a multicellular organism, spend most of their life time in such a quiescent state. The regulatory mechanisms controlling entry into or exit from quiescence, however, are still largely elusive. Because the disruption of these mechanisms is associated with cellular transformation (in multicellular organisms) or dramatically reduced life span (in unicellular organisms), research in this area will likely enhance our basic understanding of diseases such as cancer and be instrumental for the development of diagnostic and therapeutic tools to treat these diseases. To address the basic aspects of quiescence experimentally, we study the unicellular eukaryote baker’s yeast as a model system. Our current data indicate that a conserved protein complex, coined TORC1, plays a central role in coordinating both entry into and exit from G0 in response to nutrient levels. This fits well with the role of TORC1 in coupling nutrient, energy, and hormonal signals with cell growth, division, and metabolism in higher eukaryotes. Notably, amino acids are important and primeval cues that stimulate TORC1 to promote anabolic processes and inhibit catabolic processes via the conserved EGO complex. The latter assemble into heterodimeric complexes consisting of Gtr1 and Gtr2 in yeast, or RagA or RagB and RagC or RagD in mammalian cells, and are integral to larger complexes coined EGO (exit from rapamycin-induced growth arrest) complex (EGOC) in yeast or Rag-Ragulator complex in mammalian cells. In this context, our current research is focused on deciphering the amino-acid sensitive events upstream of the Rag GTPases in yeast. Due to the evolutionary conservation of the EGOC and its regulators, we expect our studies to contribute to the understanding of the molecular mechanisms leading to diseases that are associated with hyperactive mammalian TORC1 including cancer, type 2 diabetes, and neurodegeneration.
Neural development

Neural stem cells, cycling fast and slow

Dr. Boris Egger

Neural stem cell states in the brain of Drosophila melanogaster

Stem cells have the remarkable ability to proliferate, self-renew and to give rise to the great variety of different cell types in our body. Tissue-specific stem cells, such as neural stem cells generate the neurons and glial cells of the nervous system. During early brain development neural stem cells preferentially proliferate through symmetric divisions and thereby are expanding the progenitor pool. Later during development neural stem cells switch to an asymmetric division mode to self-renew and to generate daughter cells that might lose their mitotic potential and differentiate. The transitions from proliferation to differentiation are tightly regulated by a combination of cell extrinsic or environmental factors and by cell intrinsic factors. Genetic irregularities or failures in these neurodevelopmental programmes can lead to diseases such as microcephaly or brain tumours.

In our current research we focus on cell intrinsic regulators that control the different phases of the cell cycle in neural stem cells. We investigate how cell cycle regulators interact with stem cell state determinants to coordinate the transition from symmetrically to asymmetrically dividing neural stem cells.

We are also interested in how environmental factors interact with cell intrinsic regulators to determine stem cell states. Interestingly, stem cells are often found in niches that are maintained under low oxygen or hypoxia. Increased oxygen supply can be an instructive signal for the switch to genetic programmes initiating neurogenesis and differentiation.

To address our research questions, we use genetic methods and immunofluorescent labelling in the fruit fly model system Drosophila melanogaster. We monitor cell cycle phases and oxygen availability through genetically encoded biosensors and advanced live cell microscopy in the fly brain.

Many of the genetic elements controlling neural stem cell states are highly evolutionarily conserved. Therefore, our findings are relevant for the understanding of neurodevelopmental processes in healthy and diseased brains.

“Our findings are relevant for the understanding of neurodevelopmental processes in the brain”
Microbial Genomics & Metagenomics

Metagenomics: the living metaverse?

We are surrounded and populated by billions of bacteria and other microbial organisms. Any place on Earth can host a bacterial community. Metagenomics allows for the study of these communities by leveraging on next generation sequencing techniques and bioinformatics analysis pipelines. It is like entering into a fantastic metaverse of small living organisms and trying to understand its functioning.

Our group is involved in several projects focusing on metagenomics data in collaboration with other lab researchers. Here are some examples of questions we are trying to answer.

Can a saliva microbial community help to distinguish human individuals better than genomic fingerprints? E.g., distinguishing real twins? A collaboration with Profs. Uribe and Barreto, Unal, Colombia.

Is there a link between the human baby gut microbiome inherited from his/her mother and the appearance of antibiotic resistance or developing asthma later in life? A collaboration with Prof. Zimmermann, Unifr & HFR (Volery et al, 2020).

Can potato rhizospheric microbiome influence the health of the plant? E.g., by protecting the plant against pathogenic fungi. A collaboration with Profs. Weisskopf, Unifr.


We develop and extend pipelines with which several levels of analysis are performed, from taxonomic distribution, metagenome assembled genomes, antibiotic resistance genes detection, to pathways reconstruction.

We are part of the European COST Action Machine Learning for Microbiome (https://www.ml4microbiome.eu) (Moreno-Indias et al, 2021).

Other projects:
Toxin-Antitoxins in bacteria (Mansour et al, 2022; Hill et al, 2021)

Group members
Vivien Pichon, PhD student
Omer Cetiner, visiting scientist
Jeferyd Yepes Garcia, PhD student

Selected publications


How do organisms adapt to the environment? Our research seeks to understand the genetic basis of selection and adaptation, using Drosophila as an experimental system. Much of our work has focused on the adaptive role of chromosomal inversions. Inversions are structural mutations that reverse a chromosome segment (and thus gene order) relative to the normal non-inverted chromosome. The main property of inversions is that they suppress recombination in heterozygous state - this is thought to enable them to “capture” combinations of adaptive loci and protect them from being recombined away. To study the adaptive role of inversions, we have been investigating In(3R) P, a 8 Mb-long inversion spanning 1200 genes and exhibiting parallel frequency gradients (clines) on several continents, always at intermediate frequency in subtropical/tropical areas but absent in temperate areas. This compelling pattern led us to hypothesize that In(3R)P is a major driver of adaptation along latitudinal clines. Over the past 6 years, we have shown that In(3R)P is maintained by spatially varying selection; (i) undergoes seasonal fluctuations consistent with temporally varying selection; and (ii) affects major fitness traits (viability, size, stress resistance, lifespan). This inversion thus represents a ‘supergene’, a set of tightly linked loci affecting multiple complex traits. We are currently working towards elucidating its genetic architecture and the form of balancing selection that maintains it. Our research on this adaptive polymorphism contributes to the current ‘renaissance’ of the classical subject of the role of inversions in adaptation. More generally, our research program promises to yield new insights into the fundamental question of how genetic variation is being maintained.

“Little is known about the genetic basis of adaptation”

Group members
Esra Durmaz, Postdoc
Envel Kerdaffrec, Postdoc
Margot Paris, Postdoc
Marisa Rodrigues, PhD student
Fanny Gagliardi, Intern
Patrick Favre, Technician

Selected publications

Drosophila caught in a field trap close to Mont Vully. To examine genetic changes in natural populations we regularly collect flies in the wild.
Plant hormone transport

When the hormones go crazy

My group has a long-lasting interest and expertise in analyzing transmembrane transport processes in plants on a biochemical level. Over the years we were able to assign transporters of different sub-classes to distinct plant hormones by analyzing their impact on plant physiology. However, our main focus still lies on the fascinating cell-to-cell movement of the plant hormone, auxin. This event, called polar auxin transport, represents a unique, plant-specific mechanism that virtually controls all aspects of plant growth and performance and represents a hotspot in plant biology.

In 2023/22, we have demonstrated in collaboration with the Jasinski (Poznan) and Shani labs (Tel Aviv) the involvement of ABCG-type ABC transporters in the transport of the plant hormones, abscisic acid (ABA) and cytokinins. While a subset of ABA importers controls redundantly the long-distance translocation and thus ABA homeostasis (Zhang et al. 2021), ABCG56 from Medicago transports cytokinins involved in early stages of legume-rhizobia symbiosis (Jarzyniak et al. 2021).

Together with the Hegedüs lab (Budapest) we have provided a quality control for DeepMind’s AlphaFold2 machine learning method allowing for structure prediction of transmembrane proteins by using subsets of ABC transporters (Hegedüs et al. 2022). Our results strongly indicate that AlphaFold2 also performs astounding well in the case of transmembrane proteins and that the careful application of its structural models will also advance transmembrane protein-associated studies at an unexpected level.

In collaboration with the group of Leah Band (Nottingham), we addressed the long-lasting question if polar auxin transport catalyzed by ABCB- and PIN-type exporters functions independently or not. By using a systems biology approach our results revealed that ABCB and PIN proteins mediate co-dependent auxin efflux (Mellor et al. 2022).

Finally, we investigated the role of the immunophilin, TWISTED DWARF1, functioning as a co-chaperone of ABCB-type auxin transporters, during flower development. Our work indicates that TWISTED DWARF1 (green fluorescence in picture) regulates Arabidopsis stamen elongation by differential activation of ABCB-mediated auxin transport (Liu et al 2022).

Group members

Laurence Charrier, technician
Jie Liu, PhD student
Jian Xia, PhD student
Tashi Tsering, PhD student
Francesca Iacobini, PhD student

Selected publications

We study how populations (mal)adapt over space

All populations exist over geographic space and through time. As environments change with time, this inevitably leads to the movement of populations of species to novel locations, expanding their species range. With climate change, such movements are expected to be more frequent and more drastic. Whether and how these moving populations survive and adapt to new environments is the key motivator to our research. Past studies show that as populations move over geographic space, population bottlenecks that are concurrent with colonizing new habitats lead to a reduction in the efficiency of selection and increased genetic drift. This process, known as gene surfing, can lead to a phenomenon termed expansion load, the reduction in a population’s fitness due to the expansion process. This process has been observed in simulations under a wide range of parameter space and also observed in nature for many species, including humans during the out-of-Africa bottleneck in our species’ past. There is debate over the prevalence and strength of this expansion load, and in natural populations of plants, there is an additional factor of self-fertilization.

Our most recent research is investigating expansion load through simulations and also with empirical data collected from Arabis alpina, an alpine perennial that has expanded its species range from Italy northward into France and Italy since the last glacial maximum. During this expansion, the species also shifted from largely outcrossing to largely self-fertilizing. Selfing is an interesting phenomena, largely considered as an evolutionary dead-end, but still favored evolutionarily under certain situations. We hope to disentangle the effects of range expansion and selfing within our species by comparison to simulations and therefore understand if selfing provided an advantage to purge any expansion load, or if it is simply a consequence of providing faster colonization ability. We have detected load in our samples of A. alpina, and through simulations have also found differing impacts of demographic history (range expansion) in combination with a shift to selfing. The expansion largely drives a significant increase in load, and differing degrees of simulated selfing only seem to purge the most lethal and the most recessive deleterious mutations. Whether and how this may have benefitted the range expansion of A. alpina and other plant species with shifting mating systems continues to be the focus of our research along with other related projects.

Group members
Leo Zeitler, PhD student

Selected publications
Nociception and plasticity

Worms telling us how to shut off pain

Like most animals, we are able to detect damaging or potentially damaging stimuli, through a process called nociception. Nociception underlies protective behaviours to avoid injuries and facilitate healing. However, in pathological situations, pain may become persistent with no actual benefit. Chronic pain affects more than a billion people worldwide. There is an essential need for improved pain management solutions, as available drugs display either detrimental side-effects or limited efficacy. Progress in this field is hindered by a lack of mammalian models by ethical concerns, by the complexity of the nervous system, and by the difficulty to bridge the gaps in our understanding at the molecular, neuronal, and physiological/behavioural levels.

We use the simple Caenorhabditis elegans worm as a model to elucidate the mechanisms underlying nociception. We focused on recently identified human pain genes, whose functions are poorly understood. Via computer-assisted high-throughput behavioural genetic screens, we identified several dozen conserved worm mutants with impaired nociceptive processes and provided a collection of new gene-specific models for further analyses. We currently combine cutting-edge in vivo imaging techniques, proteomic, transcriptomic, optogenetics and computer-assisted analysis of behaviour to better understand pain regulatory mechanisms at the molecular, cellular and circuit levels. As a whole, our integrative research both deepens our understanding of the mechanisms underlying pain sensation and averse behaviours and brings insight on new potential drug targets for future pain treatment translational development.

Group members

Laurence Bulliard, lab technician
Georgina Gomez Saldivar, postdoc
Domenica Ippolito, Postdoc
Aurore Jordan, PhD student
Filipe Marques, Postdoc
Martina Rudgalvyte, Postdoc
Lisa Schild, lab technician
Parvathi Sushama Gopinath, PhD student
Saurabh Thapliyal, PhD Student

Selected publications

Glauser DA (2022) Temperature sensing and context-dependent thermal behavior in nematodes. Current opinion in neurobiology, 73, 102525.
Ippolito, D, Thapliyal, S, Glauser, DA. (2022) Ca2+/CaM binding to CaMKI promotes IMA-3 importin binding and nuclear translocation in sensory neurons to control behavioral adaptation. eLife, 10, e71443.
Our planet experiences climate change and associated global warming. With these conditions, plants face a challenge to grow and to produce expected yields. Looking into the future, we need to come up with good solutions how to protect plants and create stress resilient crops. Therefore, there is an urgent need to study how plants sense and respond to environmental stresses to gain insights into plant adaptation mechanisms. For example, plants close stomata (little openings in the leaves) in case of water deficiency; plants grow towards the light to increase the photosynthetic activity; roots avoid high salinity by growing away. But we still miss a deeper understanding of the main players in such adaptation mechanisms and additional circuits need to be described.

In plants, the vascular tissues transporting water and minerals (Xylem) and sugars and a myriad of signaling molecules (Phloem) play a central role in long-distance communication, distribution of vital compounds and providing a mechanical support to the plant body. These tissues are constantly produced by special meristematic cells that divide and differentiate. We aim in our research to uncover how water conducting tissue is formed and how environmental stresses affect morphology and functionality of this tissue. The previous work on xylem development uncovered key role of plant hormones like auxin and cytokinin in the early specification of vascular cells and later in differentiation of xylem. In our work, we uncover an additional layer of regulation of xylem formation, that is mediated by small signaling peptides and their cognate receptors. We could identify specific peptides that act fortifying the xylem vessels in Arabidopsis roots and we discovered a new peptide gene, that is essential for root phloem formation.

In addition to Arabidopsis, we use tomato as a plant model and we could recently identify new peptide signals. We now create mutants to be able to study the function of these new genes in tomato development and adaptation mechanisms.

*Dr. Ora Hazak*
Receptor- peptide mediated pathways shaping vascular tissues

**“Cracking the adaptation mechanisms from the very tip of the root”**

**Group members**
Samy Carbonnel, postdoc
Sara Vimercati, senior researcher assistant
Salves Cornelis, PhD student

**Selected publications**
Samy Carbonnel, Laurent Falquet and Ora Hazak (2022) Conserved mechanism for perception of root-active CLE peptides, Preprint

Confocal image of Arabidopsis thaliana root tip with the xylem-specific expression domain of CLE22 signaling peptide. The cell walls are visualized with Calcofluor staining and nuclear signal of H2B-CITRINE is driven by CLE22 promoter.
Application of genetic monitoring to the management of endangered species

Early discussions with practitioners in charge of monitoring and managing threatened populations have highlighted several gaps in knowledge on the biology and ecology of Galliformes species, although they are among the most studied species. Brainstorming and workshops between researchers and practitioners allowed to define priorities in terms of conservation and to develop research projects to estimate relevant demographic parameters. Seemingly simple questions, such as estimating the number of individuals in fact similar to the identification of criminals from partial DNA profiles in forensic science. This problem is non-trivial and remains unsolved. Dialog between research and practice allows to identify relevant research questions and to transfer recent scientific results into practice.

Research conducted since 2010 at University of Fribourg was used to establish strict guidelines for the genetic monitoring of Galliformes populations in the Jura and Vosges mountains, and in the Pre-Alps of the canton of Fribourg. Data collected in the framework of these monitoring programs allowed to estimate the demographic parameters essential for the management of the Capercaillie (Tetrao urogallus) and Hazel Grouse (Tetrastes bonasia) populations.

The genetic monitoring of Galliformes populations also allows to quantify the risk and the magnitude of inbreeding depression in wild populations. This parameter, long ignored, is critical to define conservation strategies. The work carried out at the University of Fribourg has made it possible to make managers aware of the risk posed by inbreeding and thus, to reorient the National action plan for Capercaillie in France.

Part of the research in the group is carried out by MSc students who have the opportunity to develop and carry out their own research project, from the research question to the collection and analysis of data. Students choose their topics based on personal interest and curiosity, from studying the ecology of wood ants based on intensive field work (project completed) to studying ecology and behaviour of Capercaillie, inferred from data collected in the framework of the monitoring of the species in the Jura mountains (project in progress).

Group members
Francesco Foletti, Technician

Selected publications


A regrown limb, a renewed retina, or a functionally recovered heart would be a dream for people who have experienced severe injury due to accidents or disease. By contrast, some aquatic vertebrates have the natural power to regenerate their lost body parts nearly perfectly. In our research, we investigate how zebrafish and platyfish perform self-repair of various damaged organs.

We use small tropical fish as model organisms that can be maintained in suitably equipped lab aquaria. Although they are water dwellers, they share genetic and cellular similarities to terrestrial vertebrates, including humans, due to evolutionary conservation. We analyze biological processes in their organs using microscopy, histology, multi-color fluorescence imaging and detection of gene transcription. The results can be compared between species and the findings are of biomedical relevance.

From our recent progress, we would like to highlight three publications. First, we aimed to understand the embryonic origin of the zebrafish ventricle, despite the absence of a morphological separation in this chamber. This finding hints at the existence of a cellular scaffold for evolving a cardiac septum in terrestrial vertebrates. Our second study focused on platyfish. Closer examination of their tail skeleton revealed an unconventional contribution of dorsal tissue in the caudal fin, which is normally considered a ventral appendage. This reveals evolutionary innovations of the locomotory appendages among fishes. Thirdly, we addressed a question about the impact of mechanical forces on fin regeneration in zebrafish. In collaboration with the Department of Physics in Zürich, we found that viscous shear stress modulates the regrowing rays. This suggests that mechanical forces are involved in the fine-tuning of fin shape. Altogether, our research provides new biological perspectives by integration of knowledge across disciplines to understand the mystery of organ regeneration in fish.

Group members

Catherine Pfefferli, Postdoc
Marta Wawrzyniak, Postdoc
Thomas Bise, PhD student
Hendrik Oudhoff, PhD student
Lana Rees, PhD student
Verena Zimmermann, Technician

Selected publications


Natural ecosystems are under threat, species are disappearing at a rapid pace, and with them our livelihoods. The biodiversity crisis and the climate crisis are the two great ecological challenges of our time - and in many ways two sides of the same coin. Our research group aims in exploring various aspects of biology and biogeography of the endangered and rare species in order to then efficiently protect them.

One of the most important research topics of our group are woody species (trees, shrubs and lianas). The major model organisms since nearly 12 years are trees, mainly of the following families: Ulmaceae, Juglandaceae, Fagaceae, Pinaceae, Rosaceae and Fabaceae. More recently, we are investigating the ecology, phylogeny and phylogeography of an atypical woody shrub Ptilostemon greuteri (Asteraceae) endemic to Sicily, and the woody liana Clematis alpina (Ranunculaceae) across the European continent. Second very important research topic covers the biogeography, ecology and evolution of arctic-alpine and boreo-alpine taxa such as Calamagrostis (Poaceae), Papaver (Papaveraceae), Arenaria (Caryophyllaceae) as well as selected members of monilophytes (fern and allies).

Our group is directly linked with the Botanic Garden of the University of Fribourg (G. Kozlowski is a director of the garden), as well as intensively collaborating with the Adolphe Merkle Institute (AMI), with the Natural History Museum Fribourg (NHMF) and with the Office of Forest and Nature (SFN/WNA) of the State of Fribourg. Internationally, our group is tightly associated with the Shanghai Chenshan Botanic Garden in China (Plant Systematics and Evolutionary Biology Group at the Shanghai Chenshan Plant Science Research Center of the Chinese Academy of Sciences).

Group members
Nicolas Köfler, Research Assistant
Laurence Fazan, PhD student
Yann Fragnière, PhD student
Sébastien Bihrrey, Research Assistant
Luca Champoud, Research Assistant
Benoît Clément, Technician/gardener

Selected publications

Pinus cembra is an extremely rare tree in Canton of Fribourg. Larger populations occur only along the Gastlosen chain.
Ribosomal protein homeostasis

The life cycle of ribosomal proteins

Ribosomes are the molecular machines that carry out the synthesis of all cellular proteins from mRNA templates. Eukaryotic 80S ribosomes are composed of a small 40S and a large 60S subunit, which contain a total of four different ribosomal RNAs (rRNAs) and ~80 ribosomal proteins (r-proteins). Research carried out over the last 50 years, mainly with the yeast Saccharomyces cerevisiae, revealed that the biogenesis of eukaryotic ribosomes, i.e., the accurate piecing together of these rRNAs and r-proteins, is an extremely complex process.

My laboratory is interested in understanding how r-proteins, which are synthesized in the cytoplasm, safely reach their assembly site on pre-ribosomal subunits in the nucle(ol)us and how all the different r-proteins are provided in roughly equimolar amounts. Research over the last decade has revealed that several r-proteins require so-called dedicated chaperones to be protected from aggregation and get efficiently incorporated into pre-ribosomal subunits. Expecting that additional r-proteins also rely on such selective binding partners, our current research focuses on the identification, by applying a powerful proximity-labeling approach, and functional characterization of novel dedicated chaperones. In another project, we are exploring how the co-translational binding of dedicated chaperones influences the production of the r-protein client. Interestingly, we could recently show that the abundance of the APL3 and RPL4 mRNAs decreases when the availability of the respective dedicated chaperone is limited and nascent Rpl3 and Rpl4 are instead recognized by a regulatory machinery that subjects the encoding mRNAs to degradation. Notably, deregulated expression of Rpl3 and Rpl4 leads to their massive aggregation and a perturbation of overall proteostasis in cells lacking the E3 ubiquitin ligase Tom1, which marks orphan r-proteins for degradation. We propose that this unprecedented regulatory mechanism adjusts the de novo synthesis of r-proteins to their actual consumption during ribosome assembly and, thereby, protects cells from the detrimental effects of their surplus production.

“Ribosomal protein production needs to be tightly regulated”

Group members

Benjamin Pillet, Postdoc
Alfonso Méndez-Godoy, PhD student
Sebastien Favre, PhD student

Selected publications


Evolution of social behavior

The evolution and impact of socially transferred materials

After just a few minutes of watching ants in your kitchen, you may observe them performing a behavior that looks like kissing. Upon closer inspection, you might even see droplets of fluid pass from one insect to another. This behavior is called trophallaxis.

Trophallaxis is a fluid-exchange behavior observed in ants, bees, wasps, termites, some nonsocial insects, and even in some birds and mammals. Amongst ants, some species engage in this behavior and others do not.

The fluid passed between ants during trophallaxis is rich with information beyond simply the food it contains. There are many components of trophallactic fluid produced by the ants, proteins, miRNA, nestmate recognition cues and growth hormones that enable complex communication and consensus building in ant colonies. Some of these growth-regulating components are under strong positive selection and influence larval development.

Our research harnesses this fluid exchange to study the evolution of behavior, indirect genetic effects, evolutionary economics, manipulation and control. We use proteomics, metabolomics and RNA sequencing to explore these fluids passed between individuals and quantitative behavioral and developmental tracking to see how components of these fluids flow through the colony and impact receivers. We look over the ant phylogeny at how this fluid has evolved. Using big-data, fluorescence microscopy and computer vision, we monitor each individual in the colony, from a tiny larva to the queen, and observe how trophallactic fluid flows over the social network. We also use these tools to assess the function of transmitted molecules and to explore the evolutionary economics of collective investment in care.

What began as food-for-protection mutualism between ants, plants and honeydew producing insects has evolved into an important social behavior instrumental in ants ecological dominance. The derived version of this behavior, seen in Formicine ants for example, creates a social circulatory system that enables within-colony cooperation and long-term collective decision making.

Group members
Marie-Pierre Meurville, PhD student
Matteo Negroni, Postdoc
Sanja Hakala, Postdoc
Haruna Fujiioka, Postdoc
Galitame Kuhn, animalier
Amritansh Vats, PhD student
Jeanne Brülhart, technician

Selected publications
Hakala, S; Meurville, MP; Stumpe, M; LeBoeuf, AC (2022) Biomarkers in a socially exchanged fluid reflect colony maturity, behavior and distributed metabolism. eLife 10.7554/eLife.74005
To double or not to double…

How do plant genomes evolve across heterogeneous environments?

Plants have evolved sophisticated responses to environmental changes in order to survive and reproduce, and are usually adapted to the climate and the other species that they experience across their distribution range. In our lab, we use various plant species to address the genetics of such local adaptation and how it promotes the origin of new species in the face of climate changes.

To do so, we characterize plants from natural and experimental populations using high-throughput approaches and we assess processes having shaped genomic and phenotypic variation. For instance, we have shown that a narrow endemic species, Pulmonaria helvetica growing across only 100 km² in cantons Vaud and Fribourg, originated recently through the hybridization of two species having recolonized the space left by the retreat of glaciers. In that case, 1 + 1 gave 3 species and the conservation of that new, original species is of great importance for Switzerland.

Our current focus is on the consequences of whole genome duplication (or autopolyploidy) for the evolutionary radiation of plants. It is indeed largely unknown to what extent the doubling of all chromosomes promotes or hinders plant adaptation across environmental gradients. We have thus assembled genomes and transcriptome atlases of arctic-alpine relatives of the model plant Arabidopsis thaliana to investigate how duplicated genes as well as transposable elements respond to various environmental stresses. We are now using a textbook example of autopolyploidy under climate changes (Biscutella laevigata) to investigate diploid and polyploid populations from low- vs high-elevation and to integrate the genomic and environmental drivers of plant diversification in the Alps. In that case, we still do not understand what 1 x 2 yields.

Group members

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Sandra Grüning, PhD student
Leo Zeltier, PhD student
Vera Ogi, PhD student
Annie Guillarme, PhD student
Manuel Poretti, Postdoc
Theofania Patsiou, Postdoc
Martin Côté, Postdoc
Adrian Metry, research assistant
Patrick Favre, technician
Gwenael J. acob, technician
Pascal-Antoine Christin, visiting scientist

Selected publications


How do germ cells choose their destiny?

Dr. Alessandro Puoti
Genetic networks regulating gamete sex determination in Caenorhabditis elegans

“Big decisions in a small worm”

While spermatocytes and oocytes usually originate separately from male and female organisms, the hermaphroditic nematode Caenorhabditis elegans produces spermatids during larval development and oocytes as an adult. Consequently, gametes of both sexes are derived from the same pool of precursors. A central question in our laboratory is how this decision is made at the molecular level.

The switch from spermatogenesis to oogenesis in C. elegans hermaphrodites is controlled through post-transcriptional mechanisms, comprising the stabilization or decay of specific mRNAs, the processing of pre-mRNAs, and of course the regulation of translation. Our laboratory focuses on the role of genes that have been identified through mutant screens for hermaphrodites that show abnormal gamete sex determination. For example, the mog genes are needed for the switch from spermatogenesis to oogenesis in the transition from the L4 larva to the young adult hermaphrodite. mog loss-of-function mutants never switch to oogenesis in their otherwise female body, but continue producing spermatids throughout their life. Intriguingly, C. elegans mog genes code for proteins that are homologous to vertebrate and yeast pre-mRNA splicing factors. Consequently, some aspects of sex determination in worms may depend on the splicing of specific target mRNAs. Central questions include the identification of such target mRNAs, and their respective molecular roles. In this context, we study mRNAs that are deregulated in mog mutants and the role of splicing signals for default versus alternative splicing.

With its reproductive cycle of only 3 days, C. elegans offers powerful genetic, biochemical, and molecular tools. The availability of numerous mutant alleles, and if needed, the possibility to create mutants by genome editing, allows to investigate genetic pathways and their role in regulating sex determination of germ cells.

Group members

Maria Tarca, PhD student
Aimen Sultan, PhD student
Christine Défore, Technician

Selected publications


Plant Immunity

How do plants fight microbial threats and how do microbes deal with plant defences?

Plants have a multi-layered immune system with extra- and intracellular immune receptors that sense danger signals such as microbe-derived molecules and cellular perturbations caused by the microbes. Receptor activation triggers a variety of immune responses, both locally at the site of infection and systemically throughout the plant, to control microbial colonization. To overcome this robust host immune barrier, pathogens deploy virulence factors such as effectors and toxins that undermine plant immunity and promote their proliferation. In a continuous arms race, plants evolve new immune receptors and microbes develop new virulence factors.

We focus on lipopolysaccharide, the main component of the cell wall of Gram-negative bacteria. Lipopolysaccharide is a complex and heterogeneous glycolipid that is fascinating but also challenging to work with. We have identified the immune receptor LORE in crucifers that senses bacterial 3-hydroxy fatty acids, which are released during biosynthesis of lipopolysaccharide in Pseudomonas bacteria and probably via other, yet-unknown microbial pathways. We aim for a detailed understanding of the activation and regulation of the LORE receptor complex at the molecular level. Understanding the molecular mechanisms will provide the basis for future deployment of natural plant immune mechanisms in disease resistance engineering and sustainable plant protection strategies.

“Microbes face a highly effective immune system in plants”

Group members
Katia Zbinden, Lab technician
Cheryl Pillonel, Lab technician
Priyanka Raviraj, PhD student
Bruno K.M. Smet, PhD student
Fan-Yu Yu, PhD student
Lin-Jie Shu, senior researcher

Selected publications
Recolonization of host cells is under tight control by a dedicated genetic symbiosis program.

More than a decade ago, we have isolated from Petunia hybrida a new component required for symbiotic signaling in the arbuscular mycorrhizal (AM) symbiosis. Based on its two protein domains (VAP domain and ankyrin domain), the protein has been named VAPYRIN. Two other groups in the US independently identified the orthologous gene in another AM host (Medicago truncatula), thereby confirming the conserved function of VAPYRIN in AM symbiosis. Ever since, its molecular function has been explored, however, apart from multiple interacting proteins that highlight a relation to cellular secretion (exocytosis), the molecular function of VAPYRIN remained elusive. We have recently isolated a new vapyrin allele that has a transposon insertion in close proximity to the stop codon (leaving only six codons intact, and therefore causing a complete null allele). In this new allele, we observed a general activation of cellular defense mechanisms such as cell wall reinforcement and accumulation of lignin (Chen et al., 2021). In addition, many molecular markers for defense (Pathogenesis-Related (PR) proteins) are induced in vapyrin mutants, suggesting that one of the functions of VAPYRIN is to repress defense during symbiosis.

Finally, two developmental topics that have been a focus of my lab were covered in two recent review articles. The first review deals with the developmental role of the phytohormone strigolactone in shoot architecture (Khuvung et al., 2022). This is a rather recent topic that emerged from an international COST project (STREAM, FA1206; https://www.cost.eu/actions/FA1206/). While this COST project has been terminated, a PhD student (K. Khuvung) is following up on this. Lastly, we wrote a review on phyllotaxis (Reinhardt & Gola, 2022), that marks the end of my research in this domain of plant development. This article has been highlighted by the journal editor with the selection of our proposal for a cover illustration (see image).
Eco-Evolutionary dynamics

Is eco-evolution an optimizing process?

Understanding biodiversity maintenance and how it relates to the ecosystem functioning is a key question in ecology. During the last years, we have been developing new theoretical approaches to understand coexistence in species-rich communities — the structural approach of coexistence — and to the relationship between biodiversity and ecosystem functioning (BEF). These concepts have paved the way to a new integrative view of biodiversity and ecosystem functioning.

However, evolution has shown that it can act at short time scale (Gervasi & Schiestl 2017). Moreover, co-evolved communities differ from random experimental assemblages or non-coevolved communities. This pleads that one cannot fully understand biodiversity maintenance and ecosystem functioning without incorporating evolutionary aspects.

Our group aims at understanding to what extent eco-evolutionary dynamics impacts biodiversity and ecosystem functioning, and in particular, whether eco-evolution optimizes emergent populations or communities’ properties.

In a recent contribution, we study how eco-evolution impacts population properties such as growth rates and biomass production. Contrary to the common belief that evolution climbs the fitness landscape and maximizes growth rate or biomass production — r-selection or K-selection paradigm — we argue that this is a particular case of evolutive selection. Such particular cases arise when niche differentiation does not occur along evolutionary trajectories, and therefore, they are fundamentally incompatible with the emergence of polymorphism and ultimately of biodiversity through disruptive selection.

“Evolution seldom optimizes emergent properties”

Dr. Rudolf P. Rohr
Theoretical ecology and evolution

Group members
Vasco Lepori, PhD student
Edgard Djahoui, PhD student
Phuong Nguyen, Postdoc

Selected publications


Lipid droplets (LDs) are globular intracellular structures dedicated to the storage of fat in form of neutral lipids. LDs are closely associated with the major biosynthetic organelle of the cell, the endoplasmic reticulum (ER), both in yeast and mammalian cells. Unlike other cellular compartments, however, LDs are enclosed by an unusual membrane monolayer, which is continuous with the cytoplasmic leaflet of the ER membrane. LDs contain a specific set of proteins, many of which function in neutral lipid synthesis or degradation. How these proteins are exactly targeted to the LD surface is not fully understood. To address this question, we have devised a yeast mating-based microscopic readout to monitor the transfer of LD proteins upon zygote formation in living cells using three color time-lapse imaging. The results of this analysis indicate that fusion of the ER membrane between mating partners is required for the transfer of proteins between the LDs of the two cells. Interestingly, this transfer of proteins between individual LDs is continuous, bidirectionally and affects most LDs simultaneously. In cells where otherwise LD-localized proteins are mis-localized to the ER, we observe that these proteins reach the LDs of the mating partner. These observations suggest that LDs do not fuse upon mating of yeast cells, but that they form a network that is interconnected through the ER membrane. Consistent with this, LD proteins rapidly move onto LDs of a mating partner and this protein transfer is affected by seipin, a protein important for proper LD biogenesis and the functional connection of LDs with the ER membrane.

Group members

Stéphanie Cottier, Postdoc
Aslihan Ekim Kocabey, Postdoc
Ola El Atab, Postdoc
Rasha Khaddaj, Postdoc
Jiri Stribny, Postdoc
Barkha Gupta, PhD Student
Juliette Graff, PhD Student
Zhū Han, PhD Student

Selected publications


Computational Evolutionary Biology

Computational methods to model and protect biodiversity

Biodiversity has been evolving on our planet for billions of years and has faced in the process countless challenges, including dramatic events of climate change, mass extinctions and mass diversification. Today, biodiversity is facing a number of new threats deriving from anthropogenic direct and indirect pressure. In our lab, we develop computational tools to model and understand how biodiversity and ecosystems have evolved in the past. We also implement new methods using artificial intelligence to estimate the current status of biodiversity and to optimize conservation action and policies.

Our research typically involves the development and release of opensource software implementing new models. For instance, we have recently released new programs to infer dispersal and extinction dynamics through time from fossil datasets, an R package to approximate the extinction risk of modern species based on geographic occurrence data using machine learning, and a Python program for conservation planning using reinforcement learning. We also use these tools to carry out empirical studies. For example, we have recently mapped the origination and expansion of grasslands in North America using deep learning and estimated the current extinction risk across 50,000 species of trees.

Group members

Bruna Farina, PhD student
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Omela de Gasperini, Postdoc
Torsten Hauffe, Postdoc
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Tobias Andermann, Postdoc
Zhuo Zhou, Postdoc
Carlos Calderon del Cid, PhD student
Bernard Koch, PhD student

Selected publications


Genetics and neurodegeneration

Deciphering how the brain functions: from sensory coding to neurodegeneration

The way our brain functions and what can go wrong during aging and in neurodegenerative diseases, remains still mostly a mystery. In particular with more than hundred billion neurons and a trillions of synaptic connections the human brain will remain unresolvable for decades despite rapid technical advances. Since the molecular and genetics nature of all nervous systems are shared among all animals the only way of understanding how the brain works is studying animal models with less complicated brains. In our laboratory we use diverse, impacting genetic model systems to understand the brain.

Dissecting the nervous system with single-cell resolution

The brain is without any doubt the most complex organ. How is such a complicated organ with thousands of highly interconnected cell types formed? How do cells know what how they fit into this complex puzzle? We study the genetic and molecular mechanisms that control the fate of neurons. Using single-cell transcriptomics in combination with powerful molecular genetic techniques we decipher the processes that allow neurons to diversify and how neural networks are able to function in the way they do.

Forgetting: humanizing flies to resolve dementia and neurodegeneration

While some memories are kept for years other memories are rapidly forgotten. However forgetting is not a passive, random process but underlies tightly controlled molecular machinery. Neurodegenerative diseases such as Alzheimers disease cause problems with the formation of memories or enhance the forgetting process. Studying the memory center of the fruit fly allows us to unveil these mechanisms. We therefore used CRISPR/Cas9 to convert the flies Alzheimer Precursor Protein gene to the hereditary mutations of human Alzheimer Precursor Proteins, allowing is to study the molecular and genetic processes of this disease.

Group members

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Lucia de Andres, Postdoc
Marta Sprecher-Trujillo, Scientific collaborator
Ana Humbert, PhD student
Larisa Maier, Postdoc
Abhishek Mishra, Postdoc
Noemi Sgammeglia, PhD student
Gaelle Botton-Amiot, PhD student
Al-Sayed Al Scudy, Postdoc
Nikita Komarov, PhD student
Cornelia Fritsch, Lab Technician

Selected publications


Maier GL, Komarov N, Meyenhofer F, Kwon JF and Sprecher SG. Taste sensing and sugar detection mechanisms in Drosophila larval primary taste center. eLife 8, e67844

Kaldun JC, Lone SR, Humbert Camps AM, C Fritsch C, Widmer Y, Stein JV, Tomchik SN and Sprecher SG. Dopamine, sleep, and neuronal excitability modulate amyloid-b-mediated forgetting in Drosophila. PLoS Biology 19 (10), e3001412

AK Mishra, C Fritsch, R Voutev, RS Mann, SG Sprecher. Homothorax Controls a Binary Rhodopsin Switch in
Lipid Metabolism

How is fat stored, transported, and utilized in our cells?

In our lab, we use computer simulations to understand the inner workings of cells down to molecule-by-molecule and atom-by-atom detail. Traditionally, biologists have been studying how cells work and behave in living organisms - in vivo - and in their lab tubes - in vitro - but many features are too complex and too small to understand in this way.

To overcome this limitation and understand complex biological problems with atomistic-level resolution, we develop new computational approaches to study biological systems in silico, and we combine these investigations with biochemical and biophysical approaches. Our main methodology is called molecular dynamics (MD) simulations. Using this approach, we can describe molecular systems in the range of 1-100 nanometers with atom-level accuracy. To use Feynman words, we investigate living matter by studying the “the jiggling and wiggling of atoms”.

Currently, our focus is to understand the mechanisms that determine how lipid homeostasis is maintained in the cell. In particular, we are interested in how lipids are stored, transported or mobilized to produce energy. These lipid remodelling processes are governed by the interplay between specialized proteins and membrane properties, but in most cases, we still lack a detailed molecular explanation of how these processes are controlled. Our goal is to understand these processes in molecular detail, with the ultimate goal to translate our findings to the medical domain.

There is no life without fat

Group members

- Pablo Campomanes, Senior Scientist
- Valeria Zoni, PhD student
- Emanuele Petretto, PhD student
- Shriraksha Srinivasan, PhD student
- Janak Prabhu, PhD student
- Cristian Camilo Rocha Rea, PhD student
- Ahshloth Kumar, PhD student
- Taranath Mandal, Postdoc
- Andrea Di Luca, Postdoc
- Josephine Alba, Postdoc
- Daniel Alvarez Lorenzo, Postdoc
- Arun John Peter, Postdoc
- Ashutosh Kumar, PhD student
- Taraknath Mandal, Postdoc
- Andrea Di Luca, Postdoc
- Josephine Alba, Postdoc
- Daniel Alvarez Lorenzo, Postdoc
- Arun John Peter, Postdoc
- Aksh Singh, Postdoc

Selected publications

Computational methods to infer our past

All living organisms have an evolutionary history. What is ours? Our DNA tells a large part of that story, as it does for any other species. Using modern computational and statistical methods, we seek to extract that information.

The basic idea is simple: genetic data is informative about genealogical relationships. We all have two parents, eight grandparents and more than a thousand ancestors 10 generations ago. The more recent ancestors two individuals share, the more genetically similar they are. Siblings, for instance, share half of their DNA, cousins about one-eighth.

Our goal is to link patterns of relationships to evolutionary histories. Two randomly drawn samples from a large population, for instance, should not be closely related, but they might easily turn out to be cousins if sampled from a small population (picture the locals of your favorite ski resort). But if done right, relationships tell us much more: they are informative about population size changes, migration between and mixing of past populations.

Excitingly, it is now possible to extract DNA also from fossils, which give us an even more detailed glimpse of the past. We pioneer the statistical analysis of such data, which is difficult as fossil DNA is very scarce and heavily damaged. Using our dedicated tools, we could trace back the history of the first farmers of Europe and uncovered a complex pattern of splitting into smaller groups during challenging conditions such as the last ice ages and recurrent interactions and admixture when the climate was more favorable.

What does that tell us about ourselves? Each of us traces their ancestry back to multiple, highly diverged peoples that migrated, met and interacted repeatedly over thousands of years.

“My ancestry is complicated. Just like yours.”

Who we are

Group members

Andreas Füglistaler, Postdoc
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Liam Singer, PhD student
Madiana Calafell, PhD student
Xenia Wietlisbach, PhD student
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Ermes Fotsing, PhD student
Margarida Vaz, PhD student
Aimée Freiberg, PhD student

Selected publications


Mighty Microbes

Bacteria called to plant rescue

Our group is interested in microbes living in close association with plants, either on leaves or on roots. We aim to understand how they live, which chemical language they use to communicate, and how their functions may impact plant health. We typically isolate microbes from the crops we want to protect (e.g. potato or grapevine), characterize their multifaceted abilities and try to use the strains alone or in consortia as potential alternatives to currently used fungicides.

In recent years, we have discovered that Pseudomonas associated with potato emit potent volatile organic compounds that block different developmental stages of the oomycete pathogen Phytophthora infestans, the causative agent of late blight in potato which was responsible for the Irish Famine in the middle of the 19th Century. Further work led to the discovery that such volatile compounds also have strong impact on the physiology of neighboring organisms and can thus be considered long-distance modulators of microbial behavior, influencing many functions of relevance for plant health.

While our work in the last ten years mainly focused on a particular group of multi-talented bacteria belonging to the Pseudomonas genus, we have recently learned that plants select themselves specific helper bacteria when suffering from pathogen attack.

Among the bacteria responding most strongly to this “cry for help” from infected potato plants, many Bacillus strains were identified and isolated (see one example on the picture on the right).

These newly isolated strains, some of which indeed show anti-oomycete activity in vitro, represent promising candidates for the sustainable control of plant diseases.

Group members

- Floriane L’Haridon, Lab manager
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- Mout De Vrieze, Postdoc
- Alsayed Alfiky, Postdoc
- Abhishek Anand, PhD student
- Vivien Pichon, PhD student
- Ola Abdelrahman, PhD student
- Fanny Germainier, PhD student
- Nicolas Rappo, Junior scientist
- Elissa El Feghaly, Junior scientist

Selected publications

Chromatin function

Understanding cellular reprogramming for better or worse

Every cell in a specific tissue of an organism must turn on the appropriate set of genes to function for example as a neuron, as a muscle cell or as a sperm. Defects in the regulation of the adequate gene repertoire leads cells to acquire new identities, proliferate in an uncontrolled manner and disrupt tissue function. Thus, studying this regulation is crucial to understand how cells maintain their identity and do not engage in uncontrolled proliferation and differentiation, which are processes underlying tumorigenesis.

Our lab is using the nematode Caenorhabditis elegans as model organism to study how genes are regulated to ensure proper development of an organism. Using various experimental approaches, we were able to identify several key regulators of the germline gene repertoire. The transcription factor LSL-1 is a master regulator, which is required to activate genes involved in germ cell proliferation, in meiosis and in germ cell fate maintenance. LSL-1 is functioning by antagonizing the activity of repressors, such as the heterochromatin proteins HPL-2/HP1 and LET-418/Mi2, which exert important gene regulatory functions in somatic cells. Without proper LSL-1 activity, germ cells lose their identity and reprogram into neurons. The worms become sterile and exhibit teratomas in their gonads. Altogether, our research demonstrates the importance of tightly regulating gene repertoires and provides an understanding of the underlying mechanisms. Since all these transcriptional regulators that we examined in C. elegans are conserved in human, our research has implications in regenerative medicine and tumorigenesis.

Group members
David Rodriguez Crespo, PhD student
Shweta Rajapakshie, PhD student
Magali Nanchen, PhD student
Fariba Heydari, PhD student

Selected publications


Each year, the Biochemistry Division of the Biology Department hires two apprentices, for a period of three years. Under the supervision of Julien Comelli, the apprentices’ main task is to prepare practical biochemistry work for 2nd-year students from the Faculty of Science (doctors, biologists, biochemists, chemists, BMS). These preparations enable them to learn in detail the different aspects of the profession according to the various themes/subjects/techniques specific to clinical laboratory chemistry, such as blood and its components, glucose or cholesterol, to name but the most common.

Julien Comelli’s laboratory is also responsible for preparing the practical examinations that students who have completed the practical work must pass, as well as developing new analyses/techniques/methods and various tasks common to the department.

Julien Comelli
Chief laboratory technician, responsible for apprentices

Apprentices formation

We are also a training department
Multidisciplinary Study Programmes

Our students in the Bachelor’s programmes in Biology and in Biochemistry enjoy the diversity of courses, the practical training, and the easy and informal access to our research groups. MSc students find the opportunity to apply the knowledge gained during their BSc training, and to focus on more specific aspects in Biology, Biochemistry, or Bioinformatics and computational biology. PhD students appreciate networking within different fields of research in and outside of our Department, leading them to apply for positions in the academic and private sectors. Our mission is to advance the understanding and appreciation of biology and biochemistry through cutting-edge research in a large range of fields in Life Sciences.

Bachelor studies

From 2022, the Bachelor in Biology has been streamlined and now proposes 20 ECTS of core teaching that can be completed with the two new minors, Biology-from genes to ecosystems and/or Medical and molecular life sciences, or other minors from our or other Faculties. The BSc in Biology is offered in parallel with the Bachelor in Biochemistry, which is complemented for example with minors in chemistry and/or biology.

Master studies

In 2021, the Department of Biology has successfully launched two new Master’s programmes aimed at tackling the World’s environmental and health challenges. Replacing the previous Master in Biology, the Master in Environmental Biology and the Master in Molecular Life and Health Sciences join the thriving Buhl Master in Bioinformatics and Computational Biology of our training offer. With this initiative, the Department aims at extending the study offer and at providing more visibility to its core research areas, and its technical platforms. Both Biology Masters’ programmes also offer a specific option for future teachers at secondary level II.

Master in Environmental Biology

This Master program centers on plant health and applied and evolutionary ecology. Major environmental problems, in particular global change and its consequences on biodiversity and ecosystem functioning, are intimately interconnected and pose a threat to our future. Solving these problems requires an integrative and synergistic approach in terms of both fundamental and applied research. The program ranges from fundamental concepts in ecology and evolution, to molecular aspects of plant and microbial sciences, and applied solutions for environmental policies and sustainable development. It provides students with state-of-the-art training and background in conceptual, technical, and applied aspects of environmental biology.

Master in Molecular Life and Health Sciences

This Master program focuses on the molecular mechanisms and cellular processes related to human health. The Department of Biology of the Faculty of Science and Medicine offers this multidisciplinary master programme with five different options that address molecular aspects in organisms ranging from yeast to mammals. The Master of Science in Molecular Life and Health Sciences provides a solid background including aspects on understanding human disease, neurosciences, marine sciences, biochemistry, cell biology, and animal development. This programme gives to the student the opportunity to acquire advanced theoretical background on molecular topics, hands-on experience in the laboratory, and the ability to communicate science. Master’s students are integrated in research teams and thus gain extensive experience in fundamental academic research.

FGLM Events

2022
FGLM General Assembly, Welcome Assembly, FGLM Retreat with Dr. Kaycie Butler, Dr. Raphael Gerelet, Dr. Hendrik Nolte, FGLM Autumn Assembly, FGLM Workshop “How to perform in the storm?” Dr. Thomas Teichler
FGLM Seminars: “Sharing Strange Stuff and Funky Things” Dr. Pierre Kenner / “Women Scientists in Switzerland” Dr. Claudia Kasper / “Real-time to Real-life: Sequencing and SARS-CoV-2” Dr. Emma Hodcroft

2021
FGLM General Assembly, FGLM Retreat with Dr. Samuel Jager and workshops, FGLM Autumn Assembly, FGLM Career Day with Prof. Adria Lebeer, Dr. Pierre-Marie Allard, Dr. Danièle Cassignela, Prof. Ana Marques, Dr. Mario Paul Channay, Dr. Lucía de Andres
FGLM Seminars: “Imposter syndrome” Dr. Georgia Loukatou / “Graphical abstracts and scientific illustration” Dr. Mariza Munafó / “How to write a research paper” Dr. Kaycie Butler / “From data to statement” Prof. Dr. Dan Casare Castillo-Tony / “The long road to scientific publishing” Dr. Markus Gesler / “Classification and regressions using (Bayesian) Neural Networks” Prof. Danièle Silvestro / “PhD management - mental health & project management” Dr. Pauline Fritsch / “In Search for Common Decency: The Case of CRISPR as a Powerful and Evening Genome Editing Tool” Prof. François Rochat
Department Seminars in 2021

- 02.03.21 Marc-André Selosed, CNRS
- 16.01.21 Henrique Teotonio, ENS Paris
- 23.03.21 Luc Pelerin, University of Poitiers
- 20.04.21: Ilya and Kandice Levental, University of Virginia
- 11.05.21 Luís Monteiro, Complutense University, Madrid
- 14.06.21 Frank Jiggins, University of Cambridge
- 25.05.21 Christian Münch, Goethe University Frankfurt
- 21.09.21 Mathias Beller, Heinrich Heine University Duisburg-Essen
- 03.10.21 Christian Parissod, Inaugural lecture
- 19.10.21 Pierre-Marie Allard, Inaugural lecture
- 26.10.21 Benjamin Tewbin, University of Bern
- 09.11.21 Shaul Yalovsky, Tel Aviv University
- 16.11.21 Hanna Kokko, University of Zurich
- 23.11.21 Pascal-Antoine Christia, University of Sheffield
- 30.11.21 Florian Steiner, University of Geneva
- 07.12.21 Hu-Chen Lu, Indiana University Bloomington
- 14.12.21 Markus Kühler ETHZ
- 21.12.21 Birgitta Gallet, University of Geneva

Events in 2022

- 25.03.22 Masterweek
- 31.05.22 Department Day: Bachelor Symposium, General Assembly, Barbecue
- 20-21.06.22 CUSO workshop Critical transition, early warning signs and coexistence between fixed RoH, Louis-Fle Biersier
- 01.09.2022 Swiss Chronobiology Meeting, Urs Albrecht
- 05-09.09.21 CUSO course Introduction to Bayesian Inference in Practice Beneke Silva
- 16.09.21 Getting started journal d'accueil
- 19.09.2022 Welcome Day and information for Masters students
- 21-22.11.21 CUSO workshop Identifying the fundamental differences between reproductive and introduced species to inform research and management of the groups.
- 23.11.2022 Infoday 2021 auf Deutsch
- 24.11.2022 Bachelor & Master Evening
- 25.11.2022 SNF Fellowship Interview Day
- 30.11.2022 Infoday 2021 in French
- 15.12.2022 Christmas Party

Exhibition about aging and lifespan

A major exhibition on the diversity of aging patterns, lifespans and life cycles among organisms, called “Tic Toc – The Countdown of Life”, was featured in the Natural History Museum Fribourg (NHMF).

It was conceived by NHMF director Peter Wandelner, Thomas Flatt from our department as scientific consultant, and Pia Veiga from Cattà AG. By using graphic design elements, it brought some fundamental questions closer to the public: Why do we age? Why do different organisms have such different lifespans? Are there truly immortal organisms? Can we humans escape aging? The exhibition, in part funded by a SNF AGROR grant to T. Flatt, has been widely publicized in the local and national media.

EcoLife & Evolution Groups Move in

Since 2022, the EcoLife & Evolution research groups of Sven Bacher, Louis-Félix Biersier, Thomas Flatt, Kimberly Gilbert, Christian Parissod, Rudolf Rohr and Daniel Wegmann groups are working in the former “laboratoire cantonal” building, PER23. E&E administrative Wegmann groups are working in the former “laboratoire cantonal” building, PER23.

The other E&E research groups, i.e. the Kozlowski, LeBeuf and Silvestro groups, are respectively located in PER04, PER01 and PER17.

The diverse research of the groups in E&E spans the areas of applied ecology, conservation biology and biogeography, community ecology, population genetics and genomics of adaptation, plant ecological genomics, the evolution and mechanisms of social behavior, theoretical ecology and evolution, computational evolutionary (paleo-) biology and statistical and computational biology.
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