MSCA Postdoctoral Fellowships at Sorbonne University
Call for expression of interest 2024

BIOLOGY	
Code	**Topics and supervisors / research units**
BIO1	**Resolving complex karyotypes and deciphering their roles in cellular adaptation to environmental changes** Gilles Fischer – Laboratoire de Biologie Computationnelle et Quantitative (LCQB) - Paris
	Complex karyotypes (CK) result from massive chromosome reorganization and are a hallmark of cancer progression, suggesting that the rapid accumulation of mutations could provide a unique fitness advantage. CK are also observed in natural yeast isolates, indicating that they contribute to genome evolution. Using S. cerevisiae as a model, we propose to resolve their complex genome structures using Nanopore long-read sequencing and assess their adaptive potential in stressful environments.
BIO2	**Unveiling the complex organisation of protein sequence universe** Martin Weigt – Laboratoire de Biologie Computationnelle et Quantitative (LCQB) - Paris
	Functional proteins are organised in a hierarchical way: families of homologous proteins are divided into specific subfamilies, and are part of larger superfamilies. Taking inspiration from statistical physics and generative AI, we aim at developing a coherent generative but interpretable modeling framework at all hierarchical levels, and (co-)evolutionary models exploring sequence space. Models are developed in close collaboration with experimentalists to test predictions and refine models.
BIO3	**Innovative bio-inspired cell and tissue models of genetic dilated cardiomyopathy for disease modelling and drug discovery** Onnik Agbulut - Biological Adaptation and Ageing (B2A) - Paris
	The main goal of this proposal is to develop innovative bio-inspired cellular and/or tissular models and their associated analysis tools in the perspective of high-throughput and high-content drug screening for genetic dilated cardiomyopathy. To achieve these, we generated induced pluripotent stem cells from different healthy and dilated cardiomyopathy patients and a multidisciplinary consortium which involves academic partners and companies.
BIO4	**Role of cardiomyocyte mitochondria transfer in heart homeostasis, remodeling and diseases** Onnik Agbulut - Biological Adaptation and Ageing (B2A) - Paris
	This project aims to prove that cardiomyocyte crosstalk with neighbouring cells, through the release of their mitochondria. This is considered an important mechanism by which recipient cells sense the state of cardiac organelles and thereby adapt their behaviour to the physiological/pathological conditions of the heart. To attain our objectives, we generated different animal and cellular models.

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BIO5	**Neuronal resilience-promoting strategies to fight neurodegenerative diseases** Christian Neri - Biological Adaptation and Ageing (B2A) - Paris
	Ensuring brain health is greatly challenged by the lack of knowledge of the mechanisms that enable populations of vulnerable neurons to resist neuro-degenerative diseases. Building up on compelling preliminary data, and using models of Huntington's disease (human iPS cell-derived neurons, mouse synapses on chips), the aim of the project is to study how targeted reprogramming approaches can re-instate the cellular compensation and resilience capabilities of vulnerable neurons.
BIO6	**Molecular mechanisms for the generation of hematopoietic stem cells from human induced pluripotent stem cells.** Thierry Jaffredo - Laboratoire de Biologie du Développement (LBD) - Paris
	We have developed a robust, transgene-free protocol to generate transplantable hematopoietic stem cells (HSCs) from human induced pluripotent stem cells (doi: 10.1016/j.stem.2023.11.002). The project will use bioinformatic and cell biology tools to understand how and from which progenitor cells HSCs are generated ex vivo, which cell type is transplanted in vivo, whether other cell types besides hematopoietic cells are required, and how the cells adapt to enable robust multilineage hematopoiesis.
BIO7	**Tackling Off-target Side Effects of oxaliplatin** Hélène Bertrand - Laboratoire des Biomolécules (LBM) - Paris
	Oxaliplatin (Ox) is widely used in clinic. However, the Ox-induced peripheral neuropathy (OIPN) is a major hurdle limiting its clinical use and a major societal issue. Its underlying molecular mechanisms are complex and no clinically effective treatment or prevention therapy exists. Using a multiscale (cells, in vivo models) and multidisciplinary approach (chemistry, biology, distribution), we explore molecular approaches to enhance the efficacy over toxicity ratio of Ox-based treatments.
BIO8	**The evolution of complex multicelluarity** Julien Mozziconacci – Structure et Instabilités des Génomes (StrInG) - Paris
	The appearance of complex multicellular organisms has occurred many times during evolution but only in the branch of eukaryotes, for which genome are covered with nucleosomes and folded in a very structured way. The objective of this project is to better understand how these structures enable a complex regulation of the genes by focusing on nucleosomes positions and the 3D genome folding in species of both unicellular and multicellular fungi which are close relatives at the phylogenetic level.
BIO9	**Deep learning the histone code** Julien Mozziconacci – Structure et Instabilités des Génomes (StrInG) - Paris
	In this project we will develop new deep learning to decode the histone code hypothesis, which posits that DNA transcription is partly regulated by combinatorial histone modifications. We will combine innovative models like Chromoformer and DeepHistone, that integrated 3D chromatin folding and sequence data, to understand gene regulation during cellular differentiation and disease. Computational predictions will be tested in experiments involving real cells.

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BIO10	**Dynamic control of epigenetic marks in live cells** Julien Mozziconacci – Structure et Instabilités des Génomes (StrInG) - Paris
	We wish to investigate the dynamic relationships between epigenetic modifications, chromosomal organization, and gene expression by specifically controlling the level of histone H3 lysine 9 trimethylation (H3K9me3) on different DNA repeat sequences. H3K9me3 levels will be localy modified with epigenome editing tools. The perturbations on the 1D and 3D organization of the genome and on gene expression will be monitored by imaging, Hi-C, ChiP-seq and RNA-seq.
BIO11	**Securing an original luciferin/luciferase reporting system** Yves Janin – Structure et Instabilités des Génomes (StrInG) - Paris
	From coelenterazine-using luciferases (i.e.: Renilla, Gaussia, Oplophorus, Periphylla), many bioluminescence-based reporters have been designed and are extensively used in life sciences. This project aims at providing less expensive alternatives starting with the uncharacterized Periphylla luciferase. This will involve extensive molecular biology and structure-based protein engineering to characterize this luciferase and then design adapted and efficient luciferin/luciferase reporting systems.
BIO12	**The effects of water kefir on human health** Christophe Lavelle – Structure et Instabilités des Génomes (StrInG) - Paris
	Our lab focuses on water kefir, a fermented drink made from water, sugar and fresh/dry fruits to which are added translucent grains composed of symbiotic communities of microorganisms (mainly lactic acid bacteria and yeasts). The drink conveys an image of a "healthy" product rich in probiotics, which partly contributes to its success among consumers. The aim of this project is to consolidate our knowledge of this drink, both in terms of consumption habits and its effects on human health.
MAR7	**Behavioral ecology, developmental physiology, and neuroendocrinology of a metamorphosing reef fish** Marc Besson - Biologie Intégrative des Organismes Marins (BIOM) – Banyuls, Occcitanie
	The metamorphosis of marine fishes is critical for population replenishment and resilience but this transition is vulnerable to disruption by anthropogenic stressors. Through a multidisciplinary approach, we will examine the inner molecular and developmental mechanisms responsible for the behavioral and morphological impairments caused by stressors during the metamorphosis of the spiny chromis. This project will unveil critical ecological and conservation knowledge to protect fish replenishment.
MAR8	**Coevolution of head muscles and associated motoneurons** Stéphanie Bertrand - Biologie Intégrative des Organismes Marins (BIOM) – Banyuls, Occcitanie
	The objective of the project is to bring insights into how the complex vertebrate head appeared during evolution. The candidate will focus on the mesodermal component that forms the head muscles and the neurons controlling their activity. For this purpose he/she will use the cephalochordate amphioxus as a model system and study how the oropharyngeal muscles and motoneurons develop by using several approaches (scRNA-seq, retrograde labelling, ISH, immunostaining, CRISPR/Cas9, behavior analysis).

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MAR9	**Deciphering evolutionary and developmental trajectories towards the vertebrate body plan: a chondrichthyan reference** Sylvie Mazan - Biologie Intégrative des Organismes Marins (BIOM) – Banyuls, Occcitanie
	Early embryonic architectures and cell types extensively diverge across vertebrates, yet they converge towards a highly conserved body plan, which becomes evident by gastrulation. The project aims at deciphering their underlying unity, focusing on a cartilaginous fish, the catshark Scyliorhinus canicula, and using a scRNA-seq based approach. These data should provide a comparative reference, enlightening ancestral cell states and transitions, obscured by taxa-specific diversifications.
MAR10	**Comparative study of peripheral nervous system formation in ascidians: conservation, drift and variability** Sébastien Darras - Biologie Intégrative des Organismes Marins (BIOM) – Banyuls, Occcitanie
	While EvoDevo has largely focused on the identification of conserved mechanisms regulating the formation of homologous structures, a wide range of changes may occur in the course of evolution without systematic phenotypic consequences. The current state of biology allows to access the diversity of species to document the evolution of developmental mechanisms. The project will use ascidians as models to address this question using functional genomic approaches.