



Postdoctoral position in Yeast Evolutionary Genomics

Hosting unit

Laboratory of Computational, Quantitative, and Synthetic Biology (CQSB). The [CQSB](#) is an interdisciplinary research unit within the [Institut de Biologie Paris Seine](#), supported by the [CNRS](#) and located at [Sorbonne Université](#) in central Paris. The lab operates at the interface of biology and quantitative sciences, promoting a balanced integration of theoretical and experimental approaches to explore the fundamental principles of complex biological systems.

Hosting team

Biology of Genomes (BiG). The successful candidate will join the [BiG](#) team headed by Gilles Fischer. Our research focuses at understanding the biology of eukaryotic and prokaryotic genomes. In yeast, we are interested by the relationships between mutational processes, evolution of gene content, dynamics of chromosome structure and genome evolvability across different biological scales, from cells to populations and species. We combine several approaches including, experimental evolution, long-read genome sequencing, genome engineering and computational analyses of large genomic datasets.

Recent Publications

Agier N, Vittorelli N, Ollivier L, Chaux F, Gillet- Markowska A, O'Donnell S, Pouyet F, Fischer G, Delmas S. A transient mutational burst occurs during yeast colony development [Molecular Systems Biology](#) (2025) <https://doi.org/10.1038/s44320-025-00117-1>

Miao Z, Ren Y, Tarabini A, Yang L, Li H, Ye C, Liti G, Fischer G, Li J, Yue J-X
ScRAPdb: an integrated pan-omics database for the *Saccharomyces cerevisiae* reference assembly panel. [Nucleic Acids Research](#), (2024) doi: 10.1093/nar/gkae955

S. O'Donnell, JX Yue, O. Abou Saada, N. Agier, C. Caradec, T Cokelaer, M. De Chiara, S. Delmas, F. Dutreux, T Fournier, A. Friedrich, E. Kornobis, J Li, Z. Miao, L. Tattini, J. Schacherer, G. Liti and G. Fischer. Telomere-to-telomere assemblies of 142 strains characterize the genome structural landscape in *Saccharomyces cerevisiae*
[Nature Genetics](#), 55(8):1390-1399 (2023)

Scientific project

Resolving the dynamic architecture of natural polyploid genomes in *Saccharomyces cerevisiae*. Polyploidy, characterized by organisms possessing three or more complete sets of chromosomes, is widespread across plant, animal, and fungal species. This phenomenon has garnered attention due to its profound impact on species evolution and its association with cancer development. However, understanding the genomic structure of natural polyploid populations, including their prevalence and evolutionary trajectories within species, is still in its infancy. This project aims at resolving the intricate genomic structure of polyploid genomes at the entire population level in *Saccharomyces cerevisiae*, quantifying their level of genomic instability and elucidating their adaptive capacity. We will use the latest versions of the two current long-read technologies: Oxford Nanopore Technology (ONT) and Pacific Biosciences (PACBIO) to generate fully phased Telomere-to-Telomere genome

assemblies for more than 100 natural polyploid strains. We will assess structural diversity and mutation rates for both point mutations and large-scale chromosomal rearrangements and determine whether polyploids inherently possess higher mutation rates and genome instability or if the increased number of mutational events observed during experimental evolution is due to larger genome size and/or relaxed purifying selection in polyploids as compared to diploid genomes. Finally, we will compare the adaptive potential of natural diploids and polyploids by subjecting barcoded populations to experimental evolution *via* serial passaging in challenging growth conditions. Barcode sequencing will directly estimate the relative fitness of all strains in pooled populations, while T2T assemblies of evolved clones will reveal genome-level adaptive responses.

Job information

Type of contract: fixed-term contract

Duration of contract: 24 months

Estimated start date: position available immediately

Job description: full time

Salary: €2964 to €3997 gross per month depending on experience (0 to > 3 years)

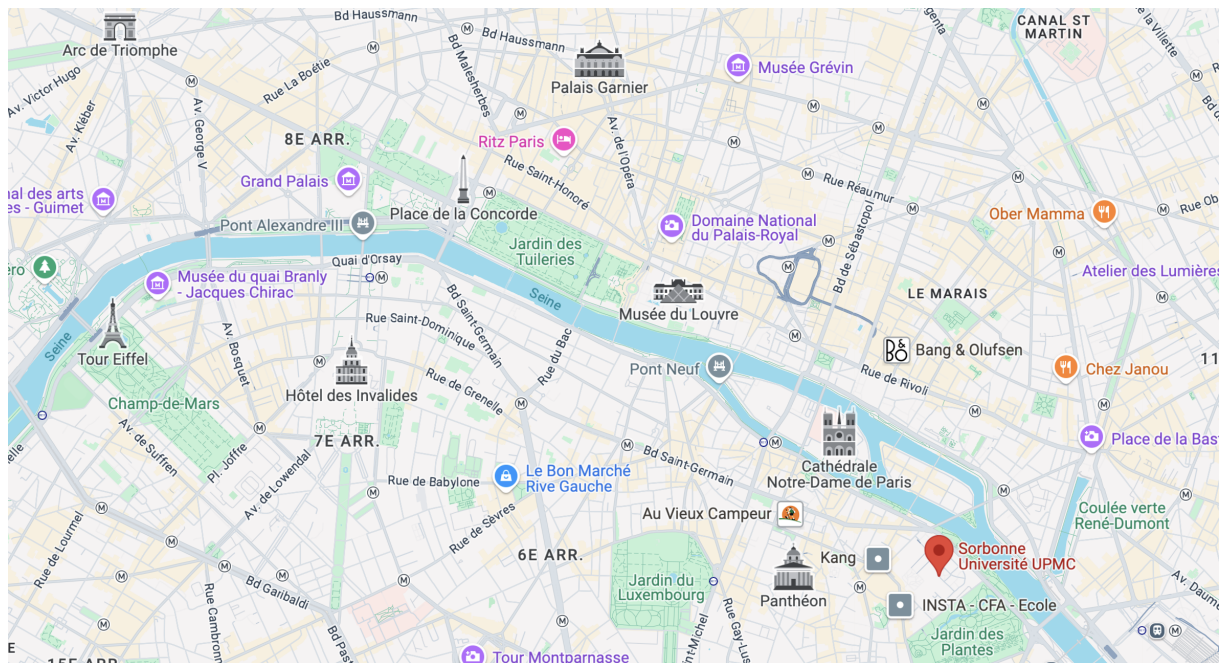
Education level: Doctorate

Requested experience: molecular biology, genetics, genomics, bioinformatics

Language skills: fluent English

Application and contact

The application should include a detailed CV, a letter of motivation and the contact details for at least two references. Candidates should send their application as a single PDF file to gilles.fischer@sorbonne-university.fr.



Sorbonne Université
Institut de Biologie Paris Seine
Computational, Quantitative and Synthetic Biology
7-9 quai Saint Bernard
75005 Paris