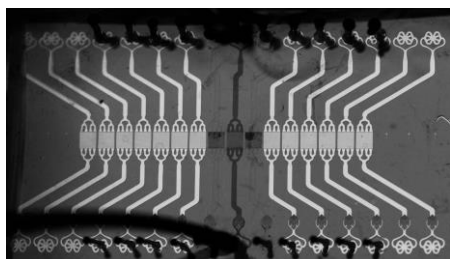


Assistant professor position in Bioinformatics (MCF0296, section 64): Role of phenotypic heterogeneity in shaping stress response strategies

Keywords: Adaptation to environmental stress, phenotypic variability, quantitative high-throughput microscopy, single-cell transcriptomic analyses, yeast genetics



Among the mechanisms by which living organisms adapt to temporal fluctuations in the environment, those that exploit phenotypic variability (whether pre-existing or stress-induced) within an isogenic population and its impact on the fate of organisms remain poorly characterized. Beyond the fundamental aspect, this issue is particularly relevant to the fight against antibiotic resistance, where the phenomenon of bacterial persistence has long been described, but remains a major therapeutic challenge. A promising approach is emerging to study in greater detail the role of phenotypic heterogeneity in response to stress, involving the temporal tracking of individual cells by microscopy/microfluidics, followed by the specific recovery of cells of interest by sorting, for large-scale 'omic' characterization. This characterization involves the use of high-throughput sequencing to determine variation in gene expression at several levels, and in particular at transcriptional level using RNA sequencing strategies. The aim is also to characterize expression variation on single cells using single-cell RNA sequencing strategies. Dissecting gene regulatory steps, in this case at the transcriptomic level, is essential to better understand the origin of phenotypic variation observed in a single cell.

In this context, the Molecular Genetics, Genomics and Microbiology Unit (GMGM, UMR7156) wishes to strengthen its research activities in quantitative biology, and more particularly in areas at the interface between high-throughput quantitative microscopy and genome expression analysis, in order to better understand the mechanisms of phenotypic variation observed in isogenic populations. The person recruited will be attached to the "Quantitative Biology of Cell Growth" team headed by Gilles Charvin, and should have a bioinformatics background. The research project should be in line with the team's thematic focus, drawing in particular on its expertise in the regulation of the response to oxidative stress or the control of proliferation in response to metabolic transitions (i.e. quiescence) in budding yeast. The project will implement state-of-the-art bioinformatics methodologies for the 'omic' characterization of large cell populations. The person will also be in charge of implementing single-cell RNA sequencing strategies. He/she must be able to work in a resolutely interdisciplinary environment at the interface with cell biology, engineering (microscopy, instrumentation, microfluidics) and bioinformatics.

We are seeking a highly motivated candidate with an excellent track record. The recruited assistant professor will teach at the University of Strasbourg, which is one of the top universities in France.

Please don't hesitate to get in touch with Gilles Charvin if you are interested in this position : charvin@unistra.fr

Relevant publications:

[Jacquel B, Kavcic B, Matifas A, Julou T, Charvin, G, biorxiv, 2023](#)

[Aspert T, Hentsch D, Charvin G, eLife, 2022](#)

[Jacquel B, Aspert T, Laporte D, Sagot I, Charvin G, eLife, 2021](#)

[Garmendia-Torres C, Tassy O, Matifas A, Molina N, Charvin G, eLife, 2018](#)

[Goulev Y, Morlot S, Matifas A, Huang B, Molin M, Toledano MB, Charvin G, eLife, 2017](#)