Engineer position in Bioinformatics / Data Science for Single-Cell Spatial Transcriptomics

Single-Cell transcriptomics allows the quantification of gene expression at the scale of individual cells, encoded in count matrices containing thousands observations (cells) and tens of thousands features (gene expression values). Furthermore, single cell gene expression can now be profiled in the context of biological tissues, making high throughput spatial transcriptomics a reality allowing to investigate the spatial heterogeneity of tumors. The analysis of such data requires new methodological frameworks, dedicated to their complexity and size.

Our project will focus on the study of pituitary tumors (PiTs), and more specifically on the interactions of tumor cells with the Tumor Micro Environment (TME). TME includes blood/lymph vessels, immune cells, cancer-associated fibroblasts, as well as extracellular matrix components, and soluble molecules. These intercellular heterogeneities result in vast possibilities of cell-to-cell interactions and cross talks that can be structured spatially to produce a specific cellular ecosystem. The present project will aim at unravelling the intricate spatial signaling networks that orchestrate the fine-tuned exchanges between tumor-cells and the TME, highlighting the role of TME in tumor biology.

The mission will be to develop analysis pipelines for quality control, processing, visualization and analysis of spatial transcriptomic data. The computing environment will be based on R, Python, Docker and NextFlow. The candidate will develop pipelines based on available software suits like Seurat or scVerse, and will also contribute to the development and diffusion of original methods developed by our group.

The candidate will be co-supervised by Franck Picard (CNRS, ENS Lyon) and Philippe Bertolino (CRCL), experts in machine learning and cancer biology. The candidate will work at the ENS de Lyon, in an interdisciplinary environment, between mathematics, computer science and biology. Moreover, the candidate will benefit from the AI4scMed PEPR project that gathers an interdisciplinary consortium in machine learning / IA dedicated to single cell genomics, with experts in machine learning, optimal transport and statistics.

Starting: from October 2023, flexible.
Duration: up to 2 years
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