Postdoctoral Fellow position at Institut Curie in Computational Biology/Cancer Genomics

Duration: 24 months with the possibility of extension, starting immediately

The Cavalli Lab is seeking a highly motivated scientist interested in deciphering tumor heterogeneity to join as Postdoctoral Fellow.
Institut Curie is one of the biggest European institutions for cancer research with strong interdisciplinary traditions. It also comprises a hospital specialized in cancer treatment, and therefore covers a continuum of expertise from fundamental research to patient care (https://institut-curie.org/). The Cavalli Lab is part of the "Bioinformatics and Computational Systems Biology of Cancer" Unit (U900 INSERM, Mines ParisTech, Institut Curie) at Institut Curie, which consists of ~90 researchers and students. It is a very active and growing interdisciplinary team of bioinformaticians, biologists, physicians, mathematicians, statisticians, physicists, and computer scientists (U900 Unit page).
The Cavalli Lab (located at Institut Curie St-Cloud, west of Paris), investigates tumor heterogeneity, targeting clinically relevant questions. The goal of our genomic approaches is to explore clinically relevant aspects of brain tumor biology. We pursue this goal using patient samples profiling, investigating temporal and intra-tumoral/spatial heterogeneity as well as tumor/tumor microenvironment interactions in gliomas. Projects in the Cavalli lab are developed within a dynamic and collaborative environment with other researchers and clinicians at Institut Curie and from the POLA network (National POLA Network for the Treatment of High-Grade Oligodendroglial Tumours). The successful candidate will be a recent PhD graduate with the ambition to tackle the complexity of tumor biology and intra-tumoral heterogeneity using computational analysis of cutting-edge sequencing datasets (single nucleus RNA-seq/ATAC-seq and spatial transcriptomics data).

Qualification
The successful candidate should hold a PhD, have a track record of creativity in developing analytic strategies, and a strong foundation of knowledge in one or more of the following: genomics, cancer biology, statistics. Excellent computational skills as well as experience with high-throughput data analysis in biology and/or single-cell data analysis is highly desirable. Must be self-motivated, capable to work in autonomy and have evidence of scientific accomplishment via peer-reviewed publications. Excellent written and verbal communication skills in English and a team spirit are essential.

Responsibilities
- Drive and develop scientific projects focused on tumor heterogeneity
- Perform end-to-end data analysis (QC, processing, normalization, visualization, interpretation, etc)
- Analyse single-cell and spatial transcriptomics datasets
- Use and develop methods and strategies to assess spatial heterogeneity from brain tumor samples
- Characterise tumor – tumor microenvironment (TME) interactions
- Perform high dimensional data analysis and integrative 'omic' data analysis

Experience / Skills
- PhD in bioinformatics, statistics, or computer science with knowledge and interest in biology
- Experience working in a Unix environment
- Experience in statistical analysis using R
- Experience with single-cell RNA-seq analysis is desirable
- Understanding of cancer cell biology is an asset as well as experience of collaboration with biologists for solving concrete biological problems

Applicants should send (1) a cover letter describing previous work, interests, and career goals, (2) CV, and (3) three letters of reference to Dr. Cavalli at florence.cavalli@curie.fr.