

Internship in Computational Biology/Cancer Genomics

Spatial transcriptomics analysis to decipher intra-tumoral heterogeneity in brain tumor samples

The Cavalli Lab is part of the "Bioinformatics, Biostatistics, Epidemiology 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.

The Cavalli Lab (located at Institut Curie St-Cloud, west of Paris), aims to decipher tumor heterogeneity. We investigate the complexity of tumor biology and temporal and intra-tumoral heterogeneity using computational analysis of data from cutting-edge sequencing efforts. The goal of our genomic approach is to explore clinically relevant aspects of brain tumor biology using patient samples.

The goal of this internship is to analyze a brand-new data type; spatial transcriptomics data (spatially resolved transcriptomics methods have been awarded as methods of the year 2020 by Nature Methods) and characterize the (spatial) intra-tumoral heterogeneity of glioma tumor samples. Spatial transcriptomics data brings a new dimension to the analysis of tumor samples allowing us to combine the full transcriptome information and the spatial localization of cells within a tumor. We are generating, in collaboration with oncologists and neuropathologists, a new spatial transcriptomics data cohort from gliomas brain tumors. New methods are becoming available to analyze this data type, the student will therefore first implement and evaluate different deconvolution methods. The student will first identify public normal and tumor single-cell RNA-seq datasets relevant to be used as a reference to analyze our 10X Visium spatial transcriptomics dataset. Following the download, processing, and quality check of the data, s/he will combine these datasets with our own single-nucleus RNA-seq data from glioma samples to create the most accurate reference to perform the analysis. S/he will then evaluate the current methods (such as Cell2Locations Kleshchevnikov et al. et SPOTlight, Elosua-Bayes et al.) to identify the cell types and states present within tumors from spatial transcriptomics data using the reference built. S/he will then characterize the different tumor cell states, taking into account their spatial context, identify if specific niches exist and their implication for the tumor's biology.

Note: Possibility to continue as PhD student.

Duration: ~6 months (M2 master project)

Starting date: Flexible

Research group:

Computational Biology and Integrative Genomics of Cancer

U900 – «Bioinformatics, Biostatistics, Epidemiology and Computational Systems. Biology of Cancer» Department

Institut Curie St-Cloud/Paris

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