



## Job description

**Title:** Bioinformatician in single cell omics analysis

**Position:** Full time

**Posted on:** 15 February 2022

**Location:** Wyss Center for Bio and Neuroengineering, Campus Biotech, Geneva, Switzerland

### About the Wyss Center for Bio and Neuroengineering

The Wyss Center is an independent, non-profit research and development organization that advances our understanding of the brain to realize therapies and improve lives. The Wyss Center staff, together with the Center's academic, clinical and industrial collaborators, pursue innovations and new approaches in neurobiology, neuroimaging and neurotechnology.

The Wyss Center advances reveal unique insights into the mechanisms underlying the dynamics of the brain and the treatment of disease to accelerate the development of devices and therapies for unmet medical needs. The Center was established by a generous donation from the Swiss entrepreneur and philanthropist Hansjörg Wyss in 2014. Additional resources from funding agencies and other sources help the Wyss Center accelerate its mission.

### Job description

The bioinformatician in single cell omics analysis will participate in collaborative projects between the Wyss Center and its academic and industrial partners, at the frontier between experimental and computational biology.

Recent years have been characterized by an exponential growth in the number and size of neuroscience-related databases, containing information on a variety of conditions, time points, and species. There is an urgent need to develop methods to unify these still largely heterogeneous datasets. In this position, the bioinformatician will build an integrated multimodal neural cell reference database.

### Key responsibilities

The candidate will be expected to perform the following tasks:

- Identify published single cells -omics neuronal/astrocytic datasets and process the raw data.
- Perform quality control, data filtering and analysis from high-throughput single-cell multi-omics data including transcriptomics (**single-cell RNA-seq**) and epigenomics (**single-cell ATAC-seq**) obtained from brain tissue or available databases.
- Integrate datasets within a common structure from different data sources such as transcriptomics (RNA-seq) and epigenomics (ATAC-seq).
- Implement an analytical "pipeline" for multimodal data integration (optical/electrical/behaviour/-omics). This will be achieved with a team of experts in signal analysis (optical/electrical/behaviour).
- Develop a visualization platform using a web-based tools like dashboard. This will be achieved in collaboration as above, to provide a common visualization output.

- Perform statistical analysis to critically assess data quality.

## **Requirements**

- PhD in neurosciences, engineering and/or in computer sciences.
- Professional experience in single cell transcriptomic data analysis using R and/or Python.
- Experience in computer science and programming using R (knowledge of python is a plus), Linux, and ability to work with version control (e.g. Git).
- Background in imaging analysis.
- Experience (theoretical and practical) in statistics and machine learning.
- Fluent in English (written / spoken).
- Superior communication, interpersonal and analytical skills.
- Positive attitude and a role model, with unquestioned integrity, work ethic and trustworthiness.

To apply, please send your CV, a cover letter and letters from two referees to [HR@wysscenter.ch](mailto:HR@wysscenter.ch) no later than April 15<sup>th</sup>, 2022.