Postdoc position in computational immunology at UCSF

The Fragiadakis Lab (Data Science CoLab, dscolab.ucsf.edu) is seeking a computationally-focused postdoc or PhD-level research scientist interested in analyzing high-dimensional immune system data and developing methods toward answering questions of immune state from patient data in different disease contexts. We have a series of collaborations studying the immune system and its response to cancer, autoimmunity, and infection — we are examining specific responses to these conditions as well as larger questions of immune organization that can be answered with this data. Through these partnerships, we are generating high-dimensional immune system data, including single-cell RNAseq and CyTOF from patient samples with associated clinical information.

We are looking for a computational biologist who is excited to delve into applied problems in immune state from data analysis, as well as methods development, perspective. Best candidates would have extensive experience working with large biological datasets, such as single-cell immune system data (single-cell RNAseq, CyTOF), with interest in working with new data types. Experience with data management, multi-modal datasets, and machine learning/statistics is preferred, along with interest in working collaboratively, teaching, and learning from both data scientists and wet-lab biologists. The position is based at UCSF Parnassus campus.

This position offers a collaborative environment comprised of a computational community in the lab, as well as close contact with wet-lab biologists through in the other CoLabs and participating UCSF labs. We also offer the possibility for co-advising with collaborating labs. Our data is generated using consistent and highly optimized workflows across projects to enable cross-data set and multi-modal analyses. Many projects have partial of full funding for a postdoctoral fellow or research scientist.

Interested candidates should contact Gabi Fragiadakis (Gabriela.Fragiadakis@ucsf.edu)

**Required qualifications**

- PhD in computational biology, bioinformatics, or similar, or PhD in biology field with a substantial computational component in thesis work
- Extensive experience working with high-dimensional biological data and large data sets
- Experience working with some subset of the following: single-cell sequencing data (scRNAseq, CITEseq, etc.), metagenomic sequencing, CyTOF or high-dimensional flow cytometry, proteomics, metabolomics
- Advanced skills in R, Python, or similar
- An interest and aptitude for learning to work with new data types and multi-modal analysis
- Version control (git), command-line tools, pipeline use/development
- Strong abilities in working as a part of a team and collaboration
- Strong skills in communicating results and documentation

**Preferred qualifications**

- Background in systems immunology
- Experience working with clinical/demographic data
- Experience developing methods for analyzing high-dimensional and multi-modal biological data
- Ability to write standalone packages/libraries for use in future projects/biological community