Postdoc position in computational immunology and microbiome at UCSF

The Spitzer lab [https://spitzerlab.ucsf.edu/](https://spitzerlab.ucsf.edu/) and the Fragiadakis Lab (Data Science CoLab) [https://dscolab.ucsf.edu/](https://dscolab.ucsf.edu/) at UCSF are collaborating on a funded project exploring human microbiome-immune interactions at the systems-level. We are hiring a computationally-focused postdoc or PhD-level research scientist interested in analyzing high-dimensional immune system and microbiome data, with a focus on developing computational and statistical methods for interrogating and integrating high-dimensional immune system and microbiome data. The work will be conducted in an established team, in coordination with senior postdoctoral researcher Joel Babdor [https://profiles.ucsf.edu/joel.babdor](https://profiles.ucsf.edu/joel.babdor). Best candidates would have extensive experience working with either microbiome data (metagenomics, 16S) and/or single-cell immune system data (single-cell RNAseq, CyTOF) and/or metabolomic data, with interest in working with new data types. Experience with data management, multi-modal datasets, and machine learning/statistics is preferred, along with a willingness to work collaboratively, teaching and learning from wet-lab biologists. The position is based at UCSF Parnassus campus.

Interested candidates please contact Gabi Fragiadakis ([Gabriela.Fragiadakis@ucsf.edu](mailto:Gabriela.Fragiadakis@ucsf.edu)) or Matt Spitzer ([Matthew.Spitzer@ucsf.edu](mailto:Matthew.Spitzer@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,16S amplicon 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 and/or microbiome analysis
- 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