Bioinformatics Postdoctoral Researcher-Krogan Lab (UCSF)

The lab of Professor Nevan Krogan at the University of California, San Francisco is seeking a dynamic, independent, and creative bioinformatic postdoctoral researcher to join his team. You will work on the develop of novel computational methods to integrate diverse high-throughput datasets produced in-house as well as publicly available datasets across a range of projects (infectious diseases, cancer, neuroscience).

The Krogan lab has pioneered a systems biology approach which combines proteomics and functional genomics to unravel mechanisms of disease and discover novel putative therapeutic targets in the areas of infectious diseases, cancer and neurobiology. As a result, you will have the opportunity to a build a diverse range of expertise, skill sets from working with cutting-edge technology, and be a partner in the Krogan lab's extensive collaborative network of leading researchers at prominent institutions across multiple fields and disciplines. The synergistic teamwork of the Krogan lab consistently publishes their findings in high-impact journals.

You will apply the appropriate algorithms, computational techniques, and statistical methodologies to analyze and visualize data primarily generated through high-throughput experiments. In-house data types are primarily global proteomics, PTM-proteomics, protein-protein interaction via AP-MS or APEX-MS. You will use and adapt in-house data analysis pipelines, written mostly in the R programming language, to perform all steps of data analysis including data quality checks, normalization, statistical tests, correction for multiple testing, as well as further downstream analyses such as functional or kinase enrichment analysis, and integrating results from varied experiments. Together with our computational team, you work with and improve upon existing data analysis pipelines and be involved in various collaborative projects within academic as well as with industry. The candidate will also collaborate with various wet lab researchers to aid in experimental and statistical design of projects, and in the biological interpretation and integration of the resulting complex data sets.

Requirements
- PhD in the fields of Bioinformatics, Biostatistics, Computational Biology or similar.
- Strong computational skills and knowledge in programming, statistics, biology.
- Experience with statistical analysis and presentation of results using the R programming language, or another language (Python, Matlab, etc.) and willingness to learn R.
- Understanding of large-scale proteomics data and placing it in a biological context, as well as experience working with other -omics data such as transcriptomics, lipidomics, and metabolomics.
- Familiarity with biological networks, their analysis and display.
- Application and validation of machine learning methods to complex data.
- Knowledge of biological network analysis, and experience with visualization tools such as Cytoscape.
- Prior experience with Unix/Linux environments.
- Experience creating packages in R.
- Team player who can thrive working on large collaborative projects.

Apply by sending the following to Kirsten Obernier, Associate Science Director to Professor Nevan Krogan (Kirsten.obernier@ucsf.edu).

- Current CV
- Cover Letter
- Two Reference Contacts

We are looking forward to hearing from you!