MASSACHUSETTS GENERAL HOSPITAL

Job Title: Bioinformatics Specialist   Job Family: Research

Job Code: Grade:

Department: Ragon Institute

GENERAL SUMMARY/ OVERVIEW STATEMENT:
The Shalek Lab (http://shaleklab.com, MIT, Broad Institute, and Ragon Institute) specializes in leveraging novel single-cell genomic approaches to understand the behavior of complex biological systems. For this position, the lab is seeking a computational postdoctoral associate will be working on projects with a specific focus on infectious disease, primarily in the study of the host response to tuberculosis infection. Research questions will center on understanding the relationship between T cell clonality and control of MTB but also extend to studies of initial granuloma formation and how cells communicate and interact with their microenvironment. The core technique learned and applied will be Seq-Well, an in-house and customizable platform for single cell RNA-sequencing scRNA-seq library generation from thousands of cells in parallel.

PRINCIPAL DUTIES AND RESPONSIBILITIES:
Seeking a bioinformatics speciaist to join collaborative projects, focusing on characterizing the host response to MTB infections, between the Shalek Lab at MIT, Broad Institute, Ragon Institute, and Harvard T.H. Chan School of Public Health. Duties will include giving updates on projects to internal and external collaborating scientists and contributing to the development and curation of new analysis pipelines and databases.

The majority of time working in the Shalek Lab under the direct supervision of Professor Alex Shalek and within the community of the clinical labs. Core techniques will include the careful annotation and deposition of data, developing and utilizing computational pipelines for large scale single- cell RNA sequencing data analysis, interpreting data within the context of each disease, and data visualization techniques.

The project will entail careful consideration of study design; interfacing with clinical teams and researchers; utilizing cloud computing platforms; data analysis involving Bash, Python, and R; interpreting and contextualizing findings; and communicating the results. The candidate will also lead the efforts on summarizing, visualizing and reporting (in the format of slides) the analysis results to the investigator and experimental collaborators. You must be capable of working in an interactive team environment while conducting self-directed research within broader goals set by group. The role will also involve some development and parallelization of efficient and user-friendly pipelines and management of databases and data storage repositories.

SKILLS/ABILITIES/COMPETENCIES REQUIRED:
Required skills:

- Knowledge of computational biology tools and techniques
- Experience working with biological data with some familiarity with next-generation sequence data analysis tools; ideally will have some prior experience with statistical methods, pipelines and tools relevant to single-cell RNAseq analysis
- Working knowledge of the NextSeq 550 sequencer to oversee management of the instruments and help troubleshoot when needed
- Experience supervising and coordinating large projects
- Proficiency in at least one modern programming language
- Experience with UNIX-based systems and command-line interfaces
- Excellent verbal and written communication skills, and the ability to explain technical/mathematical reasoning to people from non-quantitative backgrounds
- Independent, highly motivated, and highly collaborative with the ability to work together with multi-disciplinary teams of biologists, laboratory scientists, computational biologists, and physicians.
- Interest in the infectious disease or global health

Desired skills:
Experience in research lab, excellent communication skills, some basic knowledge of molecular biology, great organizational skills, enjoys working in a dynamic team environment.

- Knowledge of infectious disease field
- Experience working with clinical and single cell RNA-seq data
- Working knowledge of clinical research protocols
- Experience with cloud-based computational environments
- Experience with organizing, compressing, and transferring data on remote servers.

EDUCATION:
PhD in computational biology, or related field e.g mathematics, biostatistics required.

SUPERVISORY RESPONSIBILITY (if applicable):
Graduate and undergraduate student mentorship would be desired