

**Associate Computational Biologist  
Pellman Laboratory  
Dana-Farber Cancer Institute**

Located in Boston and the surrounding communities, Dana-Farber Cancer Institute brings together world renowned clinicians, innovative researchers and dedicated professionals, allies in the common mission of conquering cancer, HIV/AIDS and related diseases. Combining extremely talented people with the best technologies in a genuinely positive environment, we provide compassionate and comprehensive care to patients of all ages; we conduct research that advances treatment; we educate tomorrow's physician/researchers; we reach out to underserved members of our community; and we work with amazing partners, including other Harvard Medical School-affiliated hospitals.

We are looking for a highly motivated individual to join the laboratory of Dr. David Pellman at HHMI, the Broad Institute, and the single-cell genome center at Dana-Farber Cancer Institute.

The successful applicant will be responsible for analyzing single-cell whole-genome and whole-transcriptome sequencing data, and for interpreting, integrating, and relating transcriptional/genetic information to experimental data from live-cell imaging. The candidate should have a strong computational/analytical background and demonstrated knowledge of research methods and be able to adapt quickly and be part of a multi-disciplinary team. The position will focus on a new avenue of research using genomics as a tool for experimental biology, studying mechanisms that drive rapid genome evolution.

Working closely with computational and experimental colleagues to understand various methods for detecting/analyzing de novo mutations and gene expression changes at single cell level.

- Working alongside informatics colleagues to clean and analyze newly generated data and public datasets.
- Create pipelines using existing analysis tools to process data in an automated and efficient fashion.
- Application of these approaches to cancer genome analyses.
- Responsible for documentation and error reporting for existing tools.
- Ensure data quality control is constantly and consistently applied to incoming data sets.
- Create reports of data quality and communicate these to computational staff.

B.S. required in mathematics, statistics, physics, engineering, computer science, bioinformatics or other fields with quantitative knowledge. Neuroscience or psychology graduates with considerable computational experience will also be considered. Applicants with advanced degrees are also welcome to apply.

- Strong initiative and ability to take ownership of assigned tasks and projects
- Practical experience with Linux environments and proficient in a least one programming language (Java, C, Python) and one scripting language (e.g., MATLAB, R); interest in (or experience with) cloud computing a plus.
- Solid knowledge of basic statistics and statistical methods.
- Knowledge of genetic analysis and tools is preferred but not required.
- Familiarity with, or interest in studying cancer genetics and cell biology.
- Demonstrated attention to detail and analytical skills.
- Ability to work effectively in a multidisciplinary team environment.
- Excellent communication and interpersonal skills.
- Excellent written and oral presentation skills.
- Must be flexible and able to respond to shifting priorities in a dynamic setting.

Please send resume and cover letters to: [harriet\\_scott@dfci.harvard.edu](mailto:harriet_scott@dfci.harvard.edu)

Dana-Farber Cancer Institute is an equal opportunity employer and affirms the right of every qualified applicant to receive consideration for employment without regard to race, color, religion, sex, gender identity or expression, national origin, sexual orientation, genetic information, disability, age, ancestry, military service, protected veteran status, or other groups as protected by law.