

The **Pinello Lab** at **Harvard Medical School/Massachusetts General Hospital/Broad Institute of MIT and Harvard** is looking for Research Scientists/Postdoctoral Candidates/ Computational Biologists and Programmers excited about **computational challenges** in modeling biological data coming from **CRISPR genome editing, chromatin biology** and **single-cell experiments**.

Massachusetts General Hospital is a teaching hospital for Harvard Medical School and one of the top ranked hospitals nationwide. We are located in **Boston, Massachusetts** with close proximity to numerous other top-notch medical and research institutions including Harvard School of Public Health, Massachusetts Institute of Technology (MIT), The Broad Institute of MIT and Harvard, Boston Children's Hospital, Brigham and Women's Hospital, Dana-Farber Cancer Institute and Beth Israel Deaconess Medical Center, which fosters close interactions among faculty and fellows and a **strong and rich network of collaborations and intellectual exchange**.

The focus of the Pinello laboratory is to use innovative **computational approaches and cutting-edge experimental assays** to systematically analyze **sources of genetic and epigenetic variation and gene expression variability** that underlie human traits and diseases. The lab uses **machine learning, data mining** and **high-performance computing technologies** such as **parallel and GPU computing** to solve computationally challenging and **Big Data** problems associated with **next generation sequencing (NGS) data analysis**. Our mission is to use computational strategies to further our **understanding of gene regulation in development and disease etiology** and to provide a foundation for the development of **new drugs and more targeted treatments**.

The candidate(s) will work on projects developing innovative **computational approaches** to design and systematically analyze bulk and **single-cell CRISPR perturbation** experiments and integrate transcriptome, epigenome, proteome, and genome structural datasets to investigate **how genetic variants and regulatory elements control gene expression and phenotypes at an unprecedented scale**.

Read more about our research, recent publications, and software here: <http://pinellolab.org>

Requirements

- The ideal candidate(s) should have received (or expect to receive soon) a Ph.D. in Computer Science, Statistics, Genetics, Bioinformatics, Computational Biology, Mathematics, Physics, or related fields
- First (or co-first) author in one or more peer-reviewed scientific publication
- Excellent communication and writing skills
- Able to work both independently and in teams

Preferred Skills (not required)

- Proficiency in Python and/or R
- Strong statistical background and preferably statistical genetics background
- Experience with commonly used bioinformatics tools and databases
- Experience working with different types of NGS data such as ChIP-seq, RNA-seq, ATAC-seq
- Knowledge of commonly-used machine learning methods
- Experience in the analysis of single cell data and genome editing data
- Experience in developing computational pipelines with Snakemake or Nextflow
- Web development

Our lab is committed to diversity and equality; therefore, we encourage applications from underrepresented minorities.

Application process

If you are interested, please send your CV and a cover letter describing your current and future research interests, and the contact of 3 references to Luca: lpinello@mgh.harvard.edu.