

The Pinello Lab at **Massachusetts General Hospital / Harvard Medical School** is looking for Postdoctoral candidates excited about **computational challenges** in **(epi)genomics, single-cell analysis** and **CRISPR genome editing**.

Massachusetts General Hospital is a teaching hospital for Harvard Medical School and one of the top ranked hospitals nationwide. It is located in **Boston, Massachusetts** with close proximity to numerous other top-notch medical and research institutions including Harvard School of Public Health, Dana-Farber Cancer Institute, Boston Children's Hospital, Massachusetts Institute of Technology (MIT), The Broad Institute of MIT and Harvard, Brigham and Women's Hospital, Harvard Medical School, 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 candidate(s) will work on interdisciplinary projects developing innovative **computational approaches** to systematically analyze and integrate sources of **genetic and epigenetic variation and gene expression variability in 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 **disease etiology** and to provide a foundation for the development of new drugs and more **targeted treatments**. 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
- Experience with commonly used bioinformatics tools and databases
- Experience working with different types of NGS data such as CHIP-seq, RNA-seq, ATAC-seq
- Experience in the analysis of data from genome editing assays
- Experience in the analysis of single cell data
- Knowledge of commonly-used machine learning methods
- 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 2-3 references to Luca: [lpinello@mgh.harvard.edu](mailto:lpinello@mgh.harvard.edu)