Boston Children's Hospital
Division of Genetics and Genomics

Harvard Medical School
Department of Pediatrics

Postdoctoral fellows in computational genomics and bioinformatics

Two postdoctoral fellow positions are available to study transposons and somatic mutations in various human conditions at Boston Children's Hospital (Genetics & Genomics Division) and Harvard Medical School. The projects involve the development of novel computational methods for single-cell and long-read sequencing technologies as well as the integrative analysis of various types of genomic/transcriptomic/epigenetic next-generation sequencing (NGS) data.

Transposons have numerous nearly identical copies in the human genome and continuously create novel insertions in human germlines and somatic tissues. Once considered junk DNA, transposons are now recognized as playing an important role in many aspects of human biology and diseases. Somatic mutations present in a small fraction of cells or in single cells have also been implicated in various developmental and degenerative human diseases. Transposons and somatic mutations, however, are two of the most challenging biological entities to detect and validate, but recent advances in single-cell and long-read sequencing will allow us to systematically investigate them.

Alice Lee's laboratory has a track record with both transposons and somatic mutations of developing creative computational methods and performing rigorous analysis for single-cell and other high-throughput NGS data. Postdoctoral fellows will have ample opportunity to work with top experimental and clinical collaborators in the Boston area and beyond to solve real-world biomedical problems and to explore the frontiers of knowledge on transposons and somatic mutations.

Details about the laboratory can be found at http://compgen.hms.harvard.edu

Ideal candidates will have a PhD in computational biology/bioinformatics/computer science or other quantitative field and satisfy at least one of the following criteria:

- Proven ability to develop computational methods for NGS data or to perform integrative bioinformatic analysis with large NGS datasets
- Strong mathematical/statistical background and highly motivated for biomedical research
- Strong programming/cloud computing/IT background with high motivation to perform biomedical research

The Lee lab also has a *wet lab* to validate computational models/predictions within the lab. Candidates with excellent wet lab experimental skills who intend to pursue their own experiments along with training in computational research are encouraged to apply.

Interested applicants should send a CV including three references, and a brief statement of research interests along with best papers (up to three) to ealice.lee@childrens.harvard.edu with [Application] in the subject line.