 POSITION:  Postdoctoral Research Fellow

REPORTS TO:  Dr. Segrè, Lab PI

DATE:  August 2019

Postdoctoral Fellow in single cell genomics and statistical genetics of complex eye diseases
Ocular Genomics Institute, Massachusetts Eye and Ear and Harvard Medical School

POSITION SUMMARY:

We are seeking a highly motivated and creative postdoctoral fellow to join the Segrè lab interested in single cell genomics and integrative analysis of functional genomics and human genetics to uncover key causal mechanisms and pathogenic cell types for complex eye diseases. The Segrè lab is part of the Ocular Genomic Institute and the Department of Ophthalmology at Massachusetts Eye and Ear (MEE) and is affiliated with the Broad Institute of Harvard and MIT. MEE is a teaching hospital of Harvard Medical School and is an international leader for treatment and research in both Ophthalmology and Otolaryngology. The Segrè lab develops novel statistical and computational methods that integrate genome-wide association and sequencing studies (GWAS) with functional genomics (e.g., eQTLs) data from relevant tissues and cell types, to identify new causal genes and regulatory mechanisms of common eye diseases, including glaucoma, age-related macular degeneration, and diabetic retinopathy, with the ultimate goal of proposing new preventative and therapeutic targets for eye disease. To learn more about the lab please visit: https://segrelab.meei.harvard.edu/.

The successful candidate should have a strong background in statistics, statistical genetics, mathematics, computational genomics, bioinformatics, or a related quantitative field, strong programming skills, and be excited to contribute to advancing science and medicine of complex eye diseases. Research projects will involve developing statistical and computational methods for analyzing single cell RNA-seq of human eye tissues and whole genome sequencing data, and integration with genome-wide association studies to detect gene expression changes and genetic regulation associated with different ocular cell types and complex eye diseases. The project will be part of a multi-lab collaboration aimed at generating a cell atlas of the human eye from childhood to old age (https://chanzuckerberg.com/science/programs-resources/humancellatlas/seednetworks/cell-atlas-of-the-human-eye-from-birth-to-old-age/). The postdoctoral fellow will have the opportunity to develop his or her own research projects and interests within this research area, and to present ones work at local, national, and international meetings.

If interested, please send your CV, a cover letter describing your previous research experience and future research interests, and contact information for 3 references, to Dr. Ayellet Segrè: ayellet_segre [at] mee [dot] harvard [dot] edu.

CHARACTERISTIC DUTIES:

- Perform preprocessing, quality control, imputation, and phasing of whole genome sequencing (WGS) data using available and custom-built tools.
- Develop new statistical and computational methods that integrate single cell RNA-sequencing and WGS data to detect allelic imbalance and genetic regulation of gene expression at the cell type level.
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DEPARTMENT: Ophthalmology

- Develop and apply methods that integrate single cell data and other functional genomics data (e.g., expression quantitative trait loci (eQTLs), epigenetics) with genome-wide association studies (GWAS) to identify key regulatory mechanisms, genes, and pathways that affect complex eye disease risk, and to propose the underlying pathogenic cell types.
- Organize all scripts in a publicly available repository (e.g., github) with clear documentation.
- Critically review, analyze, and communicate results to our team and collaborators.
- Write up work for publications.

REQUIRED EDUCATION AND EXPERIENCE:

- Ph.D. in (bio)statistics, statistical genetics, human genetics, computational genomics, bioinformatics, mathematics, computer science, or a related quantitative discipline required.
- Strong programming skills and in-depth experience with several programming languages required, e.g., Python, R, Matlab, C++.
- Experience with Unix/Linux environments required (including shell scripting).
- Experience with large-scale data analysis, algorithm development, and statistics required; work with next-generation sequencing, single cell RNA-sequencing, GWAS, or other -omics data preferred.
- Research experience and knowledge in statistical genetics, regression models, and/or statistical learning desired.
- Demonstrate critical thinking, rigorous work, and ability to meet deadlines.
- Good publication record in peer-reviewed journals.
- Strong personal skills, and excellent verbal and written communication and presentation skills.
- Ability to work effectively both independently and collaboratively in a fast-paced, academic environment and evolving field.

WORKING ENVIRONMENT:

The Segrè lab is located in the main hospital building of Mass Eye and Ear (MEE), 243 Charles Street, in a standard research and office work space that is part of Ocular Genomics Institute at MEE. The candidate will work among a team of other computational biologists and computer scientists in the Segrè Lab and the Bioinformatics Center of the Ocular Genomics Institute, and will be part of a larger multidisciplinary research environment, which includes geneticists, clinical scientists, and experimental biologists. The candidate will have the opportunity to interact with colleagues at other universities in the fields of human genetics, single cell genomics, and functional genomics, and with the Medical and Population Genetics community at the Broad Institute of Harvard and MIT, with whom our lab is affiliated.