Postdoctoral Fellows in high-dimensional data methods applied to microbiome and integrated 'omics

DESCRIPTION OF POSITIONS

Drs. Jacqueline Starr (Brigham and Women's Hospital) and Kyu Ha Lee (Harvard T. H. Chan School of Public Health) invite applicants to join their joint laboratory group. Multiple positions range from pure biostatistical methods development to more applied methods evaluation and data analysis. This is an opportunity to work in an interdisciplinary group that values rigor and includes biostatisticians, epidemiologists, microbiologists, and imaging experts. We seek to bridge principled causal inference with high-dimensional data analysis.

NIH funding supports our work to develop novel multivariate spatial data (or other count data) models for application to microbiome data. The most immediate need is for a fellow to help develop **new multivariate spatial statistical models in a Bayesian framework**. Other possible projects include developing highly multivariate Bayesian models for analyzing sequence count data or for integrated 'omics applications involving microbiome data.

Also needed is a fellow to conduct applied methods development, e.g., comparing performance of our new methods to other approaches in simulated and real datasets. The fellow would be encouraged to identify other new applied datasets and projects.

Fellows are jointly supervised by Drs. Lee (HSPH, Nutrition and Biostatistics), Starr (BWH and Harvard Medical School), and Brent Coull (HSPH, Biostatistics). Mentors meet with fellows at least weekly and provide timely and constructive feedback to support lab members' career development goals. Fellows also participate in meetings and working groups with a much broader community of investigators.

RESPONSIBILITIES

Responsibilities will depend on the applicant's fit to each position and might include:
1) Develop Bayesian spatial statistical models for analysis of microscopic image data (especially fluorescence in situ hybridization images of microbial biofilm). This includes creating software packages to disseminate newly developed methods.
2) Apply Bayesian multivariate spatial or count data models to a) evaluate performance under different real and simulated data settings, b) compare performance to that of other approaches, and 3) perform variable selection or hypothesis testing to answer applied scientific questions.
3) Help the laboratory identify existing microbiome or other image data, help process images (e.g. image segmentation), and perform spatial statistical analysis to investigate methodologic performance and address applied scientific questions.
4) All fellows will collaborate on other methods development projects in the laboratory. The common theme is high-dimensional data analysis for variable selection and causal inference, with special emphasis on microbiome-related data and other 'omics-microbiome integration.

INSTITUTIONS

[Channing Division of Network Medicine](#) (CDNM) at [Brigham and Women's Hospital (BWH)](#)

BWH is a Harvard Medical School affiliated institution. CDNM is one of the largest research divisions within the Department of Medicine at BWH and has an outstanding track record of mentoring. The goal of CDNM is to define the etiology and reclassify complex disease using network- and systems-based approaches. CDNM has some of the largest population-based cohorts in the world, including the ongoing Nurses' Health Study. CDNM has DNA samples from more than 200,000 individuals and microbiome samples from more than 25,000 individuals.

[Harvard T. H. Chan School of Public Health](#)

[Fellows](#) may be jointly appointed at HSPH in the Department of [Nutrition](#), with additional access to the Departments of [Biostatistics](#), [Epidemiology](#), and the vibrant HSPH community.

Brigham and Women's Hospital and Harvard University seek to find, develop, promote, and retain the world's best scholars. Both are Affirmative Action/Equal Opportunity Employers that strongly encourage women, people of color, LGBTQ individuals, people with disabilities, members of ethnic minorities, foreign-born residents, and veterans to apply. Applicants will not be discriminated against because of race, color, creed, sex, sexual orientation, gender identity or expression, age, religion, national origin, citizenship status, disability, ancestry, marital status, veteran status, medical condition, or any protected category prohibited by local, state, or federal laws.

QUALIFICATIONS

- **Required**: Doctoral degree in biostatistics, statistics, computational biology, or related quantitative fields (e.g., epidemiology for the applied fellow).
- **Required**: Excellent programing skills in R, C/C++ and/or Fortran
- **Required**: Strong organizational, communication, and writing skills.
- **Preferred**: Strong skills in Bayesian modeling and Markov chain Monte Carlo methods.
- **Preferred:** Experience with multivariate analysis, variable selection methods, spatial analysis, or image analysis.

APPLICATION INSTRUCTIONS

If interested, please send your CV, research statement, and contact information for three references to Drs. Jacqueline Starr (jacqueline.starr@channing.harvard.edu) or Kyu Ha Lee (klee@hsph.harvard.edu) with the subject line "Biostatistics Postdoc 2022."