



FRED HUTCH
CURES START HERE

Staff Scientist, Biostatistics (Statistical Genetics, Omics, Genetic Epidemiology) (Job ID 18365)

Overview

Cures Start Here. At Fred Hutchinson Cancer Research Center, home to three Nobel laureates, interdisciplinary teams of world-renowned scientists seek new and innovative ways to prevent, diagnose and treat cancer, HIV/AIDS and other life-threatening diseases. Fred Hutch's pioneering work in bone marrow transplantation led to the development of immunotherapy, which harnesses the power of the immune system to treat cancer. An independent, nonprofit research institute based in Seattle, Fred Hutch houses the nation's first cancer prevention research program, as well as the clinical coordinating center of the Women's Health Initiative and the international headquarters of the HIV Vaccine Trials Network. **Careers Start Here.**

At Fred Hutch, we believe that the innovation, collaboration, and rigor that result from diversity and inclusion are critical to our mission of eliminating cancer and related diseases. We seek employees who bring different and innovative ways of seeing the world and solving problems. Fred Hutch is in pursuit of becoming an antiracist organization. We are committed to ensuring that all candidates hired share our commitment to diversity, antiracism, and inclusion.

Responsibilities

The Fred Hutchinson Cancer Research Center is recruiting a PhD level Data Scientist in the Biostatistics Program to work on high-dimensional problems in Statistical Genetics, Genetic Epidemiology, working closely alongside [Dr. Charles Kooperberg](#) and [Dr. Li Hsu](#). The Staff Scientist will carry out both methodological and applied projects under the guidance of the principal investigators. The role of the Staff Scientist involves extensive collaboration and requires the ability to function independently to support and contribute to investigator-led projects. The primary projects are conducted within the Trans-Omics for Precision Medicine (TOPMed) and the Population Architecture using Genomics and Epidemiology (PAGE) Consortia. As part of these projects we will utilize whole-genome sequencing, RNA-Seq, DNA methylation, metabolomics and proteomics data for tens of thousand participants as well as genome-wide genotyping array data for over 3M participants. A particular emphasis of our work is on identifying diseases associations and predicting risk in racially and ethnically diverse populations. We are developing novel statistical methods to improve the complex data analysis, including association testing and risk prediction.

Qualifications

The successful candidate has a PhD in Statistics, Biostatistics, Computer Science, Genetic Epidemiology or related fields.

The successful candidate will be experienced in managing and analyzing large-scale high-dimensional genetic and genomics data with existing software tools and methods and modifying/developing methods if needed. Experience with multiple types of omics data such as whole genome sequencing, methylation, and RNA-seq data is a plus.