Research Associate
MRC Biostatistics Unit University of Cambridge
United Kingdom

An opportunity has arisen for a talented biostatistician or computational biologist to work on genome-wide association and molecular QTL studies at the MRC Biostatistics Unit, Cambridge University, with Prof. Sylvia Richardson and Dr Hélène Ruffieux.

The MRC Biostatistics Unit is a leading centre of biostatistics research in Europe. It hosts four research programmes with the aim to respond to current and future scientific needs in health and biomedicine. The successful applicant will be part of the "Statistical genomics" programme which develops and applies methodological and computational approaches for complex molecular data to clarify the biological processes behind human diseases and provide actionable treatment insights.

We are seeking an ambitious and motivated individual to contribute to this research. Specifically, the proposed project will focus on analysing large datasets using in-house statistical approaches for joint QTL mapping and network modelling to study genetic regulation and mediation mechanisms in humans. Emphasis will be on establishing a map of *trans* and pleiotropic signals (QTL hotspots) genome wide, and on relating these signals to disease endpoints by interrogating and integrating diverse molecular datasets (such as transcriptomic, proteomic, metabolomic datasets).

The post-holder will be expected to develop a comprehensive analysis workflow applicable to different tissues and cell types, also leveraging public data and annotations. They will also propose a robust framework for the independent replication of both *cis* and *trans* effects. The successful candidate will take a leading role in ongoing interdisciplinary collaborations (involving biologists, clinicians, immunologists and statisticians) to tackle research questions aimed at characterising the genetic contribution to immune-mediated diseases.

The candidate must have knowledge in human genetics and demonstrated experience with the analysis of large "omics" data (ideally including genotyping data), as well as good statistical knowledge and strong programming skills. They must have a creative approach to problem-solving, as well as demonstrate excellent time management and collaboration skills.

A PhD in Computational Biology, Biostatistics, Bioinformatics, Epidemiology, Computer Science or a closely aligned discipline is required before the time of appointment. The candidate should have practical working knowledge of R/Bioconductor and code versioning tools (e.g., git). Familiarity with Python/bash/awk, command line tools and high-performance computing environments is desirable. Knowledge of low-level programming such as C++ is a plus.

This post offers opportunities to publish in high-quality scientific journals, as well as work alongside and build collaborative relationships with renowned researchers across the Cambridge Biomedical Campus and beyond. Career development support will be provided, with a range of formal courses and on-the-job training.

The position is available for 2 years in the first instance. For full details, closing date and to apply, please see the full advert at https://www.jobs.cam.ac.uk/job/32785/

For an informal discussion or more information about this post, please contact Hélène Ruffieux (email in the advert, see the above link). We welcome applications from individuals who wish to be considered for part-time working or other flexible working arrangements.