

Research Associate in computational & statistical genetics/genomics MRC Biostatistics Unit, University of Cambridge

We are seeking an ambitious and motivated individual to contribute to exciting research at the intersection of computational statistics and cutting-edge genomics. The post holder will develop Bayesian hierarchical approaches to model genetic regulation across diverse human conditions (tissues, cell types, diseases) and explore how the dynamics of this regulation contributes to disease risk and progression. He/she will conduct original research at the MRC Biostatistics Unit, Cambridge University, working with Dr H el ene Ruffieux and Prof. Sylvia Richardson.

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.

The project will focus on developing hierarchical modelling and scalable inference approaches that flexibly borrow information across related clinical/molecular traits, conditions, timepoints. It will also involve using these approaches to (1) study gene regulation mechanisms in high-dimensional networks of molecular traits and (2) understand how they relate to the temporal course of disease processes. The post holder will work with large genetic datasets in the context of genome-wide association (GWA) and molecular quantitative trait locus (QTL) problems, as well as with diverse clinical and molecular datasets (transcriptomics, proteomics, metabolomics) and public annotations. The methods will be used in ongoing collaborations with biologists and clinicians, in particular to tackle research questions aimed at characterising the genetic contribution to immune-mediated diseases.

A PhD in Biostatistics, Statistics, Computational Biology, Machine Learning or a closely aligned discipline is required before the time of appointment. The candidate should have a strong background in Bayesian statistics and computation (experience with variable selection approaches, sparse regression, graphical, longitudinal modelling and/or variational inference is a plus). They should also have good computational and software development skills (e.g., proficient in R, Julia, Python), as well as some practical working knowledge of code versioning tools (e.g., git). Experience with low-level programming such as C++ is desirable but not essential. Some knowledge in human genetics and experience with the analysis of omic data (ideally including genotyping data) is a plus, although training will be given on the basic concepts necessary to the post. The successful applicant will have a creative approach to problem-solving, and excellent time management and collaboration skills.

This post offers opportunities to publish in high-quality scientific journals, as well as 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.

We welcome applications from individuals who wish to be considered for part-time working or other flexible working arrangements. The University actively supports equality, diversity and inclusion and encourages applications from all sections of society.

For details, closing date and to apply, 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 Dr H el ene Ruffieux (helene.ruffieux@mrc-bsu.cam.ac.uk).