Institution/Company: Department of Biomedical and Molecular Sciences, Queen's University

Location: Kingston, Ontario, Canada

Job Description: Postdoctoral Fellow

A Postdoctoral fellowship position is available immediately in the Computational Genomics Laboratory (CGL) at Queen's University within the Department of Biomedical and Molecular Sciences. The CGL uses genome-wide and systems biology approaches to identify novel genomic determinants of multifactorial traits including respiratory and cardiovascular diseases, cancers, as well as inter-individual variability or adverse reactions to various medications. Specifically, our research integrates large datasets to characterize how genomic, epigenomic, and environmental factors influence transcript/protein/metabolite expression, as well as risk for diseases or drug response. There will be opportunity to generate and apply primary datasets in the laboratory using high-throughput technologies, analyze data from collaborations with other labs and networks as well as public sources. The successful candidate will work in a dynamic, trans-disciplinary environment, interacting with clinicians, biologists, biochemists, statisticians, and computer scientists at Queen's and beyond. Moreover, there will be opportunities for teaching and curriculum development for new courses aimed at providing hands-on training in computational methods applied to biomedical research.

Applicants should have a PhD or equivalent in genomics, bioinformatics, computational biology or a related field, and have extensive experience in the analysis of large-scale 'omics data. Interested candidates should send a cover letter, CV, and the contact information of at least three references to QinglingDuan (qingling.duan@queensu.ca).

Preferred qualifications and experience:
- Excellent written and verbal communication skills
- Expertise in genomics, bioinformatics, computational biology, or related areas
- Experience in analyzing large-scale genomics data, including genome-wide association studies, next-generation sequencing, DNA-methylation, gene-expression datasets
- Extensive experience in programming (e.g., UNIX, R, Python, MATLAB) and using analytic tools (e.g., Bioconductor, PLINK)
- Familiarity with methods in machine learning and systems biology analyses
- Ability to work both independently and as a team member in a trans-disciplinary environment