

Computational postdoctoral fellow in Cancer Genomics

Position Summary

We are involved in a number of cancer consortium including the International Cancer Genomics Consortium (ICGC), the Cancer Collaboratory and various Terry Fox Research Institute lead initiatives. These research and clinical-oriented projects are sequencing and generating epigenomic data from a large number of tumors because of the potential for biomarker discovery and improved treatment. Combined with the fact that third generation sequencing technologies (PacBio, Nanopore, 10X linked-reads, etc.) are becoming more mainstream, there is a need to analyze and integrate vast amounts of data but also develop new analytical methods to exploit these datasets to their full potential. This includes strategies for hybrid-assembly and structural variant detection.

The Bourque lab is seeking a computational postdoctoral fellow interested in analyzing cancer genomics and epigenomics datasets. A component of the project will be to develop new analytical methods as needed. PhD training should be in bioinformatics, computational genomics or equivalent and required skills include programming (Python or equivalent), statistics and R. Prior experience in genomics and/or epigenomics data analysis is highly desirable. Position will be funded for 2-years with possible extensions. You would join a team of more than 30 students, postdocs, bioinformaticians and software developers working at the Canadian Center for Computational Genomics, which is part of the McGill University and Genome Québec Innovation Center. You would have access to many projects that rely on state-of-art genomic technologies and computational platforms.

How to apply

If you are interested, please send a short description of your research interests and CV by **Dec 15th** to Dr. Bourque guil.bourque@mcgill.ca or until position is filled. Start date is flexible.