About Canadian COVID Genomic Network

On April 23, 2020, the Federal Government committed $40 million (http://www.cgen.ca/nr-april-23-2020) to support Genome Canada's launch of the newly formed *Canadian COVID Genomics Network* (CanCOGeN). As Canada's national facility for genome sequencing and analysis, CGEn will lead a nation-wide Host Genome Sequencing Initiative within this framework to sequence genomes of 10,000 Canadians to help understand the genomic architecture of the host response to SARS-Cov-2. CGEn is mandated to develop regional, national, and international linkages to ensure that this investment has maximal impact for the health of all Canadians.

Area of Research

The Genetic Epidemiology Committee of the CGen HostSeq project (http://www.cgen.ca/project-overview) is now looking to build a team of talented data scientists to work together to identify genetic variation that contributes to SARS-Cov-2 infection, susceptibility, and COVID-19 disease severity by supporting ongoing investigations and by addressing independent research questions. Successful candidates will join a team of internationally recognized scientists in genetic epidemiology and statistical genetics and may be located in Vancouver, Montreal or Toronto.

Position Openings

Currently, the committee is looking to hire statisticians, bioinformaticians, epidemiologists, programmers, infectious disease researchers and human geneticists for staff or post-doctoral fellowship positions, and we have several openings for these positions. We may require the work to be done remotely, and we may provide access to super computers and secure servers.

Required skills

The skills required for these roles are ***any subset*** of the following:

- Experience with imputation of missing phenotype data
- Familiarity with genotype imputation and phasing (software lines such as *IMPUTE*, *SHAPEIT*, *PHASE* and *BEAGLE*)
- Manipulating whole genome sequences using software such as *Burrows Wheeler Aligner*, *samtools*, *Rainbow* or related software (including *R* package such as *SNPAssoc*, *sequinR*)
- Computation of polygenic risk scores
- Genome-wide association studies using software such as *plink*, *plink2*, *bgenie*, *snptest, ldak* or *qctool*

- Genome-wide association studies using whole genome sequencing
- Rare and common variant analysis
- Computation of genetic correlation using software such as *LDSC/LDSR, GCTA, GEMMA* or *phenix*
- Functional annotation of genetic variants
- Imputation of HLA serotypes from sequencing data
- Database management and data preprocessing in *R*, *matlab*, *python* or *SQL*.
- Website development, including backend development using *python* or administration of *apache* servers (or prior experience with the *pheweb* software)
- X chromosome analysis (working knowledge of inactivation, formats and methods for pseudoautosomal regions, the XG blood group system, whole genome analysis of X ***or*** interaction between X and immunity)

Term

The term of the contract is up to two (2) years. The initial contract will be one (1) year, with the possibility of extending to two years based on progress.

Required Qualifications

- A Master's or PhD Degree in a relevant discipline.
- Experience analyzing genetic data or developing genetic software.
- Demonstrated problem-solving skills, time management and written and oral communication skills.
- Demonstrated ability to think and work independently solving analytic challenges.

Salary

The salary will be determined based on the position and previous experience plus benefits.

Application Instructions

Individuals interested in these openings should submit a cover letter indicating the specific skills they possess (from the *Required Skills* section, above). They should also list their interest and experience in the research area, a curriculum vitae, and a copy of a scientific paper they contributed to with a description of their role. This letter should explicitly address previous experience analyzing large scale genetic data, such as performing GWAS, calculating genetic risk scores and experience with study design. Applicants should include name and e-mail addresses of two potential referees and indicate the date they will be available to begin. All application materials must be submitted as PDFs in a single email to natalie.sun@sickkids.ca. Review of application will begin immediately and continue until the openings are filled. We appreciate all

expressed interest in these positions but only those candidates short listed for an interview will be contacted.

All qualified candidates are encouraged to apply; however, Canadians and permanent residents will be given priority.

Diversity Statement
The team is strongly committed to diversity within its community and especially welcomes applications from racialized persons / persons of colour, women, Indigenous / Aboriginal People of North America, persons with disabilities, LGBTQ persons, and others who may contribute to the further diversification of ideas.

Accessibility Statement
The team strives to be an equitable and inclusive community, and proactively seeks to increase diversity among its community members. Our values regarding equity and diversity are linked with our unwavering commitment to excellence in the pursuit of our academic mission.

We are committed to the principles of the Accessibility for Ontarians with Disabilities Act (AODA). As such, we strive to make our recruitment, assessment and selection processes as accessible as possible and provide accommodations as required for applicants with disabilities.