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CASUAL OPPORTUNITY

DALLA LANA SCHOOL OF PUBLIC HEALTH, UNIVERSITY OF TORONTO

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Date of Posting: June 15, 2022

Hours of Work: Full-time
Hourly Rate: $28-32/hour depending on experience
Length of contract: 5.5 months
EXPECTED NUMBER OF WORK HOURS PER WEEK: 36.25 HOURS

SUMMARY OF DUTIES

The Genetic Epidemiology Committee of the CGen HostSeq project (http://www.cgen.ca/project-overview) is looking to expand their team of talented data scientists working 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.

The Analyst will work under the supervision of Dr. Jennifer Brooks on several research projects in the field of genetic epidemiology, involving the linkage of genomic and administrative health data. Specifically, the Analyst will be responsible for coordination of multiple data sources, data management, statistical analysis, and presentation and interpretation of results.

The position will involve various aspects of genetic epidemiology including:
- Managing large consortium datasets, administrative health data, conducting data harmonization and maintain data integrity
- Analysis of linked genomic and administrative health data to answer multiple questions related to the long-term health effects of COVID-19
- Contribution to preparation of project reports, publications, and scientific presentations

QUALIFICATIONS:

- Master's or PhD Degree in a relevant discipline.
- Solid knowledge of epidemiological methods and designs
- Experience analyzing genome-wide association studies using plink, plink2.
- Database management and data preprocessing in R, Matlab, Python, or SQL.
- Ability to implement statistical analyses in large complex datasets
- Demonstrated problem-solving skills, time management and written and oral communication skills.
- Demonstrated ability to think and work independently solving analytic challenges.

Other beneficial skills:

- Experience working with administrative heath data
- 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
- Rare variant analysis

SUBMISSION OF APPLICATION
Please submit a one-page cover letter and Curriculum Vitae by email to: Dr. Jennifer Brooks at
jennifer.brooks@utoronto.ca by June 29th, 2022

Closing date: June 29, 2022