Job Summary

This Computational Biologist position is ideally suited to a creative individual with a strong interest in the operation and management of cutting edge software for biological applications within an academic setting. Incumbent would be responsible for data management, conversion and analysis of next-generation sequence datasets using open source informatic tools. This computational biologist position is fully grant-funded.

The incumbent works in a shared office in the Centre for High-Throughput Biology. Position requires a limited amount of national travel. Position requires some flexibility in working hours in order to meet deadlines, and to participate in conference calls in different time zones.

Organizational Status

The Computational Biologist will report to Dr. Martin Hirst, the principle investigator of the Epigenomics Group. The incumbent must be able to work independently and effectively within a collaborative team environment with national and international collaborators, researchers, industry partners and project managers.

Work Performed

- Operating and improving a state of the art next generation sequencing data analysis pipeline
- Tracking and informatics management of large volumes of data with data footprints of up to 100Gb per experiment.
- Performing sequence alignments, file merges and quality filtering using standardized tools.
- Converting sequence alignments to normalized read densities and performing pairwise differential analysis.
- Maintaining up to date documentation.
- Participation in development of standard operating procedures
- Completing performance reviews and addressing performance issues in conjunction with supervisor
- Contributing to scientific grant proposals, presentations and publications
- Other related duties as required
Supervision Received
The incumbent will work primarily under their own direction and initiative with weekly meetings with the Principle Investigator to set priorities and goals.

Supervision Given
None required

Consequence of Error/Judgement
Research data will be evaluated by both the incumbent and the Principal Investigator. Errors could result in erroneous information being communicated at research conferences and in manuscripts. Incorrect information would have a highly negative impact on ongoing or future projects.

Qualifications
Undergraduate degree in a relevant discipline. Minimum of two years experience or the equivalent combination of education and experience. - Experience working in a Unix environment, including experience with shell scripting and common command-line tools
- Expertise in one or more scripting language(s) (e.g. Python, Perl, R, awk, C)
- Familiarity with the development and maintenance of relational databases
- Experience working with next-generation sequencing data and tools would be an asset although not a requirement. (i.e. tools for alignment and variant-calling)
- Experience with statistical software, software testing, and cluster computing would also be assets
- Familiarity with epigenetics would be an asset, as would a history of publications in relevant fields.

Equity and diversity are essential to academic excellence. An open and diverse community fosters the inclusion of voices that have been underrepresented or discouraged. We encourage applications from members of groups that have been marginalized on any grounds enumerated under the B.C. Human Rights Code, including sex, sexual orientation, gender identity or expression, racialization, disability, political belief, religion, marital or family status, age, and/or status as a First Nation, Metis, Inuit, or Indigenous person.

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

Source URL: http://wwwmsl.ubc.ca/employment/technicians-research-assistants