Company Description

The SPARC BioCente is located in the Peter Gilgan Centre for Research & Learning (PGCRL) at 686 Bay Street on the 21st floor, and is a core facility of the SickKids Research Institute. SPARC is an acronym for The Sickkids Proteomics, Analytics, Robotics and Chemical (BioCentre). SPARC consists of two separate core facilities: Drug Discovery and Molecular Analysis. This posting is for SPARC Molecular Analysis, which makes use of state of the art mass spectrometry instrumentation to help investigators identify the proteins in their biological systems; this research field is often referred to as proteomics. We have been providing these services (as the Advanced Protein Technology Centre) for over 15 years at The Hospital for Sick Children (SickKids) and are staffed by experienced researchers and technicians. The newest high-resolution instruments allow us to resolve very complex samples to identify and quantitate the proteins contained therein. SPARC operates on a fee-for-service basis, servicing a range of partners representing agriculture/livestock, veterinary, fisheries, and environmental sectors, as well as many healthcare researchers. Over 50% of our users come from outside SickKids and include academic and hospital labs from disciplines like biochemistry, dentistry, pathobiology, food science, and psychiatry, as well as industrial and non-government organizations.

Job Description

Computer Science and Bioinformatics Research Assistant

We are looking for a co-op or summer student to work within SPARC Molecular Analysis, a core research laboratory that performs mass spectrometry and amino acid analysis for research scientists and industrial clients. The student will be responsible for installing and validating system suitability software on existing Windows based instruments, installing and testing software programs on a Linux based "supercomputer", processing large proteomics data sets with a well-established Python and R Studio based pipeline, and summarizing data analysis results. Depending on the skills and aptitude of the applicant and the time it takes to perform the above, the student may have opportunity to create new data analysis tools or pipelines for SPARC. This job will be a mixture of computer science and bioinformatics.

Here's What You'll Get To Do

- Install system suitability software on at least four existing mass spectrometry platforms, validate the software is working effectively, and work with SPARC scientists to establish new workflows that incorporate the software
- Install open-source software programs on a Linux based “supercomputer” and work with SPARC scientists to process proteomics data
- Process existing proteomics data with an established pipeline (Python, Jupyter, R studio based) and compare results to those from previous processing methods
- Potentially create new data processing tools or pipelines (Python, Jupyter, R studio based)

Here's What You'll Need

- Skills in software installation and validation
- Knowledge of Python, Jupyter, R studio, and Excel considered an asset
- At least some background/knowledge of biology/biochemistry/protein chemistry is an asset
- Can-do attitude and creativity toward tackling new problems
- Able to work through problems in a methodical and analytical way
- Demonstrated ability to work efficiently and effectively, both independently and within a team environment
- Good organization and time management skills
- Good interpersonal skills
- Successful applicant must agree to apply to BioTalent Canada for wage subsidy

Employment Type

Full-time, 16 weeks, 35 hours/week, hybrid (3-4 days per week on-site, 1-2 days per week work from home at supervisor’s discretion)