

Bioinformatics Analyst - Mass spectrometry based -omics

Job Description:

The Computational Immunology Research Group is seeking a Bioinformatics Analyst (with experience in machine learning and predictive modeling) to address a range of computationally complex problems at the immune-disease interface. This encompasses a broad spectrum of diseases, including cancer immunology and immunotherapy, vaccine design for both cancer and emerging diseases, and future studies in autoimmunity. We work towards the development of new immunotherapies that leverage the immune-system to eradicate the disease. Our work and findings help to improve the treatment and care for patients around the world.

Our work aims at developing novel immunotherapies and vaccines, leveraging advanced genomics, transcriptomics and proteomics pipelines to study immunity. We use the datasets we develop to better understand the immune-system towards machine-learning and artificial intelligence tasks in vaccine design. The team, comprising diverse professionals like biologists, statisticians, software engineers, and data scientists, collaborates internationally to create new therapies.

The role offers extensive training in data science and high-performance computing, with access to top supercomputers. We provide a competitive international salary and opportunities for professional growth. Join us in tackling some of the most challenging problems in immunotherapy and disease research.

The data we deal with is truly huge: individual datasets can be hundreds of terabytes, and can include numerical, textual and imaging data. The team we are building is incredibly diverse, with biologists, statisticians, software engineers, bioinformaticians, mathematicians and data scientists. Together, we are all working as a team toward the common goal of developing new therapies for cancer patients. Use your technical skills to tackle one of the hardest problems of our time as you continue to grow into data-science.

We are searching for an expert in mass-spectrometry-based -omics who is passionate about using cutting edge prediction methods to drive the next round of discovery in immunotherapeutics. We are equipped with state of the art facilities on which to develop your data-science and high performance computing skillset. This includes super computers consistently ranked among the top 500 super computers in the world. As the work is international in nature, we are constantly integrating with sistergroups around the world. There will be ample training opportunities for developers who join the team and we offer an internationally competitive salary competitive with your experience.

How to apply:

You are encouraged to contact

Dr. Javier Alfaro (Javier.Alfaro@proteogenomics.ca) before submitting an application.

Responsibilities:

A post for a Computational Biologist in proteomics is currently available within the International Computational Immunology Research Group led by Dr. Javier Alfaro. You will be (or become) an expert in a diversity of proteomics and metabolomics analysis pipelines involved in analyzing including single cell analysis, bulk-tumour analysis and blood biopsy analysis. You will support and develop grant applications within the team and provide guidance to enable best practice for experimental design. Within the bioinformatics group, you will work within a cohesive interdisciplinary team of data scientists that are located internationally in a variety of sites including Canada, UK and Poland. You will enable programs and pipelines for analysis, establish

approaches for the integration of the analysis with multiple genome-wide 'omics datasets including processed DNA, RNA and proteomics datasets. Your results will be used to explore questions in cancer vaccine science.

- experience with Amazon Web Services, Google Cloud Engine or other clouds

Responsibilities may also include:

- Provide consulting on biological data analysis for researchers within our network conducting cutting-edge molecular biology research
- Advise and help researchers with their experimental design, data analysis and interpretation of results
- Provide training (2-5 days courses) in the area of machine learning and data science in biology
- Mentorship of junior staff and co-op students
- Collaborate and interact with other scientists within our partner networks in an international, interdisciplinary, and highly collaborative work environment

Preferred Qualifications:

- Bachelor's degree (MSc preferred) or further training in Machine Learning or Bioinformatics
- Experience with version control systems (SVN, Git, Mercurial, etc)
- Experience with some of the following: R, Python, C, C++, Java
- Knowledge of UNIX/Linux environments

Beneficial skills include:

- Experience in analyzing single cell 'omics, imaging, -omics, proteomics, or microfluidics data sets
- Experience in teaching
- Experience in R as a package developer or maintainer
- Knowledge of Python or other scripting languages
- Knowledge of scientific authoring frameworks (LaTeX, Rmarkdown) and RShiny
- Experience with version control, method benchmarking, or data management technologies

Benefits

The international Computational Immunology Research Group welcomes individuals through various collaborations. Each path offers unique benefits, tailored to the path of entry. We encourage potential candidates to contact Dr. Javier Alfaro (Javier.Alfaro@proteogenomics.ca) for an initial discussion about the opportunities available. This network is a dynamic environment for skill development in machine learning and high-performance computing, with remote work compatibility. It's an ideal setting for those keen on contributing to significant challenges in immunology and disease research across a spectrum of areas.