

Software Engineer

Job Description:

I am always seeking to develop a data-science team to solve the many computationally complex problems we encounter in bioinformatics and health data science. We work towards the development of new therapeutics and immunotherapies that leverage the patient's own immune-system to eradicate the disease. Our work and findings help to improve the treatment and care for cancer patients around the world.

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 toward the common goal of developing new therapies for cancer patients and other complex diseases. 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 a software engineer passionate about applying their knowledge of software development and design to improve scientific research. We are equipped with state of the art facilities on which to develop your data-engineering and high performance computing skillset. The project has access to Cyfronet Pro- metheus (~55, 000 cores) and CI TASK Tryton (~38, 000 cores) clusters, which are consistently represented among the top 500 super computers in the world. As the work is international in nature, we are constantly integrating with sister-groups around the world. There will be ample training opportunities for developers who join the team and we offer an inter- nationally competitive salary competitive with your experience.

How to apply:

You are encouraged to contact Dr. Javier Alfaro (Javier.alfaro@proteogenomics.ca) and I will connect you to the appropriate streams through which you may apply.

Responsibilities:

The software engineer position involves the optimization of bioinformatics software prior to public distribution and the maintenance and expansion of software systems used by members of the team including the development environment for Python and R used by the team. You will play a critical role in the software development of bioinformatics tools and algorithms, which will dramatically increase the scope of our research. The software engineer also works with lab members to help write better, more maintainable code, and provides guidance in using lab resources such as the computing cluster and version control. We depend on the software engineer to continue to develop and expand their skills in data engineering and software development by attending conferences to update and consult us on the state of the art. Finally, we will encourage you to participate in polish-led software development efforts and participate in the open source community and industry partnerships.

Other responsibilities may include:

- Develop quality software and web applications
- Analyze and maintain existing software applications
- Design highly scalable, testable code
- Development of computational pipelines for analyzing big data
- Building and maintaining core infrastructure (e.g. build systems, automated code-quality assessment)

- Database schema design and management
- Web design and development
- Systems administration
- Applied machine learning
- Cloud-based workflow development and deployment
- Open-source software development and maintenance
- Mentorship of junior software engineers and co-op students
- Training of biologists and statisticians in software engineering fundamentals
- Preferred Qualifications:
- Bachelor's degree or further training in Software Engineering, Computer Science or Computer/Electrical Engineering
- Development experience with programming languages
- Experience with version control systems (SVN, Git, Mercurial, etc)
- SQL database or relational database skills
- Excellent implementation skills (high-level and low-level languages) a must
- Experience with some of the following: R, Python, C, C++, Java
- Knowledge of UNIX/Linux environments

Beneficial skills include:

- systems software
- algorithm design and analysis
- performance optimization
- SLURM or other job scheduling systems
- experience with Amazon Web Services, Google Cloud Engine or other clouds
- distributed programming
- prior exposure to molecular biology, biochemistry or bioinformatics

- prior exposure to machine learning techniques
- Relational database management systems skills (e.g. PostgreSQL)

Benefits

- You will interact internationally with researchers having state-of-the-art facilities for mass spectrometry, virology, protein biochemistry, vaccine technology and computational biology.
- Employees will have the opportunity to develop skills in machine learning and high performance computing. The center has access to Cyfronet Prometheus (~55, 000 cores) and CI TASK Tryton (~38, 000 cores) clusters, which are consistently represented among the top 500 super computers in the world.
- Our software engineers, statisticians and computer-scientists are encouraged to further develop their skills in data-science through the attendance of workshops, conferences etc.
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- As we are an international center our infrastructure is remote-work compatible. A benefit enjoyed by excellent communicators and team players.