



The Laboratory for RNA-Based Lifeforms

Full Stack Bioinformatician / Developer (Postdoc or equal)

Join “[The Laboratory for RNA-Based Lifeforms](#)” in University of Toronto’s Donnelly Centre. Together with **Dr. Artem Babaian** the work will develop the state of the art for the detection and sequence analysis of RNA viruses and virus-like agents.

(Micro)Biology is undergoing a paradigm shift in our understanding of Earth’s genetic diversity. This is being driven by the widespread adoption and exponential drop in cost of DNA/RNA sequencing, with 100+ petabytes of public sequence data available today, and growing. Our lab aims to pioneer a new-generation of computational analysis techniques optimized for exabase/exabyte-scale datasets.

Recently we’ve developed an AWS-cloud backed computing architecture, *Serratus* (<https://github.com/ababaian/serratus>), which has enabled us process 5.7 million datasets (10.2 petabytes) in only 11 days. This analysis revealed 130,000+ novel RNA viruses across the world, where only 15,000 were previously known in public databases. Learn more in our first [Nature](#) paper, or watch our [HCLS21](#) talk.

Who you are

We’re looking for a passionate, team-oriented scientist or engineer who can operate across the full stack of cloud-computing infrastructure, data analysis, through to web-deployment; or be highly talented in one dimension. Currently we’re developing the [Serratus architecture](#) (`: AWS/Terraform, python, SQL, bioinformatics software, bash`); the [Serratus.io](#) web-interface (`: AWS, CSS, JavaScript`); the *palmID* RNA virus analysis suite and API (`: R, SQL, CSS`); and several cloud-oriented analysis tools (AWS/Python). We’re open to applicants with expertise in the areas of cloud-computing, scalable algorithm development, computational virology, machine learning (why not?) or UI/UX design. You should be primarily oriented around quantitative analyses.

You will work closely with a fast-paced international research team. Our work aims to also create free and open data resources to catalyze the field of virology globally. Demonstrated development or contributions to open source projects is a major asset. Mentoring and collaboration junior scientists is expected.

(cont’d)

Qualifications

Minimum (*provide evidence please*)

- Demonstrated expertise in ≥ 1 programming language such as Python, C++, R, Perl, etc...
- Highly motivated to learn, teach and pursue science across disciplines
- Experience in the following areas:
 - Cloud infrastructure / high-performance computing systems
 - Databases (SQL)
 - Web development
 - Software engineering/documentation best practices

Preferred qualifications

- A clear vision of what you would like to pursue
- PhD or experience in computational virology, genomic or “Big Data”
- Demonstration of scientific mentorship, organizational and/or leadership skills

Where we are

The Canadian [Donnelly Centre](#) is located in the downtown (St. George) University of Toronto campus in Canada. We are embedded amongst several world-class computational biology groups and the Donnelly offers a cross-disciplinary repertoire of biological laboratories for validation/collaboration. The University of Toronto is the top Canadian university, and offers countless opportunities for extending your academic experiences.

The start date is immediate/flexible, and we encourage applicants from diverse backgrounds. The position can be full-time or contracted consultant, an ideal contact will be Toronto-local or willing to relocate, but remote work is possible for an exceptional applicant.

We will be recruiting until this vacancy is filled.

Email your application package to artem@rRNA.ca with subject **Application id0002 - bioinfo**