

David Lougheed

Full-Stack Software Developer • Bioinformatician
Montréal, Québec, Canada

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SKILLS AND LANGUAGES

Programming Languages:

- Proficient in Python and JavaScript/TypeScript.
- Some experience with Rust, R, C++, PHP.

Back-End Frameworks: FastAPI, Flask/Quart, Django, Express

Front-End Frameworks: React, React Native + Expo, Vue, D3.js

Libraries: numpy, scikit-learn, PyO3 (Rust bindings for Python), Keras

Databases and Data Stores: PostgreSQL, SQLite, MySQL, Redis

Deployment and Containerization: Docker, Compose

DevOps: GitHub Actions. Some experience with GitLab CI/CD.

Languages: Native English speaker, limited working proficiency in French.

WORK EXPERIENCE

Canadian Centre for Computational Genomics (C3G), McGill University — Montréal, QC
Software Developer 2019–2020, 2022–present

- Founding developer and system architect for the Bento Platform, which facilitates the discovery, sharing, and visualization of -omics data and associated metadata. This project is used by seven large projects, including the Québec COVID-19 Biobank, and is worked on by several full-time developers.
 - Guided the technical direction of the project, delegated tasks to other developers, and met with stakeholders.
 - **Technologies:** Python, TypeScript + React, Docker + docker compose, Flask, Django, FastAPI, GitHub Actions, PostgreSQL + PostGIS, Redis
- Principle developer on the Freezeman project from April–August 2020. Freezeman is a sample-tracking system initially created to manage samples collected during the COVID-19 pandemic. It has since grown into a laboratory information management system used by the McGill Genome Centre with over 450 000 samples.
Technologies: JavaScript + React, Python + Django, PostgreSQL
- One of two developers on the EpiVar Portal project, a data portal for censored discovery of complex genetic-epigenetic correlation data. Published in *Bioinformatics* (Lougheed *et al.* 2024).
Technologies: Node.js + Express, React, PostgreSQL, Redis

Intern, Data Team 2018–2019

- Developed three web applications, including one published as part of an article in *Nature Communications* (Grajcarek *et al.* 2019). **Technologies:** D3.js, Python + Flask, PostgreSQL
- Analyzed RNA-seq data using an in-house data processing pipeline.

Queen's University Biological Station — Kingston, ON
Field / Network Technician 2015–present (occasional)

- Assisted in deploying and maintaining a network of remote, satellite-linked climate stations.
- Deployed new Ubiquiti Unifi-based networks across multiple multi-building campuses, supporting 100+ concurrent users across 14 buildings at peak and increasing throughput by ~5x.
- Implemented software to power a interactive trail guide mobile application with 200+ installs via a custom content management system (CMS). **Technologies:** React Native + Expo, React, Python + Flask, SQLite
- Developed a Drupal theme and a WordPress theme for two of station's websites.
- Helped to maintain trails and perform general facilities maintenance.

McGill University — Montréal, QC
Course Assistant for COMP 421: Databases Jan–Apr 2019

Held office hours and graded assignment questions on relational algebra and databases.

Freelance Web Developer 2014–2015 — Kingston, ON
Developed custom web applications, websites, and Wordpress themes for clients, including a Meteor application for a local charity which managed the distribution of food to a network of partner organisations.

EDUCATION

Master of Science, McGill University
Department of Human Genetics. GPA: 4 / 4.

Montréal, QC
2020–2022

- **Select Courses:** Statistical Concepts in Genetic and Genomic Analysis, Population Genetics.

Bachelor of Science, McGill University
Joint Honours Computer Science and Biology. GPA: 3.94 / 4.

Montréal, QC
2015–2019

- **Select Courses:** Applied Machine Learning, Statistics, Honours Algorithms and Data Structures.

SELECTED PROJECTS

STRkit: A command-line application for determining the genotypes of short tandem DNA repeats in genomic data, built with Python and Rust. Described in a BioRxiv preprint (Lougheed *et al.* 2025).

SNiPe: a primer pair selection tool for environmental DNA studies, built with TypeScript and React. Published in *Environmental DNA* (Tournayre *et al.* 2024).

PUBLICATIONS

- Five publications in peer-reviewed academic journals, including one first-authored publication.
- Three manuscripts either in review or released as a preprint.

Selected Publications

- **STRkit: precise, read-level genotyping of short tandem repeats using long reads and single-nucleotide variation** (2025). [David R Lougheed](#), Tomi Pastinen, Guillaume Bourque. *BioRxiv preprint*. DOI: 10.1101/2025.03.25.645269.
- **Enhancing metabarcoding of freshwater biotic communities: a new online tool for primer selection and exploring data from 14 primer pairs** (2024). Oriane Tournayre, Haolun Tian, [David R Lougheed](#), Matthew JS Windle, Sheldon Lambert, Jennipher Carter, Zhengxin Sun, Jeff Ridal, Yuxiang Wang, Brian F Cumming, Shelley E Arnott, Stephen C Lougheed. *Environmental DNA*. DOI: 10.1002/edn3.590.
- **EpiVar Browser: advanced exploration of epigenomics data under controlled access** (2024). [David R Lougheed](#), Hanshi Liu, Katherine A Aracena, Romain Grégoire, Alain Pacis, Tomi Pastinen, Luis B Barreiro, Yann Joly, David Bujold, Guillaume Bourque. *Bioinformatics*. DOI: 10.1093/bioinformatics/btae136.