

David Lougheed

Full-Stack Software Developer • Bioinformatician
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SKILLS AND LANGUAGES

Programming & Markup Languages:

- Proficient in Python, JavaScript/TypeScript, HTML, and CSS.
- Some experience with Rust, Java, R, C++, PHP, Go.
- Comfortable with bash scripting.

Frameworks:

- **Back End:** FastAPI, Flask/Quart, Tornado, Django, Node.js + Express
- **Front End:** React, Redux, React Native + Expo, Vue

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

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

Libraries: numpy, scikit-learn, Pydantic, PyO3 (Rust

bindings for Python), Keras; socket.io; Recharts, D3.js

Standards & APIs: OAuth2 and OpenID Connect Relying Party implementation, GeoJSON, S3-compatible APIs, OpenAPI and JSON schemas.

Databases & Data Stores: PostgreSQL, SQLite, MySQL, Redis. Some experience with NoSQL databases and concepts.

Deployment & Containerization: Docker, Compose

WORK EXPERIENCE

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

- Founding developer and system architect for the Bento Platform, a microservice-based platform which facilitates the discovery, sharing, and visualization of large-scale genetic data and associated metadata. This platform is used by several large projects, including the Québec COVID-19 Biobank, and is now 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 + Redux, Recharts, Docker + Compose, Flask, Django, FastAPI, GitHub Actions, PostgreSQL + PostGIS, Redis, OAuth2
- Principal developer on the Freezeman sample-tracking system from April–August 2020, 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 of the EpiVar Portal, for the discovery and visualization 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 data exploration and visualization 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 — Kingston, ON
Bioinformatics Consultant 2019–present (occasional)

- Assisted in the creation of a chorus frog reference genome (Chen *et al.* 2024).
- Built a Python pipeline for processing polar bear GTseq genotyping data.

Software Developer, Queen's University Biological Station 2015–present (occasional)

- Implemented a content management system (CMS) to power a interactive trail guide mobile application with 200+ installs. **Technologies:** React Native + Expo, React, TypeScript, Python + Flask, SQLite
- Created a data aggregation, visualization, and download platform for semi-real-time climate data generated on-premises. **Technologies:** PostgreSQL, Python + Django, JavaScript, Vue, HighCharts
- Developed a Drupal theme and a WordPress theme for two of station's websites.

Field / Network Technician, Queen's University Biological Station 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.
- Helped to maintain trails and perform general facilities maintenance.

McGill University ————— Montréal, QC
Graduate Researcher, Department of Human Genetics 2020–2022

- Developed a novel genotyping algorithm and Python package for certain DNA patterns in human genome sequencing data.
- Created bash scripts and workflows for data analysis using high-performance computing (HPC) resources.
- Reviewed relevant literature on my topic of research and benchmarked existing genotyping approaches.
- Created data visualizations for posters and publications.

Course Assistant for COMP 421: Databases Jan–Apr 2019

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

Freelance Web Developer ————— 2013–2015 — Kingston, ON

Developed custom web applications, websites, and Wordpress themes for clients. Selected projects include:

- A Meteor application for a local charity which managed the distribution of food to a network of partner organisations.
- A PHP application for transparent peer review of scientific manuscripts, developed for a professor at Queen’s University in Kingston, ON.

EDUCATION

Master of Science, McGill University **Montréal, QC**
Department of Human Genetics. GPA: 4 / 4. 2020–2022

- **Thesis:** Using High-Fidelity Long-Read Sequencing to Better Detect and Understand Short Tandem Repeat Variation in Humans. *Supervisor: Prof. Guillaume Bourque*

Bachelor of Science, McGill University **Montréal, QC**
Joint Honours Computer Science and Biology. GPA: 3.94 / 4. 2015–2019

- **Select Courses:** Compiler Design (team co-winner for best compiler and best “peephole” optimizer), 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, Pastinen & Bourque 2025).

CTF Election System: A platform for Faculty of Science student group elections at McGill University, which during “election season” handles thousands of users. Built with Vue, Node.js, and MySQL, with an LDAP-based authentication system connected to the university Active Directory.

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

David’s Trail Guide System: A custom content management system and “white-label” mobile application for deploying trail guide apps, with trail layers provided as GeoJSON. Built using Flask, React, SQLite, and React Native + Expo, with OpenID Connect + OAuth2 (via Auth0) used for authentication and authorization.

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

- **Read-level genotyping of short tandem repeats using long reads and single-nucleotide variation with STRkit** (2026). David R Lougheed, Tomi Pastinen, Guillaume Bourque. *Accepted in Genome Res.* DOI: 10.1101/gr.280766.125.
- **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.