

# David Lougheed

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

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## SKILLS AND LANGUAGES

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### 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.

## WORK EXPERIENCE

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**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.

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<b>McGill University</b> <u>Graduate Researcher, Department of Human Genetics</u>	Montréal, QC 2020–2022
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- 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.

<u>Course Assistant for COMP 421: Databases</u>	Jan–Apr 2019
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Held office hours and graded assignment questions on relational algebra and databases.

<b>Freelance Web Developer</b>	2013–2015 — Kingston, ON
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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

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<b>Master of Science</b> , McGill University <i>Department of Human Genetics.</i> GPA: 4 / 4.	Montréal, QC 2020–2022
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- **Thesis:** Using High-Fidelity Long-Read Sequencing to Better Detect and Understand Short Tandem Repeat Variation in Humans. *Supervisor: Prof. Guillaume Bourque*

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

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**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 (Lougeed, 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

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- 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 Lougeed, 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). Orianne Tournayre, Haolun Tian, David R Lougeed, Matthew JS Windle, Sheldon Lambert, Jennifer Carter, Zhengxin Sun, Jeff Ridal, Yuxiang Wang, Brian F Cumming, Shelley E Arnott, Stephen C Lougeed. *Environmental DNA*. DOI: 10.1002/edn3.590.
- **EpiVar Browser: advanced exploration of epigenomics data under controlled access** (2024). David R Lougeed, 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.