

David Lougheed

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

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.

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

Deployment & Containerization: Docker, Compose

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

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, 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.
- Principal developer on the Freezeman sample-tracking system from April–August 2020, initially created to manage samples collected during the COVID-19 pandemic. **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

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 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

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.
- Created data visualizations for posters and publications.

EDUCATION

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

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

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.