

David Lougheed

Montréal, Québec, Canada

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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*
- **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

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.

PUBLICATIONS

Submitted & In Preprint

8. **STRkit: precise, read-level genotyping of short tandem repeats using long reads and single-nucleotide variation** (2025). [David R Loughheed](#), Tomi Pastinen, Guillaume Bourque. *BioRxiv preprint*. DOI: 10.1101/2025.03.25.645269.
7. **The BQC19 cohort: large scale, in-depth, multi-omics characterisation of Quebec COVID-19 patients** (2025). David Bujold, Solomia Yanishevsky, Tania Schramek, Mylène Bertrand, Julie Bérubé, David Brownlee, Danielle Perley, Étienne Collette, Doris Ransy, ..., [David R Loughheed](#), ..., Madelaine Durand, Simon Rousseau, Daniel Auld, Guillaume Bourque. *Under review in Scientific Data*.
6. **Insights on macrosynteny, 'rebel' genes, and a new sex-linked region in anurans from comparative genomics and a new chromosome-level genome for the western chorus frog** (2024). Ying Chen, [David R Loughheed](#), Zhengxin Sun, Jeffrey Ethier, Vance L Trudeau, Stephen C Loughheed. *BioRxiv preprint*. DOI: 10.1101/2024.10.27.620512.

Published

5. **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 Loughheed](#), Matthew JS Windle, Sheldon Lambert, Jennipher Carter, Zhengxin Sun, Jeff Ridal, Yuxiang Wang, Brian F Cumming, Shelley E Arnott, Stephen C Loughheed. *Environmental DNA*. DOI: 10.1002/edn3.590.
4. **EpiVar Browser: advanced exploration of epigenomics data under controlled access** (2024). [David R Loughheed](#), 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.
3. **Epigenetic variation impacts individual differences in the transcriptional response to influenza infection** (2024). Katherine A Aracena, Yen-Lung Lin, Kaixuan Luo, Alain Pacis, Saideep Gona, Zepeng Mu, Vania Yotova, Renata Sindeux, Albená Pramatarova, Marie-Michelle Simon, Xun Chen, Cristian Groza, [David R Loughheed](#), Romain Grégoire, David Brownlee, Yang Li, Xin He, David Bujold, Tomi Pastinen, Guillaume Bourque, Luis B Barreiro. *Nature Genetics*. DOI: 10.1038/s41588-024-01668-z.
2. **baRcodeR: An open-source R package for sample labelling** (2020). Yihan Wu, [David R Loughheed](#), Stephen C Loughheed, Kristy Moniz, Virginia K Walker, Robert I Colautti. *Methods in Ecology and Evolution*. DOI: 10.1111/2041-210X.13405.
1. **Genome-wide microhomologies enable precise template-free editing of biologically relevant deletion mutations** (2019). Janin Grajcarek, Jean Monlong, Yoko Nishinaka-Arai, Michiko Nakamura, Miki Nagai, Shiori Matsuo, [David R Loughheed](#), Hidetoshi Sakurai, Megumu K Saito, Guillaume Bourque, Knut Woltjen. *Nature Communications*. DOI: 10.1038/s41467-019-12829-8.

POSTERS AND TALKS *Presenter

6. **New genomics tools for assessing population structure in grizzly bears and testing for hybrids between grizzly and polar bears**. Oral Talk. Andrea Gómez Sánchez*, [David R Loughheed](#), Arjun Augustine, Monica Navarrete de Salgado, Stephen C Loughheed. *ArcticNet Arctic Change Conference*. 2024.
5. **Chromosome-level Genome Assembly Sheds Light on Evolution and Demographic History of Western Chorus Frog (*Pseudacris triseriata*)**. Oral Talk. Ying Chen*, [David R Loughheed](#), Zhengxin Sun, Jeffrey Ethier, Vance L. Trudeau, and Stephen C Loughheed. *10th World Herpetological Congress. Kuching, Sarawak, Borneo, Malaysia*. 2024.
4. **A chromosome-level genome assembly for Western Chorus Frog**. 2023. Ying Chen*, [David R Loughheed](#), Stephen C Loughheed. *Canadian Herpetological Society annual meeting, Carleton University*. Oral Talk.
3. **Using high fidelity long reads to better resolve short tandem repeat (STR) variation and expansion**. Poster. [David R Loughheed](#)*. *Department of Human Genetics Poster Day, McGill University*. 2022.
2. **EpiShare: an open platform to securely share epigenomic data**. Poster. David Bujold*, Ksenia Zaytseva, Palmira Granados Moreno, Hanshi Liu, Sebastian Ballesteros Ramirez, Romain Grégoire, [David R Loughheed](#), Katie Saulnier, Yann Joly. *Global Alliance for Genomics and Health Plenary Meeting*. 2020.

1. **CanDIG CHORD: Canadian Health Omics Repository, Distributed.** Oral Talk. [David R Loughheed*](#). *CANARIE Summit*. 2019.

SKILLS, LANGUAGES, AND CERTIFICATIONS

- **Scripting and Programming Languages:**
 - Proficient in Bash shell scripting, Python, and JavaScript/TypeScript.
 - Some experience with Rust, R, C++, PHP.
- **Software Development:**
 - Experience developing of data portals and web data visualizations.
 - Experience creating and using Docker and Apptainer containers.
 - **Libraries:** numpy, scikit-learn
 - **Databases and Data Stores:** Experience with SQL and document databases and GIS databases.
- **HPC:** Experience using high-performance computing (HPC) resources, e.g., Digital Research Alliance of Canada (DRAC) clusters.
- **Genomic Sequencing Data:** Experience with short- and long-read sequencing data with Illumina, Oxford Nanopore, and Pacific Biosciences HiFi platforms; experience with whole-genome variant calling, genome assembly, and GTseq (genotyping in thousands) protocols.
- **Languages:** Native English speaker, limited working proficiency in French.
- **Certifications:** Full driver's license (Class 5, Québec), pleasure craft operator card (PCOC).

AWARDS

- Tomlinson Undergraduate Award (\$300)
- J. W. McConnell Scholarship (\$3k)

FIELD EXPERIENCE

- **2015-present (*occasional*):** Helped maintain remote solar-powered satellite-linked climate monitoring stations. Tasks included regular maintenance, fault monitoring, basic electronics diagnostics and repair, and data collection.
- **Summer 2017:** Assisted in the mapping of culverts for hydrological use.