

# David Lougheed

Montréal, Québec, Canada

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## EDUCATION

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

Montréal, QC  
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  
*Joint Honours Computer Science and Biology.* GPA: 3.94 / 4.

Montréal, QC  
2015–2019

## 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, which facilitates the discovery, sharing, and visualization of -omic 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, STRkit, for short tandem repeat elements 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.

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.

## PUBLICATIONS

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### Submitted & In Preprint

8. **Long-read sequencing reveals telomere inheritance patterns from human trios** (2025). Yuxin Zhou, [David R Loughheed](#), Warren A Cheung, Isabelle Thiffault, Tomi Pastinen, Guillaume Bourque. *Submitted*.
7. **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.

### Peer-Reviewed Journal Articles

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

### Other Publications

- **An Overview and Guide to Environmental DNA Protocols and Workflows** (2025). Orianne Tournayre, Haolun (Allen) Tian, Stafford "Rotehrá:kwá" Maracle, [David R Loughheed](#), Stephen C Loughheed. *ReadTheDocs*. DOI: 10.5281/zenodo.13421371.

## POSTERS AND TALKS

\*Presenter

8. **Long-read sequencing reveals telomere inheritance patterns in human trios**. Poster. Yuxin Zhou\*, [David R Loughheed](#), Warren A Cheung, Isabelle Thiffault, Tomi Pastinen, Guillaume Bourque. (1) *American Society for Human Genetics*. Boston, MA, USA. (2) *Canadian Epigenetics, Environment and Health Research Consortium*. Banff, AB, CA. 2025.
7. **Do water courses shape microgeographic genetic connectivity in the rock hole frog in Litchfield National Park, Australia?** Poster. Stephen C Loughheed\*, [David R Loughheed](#)\*, Rute Clemente-Carvalho, Peiwen Li, Aaron Snee, Cameron Hudson. *Canadian Herpetological Society annual meeting, Université de Laval*. Québec, QC, CA. 2025.

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. Ottawa, ON, CA. 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. Ottawa, ON, CA. 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. Montréal, QC, CA. 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. Online. 2020.*
1. **CanDIG CHORD: Canadian Health Omics Repository, Distributed.** Oral Talk. [David R Loughheed](#)\*. *CANARIE Summit. Ottawa, ON, CA. 2019.*

## SKILLS, LANGUAGES, AND CERTIFICATIONS

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- **Scripting and Programming Languages:**
  - Proficient in Bash shell scripting, Python, and JavaScript/TypeScript.
  - Some experience with Rust, Java, R, C++, PHP.
- **Software Development:**
  - Experience developing data portals and web data visualisations, including with GIS data using GeoJSON and Leaflet.
  - Experience creating and using Docker and Apptainer containers.
  - **Libraries:** *Data:* numpy, polars, scikit-learn, Pydantic; *GIS:* PR0J4js, Leaflet
  - **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, and using slurm and batch bash scripts.
- **Genomics:** Extensive experience working with short- and long-read sequencing data from Illumina, Oxford Nanopore, and PacBio HiFi platforms; some experience with whole-genome variant calling, genome assembly, using GTseq and RADseq data, and performing population genetics analyses.
- **Languages:** Native English speaker, limited working proficiency in French (Québec level 4).
- **Certifications:** Full driver's license (Class 5, Québec), pleasure craft operator card (PCOC).

## VOLUNTEERING AND LEADERSHIP

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**Computer Taskforce**, McGill University ————— Montréal, QC  
Member (& Council Member, Jan-Dec 2021) Mar 2017–Apr 2023

- Created and deployed several web applications for students, including an election system which allowed student groups to run elections for free and a locker rental system for the McGill Biology Student Union.
- Participated in day-to-day operations of the organization, including organizing workshops and events, lending laptops to students, and operating a help desk.
- *As council member:* Worked with other council members to guide the direction of the organization.

Team Lead Jan 2018–Apr 2019

- Guided development of web applications which served the McGill Faculty of Science student body.
- Organized team meetings and onboarded new members.
- Fostered an inclusive environment where volunteers of varying skill levels could contribute to projects.

**McGill Robotics**, McGill University ————— Sept 2015–Apr 2017  
 Helped develop a web-based image annotation tool for training an underwater robot's computer vision system.

**TEAM Mentor**, McGill University ————— Sept–Dec 2016  
 Assisted a teaching assistant in running laboratory activities for the BIOL 111 course.

## AWARDS

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**2020-2021:** McGill Graduate Excellence Award (\$5437.50)

**2016:** Tomlinson Engagement Award for Mentoring (\$300)

**2015:** J. W. McConnell Scholarship (\$3k)

## FIELD EXPERIENCE

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- **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.