

# David Lougheed

Montréal, Québec, Canada

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## EDUCATION

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**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.
- **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

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**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 now being used or will be used by seven large projects, including the Québec COVID-19 Biobank, and is worked on by several full-time developers.
- Principle developer on the Freezeman project from April–August 2020. This project is a sample-tracking system created to manage samples collected during the COVID-19 pandemic, which later grew into a full laboratory information management system (LIMS) used by the McGill Genome Centre, with multiple full-time developers and 450 000+ samples.

*Intern, Data Team* 2018–2019

- Developed three web applications, including one published as part of an article in Nature Communications (Grajcarek *et al.*, 2019) using D3.js for complex data visualization.
- 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) using React Native, Expo, React, and Flask.

**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.

## PUBLICATIONS

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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 Lougheed](#), Zhengxin Sun, Jeffrey Ethier, Vance L Trudeau, Stephen C Lougheed. *BioRxiv preprint*. DOI: 10.1101/2024.10.27.620512.
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 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.

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, Albena 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

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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.

\*Presenter

## 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, 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.
- **Languages:** Native English speaker, limited working proficiency in French.
- **Certifications:** Full driver's license (Class 5, Québec).