

Cristian Groza

DETAILS

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Github <https://github.com/cgroza> (software projects)

EDUCATION

PhD. Quantitative Life Sciences 2019-
McGill University

BSc. Joint Computer Science and Biology 2016-2019
McGill University

DEC. Health Science 2014-2016
Dawson College

RESEARCH EXPERIENCE

Japan Society for the Promotion of Science fellowship Spring 2023
Institute for the Advanced Study of Human Biology, Kyoto, Japan

- Developed novel genome graph methods for comparative epigenomics in primate genomes with Drs. Fumitaka Inoue and Guillaume Bourque at Kyoto University from 3 April to 3 June 2023.

Research Assistant 2017 - 2019
Contract at MUGQIC, Dr. Guillaume Bourque's Lab

- Developed pipeline applying personalized genomics to hundreds of epigenomic datasets within the McGill Epigenomics Mapping Centre.

Rotating Student Fall 2019
PhD rotation in Dr Yue Li's lab
Department of Computer Science, McGill University

- Applied topic learning models to single cell transcriptomic data.

Rotating Student Summer 2019
PhD rotation in Dr Celia Greenwood's lab
Quantitative Life Sciences, McGill University

- Applied outlier detection algorithms to neuro-imaging data.

PUBLICATIONS

1. Merenciano M, Larue A, **Groza C**, Vieira C, Rebollo R and Goubert C (In preparation) Epigenetics and Genotypic Variation: a transposable elements' perspective. book: Epigenetic and Evolution, Elsevier Press

2. **Groza C**, Chen X, Wheeler T, Bourque G and Goubert C (In preparation) GraffTE: a Unified Framework to analyze Transposable-Element and Repeat-derived Structural Variants using pangenome graphs.
3. **Groza C**, Schwendinger-Schreck C, Cheung W, et al (2023) Pangenome graphs improve the analysis of rare genetic diseases. medRxiv. doi: <https://doi.org/10.1101/2023.05.31.23290808>
4. **Groza C**, Chen X, Pacis A, et al (2023) Genome graphs detect human polymorphisms in active epigenomic state during influenza infection. Cell Genomics. <https://doi.org/10.1016/j.xgen.2023.100294>
5. **Groza C**, Bourque G, and Goubert C (2023) A pangenome approach to detect and genotype TE insertion polymorphisms, In: Transposable elements, pp. 85–94 Springer. https://doi.org/10.1007/978-1-0716-2883-6_5
6. Liao W-W, Asri M, Ebler J, ..., **Groza C**, et al (2023) A Draft Human Pangenome Reference. Nature. doi: <https://doi.org/10.1038/s41586-023-05896-x>
7. **Groza C**, Kwan T, Soranzo N, Pastinen, T, Bourque G (2020) Personalized and graph genomes reveal missing signal in epigenomic data. Genome Biol 21, 124. <https://doi.org/10.1186/s13059-020-02038-8>

POSTERS & TALKS

Pangenome graphs for the analysis of rare genetic diseases <i>15min talk, American Society of Human Genetics Annual Meeting, Los Angeles, CA</i>	Oct 2022
Human Pangenome Reference Consortium Meeting <i>2min talk, poster, Bethesda, MD</i>	Oct 2022
Genome graphs detect human polymorphisms in active epigenomic state during influenza infection <i>15min talk, poster at the 8th Canadian Conference on Epigenetics, Esterel, QC, Canada</i>	Oct 2022
Genome graphs detect human polymorphisms in active epigenomic state during influenza infection <i>15min talk, Keystone Symposia Transposable Elements, British Columbia, Canada, cancelled due to COVID19.</i>	Mar 2022
Leveraging read clouds to locally assemble Alu polymorphisms <i>5min talk, poster at T2T—HPRC Towards a Complete Reference of Human Genome Diversity. Virtual.</i>	Oct 2020
Personalized and graph genomes reveal missing signal in epigenomic datasets <i>Lightning talk, poster at Genome Informatics, CSHL, NY</i>	Nov 2019
Personalized and graph genomes reveal missing signal in epigenomic datasets	Oct 2019

Talk at ATCG, McGill University

**Personalized genomes for correcting reference bias
in epigenetics**

Mar 2019

Talk at Montreal Genomics, Université de Montréal

**Impact of personalized genomes on histone ChIP-seq
peak calls**

Sep 2018

*Poster at the 5th Canadian Conference on Epigenetics,
Esterel, QC, Canada*

AWARDS AND OFFERS

Japanese Society for the Promotion of Science

2023

Short-term fellowship, 400 000 JPY

**2022 Charles J. Epstein Trainee Awards for Excellence in
Human Genetics Research, semifinalist**

2022

American Society of Human Genetics, 750 USD

Fonds de recherche du Québec

2022

Nature et technologies, 49 000 CAD, Declined

Postgraduate Graduate Scholarship - Doctoral

2022

NSERC, 63000 CAD

Graduate Excellence Award

2019

Quantitative Life Sciences, McGill University, 4500 CAD

Canada Graduate Scholarship - Master's

2019

Alexander Graham Bell, NSERC, 23000 CAD

PhD. Computer Science

Winter 2019

University of Toronto. Declined

John V Galley Scholarship

2018

McGill University, 1000 CAD

Faculty of Science Scholarship

2017

McGill University, 500 CAD

Dean's Honor List

2017, 2018

McGill University

First Class Honours

June 2016

Dawson College

3e Prix de Chimie

Jan 2014

Concurs Scientifiques Montmorency, 100 CAD

OPEN SOURCE SOFTWARE

GraffiTE

2022

Github - Software

Nextflow pipeline to detect de novo transposable element insertions.

BarcodeAsm

2020

Github - Software

Wrote a C++ program to locally assemble DNA sequences from linked-read libraries.

SeqLib

2020

Github - Accepted pull request

Added multiple features to SeqLib such as GFA output and fully adjustable assembly parameters.

TEACHING EXPERIENCE

The 8th Kyoto Course and International Symposium

1 Mar 2023

Kyoto University

Wrote the pangenomics tutorial for the graph genome section of the 8th Kyoto Course.

Pharmhackaton 2018

17 Nov 2018

StudentPharma

Helped participants with command line and programming issues in a bio/chemoinformatics themed hackaton.

SKILLS

Programming PYTHON, R, Rust, JAVA, C/++, SCALA, HASKELL, LISP, L^AT_EX
Statistics Data manipulation (*dplyr*), presentation (*ggplot2*) and statistical inference.
Bioinformatics Write and run bioinformatic software for genome assembly, pangenomics, structural variation calling and epigenomics. Process, visualize, analyze and interpret next generation sequencing data.