Luis Gerardo Fernández Luna

lgfernandezluna@gmail.com | PhD Student at McGill

Education

McGill-Kyoto University | August 2025 - present | **Mentor: Dr. Guillaume Bourque**

- Joint PhD in Genomic Medicine

National Autonomous University of Mexico (UNAM) | August 2019 – June 2023

- Bachelor of Science in Genomic Sciences
- Overall grade: 94/100; GPA scale: 3.7
- Graduated with honors
- Thesis: *"Genome-wide maps of identical repeats that can mediate complex genomic rearrangements in three human genome assemblies"*

Publications

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1. Angelica Maria Delgado-Vega, Helene Cederroth, Fulya Taylan, (..), **Luis Fernandez-Luna**, et al. Pushing the boundaries of rare disease diagnostics with the help of the first Undiagnosed Hackathon. (*Nature Genetics* DOI: 10.1038/s41588-024-01941-1 *Published*).

2. Deb SK, Kalra D, Kubica J, (..), **Luis Fernandez-Luna**, et al. The fifth international hackathon for developing computational cloud-based tools and resources for pan-structural variation and genomics. (*F1000Research* DOI: 10.12688/f1000research.148237.1 *Published*).

3. Luis Fernandez-Luna, Carlos Aguilar-Perez, Christopher M. Grochowski, Michele Mehaffey; Claudia M.B. Carvalho, Claudia Gonzaga-Jauregui. Genome-wide maps of highly‐similar intrachromosomal repeats that mediate ectopic recombination in three human genome assemblies. (DOI: https://doi.org/10.1016/j.xhgg.2024.100396 *Published at Human Genetics and Genomics Advances*).

4. Joel Cota Castro, **Luis Fernandez-Luna**, Tania Sepúlveda, Carolina I. Galaz-Montoya, Claudia Gonzaga-Jauregui.Weiss-Kruszka syndrome due to 9q31.2q31.3 deletion in a Mexican patient and analysis of *ZNF462* mutation spectrum. (*In submission*).

5.**Luis Fernandez-Luna,** Carolina Adams, Sebastián Iturbe, Diego Ortega-Del Vecchyo, Rori Rohlfs.A novel framework to infer the mutational process underlying tandem repeat evolution to understand their role in adaptation. (In preparation)

Research experience

Research assistant | Institute of Ecology and Evolution, University of Oregon | Eugene, Oregon | Research assistant | January 2023 - August 2025

Mentor: Dr. Rori Rohlfs

- Develop a simulation-based statistical tool to assess the variance of tandem repeats within and between species.
- Provide a framework based on the ancestral recombination graph to test evolutionary hypotheses regarding tandem repeat variation.

Undergraduate research student | International Laboratory for Human Genome Research (LIIGH)| UNAM **|** Quéretaro, México **|** September 2020 – December 2023
Mentor: Dr. Claudia Gonzaga-Jauregui

- Performed genome-wide analyses of repeated sequences in the human genome to understand their role in producing genomic rearrangements and structural variants.
- Performed study of the mutational spectrum of a rare disorder, Weiss-Kruszka syndrome.
- Developed a pipeline for structural variant calling in whole human genome sequence data from PacBio HiFi using GATK and Sniffles2 software.

Undergraduate research intern | Pacific Northwest Research Institute (PNRI) | Seattle, Washington **|** June 2022 – August 2022
Mentor: Dr. Claudia Carvalho

- Performed analyses of complex genomic rearrangements interrogated using genomic technologies such as optical mapping, arrays, and long-read sequencing.
- Performed bioinformatic analyses of inverted and direct repeats that mediate the potential formation of genomic rearrangements.

Undergraduate research intern | Institute of Neurobiology (INB) | UNAM **|** Quéretaro, México **|** January 2020 – March 2020
Mentor: Dr. Maria del Carmen Clapp Jimenez

- Studied hormonal regulation of blood vessels, inflammation, growth, metabolism, and tissue survival.
- Studied the effectiveness of vasoinhibins regulating the effects caused by Diabetic retinopathy

Posters and presentations

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1. Luis Fernandez-Luna, Carolina Adams, Sebastián Iturbe, Diego Ortega-Del Vecchyo, Rori Rohlfs, A Likelihood-based Framework for Inferring the Evolution of Tandem Repeats. Evolution in Athens, Georgia, Mexico. July 2025 (*Selected oral presentation*).

2. Luis Fernandez-Luna, Carolina Adams, Sebastián Iturbe, Diego Ortega-Del Vecchyo, Rori Rohlfs, SLiMulations of Tandem Repeats: Inferring the mutational process. EVO-WIBO in Blaine, Washington, Mexico. April 2025 (*Poster presentation*).

2. Luis Fernandez-Luna, Perspectives on repetitive sequences as a source of genetic variation. Guest Speaker at McGill University. October 2025 (*presentation at Guillaume Bourque's lab meeting*)

3. Luis Fernandez-Luna, Carolina Adams, Sebastián Iturbe, Diego Ortega-Del Vecchyo, Rori Rohlfs, SLiMulations of Tandem Repeats: Insights into Their Evolutionary Significance. Society for Molecular Biology and Evolution Meeting in Puerto Vallarta, Mexico. July 2024 (*Poster presentation*).

4. Luis Fernandez-Luna,Carlos Aguilar-Perez, Michele Mehaffey, Claudia Carvalho, Claudia Gonzaga-Jauregui. Bioinformatic analysis to identify identical inverted and direct repeats that mediate the potential formation of complex genomic rearrangements. ISCB-Latin America SoIBio BioNetMX Conference on Bioinformatics 2022. International Society For Computational Biology. November 2022 (*Selected oral presentation*).

5. Luis Fernandez-Luna,Carlos Aguilar-Perez, Michele Mehaffey, Claudia Carvalho, Claudia Gonzaga-Jauregui. Identification of repeats mediating the formation of complex genomic rearrangements. PNRI Monthly Meetup. Pacific Northwest Research Institute. September 2022 (*Institutional seminar*).

6. Luis Fernandez-Luna, Joel Cota Castro ,Tania Sepúlveda-Morales, Carolina I. Galaz-Montoya, Claudia Gonzaga-Jauregui. Weiss-Kruszka syndrome due to 9q31.2q31.3 deletion in a Mexican patient and analysis of *ZNF462* mutation spectrum. Wellcome Trust Genomics of Rare Disease Conference. Sanger institute. March 2022 (*Poster presentation & flash talk*).

Awards

ISCB-LA SoIBio BioNetMX Funding Fellowship (*300 USD*) | October 2022

UNAM-DGCEI International Mobility Research Scholarship (*5000 USD*) | June 2022

National Biology Olympiad (First place) | Sonora, Mexico 2018

Training and Workshops

Structural Variants in the Cloud Hackathon | Baylor College of Medicine | September 2023

Hackathon of undiagnosed diseases | Karolinska Institute | June 2023

The McKusick Short Course | The Jackson Laboratory | July 2021

Single-Cell RNA-seq Workshop| Human Cell Atlas Latin America | April 26 to May 2, 2021

Technical skills

- Experience in UNIX/Linux systems.
- Experience with HPC environments, including the use of workflow managers like gwf and Nextflow.
- Knowledge in programming languages including R, Python, Perl and bash.
- Deep experience with population genetic simulation software: SLiM and msprime.
- Experience with standard NGS bioinformatic tool sets at the command line.
- Knowledge of lab techniques including Western Blot, DNA extraction, cell culture and PCR.
- Relevant courses: Molecular Biology, Cellular Biology, Biochemistry, Mathematics 1 (Combinatorics), Mathematics 2 (Linear Algebra), Mathematics 3 (Multivariable

calculus), Mathematics 4 (Differential Equations), Programming, Computers (Scientific Programming), Bioinformatics and Statistics 1 (Frequentist Statistics) and Bioinformatics and Statistics 2 (Bayesian Inference with Calculus)

References

Dr. Rori Rohlfs, rori@uoregon.edu
Associate Professor, Department of Biology, Institute of Ecology and Evolution, University of Oregon
Dr. Claudia Gonzaga-Jauregui, cgonzagaj@gmail.com
Assistant Professor at the International Laboratory for Human Genome Research (LIIGH) at National Autonomous University of Mexico (UNAM).
Dr. Claudia M.B. Carvalho, ccarvalho@pnri.org
Assistant Investigator at Pacific Northwest Research Institute (PNRI)