

Isaac Yellan, Ph.D.

GENOMICS · COMPUTATIONAL & EVOLUTIONARY BIOLOGY

✉ isaac.yellan95@gmail.com | 🏠 imyellan.github.io | 📧 imyellan | 🌐 isaacyellan | 📧 Isaac Yellan

Professional Summary

- **Genomics** data expert with **6+** years' proven track record generating and testing new hypothesis, co-designing successful wet lab experiments, and analyzing quantitative multi-omics data (**ChIP-seq, HT-SELEX, RNA-seq**)
- Experienced integrating structural biology and regulatory genomics for **sequence-to-function prediction**, and building data analysis pipelines
- **Enthusiastic** about applying skills in complex multi-omic data integration to solve fundamental problems in biology and therapeutic discover

Experience

University of Toronto, Timothy R. Hughes Lab

Toronto, Canada

POSTDOCTORAL ASSOCIATE

Oct. 2023–

- First or co-first author on 4 scientific papers and preprints, derived from independent work and large-scale international collaborations
- **First/co-first author publications:**
 1. Implemented a reproducible (**Git & GitHub**) **R, Python, & Linux cluster-based** computational and **statistical framework** for identifying evolutionarily conserved transcription factor binding sites in the **human genome** ([Preprint, submission in preparation](#))
 2. Revealed widespread binding of transcription factors in **ChIP-seq** data to **junk DNA** and the **dark genome** ([Preprint, submission in preparation](#))

Undergraduate Research Fellowships

Toronto & Hamilton, Canada

- **McMaster U, Schellhorn Lab** Developed proof-of-concept **nanopore** sequencing pipeline for in-field toxic algae bloom **metagenomics** *Sep. 2016–May 2018*
- **SickKids, Wilson Lab** Co-developed a clinical **RNA-seq** profiling computational workflow in **R** *Sep.–Dec. 2017*
- **SickKids, Weksberg Lab** Interpreted quantitative **DNA methylation** pattern variation in Autism Spectrum Disorder *Sep.–Aug. 2016*

Education

University of Toronto, Faculty of Medicine

Toronto, Canada

PH.D. MOLECULAR GENETICS

2018–23

- Deployed computational analyses of complex genomic sequence and annotation data. Explored, visualized and presented data, orally and in written form as manuscripts and grant-applications
- **First/co-first author publications:**
 1. Independently developed a **resource** of protein domain **Hidden Markov Models**, and a multi-omic data integration pipeline (in **AlphaFold** structure prediction, **Nextflow, Python**) to discover mobile DNA **origins of human genes** (*In preparation for publication*)
 - **Designed** and analyzed results from successful **NGS-based** validation experiments
 2. Co-developed novel analysis pipeline to interpret mobile DNA's role in **human genome regulation & evolution** ([Genetics 2022](#))
 3. Characterized evolution of under-characterized transcription factor family in living fossils, including analysis of public **RNA-seq** data ([Molecular Biology and Evolution 2021](#))
- **International conferences:** **1 invited speakership** (Central America) | **3 poster presentations** (Europe & North America)
- **Major Awards:** Ontario Graduate Scholarship: 2020–21 & 22–23 (**\$30,000**) | CIHR Master's Scholarship: 2018–19 (**\$17,000**)
- **Teaching Assistant (2020–22):** Communicated concepts in genetics and fielded questions from non-expert audience
- **Organizer (2023–)** of monthly regulatory genomics journal club

McMaster University, Department of Biology

Hamilton, Canada

B.Sc. (HONS) MOLECULAR BIOLOGY & GENETICS (SUMMA CUM LAUDE)

2013–18