

Danielle Denisko

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Education

- 2020–present** **PhD program in Bioinformatics and Integrative Genomics** – Harvard University
Project title: Non-canonical roles of transposable elements in human evolution and disease
Supervisor: Dr. Alice Eunjung Lee
- 2017–2019** **MSc in Medical Biophysics (Computational Biology)** – University of Toronto
Project title: Motif elucidation in ChIP-seq datasets with a knockout control
Supervisor: Dr. Michael M. Hoffman
- 2013–2017** **Honours BSc in Mathematical and Physical Sciences** – University of Toronto (Trinity College)
Specialist: **Biological Physics**
Minor: **Mathematics**
Cumulative GPA: 3.93/4.00

Publications

■ Journal and Preprints

Hwang SY*, Kim H*, **Denisko D***, Zhao B*, Lee D, Jeong J, Kim J, Park K, Choi HJ, Kim S, Lee EA, Ahn K. Human cytomegalovirus harnesses host L1 retrotransposon for efficient replication. Submitted.

Park J, Maury EA, Oh C, Shin D, **Denisko D**, Lee EA. Genomic data processing with GenomeFlow. Accepted to BMC Bioinformatics.

Denisko D*, Viner C*, Hoffman MM. Motif elucidation in ChIP-seq datasets with a knockout control. Bioinformatics Advances (2023). 10.1101/721720

Niu YN, Roberts EG, **Denisko D**, Hoffman MM. Assessing and assuring interoperability of a genomics file format. Bioinformatics (2022): 3327-3336. 10.1093/bioinformatics/btac327

GA4GH Consortium. GA4GH: international policies and standards for data sharing across genomic research and healthcare. Cell Genomics (2021): 100029. 10.1016/j.xgen.2021.100029

Denisko D, Hoffman MM. Classification and interaction in random forests. Proc Natl Acad Sci USA (2018): 1690-1692. 10.1073/pnas.1800256115

■ Conference proceedings

Singh J, **Denisko D**, Dias A. The “LABVIDEOTORY” – Online instructional videos enhance student learning of practical skills in the undergraduate science laboratory. EdMedia Conference Proceedings (2016): 1362-1367.

Awards and Honours

- 2018–2019** Ontario Graduate Scholarship
- 2018–2019** MBP Excellence OSOTF Scholarship (University of Toronto)
- 2018** SGS Conference Grant (University of Toronto)
- 2017–2018** NSERC Canada Graduate Scholarships-Master’s
- 2017–2018** The Princess Margaret Hospital Foundation Graduate Fellowships in Cancer

	Research OSOTF
2017–2018	Graduate and Life Sciences Education Merit Entrance Scholarship (University of Toronto)
2017	The Provost's Scholar Award (Trinity College)
2016–2017	Fraser-Crawford Scholarship (Trinity College)
2016–2017	George Luste Prize in Biological Physics (University of Toronto)
2016–2017	John Samuel and Louise Mary Buscombe Bursary (Trinity College)
2016	CIHR Institute of Genetics Undergraduate Summer Studentship Award
2016	University of Toronto Summer Studentship Award
2015–2016	St. Hilda's Chancellor's Scholarship (Trinity College)
2013–2014	University of Toronto Scholar

Research Experience

Mar. 2022 – present – **Lee Lab** – Boston Children's Hospital and Harvard Medical School, Boston, MA, USA
Graduate Research Student (Supervisor: Dr. Alice Eunjung Lee)

I am investigating the hypothesis that transposable elements shape human evolution and disease in a multitude of ways distinct from the canonical view that transposable elements act through insertions disrupting or introducing coding and cis-regulatory sequences. Such non-canonical mechanisms impacting the genome and transcriptome include: formation of RNA secondary structures that interact with splicing factors and alter splicing; generation of point mutations at non-insertion genomic sites by L1 proteins; and mediation of complex large-scale chromosomal rearrangements by L1 proteins driving genomic instability and cancer.

Nov. 2021 – Feb. 2022 – **Sherwood Lab** – Brigham and Women's Hospital and Harvard Medical School, Boston, MA, USA
Bioinformatics Rotation Student (Supervisor: Dr. Richard Sherwood)

I investigated the impact of genetic variation on cholesterol metabolism by using a model combining UK BioBank patient cholesterol datasets and large-scale CRISPR knockout screens measuring low-density lipoprotein cholesterol uptake. I explored improvements to this approach by expanding the feature set used in rare coding variant burden analyses and optimizing parameters used in functional gene clustering.

Jan. 2021 – June 2021 – **Aryee Lab** – Massachusetts General Hospital, Boston, MA, USA
Bioinformatics Rotation Student (Supervisor: Dr. Martin Aryee)

I sought to address limited population variation data from non-European/underrepresented populations in Phase I/II clinical trials of CRISPR-Cas9 therapy CTX001 to treat Sickle cell disease (SCD). I leveraged recently available large-scale data from individuals of African ancestry, including whole exome/genome sequencing data, from resources such as gnomAD to more comprehensively investigate potential sgRNA off-target binding of CTX001 within SCD's largest patient demographic.

May 2016 – Nov. 2020 – **Hoffman Lab** – Princess Margaret Cancer Research Centre, Toronto, Ontario, Canada
Medical Biophysics Research Student (Supervisor: Dr. Michael M. Hoffman)

I compared statistical methods of ChIP-seq processing to identify transcription factor binding motifs. I developed a tool in Python called *peaKO* that combines differential analysis pipelines of wild-type positive and knockout negative ChIP-seq datasets. This method improves or maintains optimal motif rankings in 5 out of 8 publicly available ChIP-seq datasets. Installation instructions can be accessed at <https://peako.hoffmanlab.org>. In my undergraduate thesis project, I extended this work by investigating the performance of machine learning classifiers trained on 3D DNA shape features of wild-type and knockout datasets for improved specificity in transcription factor binding site prediction.

Oct. 2017 – Lupien Lab – Princess Margaret Cancer Research Centre, Toronto, Ontario, Canada

Nov. 2017 *Medical Biophysics Rotation Student (Supervisor: Dr. Mathieu Lupien)*

I looked for the enrichment of variant sets associated with inflammatory diseases in gained and lost chromatin regions specific to select T-cell subpopulations using R. I also investigated the differences in cancer versus normal stemness profiles by comparing open chromatin regions found in brain and blood cancers via non-negative matrix factorization.

Sept. 2017 – BHK Lab – Princess Margaret Cancer Research Centre, Toronto, Ontario, Canada

Oct. 2017 *Medical Biophysics Rotation Student (Supervisor: Dr. Benjamin Haibe-Kains)*

I investigated tumour gene fusions in the context of drug response. Using two different pipelines, I discovered gene fusions in RNA-seq datasets from various Cancer Cell Line Encyclopedia (CCLE) cell lines. I compared gene fusions to those in The Cancer Genome Atlas (TCGA) and assessed drug sensitivities by calculating the area under drug-dose response curves in R.

Sept. 2014 – Laboratory courses – Department of Human Biology, University of Toronto, Toronto, Ontario, Canada

Sept. 2016 *Pedagogical Research Assistant (Supervisor: Dr. Alistair Dias)*

I developed three online learning modules for third-year undergraduate Human Biology Program laboratory classes, involving: animal cell culture propagation, DNA microarray, and microbiological Gram staining. For each module, I created storyboards and researched key molecular mechanisms to highlight through animation. I edited video footage in Adobe Premiere Pro and created animations in Adobe Flash.

May 2015 – Cardiovascular MRI research group – Sunnybrook Research Institute, Toronto, Ontario, Canada

Aug. 2015 *Medical Biophysics Undergraduate Summer Research Student (Supervisor: Dr. Mihaela Pop)*

I analyzed electrogram signal properties (including depolarization and repolarization times, and activation-recovery intervals) in preclinical pig models of chronic myocardial infarction. I derived 3D computer activation time maps using a CARTO mapping system and compared electrical properties of cardiac cells in normal and infarcted porcine hearts under various pacing conditions.

Presentations

■ Invited

“The landscape of inverted Alu repeats in the human genome and their evolutionary implications in RNA splicing.” CSHL Transposable Elements. Cold Spring Harbor, NY, USA. 13 October 2022. Presented by Alice Lee.

“Machine Learning in Bioinformatics.” Toronto Women’s Data Group (TWDG) meetup. Toronto, ON, Canada. 29 May 2018.

■ Conference, oral presentation

“The landscape of inverted Alu repeats in the human genome and their evolutionary implications in RNA splicing.” American Society of Human Genetics (ASHG) 2023 Annual Meeting. Washington, DC, USA. 4 November 2023.

“Motif elucidation in ChIP-seq datasets with a knockout control.” Canadian Undergraduate Computer Science Conference (CUCSC). Toronto, ON, Canada. 16 June 2017.

“Analysis of bipolar voltage maps and cardiac electrograms.” Canadian Undergraduate Physics Conference (CUPC). Peterborough, ON, Canada. 23 October 2015.

■ Conference, poster presentation

"Ranking transcription factor binding motifs in ChIP-seq data without p-values." American Society of Human Genetics (ASHG) 2019 Annual Meeting. Houston, TX, USA. 15 October 2019. Presented by Lei Sun.

"Motif elucidation in ChIP-seq datasets with a knockout control." Grad Cohort for Women 2019. Computing Research Association Women (CRA-W). Chicago, IL, USA. 12 April 2019.

"Motif elucidation in ChIP-seq datasets with a knockout control." CSHL The Biology of Genomes. Cold Spring Harbor, NY, USA. 9 May 2018.

"Analysis of activation-recovery intervals from intracardiac electrograms in normal and infarcted porcine hearts." Summer Student Poster Day. Department of Medical Biophysics. University of Toronto. Sunnybrook Research Institute, Toronto, ON, Canada. 20 August 2015.

- **Workshop**

"Introduction to Bash." MBP Tech Talks. Department of Medical Biophysics. University of Toronto. Princess Margaret Cancer Research Tower. Toronto, ON, Canada. 12 October 2018.

- **Symposium organizer**

Stellar Graveyard. 12th Annual Astronomy and Space Exploration Society (ASX) Symposium. University of Toronto, Toronto, ON, Canada. 23 January 2015.

Trainees supervised

May 2019 – Yinian (Jeffrey) Niu, BSc student in Computer Science, University of Toronto
Nov. 2019 *Project title:* Corner cases in popular bioinformatics software
Co-supervisor: Dr. Michael M. Hoffman

Teaching

Fall 2022 Teaching Fellow for **MCB112 Biological Data Analysis**, Harvard College
Course broadly covers gene expression analysis with RNA-seq. Topics include: kallisto, data visualization, probability, kmeans, edgeR, regression, EM, NMF, PCA, and t-SNE.
Instructor: Dr. Sean Eddy

Additional Work and Volunteer Experience

2019–2020 **Biomedical Data Scientist** – nference Canada
2018–2019 **Organizer** – Medical Biophysics Program Tech Talks (MBP Tech Talks)
2017–2019 **Video editor** – Medical Biophysics Program Podcast Committee (MBP Podcast)
2011–2017 **Co-founder and Mentor** – Scoliosis Support Group of Ottawa
2014–2015 **Outreach director** – Astronomy and Space Exploration Society (ASX)

Other

Programming and scripting languages: Python, R, Bash, MATLAB, LaTeX

Technologies and libraries: pandas, numpy, scikit-learn, Snakemake, seaborn, ggplot2, Git/Mercurial, Slurm/SGE, GCP, Circos

Operating systems: Linux (CentOS), MacOS, Windows

Languages: English (fluent), French (fluent), Mandarin (beginner)