

Danielle Denisko

Contact

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Lab address:

📍 Princess Margaret
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Canada

Quick Links

🔗 Google Scholar

🌐 LinkedIn

📄 GitHub Pages: dcdxy

📄 GitHub: dcdxy

Programming & Scripting Languages

♥ Python (3+ and 2.7)

R

Bash

HTML (CSS)

LaTeX

Technologies & Libraries

Version control:

Mercurial, Git (Bitbucket, Github)

Data analysis:

pandas

Visualization:

ggplot2, seaborn

Workflow:

Snakemake

Machine learning:

scikit-learn

Cluster scheduler:

Slurm, SGE

Bioinformatics:

BWA, MACS2, IDR, FastQC, MultiQC, MEME Suite, BEDTools, Intervene

Data:

ChIP-seq, ATAC-seq, Hi-C, JSON, XML

Languages

English (native)

French (native)

Mandarin (beginner)

Education

- 2017–now **MSc** in Medical Biophysics (Computational Biology)
Motif elucidation in ChIP-seq datasets with a knockout control University of Toronto
- 2013–2017 **HBS** in Biological Physics (specialist) and Mathematics (minor)
Cumulative GPA: 3.93 Trinity College, University of Toronto

Projects

- 2016–now **PeaKO** (MSc project) Hoffman Lab, University of Toronto
Developed method to rank motifs in wild-type/knockout paired ChIP-seq datasets
Technologies: Python, Snakemake, Bash, MACS2, MEME-ChIP, BEDTools, Slurm, Mercurial
PyPI package: <https://pypi.org/project/peako>
Source code: <https://github.com/hoffmangroup/peako>
Web page: <https://peako.hoffmanlab.org>
Manuscript: <https://doi.org/10.1101/721720>

Papers

- 2019 **Denisko D***, Viner C*, Hoffman MM. Motif elucidation in ChIP-seq datasets with a knockout control. *BioRxiv* (2019). [Preprint]. 10.1101/721720
- 2018 **Denisko D**, Hoffman MM. Classification and interaction in random forests. *Proc Natl Acad Sci USA* (2018): 1690-1692. 10.1073/pnas.1800256115
- 2016 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.

Research experience

- 2016–now **Hoffman Lab** (Research student) Princess Margaret Cancer Research Centre, Toronto, ON
Developed peaKO by comparing statistical methods of ChIP-seq processing; implemented machine learning techniques using Python’s scikit-learn library to predict transcription factor binding using DNA shape
- 2017 **Lupien Lab** (Rotation student) Princess Margaret Cancer Research Centre, Toronto, ON
Compared cancer versus normal stemness profiles by comparing open chromatin regions found in brain and blood cancers via non-negative matrix factorization
- 2017 **BHK Lab** (Rotation student) Princess Margaret Cancer Research Centre, Toronto, ON
Discovered tumour gene fusions in RNA-seq datasets from CCLE cell lines, compared to those in TCGA, and assessed drug sensitivities in R
- 2014–2016 **Laboratory courses** (Research assistant) Department of Human Biology, University of Toronto
Developed three online learning modules using Adobe Premiere Pro and Adobe Flash
- 2015 **Cardiovascular MRI group** (Summer student) Sunnybrook Research Institute, Toronto, ON
Analyzed electrogram signal properties in preclinical pig models of chronic myocardial infarction via CARTO mapping system

Awards and honours

NSERC Canada Graduate Scholarships-Master’s • Ontario Graduate Scholarship • The Princess Margaret Hospital Foundation Graduate Fellowships in Cancer Research OSOTF • MBP Excellence OSOTF scholarship • Graduate and Life Sciences Education Merit Entrance Scholarship • SGS Conference Grant • George Luste Prize in Biological Physics • CIHR Institute of Genetics Undergraduate Summer Studentship Award • University of Toronto Summer Studentship Award