

# Danielle Denisko

## Contact

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Canada

## Quick Links

👤 Danielle Denisko  
📧 Danielle Denisko  
🐙 GitHub: dcdxy

## Programming & Scripting Languages

♥ Python (3+ and 2.7)  
R  
Bash  
HTML (CSS)  
L<sup>A</sup>T<sub>E</sub>X

## 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

## 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:** (TBA shortly on bioRxiv)

## Papers

In prep. **Denisko D\***, Viner C\*, Hoffman MM. Motif elucidation in ChIP-seq datasets with a knockout control. Manuscript in preparation.

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 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