Philip Fradkin

Email : phil.fradkin@gmail.com
Website: philechka.com

EXPERIENCE

Vector Institute   MaRS, Toronto Canada
PhD with Brendan Frey & Bo Wang labs   *September 2020 - June 2025*

- Developed Orthrus, a deep learning model for RNA property prediction, trained on 50 million sequences using a contrastive learning objective.

- Applied biologically inspired RNA augmentations, enabling Orthrus to achieve 73% of the full-data performance with only 45 training samples, demonstrating effective performance in low data regime.

- Explored the functional diversity of RNA isoforms through Orthrus's learned representations, shedding light on isoform-specific roles and behaviors.

Valence Labs, Recursion   Montral, Canada
PhD Research Intern   *September 2023 - May 2024*

- Developed MolPhenix, a multi-modal molecular phenomics model that achieved 77.33% accuracy in zero-shot molecular retrieval, an 8.1 improvement over previous methods.

- Introduced soft-weighted sigmoid locked loss (S2L) to address inactive molecule perturbations, enhancing multi-modal learning between molecular structures and phenomic experiments.

- Demonstrated robust generalization across unseen molecular scaffolds and concentrations, improving in-silico screening efficiency.

Memorial Sloan Kettering   New York, USA
Morris Lab visiting student   *Februrary 2023 - August 2023*

- Designed self-supervised learning training procedures for effective mRNA representations to improve property and function prediction.

- Investigated effectiveness of deep learning mRNA half-life models for variant effect prediction.

Deep Genomics   MaRS, Toronto Canada
Computational Biologist   *May 2016 - August 2020*

- Proposed a strategy to increase RNA half-life by modifying polyadenylation sites with antisense oligonucleotides, later verified through wet-lab experiments.

- Automated antisense oligonucleotide design by developing integrated software systems, reducing labor-intensive, error-prone processes for both wet-lab and computational teams.

- Led model benchmarking and cutoff detection for missense variant prediction, culminating in a pipeline that integrated splicing and missense predictors to detect pathogenic variants.

EDUCATION

University of Toronto (Ph.D.) Toronto, ON, Canada
Computer Science, **Vector Institute**, Brendan Frey and Bo Wang labs *2020 – Present*

   Teaching Assistant:
- Neural Networks and Deep Learning (CSC2516)
- Introduction to Machine Intelligence (ECE324)

   Select Courses:
- Neural Networks Training Dynamics (CSC2541)
- Information Theory (ECE1502)
- Trustworthy Machine Learning (CSC2559)

University of Toronto (B.Sc.) Toronto, ON, Canada
Honors Bachelor of Science *2012 – 2017*

   Computer Science Major **Computational Biology** Major

SELECT PUBLICATIONS & PRESENTATIONS

- **Orthrus: Towards Evolutionary and Functional RNA Foundation Models**
  Philip Fradkin*, Ruian Shi*, Keren Isaev, Brendan Frey, Quaid Morris, Leo J. Lee, Bo Wang
  Under review at Nature Methods; MLCB Oral 2024; NeurIPS 2024 Workshop (AIDrugX) Spotlight

- **How Molecules Impact Cells: Unlocking Contrastive PhenoMolecular Retrieval**
  Philip Fradkin*, Puria Azadi*, Karush Suri, et al.
  NeurIPS 2024, Best paper at FM4Science Workshop 2024, arXiv:2409.08302

- **A Graph Neural Network Approach to Molecule Carcinogenicity Prediction**
  Philip Fradkin, Adamo Young, Lazar Atanackovic, Brendan Frey, Leo J. Lee, Bo Wang
  Bioinformatics, 38(Suppl_1): i84âĂŞi91, 2022; Oral at ISMB 2022

- **Robustness to Adversarial Gradients: A Glimpse Into Contrastive Loss Landscape**
  Philip Fradkin, Lazar Atanackovic, Michael R. Zhang
  Poster at ICML 2022 Pre-Training Workshop

- **ATP7B variant c.1934T > G p.Met645Arg causes Wilson disease by promoting exon 6 skipping**
  Daniele Merico, Carl Spickett, Matthew OâĂŹHara, Boyko Kakaradov, Amit G. Deshwar, **Philip Fradkin**, *et al.*, Brendan J. Frey
  NPJ Genomic Medicine, 5, 16 (2020)

SERVICE & GRANTS

- **Conference Reviewing:** NeurIPS (Main Track, LMRL, MetaLearn, AI4MAT Workshops), ICML (Main Track, CB Workshop), ICLR (Main Track, Nucleic Acids, GEM bio workshops)
- **Grants:** NSERC (Total: $120,000), OGS ($15,000), Vector Research Grant ($6,000 annually)

INTERESTS

Hackathon Founding member of Toronto bioinformatics hackathon - 2017.
Outdoor Adventures In my spare time I enjoy rock climbing outdoors, and hiking. I recently completed a 100km backpacking trip in Canadian Rockies.
Reading I'm big science fiction reader. My favorites include Solaris by Stanislaw Lem and I've recently really enjoyed Malazan Book of the Fallen series.