Philip Fradkin

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EXPERIENCE

Vector Institute — MaRS, Toronto CA
PhD with Brendan Frey & Bo Wang labs — *September 2020 - Present*

- To address the challenge of RNA property prediction, we developed Orthrus, a novel deep learning method method that extends contrastive learning techniques to genomic data, trained on 50 million RNA sequences.

- Utilizing biologically inspired RNA augmentations, Orthrus learns robust RNA isoform representations, particularly effective under low-data conditions, achieving 73% of full data performance with just 45 training data points.

- Studied properties of deep learning model optima, connecting model loss landscape flatness with the training procedure. This provides insight into a possible contributor to model generalization.

Valence Labs, Recursion — Montral, CA
PhD Research Student — *September 2023 - May 2024*

- Developed MolPhenix, a molecular phenomics model that achieved 77.33% accuracy in zero-shot molecular retrievalan 8.1 improvement over previous state-of-the-art methods.

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

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

- To overcome challenges in annotation and cell type out-of-distribution detection in single-cell RNA sequencing, developed an energy-based model, that enhanced annotation accuracy and introduced OOD detection.

- Design self-supervised learning training procedures for effective mRNA representations to improve molecular phenotype prediction.

- Investigated effectiveness of deep learning mRNA half-life models in predicting variant effects. Based on these results demonstrated a richer RNA representation results in learning generalizable signal.

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

- Developed deep neural networks to predict cellular biology phenotypes. Implemented a siamese neural network to predict the stability of RNA molecules from sequence surpassing the performance of state of the art.

- Developed software systems that support both wet-lab and computational scientists, such as automation of the design of antisense oligonucleotides - short stretches of modified RNA resulting in the automation of a laborious error-prone process.

- Coordinated the experimental validation of computational insights. Based on the results of these investigations, confirmed the regulatory function of polyadenylation on RNA half-life and robustness of in-silico predictions.

EDUCATION

University of Toronto (Ph.D.)   Toronto, ON, CA
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:
- Probabilistic Learning and Reasoning (CSC2506)
- Information Theory (ECE1502)
- Trustworthy Machine Learning (CSC2559)

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

    Computer Science Major **Computational Biology** Major

SELECT PUBLICATIONS & PRESENTATIONS

- **How Molecules Impact Cells: Unlocking Contrastive PhenoMolecular Retrieval.** :
  Philip Fradkin*, Puria Azadi*, Karush Suri, Frederik Wenkel, Ali Bashashati, Maciej Sypetkowski,
  Dominique Beaini; NeurIPS 2024, https://doi.org/10.48550/arXiv.2409.08302.

- **A Graph Neural Network Approach to Molecule Carcinogenicity Prediction**:
  Publication in Bioinformatics, Oral at ISMB (2022), and LMRL - NeurIPS workshop;
  Philip Fradkin, Adamo Young, Lazar Atanackovic, Brendan Frey, Leo J Lee, Bo Wang
  Bioinformatics, Volume 38, Issue Supplement_1, July 2022, Pages i84i91,
  https://doi.org/10.1093/bioinformatics/btac266 (2022)

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

- **ATP7B Variant p.Met645Arg Causes Wilson Disease by Promoting Exon 6 Skipping**:
  Publication in NPJ Genomic Medicine;
  Daniele Merico, Carl Spickett, Matthew OHara, Boyko Kakaradov, Amit G. Deshwar, ***Philip Fradkin***,
  Shreshth Gandhi, Jiexin Gao, Solomon Grant, Ken Kron, Frank W. Schmitges, Zvi Shalev, Mark Sun, Marta
  Verby, Matthew Cahill, James J. Dowling, Johan Fransson, Erno Wienholds, Brendan J. Frey
  npj Genom. Med. 5, 16. https://doi.org/10.1038/s41525-020-0123-6 (2020)

CONFERENCE REVIEWING DUTIES & GRANTS

NeurIPS: LMRL 2022, MetaLearn 2022, Main Track 2024, AI4MAT 2024
ICML: Computational Biology Workshop 2023, Pre-Training Workshop 2022
Python: Pytorch, DGL, Keras, Tensorflow
Julia: Zygote, Distributions.jl

INTERESTS

Hackathon Founding member of Toronto bioinformatics hackathon - 2017.
Wilderness orientation Wilderness outdoor orientation program leader.
Outdoor Adventures In my spare time I enjoy rock climbing outdoors, and hiking. I recently completed a
100km backpacking trip in Canadian Rockies.