Philip Fradkin

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EXPERIENCE

BlankBio (Y Combinator S25) San Francisco, USA
Co-Founder & Chief Scientific Officer *June 2025 – Present*

- Co-founded a precision medicine company building RNA foundation models on transcript-level biology for patient stratification and diagnostics.
- Closed seed round, secured pharmaceutical partnerships, and built a founding team of research scientists and ML engineers.
- Investigated RNA foundation model scaling laws across data volume and model size, scaling architectures to 1B parameters on a distributed GPU cluster.

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

- Developed Orthrus, a 10M-parameter contrastive learning model trained on 50M RNA sequences that outperforms much larger models by encoding evolutionary conservation rather than treating genomic sequences as generic text.
- Achieved 73% of full-data performance with only 45 training samples through biologically inspired RNA augmentations, demonstrating strong few-shot generalization.
- Characterized functional diversity of RNA isoforms through learned representations, identifying isoform-specific regulatory behaviors.

Valence Labs, Recursion Montreal, Canada
PhD Research Intern *September 2023 – May 2024*

- Built MolPhenix, a multi-modal model linking molecular structures to phenomic experiments, achieving 77.33% accuracy in zero-shot molecular retrieval—an 8.1 point improvement over prior methods.
- Introduced soft-weighted sigmoid locked loss (S2L) to handle inactive molecule perturbations, improving signal from sparse phenomic readouts.
- Maintained retrieval performance across held-out concentrations and entirely unseen datasets (58.60% recall), enabling zero-shot virtual phenomics screening without retraining.

Memorial Sloan Kettering New York, USA
Morris Lab Visiting Student *February 2023 – August 2023*

- Designed a contrastive learning framework for RNA using alternative splicing and gene duplication as biological augmentations, doubling Pearson correlation in low-data settings.
- Evaluated deep learning mRNA half-life models for variant effect prediction, identifying failure modes across mutation types.

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 building integrated software systems, replacing 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 integrating 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 – 2025*

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
  Nature Methods, 2026; 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

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 a big science fiction reader. My favorites include Solaris by Stanislaw Lem and I've recently really enjoyed Malazan Book of the Fallen series.