

TUAN PHAM

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SUMMARY

Computational Biologist & AI Model Developer PhD Candidate studying **Gene Regulatory Network (GRN)** inference using **single-cell multiomics (RNA + ATAC)**. Specialized in leveraging **Foundation Models** and **Neural Networks** to decode complex transcriptional regulation. Published in *Nature Neuroscience* and *ACS Synthetic Biology*

EDUCATION

Brown University - Data Science Institute

PhD Candidate in Computational Biology

Thesis: *Gene Regulation using Integrative Multimodal Modeling with Graph Neural Networks*

Providence, RI

expected May 2027

GPA: 4.00

University of Rochester

BS in Computational Biology - Honors in Research

Minor in Computer Science

Rochester, NY

May 2022

GPA: 3.97

TECHNICAL SKILLS

- **ML/AI & GenAI:** PyTorch, PyTorch-Geometrics, Transformers, Numpy, LLMs (Gemini/OpenAI), RAG, Agentic Workflows, LoRA, Optuna, Hugging Face, GNNExplainer, SHAP, CUDA
- **Tools & Databases:** Geneformer, scGPT, scFoundation, Loki, Nicheformer, Scanpy, SCENIC+, SCENIC, Seurat, LINGER, GRNBoost2, Git, Linux, Docker, SLURM, Upstash Vector, FastAPI/Node.js

RESEARCH EXPERIENCE

Brown University

Research Projects – Deep Learning & Single-Cell Genomics

Providence, RI

Sep 2022 - Present

- Co-developing **BindGPS**, a **Graph Neural Network model** that combines signals from **Micro-C and ChIP-Seq** to predict binding sites of dosage compensation complexes, with AUROC of over 0.88 and AUPR of 0.96. Deploying **Convolutional Neural Networks** to predict **TF perturbation** and applying **GNNExplainer** with **ablation techniques** to show the importance of 3D contacts and DNA sequences.
- Deployed **neural networks** and **optimal transport** to model gene regulation of different odor-associated learning environments from lab mice using scRNA-seq with over 95% accuracy; employed **SHAP, gene perturbation, and temporal ablation** to extract important genes for learning and memory. Findings predict candidate targets in PTSD-related circuits. Manuscript in prep.
- Developed **GRIDOT**, a graph neural network framework for **single-cell multi-omic gene regulatory inference**; integrated **temporal causality** and **optimal transport** to identify TF regulatory networks across diverse modalities, **outperforming** leading methods **by 20%**.
- Co-developed **DRIFT**, a robust graph diffusion-based smoothing method to leverage **single-cell foundation models** for **spatial transcriptomic data** with zero-shot learning; outperforming state-of-the-art specialized methods in cell type annotation (**+20%**), spatial alignment (**+30%**), and clustering performance (**+20%**). **LoRA finetuning** with **reconstruction loss** increases performance by **up to 10%**.
- **Integrated scRNA-seq and ATAC-seq** data to **predict key regulatory TFs** of synaptic genes during fruit fly development - predictions were **experimentally validated** (BioRxiv preprint).
- Inferred gene trajectories of 10,000 genes in the piriform cortex during mouse neuronal differentiation by developmental **trajectory modeling for scRNA-seq** (results published in **Nature Neuroscience**).
- **Mentored** four undergraduates for their independent projects, leading to **two conference posters** and **three manuscripts**. Mentees were accepted to **top graduate programs**, including Harvard, Yale, Johns Hopkins, and the Tri-Institutional Program.

PERSONAL PROJECTS

- **Full-Stack RAG Implementation:** Engineered a **Retrieval-Augmented Generation (RAG)** pipeline using Node.js and Google Gemini embeddings, utilizing Upstash Vector for serverless similarity search to provide context-aware interactions.

University of Rochester

Undergraduate Researcher – Structural Biology & Genomics

Rochester, NY

Jan 2020-May 2022

- Designed 200 **DNA and RNA secondary structures** *in silico* with additional synthetic base pairs with RNAstructure with implications in synthesizing vaccines or aptamers, leading to a **first-author** publication in **ACS Synthetic Biology**.
- Developed a new method leveraging **NGS data** and sequence similarity networks to validate repetitive DNA homology across divergent genomes, presented results at the GLAM EVON Conference.

LEADERSHIP/TEACHING EXPERIENCE

Harvard University

Research Mentor

Boston, MA

Summer 2025

- Partnered with Harvard OpenBio to deliver COVID-focused research training for promising high school students; awarded 2nd Prize, resulting in a pending publication.

Brown University

International Student Mentor

Providence, RI

2023 - Present

- Mentored over **60** international graduate students in accessing academic and community resources, promoting a smooth transition to campus life.

Rochester Alpha Phi Omega (National Co-ed Service Fraternity)

Vice President of Service

Rochester, NY

2020-2022

- Coordinated **1,200+ hours** of service for **60+ members** in partnership with **40+ Greater Rochester-based nonprofits**, including Habitat for Humanities, US Army Reserves, and Golisano Children's Hospital.
- Raised over **\$2,500** for local nonprofits, including Make-A-Wish and House of Mercy, driving increased donor participation and expanded community outreach.

AWARDS AND HONORS

- T32 NIH BiOCN Fellowship 2025-2027
- Phi Beta Kappa (inducted 2021)
- Dean's Scholarship Recipient 2018-2022
- Student Employee of the Year Nominee 2021
- Rigby Wile Prize Recipient 2019 (annual award for a first-year class that shows proficiency in Biology)
- First Prize in Biomedical Data Science Hackathon Fall 2020 and 2021 (Undergraduate Division)

PUBLICATION

- Zeppilli, Sara, Alonso O Gurrola, Pinar Demetci, David H Brann, **Tuan M Pham**, Robin Attey, Noga Zilkha, et al. 2025. "**Single-Cell Genomics of the Mouse Olfactory Cortex Reveals Contrasts with Neocortex and Ancestral Signatures of Cell Type Evolution.**" *Nature Neuroscience*, April <https://doi.org/10.1038/s41593-025-01924-3>.
- Colin Baker, **Tuan Pham**, Pinar Demetci, Quang Huy Tran, Ievgen Redko, Bjorn Sandstede, and Ritambhara Singh. 2025. "**SCOT+: A Comprehensive Software Suite for Single-Cell alignment Using Optimal Transport.**" May. <https://doi.org/10.1101/2025.05.21.655322>
- **Pham, Tuan M.**, Terrel Miffin, Hongying Sun, Kenneth K. Sharp, Xiaoyu Wang, Mingyi Zhu, Shuichi Hoshika, et al. 2023. "**DNA Structure Design Is Improved Using an Artificially Expanded Alphabet of Base Pairs Including Loop and Mismatch Thermodynamic Parameters.**" *ACS Synthetic Biology* 12 (9): 2750–63. <https://doi.org/10.1021/acssynbio.3c00358>.

PREPRINT

- Kentro, James A., Gunjan Singh, **Tuan M. Pham**, Justin Currie, Saniya Khullar, Audrey T. Medeiros, Maria Tsiarli, Erica Larschan, and Kate M. O'Connor-Giles. 2024. "**Conserved Transcription Factors Coordinate Synaptic Gene Expression through Repression,**" October. <https://doi.org/10.1101/2024.10.30.621128>.
- Atishay Jain*, **Tuan M. Pham***, David H. Laidlaw, Ying Ma, Ritambhara Singh. 2025 "**Diffusion-based Representation Integration for Foundation Models Improves Spatial Transcriptomics Analysis.**" October. <https://doi.org/10.1101/2025.11.20.689624>