Mihir Bafna

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EDUCATION

Massachusetts Institute of Technology Ph.D. in Computer Science (Incoming)

- Interested in generative modeling for structural biology and single cell genomics
- Awarded the NSF GRFP Fellowship

Georgia Institute of Technology

B.S. in Computer Science (Machine Learning & Theory)

- GPA: 4.0
- PURA Salary/Travel Awards and first author publication for research with Dr. Xiuwei Zhang
- Head TA for Graduate Deep Learning (CS 4644/7643)
- Undergraduate Research Ambassador

PUBLICATIONS/PATENTS

- DiffRNAFold: Generating RNA Tertiary Structures with Latent Space Diffusion <u>M. Bafna</u>, V. Keerthipati, S. Kanaparthi, R. Zhang. NeurIPS MLSB & DGM4H '23
- CLARIFY: Cell-cell interaction and gene regulatory network refinement from spatially resolved transcriptomics
 <u>M. Bafna</u>, H. Li, X. Zhang
 ISMB & Bioinformatics '23
- DeepViFi: detecting oncoviral infections in cancer genomes using transformers
 U. Rajkumar, S. Javadzadeh, <u>M. Bafna</u>, D. Wu, R. Yu, J. Shang, V. Bafna
 ACM-BCB '22
- Computer-implemented methods for quantitation of features of interest in whole slide imaging N. Nguyen , L. Mora-Blanco, K. Turner, J. Wiese, J. Christiansen, <u>M. Bafna</u>
 Provisional patent PCT/US2021/022308 '21

WORK / RESEARCH EXPERIENCE

Liquid Al

Machine Learning Scientist Summer Intern

• Incoming (starting June)

Bonnie Berger Lab | Massachusetts Institute of Technology

Research Assistant

- Working on diffusion models for genome structure (via scHi-C) and protein structure conformational change.
- Accepted into the Broad Summer Research Program (BSRP) starting June

Xiuwei Zhang Lab | Georgia Institute of Technology

Research Assistant

- Developed *Clarify*: a graph autoencoder based tool for refining extracellular AND intracellular interactions (cell-cell inference, gene regulatory network prediction, subnetwork comparison) with SubGraph Neural Networks and Spatial Transcriptomics data
 - * Paper accepted to ISMB
 - * Best Poster Award at AWSOM

Cambridge, MA Sep 2024 - present

Atlanta, GA Aug 2020 - Dec 2023

Boston, MA Jun 2024 – Sep 2024

Cambridge, MA May 2023 – Jan 2024

Atlanta, GA Nov 2021 – Dec 2023

Jian Ma Lab | Carnegie Mellon University

Research Assistant

- Hypergraph Graph Neural Network model architecture (hyperSAGNN) for understanding genetic interactions, specifically trigenic, and enrichment in protein complex formation
 - * Predicted 400,000 new trigenic interactions in yeast and bounded each prediction with model uncertainty using Gaussian Processes
 - * Using AlphaFold2 and ESMFold2 Protein Sequence Embeddings to guide model in predicting trigenic interactions that are enriched in protein complex formation.
 - * $\ensuremath{\text{Preparing journal submission}}$ for a forementioned work

Boundless Bio Inc

ML/Bioinformatics Research Intern

- San Diego, CA Aug 2020 – Dec 2021
- **Provisional patent** for creating metaDetect: a computer vision algorithm for identifying metaphase spreads in stained whole slide images of cancer cells using image analysis filtering/techniques.
- Created automated pipeline for whole slide imaging \rightarrow metaDetect (CV) \rightarrow ecDNA quantification (CNN)

Awards/Honors

NSF GRFP Fellowship (Graduate Research Fellowship Award)	April 2023
Georgia Tech Faculty Honors (4.0 GPA)	Awarded Every Semester
Atlanta Workshop for Single-cell Omics (AWSOM) Best Poster Award	April 2023
Broad Summer Research Program (BSRP) Accepted	March 2023
Harvard Summer Institute for Biomedical Informatics (SBMI) Accepted	March 2023
CS 7643 Best Project Award First Place Winner	Dec 2022
Georgia Tech PURA Presidential Undergraduate Research Award (\$1500 Stipend)	May 2022
Georgia Tech PURA PURA Travel Award (\$1000)	June 2023
HealthTech Hacks @ GT First Place Winner	March 2021
Grand Challenges @ GT First Place Winner for best project idea	May 2021
Westview HS Honors Top Math Student in HS Graduating Class (600)	June 2020
Westview HS Honor Chain Top 3% GPA in HS Graduating Class (600)	June 2020

TALKS

- ISMB Oral CLARIFY: Cell-cell interaction and gene regulatory network refinement from spatially resolved transcriptomics. July 2023.
- Zhang Lab Group Meeting Overview of Generative Modeling (VAEs, Diffusion, Energy Based Models, Score Based Generative Modeling). Dec 2023.
- **GT Single Cell Genomics Journal Club** How can we learn from spatial transcriptomics data? (SPICEMIX, COMMOT methodology overview). March 2023.

POSTERS/PRESENTATIONS

- Mihir Bafna, Hechen II, Xiuwei Zhang. CLARIFY: Cell-cell interaction and gene regulatory network refinement from spatially resolved transcriptomics. *Single Cell Analyses Conference at Cold Spring Harbor Laboratory* (2023).
- Mihir Bafna, Ruochi Zhang, Bonnie Berger. Daifuku: Elucidating 3D Genome Structure via Diffusion-based scHi-C contact map imputation. Broad Summer Research Program Final Symposium (2023).
- Mihir Bafna, Vikranth Keerthipati, Subhash Kanaparthi. DiffRNAFold: Generating RNA Structures & Conformations with Latent Space Diffusion. Intelligent Systems for Molecular Biology (ISMB 2023). PURA Travel Award.
- Mihir Bafna, Hechen Ii, Xiuwei Zhang. CLARIFY: Cell-cell interaction and gene regulatory network refinement from spatially resolved transcriptomics. *Atlanta Workshop for Single-cell Omics (AWSOM 2023)*. Best Poster Award.
- Mihir Bafna, Vikranth Keerthipati, Subhash Kanaparthi. DiffRNAFold: Generating RNA Structures & Conformations with Latent Space Diffusion. Deep Learning (CS 7643) Final Project Symposium & Poster Presentation. Best Overall Project & Poster (1st out of 200).
- Mihir Bafna, Xiuwei Zhang. Benchmarking and Refining Cell-Cell Interactions with Spatial Transcriptomics and Graph Neural Networks. St. Jude's National Symposium for Undergraduate Research (NSUR 2022). Poster Presentation (52/352 selected).