# Pranav Mahableshwarkar

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## Deep Learning and Computational Genomics Research

**Pipeline for Contrastive Modality Evaluation** *(under review, JAMIA, arXiv)* Singh Lab at Brown

- Developed a scalable multi-modal contrastive learning framework for health data (MIMIC-IV/CXR).
- Evaluated all 26 modality combinations, scoring individual modality contributions in contrastive learning.
- Leveraged scores as a prior for SOTA integration of modalities in downstream fine-tuning contexts.

**Subspace Relaxation Operator for Protein Folding** *(paper in prep & Honor's Thesis)* Istrail Lab at Brown

- Used molecular dynamics to generate a 1TB dataset linking AlphaFold embeddings to improved structural outputs.
- Trained an attention-based model to apply physical transformations within the embedding space.
- Optimized training for GPU memory constraints, sharding the data/model with DDP and accumulating batches.
- Transformed structures yield context-specific (i.e. pH) structural changes and lower energy conformations.
- Collaborating with structural biologists to to experimentally validate solvent-specific structural predictions.

**BindGPS: Investigating 3D Chromatin Formation** Singh/Larschan Labs at Brown

- Designed a multiomic dataset merging 3D Micro-C data, ChIP-seq signals, and sequence information.
- Built an interpretable GNN and LoRA fine-tuned LLM for dosage compensation related classification tasks.
- Mentoring two graduate and undergraduate students.

**DNABERT-Enhancer** (*GitHub*) Ovcharenko Group at NIH

- Interpretable transformer model for robust classification (AUROC > 90%) of poised and active enhancer regions.
- Attention landscapes reveal class-specific motifs/functional enrichments along with a novel class of enhancers.

**BindCompare** *(published in Bioinformatics)* Larschan Lab at Brown

- Developed a *PyPI package* to identify locations where gene regulation and RNA processing are coupled.
- Back-end applies interval trees to rapidly select/analyze candidate co-regulators from thousands of sites.
- Working with wet lab scientists to validate candidates in-vivo using SPRITE-IP experiments.

## Experience

**Software Engineering Intern** | insitro 2024

- Developed a literature-review RAG chatbot indexing 36 million papers on PubMed; used by over 30 researchers.
- Used AWS and Python software to tightly integrate protein interactor data into ML target discovery workflows.

**Post-Bac/Undergrad ML Researcher** | Brown University 2022 - Present

- Conducting novel research in deep learning and computational biology.
- Collaborated with multiple graduate students and labs; oral and poster presentations at international conferences.

**Deep Learning Intern** | National Institutes of Health 2023

- Investigated regulatory genomics mechanisms in the Ovcharenko group using various deep learning approaches.
- Parallelized GPU infrastructure on NIH's HPC systems to decrease training time by 4X.

**Teaching and Course Development** | Brown University Computer Science & Biology 2022 – 2025

- *Deep Learning Head TA*: Led a team of 33 TAs to develop and run CS1470 for 350+ undergraduates/graduates.
- Developing a new Machine Learning in Health and Biology course with Professor Ritambhara Singh.
- *Undergraduate TA*: Advanced Algorithms in Computational Biology and Medical Informatics, Computational Molecular Biology, Fundamentals of Computer Systems, Genetics.

## Education

**Brown University** Providence, RI

*BS* in Computer Science, *BA* in Applied Math; GPA: 4.0 *2021 - 2025*

## Skills and Awards

**Languages:** Python, C/C++, Bash, SLURM, CUDA, Docker, SQL, R

**Frameworks/Libraries:** PyTorch, Pandas, Numpy, Matplotlib, Git, OpenMM, AWS, AlphaFold, RAG, Windsurf

**Awards:** Computer Science Senior Prize, Sigma Xi Inductee, 2x Undergraduate Teaching & Research Award Recipient