Aradhana

aradhana2515@gmail.com · github.com/aradhana2515 · Google Scholar · LinkedIn

EDUCATION

Ph.D. Biomedical Engineering, Duke University — *Aug 2024 – present*

M.S. Applied Cognition and Neuroscience, University of Texas at Dallas — *May 2018*

M.S. Biological Sciences, Birla Institute of Technology and Science, Pilani, India — *May 2015*

B.E. Chemical Engineering, Birla Institute of Technology and Science, Pilani, India — *May 2015*

SELECTED COMPUTATIONAL PROJECTS

Independent projects built to develop hands-on skills in ML-guided protein engineering and computational biology.

NeuroStruct github.com/aradhana2515/neurostruct

End-to-end ML pipeline for structure-aware binding affinity prediction at GABA-A and NMDA receptor subunit interfaces. Integrates ESM-2 per-residue embeddings, ESMFold-derived contact maps, and MD-derived RMSF flexibility features into a Graph Attention Network (GAT). Adding dynamics features improved Pearson r from 0.71 to 0.79 and RMSE from 1.18 to 0.98 kcal/mol over a structure-only baseline. Includes Gradio demo for real-time inference.

Python · PyTorch · ESM-2 · Graph Attention Networks · OpenMM · BindingDB · PyMOL

Specificity-Driven Active Learning for Antibody Optimization
github.com/aradhana2515/specificity-driven-active-learning

Closed-loop active learning framework that explicitly models assay physics (expression-confounded fluorescence, FACS gating), implements multi-objective acquisition with epistemic uncertainty, and demonstrates monotonic hypervolume expansion of the antibody specificity Pareto frontier across iterative rounds.

Python · scikit-learn · bootstrap ensemble regression · multi-objective optimization

Thinking in Biological Systems github.com/aradhana2515/thinking-in-biological-systems

Lightweight installable Python toolkit for simulating and classifying dynamical regimes in biological ODE models (bistability, oscillations, bifurcations). Implements custom RK4 integrator, automated regime classification, and parameter sweep heatmaps.

Python · NumPy · ODE simulation · installable package with CI

scRNA-seq Analysis: CD4 T Cell Precursors github.com/aradhana2515/scRNA-cd4-precursors

Reproducible Scanpy pipeline for identifying CD4+ transitional activation states and precursor manifolds in human immune tissue. Implements QC filtering, HVG selection, Leiden clustering, UMAP embedding, and diffusion pseudotime (DPT) to resolve a continuous naïve → transitional → effector trajectory. Designed for direct application to TIL exhaustion and autoimmune cohort datasets.

Python · Scanpy · UMAP · diffusion pseudotime · single-cell RNA-seq

Protein Engineering Web App reasonable-remarkable-jay.anvil.app *(coursework: Mathematical Modeling of Molecular Systems. Aradhana, Shruthi Subramani and Dr. Michael Lynch)*

Interactive web app for early-stage antibody specificity screening: embeds antibody and antigen sequences using ESM-2, applies nonlinear SVM on 640-dim embeddings (AUC 0.975) to rank off-target candidates across a 168-protein surfaceome panel, and cross-validates hits with AlphaFold ipTM/pTM scores. Built to identify poor specificity candidates early in the therapeutic development pipeline.

Python · ESM-2 · AlphaFold · SVM · cosine similarity · surfaceome screening

PROFESSIONAL EXPERIENCE

Graduate Research Assistant at Duke University (PI: Dr. Emma Chory) *Aug 2024 – present*

Elucidating Mechanisms of Counterselection in Immune Specificity Using Phage based Directed Protein Evolution on High-throughput Automated Robotics Platform

- Engineered IgG Fc protein sequences capable of folding and retaining binding functionality in the reducing cytosol of E. coli, overcoming a major barrier to intracellular antibody-domain engineering.
- Designed ML-guided protein interaction circuits integrating IgG Fc and Protein A/G variants, using data-driven feature selection to inform sequence choice, domain orientation, and promoter architecture prior to experimental validation.
- Built and deployed multi-component binding circuits on an automated liquid-handling turbidostat platform (Hamilton) to enable continuous, real-time quantitative measurement of binding dynamics.
- Validated protein expression, folding, and interaction specificity using Western blotting and co-immunoprecipitation assays.
- Developed stochastic and kinetic models (Monte Carlo and Gillespie simulations) to quantitatively explain time-resolved luminescence and growth dynamics across inducer regimes.
- Designing a 96-well PACE architecture where each well operates as an independent evolution lagoon on an automated robotic platform, enabling phage pIII+ positive selection and pIII- counterselection to run simultaneously at scale.
- Established a scalable, automatable intracellular counterselection framework integrating ML-guided design, protein folding constraints, binding competition, and evolutionary pressure.

Life Science Research Professional at Stanford University (PI: Dr. Michael Bassik) *Aug 2018 – Jul 2024*

Optimizing CRISPR-Cas12a system for scalable, multiplexed manipulation of human transcription

- Led an independent project to engineer optimized Cas12a vectors for highly efficient transcriptional repression and activation.
- Designed and executed a high-throughput Cas12a guide array screen to identify design rules governing combinatorial guide efficiency.
- Developed custom Python pipelines to analyze positional, combinatorial, and additive effects on guide RNA performance.
- Presented findings at CSHL Genome Engineering Conference (2023) and Stanford Genetics Retreat (2022, 2023).

High-throughput discovery and characterization of human transcriptional effectors

- Conducted large-scale recruitment screens (>100,000 effector fragments) fused to DNA-binding domains or dCas9, measuring activity using dual reporter systems.
- Optimized magnetic separation workflows to isolate ON/OFF reporter populations for downstream analysis.
- Processed samples for Illumina sequencing and identified functional domains using casTLE analysis.
- Validated individual candidates across genomic, cell-type, and DNA-binding contexts, enabling discovery of hundreds of novel activator and repressor domains.

Optimizing prime editing systems

- Evaluated several modifications of Prime Editor designs to optimize for editing efficiency.
- Characterized the most effective guide RNA designs using high-throughput screens to develop an effective prime editing system.

Identification of drug-resistant EGFR mutations using CRISPR-mediated mutagenesis (collaboration with Boehringer Ingelheim)

- Used various in vitro models to determine the efficacy of different EGFR inhibitors found in clinical trials.
- Used CRISPR-X to create a library of EGFR variants in Baf3 and PC9 cell lines; identified novel EGFR mutations contributing to drug resistance and cancer relapse.

Mitigating off-target toxicity in non-coding CRISPR screens

- Investigated growth effects of perturbing CTCF motifs near essential genes using targeted sgRNA libraries.
- Quantified growth phenotypes and transcriptional consequences of high-specificity sgRNAs.

- Generated and genotyped on-target indels in K562 cell lines.

Research Assistant at UT Dallas (PI: Dr. Jonathan Ploski) *Sep 2016 – Jun 2018*

Creating spatially and temporally inducible viral-mediated CRISPR/Cas9 system

- Developed SaCas9-compatible Cre recombinase-inducible and doxycycline-dependent AAV vectors to target the CREB gene in vivo and EMX1 gene in vitro.
- Transfected viral vectors into mammalian cells for in vitro genome editing; packaged and purified viruses for in vivo genome editing.
- Isolated genomic DNA; validated gene editing via surveyor assay achieving efficiency of 45% (SaCas9), 39% (Cre-lox), and 49% (dox-dependent) for EMX1 in vitro.
- Confirmed viral expression in vivo and in vitro by IHC and ICC respectively.

Research Assistant at InStem, NCBS, India (PI: Dr. Ravi Muddashetty) *Jun 2014 – Jun 2016*

- Investigated the role of FMRP in neural differentiation in stem cell models.
- Co-localization study of Ago2 and FMRP in cultured neurons.

Summer Intern at Grasim Industries, India *May 2012 – Jul 2012*

- Worked on increasing efficiency of biological reactors in effluent treatment plants.

PUBLICATIONS (* INDICATES EQUAL CONTRIBUTION)

1. **Aradhana***, Liu, K.*, Jain, N., Tycko, J., Yao, D., and Bassik, M. Optimizing the CRISPR-dCas12a system for scalable high-order multiplexed perturbation. (Manuscript in preparation)
2. Schwartz CI, Abell NS, Li A, **Aradhana**, Tycko J, Truong A, Montgomery SB, Hess GT. Toward optimizing diversifying base editors for high-throughput mutational scanning studies. Nucleic Acids Res. 2025 Jun 20;53(12):gkaf620. doi: 10.1093/nar/gkaf620. PMID: 40613705; PMCID: PMC12231578.
3. Tycko J*, Van MV*, **Aradhana**, DelRosso N, Ye H, Yao D, Valbuena R, Vaughan-Jackson A, Xu X, Ludwig C, Spees K, Liu K, Gu M, Khare V, Mukund AX, Suzuki PH, Arana S, Zhang C, Du PP, Ornstein TS, Hess GT, Kamber RA, Qi LS, Khalil AS, Bintu L, Bassik MC. Development of compact transcriptional effectors using high-throughput measurements in diverse contexts. Nature Biotechnology. 2024 Nov 1. doi: 10.1038/s41587-024-02442-6. PMID: 39487265.
4. Valbuena R, Nigam A, Tycko J, Suzuki P, Spees K, **Aradhana**, Arana S, Du P, Patel RA, Bintu L, Kundaje A, Bassik MC. Prediction and design of transcriptional repressor domains with large-scale mutational scans and deep learning. bioRxiv [Preprint]. 2024 Sep 24:2024.09.21.614253. doi: 10.1101/2024.09.21.614253. PMID: 39386603; PMCID: PMC11463546.
5. IGVF Consortium. Deciphering the impact of genomic variation on function. Nature. 2024 Sep;633(8028):47-57. doi: 10.1038/s41586-024-07510-0. Epub 2024 Sep 4. PMID: 39232149; PMCID: PMC11973978.
6. DelRosso, N., Tycko, J., Suzuki, P., Andrews C., **Aradhana**, Mukund A., Liongson I., Ludwig C., Spees K., Fordyce P., Bassik MC., Bintu L. (2023) Large-scale mapping and mutagenesis of human transcriptional effector domains. Nature. 616, 365–372. https://doi.org/10.1038/s41586-023-05906-y
7. Tycko, J., DelRosso, N., Hess, G.T., **Aradhana**, Banerjee, A., Mukund, A., Van, M.V., Ego, B.K., Yao, D., Spees, K., Suzuki, P., Marinov, G.K., Kundaje, A., Bassik, M.C., & Bintu, L. (2020). High-throughput discovery and characterization of human transcriptional effectors. Cell. 183, 7, 2020–2035. https://doi.org/10.1101/2020.09.09.288324
8. Ferraro, N.M., Strober, B.J., Einson, J., Abell, N.S., …**Aradhana**, …Lappalainen, T., Mohammadi, P., Montgomery, S.B. & Battle, A. (2020). Transcriptomic signatures across human tissues identify functional rare genetic variation. Science, 369(6509), eaaz5900. https://doi.org/10.1126/science.aaz5900
9. Tycko, J.*, Wainberg, M.*, Marinov, G.K.*, Ursu, O., Hess, G.T., Ego, B.K., **Aradhana**, …Snyder, M.P., Bintu, L., Greenleaf, W.J., Kundaje, A., & Bassik, M.C. (2019). Mitigation of off-target toxicity in CRISPR-Cas9 screens for essential noncoding elements. Nature Communications. 10: 4063. https://doi.org/10.1038/s41467-019-11955-7
10. Kumar, N., Stanford, W., de Solis, C., **Aradhana**, Abraham, N.D., Dao, T.-M.J., Thaseen, S., Sairavi, A., Gonzalez, C.U., & Ploski, J.E. (2018). The development of an AAV-Based CRISPR SaCas9 genome editing system that can be delivered to neurons in vivo and regulated via doxycycline and cre-recombinase. Frontiers in Molecular Neuroscience. 11, 1. https://doi.org/10.3389/fnmol.2018.00413

POSTER ABSTRACTS AND PRESENTATIONS

1. Biomedical Engineering Society Conference (BMES), San Diego, CA. 2025. Poster Presentation. **Aradhana**, Boileau, R., Golas, S., Jia, M., Ma, Q. and Chory, E. Understanding immune counterselection through robotics-assisted phage-mediated directed evolution.
2. Cold Spring Harbor Laboratory (CSHL) Genome Engineering: CRISPR Frontiers Conference, Cold Spring Harbor, NY. 2023. Poster Presentation. **Aradhana***, Liu, K.*, Jain, N., Tycko, J., Yao, D., and Bassik, M. Optimizing the CRISPR-dCas12a system for scalable high-order multiplexed perturbation.
3. Stanford Genetics Retreat, Monterey, CA. 2023. Poster Presentation. **Aradhana***, Liu, K.*, Jain, N., Tycko, J., Yao, D., and Bassik, M. Optimizing the CRISPR-dCas12a system for scalable high-order multiplexed perturbation.
4. The Impact of Genomic Variation Function (IGVF), Stanford, 2023. Oral Presentation. Optimizing Prime Editing systems.
5. Stanford Genetics Retreat, Monterey, CA. 2022. Poster Presentation. **Aradhana***, Liu, K.*, Jain, N., Tycko, J., Yao, D., and Bassik, M. Optimizing the CRISPR-dCas12a system for scalable high-order multiplexed perturbation.
6. National Centre For Biological Sciences Annual Talks, Bangalore, India. 2016. Poster Presentation. Rathod, R., **Aradhana** and Muddashetty, R. Understanding the role of FMRP in neural differentiation in stem cell models.

PROFESSIONAL SKILLS

Computational & Data Analysis

Python; PyTorch; scikit-learn; graph neural networks and graph attention networks (GAT); protein language models (ESM-2, ESMFold); AlphaFold; active learning and multi-objective Bayesian optimization; Pareto frontier methods; kinetic modeling and stochastic simulations (Monte Carlo, Gillespie); machine learning for biological data including dimensionality reduction, classification, clustering, model benchmarking, and interpretable methods; single-cell RNA-seq analysis (Scanpy, UMAP, diffusion pseudotime); next-generation Illumina sequencing and bioinformatic analysis; PyMOL; scientific figure design (Adobe Illustrator)

Experimental

High-throughput functional genomics screening and sample processing; fusion protein design and expression optimization in E. coli; directed evolution and protein–protein interaction assays; structure-guided protein design and molecular docking; automated liquid handling and continuous culture systems (turbidostat, Hamilton); CRISPR-based genome engineering (CRISPRi/a, Cas9, Cas12a, prime and base editing, HDR); AAV and lentiviral production and transduction; flow cytometry, ELISA, Western blotting, co-immunoprecipitation; mammalian cell culture; microscopy

Selected Graduate Coursework:

Structural Biochemistry · Protein Structure-Function Modeling · Mathematical Modeling of Molecular Systems · Gene Circuits · Biology by Design · Automation and High-Throughput Biology · Science Law and Policy · Business of Science

Arts & Performance:

Bharatanatyam dancer (Arangetram, 2008); classical violinist (20 years)

Current Extracurriculars:

- Sponsorships Director, Nucleate RTP
- Sponsorships Liaison, ComSciCon RTP
- Member, ACS BIOT RTP