

Neha Rao

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Profile

Computational biologist with an M.S. in Bioinformatics (Boston University) and 4+ years of hands-on experience building machine learning pipelines for large-scale multi-omics data. Developed and applied ML models (XGBoost, PyTorch) at the NCI, Boston University and Walter Reed Army Institute of Research; analyzing single-cell RNA-seq, ATAC-seq, spatial transcriptomics, and multi-modal perturbation datasets. Published in *European Neuropsychopharmacology*.

Technical Skills

- ▷ **ML / Deep Learning:** PyTorch, XGBoost, scikit-learn
- ▷ **Single-Cell & Omics:** Seurat, Scanpy, ArchR, MACS2, Bowtie2, SAMtools; scRNA-seq, ATAC-seq, CUT&RUN, spatial transcriptomics
- ▷ **Languages & HPC:** Python, R, SQL, Bash/Snakemake; Slurm HPC workflows
- ▷ **Bioinformatics Toolkits:** RELION, BWA, HOMER, EthoVision, FIJI/ImageJ, RShiny; cryoET analysis
- ▷ **Reproducible Research:** Snakemake pipelines, Git, manuscript & grant preparation

Research & Professional Experience

Data Analyst / AEOP Fellow

Feb 2025 – Sep 2025

[Walter Reed Army Institute of Research](#)

Washington, DC–Baltimore Area

- ▷ Orchestrated end-to-end multi-omics workflows (transcriptomics, metabolomics, lipidomics, microbiome) for traumatic brain injury (TBI) research.
- ▷ Integrated multi-modal patient blood biomarkers with matched controls in a clinical infection-healing study, enabling early prediction of non-union and infection trajectories across a longitudinal cohort.
- ▷ Led GI injury investigations harmonizing 4 omics layers, characterizing systemic molecular adaptations and delivering analysis-ready datasets for downstream statistical modeling.
- ▷ Performed behavioral neuroscience data analysis (EthoVision barrier assays) to quantify PTSD-like phenotypes, translating raw sensor outputs into interpretable biological signals.

Image Analysis Intern

Oct 2024 – Dec 2024

[Carnegie Mellon University](#)

Remote

- ▷ Applied PyTorch-based AI/ML models to analyze cryo-electron tomography (cryoET) images for drug discovery, gaining direct experience with HPC-deep learning workflows.
- ▷ Co-authored sections of grant proposals; identifying funding objectives, designing project plans, and aligning computational deliverables with sponsor requirements.

Cancer Research Intern (CRI-SP Fellow)

May 2024 – Aug 2024

[National Cancer Institute \(NCI/NIH\)](#)

Bethesda, MD

- ▷ Built and validated an XGBoost classifier on TCGA/ICGC transcriptomic data to identify KRAS^{G12D} transcriptional phenocopies. The model achieved discriminative performance across multi-thousand-sample cohorts and was **presented at the 2024 NIH Summer Poster Day**.
- ▷ Extended the phenocopy model to single-cell resolution: evaluated its ability to identify KRAS^{G12D}-mutant cells within non-malignant single-cell datasets, directly applying scRNA-seq analysis skills.

Database Development Intern

Jan 2024 – May 2024

[Boston University](#)

Greater Boston

- ▷ Architected and deployed **cEpiReg**, a production multi-omics database integrating bulk/single-cell ATAC-seq, RNA-seq, and ChIP-seq for Alzheimer's disease across multiple cell types and disease states (Seurat, ArchR, Scanpy).
- ▷ Engineered a cell type-specific TF-CRE-gene regulatory network framework by integrating epigenomic and transcriptional profiles, generating the data infrastructure underlying **two peer-reviewed publications**.
- ▷ Developed full-stack API services and RShiny dashboards (SQL, JavaScript, AJAX) allowing research collaborators to query multidimensional regulatory genomics layers without direct database access.

Education

Master of Science, Bioinformatics

Boston, MA

[Boston University](#)

Bachelor of Science with Honors, Biotechnology

Bangalore, India

[M.S. Ramaiah University of Applied Sciences](#)