Urmeshree Magesh

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EDUCATION

Northeastern University — Boston, MA
Master of Science in Bioinformatics; GPA: 3.78 — *Sep. 2023 – Dec 2025*
Coursework: Concentration - Data Analytics

Rajalakshmi Engineering College — Chennai, India
Bachelor of Technology in Biotechnology; GPA: 3.66 (9.15/10.0) — *Aug. 2019 – May. 2023*

TECHNICAL SKILLS

Programming Languages: R, Python, SQL, SAS, C
Data Types: Bulk RNA-seq, single-cell/snRNA-seq, spatial transcriptomics (CosMx NSCLC), NGS, clinical/EHR data
Bioinformatics Frameworks: Seurat, DESeq2, hdWGCNA, NicheNet, IPA, MAGMA, BLAST, AlphaFold2
Statistical & Visualization Tools: Tableau, Power BI, R Shiny, ggplot2, Matplotlib
Databases & Genome Resources: NCBI, Ensembl, UCSC Genome Browser, Entrez, Snowflake, SQL Server
Software & Developer Tools: Git, Snakemake, Docker, Jupyter Notebook, Nextflow, PyCharm
Wet-lab Techniques: PCR, agarose gel electrophoresis, basic cloning, cell culture

EXPERIENCE

Neurology Bioinformatics Research Intern — May 2025 – Present
Brigham & Women's Hospital/Harvard Medical School, Butovsky Lab — *Boston, MA*
- Performed bulk RNA-seq differential expression analysis to identify disease-associated genes and analyzed snRNA-seq/scRNA-seq datasets to characterize cell-type-specific transcriptional changes in Alzheimer's disease.
- Applied Seurat preprocessing workflows to generate quality-controlled objects, followed by clustering and UMAP-based dimensional reduction to visualize astrocyte and microglia transcriptional patterns.
- Developed trajectory inference approaches to characterize astrocyte and microglia state transitions, highlighting regulatory genes implicated in AD progression.
- Built integrative pipelines incorporating hdWGCNA, NicheNet, and Ingenuity Pathway Analysis (IPA) to uncover co-expression modules, signaling interactions, and enriched pathways.
- Applied NicheNet to analyze ligand–receptor interactions in human datasets and compared findings with mouse objects from MDI datasets to validate cross-species signaling relationships.
- Analyzed spatial RNA-seq datasets to evaluate molecular and cellular biomarkers, collaborating with neuroscientists to contextualize findings within neurodegenerative disease mechanisms.

Data Analytics Intern — Healthcare Technology — May 2024 – Aug 2024
Agastha Inc — *Charlotte, NC, USA*
- Integrated clinical into EHRs and developed predictive models (Python) to forecast patient trends.
- Built interactive Tableau and Power BI dashboards for hospital departments to data-driven decision-making.
- Ensured HIPAA compliance by securing patient data pipelines with AWS cloud storage and SQL backends.

Computational Biology Intern — Jan 2023 – Apr 2023
Tamil Nadu Veterinary and Animal Sciences University (TANUVAS) — *Chennai, India*
- Virtually screened ∼400,000 Coconut Database compounds to identify CDK4 inhibitors.
- Performed docking, ADMET, toxicity checks, and molecular dynamics to assess stability (LibDock 103.9).
- Built pipelines for statistical evaluation and visualization of oncology compound screening.

PROJECTS

Cellular Neighborhoods in Non–Small Cell Lung Cancer | *R, CosMx, Spatial Analysis* — Apr 2025 – Jul 2025
- Built a version-controlled workflow for CosMx NSCLC spatial data (QC, clustering, cell-state annotation).
- Mapped tumor, immune, and stromal neighborhoods to microenvironmental hetrogeneity and invasion patterns.

NeuroExome Variant Calling Workflow | *Snakemake/Nextflow, Python, R* — Jan 2025 - Mar 2025
- Implemented a NGS pipeline for QC, alignment, SNP/indel calling, and variant annotation on public exome data.
- Computed coverage and variant summary metrics to support QA and diagnostic-style review of exome results.

Comparative Genomics & Data Visualization | *R, SQL, ggplot2, Power BI* — Sep 2024 – Dec 2024
- Annotated, filtered, and prioritized NCBI/Ensembl variants for neurological disease using R/SQL workflows.
- Summarized variant burden and pathways in dashboards to support diagnostic-style genomic interpretation.

Biomarker Discovery in Breast Cancer | *DESeq2, STRING, KM Plotter, KEGG* — May 2020 – Aug 2020
- Identified differentially expressed genes and pathways linked to tumor progression.
- Performed survival analysis, highlighting novel prognostic markers (e.g., miR-21, PIK3CA).