

PRANAVA UPPARLAPALLI

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EXPERIENCE

University of Texas at Dallas

Jan 2025 - May 2025

Bioinformatics Analyst

Richardson, TX

- Ran RNA-seq and TWAS pipelines across ~1,100 human samples on SLURM HPC; delivered cohort results on schedule
- Debugged Nextflow failures (memory limits, malformed inputs, partial batches); reduced reruns and improved throughput
- Built Python QC tooling using matplotlib / pandas to validate outputs, flag normalization issues, and audit runs
- Communicated QC findings and pipeline outputs to research leads across multi-investigator projects
- Maintained FAIR-compliant version-controlled pipelines and documentation using Git for full reproducibility and traceability across the cohort

Sree Vidyanikethan Degree College

Aug 2021 - Mar 2022

Microbiologist

Tirupathi, India

- Performed antimicrobial susceptibility assays per CLSI SOPs to characterize resistant strains and refine protocols
- Centralized lab SOPs and records to improve consistency and reproducibility across experiments

PROJECTS

Spatial Transcriptomics Cohort Pipeline | [GitHub](#)

- Independently designed an end-to-end 10x Visium pipeline: spot QC, normalization, domain detection, and SVG quantification
- Ran BayesSpace resolution sweeps; validated domain stability via Adjusted Rand Index, preventing over-fragmentation
- Detected spatially variable genes via Moran's I; generated consensus top-50 spatial genes, domain stability summaries, and recurrent neighborhood adjacency matrices
- Built an interactive R Shiny dashboard for spatial domain, gene expression, and QC exploration

Colorectal Cancer TME Single-Cell Analysis | [Colorectal Cancer TME Single-Cell Analysis](#)

2024

- Built a reproducible scRNA-seq pipeline (QC, normalization, scVI batch correction, clustering); processed 63,689 cells across CRC samples
- Annotated 8 cell types across 31 clusters; identified elevated myeloid and exhausted T-cell signatures in tumor regions, indicating an immunosuppressive TME; communicated findings to collaborators

Yeast Oxidative Stress RNA-seq Pipeline | [GitHub](#)

2024

- Designed a modular Nextflow bulk RNA-seq pipeline with automated QC, alignment (STAR), and DESeq2 DE analysis; identified 783 DEGs in the oxidative stress transcriptional response
- Parameterized config profiles for reproducible SLURM execution; generated PCA plots, heatmaps, and volcano plots to validate outputs

TinyVariant: Variant Pathogenicity Benchmarking | [GitHub](#)

2023

- Designed an ML model benchmarking pipeline on ~100k ClinVar variants; evaluated logistic regression vs. neural network on ROC-AUC, precision, and recall to assess pathogenicity classification trade-offs

SKILLS

- **Programming & Scripting:** Python, R, Shell scripting, Unix/Linux, SQL, PostgreSQL, Jupyter, RMarkdown, Claude Code
- **Workflow & Infrastructure:** Nextflow, nf-core, Snakemake, Git, GitHub Actions, Docker, Singularity, Conda, CI/CD
- **HPC & Cloud:** SLURM-based HPC, Linux systems, AWS (S3, EC2, Batch), reproducible workflows, FAIR data principles
- **NGS & Omics Data:** RNA-seq, scRNA-seq, snRNA-seq, ATAC-seq, spatial transcriptomics (10x Visium, Xenium, CosMx, MERFISH, Slide-seq), TWAS, multi-omics analysis
- **Data Formats:** FASTQ, BAM/SAM, GTF/GFF3, VCF, BED, H5AD, JSON
- **Alignment & QC Tools:** STAR, salmon, kallisto, FASTQC, MultiQC, Samtools, Bedtools, PrediXcan, IGV
- **Omics Tools:** Scanpy, Seurat, scVI, Squidpy, BayesSpace, Harmony, DESeq2, edgeR, limma, CellChat, NicheNet
- **Databases & Repositories:** GEO, NCBI, Ensembl, UCSC Genome Browser, ENCODE, SRA, TCGA, KEGG, cBioPortal
- **Statistical & ML Methods:** Differential expression, GSEA, pathway enrichment, gene ontology, statistical QC, ML model benchmarking, PCA, clustering, regression, scikit-learn, metadata harmonization, data interpretation
- **Data Visualization:** matplotlib, pandas, seaborn, ggplot2, R Shiny, UMAP/tSNE

EDUCATION

University of Texas at Dallas

Aug 2023 - May 2025

M.S., Bioinformatics and Computational Biology

Richardson, TX

Bharati Vidyapeeth University

Aug 2022 - May 2023

Advanced Diploma, Bioinformatics

Pune, India

Sri Venkateshwara University

Jun 2019 - May 2022

B.S., Microbiology, Biochemistry & Chemistry

Tirupathi, India