

PRANAVA UPPARLAPALLI

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Summary

A bioinformatics professional with a recent Master of Science degree, passionate about translating complex data into meaningful discoveries. I specialize in building scalable genomic workflows for transcriptomics and multi-omics analysis using Python, R, and Nextflow. My strong research background has equipped me with proven problem-solving and analytical skills.

Education

- University of Texas at Dallas, Richardson, TX** Aug 2023 – May 2025
Master of Science in Bioinformatics and Computational Biology
- Bharati Vidyapeeth University, Pune, MH, India** Aug 2022 – May 2023
Advanced Diploma, Bioinformatics
- Sri Venkateshwara University, Tirupati, AP, India** June 2019 – May 2022
Bachelor of Science in Microbiology, Biochemistry, and Chemistry

Work Experience

- Graduate Student Researcher, Xuan lab, The University of Texas at Dallas** Jan 2025 – May 2025
 - Tested a GWAS-based machine learning algorithm based on PrediXcan using genomic data to accurately predict gene expression in different tissues, leveraging eQTL models and GTEx database.
 - Analyzed the role of trans SNPs using HI-C data, to decipher the relationship between genotype and phenotype using SNP variants.
 - Created pipelines and provided efficient data analysis using Bash scripting and HPC computing.
- Undergraduate Research - Sree Vidyanikethan Degree College** Aug 2020 – Mar 2021
 - Researched and characterized the antioxidant properties of *Biancaea sappan*, employing advanced biochemical assays for compound analysis.
 - Designed and executed lab experiments that increased compound yield efficiency by 15%.
 - Optimized growth conditions by formulating specialized media and conducting antibacterial assays.

Projects

- Cancer RNA-Seq Expression Analysis** May 2025 – Jun 2025
 - Explored gene expression across five major cancer types using RNA-Seq data. Built a complete R-based pipeline to perform QC, normalization, and differential expression analysis using DESeq2.
 - Generated heatmaps, PCA plots, and volcano/MA plots to identify biomarkers and clustering patterns across BRCA, KIRC, LUAD, COAD, and PRAD.
- Yeast-Stress Analysis** Dec 2024 – Jan 2025
 - Designed a reproducible RNA-Seq analysis pipeline using Nextflow and Docker, incorporating Fastp for QC, HISAT2 for alignment, SAMtools for BAM processing, and FeatureCounts for quantification.
 - Performed differential expression analysis using edgeR to investigate transcriptomic changes in yeast under oxidative stress, followed by pathway enrichment and visualization with volcano plots and heatmaps.
- Gleason Score Classification Using ResNet-50** Sep 2024 – Dec 2024
 - Designed a deep learning pipeline using ResNet-50 for prostate cancer classification, achieving 90% classification accuracy.
 - Implemented data augmentation techniques to improve model robustness and generalizability.

Skills

- Bioinformatics & Genomic Analysis:** RNA-Seq, Single-Cell RNA-Seq, TWAS, GWAS, eQTL Analysis, Differential Gene Expression (DGE), MetaXcan, DESeq2, edgeR, PLINK, GSEA, FeatureCounts, FastQC, MultiQC, Trimmomatic, Samtools, BEDTools, HISAT2
- Programming & Workflow Automation:** Python, R, Bash/Shell Scripting, SQL, Nextflow, Docker, Conda, Git, Galaxy
- Computational Biology & Structural Tools:** Molecular Docking, Protein-Ligand Interaction, AlphaFold 3, PyMOL
- Databases & Resources:** GEO, dbSNP, Ensembl, SRA, GWAS Catalog, UCSC Genome Browser, KEGG, NCBI
- Molecular Biology Techniques:** DNA/RNA Extraction, Quantitative PCR (qPCR), CRISPR-Cas9, Gel Electrophoresis, Western Blotting

Relevant Courses

- Applied Bioinformatics | Analysis of Data Structures and Algorithms | Big Data | Molecular Biology | Biochemistry | Probability & Statistics