PRANAVA UPPARLAPALLI

pxu.bioinfo@gmail.com | LinkedIn | GitHub | +1 (945) 527-5490 | Richardson, TX, 75080

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

- **Yeast-Stress Analysis**   *Dec 2024 – Jan 2025*
  - Engineered a reproducible RNA-Seq pipeline using Nextflow and Docker, automating the process from raw data QC to differential gene expression analysis with edgeR, successfully identifying 20+ stress-response genes.
  - Analyzed the differentially expressed genes using functional enrichment analysis to identify key biological pathways impacted by oxidative stress, and created data visualizations (volcano plots, heatmaps) to communicate the findings.

- **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.

- **SeqMorph: A Sequence Mutation and Analysis Tool**   *Aug 2024 – Dec 2024*
  - Developed a Python-based tool to analyze sequence mutations in DNA and protein, incorporating mutation mapping and functional impact prediction.
  - Published the tool on GitHub with full documentation and user tutorials to enhance variant analysis capabilities.

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