

# PRANAVA UPPARLAPALLI

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## SUMMARY

Driven by curiosity to uncover insights from biological data, I create tools and workflows that accelerate genomics and medical research—turning complex data into meaningful discoveries.

## PROFESSIONAL EXPERIENCE

- Graduate Researcher - Dr.Xuan's Lab**, University of Texas at Dallas, Richardson, Tx Jan 2025 – Present
- Developed Elastic Net models using MetaXcan on Skin and Whole Blood gene expression data to conduct a TWAS study, identifying 12 novel risk alleles and loci, resulting in a 40% increase in gene-trait association discovery precision.
  - Automated workflows with SnakeMake, Python, and R, boosting data processing and visualization efficiency by 25%.
  - Integrated multi-omics datasets (RNA-Seq, GWAS, spatial HiC) to enhance and validate gene-trait association discovery.
- Undergraduate Researcher – Microbiology Lab**, Sree Vidyanikethan Degree College, India Aug 2020 – Mar 2021
- Researched antioxidant properties of *Biancaea sappan*, optimizing compound extraction efficiency by 15%.
  - Established the potential use of *Biancaea sappan* heart wood for water purification by eliminating harmful microbes**, highlighting its possible application in **gut health treatment** due to its antimicrobial properties
  - Designed and conducted antibacterial assays to assess bioactive compound effectiveness.

## EDUCATION

- Master of Science in Bioinformatics and Computational Biology** May 2025  
The University of Texas at Dallas, Richardson, TX **GPA 3.2**
- Advanced Diploma, Bioinformatics** May 2023  
Bharati Vidyapeeth University, Pune, MH, India **GPA 3.7**
- Bachelor of Science, Microbiology, Minor: Biochemistry, Chemistry** May 2022  
Sri Venkateshwara University, Tirupati, AP, India **GPA 3.5**

## SKILLS

- Programming & Scripting:** Python, R, Java, Matlab, Bash (Shell Scripting).
- Data Analysis & Bioinformatics tools:** PLINK, BEDTools, SamTools, edgeR, FastQC, HISAT2, MetaXcan, MultiQC, PyMOL, Chimera, AutoDock Vina, PEER tool, DDSEQ2 Analysis, Bioconductor. AlphaFold (Protein prediction)
- Databases:** GWAS Catalog, dbSNP, Ensembl, GEO, KEGG, NCBI, SRA, UCSC Genome Browser.
- Workflow Automation:** SnakeMake, Nextflow, Docker, Git/GitHub.
- Database Management:** PySpark, MySQL.
- Techniques:** RNA-Seq Analysis, sc - RNA-Seq, GWAS, TWAS, Molecular Docking, Differential Gene Expression Analysis, Protein-Ligand Interaction Studies, DNA/RNA Extraction, Functional Enrichment Analysis. RMSD Analysis

## PROJECT EXPERIENCE

- Yeast-Stress RNA-Seq Analysis**, [GitHub](#) Dec 2024 – Jan 2025
- Developed an RNA-Seq pipeline to analyze yeast response to oxidative stress, improving processing efficiency by **30%**.
  - Identified 20+ differentially expressed genes** involved in **stress adaptation and survival mechanisms**, providing insights into **oxidative damage response pathways**.
- SeqMorph: Sequence Mutation & Analysis Tool**, [GitHub](#) Aug 2024 – Dec 2024
- Developed a **Python-based tool for analyzing DNA and protein mutations**, enabling faster and more accurate **variant annotation**.
  - Reduced **mutation analysis time by 30%** through automated impact prediction, improving the identification of functionally significant variants.

## RELEVANT COURSES

- Applied Bioinformatics
- Probability & Statistics
- Molecular Biology
- Biochemistry
- Big Data
- Algorithm Analysis and Data Structure