

# Vishnu Priya Nuthanapati

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## Summary

Highly motivated graduate in bioinformatics and biomedical engineering, with strong expertise in NGS data processing, Transcriptomics, and omics data analysis. Proficient in various software tools and computational techniques for large-scale data analysis and workflow automation. Experienced in developing efficient data pipelines and conducting comprehensive analyses to extract meaningful biological insights. Seeking a role to apply skills and contribute to innovative scientific advancements

## Education

### Northeastern University

Boston, MA

*Master of Science in Bioinformatics ; GPA: 3.9/4.0*

*Expected Dec 2024*

- **Coursework:** Bioinformatics Computational & Statistical Methods, Advanced Genomics, Omics, ML & AI

### Osmania University, College of Engineering

Telangana, India

*Bachelor of Engineering in Bio-Medical Engineering ; GPA: 4.0/4.0*

*Aug 2017 - Jul 2021*

- **Coursework:** Biomedical Instrumentation, Cell-Tissue Engineering, Human Physiology, Biomedical Signal Analysis

## Relevant Technical Skills

- |                         |                           |                        |
|-------------------------|---------------------------|------------------------|
| • R/BioConductor/RShiny | • Docker                  | • Snowflake            |
| • JupyterHub/Notebooks  | • SQL/MySQL               | • Cloud Services (AWS) |
| • HPC Computing (Slurm) | • Mage/NextFlow           | • Web Technologies     |
| • Python/BioPython      | • Conda/PositConnect      | • Rest APIs            |
| • Unix/Shell/Bash       | • Pandas/Streamlit/Plotly |                        |
| • GitHub/BitBucket      | • Matlab                  |                        |

## Domains Worked In

- |                            |                         |                               |
|----------------------------|-------------------------|-------------------------------|
| • NGS                      | • Machine/Deep Learning | • RNASeq (bulk, sc)           |
| • Benchling                | • Transcriptomics       | • Visualization (Cytoscape)   |
| • Probability & Statistics | • Cite-Seq/Chip-Seq     | • Mutation Analysis (Vartrix) |

## Work Experience

### VOR BIOPHARMA.INC

Jan 2024 – Jul 2024

*Quantitative Biology Co-op*

*Massachusetts, USA*

- Utilized Nextflow pipelines to analyze long-read sequencing data, identifying AML mutations at single-cell resolution with a 15% increase in detection sensitivity
- Leveraged algorithms to track AML blast evolution from diagnosis to relapse, improving mutation tracking accuracy by identifying an additional 20 mutations and providing deeper insights into disease progression
- Developed a data validation pipeline to enrich sequencing data, reducing error rates by five times and enhancing the accuracy of genetic sequencing analysis for more reliable biological insights
- Built ETL pipelines using Mage, reducing data processing time from 12 to 2 hours and improving access to thousands of records daily via REST APIs for biological analysis
- Partnered with the process development team to design, build, and deploy dashboards for biological sample inventory management, achieving a 40% increase in process efficiency and enabling real-time tracking of inventory
- Assessed CRISPR ABE edits from NGS samples and developed visualizations, enabling wet-lab scientists to analyze 200+ samples daily and improving workflow efficiency
- Coordinated with the business development team to develop a comprehensive database of registered sequence listings, streamlining access to over 5,000 records and improving IP management efficiency by 30%

### ACCENTURE PRIVATE SOLUTIONS

Aug 2021 - Jun 2022

*Associate Software Engineer*

*Telangana, India*

- Collaborated with the DevOps team to automate DocuSign Access requests using PowerBI, processing 50+ requests daily and reducing manual effort
- Led patching on client servers, overseeing scheduling, testing, and deployment of updates for the client operations team

- Streamlined access to GAMS (Global Asset Management System) by managing user accounts with SQL, improving client request response time by 25% and account management efficiency by 30%
- Supervised clients by providing permissions for information on terminated employees, viewing, and tracking assets globally

## **CAMPUS FELLOWSHIPS MENTORSHIP PROGRAM**

**Nov 2020 - Jun 2021**

*Bioinformatics Research Intern*

*Telangana, India*

- Performed NGS data processing using RSEQREP in AWS, handling large datasets and optimizing pipelines to process thousands of samples faster and improve overall data accuracy for genomic analysis
- Optimized transcriptomic data processing pipelines, including QC (fast QC, multiQC), alignment, and expression quantification, ensuring efficient handling of large-scale datasets and high-quality data for downstream analysis
- Directed downstream genomic data analysis, identifying key regulatory pathways and novel gene targets through differential expression and pathway enrichment
- Designed a mentorship program website with HTML, CSS, NodeJS, and Balsamic, resulting in a 35% increase in student outreach

## **KNOWLEDGE SOLUTIONS INDIA**

**Aug 2020 - Oct 2020**

*Research Intern*

*Hyderabad, India*

- Developed an insurance premium prediction engine using an ensemble of Multi-Linear and Random Forest Regressor, improving prediction accuracy and aiding in better decision-making
- Implemented feature selection using Principal Component Analysis and achieved ~1.5% MAPE on predictions

## **GOWRI GOPAL HOSPITAL**

**Aug 2020 - Oct 2020**

*BioMedical Intern*

*Kurnool, India*

- Initiated an orientation program on handling basic errors in medical devices with bio-medical professionals for medical interns and doctors across all departments
- Calibrated medical devices and instruments with calibration tools using calibration kits and reduced error rate by 5%

## **Projects**

### **Functional Annotation and Evolutionary Analysis of Apoe Orthologs**

**Feb 2023**

- Performed multiple sequence alignment (MSA) of APOE orthologs across species using Clustal Omega, identifying 85% conserved regions
- Annotated 95% of predicted proteins using BLAST and KEGG API, mapping them to known biological pathways
- Conducted evolutionary and functional studies of conserved regions, providing insights into gene functionality across species

### **Transcriptome Assembly And Analysis of Aiptasia Pallida RNASeq Data**

**Oct 2022**

- Processed Aiptasia pallida RNA-Seq data using Trimmomatic, GSNAP, and Samtools, achieving mapping of over 20 million reads and generating sorted BAM files for further analysis
- Assembled transcriptomes with Trinity, improving the N50 metric to over 2,000 base pairs, enhancing the quality of gene expression reconstruction
- Predicted coding regions using TransDecoder, identifying more than 15,000 potential open reading frames (ORFs) for detailed analysis of gene function and protein-coding potential

### **Mapping of miRNA-Gene regulatory Networks in Schizophrenia Across Tissue**

**Jul 2021**

- Generated comprehensive network map of miRNA-gene interactions in Schizophrenia using the TargetScan prediction framework
- Identified several active slices of this network across multiple tissues using contextual expression-based parameters
- Integrating the tissue-specific network maps, identified genes with maximum convergence across tissues as well as existing FDA-approved drugs targeting them for drug-repositioning

## **Conference & Volunteer Activities**

- Presented Poster at the Experimental Biology 2021 Conference
- Volunteered at IEEE, Hyderabad section as a marketing volunteer (EMBS society)
- Participated in NSS, contributing to community outreach and organizing social welfare initiatives