TUSHARIKA RASTOGI

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EDUCATION

University of Michigan **Ann Arbor, MI**
MS in Bioinformatics *(GPA: 3.65/4.00)* *December 2022*
Coursework: *Bioinformatics Concepts and Algorithms, Programming Laboratory in Bioinformatics, Applied Biostatistics, High-throughput Molecular Genomic and Epigenomic Data Analysis*

Amity University **Noida, U.P. India**
B.Tech in Bioinformatics *(GPA: 4.0/4.0)* *June 2021*

SKILLS

Programming Language: R, Python, Shell Scripting
Cloud Computing: AWS S3, AWS Batch, AWS EC2, High-performance Computing (HPC), Nextflow Tower(nf-tower)
Operating Systems: Windows, Unix/Linux, Ubuntu, MacOS
Bioinformatics Tools & Packages: Seurat, Numpy, DESeq2, Limma, Maftools, Pandas, Matplotlib, SciPy, dplyr, ggplot2, gprofiler, enrichplot, org.HS.eg.db, clusterProfiler, pheatmap, ComplexHeatmap, EnhancedVolcano, Plotly, UpsetR, BLAST, ORF Finder, SRAToolkit, FASTQC, Trimmomatic, HISAT2, StringTie, BowTie2, SAMTools, Xengsort, SigProfiler, Sequenza
Databases: Entrez (NCBI), GenBank, RefSeq, EnsEMBL, TCGA, GDC Data Portal, miRbase, KEGG Pathway Database, UCSC Genome Browser, GENCODE, RCSB PDB, UniProt, SwissProt, STRING, GEO, SRA, COSMIC, ClinVar, dbNSFP
Scientific Communication: Translate complex bioinformatics analyses into clear, actionable insights, bridging the gap between computational biologists, wet lab scientists, and clinicians to drive informed decision-making.

EXPERIENCE

Michigan Medicine **Ann Arbor, MI**
Bioinformatics – Computational Biologist Intermediate May 2023 - *Present*

- **Automated bioinformatics workflows** with **Nextflow** (**Sarek** for DNA Variant Analysis, **RNAseq**, and **RNAfusion**), **reducing processing time by 60-80%** and ensuring **scalability on AWS Batch/HPC** for high-throughput genomic analysis. Enhanced reproducibility and efficiency, enabling accurate and reliable large-scale data analysis.
- **Leveraged VarSeq** for comprehensive **variant annotation**, adhering to **GATK Best Practices** for high-quality genomic analysis, to identify clinically relevant genetic variants, supporting precision medicine and research.
- **Performed copy number variation (CNV)** analysis using **Sequenza** on **100+ tumor samples**, **with and without matched normal controls**, to identify chromosomal alterations and infer tumor purity and ploidy, providing critical insights for cancer characterization.
- Conducted **proteomics analysis** to compare plasma protein profiles across experimental conditions, performing **differential abundance analysis using limma** and calculating dynamic range to evaluate protein variability.
- Performed **mutational signature analysis** using computational frameworks like **SigProfiler** to uncover underlying mutational processes in tumor samples, **deconvolute signature contributions** to distinguish endogenous vs. exogenous mutation sources, providing key insights into tumor etiology and potential carcinogenic influences.
- **Developed automation scripts**, including the dbNSFP Prediction Aggregation tool and Jaccard Index, to **streamline bioinformatics workflows**. Engineered automated functions that **reduced manual review and data processing time by over 50%**, enhancing efficiency and scalability for genomic analysis.
- Deliver bioinformatics insights in **weekly team meetings**, driving **workflow development**, **data analysis** progress, and **troubleshooting**. Present research in monthly lab meetings, distilling **complex computational results into actionable insights** for interdisciplinary teams, including wet lab scientists and clinicians, to enhance collaboration and decision-making.

Michigan Medicine **Ann Arbor, MI**
Bioinformatics Specialist *November 2022 – December 2022*

- **Analyzed** scRNASeq and snRNASeq data using **Seurat** in **R** to identify distinct cell populations in visceral vs. subcutaneous adipose tissue across disease conditions. Provided insights into metabolic disease mechanisms and tissue-specific immune responses, supporting research on obesity and therapeutic interventions.

Indian Institute of Technology **Gandhinagar, India**
Summer Intern *May 2022 – July 2022*

- **Developed and implemented** an R-based pipeline for comprehensive HNSCC data analysis, identifying 895 differentially expressed genes (**DEGs**) and 69 differentially expressed miRNAs (**DEMs**). Provided insights into key regulatory pathways, potential biomarkers, and therapeutic targets for cancer research.
- Conducted **predictive analysis** to identify 177 DEGs inversely correlated with differentially expressed miRNAs, providing insights into HNSCC regulatory mechanisms, thus demonstrating an ability to derive meaningful biological insights from complex data sets.

ACADEMIC PROJECTS

Comparative analysis of transcriptomic signatures identified in preterm and normal term births *January 2022 – April 2022*

- Developed an **RNA-seq** pipeline integrating **FASTQC, Trimmomatic, BowTie2, StringTie, DESeq2, and PantherDB** to identify upregulated placental maturation markers in preterm births. Ensured data accuracy through interdisciplinary collaboration and provided actionable insights to support therapeutic research in maternal-fetal health.

Distinct Role of FOXA1 mutants in mouse prostate tumirogenesis *August 2021 – December 2021*

- Conducted **bulk RNA-seq analysis** to assess FOXA1 overexpression effects in prostate organoids, identifying 331 differentially expressed genes with high concordance across **STAR** and **SALMON** aligners. Automated pre-processing with shell scripts to streamline workflow efficiency. Performed **GSEA** and **Enrichr pathway analysis**, visualizing hallmark pathways disrupted by FOXA1 mutations to highlight potential therapeutic targets for prostate cancer.

PUBLICATIONS

- Examining Molecular Features of Rare Brain Metastases Patient-Derived Xenograft Models *March 2025*
- Examining molecular landscape and drug sensitivity profiles of patient-derived xenografts from resected brain metastases *August 2024*