

Tejas Temker

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EDUCATION

Northeastern University

Master of Science in Bioinformatics

Relevant Coursework: Data structures and Algorithms, Introduction to Data Mining/Machine Learning, Genomics, Biostatistics

Boston, USA

Dec 2024

Reva University

Bachelor of Science in Bioinformatics

Relevant Coursework: Computational Methods -1, Python Programming, Statistics & Data Science, Evolutionary Bioinformatics

Bangalore, India

Jul 2022

EXPERIENCE

Research Associate | Northeastern University | Boston, USA

Sep 2023 – Dec 2023

- Implemented pipeline to map Oxford Nanopore long-read sequencing data to accurately map reads to complex genomic regions
- Development and maintenance of automated pipelines/tools to analyze large NGS data produced internally
- Automated a pipeline using Snake make to compare the gene expression data obtained by various pseudo aligners
- Predicted differentially expressed genes and presented findings using heat maps and color-coded KEGG pathways
- Implemented and developed scalable motif finding algorithm to analyze biological data

Computational Biologist Intern | Ocean Genomics | Pittsburgh, USA

May 2023 - Aug 2023

- Improved transcriptome data quantification to improve isoform identification by resolving over 500 unique code anomalies in Rust
- Developed pipeline to quantify ScRNA-Seq data to validate BAM files by integrating tools alevin, STARsolo, and mudskipper
- Collaborated to refine Salmon tools algorithm, to adjust quantification logic to ONT- Seq data by improving existing bias model in C
- Applied bioinformatics tools to visualize, analyze, manipulate, or interpret genomic data

Research Associate | Northeastern University | Boston, USA

Jan 2023 – May 2023

- Enhanced the prediction of proteins to boost identification of protein peptides in Mass Spectrometry data using machine learning models
- Controlled false discoveries in sensitive Plex DIA experiments to increase the detection of protein peptides
- Predicted the genotype and the class of mice gene expression data using various machine learning models boosting the accuracy on reduction of RMSE by 20%
- Utilized R for data analysis of large datasets to create visualizations

Bioinformatics Engineer | BioNome | Bangalore, India

Jan 2021 – Jun 2022

- Complete high resolution denovo assembly of a model organism using long read technologies to study phylogenetic properties
- Analyzed genomic data to assess phenotypic differences, using variants calling tool GATK to identify various structural variants
- Organized various biological data such as genome sequences, genotyping, and phenotyping data to reduce manual retrieval
- Leveraged tools FastQC, Trimmomatic, and Bowtie, to perform RNA-seq analysis on yeast samples, to analyze gene expression
- Developed coding and non-coding model to analyze evolutionary significance of sequences using Hidden Markov Models (HMM) to identify conserved domains
- Analyzed DNA sequences into coding or non-coding categories to analyze gene functions by statistical analysis and creating ROC curves using Matplotlib

SKILLS

Bioinformatics Tools:	Gapseq, MiniMap2, BWA, SAM Tools, IGV, Docker, STAR, HISAT2, Kallisto, Bowtie2, TransDecoder
Languages:	R-script, RUST, Python, Linux, Perl, SQL, and SAS
Databases:	NCBI, UCSC Genome Browser, DepMap, BioBank, TCGA, Ensemble, and GEO
Libraries:	BioPython, Seurat, PyTorch, NextFlow, TensorFlow, DESeq2, Pandas, NumPy, Bioconductor, Matplotlib
Biological knowledge:	Single cell data analysis, RNA seq data, HIPAA, Variant Calling, WES, GWAS, Evolutionary Analysis, Regression, Clustering, Predictive Analysis

ACADEMIC PROJECTS

Microarray Metanalysis of Alzheimer's disease datasets

- Performed microarray Meta analysis to Predict differentially expressed genes and metabolic pathways in R using package Limma
- Identified DNMT1 as a functional biomarker for Alzheimer's using online database's such as TOPPFUN, DAVID and KEGG

Transcriptome assembly of Streptococcus pneumoniae Serotype 20

- Constructed robust pipeline of Streptococcus Pneumoniae Serotype 20 genome, utilizing computational tools Spade, Trinity assembler to ensure robust genomic data analysis
- Achieved transcriptome assembly with Trinity, ensuring a comprehensive quality examination of gene expression dynamics to enhance research outcomes