Shalini Karthyk

• +1 617-373-0081 • karthyk.shalini@gmail.com • LinkedIn • Portfolio • Boston, MA

Bioinformatics Scientist

Experienced bioinformatics and data science professional with **5 years** in academia and industry. Proven in data engineering, bioinformatics pipelines, and real-world data analytics, focusing on molecular biology, Computational Biology, and Machine learning. Skilled in cross-functional collaborations and driving innovative mRNA research in biotech and pharma R&D.

EDUCATION

Master of Science in Bioinformatics | Graduate Certificate in Data Analytics **January 2022 - June 2024**
Northeastern University, Boston, MA **GPA: 4.0/4.0**

Bachelor of Technology in Bioinformatics **July 2015 - July 2019**
SASTRA University, Tanjore, TN, India

TECHNICAL SKILLS

Bioinformatics Databases: BLAST, NCBI, GenBank, PDB, EMBL, Entrez, SwissProt, UniProt, ENCODE, GENCODE, Ensembl.
Genomic Analysis: GWAS, Exome, Whole Genome, Transcriptomics, Epigenetics, Structural Variants, Functional Genomics.
Programming Languages: R, Python, SQL, NoSQL, MATLAB, C, C++, Java, Perl, PHP, HTML, Bash, Shell Scripting.
Machine Learning: Classification (DT, Random Forest, SVM, KNN, Neural Networks), Regression (Ridge, Lasso), Clustering.
Computing: High-Performance Computing (Linux/Unix, Cluster), Cloud (AWS, Code Ocean), Docker, Version Control (Git/GitHub).
Project Management: Trello/JIRA, Benchling, LabArchive.

PROFESSIONAL WORK EXPERIENCE

The Institute for Experiential AI **Boston, MA**
Bioinformatics and Machine Learning Analyst Co-op **January 2024 – June 2024**

- Led team to accelerate personalized cancer immunotherapies development by identifying key CD8+ T cell transcriptional drivers, utilizing **DESeq, DEXSeq, GSEA**, and novel microfluidics approach.
- Developed **ETL** pipeline for ENCODE shRNA RNA-binding protein (RBP) Knockdown data, improving differential splicing analysis by 60% for over 10,000 splice junctions.
- Orchestrated ML pipeline (**XGBoost, SHAP**) to boost genomics research prediction accuracy by 20% and **innovative graph structure** for mRNA splicing analysis, advancing understanding of 200+ RBPs in post-transcriptional regulation.

Northeastern University **Boston, MA**
Data Validation Assistant **January 2022 – December 2023**

- Streamlined the ALERT video analytics data tool with a revamped **MATLAB** data structure, reducing report generation time by 50% and enhancing usability.
- Automated video annotation software using **advanced tracking algorithms**, resulting in a **70%** increase in productivity.
- Engineered robust **QA testing** measures, enabling re-coding of 50+ bugs and a 30% decrease in overall bug recurrence rate.

Fulcrum Therapeutics **Cambridge, MA**
Bioinformatics Associate Intern **June 2023 – August 2023**

- Pioneered **high-throughput** erythroid differentiation, boosting CRISPR and small molecule screening for drug development by 30% for 150 compounds in hematological disease research.
- Devised proprietary **R Shiny** algorithm to identify erythroid lineage markers using 10X genomics single-cell technology and qPCR, with 40% higher precision than existing methods, reducing potential targets to top 3 sure marker genes.
- Optimized flow cytometry for co-positivity analysis and sorting with a novel gating strategy, increasing cell purity by 35%.

Brigham and Women's Hospital **Boston, MA**
Technical Research Assistant **September 2019 - September 2021**

- Implemented **Next-Generation Sequencing** (NGS) pipelines with **Nextflow** to examine kidney organoid transcriptomes, revealing 1,500+ genetic variations and profiling gene expression levels for 7,000 genes.
- Directed a 3-person team 2qusing **AAV-CRISPR** to excise 100 kb in a DMD mouse model, improving partial muscle function.
- Amplified **SARS-CoV-2** variant detection by 40% through the implementation of **immuno-PCR** techniques and isolating immune cells and specific antibodies against COVID-19.
- Identified 8 nephrotoxicity-related genes in kidney organoids using genomic and epigenetic analysis of 20M reads in R.
- Enhanced **multiplex assay** efficiency by 25% for 18 biomarkers using Luminex, MSD, and Randox, retaining 90% sensitivity.

Harvard Medical School, Department of Genetics **Boston, MA**
Research Intern **February 2019 – June 2019**

- Built **Seurat** pipeline for **single-cell RNASeq** in kidney organoids, identified 5 subtypes, and mapped cell fate with Monocle.
- Executed CRISPR/Cas9 mediated mutation of 6 kidney disease genes in iPSC lines and rescued disease phenotype, quantifying **post-treatment gene expression** changes across 5000 genes by Bulk RNA-seq analysis.
- Enhanced RNA-seq alignment and genetic screen analysis with **BLAST, BWA, and Samtools**, improving data interpretation.

PUBLICATIONS

- J. Estevam, M. Finocchiaro, **S. Karthyk,** A. Paul, and T. Konry**, "**An innovative single-cell function-to-omics platform to characterize bispecific antibodies," *submitted and under review*.
- Y. Raghava, A. Paul, **S. Karthyk,** J. Vyas, Z. Xu, J. Dy, J. Platig, and P. Castaldi, **"**Charting the role of RBPs in tissue-specific alternative splicing using machine explanations," *in progress.*