Arshia Kapil

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EDUCATION

- **Masters of Science** — **University of California, Santa Cruz**
  Biomolecular Engineering and Bioinformatics   *Sept. 2023-Mar. 2025*
  - Relevant courses - RNA Bioinformatics, Evolutionary Genomics, Entrepreneurship in Biotechnology
- **Bachelor of Science** — **University of California, Santa Cruz**
  Biomolecular Engineering and Bioinformatics - GPA: 3.78/4   *Sept. 2019-Aug. 2023*
  - Relevant courses - Bioinformatics Models and Algorithms, Introduction to Database Management Systems

WORK EXPERIENCE

- **Graduate Research Assistant — UCSC Paleogenomics Lab**   *Jan. 2024 - Present*
  - Engineered a Nextflow pipeline that streamlined genome assembly by identifying key repeat sequences, solving computational bottlenecks in genomic research.
  - Leveraged bioinformatics tools (KMC, Jellyfish, Fastk, Meryl) to process large-scale genomic datasets, and performed metrics ensuring accurate repeat identification for assembly refinement.
  - Optimized high-throughput data processing in a Linux-based server environment using Bash scripting, reducing computational runtime by 40%, accelerating genomic analysis workflows.
- **Research Assistant — Institute for the Biology of Stem Cells**   *Jun. 2022 - Aug. 2023*
  - Applied Python and R to conduct differential expression analysis on RNA-seq and ATAC-seq datasets, uncovering differentially expressed genes and regulatory patterns in stem cell differentiation during early human embryonic development.
  - Developed a custom Python script using Scanpy, Seaborn, and Matplotlib to detect paired adhesion molecules across tissue samples, enhancing our understanding of cell-cell interactions using statistical methods.
- **Biology/Chemistry Intern — Unnatural Products Inc.**   *Jun. 2022 - Jun. 2023*
  - Increased drug synthesis efficiency by 50% by refining chemical screening methods, ensuring faster and more precise selection of monomers.
  - Applied advanced drug screening techniques using DSF, FP, TR-FRET, and gel electrophoresis, contributing to drug discovery.
  - Acquired wet lab expertise in bacterial transformation, including media preparation and cell centrifugation in a drug discovery start-up.

PROJECTS

- **Exploring tRNA dynamics :** Analyzed the effects of quorum sensing on biofilm production in pathogenic bacterial species. Implemented tRAX pipeline(incorporates Bowtie2 and Deseq2) on OTTR-seq data for comprehensive QC, normalization, Exploratory Analysis, and differential expression analysis of tRNAs in stationary, exponential, and biofilm phases of Vibrio Cholerae.

- **Machine Learning and Molecular Dynamics :** Applied diverse machine learning techniques in molecular dynamics simulations to optimize computational modeling. Leverage coarse graining and graph neural networks trained on proteins to create protein visualizations.

- **StructHunt :** First place winner of QBI Hackathon, with project StructHunt. Collaborated with an interdisciplinary team, winning $10K for further research toward a publication. Developed a tool monitoring bioRxiv and medRxiv archives, integrating new papers on biomolecular structures into RCSB Protein Data Bank. Gained insights into biomolecular integrative structures and LLM techniques within 36 hours. Deployed a fully functional prototype integrated with GoogleDocs and email notifications on AWS with 82% accuracy.

SKILLS

Computational: Python, R, RNA-seq, Pytorch, Tensorflow, UCSC Genome Browser, matplotlib, Linux, Bash, Conda