Devansh Pancholi

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PROFILE SUMMARY

Bioinformatics graduate with research experience in computational genomics, sequencing-data analysis, RNA biology, and machine learning. Developed scalable HPC workflows for WGS, fragmentomics, epigenomics, and AI-driven structure prediction using Python, C++, and deep learning frameworks. Experienced in high-throughput sequencing analysis, biological data interpretation, and computational pipeline development for large-scale omics datasets. Interested in computational genomics, genome regulation, transcriptomics, and applying machine learning to complex biological systems.

RESEARCH INTERESTS

Computational genomics, cancer genomics, sequencing-data analysis, epigenomics, RNA biology, transcriptomics, genome regulation, machine learning for biological systems, and scalable bioinformatics workflow development.

https://devansh-pancholio-portfolio.netlify.app/

EDUCATION

Master of Science in Bioinformatics | Saint Louis University, USA **May 2026**

Coursework: Bioinformatics I & II, Genomics,Machine Learning, Deep Learning, Algorithms for BCB, Biochemical Pharmacology

Bachelor of Engineering in Biomedical Engineering | L.D. College of Engineering, India **June 2023**

Coursework: Python, C++, Embedded Systems, AI Fundamentals, Circuit Python, Signal Processing, Diagnostic Instrumentation

TECHNICAL SKILLS

Deep Learning & ML: GNN (Message Passing), Denoising Diffusion (DDPM), Transformer Encoders, RiNALMo (RNA Language Models), ESM-2 (Protein LM), XGBoost, Scikit-learn, SHAP

Programming: Python, C++, R, Bash/Shell, MATLAB, SQL, MySQL

Bioinformatics & Genomics: NGS Analysis, fragmentomics, epigenomics (5hmC), Bulk RNA-seq, scRNA-seq - analysis, Alignment, Genome Assembly, Pipeline Development,

Bioinformatics Tools: BWA , BAM/SAMtools, STAR, Bowtie2, IGV, UCSC Genome Browser, BLAST, Clustal Omega, Scanpy

Datasets: GWAS, TCGA, WGS, SRA and more

Structural Biology: RMSD, TM-score, Kabsch Alignment, RNA motif modeling, PyMOL, Chimera

Data Visualization: Matplotlib, Seaborn, Jupyter Notebook, Ggplot

HPC & Infrastructure: Linux/UNIX, SLURM, Docker, Nextflow, Snakemake

RESEARCH EXPERIENCE

Research Assistant (WashU)| Advisor: Dr. Maher **Jan 2025 - Present**

Fragmentomics and Epigenomics | Washington University in Saint Louis

Worked on large-scale fragmentomics and epigenomics analysis to investigate cancer-associated DNA fragmentation and chromatin organization using high-throughput sequencing data.

- Designed and implemented HPC-based bioinformatics pipelines for WGS and 5hmC datasets using BWA, samtools, Docker/LSF, and scalable cluster workflows.
- Performed fragment-length distribution analysis to investigate cancer-associated chromatin organization, nucleosome positioning, and cohort-level fragmentation variability.
- Developed analytical frameworks for short/long fragment ratio estimation, nucleosome peak enrichment, and healthy-versus-cancer fragmentation profiling.
- Implemented end-motif (4-mer and 5-mer) analysis pipelines from FASTQ data to investigate fragmentation mechanisms and epigenetic regulation.

- Built reproducible BAM-processing and TLEN-based extraction workflows for cohort-scale sequencing analysis across multiple biological conditions.
- Generated publication-quality visualizations including normalized fragment distributions, variability summaries, violin/box plots, and comparative cohort analyses.
- Investigated pre-analytical effects (EDTA vs Streck) on fragmentation patterns and downstream biological interpretation

Research Assistant (SLU)| Advisor: Dr. Hou **Mar 2025 – Present**

- Developed computational pipelines for RNA motif extraction, structural alignment, hierarchical RMSD clustering, and template-based assembly using C++ and Python.
- Built RNAMotifDB integrating RNA sequence, secondary structure, and template-derived tertiary structure information for motif-level structural analysis.
- Developed template-search frameworks using sequence similarity, RMSD, and TM-score metrics with parallelized HPC execution for scalable structural comparison.
- Extended deep-learning–based RNA structure prediction workflows using GNN + diffusion frameworks, integrating RiNALMo embeddings, motif-aware structural representations, and residue-level alignment strategies for template-guided 3D prediction.
- Benchmarked OpenFold3 and Boltz-style RNA structure prediction workflows using template-guided and synthetic MSA strategies on RNA structural datasets, achieving improved structural consistency and RMSD reductions of up to ~35% for larger RNA systems.
- Developed scalable Nextflow-based HPC workflows for preprocessing, template extraction, model inference, PDB generation, and structural evaluation.
- Implemented automated structural repair and coordinate-mapping methods to address missing residues, variable-length inputs, and alignment consistency issues.
- Validated AI-driven RNA structure prediction workflows across RNA structures ranging from 30–238 nucleotides while resolving NaN instability and inference-related issues.

Course Project | Advisor: Dr. Ted **Feb 2025 – Apr 2025**

Protein Sequence–Disease Classifier |

- Built an ML pipeline using ESM-2 embeddings for ~20,000 protein sequences.
- Engineered multimodal biological features including disorder prediction and PTM-associated signals.
- Achieved ROC-AUC ~0.80 with strong precision/recall performance using ensemble machine-learning models.
- Developed interpretable prediction workflows using SHAP-based feature interpretation

Publications & Technical Projects

Smart Stethoscope - IoT-enabled Medical Device |

- Developed and presented an IoT-enabled smart stethoscope system integrating signal-processing pipelines, amplification/filtering circuitry, and Arduino-based acquisition workflows for low-cost biomedical monitoring; published at IEEE ASIANCON 2023 (IEEE Xplore).

Soft Skills

- Strong communication (written and verbal fluency), effective time management and organizational skills, and the ability to work both collaboratively in team environments and independently to complete Projects successfully.