

EDUCATION

Northeastern University <i>Master of Science in Bioinformatics (GPA: 3.62)</i> <ul style="list-style-type: none">Course work: Bioinformatics Programming, Computational Methods-1, Computational Methods-2, Statistics using R, Collecting Storing and Retrieving Data, Genomics, Introduction to Machine Learning.	Boston, MA <i>Sept 22 – Dec 24</i>
Vellore Institute of Technology (VIT) <i>Integrated Biotechnology</i> <ul style="list-style-type: none">Course work: Biochemistry, Cell Biology, Molecular Biology, Genetic Engineering, Fundamentals of Mathematics, Introduction to Bioinformatics.	Vellore, India <i>July 17 – May 22</i>

SKILLS

Operating skills:	Linux/Unix, HPC (Slurm, LSF), Google Cloud (GCP).
Programming skills:	Python, BioPython, R, Shell scripting.
Bioinformatics skills:	Whole Genome Analysis (WGS), Genome Assembly, GWAS, scRNA-seq, ChIP-seq, RNA-seq, DNA-Methylation Analysis, Transcriptome Assembly, Differential Gene Expression Analysis, KEGG and Gene Set Enrichment Analysis, String Network Analysis, Phylogenetic Tree Analysis.
Bioinformatics Tools:	Plink, Hail, Nextflow, Trimmomatic, SPAdes, QUAST, Cell Ranger, STAR, DoubletFinder, Seurat, Harmony, HISAT2, featureCounts, Bowtie2, GATK, Trinity, DESeq2, ClusterProfiler, BLAST, Clustal Omega, BEAST2.
Machine Learning:	K-Nearest-Neighbours (KNN), Support Vector Machine (SVM), Artificial Neural Network, Lasso, Ridge, and Elastic Regression.
Data Analysis Platform:	All of Us Research, UK Biobank.
Wet lab Techniques:	PCR, qPCR, cDNA Synthesis, Gel Electrophoresis, DNA/RNA Isolation.

WORK EXPERIENCE

Bioinformatics Research Analyst <i>Brigham and Women's Hospital</i> Title: Single-cell Transcriptomic Profiling of PBMCs Following Treatment. <ul style="list-style-type: none">Objective: To profile immune cell populations and assess transcriptional dynamics across biological conditions using single-cell RNA sequencing of PBMCs.Responsibilities:<ul style="list-style-type: none">Performed alignment of sequenced reads using Cell Ranger to generate count matrices from scRNA-seq data.Conducted quality control and downstream analyses using DoubletFinder, Seurat and Harmony for data integration, normalisation and dimensionality reduction.Identified and annotated immune cell types and executed clustering, UMAP visualization, and differential abundance testing to compare cell-type proportions across experimental groups.Performed differential gene expression analysis and generated volcano plots to identify key transcriptional markers and pathways of interest.Interpreted immune cell shifts and gene signatures to support broader biological hypotheses.	<i>Jan 25 - Present</i>
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Bioinformatics Research Analyst Coop <i>Brigham and Women's Hospital</i> Title: Genetic Mimics of GLP-1Ra and SGLT2i Therapy, Heart Failure and Chronic Kidney Disease Outcomes. <ul style="list-style-type: none">Objective: Evaluated the impact of genetic mimics of GLP1-Ra and SGLT2i therapies on heart failure (HF) and chronic kidney disease (CKD) outcomes using Whole Genome Sequencing (WGS) data from 317,964 participants in the All of Us Research Program.Responsibilities:<ul style="list-style-type: none">Preprocessed and analyzed large-scale WGS datasets to extract high-quality genotype data for downstream analyses.Applied elastic net regression to identify significant genetic variants associated with reduced hemoglobin A1c (HbA1c) levels and performed linkage disequilibrium pruning to reduce collinearity among variants.Developed and validated polygenic risk scores to model lifelong genetic mimics of GLP-1Ra and SGLT2i against cardiometabolic traits, confirming the validity and strength of the genetic instruments.Evaluated efficacy outcomes including HF, CKD, CAD and safety outcomes such as multiple endocrine neoplasia and thyroid cancer.Conducted phenome-wide association study (PheWAS) using logistic regression to explore the broader clinical implications.	<i>Jan 24 – Nov 24</i>
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Computational Biology Intern <i>Carpenter Lab, Indiana University</i> Title: Integrative Analysis of RNA-seq Data of Breast Cancer: A Bioinformatics Approach for Gene Expression Profiling and Pathway Analysis. <ul style="list-style-type: none">Objective: Analyzed RNA-seq data to identify key genes and pathways involved in breast cancer, contributing to a deeper understanding of its molecular mechanisms.Responsibilities:<ul style="list-style-type: none">Utilized Bash and bioinformatics tools for RNA-seq data preprocessing and quality control, ensuring high-quality input data for downstream analysis and reducing technical variability.Conducted RNA-seq alignment and quantification using HISAT2 and featureCounts, achieving a high mapping rate and accurate quantification of gene expression.Performed differential gene expression analysis, KEGG pathway analysis, and gene set enrichment analysis using DESeq2 and ClusterProfiler and visualized results using heatmaps, volcano plots, and pathway maps, effectively summarizing findings for presentation and facilitating hypothesis generation.	<i>May 23 - Aug 23</i>
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RESEARCH PROJECTS

<ul style="list-style-type: none">Performance Comparison of Machine Learning Algorithms to Predict Chronic Kidney Disease.Performing Genome Assembly, Transcriptome Assembly, Gene Annotation and Protein Function Prediction of <i>Escherichia coli</i> Genome using Bioinformatic Pipeline.Phylogenetic trees construction for organisms chosen based on similarity of Protein to find conserved regions in gene sequences and to study evolution by constructing phylogenic trees using Bioinformatic tools.

CONFERENCE / RESEARCH

<ul style="list-style-type: none">Subbaramireddy Remala, Liming Liang, Amil M. Shah, Leo F. Buckley. Long-Term Efficacy and Safety of GLP-1R Agonist and SGLT2 inhibitor Therapy General Population: A 2x2 Factorial Mendelian Randomization Study". Presenting at Gordon Research Conference on Human Genetics and Genomics 2025.Subbaramireddy Remala, Liming Liang, Amil M. Shah, Leo F. Buckley. "Genetic Mimics of GLP-1Ra and SGLT2i Therapy, Heart Failure and Chronic Kidney Disease Outcomes". Presented at American Heart Association Scientific Sessions 2024.Bhavya Chebrolu, PharmD, MS, Subbaramireddy Remala and Leo Buckley, PharmD, MPH. "Whole Genome Sequencing in a Diverse Cohort Identifies Genetic Predictors of Response to SGLT2i". Presented at American College of Clinical Pharmacy Annual Meeting 2024.
