

**EDUCATION****Northeastern University****Boston, MA***Master of Science in Bioinformatics with Omics concentration***Sept 22 – Dec 24**

- Relevant course work: Bioinformatics Programming, Computational Methods-1, Computational Methods-2, Statistics using R, Collecting Storing and Retrieving Data, Genomics, Introduction to Machine Learning.

**SKILLS****Operating skills:** Linux/Unix, Windows, HPC cluster.**Version Control:** Git.**Programming skills:** Python, BioPython, R, shell scripting, SQL.**Bioinformatics skills:** Whole Genome Analysis (WGS), Whole Exome Analysis (WES), 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, Trimmomatic, SPAdes, QUAST, Seurat, STAR, HISAT2, FeatureCounts, HTseq, Bowtie2, GATK, Trinity, DESeq2, ClusterProfiler, BLAST, Clustal Omega, BEAST2.**Data Analysis Platform:** All of Us Research, UK Biobank.**Wet lab Techniques:** PCR, qPCR, cDNA Synthesis, Gel Electrophoresis, DNA/RNA Isolation.**WORK EXPERIENCE****Research Analyst I Coop (Bioinformatics)****Jan 24 - Present****Brigham and Women's Hospital - Harvard Medical School****Project 1**

Genetic Mimics of GLP-1Ra and SGLT2i Therapy, Heart Failure and Chronic Kidney Disease Outcomes

- Analyzed whole Exome Sequencing data from the All of Us Research Program to evaluate the impact of genetic mimics of GLP1-Ra and SGLT2i therapy on cardio-kidney outcomes.
- Applied elastic net regression and linkage disequilibrium pruning to identify variants linked to lower hemoglobin A1c levels.
- Developed polygenic risk scores to simulate lifelong GLP1-Ra and SGLT2i treatment, encompassing 245,388 participants with varied demographics.
- Demonstrated that higher GLP1-Ra genetic scores significantly reduced the risk of coronary artery disease, heart failure, and chronic kidney disease, with these associations not modified by the SGLT2 inhibitor genetic score.

**Project 2**

Whole Genome Sequencing in a Diverse Cohort Identifies Genetic Predictors of Response to SGLT2i.

- Analyzed Whole Exome Sequencing data from the All of Us Research Program to identify genetic variants within the SLC5A2 gene that predict response to SGLT2 inhibitors.
- Utilized elastic net regression and cross-validation techniques to identify significant genetic variants associated with improved HbA1c reduction following SGLT2i therapy.
- Assessed the impact of genetic variation on drug efficacy in a diverse cohort, including 80% participants from underrepresented populations.

**Computational Biology Intern****May 23 - Aug 23***Carpenter Lab, Indiana University*

Integrative Analysis of RNA-seq Data of Breast Cancer: A Bioinformatics Approach for Gene Expression Profiling and Pathway Analysis.

- Utilized Python and Bioinformatics tools for RNA-seq data preprocessing and quality control.
- Conducted RNA-seq alignment and quantification using HISAT2 and featureCounts.
- Performed Differential Gene Expression Analysis, KEGG Pathway Analysis and Gene Set Enrichment Analysis using DESeq2 and ClusterProfiler.
- Visualized results using heatmaps and volcano plots, and effectively communicated findings to the supervisor.

**RESEARCH PROJECTS**

- Performance Comparison of Machine Learning Algorithms to Predict Chronic Kidney Disease.
- Performing Genome Assembly, Transcriptome Assembly, Gene Annotation and Protein Function Prediction of *Escherichia coli* 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 phylogenetic trees using Bioinformatic tools.
- Isolation of Chitosan using shrimp shells using biological method.

**CONFERENCE / RESEARCH**

- 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".  
Presenting 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.

**LEADERSHIP SKILLS****Society of Manufacturing Engineers (SME-VIT)**

Vice Chair-person Management

**May 2018 – May 2019****VIT School of Biosciences and School of Technology**

Program Representative

**July 2017 – April 2019**