SUBBARAMIREDDY REMALA
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EDUCATION

Northeastern University   **Boston, MA**
Master of Science in Bioinformatics with Omics concentration (GPA: 3.62)   *Sept 22 – Dec 24*
- 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, Google Cloud (GCP).
Programming skills:	Python, BioPython, R, Shell scripting.
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, Nextflow, Trimmomatic, SPAdes, QUAST, Seurat, STAR, HISAT2, FeatureCounts, HTseq, Bowtie2, GATK, Trinity, DESeq2, ClusterProfiler, BLAST, Clustal Omega, BEAST2.
Machine Learning:	K-Nearest-Neighbors (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 Coop   *Jan24 – 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.
- **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 Exome Sequencing (WES) data from 245,388 participants in the All of Us Research Program.
- **Responsibilities:**
  - Preprocessed and analyzed large-scale WES datasets to extract high-quality genetic 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 exposure to GLP-1Ra and SGLT2i genetic mimics, ensuring reproducibility across diverse demographic subgroups.
  - Demonstrated that GLP-1Ra genetic scores significantly reduce heart failure and chronic kidney disease risks, while SGLT2i genetic scores reduce heart failure risk, with additive protective effects when combined.

Project 2
Whole Genome Sequencing in a Diverse Cohort Identifies Genetic Predictors of Response to SGLT2i.
- **Objective:** Explored SLC5A2 genetic variants predictive of response to SGLT2 inhibitors (SGLT2i) therapy using Whole Exome Sequencing (WES) data from a diverse cohort of over 80% underrepresented populations, focusing on precision medicine approaches.
- **Responsibilities:**
  - Conducted data preprocessing and rigorous quality control to ensure accuracy in variant identification
  - Applied elastic net regression and cross-validation to pinpoint variants associated with improved HbA1c reduction following therapy.
  - Employed elastic net regression and cross-validation to identify key genetic variants within SLC5A2 associated with enhanced HbA1c reduction in response to SGLT2i therapy.

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.
- **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:**
  - 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.

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 phylogenic 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".
  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.

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*