SUBBARAMIREDDY REMALA

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EDUCATION

Northeastern University

Boston, MA

Master of Science in Bioinformatics with Omics concentration

September 2022 - Present

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

Vellore Institute of Technology (VIT)

Vellore, IN

Master of Science in Integrated Biotechnology

• Relevant Course work: Molecular Biology and Cell Biology, Microbiology, Immunology, Genetic Engineering, Bioprocess, Aquatic Biotechnology, Cell culture Technology, Fundamentals of Mathematics.

SKILLS

Operating skills: Linux/Unix, Windows, HPC cluster.

Version Control: Git.

Programming skills: Python, BioPython, Hail, R, shell scripting.

Bioinformatics skills: Genome Assembly, GWAS, scRNA-seq, ChIP-seq, Bulk 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, Trimmomatic, SPAdes, QUAST, Seurat, STAR, HISAT2, FeatureCounts, HTseq, Bowtie2, 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

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 genetic 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.

Computational Biology Intern

May 23 - August 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

- 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 ABSTRACTS / 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". Submitted to American Heart Association Scientific Sessions 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