

SRUJANA PRASANNA NEELAVAR

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EDUCATION

Carnegie Mellon University, Pittsburgh, PA May 2024
Master of Science in Computational Biology
Relevant Coursework: *Programming for Scientists, Algorithms and Data Structures, Essential Mathematics and Statistics, Machine Learning, Computational Genomics, Advanced Microbiology, Modeling and Simulation*
Visvesvaraya Technological University, Bangalore, India Aug 2021
Bachelor of Engineering in Biotechnology
Major GPA: 9.40/10.00 Rank: 1/45 (Department Gold Medalist)

RELATED EXPERIENCE

Graduate Research Assistant, Pittsburgh, PA Jan 2023 – Present
Hiller Lab, Carnegie Mellon University

- Conducted a comparative genomics analysis to assess the covariance between the regulator Rgg144 and its corresponding signal peptides, namely SHP144, rio120, rio121, and rio122 in *Streptococcus pneumoniae*.
- designed and generated a network diagram to elucidate the specificity of interactions between the regulator and the signal peptides.

Summer Research Fellow, Bangalore, India Jun 2021 – Aug 2021
Jawaharlal Nehru Center for Advanced Scientific Research

- Performed coevolutionary analysis on the receptor binding domain of SARS CoV-2 genome using Shell scripting.
- Generated the positive and negative datasets for the analysis of the SARS CoV-2 genome from over 2.5 million sequences deposited on the database by predicting the possible sequence space using Python.

Research Intern, Bangalore, India Aug 2020 – Sep 2020
Center of Excellence Computational Genomics, RV College of Engineering

- Identified hit compounds from *Citrus limon* as potential natural GPVI receptor antagonists through High Throughput Screening using bioinformatics tools like BLAST, MEGA X, Clustal W and AutoDock Tools.
- Examined the interaction of hit compounds and GPVI receptor through MDS using GROMACS.

TECHNICAL SKILLS

Programming Languages and Cloud: Python (NumPy, Pandas, Scikit-learn), Go, Bash, HTML, Google Cloud Platform - Compute Engine, Github, PSC Bridges Supercomputing System
Bioinformatics Tools: BLAST, MEGA X, ClustalW, AutoDockTools, GROMACS, AUGUSTUS, samtools, bamtools
Biotechnology: Isolation and quantification of DNA, RNA and proteins, Isolation and fusion of protoplasts, electrophoresis, ELISA

PROJECT EXPERIENCE

A Pipeline to Annotate the Transcriptome of *Pongo pygmaeus*, Pittsburgh, PA Mar 2023 – May 2023
Course Project/ Team Member

- Developed a pipeline using tools such as FastQC, minimap2, samtools, stringtie, AUGUSTUS, GFFRead and OmicsBox to annotate the publicly available RNA-Seq data of *Pongo pygmaeus*.

Prediction of Diabetes Based on Multiple Diagnostic and Lifestyle Features, Pittsburgh, PA Mar 2023 – May 2023
Course Project/ Team Member

- Created predictive Machine Learning models (k-NN and Multiclass Logistic Regression) to forecast diabetes using CDC's BRFSS 2015 survey data, while mitigating class imbalance with SMOTE.

In silico approach for the bioremediation of hexavalent chromium by structure prediction and docking studies of chromium(VI) reductase from *Pseudomonas* sp. G1 strain, Bangalore, India Feb 2021 – Jun 2021
Major Project/ Team Lead

- Generated the 3D structure of chromium(VI) reductase from *Pseudomonas* sp. G1 strain and studied the molecular interactions between chromate/dichromate and chromium(VI) reductase using iGemDock.
- Studied the importance of active site residues by preparing *in silico* mutants using tools such as I-Mutant and Dynamut.

PUBLICATION

- Narsing Rao MP, Neelavar S, Li WJ et al. Description of *Paenibacillus yunnanensis* sp. nov., Isolated from a Tepid Spring. *Current Microbiology*. 2020 Oct. 77(10):3174-3178.