

SRAVYA SRI MALLAMPALLI

Bioinformatics Research Intern

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Education

Indian Institute of Information Technology, Sricity

2022 - Present

B.Tech in Computer Science and Engineering

Experience

Bioinformatics Research Intern

2023 - Present

IIIT Sri City, Under the Guidance of Assistant Prof. Dr. Chandramohan Dasari

Sricity, India

- Conducted genomic variant classification for MECP2 mutations related to Rett Syndrome.
- Developed machine learning models (XGBoost, Random Forest) achieving 97.5% accuracy.
- Worked with genomic databases like ClinVar and used computational tools.

Research Works

Genomic Variant Classification for MECP2 Mutation Pathogenicity

2025



- Sravya Sri Mallampalli, Chandra Mohan Dasari. *Genomic Variant Classification for MECP2 Mutation Pathogenicity*.
- Accepted at the PM4B 2025 workshop of the PAKDD 2025 conference.
- Classified genomic variants in the MECP2 gene associated with Rett syndrome using computational analysis.
- Tools and Software: XGBoost, Random Forest, One-Hot Encoding

Deletion-Insertion Analysis with RNN for MECP2 and FOXP1 in Rett Syndrome Feb 2025 - Present



- Developed an RNN-based model to predict deletion-insertion effects in MECP2 and FOXP1 genes linked to Rett Syndrome.
- Utilized deep learning techniques to analyze sequence variations and their regulatory impact.
- Tools and Software: TensorFlow, Keras, Biopython, PyTorch.

Machine Learning & Deep Learning Projects

Mouse Mammary RNA-Seq Analysis

April 2024



- Analyzed RNA-seq data from 12 mouse mammary tissue samples to identify differentially expressed genes and explore pathways relevant to breast cancer.
- Tools and Software: HISAT2, featureCounts, edgeR, DESeq2, ggplot2.

Computational Drug Discovery Regression Model with RF

Dec 2024



- Developed a Random Forest-based regression model to predict drug-target interactions for computational drug discovery. Trained on molecular descriptors and biological activity data to improve lead identification efficiency.
- Tools and Software: Scikit-learn, RDKit, Pandas, NumPy, Matplotlib.

FASTA to 3D Protein Structure Prediction

Jan 2025 - Present



- Developed a pipeline to predict 3D protein structures from FASTA sequences.
- Tools and Software: AlphaFold, MODELLER, PyMOL.

Software-Based Projects

DNA Sequence GC Content Calculator

2023



- Created a Python script to calculate GC content across large DNA sequences to study genome stability.
- Tools and Software: Biopython, Matplotlib, Pandas.


Comprehensive Analysis of SARS-CoV-2

Oct 2024



- Conducted genome assembly, variant classification, and structural prediction of the SARS-CoV-2 spike protein.
- Tools and Software: SPAdes, Nextclade, PyMOL, AlphaFold.

Certifications

Specialization in Bioinformatics(Coursera, UC SanDiego) 

Genomic Data Science Specialization (Coursera, Johns Hopkins University)

Python for Data Science and AI (IBM)

Technical Skills

Programming Languages: Python, R, SQL, Bash, JavaScript, Java, MATLAB

Data Analysis and Machine Learning: Pandas, NumPy, SciPy, TensorFlow, Scikit-learn

Genomics Tools: BLAST, BWA, HISAT2, edgeR, MEGA

Visualization: ggplot2, Matplotlib, Cytoscape

Version Control and Cloud Platforms: Git, GitHub, AWS, Google Cloud