

JOHN REDDY PEASARI

Bioinformatics Student & Research Assistant

@ johnreddy.peasari@slu.edu

+1-207-299-2199

Saint Louis, MO USA

johnreddy.me

linkedin.com/in/JohnPeasari

EDUCATION

Saint Louis University

Masters in Bioinformatics and Computational Biology

Aug 2019 – Present

Saint Louis, MO, USA

- GPA: 3.92 - Graduate Scholarship - Graduate assistant ship

Sreenidhi Institute of Science and Technology

Bachelors in Biotechnology, B.TECH

Sep 2014 – April 2018

Hyderabad, India

- GPA: 3.70 - Best Student of Biotechnology

EXPERIENCE

Donald Danforth Plant Science Center-Intern

The Slotkin Laboratory

June 2020 – August 2020

Saint Louis, MO, USA

- Performed the analysis of amplicon deep sequencing samples in various transgenic plants. Developed a tool to quantify the methylation status of each cytosine from the Kismeth program generated output.

Graduate Research Assistant

Saint Louis University

September 2019 – Present

Saint Louis, MO, USA

- Performed Bulk RNA Seq analysis of Yeast sequencing data. Developed a pipeline to predict 3' UTR ends from the RNA seq data and compared UTR diversity across the samples. Phylogenetic studies of wtf genes in schizosaccharomyces species.

Scientific Assistant

BhaPra Biosolutions

October 2018 – June 2019

CCMB, Hyderabad, India

- Worked in the project titled "Development of Mosquito repellent military uniform impregnated with mosquito repellent formulations in meso porous silico nano particles. Synthesized Mesoporous silica nano particles and standardized mosquito repellents.

Undergraduate Researcher

Department of Biotechnology, India

Sep 2018 – Aug 2019

SNIST, Hyderabad, India

- Successfully finished multiple projects in Bio process lab. Involved in the cultivation of algae and spirulina for biomass production, lipid enhancement and astaxanthin extraction.

LANGUAGES

Telugu, English

Hindi



TECHNICAL SKILLS

Python, Linux, BASH, R, NGS Tools, SQL, Git
C++, SAS, HPC
HTML



PROJECTS

Predicting 3'UTR ends from RNA-Seq data

3 UTR ends were predicted using the single ends reads sequencing depth

Quantifying RdDM strength based on the methylation pattern

Used Python and Open CV library to accurately quantify the RNA directed DNA methylation strength. This tool was made user friendly to be used by anyone

Measuring poly(A) tail length variation in Arabidopsis thaliana SOC1 gene

Automated pipeline to measure Poly (A) and Poly (T) homo polymers lengths across 20 deep sequenced transgenic samples

Health Care Organisation Database

End to end database was created using MS SQL Server-19, PostgreSQL and SQLite

Detection of Facial Expression in Real-Time using Convolution Neural Networks

Optimization of stress conditions in Chlorella sorokiniana for enhanced lipid and PUFA content

Growth of Chlorella sorokiniana in small scale race way pond using grape pomace as a nutrient source for bio diesel production

PUBLICATIONS

- Phytochemical screening and in silico studies of flavonoids from Chlorella pyrenoidosa.
- Chromatographic analysis of phytochemicals in costus igneus and computational studies of flavonoids.
- Simultaneous Production of Astaxanthin and Lipids from Chlorella Sorokiniana in presence of Reactive Oxygen Species.
- An siRNA-guided ARGONAUTE protein directs RNA Polymerase V for the first round of RNA-directed DNA methylation - InReview

ACHIEVEMENTS

- CAMDA challenge - Participated in ISMB 2020 virtual conference
- Received a fellowship award for ISMB 2020
- President of Technical Association of Biotechnology club.
- Awarded Nova Scotia Graduate Scholarship -Dalhousie University.

For more info please click here: johnreddy.me.