

John Reddy Peasari

Technical Skills: Windows, Linux, Python, R, SQL, BASH, SAS, HPC, C++, Git, ML, Biometry
NGS analysis: QC tools, alignment tools, quantification tools, DGE, IGV, GATK, WES, RNA Seq, DNA seq data analysis, Bioconductor, Samtools, Deeptools, Bedtools, Bcftools, Blast (command line), Schrodinger suite, Pymol, Auto dock etc....

Experience

- Bioinformatics Analyst, University of Oklahoma Health Sciences Center**

July 2021 – Present

 - Bioinformatics analyst under Dr. William Sonntag at OUHSC in the Geroscience and Healthy Brain Imaging Center core.
 - Responsible for various NGS analysis for the PJI’s at the core. Analyzing the animal behavior data, ingenuity analysis pathway.
- Graduate Research Assistant, Saint Louis University**

September 2019 – May 2021

 - Working as a graduate research assistant under Dr. Zhenguo Lin on the next generation sequencing data analysis.
 - Identifying differentially expressed genes in the Bulk RNA sequencing data of yeast.
 - Phylogenetic studies, studying the 3 ‘UTR polymorphisms across the genes.
- Research Intern, Donald Danforth Plant Science Center**

June 2020 – August 2020

 - Employed as a summer research intern by Dr. R. Keith Slotkin to work with deep sequencing data of plants.
 - Collaborated with post-doctoral research associates in Keith’s lab and successfully executed two informatics projects.
 - A program was developed to analyze various dot plots using Python OpenCV to quantify methylation strength.
- Scientific Assistant, BhaPra BioSolutions Pvt Ltd**

October 2018 – May 2019

 - Worked under the guidance of Dr. Janapala Venkateswara Rao, CEO & Retired Chief Scientist.
 - My responsibilities were: planning, executing experiments, analyzing the results, and presenting to the CEO. Also includes, maintaining SOP’s, lab records, paperwork, writing quarterly project reports and guiding a research intern in the lab.
- Undergraduate Researcher, SNIST**

September 2017 – August 2018

 - Worked as an in the bioprocess laboratory under Dr. Yadavalli Rajasri with algae cultivation.
 - Designed multiple experiments, performed, and published my research work in reputed journals.
 - Involved with the cultivation of algae and Spirulina for biomass production, lipid extraction and astaxanthin extraction.

Projects

- Quantifying RNA directed DNA Methylation Strength (RdDM) based on the methylation pattern.**

 - Analyzed the methylation dot plots of various transgenic plants.
 - RdDM strength was quantified and compared across various Kismeth generated methylated dot plots.
 - A tool was developed using Python, OpenCV, and Jupyter Notebook that will produce various distribution of the dot plot.
- Measuring poly(A) tail length variation in various transgenic Arabidopsis thaliana plants SOC1 gene**

 - Analyzed amplicon deep sequencing data from twenty plants generated using ePAT technique.
 - Compared poly A and poly T length distributions across the samples.
 - Used various next generation sequencing data analysis tools to achieve the final goal of the project.
 - Python was used to build automated scripts and R was used to generate various distribution plots.
- Identifying 3 ‘UTR end coordinates and quantifying read coverage across all the predicted 3 ‘UTR from the saccharomyces cerevisiae RNA sequencing data.**

 - 3 ‘UTR coordinates and the read coverage of the of all the genes in saccharomyces cerevisiae were predicted.
 - Developed a pipeline using BASH and Python.
 - Comparison of 3 ‘UTR diversity across 18 different conditions. Working on to optimize the pipeline.
- Analyzing Bulk RNA sequencing data of saccharomyces cerevisiae species.**

 - Used edgeR, Deseq2 to identify various differentially expressed genes.

- CMap Drug Safety Challenge: CAMDA – Improving deep learning accuracy on prediction of drug induced liver injury.**

 - Camda -2020 challenge focusses on understanding or predicting a drug’s potential to cause acute liver failure i.e., DILI and the conference provided gene expression data from six different cell lines.
 - we aimed to improve the performance of deep learning on this challenge by investigating different methods of preprocessing data and network architectures.

Education

- Saint Louis University, MO, USA, GPA 3.93/ 4.00**

August 2019 – May 22, 2021

MS Bioinformatics and Computational Biology
- Sreenidhi Institute of Science and Technology, India, GPA 3.70/ 4.00**

September 2014 – April 2018

Bachelors (BTech) Biotechnology

Publications

- Phytochemical screening and in silico studies of flavonoids from *Chlorella Pyrenoidosa*, Informatics in Medicine Unlocked.
- Simultaneous production of astaxanthin and lipids from *Chlorella Sorokiniana* in the presence of reactive oxygen species.
- Chromatographic analysis of phytochemicals in *Costus Igneus* and computational studies of flavonoids.
- An siRNA-guided ARGONAUTE protein directs RNA Polymerase V for the first round of RNA-directed DNA methylation.

Accomplishments

- Graduate research assistant and graduate scholarship during my master’s at SLU.
- CAMDA challenge - Participated in ISMB 2020 virtual conference and received a fellowship award for ISMB 2020.
- Best student of biotechnology and president of Technical Association of Biotechnology club.

For more information, please click here: johnreddy.me