PEASARI JOHN REDDY

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Objective: To be a successful professional in the rapidly growing technology, research and contribute my part for the better of technology and society.

Educational Qualifications:

Saint Louis University, Missouri, USA

August 2019 – May 2021

Master's in Bioinformatics and Computational Biology: 3.93 GPA

Sreenidhi Institute of Science and Technology, Telangana, India.

September 2014 - April 2018

Bachelor of Technology in Biotechnology, Percentage: 3.70 GPA

Board of Intermediate, Telangana, India

June 2012-March 2014

Major in Mathematics, Physics & Chemistry, Percentage: 95%

Secondary School Certificate, Telangana, India.

June 2011- March 2012

10th Grade, GPA: 9.8/10

Research Experience:

Bioinformatics analyst – University of Oklahoma Health Sciences Center, USA

July 20 – Present

Working as a full-time bioinformatics analyst under Dr. William Sonntag in the GeroScience and Healthy Brain Imaging Center. I am responsible for all the bioinformatics analysis conducted by the PI's and PJI's at the core center. Mostly, I deal with the next generation sequencing data like RNA Sequencing, Whole DNA sequencing, Whole Exome Sequencing etc.

Other works include: Ingenuity pathway analysis or IPA, Image analysis, analyzing animal behavior data, other data analysis. Assisting with the visualization, publication ready figures, and manuscript.

Research Intern – Donald Danforth Plant Science Center, USA

June 2020 – August 2020

Employed as a research intern last summer in The Slotkin Laboratory. Collaborated with post-doctoral research associates in Dr. Keith's lab and successfully finished two projects. Used various tools in analyzing deep sequencing samples of transgenic plants. A program was developed to quantify RNA-directed DNA Methylation strength of various dot plots generated from various samples using Python and it is made user-friendly to be used by anyone in the lab. Attended weekly lab meetings and presented my work to lab members at the end. Wrote my contributions for the paper that is in review at Nature Genetics.

Worked as a GRA under the supervision of Dr. Zhenguo Lin in the biology program on next-generation sequencing analysis. Initially, I was exposed to various NGS tools and software and explored them to acquaint myself with those tools. Performed phylogenetic studies, RNA seq analysis, predicting 3 UTR ends from RNA single-end data. Variant calling analysis (In progress). A pipeline was developed using BASH and Python that predicts 3'UTR coordinates and the read coverage across the 3'UTR regions in saccharomyces cerevisiae RNA seq data.

Scientific Assistant - BhaPra BioSolutions, India

October 2018 – June 2019

Employed as a Junior Scientific Assistant with BhaPra BioSolutions Pvt. Ltd, under the guidance of Dr. Janapala Venkateswara Rao (Chief Scientist, Indian Institute of Chemical Technology, IICT). I worked on the project "Development of Mosquito repellent military uniform impregnated with mesoporous silico nanoparticles". My role was to optimize the protocol to produce mesoporous silica nanoparticles. My responsibilities include planning, executing experiments and presenting them to the CEO and analyzing the results. Also includes, maintaining SOP's, lab records, paperwork, writing quarterly project reports and guiding research intern in the lab.

Undergraduate Researcher - SNIST, India

September 2017 – September 2018

Worked as an undergraduate researcher under Dr. Rajasri Yadavalli (Associate Professor) in the bioprocess laboratory with algae. I designed multiples experiments, executed them, and published my research work in reputed international journals. Responsibilities include are: Plan experiments, perform experiments, discuss progress with the PI weekly, maintain the lab facilities, guide fellow lab mates, write reports, present work at various international conferences, and publish work. My work here got me a research award, a prize for poster presentation and finally, I am here at SLU with funding because of this work.

Publications:

- 1. Rajasri Yadavalli, <u>John Reddy Peasari</u>, Priyadarshini Mamindla, Praveenkumar, Sri Mounika, Jayasree Ganugapati, Phytochemical screening and in silico studies of flavonoids from *Chlorella pyrenoidosa*, Informatics in Medicine Unlocked, Volume 10, 2018, Pages 89-99, ISSN 2352-9148.
- 2. Yadavalli, Rajasri, Hariprasad Ratnapuram, <u>John Reddy Peasari</u>, C. Nagendranatha Reddy, Veeramuthu Ashokkumar, and Chandrasekhar Kuppam. "Simultaneous production of astaxanthin and lipids from Chlorella sorokiniana in the presence of reactive oxygen species: a biorefinery approach." Biomass Conversion and Biorefinery (2021): 1-9.
- 3. **John reddy Peasari,** Sneha Sri Motamarry, Karthikeya Srinivasa Varma, P. Anitha, Ravindra Babu Potti, Chromatographic analysis of phytochemicals in *costus igneus* and computational studies of flavonoids, Informatics in Medicine Unlocked, 2018, ISSN 2352-9148.

4. An siRNA-guided ARGONAUTE protein directs RNA Polymerase V for the first round of RNA-directed DNA methylation.

Course Work:

Masters: Genomics, bioinformatics 1, data structures, biometry, machine learning, bioinformatics II, databases, algorithms, and computational biology, SAS, Health care data science- High Performance computing.

Bachelors: Microbiology, biochemistry, cell biology, genetics, molecular biology, genetic engineering, immunology, bioinformatics, instrumental methods of analysis, bioprocess engineering, plant biotechnology, animal biotechnology, environmental studies, biochemical reaction engineering, process engineering calculations, mass transfer and separations, momentum and hear transfer, food science and technology, managerial economics and financial analysis, (bioethics, biosafety and IPR), computational molecular biology, biosensors and nanobiotechnology, downstream processing, management science.

Projects:

Identifying 3'UTR coordinates and quantifying read coverage across all the predicted 3'UTR ends from saccharomyces cerevisiae RNA sequencing data.

- 3'UTR coordinates of all the genes in saccharomyces cerevisiae were predicted.
- Read coverage was calculated across all the 3'UTR ends.
- Built a pipeline using BASH and Python.
- 3'UTR diversity was compared across 18 different conditions. Working on to optimize the pipeline.

Measuring the poly-A and poly-T tail length variation in various transgenic *Arabidopsis thaliana* SOC1 gene.

- Analyzed amplicon deep sequencing data from twenty samples.
- Compared poly A and Poly T length distribution across the samples.
- Used various bioinformatics tools to achieve this task.
- Python was used to build scripts that automates this analysis.
- R was used to generate various distribution plots.

Quantifying RNA directed DNA Methylation Strength (RdDM) from various methylation patterns.

- Analyzed the methylation dot plots of various transgenic plants.
- RdDM strength was quantified and compared across various Kismeth dot plots.
- A tool was developed using Python and OpenCV library.
- R was used to generate violin plots and box plots to show the distribution of the RdDM strength.

End to end RNA sequencing analysis of saccharomyces cerevisiae data.

- Successfully implemented pipeline for the bulk RNA sequencing analysis.
- Employed BASH and various tools to achieve this task.
- Used Deseq2 to identify various differentially expressed genes.

Designed and built health care organization database.

- End to end health care organization database was created.
- Constructed initial ERD, relational schema, and performed Normalization.
- Used SQL, Microsoft SQL Server 2019, Postgress SQL, sqlite.

Improving Deep Learning Performance on Prediction of Drug-Induced Liver Injury

- The annual international conference on Critical Assessment of Massive Data Analysis (CAMDA) releases challenges each year to tackle big data problems in the life sciences; the CMap Drug Safety challenge focuses on the prediction of DILI.
- This year (2020), we seek to improve the performance of deep learning on this challenge by investigating different methods of preprocessing data and network architectures.
- Our current leading model was able to predict severe DILI more accurately than previous deep learning results.

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

- In this study, various stress conditions were optimized to obtain high lipid content in Chlorella sorokiniana.
- C.sorokiniana was cultured under the mixotrophic condition in modified BG-11 media.
- Lipids were extracted by Bligh-Dyer method and trans esterified samples from C. sorokiniana were analyzed by Gas chromatography.

Growth of *Chlorella sorokiniana* in small scale raceway pond using Grape Pomace as a nutrient source in a fed-batch mode for biodiesel production.

- Emerging economies and growing world population heavily rely on natural sources of the earth.
- As sustainable production methods for food and energy are necessary, so cultivation of microalgae can be an important contribution for transition into a more sustainable society.
- To decrease negative impact on the environment, fruit waste like grape pomace can be used as one of the alternative sources as a growth medium.
- C.sorokiniana was cultivated, lipids were extracted and analyzed.

Technical Skills

Operating System: Microsoft Windows and Linux

Programming Languages: Python, R, C++, SQL, and BASH scripting

Statistical programming: SAS

Version control: Git

NGS Tools: NCBI SRA Toolkit, FastQC, fastp, MultiQC, STAR, Bowtie2, Tophat, Velvet, CANU, Hisat2, BWA, Salmon, SPAdes, Quast, IGV, HTSeq, featureCounts, StringTie, SAMtools, bedtools, deeptools, Bioconductor, BBDuk, trimmomatic, BBMap, Cutadapt, Galaxy, BLAST (command line), GATK, Genedoc, MEGA, ClustalW, Schrodinger maestro, Desmond maestro, Pymol, Chimera, Modeller, HMMER, Discovery studio, Autodock.

Databases: NCBI, UCSC Genome Browser, SGD, Uniprot, PDB.

Conferences & Symposiums:

- Participated in CAMDA 2020 (*Critical Analysis of Massive Data Analysis*) virtual conference from July 26, 2020 July 27, 2020.
- Poster Presentation on <u>In-silico approach to design a drug for Osteoarthritis</u> in International Conference on Biotechnology and Bioengineering- Trends organized by CBT, IST, JNTUH & DBT, SNIST held from 23rd-25th March 2017.
- Oral presentation on "<u>Production of Mosquitocidal Endotoxins by Degradation of Chicken Feather</u> waste" at BITS Pilani Hyderabad organized by ATMOS held from 14th -16th October 2011.
- Presented a poster in World Health Congress, Hyderabad in the month of August 2017.
- Presented a poster titled "<u>Phytochemical Screening and Insilco studies of Flavonoids from Chlorella pyrenoidosa</u>" at the XIV BRSI Convention and International Conference, organized by Council of Scientific and Industrial Research-National Environmental Engineering Research Institute (CSIR-NEERI) Nagpur, 2017.
- Received 2nd prize for Poster Presentation entitled "Growth of Chlorella sorokiniana In Small Scale Race Way Pond Using Grape Pomace as Nutrient Source in Fed-Batch Mode for Biodiesel Production" in the National Symposium on "Emerging Environmental Challenges: An Engineering Approach (EEC-2018)" held on 16th February 2018 at BITS-Pilani, Hyderabad Campus in collaboration with CSIR-NEERI.
- The abstract titled "Homology modeling and Molecular Dynamic simulations of Human Sulfonylurea receptor1: A Pancreatic Protein" is selected for International Conference on Biotechnological Research and Innovation for Sustainable Development, XV BRSI Convention 22-25 November 2018 organized by CSIR-IICT in association with Biotech Research Society, India (BRSI).

Educational Accomplishments:

- Received graduate scholarship for 2 years from Saint Louis University College of Arts and Sciences.
- Received graduate research assistant to work under bioinformatics and computational biology department.
- Appointed as a research intern at the Donald Danforth Plant Science Center last summer to work in Dr. Keith's lab.
- Received fellowship from ISMB CAMDA 2020 to attend the virtual conference.
- Recipient of **Research Ratna Award 2019** (Best Researcher) by RULA awards for one of my publication.
- Accredited member of World Research Council in compliance with Accreditation number WRC-RRF-IND-1079 for the year 2019-20.
- Nominated for Student Innovation Award 2019 by the faculty of the department of Biotechnology, SNIST.
- Cleared SAP online assessment test conduct by TASK, Government of Telangana.
- Received full fee waiver from 'The Princeton Review' for Undertaking GRE in the year 2017.
- Received Best student of the biotechnology award for the academic year 2015-2016 on an annual day from the head of the department Dr. K.S.R Siva Sai.
- Stood in third place with 3.70 GPA in bachelors.
- Overall performance award in class 10th.

Other Activities:

- Certificate of Achievement for securing the second position at Sports Bout 2018 (State level Inter College Tournament) held during 5th and 6th January 2018.
- Elected as President of the biotechnology club, **TAB** (Technical Association of Biotechnology).
- Worked as an Organizer for Rigolade 2017 in Sreevision cultural fest at SNIST.
- Organized **Bio-Mania** 2017 event during Sreevision 2017.
- Participated in **Bio-Mania** guiz conducted in Sreevision in the year 2016.
- Received participation certificate for Bio-war (Quiz) conducted in Sreevision cultural fest in the year 2014.
- Designed a customized mini raceway pond for Algal Cultivation.
- Selected for Nova Scotia Graduate Scholarship from Dalhousie University.

Yours sincerely, John Reddy Peasari