




Sai Hariharan Sankara Subramanian

Computational Biologist/NGS Data analyst

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ABOUT ME

Bioinformatician/ Computational Biologist having 5+ years of experience in the field of Metagenomics, NGS data analysis, and Computational Drug Discovery. Published 5 research publications in reputed journals including nature communications. Skilled in various programming languages, Workflow scripting languages, statistical tools and molecular biology techniques. Strong research professional with a Master of Technology (M.Tech.) in Bioinformatics from SASTRA having done a Master's thesis at the University of Texas at Austin.

PROFESSIONAL EXPERIENCE

Senior Bioinformatician, Decode Age

Mar 2022 – present
Bengaluru, India

- Developed end-to-end metagenomic pipelines for analyzing gut microbial profiles and generating personalized reports for customers.
- Supervising a bioinformatics team for building scalable automated pipelines, creating storage repositories, and curating gut microbial information.
- Experience in developing microbiome bioinformatics and metagenomics pipelines for NGS (ONT and Illumina) datasets using WSL such as Nextflow and Snakemake.
- High proficiency in computational and programming languages, including a working knowledge of R, bash, and Python.
- Interpretation and visual representation of large metagenomic datasets using various R packages.
- Understanding the role of the gut microbiome in disease etiology and Aging to device strategies for extending healthspan.
- Submitted abstracts to two major conferences (7th International Conference on Gastroenterology and Aging and gerontology conference, Hungary)

Senior Research Fellow, National Institute of Ocean Technology (NIOT)

Sep 2018 – Mar 2022
Chennai, India

- Developed a semi-automated pipeline to identify bioremediation enzymes from high-throughput metagenomic datasets using python and shell script on a Linux platform.
- Conducting and optimizing both 16S rRNA gene sequencing and whole metagenome sequencing experiments, using Illumina and/or nanopore platforms.
- Analyzing metagenomic sequencing data to identify and profile microbial communities, including taxonomic classification of microbes using 16S rRNA gene sequences, as well as functional annotation of metagenome-assembled genomes (MAGs) or gene catalogs.
- Expertise in molecular biology techniques to extract DNA from deep-sea water, sediment, and bacterial samples, characterise and analyze them at both sequence and structure levels.
- Experience in Developing web portals and MySQL databases.

- Participated in a cruise on NIOT research vessel "ORV Sagar Nidhi" for collecting deep-sea sediment and water samples.

Project Trainee, Jubilant Biosys Limited ☑

Jul 2018 – Sep 2018
Bengaluru, India

- Analysed and studied protein-ligand complex using computational chemistry tools and methods to identify a potential compound for a specific target.

- Experience in working on tools such as Schrodinger, Cresset, pyMol, pyRx.

Research Scholar, The University of Texas at Austin (UT Austin) ☑

Jan 2017 – Jul 2017
Austin, USA

- Performed Virtual Screening of over 3.6M compounds for identifying potential drug candidates to inhibit the role of a protein of interest involved in DNA damage repair pathway associated with the etiology of human cancer.

- Modelled interaction of non-B-DNA structures with DNA damage repair proteins and elucidated the key residues for its mechanism of action.

- Experience in Virtual Screening, Docking, Modelling protein-DNA interaction, and Energy minimization related studies

EDUCATION

M.Tech Bioinformatics, SASTRA University ☑

2012 – 2017
Tanjavur, India

- Grade: CGPA: 7.489/10

- Integrated (5yr) M.Tech in Bioinformatics. Aced in key courses such as Machine Learning, Drug Design, NGS with projects in Network pharmacology.

- Activities and societies: University Football team, Organised symposium, Music band.

PUBLICATIONS

Microbial community structure and exploration of bioremediation enzymes:

18 Mar 2023

functional metagenomics insight into Arabian Sea sediments,

Molecular Genetics and Genomics

Deep-sea sediment metagenome from Bay of Bengal reveals distinct microbial

22 Nov 2022

diversity and functional significance, Genomics ☑

Vertical Microbial Profiling of Arabian Sea Oxygen Minimal Zone Reveals Complex

23 Feb 2022

Bacterial Communities and Distinct Functional Implications, Microbial Ecology ☑

Distinct DNA repair pathways cause genomic instability at alternative DNA

13 Jan 2020

structures, Nature Communications ☑

RemeDB: Tool to predict Bioremediation related enzymes from High-throughput

01 Dec 2019

metagenomic datasets, Journal of Computational Biology ☑

INTERESTS

Football (University Football Team) | **Cooking** ☑ (Commercial scale)

Music (Percussionist, performed at several events)