

# NIKHIL YENGALA REDDY

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## OBJECTIVE

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Innovative and analytical specialist with a solid background in data analysis and bioinformatics, as well as a great passion for UI/UX design. Possesses extensive experience in interpreting complex biological data and turning discoveries into apps that are easy for users to utilize. Eager to use experience in bioinformatics and data science to further the creation of user-friendly, data-driven products and platforms. Seeks to improve user experiences in scientific research or healthcare technologies by fusing analytical skills with design thinking. Ultimately will lead to the development of refined, friendly, and vital data visualization and interpretation.

## EDUCATION

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### MS in Bioinformatics

*Johns Hopkins University, Maryland*

08/2021-05/2023

### BS in Molecular Biology, Minor Chemistry

*San Jose State University, California*

08/2021-05/2023

## RELEVANT EXPERIENCE AND PROJECTS

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### Github Project | [rnikhil10.github.io](https://github.com/rnikhil10) | Personal Project

2022-2023

A meticulously curated showcase of my interdisciplinary expertise at the intersection of bioinformatics, data science, and UI/UX design, my portfolio demonstrates a deep commitment to leveraging technology for solving complex biological problems and enhancing user experience in scientific applications. It reflects my proficiency in a range of technical skills, from advanced data analysis to intuitive web design, underpinned by a solid educational foundation in bioinformatics from Johns Hopkins University.

### Research | Department of Microbiology and Bioinformatics | San Jose State University

2020-2020

Worked on Multidrug Resistance (MDR) genes to identify species from which they originate and to further understand the structure and mechanism through which it functions. The genes belonged to a family of proteins known as the major facilitator superfamily (MFS). Used Biopython to obtain large genomic data from PDB. The tools, such as MABL and UNIPROT, were used to understand the gene's origination through multiple sequence alignment with related species and then constructed a phylogenetic tree. Another tool such as Pymol was used to analyze the structure of MDR proteins.

### Bioinformatics Academic Project | Department of Bioinformatics | San Jose State University

2019-2019

Identified and analyzed conserved regions in the Rhodopsin protein sequence among the various species. Performed series of data collection through the NCBI data bank. The tools, such as Galaxy and UCSC Genome Browser, was used to perform for NGS data analysis. In addition, the tool, WEBLOGO3, was used to make motif sequence to find highly conserved regions.

## VOLUNTEER EXPERIENCE

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### Sinai Hospital | Baltimore, Maryland

2022-2023

- Collaborated with healthcare staff to ensure smooth patient flow and efficient operations.
- Demonstrated strong communication skills while interacting with diverse patient populations.

### Stanford University Medical Center Hospital | Stanford, California

2015-2015

- Interacted with supervisor to ensure the patients are comfortable.

## INVOLVEMENT

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### BSA Advisory Board Chair and Student Member

2019-2021

*Biological Student Association (BSA), San Jose State University, San Jose, CA*

- BSA Advisory Board is a program run by junior and senior students designed to advise students majoring in biology
- Chair of BSA Advisory Board and served as a mentor to new and fellow students

## SKILLS

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Python (Pandas, Spark, Jupyter), Java, HTML, CSS, JS, SQL, R (ggplot), Linux/UNIX, NGS, Tableau, Github