SAINADH JAMMIGUMPALA

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EDUCATION

National Institute Of Technology Calicut, India **CGPA - 8.54**

BTech(Computer Science and Engineering),2023

Coursework: Data Structure, Design, and Analysis of Algorithms, Operating System, DBMS

WORK EXPERIENCE

- **Variant Curation Service – (SDE, Strand Life Sciences)** **Feb 2024 - Present**

  Next.js, MUI, Node.js with NestJS framework
  - Developed the VIQ Scoring Wizard to automate variant classification by enforcing SOP guidelines, standardizing evidence scoring, and minimizing human error.
  - Built a rule-based curation engine using custom JSON rules to assess variant pathogenicity, significantly improving curation workflow efficiency.
  - Designed interactive UI components, backend APIs, and modular database schemas; implemented migration logic to manage evolving rule sets.
  - Optimized MongoDB indexing and schema design to enable real-time variant data retrieval, supporting penetrance models for gene and variant classification
- **Disease Allele Frequency – (SDE, Strand Life Sciences)** **Aug 2023 - Feb 2024**

  Next.js, MUI, Node.js with NestJS framework, AWS Athena
  - Developed an automated DAF platform that reduced gene-wise, transcript-level variant frequency analysis from days to minutes by integrating data from gnomAD, ClinVar, and internal databases.
  - Engineered scalable backend APIs with AWS Athena to efficiently query and process large-scale genomic datasets.
  - Built robust backend schemas, UI components, and parsers for ClinVar API and gnomAD VEP annotations to support automated frequency calculations.
  - Enhanced performance and data accuracy through variant filtering pipelines.
- **Genome Sequencing & Color Blindness Analysis – (SDE, Strand Life Sciences)** **Jul - Aug 2023**

  Python, Genomics, BWT, Suffix Trees, Read Alignment
  - Implemented custom read alignment algorithms using both Suffix Trees and Burrows-Wheeler Transform (BWT) to analyze over 3 million DNA reads from Chromosome X.
  - Reduced alignment time to under 1 second per read using optimized rank/select structures and memory-efficient delta parameters.
  - Identified genetic anomalies responsible for color blindness by comparing exon-level read counts and simulating theoretical mutation mosaics.
  - Parsed and visualized complex genomic data (FASTA, BWT, mapping files) to detect exon-level imbalances, supporting X-linked inheritance mutation theories.
- **Article Similarity Index – (Intern, Strand Life Sciences)** **May – Jul 2022**

  React, Redux, MUI, Flask, NetworkX, Obonet
  - Built a search platform that displays the top 20 articles ranked by relevance to user-submitted phenotypes.
  - Enhanced matching logic inspired by PMC6128307, improving phenotype-to-article scoring accuracy.
  - Integrated caching and optimized graph traversal for fast, scalable similarity computation on large biomedical datasets.
  - Designed a responsive UI with multi-phenotype support and dynamic relevance-based result ranking.

TECHNICAL SKILLS

- Languages: C/C++, Javascript, Python
- Full Stack Development: HTML, CSS, Javascript, ReactJs, NextJs, NestJs, Flask, MUI, Bootstrap
- Database: Mysql, MongoDB
- Data Science: Standard Ml Algorithms(Regression, Classification, Clustering)
- Data Analysis: Numpy, Pandas, NetworkX, Obonet
- Developer Tools: VS Code, Git, Postman

HONORS AND AWARDS

- Selected for the Engineering Leadership Program; currently leading a team of 4 developers.
- Solved 600+ problems on Codeforces, Leetcode, Geeksforgeeks and Interviewbit.