

Mahesh Vangala

I'm a hands-on full-stack web developer and data engineer building scalable web applications, data platforms, and AI-driven automation systems. I focus on solving complex technical problems, designing reliable architectures, and delivering systems that perform in real-world production environments.

Experiences

- 2025
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present
- **App Developer**
[Lifez](#) Boston, MA
 - **Sr. Software Eng. - Data Analytics & Software Development**
Institute for Protein Innovation Boston, MA
 - **Data Scientist**
UMass Chan Medical School Worcester, MA
 - **Sr. Computational Biologist**
Dana-Farber Cancer Institute Boston, MA
 - **Bioinformatics Research Associate**
Vermont Genetics Network, University of Vermont Burlington, VT
 - **Bioinformatics Software Engineer**
Institute for Genome Sciences, University of MD School of Medicine Baltimore, MD

Selected Projects

- 2020
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2022
- **[National COVID Cohort Collaborative \(N3C\)](#)**
UMass Chan Medical School
 - Led the project from plan to prototype to production in under 2 months.
 - Designed and delivered end-to-end automation of weekly data transfers.
 - Continuous integration of feature updates using Docker and AWS Fargate stack.
 - Automated email notifications of data quality metrics.
 - **[Conquering Diseases](#)**
UMass Chan Medical School
 - Re-architected a monolithic .NET data access layer into a decoupled Python GraphQL service, containerized via Docker and deployed on AWS using a custom VPC, enabling secure, scalable data consumption across multiple departments.
 - Implemented a custom authentication and authorization system using JWT and OAuth, ensuring secure access to sensitive data.
 - Developed a custom data model and API for the GraphQL service, enabling secure, scalable data consumption across multiple departments.
 - **Visualization Pipeline for RNA-seq data (VIPER)**
Dana-Farber Cancer Institute
 - A comprehensive solution that performs most standard RNA-seq analyses quickly and effectively.
 - Published work in peer reviewed journal. <https://doi.org/10.1186/s12859-018-2139-9>
 - Played a vital role in devising and developing snakemake-module based pipeline design pattern.
 - **[CloVR: a virtual machine for automated and portable sequence analysis from the desktop using cloud computing](#)**
University of MD School of Medicine
 - CloVR supports use of remote cloud computing resources to improve performance for large-scale sequence processing.
 - Published work in peer reviewed journal. <https://doi.org/10.1186/1471-2105-12-356>
 - My work into comparative genomics pipeline in CloVR resulted in further funding of the project.

Education

- 2008
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2010
- **Professional Science Masters in Bioinformatics (Genomics track)**
Virginia Commonwealth University Richmond, VA

Contact Info

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Skills

Rust
Python
Java
Perl
Bash

Angular
GraphQL

Docker
Kubernetes

Snakemake
Apache Beam
Apache Spark
Dagster

RabbitMQ
Redis
Apache Kafka

SQL Server/MySQL/Postgres
Neo4j
Cassandra
Bigquery
Athena
DynamoDB

AWS
GCP
Terraform