

Mahesh Vangala

I'm a hands-on full-stack 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 present	● Founder & Builder Lifez App	 Boston, MA
2022 2025	● Sr. Software Eng. - Data Analytics & Software Development Institute for Protein Innovation	 Boston, MA
2017 2022	● Data Scientist UMass Chan Medical School	 Worcester, MA
2014 2017	● Sr. Computational Biologist Dana-Farber Cancer Institute	 Boston, MA
2012 2014	● Bioinformatics Research Associate Vermont Genetics Network, University of Vermont	 Burlington, VT
2010 2012	● Bioinformatics Software Engineer Institute for Genome Sciences, University of MD School of Medicine	 Baltimore, MD

Selected Projects

2020 2022	● National COVID Cohort Collaborative (N3C) UMass Chan Medical School <ul style="list-style-type: none">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.
2019 2022	● Conquering Diseases UMass Chan Medical School <ul style="list-style-type: none">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.
2015 2017	● Visualization Pipeline for RNA-seq data (VIPER) Dana-Farber Cancer Institute <ul style="list-style-type: none">A comprehensive solution that performs most standard RNA-seq analyses quickly and effectively.Published work in peer reviewed journal. https://doi.org/10.1186/s12859-018-2139-9Played a vital role in devising and developing snakemake-module based pipeline design pattern.
2010 2012	● CloVR: a virtual machine for automated and portable sequence analysis from the desktop using cloud computing University of MD School of Medicine <ul style="list-style-type: none">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/10.1186/1471-2105-12-356My work into comparative genomics pipeline in CloVR resulted in further funding of the project.

Education

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