

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.	Docker Kubernetes
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.	Snakemake Apache Beam Apache Spark Dagster
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.	RabbitMQ Redis Apache Kafka
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.	SQL Server/MySQL/Postgres Neo4j Cassandra Bigquery Athena DynamoDB

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