

Mahesh Vangala

I'm a full-stack and data engineering leader with a hands-on approach to building systems that work in the real world — from scalable web applications to AI-driven solutions and automation pipelines.

I'm passionate about solving complex technical problems, connecting technology with tangible outcomes, and continually learning along the way.

But technology alone isn't enough. I believe the true measure of leadership is not titles or control, but the ability to empower doers, cultivate accountability, and foster a culture where innovation and integrity thrive.

Having navigated challenging environments, I've seen how leadership can be a force multiplier of talent, and I strive to create workplaces where people can grow, contribute, and be celebrated for their work.

I combine technical mastery with ethical leadership, advocating for environments that value both innovation and human dignity — where results come from empowered teams.

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.
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 module based 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
Neo4j
Cassandra
Bigquery
Athena
DynamoDB

AWS
GCP