

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