

# 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	<b>Founder &amp; Builder</b> <a href="#">Lifez App</a>	📍 Boston, MA
2022   2025	<b>Sr. Software Eng. - Data Analytics &amp; Software Development</b> Institute for Protein Innovation	📍 Boston, MA
2017   2022	<b>Data Scientist</b> UMass Chan Medical School	📍 Worcester, MA
2014   2017	<b>Sr. Computational Biologist</b> Dana-Farber Cancer Institute	📍 Boston, MA
2012   2014	<b>Bioinformatics Research Associate</b> Vermont Genetics Network, University of Vermont	📍 Burlington, VT
2010   2012	<b>Bioinformatics Software Engineer</b> Institute for Genome Sciences, University of MD School of Medicine	📍 Baltimore, MD

## Selected Projects

2020   2022	<b>National COVID Cohort Collaborative (N3C)</b> UMass Chan Medical School <ul style="list-style-type: none"><li>• Led the project from plan to prototype to production in under 2 months.</li><li>• Designed and delivered end-to-end automation of weekly data transfers.</li><li>• Continuous integration of feature updates using Docker and AWS Fargate stack.</li><li>• Automated email notifications of data quality metrics.</li></ul>
2015   2017	<b>Visualization Pipeline for RNA-seq data (VIPER)</b> Dana-Farber Cancer Institute <ul style="list-style-type: none"><li>• A comprehensive solution that performs most standard RNA-seq analyses quickly and effectively.</li><li>• Published work in peer reviewed journal. <a href="https://doi.org/10.1186/s12859-018-2139-9">https://doi.org/10.1186/s12859-018-2139-9</a></li><li>• Played a vital role in devising and developing module based design pattern.</li></ul>
2010   2012	<b>CloVR: a virtual machine for automated and portable sequence analysis from the desktop using cloud computing</b> University of MD School of Medicine <ul style="list-style-type: none"><li>• CloVR supports use of remote cloud computing resources to improve performance for large-scale sequence processing.</li><li>• Published work in peer reviewed journal. <a href="https://doi.org/10.1186/1471-2105-12-356">https://doi.org/10.1186/1471-2105-12-356</a></li><li>• My work into comparative genomics pipeline in CloVR resulted in further funding of the project.</li></ul>

## Education

2008   2010	<b>Professional Science Masters in Bioinformatics (Genomics track)</b> 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