

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
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present
- **Founder & Builder**
[Lifetz App](#) 📍 Boston, MA
- 2022
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2025
- **Sr. Software Eng. - Data Analytics & Software Development**
Institute for Protein Innovation 📍 Boston, MA
- 2017
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2022
- **Data Scientist**
UMass Chan Medical School 📍 Worcester, MA
- 2014
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2017
- **Sr. Computational Biologist**
Dana-Farber Cancer Institute 📍 Boston, MA
- 2012
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2014
- **Bioinformatics Research Associate**
Vermont Genetics Network, University of Vermont 📍 Burlington, VT
- 2010
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2012
- **Bioinformatics Software Engineer**
Institute for Genome Sciences, University of MD School of Medicine 📍 Baltimore, MD

Selected Projects

- 2020
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2022
- **[National COVID Cohort Collaborative \(N3C\)](#)**
UMass Chan Medical School
- 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
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2022
- **[Conquering Diseases](#)**
UMass Chan Medical School
- 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
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2017
- **Visualization Pipeline for RNA-seq data (VIPER)**
Dana-Farber Cancer Institute
- A comprehensive solution that performs most standard RNA-seq analyses quickly and effectively.
 - Published work in peer reviewed journal. <https://doi.org/10.1186/s12859-018-2139-9>
 - Played a vital role in devising and developing snakemake-module based pipeline design pattern.
- 2010
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2012
- **[CloVR: a virtual machine for automated and portable sequence analysis from the desktop using cloud computing](#)**
University of MD School of Medicine
- 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/10.1186/1471-2105-12-356>
 - My work into comparative genomics pipeline in CloVR resulted in further funding of the project.

Education

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

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