

# 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**  
[Lifez 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