

# Mahesh Vangala

A programming enthusiast with full stack expertise bringing ideas to life, using but not limited to, Angular/Python/Beam/Kafka/(Neo4j, Cassandra)/Docker/Kubernetes/(AWS, GCP).

With 10+ years of hands on experience in academic, research and clinical settings working with genomic and clinical data, I bring broad spectrum of skills ranging from Data Engineering, Data Science and Dev/Ops.

Creative and goal oriented, I take immense pride in end-to-end automation of operational tasks and a big believer of the quote "you don't know it until you teach it to a computer".

Looking forward to the opportunities to prove and enhance my leadership and technical expertise.

## Experiences

2017   present	<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
2005   2007	<b>M.S in Biophysics</b> University of Madras	Chennai, India
2001   2004	<b>B.S. in Biotechnology</b> Osmania University	Hyderabad, India

## Contact Info

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## Skills

Rust  
Python  
Java  
Perl  
Bash  
  
Angular  
GraphQL  
  
Docker  
Kubernetes  
  
Snakemake  
Apache Beam  
Apache Spark  
  
RabbitMQ  
Redis  
Apache Kafka  
  
SQL Server/MySQL  
Neo4J  
Cassandra  
Bigquery  
Athena  
DynamoDB  
  
AWS  
GCP