

# 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<br> <br>present | <b>Data Scientist</b><br>UMass Chan Medical School  | Worcester, MA  |
| 2014<br> <br>2017    | <b>Sr. Computational Biologist</b><br>Dana-Farber Cancer Institute  | Boston, MA     |
| 2012<br> <br>2014    | <b>Bioinformatics Research Associate</b><br>Vermont Genetics Network, University of Vermont                   | Burlington, VT |
| 2010<br> <br>2012    | <b>Bioinformatics Software Engineer</b><br>Institute for Genome Sciences, University of MD School of Medicine | Baltimore, MD  |

## Selected Projects

|                   |  |
|-------------------|--|
| 2020<br> <br>2022 | <b>National COVID Cohort Collaborative (N3C)</b><br>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<br> <br>2017 | <b>Visualization Pipeline for RNA-seq data (VIPER)</b><br>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<br> <br>2012 | <b>CloVR: a virtual machine for automated and portable sequence analysis from the desktop using cloud computing</b><br>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<br> <br>2010 | <b>Professional Science Masters in Bioinformatics (Genomics track)</b><br>Virginia Commonwealth University | Richmond, VA     |
| 2005<br> <br>2007 | <b>M.S in Biophysics</b><br>University of Madras   | Chennai, India   |
| 2001<br> <br>2004 | <b>B.S. in Biotechnology</b><br>Osmania University   | Hyderabad, India |

## Contact Info

✉ [vangalamaheshh@gmail.com](mailto:vangalamaheshh@gmail.com)  
in [linkedin.com/in/maheshvangala](https://www.linkedin.com/in/maheshvangala)  
github [github.com/vangalamaheshh](https://github.com/vangalamaheshh)  
🌐 [vangalamaheshh.github.io](https://vangalamaheshh.github.io)  
☎ [\(443\)326-1957](tel:(443)326-1957)

## 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