

## OBJECTIVE

To work on challenging interdisciplinary bioinformatics projects with an opportunity to prove and enhance my skill sets.

## SUMMARY OF QUALIFICATIONS

**Computational:** Cloud Deployment (AWS EC2, Google Compute Engine, Google Container Engine), Kubernetes (Cluster Orchestration), Full stack web development (MongoDB, NodeJs, AngularJS (Angular2), Bootstrap), Parallel Programming, Informatics Pipeline Development, Data Visualization Using R, Highcharts & D3Js, VegaLite.

**Bioinformatics:** NGS data analysis, RNASeq pipeline development and analysis, CRISPR analysis, Google Genomics Framework, Google Big Query, Single-Cell RNASeq Analysis, Metagenomics, Metatranscriptomics and Microbial Genomics data analysis.

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## EMPLOYMENT

University of Massachusetts Medical School <b>Data Scientist</b>	March, 27, 2017 - Present
Dana-Farber Cancer Institute <b>Sr. Computational Biologist</b>	June-16-2014 – March, 24, 2017
Vermont Genetics Network <b>Bioinformatics Research Associate</b>	April, 30, 2011 – June, 13, 2014
Institute for Genome Sciences, Univ. of MD School of Medicine <b>Bioinformatics Software Engineer</b>	September, 15, 2010 – April, 27, 2011
Institute for Genome Sciences, Univ. of MD School of Medicine <b>Bioinformatics Intern</b>	June, 14, 2010 – August, 31, 2010
Virginia Commonwealth University <b>Graduate Teaching Assistant</b>	August, 17, 2009 – May, 12, 2010
S.S.N College, Ongole, India <b>Lecturer</b>	June, 04, 2007 – May, 30, 2008

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## EDUCATION

Center for the study of Biological Complexity, Virginia Commonwealth University <b>M.S in Bioinformatics (Genomics track)</b>	2010
University of Madras, Chennai, India <b>M.Sc. in Bioinformatics</b>	2007
Osmania University, Hyderabad, India <b>B.Sc. in Biotechnology</b>	2004

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## PUBLICATIONS

- Michelle A. Lutz, Scott Tighe, **Mahesh Vangala**, Heather Driscoll, Timothy Hunter, Minoru Takeda, Steven R. Corsi. Environmental factors affecting biofilm abundance, community structure, and gene expression in streams receiving organic deicer runoff, *Environmental Science & Technology*, 2016. (Manuscript submitted.)
  - Sonia Agrawal, Cesar Arze, Shaun Adkins, Jonathan Crabtree, David Riley, **Mahesh Vangala**, Kevin Galens, Claire Fraser, Hervé Tettelin, Owen White, Samuel V. Angiuoli, Anup Mahurkar, W. Florian Fricke. CloVR - Comparative: Automated, cloud-enabled comparative microbial genome sequence analysis pipeline, *BMC Genomics*, 2016.
  - John Stanton-Geddes, Andrew Nguyen, Lacy Chick, James Vincent, **Mahesh Vangala**, Robert R. Dunn, Aaron M. Ellison, Nathan J. Sanders, Nicholas J. Gotelli and Sara Helms Cahan. Thermal reactionomes reveal divergent responses to thermal extremes in warm and cool-climate ant species, *BMC Genomics*. 2016
  - Angiuoli SV, Matalaka M, Gussman G, Galens K, **Vangala M**, Riley DR, Arze C, White JR, White O and Fricke WF. CloVR: A virtual machine for automated and portable sequence analysis from the desktop using cloud computing. *BMC Bioinformatics*. 2011 Aug;12:356.
  - White JR, Arze C, Matalaka M, **The CloVR Team**, Angiuoli SV & Fricke WF. CloVR-Metagenomics: Functional and taxonomic microbial community characterization from metagenomic whole-genome shotgun (WGS) sequences – standard operating procedure, version 1.0. *Nature Precedings*. 05 April 2011.
  - White JR, Arze C, Matalaka M, **The CloVR Team**, Angiuoli SV & Fricke WF. CloVR-16S: Phylogenetic microbial community composition analysis based on 16S ribosomal RNA amplicon sequencing – standard operating procedure, version 1.0. *Nature Precedings*. 05 April 2011.
  - Galens K, White JR, Arze C, Matalaka M, Gwinn MG, **The CloVR Team**, Angiuoli SV & Fricke WF. CloVR-Microbe: Assembly, gene finding and functional annotation of raw sequence data from single microbial genome projects – standard operating procedure, version 1.0. *Nature Precedings*. 05 April 2011.
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## ABSTRACTS

1. R. Kishore, A. Hakobyan, **M. Vangala**, V.N.S Garikipati, A. Khachatryan, L. Nersisyan, P. Mill, M. A. Zuriaga - Herrero, K. Walsh, A. Arakelyan & D. A. Goukassian. Effect of Space Flight on Astronauts Plasma-Derived Exosomal miRNA Expression: Implications for Biomarker Development – Omics, Human Research Program, NASA. 23 Jan 2017.
  2. **M. Vangala**, K. Okamoto, J. Miller, J.P. Dustin, S. Matar, S.M. Ní Chadhain, S. Jones & L.A. Launen. A metagenomic study of the bioremediation potential of sediment microbial communities in an urban estuary – American Society for Microbiology, 114<sup>th</sup> General Meeting. 17 May 2014.
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## **PRESENTATIONS**

1. “ViPeR: Visualization Pipeline for RNASeq Data Analysis.” Center for Functional Cancer Epigenetics, Dana-Farber Cancer Institute, Boston, MA, March, 2016.
  2. “A Metagenomic Study of The Bioremediation Potential of Sediment Microbial Communities in An Urban Estuary.” IDeA Networks of Biomedical Research Excellence, University of Delaware, Newark, DE, August 2013.
  3. “Community Resource Solutions to Analyze Large Genomic Datasets.” Association of Bio Molecular Resource Facilities conference, Palm Springs, CA, March 2013.
  4. “Bioinformatics Project Management: Integrated Workflows, Project Tracking, and User Results.” Association of Bio Molecular Resource Facilities conference, Palm Springs, CA, March 2013.
  5. “Vermont Genetics Network Bioinformatics Core Facility.” Association of Bio Molecular Resource Facilities conference, Palm Springs, CA, March 2013.
  6. “Vermont Genetics Network Bioinformatics Core Facility.” Northeast Regional Life Sciences Core Directors Meeting, Mountain View Grand Resort, Whitefield, New Hampshire, October, 2012.
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## **COMPUTATIONAL SKILLS**

- SYSTEMS – Unix/Linux, Mac, Windows.
- LANGUAGES – Bash shell, Perl, Java, Ruby, Rails, Python, R, JavaScript, Ext-js, AJAX, XML, HTML, CSS.
- DATABASES – MySQL, Normalization, E/R Diagram, Database theory.

## **LAB SKILLS**

- PCR
  - DNA cloning
  - Gel electrophoresis
  - Cell culturing.
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