Uma M. Vangala (Mahesh Vangala)
Boston, MA. **Ph. 443-326-1957**
vangalamaheshh@gmail.com
Website: mvangala.com

OBJECTIVE

To work on challenging interdisciplinary projects in the field of NextGen Research, with an opportunity to prove and enhance my skill sets.

SUMMARY OF QUALIFICATONS

Computational: Cloud Deployment (AWS EC2, Google Compute Engine, Google Container Engine), Full stack web development (MongoDB, NodeJs, AngularJS, Bootstrap), Parallel Programming, Informatics Pipeline Development, Data Visualization Using R.

Bioinformatics: NGS data analysis, RNASeq pipeline development and analysis, CRISPR analysis, Google Genomics Framework, Metagenomics and Metatranscriptomics data analysis, Microbial Genomics data analysis.

Websites built: http://mvangala.com, http://mbcf.dfci.harvard.edu

EMPLOYMENT

Dana-Farber Cancer Institute   June, 16, 2014 - present
Bioinformatics Analyst

Vermont Genetics Network   May, 2012 – June, 13, 2014
Bioinformatics Research Associate

Institute for Genome Sciences, Univ. of MD School of Medicine   September, 2010 – April, 2012
Bioinformatics Software Engineer

Institute for Genome Sciences, Univ. of MD School of Medicine   June, 2010 – August, 2010
Bioinformatics Intern

Virginia Commonwealth University   August, 2009 – May, 2010
Graduate Teaching Assistant

S.S.N College, Ongole, India   June, 2007 – May, 2008
Lecturer

EDUCATION

Center for the study of Biological Complexity, Virginia Commonwealth University   2010
M.S in Bioinformatics (Genomics track)

Univeristy of Madras, Chennai, India   2007
M.Sc in Bioinformatics

Osmania University, Hyderabad, India   2004
B.Sc in Biotechnology

PUBLICATIONS

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, Matalka 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, Matalka 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, Matalka 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, Matalka 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.

PRESENTATIONS

- "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.

- "Community Resource Solutions to Analyze Large Genomic Datasets." Association of Bio molecular Resource Facilities conference, Palm Springs, CA, March 2013.

- "Bioinformatics Project Management: Integrated Workflows, Project Tracking, and User Results." Association of Bio molecular Resource Facilities conference, Palm Springs, CA, March 2013.

- "Vermont Genetics Network Bioinformatics Core Facility." Association of Bio molecular Resource Facilities conference, Palm Springs, CA, March 2013.

- "Vermont Genetics Network Bioinformatics Core Facility." Northeast Regional Life Sciences Core Directors Meeting, Mountain View Grand Resort, Whitefield, New Hampshire, October, 2012.

COMPUTATIONAL SKILLS

- SYSTEMS – Unix/Linux, Mac, Windows.
- LANGUAGES – Bash shell, Perl, Python, R, MEAN application stack (web-development).
- RELATIONAL DATABASES – MySQL, Normalization, E/R Diagram, Database theory.
- GRAPH DATABASES – Neo4j
- PARALLEL PROGRAMMING – Snakemake, CloVR, Ergatis
- CLOUD COMPUTING – Docker, AWS

LAB SKILLS

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