

Viswanadham Sridhara

CONTACT

Viswanadham.Sridhara@gmail.com

Tel: (724) 590 2170

Google Scholar | LinkedIn | Github | BitBucket | Blog | DockerHub

PROFILE

I am a computational scientist with modeling and simulation experience in engineering and life sciences domain. Post-PHD, I have 12+ years' experience analyzing high-dimensional datasets.

Till date, my research work has resulted in ~20 peer-reviewed publications and numerous conference proceedings and poster presentations (google scholar citations: ~580, h-index=11).

EDUCATION

2003 - 2007

PhD, Electrical and Computer Engineering, ODU, Norfolk, VA

Dissertation: Molecular dynamics simulations to probe effects of ultra-short high-intensity electric pulses on biological suspensions

2001 - 2003

MS, Electrical and Computer Engineering, ODU, Norfolk, VA

Thesis: Monte carlo analysis of millimeter-wave GaN Gunn diodes

SKILLS

Machine learning

Regression, Classification, Regularization, Hierarchical Clustering, Discriminant analyses

Programming

Python (numpy, pandas, scikit-learn, matplotlib, tensorflow, keras), R (tidyverse, ggplot), MATLAB, Perl, C, C++, Fortran

Other skills

Git, Snakemake, Docker, UNIX, MacOS, LaTeX, SQLite

Engineering

Monte-carlo models [MS Thesis focus], Molecular dynamics simulations for atomic modeling [PHD Dissertation focus]

PROFESSIONAL EXPERIENCE

Oct '18 - Present

Consultant

Universities, Hospitals and Startups

In my current role, I am working for a proteomics software company.

In previous roles as Independent Consultant (part of 2016, 2017 and 2018) for MGH, WRI and biofuel startup

- Improved primer design for a proof-of-principle assay to capture long genomic regions.
- Built NGS pipeline and developed new computational methods for downstream analyses.
- Set-up in-house Jbrowse genome browser and Sequenceserver (blast+ web server).

Mar '18 - Nov '18

Bioinformatics Systems Developer

Booz Allen Hamilton

- Automated preprocessing of gene expression data (microarray and RNA-seq) for placental datasets using raw data stored in NCBI's GEO repository (PAT - Placental Atlas Tool).

- Improved analytics of differential expression, gene ontology and pathway analyses of the above preprocessed placental datasets (>20 RNA-seq and >300 microarray datasets).

Aug '15 - Apr '16

Computational Biologist

UT Southwestern Medical Center – PROTEOMICS CORE FACILITY

- Protein identification and quantitation using bioinformatics tools.
- Bioinformatics proteomics consultant work with UT Southwestern investigators.

Dec '12 - Aug '15

Research Engineering/Scientist Associate V

The University of Texas at Austin – CENTER FOR COMPUTATIONAL BIOLOGY AND BIOINFORMATICS

- Built machine learning models using LASSO regression to predict bacterial growth conditions from *in-silico* metabolic fluxes generated from metabolic network based flux balance analyses (FBA) methods.
- Collaborated with multiple labs with proteomics bioinformatics consulting and short-term contracts.
- Taught computational mass-spectrometry in Big Data Summer School organized by CCB (Center for Computational Biology and Bioinformatics) every summer – 4 day course)

Jun '07 - Jan '12

Visiting Research Fellow

National Center for Biotechnology Information (NCBI)

- Part of NCBI OMSSA (Open Mass Spectrometry Search Algorithm) project:
 - a. Improved noise filtering routines/filters to accommodate high-resolution mass-spectrometry data.
 - b. Optimized algorithm for ETD data analysis (ion-types, precursor peak filtering).
- Integration of sequence data & high-throughput phosphoproteomics data.
- Developed a prototype for new class of peptide identification search algorithm OMSSA-SIM.
 - b. Preliminary work in ASMS 2011 (oral presentation in computational mass-spectrometry).

Summer '06

Student Volunteer

Old Dominion University - Aerospace Engineering

- Helped improve programming drives for a test bogie run on MAGLEV (train using magnetic levitation).

Summer '04

Intern

Siemens Limited. Siemens Vdo Automotive

- Finite element analyses (2D) to improve fuel injection solenoid models using Ansoft software.

SAMPLE CODE

Jupyter

<https://sivome.github.io/Jupyter>

R Markdown

<https://sivome.github.io/R-markdown>

LDA

<https://www.ncbi.nlm.nih.gov/pubmed/22321509>

Regularization

<https://www.ncbi.nlm.nih.gov/pubmed/25502413>

Visualization-R

<https://www.ncbi.nlm.nih.gov/pubmed/29152409>

DockerHub sample

<https://sivome.github.io/DockerHub-sample>

SELECTED TALKS

1. Large-scale analysis of PTMs @ UT-Austin, Thermo Fisher Scientific, MD Anderson Cancer Center
2. Using subspectral interval matches to make novel identifications of ETD tandem mass spectra @ ASMS 2011
3. Predicting bacterial growth conditions from bacterial physiology @ Center for Systems and Synthetic Biology, UT-Austin
4. Open Mass Spectrometry Search Algorithm @ George Washington University

SELECTED PUBLICATIONS

1. Tosi, L., Sridhara, V., Yang, Y., et. al., "Engineered DNA Capture Probes for Massively Multiplexed Cloning of Kilobase-Sized Genome Regions", *Nature Biomedical Engineering*, 2017;1. pii: 0092. doi: 10.1038/s41551-017-0092. Epub 2017 Jun 26.
2. Sridhara, V., Meyer AG, Rai P, Barrick JE, Ravikumar P, Segre D, and Wilke C.O. "Predicting growth conditions from internal metabolic fluxes in an in-silico model of *E. coli*." (*PLoS One*. 2014 Dec 12;9(12):e114608.).
3. Sridhara, V., Joshi, R. P. "Evaluations of a mechanistic hypothesis for the influence of extracellular ions on electroporation due to high-intensity, nanosecond pulsing." *Biochimica Biophysica Acta - Biomembranes*, Vol. 1838, no. 7, Jul 2014, pp. 1793-1800.
4. Sridhara, V., Joshi, R. P. "Numerical study of lipid translocation driven by nanoporation due to multiple high-intensity, ultrashort electrical pulses." *Biochimica Biophysica Acta - Biomembranes*, Vol. 1838, no. 7, Mar 2014, pp. 902-909.
5. Sridhara, V., Dina L. Bai, An Chi, Jeffrey Shabanowitz, Donald F. Hunt, Stephen H. Bryant and Lewis Y. Geer "Increasing peptide identifications and decreasing search times for ETD spectra by pre-processing and calculation of parent precursor charge." *Proteome Science* 2012, 10:8.
6. Sridhara, V., Aron Marchler-Bauer, Stephen H. Bryant and Lewis Y. Geer, "Automatic annotation of experimentally derived, evolutionarily conserved post-translational modifications onto multiple genomes." *Database* (Oxford), 2011, bar019.

CONFERENCE PROCEEDINGS

1. Sridhara, V., Joshi, R.P., Hu, Q., Nguyen, A., and Schoenbach, K.H. "Simulations of cell response to high intensity, ultrashort electrical pulses" (invited paper) *Bio-Electromagnetic Society Conference*, Cancun, Mexico, June 11-15, 2006.
2. Pliquett, U., et. al., "Monitoring intracellular changes in Jurkat cells after nanosecond pulsed electric field application." *Electromed 2005 Conference*, Portland, OR, May 15-18, 2005.
3. Garner, A.L., et. al., "Changes in the Dielectric Properties of Jurkat and HL-60 cells after Electrical Pulses." *Electromed 2005 Conference*, Portland, OR, May 15-18, 2005.

POSTERS

AACR 2017, Proceedings of the AACR 2016, EMBL Conference 2014, Synthetic Biology: Engineering, Evolution and Design (SEED), ASMS 2010, ASMS 2009, ASMS 2008