



Viswanadham (Vish) Sridhara

CONTACT

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

PROFILE

- [1] Experienced bioinformatics data scientist with over **12 years of experience** in next-generation sequencing (NGS) and mass-spectrometry software applications.
- [2] Skilled in using machine learning and deep learning methods for high-dimensional biological datasets, including **proteogenomics, multi-omics and single-cell applications**.
- [3] Adept in utilizing high-performance computing methods and technologies such as **snakemake, docker containerization, and cloud computing**.
- [4] Proven ability to work effectively in both small and large groups, utilizing **agile project management methodologies**.
- [5] Track record of producing high-quality results with **~20 peer-reviewed publications** (google scholar citations: ~900, h-index=14, incl. Nature Biomedical Engineering IF=27.0).

EDUCATION

2003 - 2007: PHD, Electrical and Computer Engineering (**Biophysics**), ODU, Norfolk, VA
Dissertation (funded by Department of Defense MURI grant): Molecular dynamics simulations to probe effects of ultra-short high-intensity electric pulses on biological suspensions to understand how nano-second pulsed electric fields (nsPEFs) kill cancer cells.

2001 - 2003: MS, Electrical and Computer Engineering, ODU, Norfolk, VA
Thesis: Monte carlo analysis of millimeter-wave GaN Gunn diodes.

TECHNICAL SKILLS

Programming: Python, R (tidyverse), SQL, MATLAB, Shell Scripting
Machine learning: Regression, classification, clustering, deep learning
NGS: Bulk RNA-seq, Single cell RNA-seq, Long read sequencing, DNA-seq/WGS
Mass spectrometry: Identification, Quantitation, PTMs, PPIs, DDA, DIA
Structure and SysBio: AlphaFold2, MetaCyc, SAINT, GROMACS, NAMD, VMD
Pipelines / Data Portals: Snakemake, Nextflow, ICGC, COSMIC, Tranche
DevOps / MLOps: Git, Docker, CI/CD, Databricks (Azure), Sagemaker (AWS)

PROFESSIONAL CERTIFICATES

- [1] Microsoft Azure Databricks for Data Engineering (Microsoft)
- [2] Data structures and Algorithms Specialization (UCSD)
- [3] Google Cloud Fundamentals: Core Infrastructure (Google)
- [4] Foundations of Project Management (Google)

PROFESSIONAL EXPERIENCE

Jul '22 - Feb '23

6 months career break

- Leveraged online learning platforms and resources to gain new skills and knowledge in relevant areas, including deep learning, cloud computing etc.

Apr '21 - Jul '22

Bioinformatics Test Engineer and Technical Writer

Protein Metrics, a Dotmatics company, Cupertino, CA

- Conducted FDR sensitivity calculations for Byonic CI/CD version testing.
- Developed and implemented automated command-line interface (CLI) tests for Byos applications, with a focus on antibody de novo assembly, hydrogen-deuterium exchange (HDX) studies and other proteomics applications.
- Routinely updated customer-facing product manuals (15+) and release notes.

Jun '19 -Mar '21

Senior Bioinformatics Scientist

Food and Drug Administration (Argentys contractor), Silver Spring, MD

- Built an RNA-seq pipeline for bulk processing of large-scale genomics datasets using fastp, HISAT2, featureCounts, and DESEQ2.
- Developed a single-cell RNA-seq pipeline prototype for analyzing 10X datasets using Cell Ranger, SAVER, Seurat/Monocle, fastMNN, and R packages.
- Characterized immune-driven (CD4/CD8 T cells) drug hypersensitivity using single-cell RNA sequencing technologies (10X Genomics).
- Identified molecular features of neural stem cells during different stages of differentiation.
- Conducted single-cell RNA-seq/ATAC-seq analyses (10X Genomics) of bone-marrow and adipose-derived MSCs using Cell Ranger, Monocle, CICERO and other related packages.

Nov '18 - May '19

Part-time Test Engineer

Protein Metrics, a Dotmatics company, Cupertino, CA

- Benchmarking of different Byos applications and comparative studies with leading proteomics software.
- Advanced intact protein analysis for data coming from different instruments.

Feb '18 - Nov '18

Bioinformatics Systems Developer

Booz Allen Hamilton, Rockville, MD

- Participated in design of cloud-based tools using EC2, S3, and Lambda (AWS technologies), to create scalable and cost-effective solutions for data storage, processing, and analysis.
- Developed a genomics pipeline using Snakemake, R packages, and Python modules for PAT, a cloud-based placental atlas tool that uses raw data from the NCBI GEO database.
- Improved analytics for differential expression, gene ontology and pathway analysis for the PAT tool (>12500 datasets for >20 RNA-seq and >300 microarray projects).

Apr '16 - Dec '17

Independent Contractor

Universities, Hospitals and Startups (Remote)

Independent Consultant / Contractor for MGH, WRI and Mascoma

Tools used: Bowtie, samtools, bedtools, BCFtools, LUMPY, GATK (Mutect2, HaplotypeCaller), MUMmer, SPAdes

Mass General Hospital: Designed primers/probes for a new assay, built an end-to-end bioinformatics pipeline and developed new methods to assess metrics for a long genomic region capture protocol at Mass General Hospital. Resulted in a co-first author publication in Nature Biomedical Engineering.

Windber Research Institute: Developed novel statistical methods to integrate multi-omics data of breast tumors at Windber Research Institute, utilizing a combination of machine learning models, clustering methods, and data from DrugBank.

Mascoma: Built custom RNA-seq pipeline, analyzed WGS data, and set-up in-house genome browser and blast+ web server for biofuel production at Mascoma.

Dec '12 - Apr '16

THE UNIVERSITY OF TEXAS SYSTEM (UT AUSTIN, UTSW MEDICAL CENTER DALLAS)

Research Engineering/Scientist Associate V Dec '12 - Aug '15

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

- Worked on a multi-university Army research office MURI grant to build mathematical models for E. coli multi-omics data inference (34 growth conditions, 9 time points).
- Developed a computational method for unbiased identification and characterization of new post-translational modifications using MODa, Python and R scripts.
- Conducted 13C metabolic flux analyses for E. coli samples using FiatFlux software.
- Developed and optimized machine learning models, including LASSO (elastic net) models, to predict bacterial growth conditions based on in-silico metabolic fluxes (FBA).
- Provided proteomics bioinformatics consulting and taught computational mass-spectrometry in a 4-day course at the Big Data Summer School organized by CCBB.
- Managed and oversaw the development of computational infrastructure, including high-performance computing clusters, storage systems, and software tools, ensuring optimal performance and availability for research and development activities.

Computational Biologist Aug '15 - Apr '16

UT Southwestern Medical Center – PROTEOMICS CORE FACILITY

- Conducted protein identification, quantitation, PTM and protein-protein interaction analyses using FAIR data principles with different bioinformatics tools e.g., OMSSA, MASCOT, Sequest, X!Tandem, ProteomeDiscoverer, MaxQuant, SAINT.
- Provided expert bioinformatics and proteomics consulting for UT Southwestern investigators (in compliance with CAP/CLIA regulations), specializing in the analysis of data related to immunology, oncology, and neurological disorders.

Jan '12 - Dec '12

Scientific Programmer

Samuel Roberts Noble Foundation, Ardmore, OK

- Assisted in integrating GenoLogics LIMS system with mass-spectrometry equipment.
- Built pathway databases using MetaCyc and PathwayTools.

Jun '07 - Jan '12

Postdoctoral Fellow

National Center for Biotechnology Information (NCBI), Bethesda, MD

- Improved noise filtering routines and optimized data analysis algorithms for OMSSA (open source mass-spectrometry search engine), utilizing ML models such as LDA to achieve robust and accurate identification and quantification of target peptides.
- Provided OMSSA user support for quantitative proteomics techniques (iTRAQ, TMT 6-plex) by adding requested enzymes, modifications and ion-types.
- Developed a new method for annotating post-translational modifications (PTMs) on genomes using high-throughput proteomics data, protein family domain definitions, and NCBI resources. This method enables large-scale annotation of conserved PTM sites and identification of novel evolutionarily conserved PTMs.
- Developed a prototype to overcome limitations in present-generation sequence library search algorithms, such as exact precursor mass match and unknown PTMs. Presented preliminary work (oral presentation) at ASMS 2011.

Aug '03 - May '07

OLD DOMINION UNIVERSITY (JOSHI LAB, FRANK REIDY RESEARCH CENTER FOR BIOELECTRICS)

Graduate Research Assistant Aug '03 - May '07

COMPUTATIONAL RESEARCH LAB - BIOELECTRICS, Norfolk, VA

- Conducted research under DoD MURI grant (multi university, incl. MIT) to model and simulate the effect of nano-second pulsed electric fields (nsPEFs) on cancer cells.
- Conducted intense Molecular Dynamics simulations to understand nanopore formation in lipid bilayers using GROMACS (analysis) and VMD (visualization).
- Computed permittivities and diffusion coefficients of local lipid membranes.
- Studied the effects of sodium and calcium ions on pore formation in biological suspensions.
- Mentored and trained graduate students, providing guidance and support for research projects and career development.

FRANK REIDY RESEARCH CENTER FOR BIOELECTRICS, Norfolk, VA

- Conducted Time Domain Dielectric Transient Spectroscopy (TDDS) measurements to monitor structural changes in leukemic cells after nsPEF application.
- Analyzed TDDS data with MATLAB signal processing toolbox.

Summer '04

Internship

Siemens Limited. Siemens Vdo Automotive, Chesapeake, VA

- Conducted 2D-FEA using Ansoft software to improve fuel injection solenoid models.

SELECTED

TALKS

1. Engineered DNA Capture Probes for Massively Multiplexed Cloning of Kilobase-Sized Genome Regions, presented at FDA.
2. Using subspectral interval matches to make novel identifications of ETD tandem mass spectra, presented at the 2011 American Society for Mass Spectrometry (ASMS) conference.
3. Predicting bacterial growth conditions from bacterial physiology, presented at the Center for Systems and Synthetic Biology at UT-Austin.

PUBLICATIONS

1. Tosi, L., Sridhara, V., et. al., Nature Biomedical Engineering, 2017.
2. Caglar, M. U., et. al., Scientific Reports 2017.
3. Brown, C. W., Sridhara, V., et. al., BMC Genomics 2017.
4. Kalantari, R., et. al., RNA 2016.
5. Houser, J. R., et. al., PLOS Computational Biology 2015.
6. Sridhara, V., et. al., PLoS One 2014.
7. Sridhara, V., Joshi, R. P. Biochimica Biophysica Acta - Biomembranes 2014.
8. Sridhara, V., Joshi, R. P. Biochimica Biophysica Acta - Biomembranes 2014.
9. Sridhara, V., et. al., Proteome Science 2012.
10. Sridhara, V., et. al., Database (Oxford) 2011.
11. Joshi, R.P., et. al., IEEE Trans. Dielectrics & Electrical Insulation 2009.
12. Allen L. Garner, et. al., Biochemical Biophysical Research Communications 2007.
13. Joshi, R.P., et. al., Physical review. E, Statistical, nonlinear, and soft matter physics 2007.
14. Pliquett, U., et. al., Bioelectrochemistry 2006.
15. Joshi, R.P., Sridhara, V., et. al., Biochemical Biophysical Research Communications 2006.
16. Qin Hu, Sridhara, V., et. al., (invited paper) IEEE Transactions on Plasma Science 2006.
17. Hu, Q., Sridhara, V., et. al., Physical Review E - Statistical, Nonlinear, and Soft Matter Physics 2005.
18. Joshi, R. P., Sridhara, V., et. al., Journal of Applied Physics 2003.
19. Joshi, R. P., Sridhara, V., et. al., Journal of Applied Physics 2003.

CONFERENCE

PROCEEDINGS

1. Sridhara, V., et. al., (invited paper) Bio-Electromagnetic Society Conference 2006.
2. Pliquett, U., et. al., Electromed 2005 Conference.
3. Garner, A.L., et. al., Electromed 2005 Conference.

POSTERS

SCD(FDA) 2020, AACR 2017, Proceedings of the AACR 2016, EMBL Conference 2014, Synthetic Biology: Engineering, Evolution and Design (SEED), ASMS '08-'10

GRANT REVIEWER

National Science Foundation (NSF)

JOURNALS REFEREED

JPR, PLoS Pathogens, Journal of Theoretical Biology, Biology Direct, PLoS Computational Biology, International Journal of Bioinformatics Research and Applications

PROFESSIONAL MEMBERSHIPS

American Association for Cancer Research, American society for mass spectrometry

AWARDS

- 2007: NIH Postdoctoral Fellowship
- 2007: Outstanding Graduate Researcher Award, Old Dominion University
- 2006: BCET Scholarship, Old Dominion University
- 2006: Honorary Mention, ODU Research Foundation Day Poster Presentation
- 1996-2000: National Merit Scholarship, College of Engineering, Osmania University
- 1994-1996: College Scholarship, St. Thomas Samhita Jr. College
- 1994: Certificate of Merit in Mathematics

SAMPLE PROJECTS

Machine Learning

PLoS One paper - Regularization and metabolic network models.
Link to Python code - FBA and sklearn | Link to R markdown - GLMNET predictions

Visualization

Nature Biomedical Engineering paper - Designing probes for genome capture.
Link to R markdown - advanced analysis and Visualization

Cancer Multi-omics

[URL: https://sivome.github.io/Poster_PDFs/Proteogenomic_AACR_Poster.pdf]

Single-cell work

[URL: https://sivome.github.io/Poster_PDFs/SingleCellMSC_SCD_Poster.pdf]

Deep Learning

Link to Python Jupyter notebook - [URL: <https://sivome.github.io/genomics/2019/11/17/Denoising-Single-Cell-Data-With-Autoencoders.html>]