Saradha Venkatachalapathy

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SUMMARY

I am a Ph.D. student specializing in microscopy, genomics and computer vision. My research focuses on using machine learning models to interpret causal relationships in highly variable biological processes. I have experience leading interdisciplinary projects with pathologists and mathematicians to guide the design of experiments and modeling.

EDUCATION

Ph.D, Mechanobiology National University of Singapore	Sep 2016 - Present
B.Tech Biotechnology (Distinction) SASTRA University	Jul 2011 - May 2015

WORK EXPERIENCE

Visiting Researcher Paul Scherrer Institute & ETH Zürich	Sep 2020 - Present
Consultant, Computer Vision Qritive	Sep 2019 - Dec 2019
Research Assistant, National University of Singapore	Sep 2015 - Jul 2016

SKILLS

Statistics: Multivariate Statistics, Linear Algebra, Diffusion maps, Pattern recognition and Machine Learning.

Computer Vision: Segmentation, Feature generation and Particle tracking

Computational Biology: Analysis of bulk and single cell Microarray, RNA-Seq and HiC data.

Experimental Skills: Microscopy, Tissue engineering and mechanical manipulation of cells.

Tools: R, ImageJ, MATLAB, Python, QuPath, Git, LaTeX and Inkscape.

SELECTED RESEARCH PROJECTS

Automated segmentation and feature generator for 3D images

- Built an automatic image processing pipelines for segmentation and feature generation that reduced the processing time by 60%.
- Engineered features for morphology, textural and spatial distribution of objects in images.
- Integrated multi-domain features such as protein expression, RNA seq and image features to enable deduction of functional links.

Digital pathology platform for grading breast cancer stages at single cell resolution

- Performed instance segmentation of singe nuclei from patient tissue biopsies using U-Net based CNN and extracted geometric and textural features of nuclei.
- Built machine learning models to diagnose breast cancer stages at single cell resolution from patient breast tissue biopsies with 80% accuracy.
- Developed a single cell tumorigenesis score that characterises tumor progression.
- Identified regions of tissue tension using spatial statistics of nuclear images.

Deconvolving cell variability in cancer

- Developed a 3D in-vitro organoid tissue model for cancer progression amenable to high-resolution imaging.
- Implemented a classifier to predict cell shape with an accuracy of 95% and used the latent feature vectors along with regression models to show that cell shape is coupled to its function.
- Demonstrated a causal relationship between cell shape and activation by cancer cells using multimodal-multivariate analysis.
- Established the use of tissue model to assay the treatment efficacy of radiotherapy.

Trajectory inference to accelerate reprogramming of skin cells to stem cells

- Developed a novel technique to reprogram skin cells to stem cells with high efficiency.
- Performed statistical tests and pathway analysis on RNA seq data to characterize the temporal changes in the transcription profile during reprogramming.

- Modeled trajectories of reprogramming cells using clustering and diffusion models of single cell image features.
- Identified sources of low efficiency in large noisy image data which were experimentally validated to accelerate stem cell generation.

DNA structure informs cellular state

- Identified latent immune cells based on micorscopy image based radial DNA distribution within the nucleus and clustering large single cell RNA-Seq dataset.
- Predicted DNA structure from integrating RNA-Seq and ChIP-Seq data and validated the robustness using experiments and HiC data.

Cell shape modulates cellular response to stimuli

- Aligned, analyzed, visualized and interpreted differential gene expression patterns in RNA-Seq and microarray data. Also performed statistical tests and pathway analysis.
- Demonstrated the cell shape can modulate the transcriptional response to compressive load and inflammation.

Identification of dead (Apoptotic) cancer cells in a high-content screen

- Setup preliminary high content screen to characterize cancer cell survival in the presence of various drugs.
- Developed automatic image feature extraction from high content drug screens on cancer cells.
- Deployed multiple machine learning methods for classifying cancer cells as either dead (apoptotic) or live. Achieved identification accuracy of over 90%.

PEER REVIEWED PUBLICATIONS

- Dai Yang, K., Belyaeva, A., **Venkatachalapathy, S.**, Damodaran, K., Katcoff, A., Radhakrishnan, A., Shivashankar GV and Uhler, C. (2021). Multi-domain translation between single-cell imaging and sequencing data using autoencoders. *Nature Communications*, 12(1), 1-10;;[PMID: 33397893]
- Dai Yang, K., Damodaran, K., **Venkatachalapathy**, **S**., Soylemezoglu, A. C., Shivashankar, G. V., and Uhler, C. (2020). Predicting cell lineages using autoencoders and optimal transport. *P*LoS computational biology, 16(4), e1007828;[PMID: 32343706]
- Venkatachalapathy S, Jokhun DS, and Shivashankar GV. Multivariate analysis reveals activation-primed fibroblast geometric states in engineered 3D tumor microenvironments. Mol. Biol. Cell.2020;:mbcE19080420. [PMID:32023167]
- Damodaran K*, **Venkatachalapathy S***, Alisafaei F, Radhakrishnan AV, Sharma Jokhun D, Shenoy VB, and Shivashankar GV. Compressive force induces reversible chromatin condensation and cell geometry dependent transcriptional response. *Mol. Biol. Cell.*2018;:mbcE18040256. [PMID:30256731]
- Roy B, **Venkatachalapathy S**, Ratna P, Wang Y, Jokhun DS, Nagarajan M, and Shivashankar GV. Laterally confined growth of cells induces nuclear reprogramming in the absence of exogenous biochemical factors. *Proc.* Natl. Acad. Sci. U.S.A.2018;. [PMID: 29735717]
- Belyaeva A, **Venkatachalapathy S**, Nagarajan M, Shivashankar GV, and Uhler C. Network analysis identifies chromosome intermingling regions as regulatory hotspots for transcription. *Proc.* Natl. Acad. Sci. U.S.A. 2017;.[PMID:29229825]
- Mitra A, Venkatachalapathy S, Ratna P, Wang Y, Jokhun DS, and Shivashankar GV. Cell geometry dictates TNFαA-induced genome response. Proc. Natl. Acad. Sci. U.S.A.2017; [PMID:28461498]
- Radhakrishnan AV, Jokhun DS, **Venkatachalapathy S**, and Shivashankar GV. Nuclear Positioning and Its Translational Dynamics Are Regulated by Cell Geometry. *B*iophys.J.2017;112(9):1920-1928;[PMID:28494962]

* indicates equal contribution

Complete List of publications: Here

CONFERENCE: TALKS AND POSTERS

• 64th Annual Biophysical Society Meeting

San Diego, Feb 2020

Talk: "Cell Geometry Modulates the Activation of Fibroblasts in 3D Tumor Microenvironment

• Drug Discovery 2019 – Looking Back To The Future Liverpool, Nov 2019

Talk: Invited Speaker: "Mechano-Genomics: from Cell-Fate Decisions to Biomarkers"

• International Conference on Genomes and AI: From Packing to Regulation Singapore, Oct 2019

Talk: "Multivariate analysis of fibroblast activation in engineered 3D tumor microenvironments"

• Mechanobiology after 10 Years: The Promise of Mechanomedicine Singapore, Nov 2018

Poster: "Heterogeneity in cell geometric states regulate the selective activation of fibroblasts"

• Nuclear Mechanogenomics, EMBO Workshop

Singapore, Apr 2018

Talk: Role of cell geometry and 3D chromatin structure in differential genome regulation"

• The 3rd International Symposium on Mechanobiology

Singapore, Dec 2017

Talk: "Role of 3D chromatin architecture in differential genome regulation"

• Mechanobiology of Disease, MBI-BioPhysical Society meeting

Singapore, Sep 2016

Poster: "Nuclear positioning and its translation dynamics is regulated by cell geometry"

TEACHING AND LEADERSHIP EXPERIENCE

• Graduate Teaching Assistance

2016-2018

Assisted in the instruction and evaluation of 30 students in the Nuclear Mechanics and Genome Regulation module and was a MATLAB instructor for Mechanobiology Bootcamp.

• Image Analysis for dummies workshop

May, 2015

Designed and instructed a class on Automating image processing with ImageJ to 30 researchers.

• Supervised and mentored 2 students in the lab for their undergraduate or masters thesis.

HONORS AND AWARDS

• Dean's Merit list given to the top 2-10% students in the University	2015
• Inspirational Mentorship Award, NUS High School	2017
• Best Oral Presentation Award, Genomes and AI: From Packing to Regulation	2019

PAST EXPERIENCES

Intern, Biophysics laboratory, Raman Research Institute (RRI)

Winter, 2013

Developed algorithms to identify and track vesicles in axons.

Medical Intern, Kanmani Fertility Clinic, Raju Hospitals

Summer. 2013

Performed androgen characterisation, leukocyte culture, karyotyping and follicular study on patient samples.

Undergraduate researcher, Chromatin Epigenetics laboratory, SASTRA University

2012-20

Developed algorithms to identify apoptotic cells with an accuracy of over 90% in a high content screen.