Saradha Venkatachalapathy

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SUMMARY

Ph.D. student at the Mechanobiology Institute, NUS specializing in genomics and computer vision. Extensive background in developing algorithms and implementing statistical models to interpret causality in highly variable processes. Experienced in leading interdisciplinary collaborative projects with biologists and mathematicians to guide the design of experiments and modeling.

EDUCATION AND WORK EXPERIENCE

Ph.D, Mechanobiology National University of Singapore GPA 4.7/5	Sep 2016 - Present
B.Tech Biotechnology (Distinction) SASTRA University GPA 8.1/10	Jul 2011 - May 2015
Consultant, Computer Vision Qritive	Sep 2019 - Dec 2019
Research Assistant, National University of Singapore	Sep 2015 - Jul 2016

SKILLS

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

Computer Vision: Segmentation, Feature generation and Particle tracking

Computational Biology: Analysis of bulk and single cell Microarray, RNA-Seq and HiC. Experimental Skills: Microscopy, Tissue engineering and mechanical manipulation of cells. Tools: R, MATLAB, Python (pandas, scikit, PyTorch), SQL, Git, LATEX and Inkscape.

SELECTED RESEARCH PROJECTS

Automated feature generator for 3D images

- Built an in-house automatic image processing pipeline for segmentation and feature generation.
- Developed novel parameters that measure morphology, textural and spatial distribution of objects.
- Integrated multi-domain features such as protein expression, RNA seq and image features for deducing functional links.
- This reduced the processing time from 48 hours to 3 hours.

Deconvolving cell variability in cancer

- Only a subset of cells are activated by cancer signals in engineered breast cancer tissue.
- Developed a linear classifier to predict cell shape with an accuracy of 95%.
- Established the existence of activation primed cell shapes using multimodal-multivariate analysis.
- Demonstrated a causal relationship between cell geometry and activation [MBoC,2020].

Time series analysis of reprogramming

- Developed a novel method to reprogram fibroblasts to iPSC-like cells.
- Aligned, analyzed and visualized the transcriptome during mechanically induced de-differentiation. Performed statistical tests and pathway analysis to characterize the temporal changes in the transcription profile and infer the biological relevance [PNAS,2018].
- Implemented pseudo-temporal ordering of single cell data to identify variable trajectories during the generation of stem cells.

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

Complete List of publications Here