Sayane Shome

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PROFESSIONAL SUMMARY

Computational researcher with over 12 years of versatile research experience handling different types of biological data, including NGS data (Single-cell/Bulk RNA-seq, WGS, exome, Abseq, Hi-C data), proteins, clinical and radiology imaging data. Adept at AI/ML and statistical approaches to solve complex biological and healthcare problems. Proven ability to deliver results under highly dynamic, fast-paced research and clinical environments with professionalism and impact.

EDUCATION

Ph.D. in Bioinformatics and Computational Biology | Iowa State University, Ames, IA, USA *(2015- 2021)*

Completed graduate-level coursework *in Bioinformatics, Molecular Biology, Computational Algorithms, Machine learning, Probability and Statistics*

Bachelor of Technology in Bioinformatics | Vellore Institute of Technology, Vellore, India *(2009-2013)*

EXPERIENCE HIGHLIGHTS

Postdoctoral Fellow, Dept of Anesthesia and Pediatrics, STANFORD UNIVERSITY 2021 to Current

- Contributing to genomics and AI projects focused on newborn health, including both mouse models and human infant data.
- **Analyzing high-throughput datasets** (Bulk RNA-seq, scRNA-seq, Ab-seq, Hi-C) to study BPD progression and supporting biomedical experimental research in lab; collaborating with experimental biologists and clinicians at Stanford Hospitals.
- Carried out **multi-omics analysis** of lipidomics and transcriptomics samples of human tracheal aspirate samples collected from Stanford Hospitals.
- Working with **Electronic Health Records** (EHR) of newborns to investigate postnatal blood count variations.
- Implementing **machine learning** (random forest, Xgboost etc.) and **statistical models** (regression models, statistical tests, correlation networks) on **genomic and clinical datasets** to understand role of Sp3 transcription factor in fetal lung development.
- Building **generative AI models** for image/text to image (e.g., GANs, diffusion models) or image to text translation (using Blip2) for prognosis **using medical imaging data.**
- Experience working with open source/public clinical imaging datasets and from Stanford hospitals for predictive modelling.

Research Assistant, Dept of Biochemistry, Biophysics and Molecular Biology, IOWA STATE UNIVERSITY 2016 to 2021

Led and contributed to several collaborative projects with experimental biologists related to computational biophysics and genomics, which resulted in six peer-reviewed publications and contributed to five grants on topics such as understanding biological systems of membrane and transmembrane proteins using MD simulations and finding the impact of dairy processing stages on miRNA expression levels in cow milk samples.

External Student Researcher, FCITR, KING ABDULAZIZ UNIVERSITY OF SCIENCE AND TECHNOLOGY 2013 to 2015

Carried out a virtual collaborative project with the university in Saudi Arabia to determine the impact of single nucleotide variants on Ephrin-binding protein-2, I carried out molecular dynamics simulations and other computational analysis to compare the native and mutant protein dynamics and binding properties. Further, I worked on a project involved in drug designing for the regulation of the BCL-2 protein family, which is associated with Autism disease. The research work resulted in two manuscripts published in international peer-reviewed journals. I also assisted the supervising professor in grant application writing and content for chapter writing.

Project Trainee, INSTITUTE OF STATISTICAL SCIENCES, ACADEMIA SINICA 2013

Worked as trainee at premier scientific institute of Taiwan to determine the correlation between multiple gene expression, I carried out analysis to predict transcriptional interactions between gene pairs based on time-regulated microarray gene expression data from medulloblastoma patients using an in-house PARE server developed by the lab.

Intern, XCODE LIFESCIENCES, VIT – TECHNOLOGY BUSINESS INCUBATOR, INDIA 2011

Supported a collection of SNPs-related to hereditary traits and disease risks such as diabetes and cardiac arrest from multiple databases inclusive of GWAS, dbSNP, SNPedia determining the risk probability for the genotype and phenotypic composition. Led the data curation assisting in-house X-DNA project focused on genotyping of saliva samples from Indian patients mainly based on

five disease risks, including Diabetes type-2 and cardiovascular diseases. The company's CEO was awarded MIT's TR35 India 2013.

TECHNICAL PROFICIENCIES

COMPUTING SKILLS

Programming Languages: Python, R, Bioconductor, Perl, Matlab, Unix/Shell/Bash Scripting,C
Machine learning packages: Tensorflow, PyTorch, Keras, Sklearn,Pillow
Statistical techniques: PCA, SVM, Random forest, regression modelling, clustering, dimensionality reduction,classification methods,gradient descent,genetic algorithms,linear-effect models
Generative AI models : GANs, Diffusion Models
Computational expertise: HPC clusters, CUDA infrastructure
Website development: HTML,CSS,Wordpress

COMPUTATIONAL BIOLOGY SOFTWARES

NGS data analysis: BWA, Samtools, GATK, Trinity, Galaxy, Kallisto, Scanpy, Seurat, Velocyto, Scvelo, CellChat, Cooltools
Network Analysis and visualization: Cytoscape, Circos, Ggplot2, Plotly, Networkx, Jupyter notebook, R Markdown, Shiny app
Wet-lab experimental experience and familiarity *(not expertise):* Genotyping, PCR, Flow cytometry, working with mouse models and dissections, bronchoalveolar lavage, histology, antibody staining, Merfish and Spatial transcriptomics

PROFESSIONAL CERTIFICATIONS

Stanford Ignite Program, Stanford Graduate School of Business| Stanford University, Stanford, CA, USA *(2023- 2023)*

SELECTED RESEARCH PUBLICATIONS (full list)

(GOOGLE SCHOLAR : H-INDEX = 9)

1. **Shome, S.**, Jernigan, R. L., Beitz, D. C., Clark, S., Testroet, E. D. (2021). Non-coding RNA in raw and commercially processed milk and putative targets related to growth and immune response. *BMC Genomics*, 22:749.

2. **Shome, S.**, Jia, K., Sivasankar, S., Jernigan, R. L. (2023). Characterizing interactions in E-cadherin assemblages. *Biophysical Journal*, 122(15): 3069–3077.

3. McCoy, A. M., Lakhdari, O., **Shome, S.**, et al. (2023). Sp3 is essential for normal lung morphogenesis and cell cycle progression during mouse embryonic development. *Development*, 150(5): dev200839.

4. Becker, M., Espinosa, C., Stelzer, I., **Shome, S.**, et al. (2023). Large-scale correlation network construction for unraveling the coordination of complex biological systems. *Nature Computational Science*, 3: 346–359.

5. **Shome, S.**, Sankar, K., Jernigan, R. L. (2021). Simulated drug efflux for the AbgT family of membrane transporters. *Journal of Chemical Information and Modeling*, 61(11): 5673–5681.

AWARDS & DISTINCTIONS

- Stanford Postdoc Champions: Community Impact Award (2024)
- NSF I-Corps Northeast Hub Regional program (2023)
- Infosys Most energy efficient/Sustainable Energy hack, Treehacks 2020, Stanford University (2020)
- URSSI Winter School Travel Award, University of Washington (*2019)*
- CPLC Summer School Travel Award, University of Illinois at Urbana-Champaign (2019)
- ISCB Travel Award, Intelligent Systems for Molecular Biology Conference (2018,2017,2016)
- Diane Brandt Fellowship Award, Iowa State University (2015 to 2016)
- Taiwan International Graduate Program – IIP Fellowship, Academia Sinica, Taiwan (2013)

SCIENCE COMMUNICATION

Sayane Shome

- Gave a presentation on **Generative AI in imaging** at the Fundamental Physics Directorate (FPD) seminar series at SLAC National Accelerator Laboratory (Stanford University and DOE).
- Organized a day-long tutorial on **protein sequence analysis using transformer-based LLMs** at ISMB/ECCB 2023(France) and AMIA 2024(USA).
- Was a panelist at 'Asian Women in CompBio' in ISCB-Asian SCS 2022 and introduced programming basics to college students at Berea College, Kentucky, USA in March 2022.
- Participated as a panelist on 'Mental Health in Academia' at the ECCB-SCS 2022(Hybrid). Selected as Judge for ISCB Wikipedia Competition from 2017-2021.
- Contributed as a science writer for the ISCB Fellows Workshop and a senior blogger for PloS Computational Biology Field Reports.
- Also engaged as a student speaker for Women in Science and Engineering programs at Iowa State University from 2016-2018.

COMMUNITY LEADERSHIP

- Council member At-Large, AAAS Council 2023 - 2025
  American association of the advancement of Sciences
- Core-committee member, Stanford Immunology Postdoctoral Association 2022-2024
  Stanford University
- Co-chair, Data Science Committee 2023,2022
  Grace Hopper Celebration in Computing, AnitaB.org
- Chair, RSG Committee and Executive Team Member-Student Council 2015-2021
  International Society of Computational Biology
- Advisor and Organizing Team Member, Student Council Symposium – Africa 2017,2019
  Student Council, International Society of Computational Biology
- Co-Chair, Platform Session: Molecular Dynamics Session-I 2018
  Biophysical Society Annual Meeting
- BCB Department Senator and Member of University Relations and Affairs Committee 2018-2019
  Graduate and Professional Students Senate, Iowa State University