

Shan A. Sabri

BIOINFORMATICS SCIENTIST · COMPUTATIONAL BIOLOGIST

630-201-1911 | ShanASabri@gmail.com | ShanSabri.github.io | ShanSabri | ShanSabri | Publications

Summary

Computational scientist with expertise in performing end-to-end data analysis, visualization, and interpretation of data from various NGS-based technologies. Actively developing innovative, sophisticated computational methods and tools for data analysis. Strong interpersonal, written and oral communication skills as evidenced by multiple collaborations, fellowships, and presentation awards.

Education

University of California, Los Angeles

Ph.D. in Bioinformatics, Emphasis Machine Learning ([Dissertation](#))

Los Angeles, CA

June 2020

Johns Hopkins University

M.Sc. in Bioinformatics

Baltimore, MD

Dec. 2013

Loyola University Chicago

B.Sc. in Bioinformatics and Mathematics, Minor Biostatistics

Chicago, IL

May 2012

Experience

Sana Biotechnology

Lead Computational Biologist, Embedded

Chicago, IL

Jan. 2023 – Present

- Partner with the Islet Biology Research team to mature a series of release assays that characterizes cell differentiation purity and conversion efficiency
- Build and streamline production-quality quality-control pipelines, reporting tools and interactive dashboards for analyzing scRNA/RNA-seq data

ArsenalBio

Scientist II → Senior Scientist I, Computational Biology & Machine Learning

South San Francisco, CA

Aug. 2020 – Sept. 2022

- Built infrastructure, computational pipelines and statistical workflows to assess CRISPR-Cas9 editing efficiency, specificity and safety via targeted amplicon sequencing, enrichment and WGS; prepare IND-enabling data packages in alignment with pre-clinical development objectives
- Developed and deployed custom pipelines and visualization applications that deliver data and results to industry and academic partners; including an interactive TME atlas of >1.2M single cell transcriptomes

Ernst & Plath Labs

Graduate Student Research

Los Angeles, CA

Aug. 2014 – June 2020

- Applied multi-omics assays and computational methods to decipher the changes that occur during cell-fate transition using somatic-to-iPSC conversion as a platform
- Developed a computational method that leverages a stacked ensemble of regression models to predict single-cell chromatin landscape using an atlas of population-level data, alleviating the need for additional assays

Genentech

Computational Biology Research Intern

South San Francisco, CA

June 2018 – Sept. 2018

- Performed integrated computational analyses from various data modalities (scRNA-/RNA-/ATAC-seq) to unravel the metastatic process of CRC

Sample Projects

deconR R package to deconvolve cell type profiles from bulk assays using an ensemble of regressions ([github](#))

JubRi R package to perform keyword enrichment analysis based on published literature; also see [PubMedScrapeR](#) ([github](#))

Levenshtein An efficient dynamic programming algorithm of the Sequence-Levenshtein distance written in Cython ([github](#))

SSFold An algorithm for predicting the optimal RNA secondary structure written in Python ([github](#))

Skills

Programming

R, Python, BASH, Jupyter; working knowledge of SQL & Apache Spark and Hadoop frameworks; expertise developing Dash & Shiny dashboards and software packages

Bioinformatics

RNA-/ChIP-/DNase-/ATAC-seq, single-cell RNA-/ATAC-seq, Whole genome sequencing & promoter-capture HiC processing & analysis techniques; variant calling, batch correction, gene regulatory networks & data visualization

Machine Learning

Classification, regression, hyperparameter tuning, feature selection; Scikit-learn, TensorFlow, PyTorch

Applications

LaTeX, Git/Subversion, AWS/Cloud computing platforms, Docker/Gradle build tools; Snakemake; Linux/Unix; Benchling & Jira

Publications

(SELECTED OF 20)

CRISPR/Cas9-based Integration of a Large and Modular Cassette into a Safe Harbor Site to Improve CAR T cell Therapy Efficacy and Safety

B. Galvin, G. Zheng, R. Moot, M. Nguyen, M. Tan, R. Sit, L. Berthoin, D. DeTomaso, S. K. Panagiotopoulou, **S. Sabri**, J. Feng, M. Ku, A. Yao, A. Liu, *et al.*
J Immunother Cancer 10(Suppl 2 (Nov. 2022) A349. Society for Immunotherapy of Cancer (SITC)

Single-cell Multi-omic Profiling and Clonal Tracing of the Human Gynecological Tumor Microenvironment

V. Liu, K. Sandor, B. Daniel, L. Berthoin, **S. Sabri**, S. Panagiotopoulou, Y. Yin, K. Hiam-Galvez, R. Sit, Z. Fan, B. Galvin, O. Khan, N. Bezman, *et al.*
Cancer Research 82.12 (June 2022) p. 1701. American Association for Cancer Research (AACR)

Defining the Nature of Human Pluripotent Stem Cell-derived Interneurons via Single-cell Analysis

T. Allison, J. Langerman, **S. Sabri**, M. Otero-Garcia, A. Lund, J. Huang, X. Wei, R. A. Samarasinghe, D. Polioudakis, *et al.*
Stem Cell Reports 16.10 (Oct. 2021) pp. 2548–2564

Transcriptional Analysis of Cystic Fibrosis Airways at Single-cell Resolution Reveals Altered Epithelial Cell States and Composition

G. Carraro*, J. Langerman*, **S. Sabri**, Z. Lorenzana, A. Purkayastha, G. Zhang, B. Konda, C. J. Aros, B. A. Calvert, A. Szymaniak, *et al.*
Nature Medicine 27.5 (May 2021) pp. 806–814

A Human Skeletal Muscle Atlas Identifies the Trajectories of Stem and Progenitor Cells across Development and from hPSCs

H. Xi, J. Langerman, **S. Sabri**, P. Chien, C. S. Young, S. Younesi, M. Hicks, K. Gonzalez, W. Fujiwara, J. Marzi, S. Liebscher, M. Spencer, *et al.*
Cell Stem Cell 27.1 (July 2020) pp. 158–176

Reduced MEK Inhibition Preserves Genomic Stability in Naïve Human ES Cells

B. D. Stefano, M. Ueda, **S. Sabri**, J. Brumbaugh, A. J. Huebner, A. Sahakyan, K. Clement, K. J. Clowers, A. R. Erickson, K. Shiota, *et al.*
Nature Methods 15.9 (Aug. 2018) pp. 732–740

Cooperative Binding of Transcription Factors Orchestrates Reprogramming

C. Chronis*, P. Fiziev*, B. Papp, S. Butz, G. Bonora, **S. Sabri**, J. Ernst, K. Plath
Cell 168.3 (Jan. 2017) pp. 442–459

Honors & Awards

PROFESSIONAL RECOGNITION

2022	Recipient , ArsenalBio Excellence Recognition	South San Francisco, CA
2019	Finalist , 1st Annual AI LA Life Summit	Pasadena, CA
2019	Recipient , Outstanding Mentor Award, Bruins-In-Genomics (B.I.G.) Summer Research Program	Los Angeles, CA
2019	Recipient , Travel Award, Deep learning for Science at Lawrence Berkeley National Laboratory	Berkeley, CA
2019	Finalist , Citadel & Correlation One Datathon	Berkeley, CA
2018	Finalist , Citadel & Correlation One Datathon	Pasadena, CA
2017	Recipient , Molecular Biology Institute (MBI) Outstanding Poster Presentation Award	Los Angeles, CA
2017	2nd Place , Broad Stem Cell Research Center (BSCRC) Elevator Pitch (video source)	Los Angeles, CA
2017	3rd Place , Citadel & Correlation One Datathon (\$2,500 cash prize; report)	Pasadena, CA
2016	Recipient , Best Research Pitch Award at Cornell University's ACLS International Summer School	New York, NY

ACADEMIC FELLOWSHIPS

2019	Recipient , UCLA Dissertation Year Fellowship (\$37,272/year)	Los Angeles, CA
2016–2018	Recipient , Broad Stem Cell Research Center (BSCRC) Fellowship (\$40,000/year)	Los Angeles, CA
2017	Recipient , Philip J. Whitcome Fellowship (awarded but declined; \$29,376/year)	Los Angeles, CA
2013	Recipient , Noblis Bioinformatics Scholarship (\$9,750/year)	Baltimore, MD
2008–2012	Recipient , Trustee Academic Scholarship (\$10,000/year)	Chicago, IL

Teaching & Mentorship

Sum. 2022	Internship Mentor , Bilge Gungoren (Caltech, B.Sc. Chemical Eng.)	South San Francisco, CA
Spg. 2020	Research Mentor , Jingyuan Fu (UCLA, Ph.D. Computer Science)	Los Angeles, CA
Sum. 2019	Research Mentor , Jeremy Wang (Brown Univ., B.Sc. Mathematics)	Los Angeles, CA
Sum. 2019	Research Mentor , Rebecca Castillo (Univ. of New Mexico, B.Sc. Computer Science)	Los Angeles, CA
Win. 2017	Research Mentor , Harry Yang (UCLA, Ph.D. Bioinformatics)	Los Angeles, CA
Fall 2015	Research Mentor , Kiku Koyano (UCLA, Ph.D. Bioinformatics)	Los Angeles, CA
Fall 2015	Teaching Assistant , Intro to Bioinformatics and Genomics; student evaluation rating of 8.94/10	Los Angeles, CA
Fall 2014	Teaching Assistant , Computer Concepts for Bioinformatics; student evaluation rating of 11.21/12	Baltimore, MD
Fall 2013	Teaching Assistant , Computational Genomics; student evaluation rating of 10.60/12	Baltimore, MD