Shan A. Sabri

BIOINFORMATICS SCIENTIST · COMPUTATIONAL BIOLOGIST

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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 *Los Angeles, CA*
PH.D. IN BIOINFORMATICS, EMPHASIS MACHINE LEARNING (DISSERTATION) *June 2020*

Johns Hopkins University *Baltimore, MD*
M.SC. IN BIOINFORMATICS *Dec. 2013*

Loyola University Chicago *Chicago, IL*
B.SC. IN BIOINFORMATICS AND MATHEMATICS, MINOR BIOSTATISTICS *May 2012*

Experience

Sana Biotechnology *Chicago, IL*
LEAD COMPUTATIONAL BIOLOGIST, EMBEDDED *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
- Develop and streamline quality-control pipelines, reporting tools, and interactive dashboards for analyzing scRNA/RNA-seq data; reducing QC turnaround time by 85%

ArsenalBio *South San Francisco, CA*
SENIOR SCIENTIST I, COMPUTATIONAL BIOLOGY & MACHINE LEARNING *March 2022 - Sept. 2022*
SCIENTIST II, COMPUTATIONAL BIOLOGY & MACHINE LEARNING *Aug. 2020 - March 2022*

- Built infrastructure, computational pipelines and statistical workflows to assess CRISPR-Cas9 editing efficiency, specificity and safety via targeted amplicon sequencing, enrichment and WGS; wrote study reports for IND submission
- 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 *Los Angeles, CA*
GRADUATE STUDENT RESEARCH *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 *South San Francisco, CA*
COMPUTATIONAL BIOLOGY RESEARCH INTERN *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 preform keyword enrichment analysis based on published literature; also see PubMedScrapeR (github)
`modified-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, Jypyter; 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 modeling, hyperparameter tuning & optimization, feature selection; Scikit-learn & TensorFlow
Applications	LaTeX, Git/Subversion, AWS/Cloud computing platforms, Docker/Gradle build tools; Snakemake; Linux/Unix; Benchling & Jira

Publications

(Selected of 20)

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) pp. 1701–1701. American Association for Cancer Research (AACR)

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) A1–A1603. Society for Immunotherapy of Cancer (SITC)

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. Shioda, *et al.*
Nature Methods 15.9 (Aug. 2019) 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**, Practical 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*