

Shan A. Sabri

BIOINFORMATICS SCIENTIST

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Summary

Computational biologist with expertise in performing end-to-end data analysis, visualization, and interpretation of data from various NGS-based platforms (ChIP-/ATAC-/RNA-seq, single cell RNA-/ATAC-seq, HiC). 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. A complete academic vitae can be found [here](#).

Education

University of California, Los Angeles

PH.D. IN BIOINFORMATICS

Los Angeles, CA

Aug. 2014 - Est. Spring 2020

- Thesis: Investigating Cell Fate Transition Dynamics at Single Cell Resolution
- Advisors: Kathrin Plath, Ph.D. and Jason Ernst, Ph.D.

Johns Hopkins University

M.Sc. IN BIOINFORMATICS

Baltimore, MD

Aug. 2012 - Dec. 2013

Loyola University Chicago

B.Sc. IN BIOINFORMATICS AND MATHEMATICS, MINOR BIOSTATISTICS

Chicago, IL

Aug. 2008 - May 2012

Experience

University of California, Los Angeles

GRADUATE STUDENT RESEARCHER, PLATH AND ERNST LABS

Los Angeles, CA

Aug. 2013 - Present

- Applying genomic (ATAC-seq, ChIP-seq, bulk RNA and single cell-seq) and computational methods (trajectory inference, gene regulatory network reconstruction, imputation, ChromHMM modeling) to describe the cell state changes induced by reprogramming transcription factors during the conversion of somatic cells to induced pluripotent stem cells (iPSCs)
- Developing a computational method that utilizes machine learning approaches to deconvolve single cell chromatin features using population-level chromatin and gene expression data
- Deploying data processing and analysis pipelines for single cell RNA-seq that are being used as a standard in our labs and among collaborators

Genentech

BIOINFORMATICS & COMPUTATIONAL BIOLOGY RESEARCH INTERN

South San Francisco, CA

June 2018 - Sept. 2018

- Integrated information from RNA-seq, ATAC-seq, and scRNA-seq to gain insights into the metastatic process of colorectal cancer profiling
- Wrote production grade software packages in R to characterize the cellular composition and chromatin landscape of tumors at primary and metastatic sites and identified potential shifts in population numbers due to targeted depletion of cancer stem cells

Google

SUMMER STUDENT DEVELOPER THROUGH GOOGLE SUMMER OF CODE (GSOC)

Chicago, IL

May 2012 - Aug. 2012

- Bioinformatic analyses of the Geuvadis RNA-sequencing project (Lappalainen *et al.*, 2013) to determine if RNA-editing can be used to effectively define population structure
- Wrote software in Python and C++ to identify and correlate RNA-editing levels with gene expression levels to determine sites that impose a cis-regulation on gene expression

Skills

Machine Learning

Classification & regression modeling, hyperparameter tuning & optimization, feature selection; Keras, PyTorch, Scikit-learn, & TensorFlow frameworks

Bioinformatics

RNA-/ChIP-/ATAC-seq, single-cell RNA-/ATAC-seq, Whole genome sequencing, and promoter-capture HiC processing and analysis techniques; variant calling, batch correction, gene regulatory networks, data visualization; Expertise on iPSC reprogramming systems and epigenetics

Programming

R, Python, BASH; working knowledge of C++, SQL & Java; experience developing R Shiny web applications and packages

Applications

TeX, Git/Subversion, AWS/Cloud computing platforms; Linux/Unix; common spreadsheet and presentation software

Publications

JOURNAL ARTICLES (SELECTED OF 11)

Single Cell Sequencing Reveals a Poised Expression State on the Path to iPSCs that Emerges Upon Somatic Program Shutdown

J. Langerman*, S. Sabri*, C. Chronis, J. Ernst, K. Plath

Nature; in revision (July 2019)

Defining Features of Human Interneuron Maturation

T. Allison, **S. Sabri**, A. Lund, M. Otero, D. Poulakis, J. Langerman, M. Cobos, D. Geschwind, K. Plath, W. Lowry
Cell Stem Cell; in review (June 2019)

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, S. P. Gygi, H. Gu, T. Shioda, A. Meissner, Y. Takashima, K. Plath, K. Hochedlinger
Nature Methods 15.9 (Aug. 2019) pp. 732–740

Identification and Single-Cell Functional Characterization of an Endodermally Biased Pluripotent Substate in hESCs

T. F. Allison, A. J. Smith, K. Anastassiadis, J. Sloane-Stanley, V. Biga, D. Stavish, J. Hackland, **S. Sabri**, J. Langerman, M. Jones, K. Plath, D. Coca, I. Barbaric, P. Gokhale, P. W. Andrews
Stem Cell Reports 10.6 (June 2018) pp. 1895–1907

Analysis of Cardiomyocyte Clonal Expansion during Mouse Heart Development and Injury

K.-I. Sereti, N. B. Nguyen, P. Kamran, P. Zhao, S. Ranjbarvaziri, S. Park, **S. Sabri**, J. L. Engel, K. Sung, R. P. Kulkarni, Y. Ding, T. K. Hsiai, K. Plath, J. Ernst, D. Sahoo, H. K. Mikkola, M. L. Iruela-Arispe, R. Ardehali
Nature Communications 9.1 (Feb. 2018) p. 754

Human Naive Pluripotent Stem Cells Model X Chromosome Dampening and X Inactivation

A. Sahakyan, R. Kim, C. Chronis, **S. Sabri**, G. Bonora, T. W. Theunissen, E. Kuoy, J. Langerman, A. T. Clark, R. Jaenisch, K. Plath
Cell Stem Cell 20.1 (Jan. 2017) pp. 87–101

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) 442–459.e20

Honors & Awards

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

EXTERNAL

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 (source)	Los Angeles, CA
2017	3rd Place , Citadel & Correlation One Datathon (\$2,500 cash prize)	Pasadena, CA
2016	Recipient , Best Research Pitch Award at Cornell University's ACLS International Summer School	New York, NY

Teaching & Mentorship

Sum. 2019	Research Mentor , Undergraduate students Jeremy Wang (Brown U.) & Rebecca Castillo (U. of New Mexico)	Los Angeles, CA
Win. 2017	Research Mentor , Bioinformatics graduate student Harry Yang	Los Angeles, CA
Fall 2015	Research Mentor , Bioinformatics graduate student Kiku Koyano	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