

Shan A. Sabri

DATA SCIENTIST · RESEARCH SCIENTIST

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Summary

Computational scientist with expertise in solving analytical problems using quantitative approaches on large, complex data sets. Actively developing innovative, sophisticated computational methods and tools for data analysis and interpretation. Strong interpersonal, written and oral communication skills as evidenced by multiple collaborations, fellowships, and presentation awards. A complete vitae can be found [here](#).

Education

University of California, Los Angeles

Los Angeles, CA

PH.D. IN BIOINFORMATICS/COMPUTATIONAL BIOLOGY (GPA: 3.85/4)

Est. Spring 2020

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

Johns Hopkins University

Baltimore, MD

M.SC. IN BIOINFORMATICS/COMPUTATIONAL BIOLOGY (GPA: 3.93/4)

Dec. 2013

Loyola University Chicago

Chicago, IL

B.SC. IN BIOINFORMATICS AND MATHEMATICS, MINOR BIOSTATISTICS (GPA: 3.66/4)

May 2012

Experience

University of California, Los Angeles

Los Angeles, CA

GRADUATE STUDENT RESEARCHER, PLATH AND ERNST LABS

Aug. 2013 - Present

- Applying computational methods (trajectory and causal inference, gene regulatory network reconstruction, imputation, predictive modeling) to genomics data to understand cell fate transitions during the conversion of somatic cells to induced pluripotent stem cells (iPSCs)
- Developing a computational method that utilizes K-Nearest-Neighbor (KNN) Regression to deconvolve single cell chromatin features using population-level chromatin and gene expression data
- Writing R packages ([JubRi](#) and [PubMedScrapeR](#)) to perform literature-based NLP topic modeling of genes using latent Dirichlet allocation (LDA)
- 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

South San Francisco, CA

BIOINFORMATICS & COMPUTATIONAL BIOLOGY RESEARCH INTERN

June 2018 - Sept. 2018

- Performed integrated analyses on information from various genomic data platforms (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

Chicago, IL

SUMMER STUDENT DEVELOPER THROUGH GOOGLE SUMMER OF CODE (GSOC)

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

Sample Projects

deconR	R package to deconvolve cell type profiles from bulk assays using K-Nearest-Neighbor Regression (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)
oriFinder	A method to pinpoint the origin of replication for bacterial genomes (github)

Skills

Machine Learning

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

Bioinformatics

Next-gen sequencing data processing and analysis techniques; variant calling, batch correction, gene regulatory networks, high-dimensional data visualization

Programming

R, Python, BASH; working knowledge of SQL, C++ & 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 (Sept. 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)

A Single-Cell Transcriptomic Atlas of Human Neocortical Development during Mid-gestation

D. Polioudakis, L. Torre-Ubieta, J. Langerman, A. Elkins, X. Shi, J. Stein, C. Vuong, S. Nichterwitz, M. Gevorgian, C. Opland, D. Lu, W. Connell, E. Ruzzo, J. Lowe, T. Hadzic, F. Hinz, **S. Sabri**, W. Lowry, M. Gerstein, K. Plath, D. Geschwind
Neuron 103.5 (Sept. 2019) pp. 785–801

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 Naïve 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	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 (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