

**Shan A. Sabri**

CONTACT INFORMATION	1831 Sawtelle Blvd Unit: PH2 Los Angeles, CA 90025 USA (630) 201-1911 <a href="mailto:ShanASabri@gmail.com">ShanASabri@gmail.com</a> <a href="https://www.linkedin.com/in/ShanSabri">www.Linkedin.com/in/ShanSabri</a> <a href="https://www.github.com/ShanSabri">www.github.com/ShanSabri</a>
RESEARCH INTERESTS	Big data analytics, time-series analysis, predictive modeling, machine learning, data visualization, clustering algorithms, data science, single cell RNA-sequencing, cell and molecular biology
EDUCATION	<b>University of California, Los Angeles</b> , Los Angeles, California USA Ph.D., Bioinformatics (expected graduation date: Spring 2020) GPA 3.85/4.00 <ul style="list-style-type: none"> <li>Dissertation Topic: Investigating Cell Fate Transition Dynamics at Single Cell Resolution</li> <li>Advisors: Kathrin Plath, Ph.D. and Jason Ernst, Ph.D.</li> </ul> <b>Johns Hopkins University</b> , Baltimore, Maryland USA M.S., Bioinformatics, December 2013 GPA 3.93/4.00 <b>Loyola University Chicago</b> , Chicago, Illinois USA B.S., Bioinformatics and Mathematics, minor Biostatistics, May 2012 GPA 3.66/4.00
HONORS AND AWARDS	UCLA Dissertation Year Fellowship - \$37,272/year, 2019-present Broad Stem Cell Research Center (BSCRC) & Rose Hills Fellowship - \$40,000/year, 2016-2019 Deep learning for Science Travel Award, Lawrence Berkeley National Laboratory, 2019 Citadel & Correlation One Datathon at UC Berkeley, Qualified contestant, 2019 Citadel & Correlation One Datathon at Caltech, Qualified contestant, 2018 Citadel & Correlation One Datathon at Caltech, 3rd place (\$2500 cash prize), 2017 Broad Stem Cell Research Center (BSCRC) Elevator Pitch, 2nd place, 2017 ( <a href="#">source</a> ) Molecular Biology Institute (MBI) Outstanding Poster Presentation Award, 2017 Philip J. Whitcome Pre-doctoral Fellowship (awarded but declined) - \$29,376/year, 2016-2017 Best Research Pitch Award, Cornell University's ACLS International Summer School, 2016 First year Bioinformatics IDP Reserach Fellowship, 2014-2015 Noblis Bioinformatics Scholarship, 2012-2013 Google Summer of Code Project Showcase, 2012 Johns Hopkins University: graduated Summa Cum Laude, 2013 Loyola University Chicago: graduated Cum Laude, Merit Trustee Scholarship recipient 2008-2012
ACADEMIC EXPERIENCE	<b>University of California, Los Angeles</b> , Los Angeles, California USA <i>Doctoral Candidate</i> <b>August, 2014 - present</b> Includes current Ph.D. research, Ph.D. and Masters level coursework and research/consulting projects.  Thesis project: I aim to uncover the temporal sequence of cell state transitions as somatic cells reprogram to induced pluripotent stem cells by identifying genes that are activated or inactivated during these transitions. I am developing methods that reconstruct the transcriptional transitions in those cells moving towards the pluripotent state by utilizing ordered expression profiles with unsupervised, network based algorithms at the transcriptomic level.  <i>Teaching Assistant</i> <b>August - December, 2015</b> CM221 Introduction to Bioinformatics and Genomics, Fall 2015: Supported instruction of graduate level course in Computer Science (cross-listed with Bioinformatics) for 74 students. Shared

responsibility for lectures, exams, homework assignments, and grades. Developed interactive course activities to engage students and increase participation. Course topics include: probabilistic modeling, HMMs, evolutionary models, and sequence analysis. Received an overall student evaluation rating of 8.94/10.

**Johns Hopkins University**, Baltimore, Maryland USA

*Graduate Student*

**August, 2012 - December 2013**

Includes Masters level coursework and research projects.

*Teaching Assistant*

**May - August, 2013**

605.453 Computational Genomics, Summer 2013: Held office hours and leading bi-weekly computer lab exercises and discussions. Course topics include: prediction models, genomic evolution, sequence assembly, and Python programming. Received an overall student evaluation rating of 10.60/12.

## PUBLICATIONS

- [1] Takahashi R\*, Grzenda A\*, Allison T\*, Rawnsley J, Balin S, **Sabri S**, Plath K, Lowry W. Defining Transcriptional Signatures of Human Hair Follicle Cell States. *Journal of Investigative Dermatology*. *Accepted*.
- [2] Polioudakis D, Torre-Ubieta L, Langerman J, Elkins A, Shi X, Stein J, Vuong C, Nichterwitz S, Gevorgian M, Opland C, Lu D, Connell W, Ruzzo E, Lowe J, Hadzik T, Hinz F, **Sabri S**, Lowry W, Gerstein M, Plath K, Geschwind D. A Single Cell Transcriptomic Atlas of Human Neocortical Development during Mid-gestation. *Neuron*, 103, 1—17. DOI:10.1016/j.neuron.2019.06.011
- [3] Stefano B, Ueda M, **Sabri S**, Brumbaugh J, Huebner A, Sahakyan A, Clement K, Clowers K, Erickson A, Shioda K, Gygi S, Gu H, Shioda T, Meissner A, Takashima Y, Plath K, Hochedlinger K. Reduced MEK Inhibition Preserves Genomic Stability in Nave Human ES Cells. *Nature Methods*, 15(9), 732—740. DOI:10.1038/s41592-018-0104-1
- [4] Allison T, Smith A, Anastassiadis K, Sloane-Stanley K, Biga V, Stavish D, Hackland J, **Sabri S**, Langerman J, Jones M, Plath K, Barbaric I, Gokhale P, Andrews P. Identification and Single Cell Functional Characterization of a Novel Endodermally Biased Pluripotent Sub-state in Human Embryonic Stem Cells. *Stem Cell Reports*, 10(6), 1895—1907. DOI:10.1016/j.stemcr.2018.04.015
- [5] Sereti K\*, Nguyen N\*, Kamran P\*, Zhao P, Ranjbarvaziri S, Park S, **Sabri S**, Engel J, Sung K, Kulkarni R, Ding Y, Hsiai T, Plath K, Ernst J, Sahoo D, Mikkola H, Iruela-Arispe L, Ardehali R. Clonal Analysis of Cardiomyocyte Generation During Development and Injury using the Rainbow Model. *Nature Communications*, 9(1). DOI:10.1038/s41467-018-02891-z.
- [6] Sahakyan A, Kim R, Chronis C, **Sabri S**, Bonora G, Theunissen TW, Kuoy E, Clark AT, Jaenisch R, Plath K. Human Nave Pluripotent Stem Cells Model X Chromosome Dampening and X Inactivation. *Cell Stem Cell*, 20(1), 87—101. DOI:10.1016/j.stem.2016.10.006.
- [7] Chronis C\*, Fiziev P\*, Papp B, Bonora G, **Sabri S**, Ernst J, Plath K. Cooperative Binding of Transcription Factors Orchestrates Reprogramming the induction of pluripotency. *Cell*, 68(3), 442—459.e20. DOI:10.1016/j.cell.2016.12.016.
- [8] **Sabri, S**. The Fundamentals of Discrete Mathematics. 1st ed. Addison: Shan A. Sabri. *Lulu Com*, 2013. ISBN:9781304049032.

## PAPERS IN PREPARATION

- [1] Langerman J\*, **Sabri S**\*, Chronis C, Ernst J, Plath K. Single Cell Sequencing Reveals a Poised Expression State on the Path to iPSCs that Emerges Upon Somatic Program Shutdown. *Nature*. *In revision*.
- [2] Allison T, **Sabri S**, Lund A, Otero M, Poulakis D, Langerman J, Cobos M, Geschwind D, Plath K, Lowry W. Defining Features of Human Interneuron Maturation. *Cell Stem Cell*. *Submitted & In review*.

CONFERENCE  
PRESENTATIONS

- [3] Zhang R, Jelinek D, Xie X, Guo N, Ambrus A, Vo A, Kesaf A, Sevier P, Karsli-Uzunbas G, Poillet-Perez L, Wang X, Smith D, Morselli M, **Sabri S**, Ing N, Pellegrini M, Plath K, Ernst J, Gertych A, Knudsen B, Balzer B, Mehnert J, Scumpia P, Yang L, White E, Collier H. Autophagy in Melanoma-Associated Stroma Promotes Tumor Growth by Maintaining ECM Formation and Suppressing Th1-Type Immune Responses. *Cancer Cell. In revisions.*
- [1] **Sabri S**, Langerman J, Ernst J, Plath K. Deconvolution of Single Cell Chromatin Features using Population-level Chromatin and Single Cell RNA-seq Data. Southwestern Bioinformatics Conference (SBC), May 2019, San Diego, California. *Oral presentation.*
- [2] **Sabri S**, Langerman J, Ernst J, Plath K. Deconvolution of Single Cell Chromatin Features using Population-level Chromatin and Single Cell RNA-seq Data. International Society for Stem Cell Research (ISCCR), June 2019, Los Angeles, California. *Poster presentation.*
- [3] **Sabri S**, Langerman J, Ernst J, Plath K. Inferring Individual Cell Type ChIP-seq Profiles from Population ChIP-seq and Single Cell RNA-seq Data. UCLA Computational Medicine & Amazon Web Services (AWS) Symposium, February 2019, Los Angeles, California. *Poster presentation.*
- [4] **Sabri S**, Langerman J, Chronis C, Ernst J, Plath K. Single Cell Sequencing Reveals the Expression Changes Underlying Reprogramming to iPSCs and Conserved Mechanisms of Reprogramming Processes. 15th Annual Stem Cell Conference on B2B - Bench to Bedside, February 2019, Los Angeles, California. *Poster presentation.*
- [5] **Sabri S**, Langerman J, Plath K, Ernst J. Inferring Individual Cell Type ChIP-seq Profiles from Population ChIP-seq and Single Cell RNA-seq Data. Keystone Symposia Single Cell Biology, January 2019, Breckenridge, Colorado. *Poster presentation.*
- [6] **Sabri S**, Piskol R, Boumahdi S, de Sousa e Melo F, de Sauvage F. Gaining Insights into the Metastatic Process of Colorectal Cancer using Multi-omics Profiling. Genentech Research & Development (gRED) Poster Event, August 2018, South San Francisco, California. *Poster presentation.*
- [7] **Sabri S**, Langerman J, Chronis C, Ernst J, Plath K. Single cell Transcriptomics Identifies an Expression State Poised for Gene Expression from Various Lineages on the Path to Induced Pluripotency. 14th Annual Stem Cell Conference on Transforming Medicine, February 2018, Los Angeles, California. *Poster presentation.*
- [8] **Sabri S**, Langerman J, Chronis C, Ernst J, Plath K. Single cell Transcriptomics Identifies an Expression State Poised for Gene Expression from Various Lineages on the Path to Induced Pluripotency. Cold Spring Harbor Laboratory (CSHL) Single Cell Meeting, November 2017, Cold Spring Harbor, NY. *Oral presentation.*
- [9] **Sabri S**, Langerman J, Chronis C, Ernst J, Plath K. Single cell Transcriptomics Identifies an Expression State Poised for Gene Expression from Various Lineages on the Path to Induced Pluripotency. 3rd Annual Institute for Quantitative and Computational Biosciences (QCBio) Retreat, September 2017, Santa Monica, California. *Oral presentation.*
- [10] **Sabri S**, Langerman J, Ernst J, Plath K. Reconstructing Reprogramming Dynamics Using High-throughput Single-cell Transcriptomes. 2017 Annual Molecular Biology Institute (MBI) Retreat, April 2017, Ventura, California. *Poster presentation.*
- [11] **Sabri S**, Langerman J, Ernst J, Plath K. Reconstructing Reprogramming Dynamics Using High-throughput Single-cell Transcriptomes. 13th Annual Stem Cell Conference on Transforming Medicine, February 2017, Los Angeles, California. *Oral and Poster presentation.*
- [12] Smith B, Chronis K, **Sabri S**, Sokolov A, Uzunangelov V, Cheng D, Wei W, Stuart J, Plath K, Witte O. Single Cell Analysis of Normal Basal Cells Reveals Cellular Heterogeneity and Link to Aggressive Prostate Cancer Phenotypes. 23rd Annual Prostate Cancer Foundation (PCF) Scientific Retreat, October 2016, Carlsbad, CA. *Poster presentation.*

- [13] **Sabri S\***, Langerman J, Ernst J, Plath K. Reconstructing Reprogramming Dynamics Using High-throughput Single-cell Transcriptomes. Cornell University's Academy of Computational Life Sciences (ACLS) International Summer School, August 2016, New York City, New York. *Oral and poster presentation.*
- [14] **Sabri S\***, Copp A\*, Blansit K\*, Tao Y, Kaboodrangidaem A, Le N.K, Yang W. OncoSolutions: A way to Aid Oncologists' Clinical Decision Making. BCLA's 2nd Annual Entrepreneurship Summit, June 2016, Los Angeles, California. *Oral and poster presentation.*
- [15] **Sabri S**, Langerman J, Ernst J, Plath K. Reconstructing Reprogramming Dynamics Using High-throughput Single-cell Transcriptomes. 3rd Annual UCLA Bioinformatics IDP Retreat, May 2016, Big Bear Lake, California. *Oral presentation.*
- [16] **Sabri S**, Langerman J, Ernst J, Plath K. Reconstructing Reprogramming Dynamics Using High-throughput Single-cell Transcriptomes. UCLA Monday Biological Chemistry Seminar Series, April 2016, Los Angeles, California. *Oral presentation.*
- [17] **Sabri S**, Langerman J, Ernst J, Plath K. Reconstructing Reprogramming Dynamics Using High-throughput Single-cell Transcriptomes. 20th Annual International Conference on Research in Computational Molecular Biology (RECOMB), April 2016, Santa Monica, California. *Poster presentation.*
- [18] **Sabri S**, Langerman J, Ernst J, Plath K. Reconstructing Reprogramming Dynamics Using High-throughput Single-cell Transcriptomes. 6th Annual International Conference on Research in Computational Molecular Biology Satellite Workshop on Massively Parallel Sequencing (RECOMB-Seq), April 2016, Los Angeles, California. *Oral presentation.*
- [19] **Sabri S**, Quach B, Ghazali D, Al-Eneze Y, Patel R, Reisman S, Vlahos T, Putonti C. Discovering the Source of Metagenomic Reads from Compositional Properties. 8th Annual Research Symposium for the Center for Biotechnology Education. May 2013, Rockville, Maryland. *Oral and poster presentation.*
- [20] Kelly, J, **Sabri S**, Peterson E, Winkelman J, Putonti C, Rier S, Tuchman N. Elevated Atmospheric Carbon Dioxide Alters the Composition of Soil Microbial Communities. 3rd Annual Argonne Soil Metagenomics Workshop, October 2011, Bloomingdale, Illinois. *Oral presentation.*

## PROFESSIONAL EXPERIENCE

### **Genentech**, South San Francisco, California USA

*Bioinformatics & Computational Biology Research Intern*

**June, 2018 - September, 2018**

Gained insights into the metastatic process of colorectal cancer using multi-omics profiling. I characterized 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, Illinois USA

*Summer Student Developer*

**May, 2012 - August, 2012**

Summer of Code (GSoC) project involving informatic analyses of the Geuvadis RNA-sequencing project (Lappalainen *et al.*, Nature 2013) to determine if RNA-editing can be used to effectively define population structure. I have identified and correlated RNA-editing levels with gene expression levels to determine sites that impose a cis-regulation on gene expression.

### **Precision Plating Company**, Chicago, Illinois USA

*Laboratory Specialist*

**October, 2010 - May, 2012**

Performed wet chemistry analyses to test and troubleshoot production materials for effectiveness and functionality. I have also wrote software to automate daily operations and boost production efficiency.

- TECHNICAL SKILLS  
AND COMPETENCES
- Machine Learning: Experience developing and optimizing regression models for prediction
  - Bioinformatics: Expert level knowledge of scRNA-seq; extensive use of RNA-seq, ChIP-seq, Hi-C/5C/4C/3C and microarray data for analyses; acquainted with NGS platforms
  - Computer Languages: Python, Perl and Unix shell; familiar with C++, Java and SQL
  - Statistical Software: R; some experience with MATLAB, SAS and S-Plus
  - Applications: L<sup>A</sup>T<sub>E</sub>X, version control software, command line usage; comfortable with common database, spreadsheet, and presentation software
  - Operating Systems: Unix/Linux, OSX, Windows