

SHAILA A. MUSHAROFF

University of California San Francisco, Department of Medicine, San Francisco, CA
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EDUCATION

- 2015 **Stanford University**, Stanford, California
Ph.D. in Genetics
Doctoral advisor: Dr. Carlos D. Bustamante
Committee: Drs. Marcus Feldman, Dmitri Petrov, Hua Tang, Stephen Montgomery
Dissertation Title: "Non-equilibrium population genetics: sex-biased demography and mutational load"
- 2009 **New York University**, New York, New York
Master of Science in Computer Science
Research advisor: Dr. Bhubaneswar (Bud) Mishra
- 2005 **Rutgers University**, New Brunswick, New Jersey
Bachelor of Science in Genetics and Computer Science
Thesis advisor: Dr. Martin Nemeroff
Thesis title: "Predicting Protein Structure with Genetic Algorithms"

RESEARCH EXPERIENCE

- Postdoctoral Scholar, University of California San Francisco**, San Francisco, CA 2015 - Present
Dr. Noah Zaitlen
- Demonstrated that there is population structure in phenotypic variance and developed a statistical method to correct for this structure, increasing power and reducing bias of genetic association tests
 - Developing statistical genetic methods for admixed populations and large datasets
- Graduate Student, Stanford University**, Stanford, CA 2010 - 2015
Dr. Carlos D. Bustamante
- Developed methods to accurately infer sex-biased demographic parameters for populations which have changed in size. Collaborator: Dr. Sohini Ramachandran, Brown University
 - Performed population genetic analysis on a large sample of admixed whole-genome sequences
 - Studied patterns of deleterious alleles in diverse human populations from the Human Genome Diversity Panel (HGDP), Thousand Genomes, as well as in orangutans
- Graduate Student, Cornell University**, Ithaca, NY 2009 - 2010
Dr. Carlos D. Bustamante
- Analyzed the first admixed whole-genome sequences and assessed the impact of ancestry on the retention of deleterious alleles
- Dr. Andrew Clark
- Characterized the population structure and demographic history of individuals from Qatar
- Research Intern, IBM Watson**, Yorktown Heights, NY Summer 2007
Dr. Isidore Rigoutsos, Bioinformatics and Pattern Discovery Group
- Developed a parallelized biclustering method for use on gene expression microarray data
 - Analyzed time course experiments with variable time steps and identified co-expressed genes
- Research Assistant, New York University**, New York, NY 2008 - 2009
Dr. Edo Kussell, Center for Comparative Functional Genomics
- Characterized inteins ("internal proteins") in bacteria-host phage interaction based on bacterial endonuclease and phage cut-site nucleotide sequence similarity

- Wrote segmentation program in MATLAB for confocal microscope images of *D. melanogaster* eyes

Research Assistant, New York University, New York, NY 2007 - 2008

Dr. Richard Bonneau, Center for Comparative Functional Genomics

- Contributed to cMonkey, a multi-species regulatory module detection method
- Used neural networks to predict disordered protein regions of *P. falciparum* and *P. vivax* from sequence data

Research Assistant, New York University, New York, NY 2006 - 2007

Dr. Bud Mishra, Bioinformatics Lab

- Contributed to oncogene detection method based on copy number variation

PUBLICATIONS

Mathias R.A., Taub M.A.*, Fu W.*, **Musharoff S***, O'Connor T.D.*, et al. "A continuum of admixture in the Western Hemisphere revealed by the African Diaspora genome." *Nature Communications*. October 2016. **Equal contribution by these authors (MAT, WF, SM, and TDO)*

Henn BM, Botigué LR, Peischl S, Dupanloup I, Lipatov M, Maples BK, Martin AR, **Musharoff S**, Cann H, Snyder MP, Excoffier L, Kidd JM, Bustamante CD. "Distance from sub-Saharan Africa predicts mutational load in diverse human genomes." *PNAS*. 2016 Jan 26.

Ma X, Kelley JL, Eilertson K, **Musharoff S**, et al. "Population genomic analysis of ten genomes reveals a rich speciation and demographic history of orang-utans (*Pongo pygmaeus* and *Pongo abelii*)." *PLoS One*. 2013 Oct 23.

Kidd JM, Gravel S, Byrnes J, Moreno-Estrada A, **Musharoff S**, et al. "Population genetic inference from personal genome data: impact of ancestry and admixture on human genomic variation." *American Journal of Human Genetics*. 2012 Oct 5.

Danecek P, Auton A, Abecasis G, Albers CA, Banks E, DePristo MA, Handsaker RE, Lunter G, Marth GT, Sherry ST, McVean G, Durbin R; **1000 Genomes Project Analysis Group**. "The variant call format and VCFtools." *Bioinformatics*. 2011 Aug 1.

Hunter-Zinck H, **Musharoff S**, Salit J, Al-Ali KA, Chouchane L, Gohar A, Matthews R, Butler MW, Fuller J, Hackett NR, Crystal RG, Clark AG. "Population genetic structure of the people of Qatar." *American Journal of Human Genetics*. 2010 Jul 9.

MANUSCRIPTS

Musharoff S., S. Shringarpure, C.D. Bustamante, S. Ramachandran, "Modeling population size changes leads to accurate inference of sex-biased demographic events." (under review at PLoS Genetics)

Musharoff S., D. Park, J. Galanter, X. Liu, S. Huntsman, C. Eng, E.G. Burchard, J.F. Ayroles, N. Zaitlen. "Existence and implications of population variance structure." (in preparation)

M. Daya, N. Rafaels, ..., **CAAPA Consortium**. "Association study in African-admixed populations across the Americas recapitulates asthma risk loci in non-African populations." (submitted)

INVITED TALKS

Musharoff S. "Modeling ancestry-dependent phenotypic variance accurately corrects for population structure and detects variance effects." Population, Evolutionary and Quantitative Genetics Conference, May 13-1, 2018.

Musharoff S. “Modeling ancestry-dependent phenotypic variance reduces bias and increases power in genetic association studies.” SMBE Satellite Meeting on the Genetics of Admixed Populations. San Antonio, Texas, May 18-20, 2016.

Musharoff S., Shringarpure S., Bustamante C.D., Ramachandran S. “Modeling population size changes leads to accurate inference of sex-biased demographic events.”

- Society for Molecular Biology and Evolution, Vienna, Austria, July 12, 2015
- Evolgenome Seminar. Stanford, CA. April 1, 2015

Musharoff S. “Inferring sex-biased demography from genomic data.” Stanford 5th Annual Symposium on Genomics and Personalized Medicine. April 2015.

Musharoff S. Human Genomics, Health, Disease, and Demography. Stanford University EXPLORE: A Lecture Series on Biomedical Research, Stanford, CA, June 2013.

Musharoff S. Incorporating Sex in Chromosome X GWAS and Estimating Sex-Bias from Whole-Genome Sequence Data. Stanford Whole Genome Sequencing Club. February 2012.

Musharoff S. The Inference of Sex-Biased Human Demography. Current Issues in Genetics: Stanford Genetics Department Seminar, Stanford, CA, May 17, 2013.

Musharoff S., Waltman P., Bonneau R. Multi-Species Integrated Biclustering. NYC Area Microbial Evolution & Genomics Workshop, New York, NY, January 25, 2008

CONFERENCE POSTERS

S. Musharoff, N. Zaitlen. Modeling ancestry-dependent phenotypic variance increases power in multi-ethnic association studies and enables detection of variance effects. American Society of Human Genetics Annual Meeting, Orlando, FL, October 17, 2017.

S. Musharoff, S. Shringarpure, C.D. Bustamante, S. Ramachandran. A novel likelihood ratio test for sex-biased demography and its application to human genomic data

- American Society of Human Genetics Annual Meeting, San Diego, CA, October 18, 2014.
- Society for Molecular Biology & Evolution, San Juan, Puerto Rico, June 8, 2014.
- American Society of Human Genetics Annual Meeting, Chicago, 2013.

S. Musharoff, J. M. Kidd, B. M. Henn, S. Gravel, B. Maples, K. Eilertson, M. C. Yee, H. M. Cann, G. Euskirchen, M. Snyder, C. D. Bustamante, S. Ramachandran. A likelihood ratio test for sex-bias and its application to whole-genome sequencing data of a set of globally-distributed populations. American Society of Human Genetics Annual Meeting, San Francisco, CA, November 7th, 2012.

S. Musharoff, J. M. Kidd, B. M. Henn, M.C. Yee, H. M. Cann, G. Euskirchen, M. Snyder, D. Bustamante, S. Ramachandran. Characterizing patterns of variation on the human X chromosome of eight globally distributed populations using whole genome sequencing. The Biology of Genomes, Cold Spring Harbor Laboratory, Cold Spring Harbor, NY, May 9th, 2012.

S. Musharoff, S. Ramachandran, J.M. Kidd, B.M. Henn, M.C. Yee, H.M. Cann, G. Euskirchen, M. Snyder, C.D. Bustamante. Comparison of the X Chromosome to Autosomes of Diverse Human Genomes and the Analysis of Sex-Specific Processes. American Society of Human Genetics Meeting, Montreal, Canada, October 11th, 2011.

S. Musharoff, J. Kidd, B. Henn, M.C. Yee, M. Snyder, F. De La Vega, C. D. Bustamante. Distribution of Deleterious Alleles Across Diverse Populations. American Society of Human Genetics Annual Meeting, Washington D.C., November 2nd, 2010.

HONORS AND FELLOWSHIPS

2016 Awarded UCSF PRESCIENT Fellowship (declined)
2010-2014 Stanford Genetics Training Grant
2008 NYU Presidential Service Award for Women in Computing
2000 Rutgers Dean's List
1999 Rutgers General Honors Program
1999 National Society of Collegiate Scholars
1999-2000 National Merit Scholarship

TEACHING EXPERIENCE

2017 Teacher, Summer Short Course on Human Population Genomics, University of Chile
Designed and co-taught a week-long 40-hour course on population and statistical genetic theory and methods to Chilean undergraduate and graduate students

2016, 2017 Lecturer, Graduate Biostatistics course, UCSF
Delivered four 4-hours lectures to Ph.D. students. Designed and taught coding examples.

2012 Full Teaching Assistant & Lecturer, Stanford University, Spring 2012
Course: "GENE 209: Statistical Genetics"

- Taught and designed weekly sections, statistics reviews, and delivered one lecture
- Aided in course design, wrote and graded homework assignments, held office hours

2013, 2012 Institutes of Medicine Summer Research Program, Stanford, CA
Taught single-day course: human population genetics (2013) and personalized medicine (2012)

2008-2010 Teacher, Stanford University Splash!
Taught a biannual single-day course on introductory population genetics to high school students

2008 Teacher, New York University cSplash!
Taught a single-day course on mathematics of parasite-host interactions to high school students

EXTRACURRICULAR AND UNIVERSITY SERVICE

2012-2014 Mentor, Stanford Biosciences Student Association (SBSA)
Spring 2014 Co-teacher, Stanford d.school Research as Design course
Spring 2013 Consultant, SAP. Implementing genomics operations on custom hardware
2014 Organizer, Academic Career Development Chats (ACDC) for diverse graduate students
2014 Organizer, Stanford 15th Annual Biomedical Computation at Stanford (BCATS) Symposium
2013 Diversity Host, Stanford Biosciences Ph.D. Recruitment
2012 Presenter and Volunteer, Standout Diversity Poster Event
2012 Co-organizer, Stanford Genetics Department Ph.D. Recruitment
2011 Host, Stanford Genetics Department Ph.D. Recruitment
2006-2008 President/VP, NYU Women in Computing (WinC) student organization; organized outreach events for high school girls from underserved groups

MEMBERSHIP

2009-Present American Society for Human Genetics
2009-Present Society of Molecular Biology and Evolution
2014-2015 Stanford Geneticists for Diversity in Science (GDS)
2013-2014 Stanford Women In Science and Engineering (WISE)
2010-2011 Association for Women in Science (AWIS)
2009-2010 Cornell Asian-American Student's Association

PROGRAMMING LANGUAGES

R, Python, C, C++, Unix tools, Matlab, Java, lisp