

# SHAILA A. MUSHAROFF

Stanford University, Department of Genetics, Stanford, CA  
shailam@stanford.edu

## EDUCATION

Expected 2015

**Stanford University**, Stanford, CA

**PhD** in Genetics

Doctoral Advisor: Dr. Carlos D. Bustamante

Doctoral Committee: Drs. Marcus Feldman, Dmitri Petrov, Hua Tang, Stephen Montgomery

Dissertation Title: “Demography-aware inference of sex-bias, substructure, and deleterious mutation load”

2009

**New York University**, New York, NY

**Master of Science** in Computer Science

Research adviser: Bud Mishra

2006

**Rutgers University**, New Brunswick, NJ

**Bachelor of Science** in Genetics and Computer Science

Thesis adviser: Martin Nemeroff

Thesis title: “Predicting Protein Structure with Genetic Algorithms”

## RESEARCH EXPERIENCE

**Graduate Student, Stanford University**, Stanford, CA

2010 - Present

Dr. Carlos D. Bustamante Laboratory

- Developed methods accurately infer sex-biased demography from genomic data for populations of non-constant size. Collaborator: Dr. Sohini Ramachandran, Brown University
- Leading subgroup to call X chromosome variants and perform X vs autosome analysis on large sample of whole-genome sequences of admixed individuals for CAAPA (Consortium on Asthma among African-ancestry Populations in the Americas)
- Studied patterns of deleterious allele retention in diverse human populations from the Human Genome Diversity Panel (HGDP), Thousand Genomes, and in orangutans

**Graduate Student, Cornell University**, Ithaca NY

2009 - 2010

Dr. Carlos D. Bustamante Laboratory

- Analyzed whole-genome sequences of two individuals of admixed descent and assessed the impact of ancestry on retention of deleterious alleles

Dr. Andrew Clark Laboratory

- Characterized the population structure and demographic history of individual from Qatar and recovered population substructure using statistical genetic methods

**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 validated functional enrichment using GO terms.

**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 MATLAB program to annotate confocal microscope images of *Drosophila melanogaster* eye development

**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 deep learning (neural net) 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 method to detect oncogenes from aCGH data based on copy number variation

### FUNDING AND FELLOWSHIPS

2010-2014 Stanford Genetics Training Grant

1999-2000 National Merit Scholarship

### HONORS AND AWARDS

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

### PUBLICATIONS

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, Shringarpure S, Bustamante C.D., Ramachandran S., "Modeling population size changes leads to accurate inference of sex-biased demographic events" (in preparation)

Brenna M. Henn\*, Laura R. Botigué\*, ...Shaila Musharoff, et al. "Distance from Sub-Saharan Africa Predicts Mutational Load in Diverse Human Genomes" (in preparation)

### INVITED TALKS

**S. Musharoff**, S. Shringarpure, C.D. Bustamante, S. Ramachandran. "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,** S. Shringarpure, C.D. Bustamante, S. Ramachandran. A Novel Likelihood Ratio Test Framework for Sex-Biased Demography and its Application to Human Genomic Data

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

**S. Musharoff,** S. Shringarpure, C.D. Bustamante, S. Ramachandran. A Novel Likelihood Ratio test for Sex-Bias and the Effect of Cryptic Sex-Bias on the Estimation of Demographic Parameters. 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, S. Gravel, B. Maples, K. Eilertson, M. C. Yee, H. M. Cann, G. Euskirchen, M. Snyder, C. D. Bustamante, S. Ramachandran. Assessing the Relative Effects of Demography versus Selection on the Human X Chromosome Using Next-Generation Sequencing. Society for Molecular Biology & Evolution, Dublin, Ireland, June 25th 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 Annual Meeting, Montreal, Canada, October 11th 2011.

**S. Musharoff,** J. Kidd, B. Henn, MC. 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.

#### TEACHING EXPERIENCE

- 2012 Full Teaching Assistant & Lecturer, Stanford University, Spring 2012  
 Course: "GENE 209: Statistical Genetics"
- Taught and designed weekly sections, statistics reviews, and gave a 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 biannual single-day course on introductory population genetics to high school students
- 2008 Teacher, New York University cSplash!  
 Taught 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 PhD Program Recruitment  
 2012 Presenter and Volunteer, Standout Diversity Poster Event  
 2012 Co-organizer, Stanford Genetics Department PhD Recruitment  
 2011 Host, Stanford Genetics Department PhD Recruitment  
 2006-2008 President / VP, NYU Women in Computing (WinC) student organization; organized outreach events for low income, minority high school girls

### **MEMBERSHIP**

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

### **PROGRAMMING LANGUAGES**

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