

Curriculum Vitae
Sohini Ramachandran

Ecology and Evolutionary Biology
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Position: Assistant Professor, Ecology and Evolutionary Biology and Center for Computational Molecular Biology, Brown University.

Education

2002 - 2007: Ph.D., Stanford University, Department of Biological Sciences (Population Genetics).
Doctoral advisor: Professor Marcus W. Feldman.
Dissertation title: "The signature of historical migrations on human population genetic data."
1998 - 2002: B.S. with honors, Stanford University, Mathematical and Computational Sciences.
Advisor: Professor Bradley Efron.

Professional appointments

July 1, 2015 - present: Manning Assistant Professor of Ecology and Evolutionary Biology, Brown University.
July 2010 - June 30, 2015: Assistant Professor, Brown University.
2007 - 2010: Junior Fellow, Harvard University Society of Fellows. Postdoctoral work with Professor John Wakeley (Department of Organismic and Evolutionary Biology).

Completed Publications

Chapters in books

Soemedi, R., Vega, H., Belmont, J. M., **Ramachandran, S.** and Fairbrother, W. G. (2014) 'Genetic variation and RNA binding proteins: tools and techniques to detect functional polymorphisms', ed. G. Yeo, In: *Advances in Experimental Medicine and Biology* 825:227-266.

[SR co-wrote the chapter, particularly discussing implications of alternative splicing in population genetics.]

Ramachandran, S., Tang, H., Gutenkunst, R. and Bustamante, C. D. (2010), 'Genetics and Genomics of Human Population Structure', Pages 589-616 In: *Vogel and Motulsky's Human Genetics: Problems and Approaches, 4th ed.*, eds. M. Speicher, S. E. Antonarakis and A. G. Motulsky. Springer.

Ramachandran, S. and Feldman M. W. (2009), 'Theory of migration: Implications for linguistic evolution', Pages 21-30 In: *Ancient Human Migrations: A Multidisciplinary Approach*, eds. P. N. Peregrine, I. Peiros, and M. W. Feldman. University of Utah Press.

Refereed journal articles (* indicates undergraduate coauthor)

Alpert Sugden, L. and **Ramachandran, S.** (2016) 'Integrating the signatures of demic expansion and archaic introgression in studies of human population genomics'. *Current Opinion in Genetics and Development* Vol. 41: 140-149.

[SR is corresponding author.]

Nakka, P., Raphael, B. J., and **Ramachandran, S.** (2016) 'Gene and network analysis of common variants reveals novel associations in multiple complex traits'. *Genetics* Vol. 204: 783-798.

[SR and BJR are corresponding authors; chosen by *Genetics* editors as one of the October 2016 issue highlights: www.genetics.org/content/204/2/NP]

Behr, A. A.*, Liu-Fang, G.*, Liu, K. Z.*, Nakka, P., and **Ramachandran, S.** (2016) 'PONG: fast analysis and visualization of latent clusters in population genetic data'. *Bioinformatics* Vol. 32:2817-2823.

Palacios, J. A., Wakeley, J., and **Ramachandran, S.** (2015) 'Bayesian nonparametric inference of population size changes from sequential genealogies'. *Genetics* Vol. 201:281-304.

[SR and JAP are corresponding authors; chosen by *Genetics* editors as one of the September 2015 issue highlights: www.genetics.org/content/201/1/NP]

Creanza, N., Ruhlen, M., Pemberton, T. J., Rosenberg, N. A., Feldman, M. W., and **Ramachandran, S.** (2015) 'A comparison of worldwide phonemic and genetic variation in human populations.' *Proceedings of the National Academy of Sciences USA* Vol. 112:1265-1272.

[SR is the PI of this project, conceived of the study with MR and MWF, designed the research with NC and MWF, prepared and analyzed the linguistic data with NC, and wrote the paper with input from all authors. Commentaries published in *PNAS* (Vol. 112:1919-1920; www.pnas.org/content/112/7/1919.full.pdf) and *Nature Reviews Genetics* (Vol. 16:128-129; www.nature.com/nrg/journal/v16/n3/full/nrg3911.html).]

Smith, K.F., Goldberg, M.*, Rosenthal, S., Carlson, L., Chen, J.*, Chen C., **Ramachandran, S.** (2014) 'Global diversity and risk of human infectious disease outbreaks.' *J Roy Soc Interface* Vol. 11:20140950.

[SR co-designed the project with KFS and CC, supervised MG and co-advised JC in their analyses of the data. Press coverage from Yahoo! and Voice of America, among others.]

Leiserson, M. D. M., Eldridge, J., **Ramachandran, S.**, and Raphael, B. J. (2013) 'Network analysis of GWAS data', *Current Opinion in Genetics and Development* Vol. 23:602-610.

[SR co-wrote the paper, focusing on limitations of current GWAS analyses and applications of network analyses to GWAS data. Featured on the journal cover.]

Porder, S. and **Ramachandran, S.** (2012), 'The phosphorus content of common rocks - a potential driver of ecosystem P status'. *Plant and Soil* Vol. 367:41-55.

[SR conducted the data analysis for this paper and wrote the methods.]

Wakeley, J., King, L., Low, B. S. and **Ramachandran, S.** (2012), 'Gene genealogies within a fixed pedigree, and the robustness of Kingman's coalescent', *Genetics* Vol. 190:1433-1445.

[SR is co-PI on this project, co-designed the project, co-wrote the pedigree-coalescent simulation software, and derived analytical results along with JW.]

Ramachandran, S. and Rosenberg, N. A. (2011), 'A test of the influence of continental axes of orientation on patterns of human gene flow', *American Journal of Physical Anthropology* Vol. 146:515-529.

[Cover article; discussed in *Science* <http://www.sciencemag.org/content/333/6050/1692.full>; press coverage by American Archaeology, Scientific American and Discovery News; one of *AJPA*'s five most-downloaded articles of 2011.]

Novembre, J.* and **Ramachandran, S.*** (2011), 'Perspectives on human population structure at the cusp of the sequencing era', *Annual Review of Genomics and Human Genetics* Vol. 12:245-274. (*contributed equally to this manuscript)

Henn, B. M., Gignoux, C. R., Jobin, M., Granka, J. M., Macpherson, J. M., Kidd, J. M., Rodríguez-Botigué, L., **Ramachandran, S.**, Hon, L., Brisbin, A., Lin, A. A., Underhill, P., Comas, D., Kidd, K. K., Parham, P., Norman, P. J., Bustamante, C. D., Mountain, J. L., and Feldman, M. W. (2011), 'Feature Article: Hunter-gatherer genomic diversity suggests a southern African origin for modern humans', *Proceedings of the National Academy of Sciences USA* Vol. 108: 5154-5162.

[SR designed and conducted data analysis for the origin of the human expansion and co-wrote the paper with all authors.]

[Press coverage by NatureNews and BBC News]

Casto, A. M., Li, J. Z., Absher, D., Myers, R., **Ramachandran, S.** and Feldman, M. W. (2010), ‘Characterization of X-linked SNP genotypic variation in globally distributed human populations’, *Genome Biology* Vol. 11:R10.

Ramachandran, S., Rosenberg, N. A., Feldman, M. W. and Wakeley, J. (2008), ‘Population differentiation and migration: coalescence times in a two-sex island model for autosomal and X-linked loci’, *Theoretical Population Biology* Vol. 74: 291-301.

Li, J. Z., Absher, D. M., Tang, H., Southwick, A. M., Casto, A. M., **Ramachandran, S.**, Cann, H. M., Barsh, G. S., Feldman, M., Cavalli-Sforza, L. L. and Myers, R. M. (2008), ‘Worldwide human relationships inferred from genome-wide patterns of variation’, *Science* Vol. 319: 1100-1104.

Wang, S., Lewis Jr., C. M., Jakobsson, M., **Ramachandran, S.**, Ray, N., et al. (2007), ‘Genetic variation and population structure in Native Americans’, *Public Library of Science Genetics* Vol. 3: e185.

[As of October 2015, among the top ten downloaded PLoS Genetics articles of all time. See a commentary at: <http://journals.plos.org/plosgenetics/article?id=10.1371/journal.pgen.1005557>]

Rosenberg, N. A., Mahajan, S., **Ramachandran, S.**, Zhao, C., Pritchard, J. K. and Feldman, M. W. (2005), ‘Clines, clusters, and the effect of study design on the inference of human population structure’, *Public Library of Science Genetics* Vol. 1: e70.

Ramachandran, S., Deshpande, O., Roseman, C. C., Rosenberg, N. A., Feldman, M. W. and Cavalli-Sforza, L. L. (2005), ‘Support from the relationship of genetic and geographic distance in human populations for a serial founder effect originating in Africa’, *Proceedings of the National Academy of Sciences USA* Vol. 102: 15942-15947.

[Recognized by the Faculty of 1000 <http://f1000biology.com/article/id/1029413/evaluation>]

Macpherson, J. M., **Ramachandran, S.**, Diamond, L. and Feldman, M. W. (2004), ‘Demographic estimates from Y-chromosome microsatellite polymorphisms: analysis of a worldwide sample’, *Human Genomics* Vol. 1: 345-354.

Ramachandran, S., Rosenberg, N. A., Zhivotovsky, L. and Feldman, M. W. (2004), ‘Robustness of the inference of human population structure: a comparison of X-chromosomal and autosomal microsatellites’, *Human Genomics* Vol. 1: 87-97.

Non-refereed journal articles

Chen, L-L, Claw, K. G., and Ramachandran S. (2016), ‘A two-fold challenge: the experience of women of color in genomics’, *Genome Biology* Vol. 17: 210.

[All authors contributed equally to this manuscript.]

Bustamante, C. D.* and **Ramachandran, S.*** (2009), ‘Evaluating signatures of sex-specific processes in the human genome’, *Nature Genetics* (News and Views) Vol. 41: 8-10. (*contributed equally to this manuscript)

Abstracts

2016 - P. Nakka, B. J. Raphael, and S. Ramachandran; contributed talk, “Gene and network analysis of common variants reveals novel associations in multiple complex diseases”; RECOMB-Genetics satellite meeting

2016 - S. Ramachandran, and L. A. Sugden; invited talk, “A novel, probabilistically interpretable framework for localizing genomic elements underlying adaptive evolution”; American Association of Physical Anthropology annual meeting.

2015 - J. A. Palacios Roman, J. Wakeley, and S. Ramachandran; contributed talk, “Inference of population size trajectories with Tajima’s coalescent”; Probabilistic Modeling in Genomics, Cold Spring Harbor Laboratory

2015 - L. Alpert and S. Ramachandran; contributed talk, “Novel probabilistically interpretable methods for localizing targets of selective sweeps”; Society of Molecular Biology and Evolution annual meeting

2015 - S. Musharoff, S. Shringarpure, C. D. Bustamante, and S. Ramachandran; contributed talk (SM), “Modeling population size changes leads to accurate inference of sex-biased demographic events”; Society of Molecular Biology and Evolution annual meeting

2015 - N. Creanza, M. Ruhlen, T. J. Pemberton, N. A. Rosenberg, M. W. Feldman, and S. Ramachandran; contributed talk (NC), “A comparison of worldwide linguistic and genetic variation in human populations”; Human Behavior and Evolution Society (HBES) annual meeting. *NC won the HBES Postdoctoral Award for her talk.*

2015 - L. Alpert and S. Ramachandran; contributed talk (LA), “A novel probabilistically interpretable method for identifying targets of selective sweeps”; Society of Molecular Biology and Evolution satellite meeting on “Investigating biological adaptation with NGS: data and models”

2015 - S. Ramachandran, N. Creanza, M. Ruhlen, T.J. Pemberton, N.A. Rosenberg, and M.W. Feldman; invited symposium presentation, “Studying modern human migrations with integrated analyses of genetic and linguistic data”; American Association of Physical Anthropology annual meeting

2014 - N. Creanza, M. Ruhlen, T. J. Pemberton, N. A. Rosenberg, M. W. Feldman, and S. Ramachandran; invited symposium presentation (NC), “Worldwide linguistic and genetic variation”; Society of Molecular Biology and Evolution annual meeting

2013 - S. A. Musharoff, C. D. Bustamante, and S. Ramachandran; invited symposium presentation (SR), “Modeling and inference of sex-biased demographic processes, applied to human population-genomic data”; Society of Molecular Biology and Evolution annual meeting

2013 - N. Creanza and S. Ramachandran; contributed talk title (NC), “Worldwide phonemic variation: evolutionary analyses and genomic comparisons”; Evolution annual meeting

2012 - S. Ramachandran, L. King, B. S. Low, P. Wilton, and J. Wakeley; contributed symposium presentation, “The Ties That Bind: Gene genealogies within a fixed pedigree”; Society of Molecular Biology and Evolution annual meeting

2011 - S. Ramachandran, D. Nadkarni, and M. Harrison; contributed talk title, “Detecting gene flow with low-dimensional summaries of genotype data”; Society of Molecular Biology and Evolution annual meeting

2010 - J. Wakeley and S. Ramachandran; talk title (JW), “Sources of variation in ancestral genetic processes”; Institute of Mathematical Statistics annual meeting

2010 - S. Ramachandran and N. A. Rosenberg; invited talk title, “Continental axes of orientation influence patterns of human gene flow”; American Association of Physical Anthropologists annual meeting, Wiley-Blackwell symposium

2009 - S. Ramachandran, N. A. Rosenberg, M. W. Feldman, and J. Wakeley; contributed talk title, “Coalescence times in a two-sex island model for autosomal and X-linked loci”; Society of Molecular Biology and Evolution annual meeting

2008 - S. Ramachandran, and N. A. Rosenberg; platform presentation, “The influence of continental axes of orientation on patterns of human gene flow”; American Society of Human Genetics annual meeting

2007 - D. Absher, J. Li, H. Tang, S. Ramachandran, A. Southwick, G. Barsh, M. W. Feldman, L. Cavalli-Sforza, and R. M. Myers; platform presentation (DA), “High-resolution genetic characterization of 51 unique human populations from the Human Genome Diversity Panel”; American Society of Human Genetics annual meeting

2006 - S. Ramachandran, N. A. Rosenberg, and M. W. Feldman; contributed talk title, “Models for comparing male and female demographic histories using autosomal and X-chromosomal microsatellites”; Evolution annual meeting

2005 - S. Ramachandran, N. A. Rosenberg, L. A. Zhivotovsky, and M. W. Feldman; contributed talk title, “Comparing male and female demographic histories using autosomal and X-chromosomal microsatellites”; American Association of Physical Anthropology annual meeting

2005 - N. A. Rosenberg, S. Ramachandran, L. A. Zhivotovsky, and M. W. Feldman; contributed talk title (NAR), “Models for predicting patterns of X-chromosomal genetic variation from autosomal variation”; American Association of Physical Anthropologists annual meeting

2005 - S. Ramachandran, C. C. Roseman, N. A. Rosenberg, M. W. Feldman, and L. L. Cavalli-Sforza; contributed talk title, “Geographic distance predicts genetic distance in human populations”; Evolution annual meetings

In addition to the above, I have been an author on poster presentations: 2016, Biology of Genomes (senior author), Evolution annual meeting (senior author); 2015, Pew Scholars annual meeting (senior author), Society of Molecular Biology and Evolutionary (senior author on two posters); 2014, Society of Molecular Biology and Evolution (senior author), Biology of Genomes (senior author), Pew Scholars annual meeting (senior author); 2013, American Society of Human Genetics (first author); 2012, Biology of Genomes (senior author); 2011, American Society of Human Genetics (coauthor); 2004, Gordon Research Conferences, Molecular Evolution (first author).

Invited lectures

2017 (scheduled)

Arizona State University, School of Life Sciences seminar series
Stanford University, Center for Computational, Evolutionary, and Human Genomics
University of California, Los Angeles, Genetics and Genomics Seminar Series
Brown University, Pathology and Laboratory Medicine Grand Rounds
Cornell University, Department of Biomedical Sciences
University of Pennsylvania, Department of Biology

2016

Washington University in St. Louis, Department of Biology
UCLA Computational Genomics Summer Institute, an NIH-funded program jointly hosted by UCLA and the Institute of Pure and Applied Mathematics (IPAM)
National Academy of Sciences’ 28th Annual Kavli Frontiers of Science Symposium; Session on “Resurrecting the Past: Genomic Reconstructions of Human History”

2015

University of Kentucky, Lexington, Department of Biology, Ribble Seminar Series
Harvard University, Department of Organismic and Evolutionary Biology, Hoekstra Lab
Boston Evolution Supergroup (member institutions are Harvard University, Harvard Medical School, and the Broad Institute)
Pennsylvania State University, Biology Department
University of Massachusetts-Amherst, Molecular and Cellular Biology and Organismic and Evolutionary Biology (joint seminar)
University of North Carolina at Charlotte, Department of Bioinformatics and Genomics
University of Idaho, Center for Modeling of Complex Interactions

2014

SUNY Binghamton, Department of Biology
Brown University, Department of Cognitive, Linguistic & Psychological Sciences, Linguistics and Language Lunch
University of Leicester, UK, EMBO-sponsored conference “Human Evolution in the Genomic Era” (Plenary speaker)
University of Toronto, Ecology and Evolutionary Biology
Emory University, Population Biology, Ecology, and Evolution program
University of Washington, Seattle, Department of Genome Sciences

2013

Pew Scholars Program in the Biomedical Sciences Annual Meeting
Massachusetts Institute of Technology, Bioinformatics Seminar
University of California, Los Angeles, Bioinformatics Seminar series
SUNY Stony Brook, Ecology and Evolution colloquium series
University of Pennsylvania, Department of Genetics

2012

The Royal Swedish Academy of Sciences, Symposium on “Modern Human Genetic Variation” (one of 13 invited speakers)

2011

Brown University, Department of Applied Mathematics, Pattern Theory Seminar series
St. Jude Children’s Research Hospital, PAAR4Kids Annual Meeting

2010

University of New Mexico, Seminar in Interdisciplinary Biological and Biomedical Sciences (SiBBs)
National Institute of Biomedical Genomics, Kalyani, India

2009

Harvard Medical School, Department of Genetics
Cornell University, Biological Statistics and Computational Biology
University of California San Francisco, Institute for Human Genetics
Brown University, Center for Computational Molecular Biology
New York University, Department of Biology
University of Michigan, Department of Human Genetics
University of Michigan, Bioinformatics Program
St. Jude Children’s Research Hospital, Department of Pharmaceutical Sciences
University of Rochester, Department of Biology

2008

23andme, Mountain View, CA
University of Michigan, Department of Genetics, Interdisciplinary Group Seminar

2007

Brown University, Ecology and Evolutionary Biology Department Seminar

2006

Santa Fe Institute, invited colloquium
University of Michigan, Department of Human Genetics Journal Club

Work in progress (* indicates undergraduate coauthor)

Musharoff, S. A., Bustamante, C. D., and **Ramachandran, S.**, ‘Inference of sex-biased demography from whole-genome data’. In prep for *PLoS Genetics*.

[SR is co-PI of this project and designed the research with CDB and SAM.]

Sugden, L. A., Atkinson, E., Henn, B., and **Ramachandran, S.**, ‘Novel probabilistically interpretable methods for identifying and localizing adaptive mutations’. In prep for *PLoS Biology*.

Research Grants

“Novel statistical methods to localize genomic elements underlying adaptive evolution”, National Institutes of Health R01 GM118652 (PI). Anticipated total costs over 5 years: \$1,607,269 (6/6/2016 – 5/31/2021).

“Project 1: Incorporating Ethnic and Gender Disparities in Genomic Studies of Disease”, National Institutes of Health P20 GM109035-01A1 (PI). Project 1 in Brown University’s “COBRE: Center for Computational

Biology of Human Disease”, (PI: Rand; 6/1/2016 – 2/28/21). Total costs to PI Ramachandran in Fiscal Year 1 are \$279,489.

“CAREER: Next-generation inference of evolutionary parameters from genome-wide sequence data”, National Science Foundation DBI-1452622 (PI). \$1,029,319 (2/15/2015 – 1/31/2020).

REU Supplement to “CAREER: Next-generation inference of evolutionary parameters from genome-wide sequence data”, National Science Foundation DBI-1452622 (PI). \$5,376 (6/13/2016 for summer 2016), used to fund Annie Fischer '17 (Applied Math-Bio) and Katherine Liu '17 (Computer Science and Religious Studies).

Pew Scholars Program in the Biomedical Sciences (PI). \$240,000 (8/2012 – 8/2016).

Completed grants

“Effects of Climate and Land-Cover Change on Human Infectious Disease Outbreaks”, Brown University Institute for the Study of Environment and Society (co-investigator). \$150,000 (7/2014 – 6/2016).

Alfred P. Sloan Foundation (PI). \$50,000 (9/2012 – 9/2015)

REU Supplement to “CAREER: Next-generation inference of evolutionary parameters from genome-wide sequence data”, National Science Foundation DBI-1452622 (PI). \$4,312 (4/27/2015 for summer 2015), used to fund Gracie Liu-Fang (Wellesley '17, Computer Science).

“Communications and Socio-Environmental Drivers of Disease Outbreaks”, Brown University Environmental Change Initiative (co-investigator). \$20,000 (9/2013 – 7/2014).

“Detecting signatures of selection and historical migrations on human population genetic data”, William H. Milton Fund of Harvard University (PI). \$30,204 (1/1/2008 – 12/31/2009).

Grants awarded to trainees

2016 – Stephen Rong, National Science Foundation Graduate Research Fellowship

2016 – Tyler Dae Devlin '17, Summer Research Assistantship, Brown University Program in Liberal Medical Education

2016 – Katherine Liu '17, Karen T. Romer UTRA, Brown University

2014-2015 – Priyanka Nakka (graduate student), Oliver Cromwell Gorton Arnold predoctoral fellowship, Brown University

2014 – Aaron Behr '15, Karen T. Romer UTRA, Brown University

2013 – Dr. Julia Palacios, Conacyt Postdoctoral fellowship (Estancia Postdoctoral en el Extranjero, National Council for Science and Technology, Mexico)

2013 – Maya Ramchandran '15 and Natalie Van Houten '14, Karen T. Romer UTRA (Team UTRA for multiple students), Brown University.

2012 – Michael Goldberg '13, Karen T. Romer UTRA, Brown University.

2011 – Alyna Khan '12, Karen T. Romer Undergraduate Teaching and Research Award (UTRA), Brown University.

Service

To the department/university

Invited faculty panelist, “The Road Taken - Mastering the Journey from Here to There”, Office of Women in Medicine and Science Annual Professional Development Program, Brown University (June 2016).

Director of Undergraduate Studies, Computational Biology concentration, July 2015 - present. Led the design of the Bachelor of Arts in Computational Biology (approved December 2015). Concentration advisor for 8 advisees to date and overseer of concentration requirements for 5 graduates to date (2015-present).

Member, Diversity Advisory Board, Brown University. A central goal of the Board is to work with and advise the Vice President for Academic Development, Diversity and Inclusion and other senior officers as appropriate concerning the promotion of diversity and the development of a welcoming and inclusive campus climate.

Biology senior prize and thesis award committee, Brown University, Spring 2015.

Evening Lectures to Brown University Club (alumni): "How DNA Shapes Our Lives"; Seattle - October 28, 2014; Raleigh/Durham Triangle - November 10, 2014.

Advisory Board member, Office of Women in Medicine and Science. 9/2014 - present.

Concentration advisor, Applied Math-Biology, 2014-2017. 27 advisees to date (2014-present).

Member, Rhodes, Marshall, Mitchell Fellowships committee, Brown University: 2012, 2016.

Center for Computational Biology graduate admissions committee: Spring 2011, Spring 2015.

To the profession

Study section member: Advances in Biological Informatics, NSF (10/2015).

Associate Editor, Genetics (Population and Evolutionary Genetics Theory), 9/2014 - present

2014 - Symposium co-organizer, "Out of Africa: Humans, commensals, pathogens, oh my!", Society of Molecular Biology and Evolution annual meeting

Faculty Member, Evolutionary/Comparative Genetics section, Faculty of 1000, 4/2013 - present

Editorial Board member, Investigative Genetics, 3/2012 - 4/2016 (ended due to journal closure).

Temporary member: Genetic Variation and Evolution (GVE) study section, NIH (10/2012).

Associate Editor, Molecular Biology and Evolution, 1/2011 - 9/2015

2009 - Symposium co-organizer, "Sex-specific demography using the X", Society of Molecular Biology and Evolution annual meeting

Ad hoc reviewer for journals including: American Journal of Human Genetics, Genetics, Genome Research, Molecular Biology and Evolution, Nature, Nature Genetics, PLoS Genetics, PNAS, Theoretical Population Biology. *Ad hoc* reviewer for Evolutionary Genetics Program, NSF (2016).

Memberships: American Society of Human Genetics, American Association for the Advancement of Science, Society for Molecular Biology and Evolution; affiliate member, Pharmacogenomics Research Network (January 2013 - present)

To the community

Invited faculty speaker, "Biomedical Informatics and Data Science for Biomedicine and Health Care", Summer@Brown course for high school students.

Invited faculty panelist, 2016 Young Scholars Conference, Brown University. A professional development workshop for diverse graduate students and postdocs from STEM fields.

Invited faculty speaker, Catalyst 2015, Brown University. Catalyst is a pre-orientation program that aims to prepare under-represented and disadvantaged students for science at Brown University.

Parent Support Board Member, East Side/Mount Hope YMCA Childcare Center, Providence, RI. June 2014 - present.

Faculty speaker, The Artemis Project (2013, 2014, 2016). The Artemis Project is a free, five-week summer day camp for rising 9th grade girls in Providence who are interested in computing.

Invited faculty speaker, MathWiSE (Math/Applied Math Department's affinity group of Brown Women in Science and Engineering), April 2013.

Invited panelist, "She Blinded Me With Science: the (r)evolutionary biology and relationships of *The How and the Why*", Trinity Repertory Company, Providence RI (December 2012).

(Video link available at: http://www.trinityrep.com/box_office/on_stage/hw.php)

Keynote speaker, Brown Women in Science and Engineering (WiSE) mentoring social, Fall 2012.

Member of the Faculty Network for the African American, Latino, Asian/Asian American, Native American (ALANA) Mentoring Program, 2012-2013.

Service prior to 2010

Search committee member, Vice Provost for Graduate Education and Vice Provost for Research, Stanford University. Appointed to committee by Provost's office, Winter and Spring 2006.

Graduate Student Representative, Stanford Alumni Association Board of Directors. Fall 2003 – Spring 2006.

At-large elected representative, Stanford University Graduate Student Council (Spring 2004 – Spring 2005).

Academic honors and fellowships

Interviewed and profiled by *Genome Biology*, October 2016, in “A two-fold challenge: the experience of women of color in genomics”.

Henry Merritt Wriston Fellowship winner, 2016-2017. Recognizes junior faculty who are fulfilling Brown University's dual mission of excellence in both teaching and research. Includes one semester's leave on special assignment at full pay.

Manning Assistant Professor, Brown University, July 2015 – present. Includes annual research funds in the amount of \$2,000.

SimBank Catalysis meeting, National Evolutionary Synthesis Center, Durham NC, invited participant (11/2014)

2013 Career Enhancement Fellowship (Declined), Woodrow Wilson National Fellowship Foundation.

Interviewed and profiled as a “Scientist to Watch” (*The Scientist*, June 2012, featuring scientists under 40 years of age) and in “Turning point” (*Nature* 488:547, August 22 2012).

2012 Pew Scholar, Program in Biomedical Sciences, Pew Charitable Trusts; \$240,000 (8/2012-8/2016)

Alfred P. Sloan Research Fellow, Alfred P. Sloan Foundation; \$50,000 (9/2012 - 9/2014).

Women Evolving Biological Sciences (WEBS), National Evolutionary Synthesis Center, Durham NC, invited workshop participant (11/2011)

Center for Computational Molecular Biology Seed Award, Brown University, \$5,000 (10/5/2010).

Samuel Karlin Prize in Mathematical Biology, Stanford University Department of Biological Sciences (for dissertation work, awarded at Commencement 2008).

Junior Fellow, Harvard University Society of Fellows, July 2007 – July 2010.

Fellowship recipient, Stanford Genome Training Program, Fall 2005 – Spring 2007.

Excellence in Teaching Award, Stanford University of Department of Biological Sciences (2005).

National Defense Science and Engineering Graduate Fellow, 2002-2005. Administered by the Department of Defense, Army Research Office, and American Society for Engineering Education.

2002 Lloyd W. Dinkelspiel Award for Outstanding Contributions to Undergraduate Education, Stanford University. (Nomination procedure, one of four recipients, only two of which are undergraduates).

2002 J.E. Wallace Sterling Award for Outstanding Service to the Stanford Community, Stanford University Alumni Association. (First student in history of Sterling and Dinkelspiel awards to win both.)

Fourth place scholar in 1998 Westinghouse Science Talent Search. Recipient of \$15,000 scholarship.

Teaching

Statistical Analysis of Biological Data: BIOL0495 (Spring semester, every year), Brown University. 60 undergraduate and graduate students; introductory biostatistics course covering probability theory, estimation,

hypothesis testing, regression, correlation, and analysis of variance. Course features a weekly computational lab where students learn to program in R. All labs are designed by the instructor.

Human Population Genomics: BIOL1465 (Fall semester, even years), Brown University. 18 undergraduates and graduate students; upper-division course covering recent primary literature on human genomics and classic theory in population genetics. Course structure includes one lecture per week and one student-led discussion on primary articles.

Program faculty member, 2016 UCLA Computational Genomics Summer Institute (an NIH-funded program jointly hosted by UCLA and the Institute of Pure and Applied Mathematics (IPAM)). Tutorial entitled “Genomic reconstructions of deep human history”.

Coalescent Theory: BIOL 2430-02 (Fall 2015), Brown University. Graduate seminar covering coalescent theory and algorithms for implementing coalescent-based inference of evolutionary processes from sequence data. Computational work was done in R; this course was co-taught with postdoctoral fellow Dr. Julia Palacios.

Personalized Medicine: Promises and Future Goals (GISP0014, Spring 2014), Brown University. 5 undergraduates.

Statistical Computing in R: BIOL 2430-03 (Fall 2013), Brown University. Graduate seminar covering applied statistics and focusing on implementation of methods in the statistical programming language R. Concepts covered was determined by the interests of class members, who developed exercises for the class as final projects for the course.

Independent Studies

BIOL1960: Spring 2011 – Alyna Khan '12; Spring 2012 – Milan Kantesaria '13, Alyna Khan '12; Spring 2014 – Natalie Van Houten '14; Spring 2015 – Aaron Behr '15.

BIOL 1950: Fall 2012 – Michael Goldberg '13, Nicholas Sinnott-Armstrong '13.5; Fall 2013 – Natalie Van Houten '14; Fall 2014 – Aaron Behr '15, Maya Ramchandran '15.

Theses advised

Honors theses: Alyna Khan '12, Michael Goldberg '13 (co-advised), Aaron Behr '15, Maya Ramchandran '15; External Reader: Chris Baker '12, Vishesh Jain '14, Eliza Dexter Cohen '15

Mentoring experience

Postdoctoral scholars: Dr. Julia Palacios (9/2013-9/2016; tenure-track Assistant Professor in Statistics and Biomedical Data Science at Stanford University); Dr. Lauren Alpert (7/2014-present)

Doctoral students: Priyanka Nakka (2013-present; advanced to candidacy 12/2015); Stephen Rong (2014-present)

Dissertation committees: Max Leiserson (Computer Science, Brown University); Chris Graves; Emily Holtenbeck; Yinghong Lan; Kim Cohen Neil; Kealoha Kinney; Adam Spierer.

External dissertation committee member: Sophie Ran Wang (PhD, Harvard Medical School, 2014); Agnes Sjostrand (MS, École normale supérieure de Lyon, France, 2011)

High school researchers: Kathleen Lilla Hai-Salasz (summer 2012 - summer 2014; undergraduate at Emory University); Madalyn Redding (2015 - present)

Other teaching

Lecturer: Human Population Genetics, Henry Stewart Talks. Provided invited lecture on genetic drift for an online flipped-teaching course organized by Professors Rasmus Nielsen (UC Berkeley) and Noah Rosenberg (Stanford).

Guest lecturer: Darwinian Medicine (Brown University, Fall 2010); Biostatistics (Stanford University, Winter 2005); Theoretical Population Biology (graduate course, Stanford University, Winter 2006, Spring 2006)