

**Curriculum Vitae**  
**Sohini Ramachandran**

Ecology and Evolutionary Biology  
Center for Computational Molecular Biology  
Brown University  
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**Current positions**

Associate Professor of Ecology and Evolutionary Biology,  
Associate Professor of Computer Science,  
and Director, 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**

January 2019 - July 2019: Fellow, Natural Sciences Programme/Theoretical Biology, Swedish Collegium for Advanced Study, Uppsala, Sweden.

July 1, 2017 - present: Associate Professor of Ecology and Evolutionary Biology, Associate Professor of Computer Science, Brown University.

July 1, 2017 - present: Director, Center for Computational Molecular Biology, Brown University. Served as Interim Director during Spring semester, 2017. On sabbatical July 1, 2018 - June 30, 2019.

July 1, 2015 - June 30, 2017: Manning Assistant Professor of Ecology and Evolutionary Biology, Brown University.

July 2010 - June 30, 2015: Assistant Professor of Ecology and Evolutionary Biology, 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 (Underlined authors are trainees, † indicates undergraduates, \* indicates joint first or last authors)**

Musharoff, S. A., Shringarpure, S., Bustamante, C. D.\*, and **Ramachandran, S.\***, ‘Inference of sex-biased demography from whole-genome data’. Editorially accepted, *PLoS Genetics*.

[SAM and SR are co-corresponding authors.]

Atkinson, E. G., Audesse, A. J., Palacios, J. A., Smith, G. T., Bobo, D., Webb, A. E., **Ramachandran, S.**, and Henn, B. M. (2018) ‘No evidence for recent selection at FOXP2 among diverse human populations’. *Cell* 174:1424-1435.

[Coverage in Nature: <https://www.nature.com/articles/d41586-018-05859-7>;

Nature Reviews Genetics: <https://www.nature.com/articles/s41576-018-0046-6>;

Science News: <https://www.sciencenews.org/article/language-gene-foxp2-no-humans-evolution-boost>]

Alpert Sugden, L., Atkinson, E. G., Fischer, A. P.†, Rong, S., Henn, B. M., and **Ramachandran, S.** (2018) ‘Localization of adaptive variants in human genomes using Bayesian one-dependence estimation’. *Nature Communications* 9: 703.

[LAS and SR are corresponding authors.]

Feldman, M. W. and **Ramachandran, S.** (2018) ‘Missing compared to what? Revisiting heritability, genes and culture’. *Philosophical Transactions of the Royal Society B* 373: 20170064.

Nakka, P., Archer, N. P., Xu, H., Lupo, P. J., Raphael, B. J., Yang, J. J., **Ramachandran, S.** (2017) ‘Novel gene and network associations found for acute lymphoblastic leukemia using case-control and family-based studies in multi-ethnic populations’. *Cancer Epidemiology, Biomarkers & Prevention* doi: 10.1158/1055-9965.EPI-17-0360.

[SR is corresponding author.]

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.

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

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

[AAB and SR are corresponding authors.]

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](http://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](http://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](http://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!, NPR, 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.

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.

### Abstracts

2019 - L. A. Sugden, S. Ramachandran; contributed talk, "Leveraging linkage disequilibrium to localize genomic targets of adaptation", Workshop on quantitative methods for excavating the past from genomes, Swedish Collegium for Advanced Study and Uppsala University Evolutionary Biology Center

2018 - M. McGuire<sup>#</sup>, S. P. Smith<sup>#</sup>, B. Sandstede\*, S. Ramachandran\* (<sup>#</sup>=joint first authors, \*=joint senior authors); contributed talk (SPS), "Hierarchical clustering reveals differential genetic architecture between immunological and metabolic phenotypes", Probabilistic Modeling in Genomics, Cold Spring Harbor Laboratory

2018 - L. A. Sugden, S. Ramachandran; invited talk (SR/LAS), "Integrating selection scans across different genomic scales into a single hidden Markov model framework", Probabilistic Modeling in Genomics, Cold Spring Harbor Laboratory

2018 - S. Shahamatdar, M. Xiao, E. Van Allen\*, S. Ramachandran\* (\*=joint senior authors); platform presentation (SS), "Germline variants associated with immune infiltration in solid tumors", American Society of Human Genetics annual meeting

2018 - P. Nakka, K. McManus, 23andMe Research Team, A. O'Donnell-Luria, U. Francke, J. Mountain, S. Ramachandran\*, F. Sathirapongsasuti\* (\*=joint senior authors); featured plenary oral presentation (PN), "Incidence of uniparental disomy in 2 million individuals from the general population", American Society of Human Genetics annual meeting

2018 - S. Ramachandran, L. A. Sugden, M. C. Turchin; invited talk (SR), "Modeling the interaction between population structure and selection"; Symposium on "Improving inference frameworks by accounting for population structure"; Society of Molecular Biology and Evolution annual meeting

2018 - L. A. Sugden, E. G. Atkinson, A. P. Fischer, S. Rong, B. M. Henn, S. Ramachandran; contributed talk (LAS), "Statistical inference frameworks for detecting adaptive evolution of variants and genes"; Symposium on "Machine learning approaches in evolutionary genetics"; Society of Molecular Biology and Evolution annual meeting

2018 - P. Nakka, K. McManus, 23andMe Research Team, A. O'Donnell-Luria, U. Francke, S. Ramachandran, J. Mountain, F. Sathirapongsasuti; platform presentation (PN), "Incidence of uniparental disomy in 2 million individuals from the general population", New York Population Genomics Workshop, Cold Spring Harbor Laboratory

2017 - L. A. Sugden and S. Ramachandran; contributed talk (SR), “New methods for localizing adaptive mutations from genomic data”; Feldmania 2017, Stanford, CA

2017 - L. A. Sugden, E. G. Atkinson, A. P. Fischer, S. Rong, B. M. Henn, S. Ramachandran; contributed talk (LAS), “Novel Bayesian frameworks for inference of adaptive evolution acting on variants, genes, and pathways”; Probabilistic Modeling in Genomics, Aarhus University, Denmark

2017 - N. Creanza, A. Surowiec, S. Ramachandran, M. W. Feldman; contributed talk (NC), “Mother tongues? A global study of sex-biased cultural transmission of language”; Cultural Evolution Society inaugural conference

2017 - L. A. Sugden, E. Atkinson, B. M. Henn, and S. Ramachandran; contributed talk (LAS), “An interpretable, dependence-aware composite classification framework for hard sweep detection and localization, with application to a Southern African population”; New York Area Population Genomics Workshop

2016 - P. Nakka, B. J. Raphael, and S. Ramachandran; contributed talk (PN), “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 (SR/LAS), “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 (JAP), “Inference of population size trajectories with Tajima’s coalescent”; Probabilistic Modeling in Genomics, Cold Spring Harbor Laboratory

2015 - L. Alpert and S. Ramachandran (SR); 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 (SR), “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 (SR), “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 (SR), “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 (JW), “Sources of variation in ancestral genetic processes”; Institute of Mathematical Statistics annual meeting

2010 - S. Ramachandran and N. A. Rosenberg; invited talk (SR), “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 (SR), “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 (SR), “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 (SR), “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 (SR), “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 (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 (SR), “Geographic distance predicts genetic distance in human populations”; Evolution annual meetings

In addition to the above, I have been an author on poster presentations: 2018, ASHG (senior author), SMBE (senior author, and coauthor), Population, Evolutionary and Quantitative Genetics (senior author); 2016, Biology of Genomes (senior author), Evolution annual meeting (senior author); 2015, Pew Scholars annual meeting (senior author), SMBE (senior author on two posters); 2014, SMBE (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, ASHG (coauthor); 2004, Gordon Research Conferences, Molecular Evolution (first author).

## **Invited lectures**

### **2020**

Statistical Genetics Seminar Series, Duke University (scheduled)

### **2019**

International Laboratory for Human Genome Research, Universidad Nacional Autónoma de México (scheduled)

Uppsala University, Human Evolution group meeting

Swedish Collegium for Advanced Study, Uppsala, Sweden

University of California, Berkeley; Center for Computational Biology seminar series, graduate student invited speaker

### **2018**

Brown University and Rhode Island Hospital, Dermatology Research Lecture Series  
Brown University, NIH COBRE Center for Computational Biology of Human Disease  
Brown University, Department of Applied Mathematics, Pattern Theory Seminar series  
Vanderbilt University, Biological Sciences Seminar  
Cornell University, Cornell Center for Comparative and Population Genomics (3CPG) Seminar series  
Brown University; Department of Molecular Biology, Cell Biology and Biochemistry graduate program seminar series  
UCLA Computational Genomics Summer Institute, an NIH-funded program jointly hosted by UCLA and the Institute of Pure and Applied Mathematics (IPAM)  
University of California, Davis, Ecology and Evolution Seminar Series  
The Broad Institute of MIT and Harvard, Medical and Population Genetics seminar series

### **2017**

Arizona State University, School of Life Sciences seminar series  
Stanford University, Center for Computational, Evolutionary, and Human Genomics  
Brown University, Pathology and Laboratory Medicine Grand Rounds  
Brown University, Department of Computer Science  
Women in Data Science and Mathematics Research Collaboration Workshop (WiSDM), the Institute for Computational and Experimental Research in Mathematics (ICERM)  
University of California, Los Angeles, Genetics and Genomics Seminar Series  
Michigan State University, “Science at the Edge” seminar series  
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, NIH COBRE 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 (Underlined authors are trainees, † indicates undergraduates, \* indicates joint first or last authors)**

Nakka, P., Smith, S. P., O’Donnell-Luria, A. H., McManus, K., 23andMe Research Team, Mountain, J., **Ramachandran, S.\***, and Sathirapongsasuti, F\*, ‘Characterization of prevalence and health consequences of uniparental disomy in four million individuals from the general population’. Under revision. Preprint available at: <https://www.biorxiv.org/content/10.1101/540955v1>

[SR, and FS are joint senior authors.]

Cheng, W., **Ramachandran, S.\***, and Crawford, L.\*, ‘Epsilon-genic effects bridge the gap between polygenic and omnigenic complex traits’. Under revision. Preprint available at: <https://www.biorxiv.org/content/early/2019/04/04/20190404>

[SR and LC are co-corresponding authors.]

Palacios, J. A., Veber, A., Cappello, L., Wang, Z., Wakeley, J., and **Ramachandran, S.**, ‘Bayesian estimation of population size changes by sampling Tajima’s Trees’. Under revision. Preprint available at: <https://www.biorxiv.org/content/10.1101/605352v1>

[JAP is corresponding author.]

McGuirl, M. R.\*, Smith, S. P.\*, Sandstede, B.\*, **Ramachandran, S.\***, ‘Hierarchical clustering of gene-level association statistics reveals shared and differential genetic architecture among traits in the UK Biobank’. Under revision. Preprint available at: <https://www.biorxiv.org/content/10.1101/565903v1>

[MRM and SPS are joint first authors; BS and SR are co-corresponding authors.]



Shahamatdar, S., He, M. X., Reyna, M., Gusev, A., AlDubayan, S. H., Van Allen, E. M.\*, and **Ramachandran, S.\***, ‘Germline features associated with immune infiltration in solid tumors’. Under revision.

[EMVA and SR are co-corresponding authors.]

Rong, S. and **Ramachandran, S.**, ‘Soft sweep detection is sensitive to assumptions about sweep prevalence’. In prep.

### Active grants

“Predoctoral Training Program in Biological Data Science at Brown University”, National Institutes of Health T32 GM128596 (Contact PI; MPIs are Bjorn Sandstede, Eliezer Upfal, Zhijin Wu). Anticipated total costs over 5 years: \$942,600 (7/1/2018 – 6/30/2023).

“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).

“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).

### Completed grants

“Project 1: Incorporating ethnic and gender disparities in genomic studies of disease”, National Institutes of Health P20 GM109035-01A1 (PI: 6/1/2016 – 2/28/2018). Project 1 in Brown University’s “COBRE: Center for Computational Biology of Human Disease”, (PI: Rand; 6/1/2016 – 2/28/21). Total direct costs to PI Ramachandran during the two years of funding were \$410,379.

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

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).

“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

2018 – Sam Smith, trainee on NIH predoctoral training grant “Predoctoral Training Program in Biological Data Science at Brown University” (T32GM128596); Sahar Shahamatdar, Sidney Frank Fellowship, Brown University and 2018 ASHG/Charles J. Epstein Trainee Award for Excellence in Human Genetics Research - Semifinalist; Kaileigh Ahlquist, trainee on NIH predoctoral training grant “Training in Molecular and Cell Biology and Biochemistry” (T32GM0007601); Priyanka Nakka, 2018 ASHG/Charles J. Epstein Trainee Award for Excellence in Human Genetics Research - Finalist

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, 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**

Faculty speaker, New Faculty Orientation at the Sheridan Center for Teaching and Learning, August 2019.

Member, Internal Advisory Committee, NIH COBRE Center for Computational Biology of Human Disease, Brown University. Fall 2019 - present.

Faculty speaker, junior faculty Responsible Conduct of Research course session on "How to Run a Lab", Brown University Division of Biology and Medicine (December 2018).

Invited faculty panelist, "How Involvement in Professional Societies and National Organizations Can Propel Your Career", Office of Women in Medicine and Science Annual Professional Development Program, Brown University (June 2018).

Panelist, Faculty of Color network and support panel, 2018 Super Monday; Brown University's annual spring recruitment event for underrepresented minority students.

Invited faculty speaker on "Approaches to Studying Race and Health", Academy in Context, February 2018 dinner seminar hosted by the Graduate School at Brown University.

Committee member, Research Achievement Awards (2017-2018), Brown University Office of the Vice President of Research.

Member, Brown University Committee on Commencement Speakers (July 2017- July 2020).

Panel moderator, "Edging Ahead in Study Section as an Applicant and Reviewer", Office of Women in Medicine and Science Annual Professional Development Conference, Brown University (June 2017).

Invited faculty panelist, "Data Science as a Liberal Art", 2017 Commencement Forum, Brown University (May 2017).

Member, Henry Merritt Wriston Fellowship award committee (2017). Recognizes junior faculty who are fulfilling Brown University's dual mission of excellence in both teaching and research.

Faculty speaker, New Employee Advisory Program (NEAP), Brown University (March 2017). Series provides monthly Brown bag lunch sessions to new staff to help them get acclimated to the 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, 2017.

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

### **To the profession**

Session co-chair, Personal and Medical Genomics, 2019 meeting on Genome Informatics, Cold Spring Harbor/Wellcome Trust.

Keynote speaker, 2019 meeting on Probabilistic Modeling in Genomics, Aussois, France.

Organizing committee member; 2020 Population, Evolutionary and Quantitative Genetics meeting, Washington, DC.

Co-organizer, Workshop: "Quantitative methods for excavating the past from genomes", Swedish Collegium for Advanced Study, May 27-28, 2019. International meeting with 45 attendees from four countries, co-sponsored by Uppsala University's Evolutionary Biology Center.

Session co-chair, Population Genetics II: Natural Selection, 2018 meeting on Probabilistic Modeling in Genomics, Cold Spring Harbor Laboratory.

Standing member: Genetic Variation and Evolution (GVE) study section, NIH (7/2018-6/2024).

Co-organizer, SMBE Satellite Meeting on Modern Methods for the Study of Ancient DNA, April 4-6 2018. International meeting with 60 attendees from seven countries, co-sponsored by Brown University's Center for Computational Molecular Biology.

Faculty speaker, Women in Data Science and Mathematics (WiSDM) workshop, Institute for Computational and Experimental Research in Mathematics.

Faculty advisor, 2017 Young Scholars Conference, Brown University. A professional development workshop for diverse graduate students and postdocs from STEM fields.

*Ad hoc* reviewer for Experimental Program to Stimulate Competitive Research, EPSCoR Research Fellows Solicitation, NSF (2017).

*Ad hoc* reviewer for Evolutionary Genetics Program, NSF (2016).

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.

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**

Moderator and panelist, Women of Color in STEM, sponsored by Brown University's Initiative to Maximize Student Development (IMSD)

smallskip

Invited faculty speaker, WiSE (Brown Women in Science and Engineering), November 2017.

Invited faculty speaker, "Biomedical Informatics and Data Science for Biomedicine and Health Care", 2016 and 2017 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, 2018). 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](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**

Presidential Early Career Award in Science and Engineering, awarded July 2019, nominated by the Department of Health and Human Services (National Institutes of Health).

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, 2018 UCLA Computational Genomics Summer Institute (an NIH-funded program jointly hosted by UCLA and the Institute of Pure and Applied Mathematics (IPAM)). Tutorial entitled “Applications of Latent Dirichlet Allocation in genomics”.

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, Jonathan Chang '18

### **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 Sugden (7/2014-8/2019; tenure-track Assistant Professor of Statistics at Duquesne University); Dr. Michael Turchin (10/2017-present); Dr. Katherine Brunson (7/2018-present); Dr. Greg Darnell (9/2019-present).

**Doctoral students:** Priyanka Nakka (2013-2018; now a postdoctoral researcher with Joel Hirschhorn at The Broad Institute); Stephen Rong (2014-2017; advanced to candidacy 4/2017, now in William Fairbrother's lab at Brown University); Wei Cheng (2017-present); Sahar Shahamatdar (2017-present; MD/PhD student in doctoral phase); Samuel Smith (2017-present); Kaileigh Ahlquist (rotation student, Jan-March 2018; graduate student starting June 2018); Elizabeth (Elsie) Gibson (2019-present).

Dissertation committees: Max Leiserson (Computer Science, Brown University; graduated 5/2016); Chris Graves (graduated 5/2017); Emily Hollenbeck Heyne (graduate 12/2018); Yinghong Lan (graduated 8/2018); Kim Cohen Neil; Kealoha Kinney (graduated 5/2016); Adam Spierer; William Jordan (Molecular Biology, Cell Biology, and Biochemistry, Brown University; graduated 5/2019); Joaquin Nunez; Hannah Weller (doctoral advisory committee); Patrick Freeman (doctoral advisory committee); Gryte Satas (Computer Science, Brown University); Alyssa Funk (Molecular Biology, Cell Biology, and Biochemistry, Brown University).

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: Evolutionary Biology (Brown University, Fall 2017); Diversity of Life (Brown University, Fall 2017); Living Biology at Brown and Beyond (Brown University, Fall 2017); Darwinian Medicine (Brown University, Fall 2010); Biostatistics (Stanford University, Winter 2005); Theoretical Population Biology (graduate course, Stanford University, Winter 2006, Spring 2006)