Curriculum Vitae

Sohini Ramachandran

Ecology, Evolution and Organismal Biology
Brown University
Box G-W
Providence, RI 02912

Office: (401) 863-9701
Fax: (401) 863-2166
sramachandran@brown.edu
www.brown.edu/Research/Ramachandran_Lab

Current positions

Hermon Carey Bumpus Professor of Biology,
and courtesy faculty appointed in Computer Science, 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, 2023: Founding Director, Data Science Institute, Brown University. Completed service September 1, 2024.

January 1, 2023 - present: Hermon Carey Bumpus Professor of Biology, Brown University.

July 1, 2021 - present: Professor; Ecology, Evolution and Organismal Biology, Brown University.

July 1, 2021 - June 30, 2023: Director, Data Science Initiative, Brown University. On sabbatical January 1, 2022-June 30, 2022.

August 24, 2020 - June 30, 2021: interim director, Data Science Initiative, Brown University.

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

July 1, 2017 - June 30, 2021: Associate Professor of Ecology and Evolutionary Biology, Associate Professor of Computer Science, Brown University.

July 1, 2017 - June 30, 2022: Director, Center for Computational Molecular Biology, Brown University. Served as Interim Director during Spring semester, 2017. On sabbatical July 1, 2018 - June 30, 2019; on sabbatical January 1, 2022-June 30, 2022.

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

July 1, 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 JM, **Ramachandran S**, and Fairbrother WG. (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 CD. (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, SE Antonarakis and AG Motulsky. Springer.

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

Refereed journal articles (Underlined authors are trainees, † indicates undergraduates, * indicates joint first or last authors)

Moody N, Williams CM, **Ramachandran S**, and Fuxjager MJ. ‘Social mates dynamically coordinate aggressive behavior to produce strategic territorial defense’. Editorially accepted at *PLoS Computational Biology.*

Liu X, Crawford L, and **Ramachandran S**. ‘ML-MAGES: A machine learning framework for multivariate genetic association analyses with genes and effect size shrinkage’. (2025) *RECOMB: 29th Annual International Conference on Research in Computational Molecular Biology.* Acceptance rate is 15.9%.

Smith SP*, Darnell G*, Udwin D, Stamp J, Harpak A, **Ramachandran S***, and Crawford L*. ‘Discovering non-additive heritability using additive GWAS summary statistics’. (2024) *eLife* doi: https://doi.org/10.7554/eLife.90459. Accepted under the original “review, then publish” eLife model.

[SPS and GD are joint first authors; SR and LC are joint senior authors; LC is corresponding author.]

Shahamatdar S*, Saeed-Vafa D*, Linsley D, Khalil F, Lovinger K, Li L, McLeod H, **Ramachandran S**, and Serre T. ‘Deceptive learning in histopathology’. (2024) *Histopathology* doi: https://doi.org/10.1111/his.15180.

[DL is corresponding author.]

Lappalainen T, Li YI, **Ramachandran S**, and Gusev A. ‘Genetic and molecular architecture of complex traits’. (2024) *Cell* 187:1059-1075. doi: 10.1016/j.cell.2024.01.023.

[TL is corresponding author.]

Chevy ET, Huerta-Sánchez E*, and **Ramachandran S***. ‘Integrating sex-bias into studies of archaic admixture on chromosome X’. (2023) *PLoS Genetics* 19:e1010399. https://doi.org/10.1371/journal.pgen.1010399.

[ETC and SR are co-corresponding authors; EH-S and SR are joint senior authors.]

Ahlquist KD, Sugden LA*, and **Ramachandran S***. ‘Enabling interpretable machine learning for biological data with reliability scores’. (2023) *PLoS Computational Biology* 19:e1011175.

[KDA and LS are co-corresponding authors; LS and SR are joint senior authors.]

Atkinson EG, Dalvie S, Pichkar Y, Kalungi A, Majara L, Stevenson A, Abebe T, Akena D, Alemayehu M, Ashaba FK, Atwoli L, Baker M, Chibnik LB, Creanza N, Daly MJ, Fekadu A, Gelaye B, Gichuru S, Injera WE, James R, Kariuki SM, Kigen G, Koen N, Koenen KC, Koenig Z, Kwobah E, Kyebuzibwa J, Musinguzi H, Mwema RM, Neale BM, Newman CP, Newton CRJC, Ongeri L, **Ramachandran S**, Ramesar R, Shiferaw W, Stein DJ, Stroud RE, Teferra S, Zingela Z, Martin AR, NeuroGAP-Psychosis Study Team. (2022) ‘Genetic structure correlates with ethnolinguistic diversity in eastern and southern Africa’. *American Journal of Human Genetics* 109:1667-1679. doi: 10.1016/j.ajhg.2022.07.013.

Menghini C, Uhr J, Haddadan S, Champagne A, Sandstede B, and **Ramachandran S**. (2022) ‘The Drift of #MyBodyMyChoice Discourse on Twitter’. *WebSci22: the 14th ACM Web Science Conference 2022*:110-117. https://doi.org/10.1145/3501247.3531570.

[Runner-up for the best paper award at WebSci22.]

Cheng W, **Ramachandran S**, and Crawford L. (2022) ‘Uncertainty Quantification in Variable Selection for Genetic Fine-Mapping using Bayesian Neural Networks’. *iScience* 25, 104553.

[This paper was awarded a spotlight talk at RECOMB-Genetics 2022.]

Gopalan S, Smith SP, Korunes K, Hamid I, **Ramachandran S***, and Goldberg A*. (2022) 'Human genetic admixture through the lens of population genomics'. *Philosophical Transactions of the Royal Society B*, special issue on 'Celebrating 50 years in Lewontin's apportionment of human diversity'. Volume 377: 20200410. https://doi.org/10.1098/rstb.2020.0410arXiv.

Smith SP, Shahamatdar S, Cheng W, Zhang S†, Paik J†, Graff M, Haiman CA, Matise TC, North KE, Peters U, Kenny E, Gignoux CR, Wojcik GL, Crawford L*, and **Ramachandran S***. (2022) 'Enrichment analyses identify shared associations for 25 quantitative1traits in over 600,000 individuals from seven diverse ancestries'. *American Journal of Human Genetics* 109:1-14. https://doi.org/10.1016/j.ajhg.2022.03.005

[SR is corresponding author. SPS and the paper were chosen by the editorial board of AJHG as one of two 2022 CW Cotterman Award winners, given to two trainee-authored articles published in AJHG in the previous year that best represent outstanding scientific contributions to the field of human genetics.]

Demetci P*, Cheng W*, Darnell G, Zhou X, **Ramachandran S**, and Crawford L. (2021) 'Multi-scale inference of genetic trait architecture using annotated neural networks'. *PLoS Genetics* 17:e1009754.

Spierer A, Mossman JA, Smith SP, Crawford L, **Ramachandran S**, and Rand DM. (2021) 'Natural variation in the regulation of neurodevelopmental genes modifies flight performance in Drosophila'. *PLoS Genetics* 17:e1008887.

[SPS and SR provided guidance to AS for extending PEGASUS software from the Ramachandran Lab to analyze Drosophila genomes.]

Cheng W, **Ramachandran S***, and Crawford L*. (2020) 'Estimation of non-null SNP effect size distributions enables the detection of enriched genes underlying complex traits'. *PLoS Genetics* 16:e1008855.

[WC is SR's graduate advisee and led analysis; SR and LC are co-corresponding authors and designed the research together.]

McGuirl MR*, Smith SP*, Sandstede B*, and **Ramachandran S*** (2020) 'Hierarchical clustering of gene-level association statistics reveals shared and differential genetic architecture among traits in the UK Biobank'. *Genetics* 215:511-529.

[MRM and SPS are joint first authors, SPS is SR's graduate advisee and led analysis of UK Biobank genotype and phenotype data; BS and SR are co-corresponding authors, designed the research together, and co-mentored the first authors. Chosen by Genetics editors as one of the June 2020 issue highlights: https://www.genetics.org/content/215/2/NP.]

Shahamatdar S, He MX, Reyna M, Gusev A, AlDubayan SH, Van Allen EM*, and **Ramachandran S***. (2020) 'Germline features associated with immune infiltration in solid tumors'. *Cell Reports* 30:2900-2908.

[SS is SR's graduate advisee and led analyses; EMVA and SR are co-corresponding authors, EMVA advised on clinical relevance of research and SR and EMVA co-designed the research.]

Nakka P, Smith, SP, O'Donnell-Luria AH, McManus K, 23andMe Research Team, Mountain J, **Ramachandran S***, and Sathirapongsasuti F*. (2019) 'Characterization of prevalence and health consequences of uniparental disomy in four million individuals from the general population'. *American Journal of Human Genetics* 105:921-932.

[PN was SR's graduate advisee during the development of this publication and led all analyses of 23andMe Inc. consented research participants; SPS is SR's graduate advisee and conducted analyses in UK Biobank samples; SR and FS are joint senior authors and designed the research together; PN and FS are co-corresponding authors.]

Palacios JA, Veber A, Cappello L, Wang Z, Wakeley J, and **Ramachandran S** (2019) 'Bayesian estimation of population size changes by sampling Tajima's Trees'. *Genetics* 213:967-986.

[JAP is corresponding author and was SR's postdoctoral advisee when the research was initially designed; SR led the initial design of the research and co-led writing of the paper with JAP.]

Musharoff SA, Shringarpure S, Bustamante CD*, and **Ramachandran S*** (2019) 'Inference of sex-biased demography from whole-genome data'. *PLoS Genetics* 15:e1008293.

[SAM and SR are co-corresponding authors; SR co-designed research with CDB and SAM while SAM was CDB's graduate advisee; SAM and SR co wrote the paper.]

Atkinson EG, Audesse AJ, Palacios JA, Smith GT, Bobo D, Webb AE, **Ramachandran S**, and Henn BM. (2018) 'No evidence for recent selection at FOXP2 among diverse human populations'. *Cell* 174:1424-1435.

[JAP did ancestral recombination graph reconstruction, advised by SR; SR co-led selection scan analyses with EGA and BMH; SR coordinated collaboration with AJA and AEW on this project.
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 EG, Fischer AP†, Rong S, Henn BM, 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, co-designed the research and co-wrote the paper; LAS was SR's postdoctoral advisee during this project; SR also advised undergraduate APF's contribution on validation in published literature of selection scan results, as well as graduate student SRong's simulations for soft sweeps.]

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

[MWF is corresponding author.]

Nakka P, Archer NP, Xu H, Lupo PJ, Raphael BJ, Yang JJ, **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, designed the research, advised PN on all analyses, and coordinated the collaboration of all authors; BJR consulted on applications of HotNet; PJL and JJY provided samples for analysis and helped write the paper with PN and SR.]

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, designed the research, and co-wrote the paper with LAS; LAS conducted all analyses.]

Nakka P, Raphael BJ, 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]

Behr AA†, Liu KZ†, 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 JA, 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 TJ, Rosenberg NA, Feldman MW, 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 KF, 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 MDM, Eldridge J, **Ramachandran S**, and Raphael BJ. (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 BS, and **Ramachandran S**. (2012), 'Gene genealogies within a fixed pedigree, and the robustness of Kingman's coalescent', *Genetics* Vol. 190:1433-1445.

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

Ramachandran S, and Rosenberg NA. (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 BM, Gignoux CR, Jobin M, Granka JM, Macpherson JM, Kidd JM, Rodríguez-Botigué L, **Ramachandran S**, Hon L, Brisbin A, Lin AA, Underhill P, Comas D, Kidd KK, Parham P, Norman PJ, Bustamante CD, Mountain JL, and Feldman MW. (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 AM, Li JZ, Absher D, Myers R, **Ramachandran S** and Feldman MW. (2010), 'Characterization of X-linked SNP genotypic variation in globally distributed human populations', *Genome Biology* Vol. 11:R10.

Ramachandran S, Rosenberg NA, Feldman MW 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 JZ, Absher DM, Tang H, Southwick AM, Casto AM, **Ramachandran S**, Cann HM, Barsh GS, Feldman M, Cavalli-Sforza LL, and Myers RM. (2008), 'Worldwide human relationships inferred from genome-wide patterns of variation', *Science* Vol. 319: 1100-1104.

Wang S, Lewis Jr CM, 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 NA, Mahajan S, **Ramachandran S**, Zhao C, Pritchard JK, and Feldman MW. (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 CC, Rosenberg NA, Feldman MW, and Cavalli-Sforza LL. (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 JM, **Ramachandran S**, Diamond L, and Feldman MW. (2004), 'Demographic estimates from Y-chromosome microsatellite polymorphisms: analysis of a worldwide sample', *Human Genomics* Vol. 1: 345-354.

Ramachandran S, Rosenberg NA, Zhivotovsky L, and Feldman MW. (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

Carlson J*, Henn BM*, Al-Hindi DR, and **Ramachandran S***. (2022) "Counter the weaponization of genetics research by extremists", *Nature* 610:444-447.

Edge MD, **Ramachandran S**, and Rosenberg NA. (2022) "Celebrating 50 years since Lewontin's apportionment of human diversity", *Philosophical Transactions of the Royal Society B*, special issue. Volume 377: 20200405.

Ramachandran S, Otto SP, Uyenoyama M, and Van Cleve J. (2019), "Any news?" Special issue in honor of Marcus Feldman's 75th birthday, *Theoretical Population Biology* 129:1-3.

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

Bustamante CD*, and **Ramachandran S***. (2009), 'Evaluating signatures of sex-specific processes in the human genome', *Nature Genetics* (News and Views) Vol. 41: 8-10.

Abstracts

2025 - S Ramachandran; invited talk, Center in Genomics & Systems Biology annual symposium, New York University Abu Dhabi

2025 - S Ramachandran; invited talk, Horizons in Genomic Sciences 2025 (international colloquium organized by the International Laboratory for Human Genome Research at the National Autonomous University of Mexico), Queretaro, Mexico

2024 - S Ramachandran; invited talk, Biological Data Science meeting, Cold Spring Harbor Laboratory

2024 - CM Williams, S Ramachandran; invited talk (SR), "Family ties: methodological challenges and opportunities generated by relatives in biobanks", Biology of Genomes annual meeting, Cold Spring Harbor Laboratory

2023 - S Ramachandran; invited talk, Symposium on "Computational evolutionary genomics in the era of machine learning", SMBE 2023 annual meeting

2023 - S Ramachandran; invited keynote, RECOMB 2023

2022 - S Ramachandran; invited distinguished keynote 2022 Youth Bioinformatics Symposium, International Society for Computational Biology

2021 - S Ramachandran; invited keynote lecture on Evolutionary and Population Genomics, 6th annual Danish bioinformatics conference

2020 - G Darnell, L Crawford, S Ramachandran; platform presentation (GD), "Finding missing epistasis: partitioning marginal epistasis deconvolves nonlinear interactions from additive effects in GWA summary statistics", American Society of Human Genetics annual meeting

2020 - N Swinford, K Ahlquist, G Harrison, P Norman, S Ramachandran, BM Henn; contributed talk, "Searching for signatures of recent balancing selection in the HLA genomic region within the Khomani and Nama of South Africa", Society of Molecular Biology and Evolution annual meeting (meeting was cancelled due to COVID-19 pandemic)

2020 - SP Smith, W Cheng, L Crawford, S Ramachandran; contributed talk, "Redefining replication in multiethnic genome-wide association", Society of Molecular Biology and Evolution annual meeting (meeting was cancelled due to COVID-19 pandemic)

2020 - S Ramachandran; invited talk, "Integrating germline inheritance into cancer genomics", Major Symposium on Germline Influence on Immunotherapy Outcomes, American Association for Cancer Research annual meeting (meeting was cancelled due to COVID-19 pandemic)

2019 - S Ramachandran; invited talk, "Characterization of prevalence and health consequences of uniparental disomy in four million individuals from the general population", Wellcome Trust/CSHL Genome Informatics annual meeting, Cold Spring Harbor Laboratory

2019 - S Ramachandran; invited keynote lecture, "Leveraging linkage disequilibrium in human population-genetic analyses", Probabilistic Modeling in Genomics annual meeting, Aussois, France

2019 - LA 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 McGuirl$^{\#}$, SP Smith$^{\#}$, B Sandstede*, S Ramachandran* ($^{\#}$=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 - LA 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, LA Sugden, MC. 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 - LA Sugden, EG Atkinson, AP Fischer, S Rong, BM 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 - LA Sugden and S Ramachandran; contributed talk (SR), "New methods for localizing adaptive mutations from genomic data"; Feldmania 2017, Stanford, CA

2017 - LA Sugden, EG Atkinson, AP Fischer, S Rong, BM 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, MW Feldman; contributed talk (NC), "Mother tongues? A global study of sex-biased cultural transmission of language"; Cultural Evolution Society inaugural conference

2017 - LA Sugden, E Atkinson, BM 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, BJ 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 LA 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 - JA 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, CD 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, TJ Pemberton, NA Rosenberg, MW 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, TJ Pemberton, NA Rosenberg, and MW 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, TJ Pemberton, NA Rosenberg, MW Feldman, and S Ramachandran; invited symposium presentation (NC), "Worldwide linguistic and genetic variation"; Society of Molecular Biology and Evolution annual meeting

2013 - SA Musharoff, CD 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, BS 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 NA 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, NA Rosenberg, MW 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 NA 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, MW Feldman, L Cavalli-Sforza, and RM 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, NA Rosenberg, and MW Feldman; contributed talk (SR), "Models for comparing male and female demographic histories using autosomal and X-chromosomal microsatellites"; Evolution annual meeting

2005 - S Ramachandran, NA Rosenberg, LA Zhivotovsky, and MW Feldman; contributed talk (SR), "Comparing male and female demographic histories using autosomal and X-chromosomal microsatellites"; American Association of Physical Anthropology annual meeting

2005 - NA Rosenberg, S Ramachandran, LA Zhivotovsky, and MW 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, CC Roseman, NA Rosenberg, MW Feldman, and LL 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: 2024, ASHG (senior author, abstraction selected as "Reviewer's Choice", in top 10% of scored abstracts); 2024, SMBE (senior author); 2024, Probabilistic Modeling in Genomics (senior author); 2020, ASHG (senior author, abstraction selected as "Reviewer's Choice", in top 10% of scored abstracts); 2019, 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, ASHG (senior author; abstract selected as "Reviewer's Choice", in top 10% of scored abstracts),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

2025 Department of Quantitative and Computational Biology, University of Southern California (scheduled)
Department of Biology, Johns Hopkins University (scheduled)

2024 Laboratory of Genetics, University of Wisconsin-Madison

2023 Department of Biology, New York University

2022 Institute for Organismal Biology frontiers seminar, Uppsala University; PAGE All Investigators Meeting (virtual); Evolutionary Studies Initiative, Vanderbilt University; Ecology and Evolutionary Biology, Princeton University

2021 New York Area Population Genetics Working Group; Center for Genetic Epidemiology, University of Southern California; Computational Genomics Summer Institute quarterly meeting, UCLA; Biostatistics-Biomedical Informatics B3D Seminar Series, presented by the Departments of Biostatistics (Harvard School of Public Health) and Biomedical Informatics (Harvard Medical School); Ecology and Evolutionary Biology seminar series, University of Calgary; Center for Study of Race and Ethnicity, Brown University; Panelist along with Lorin Crawford and C. Brandon Ogbunu on Race and Genetics in America
(https://digitalpublications.brown.edu/projects/race-and-genetics-in-america);
University of Connecticut, Ecology and Evolutionary Biology seminar series;

Race and Technology: A Research Lecture Series, Microsoft Research (https://www.microsoft.com/en-us/research/videos/race-and-technology-a-research-lecture-series/)

2020 Center for Statistical Genetics and Genomics Seminar Series, Duke University; Population Science Program Meeting, Cancer Center at Brown University; Colloquium on the Biology of Populations Seminar Series, Department of Ecology and Evolutionary Biology, Princeton University; Department of Biology, University of Rochester

2019 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

Preprints posted (Underlined authors are trainees, † indicates undergraduates, * indicates joint first or last authors)

Williams CM, Scelza BA, Slack SD, Mathias RA, Watson H, Barnes KC, Lange E, Johnson RK, Gignoux CR, **Ramachandran S**, Henn BM. 'A rapid, accurate approach to inferring pedigrees in endogamous populations'. bioRxiv doi: https://www.biorxiv.org/content/10.1101/2020.02.25.965376v3.

[BM Henn is corresponding author.]

Williams CM, OĆonnell J, Freyman WA, 23andMe Research Team, Gignoux CR, **Ramachandran S***, Williams AL*. 'Phasing millions of samples achieves near perfect accuracy, enabling parent-of-origin classification of variants'. bioRxiv doi: https://www.biorxiv.org/content/10.1101/2024.05.06.592816v1. Submitted to *PLoS Biology.*

[SR and ALW are joint senior authors; CMW, SR, and ALW are corresponding authors.]

Chevy ET, Min J, Caudill V, Champer SE, Haller BC, Rehmann CT, Smith CCR, Tittes S, Messer PW, Kern AD, **Ramachandran S**, Ralph PL. 'Population genetics meets ecology: a guide to individual-based simulations in continuous landscapes'. bioRxiv doi: https://www.biorxiv.org/content/10.1101/2024.07.24.604988v1. Submitted to *Ecology and Evolution.*

[PLR is corresponding author.]

Active grants

"Novel population-genetic methods for localizing targets of natural selection in diverse human genomes", National Institutes of Health R35 GM139628 (PI). Anticipated total costs over 5 years: $1,758,959 (1/1/2021-12/31/2025).

"Predoctoral Training Program in Biological Data Science at Brown University", National Institutes of Health T32 GM149433-01A1 (awaiting notice of award; Contact PI; MPIs are Lorin Crawford, Emilia Huerta-Sanchez, and Bjorn Sandstede). Total costs requested over 5 years: $3,123,975 (7/1/2024 – 6/30/2029).

Pending grants

"Population-genetic methods for inferring recent histories and targets of selection in the biobank era", National Institutes of Health R35 GM139627 renewal (PI). Anticipated totals costs over 5 years: $2,999,985. Impact score of 13 received in October 2024.

Completed grants

“PIPP Phase I: Mobility Analysis for Pandemic Prevention Strategies (MAPPS)”, National Science Foundation CBET-2154941 (co-PI). $999,211 (8/1/2022 – 1/31/2024).

“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). Total costs over 5 years, included awarded supplements: $1,540,019 (7/1/2018 – 6/30/2023).

“Novel statistical methods to localize genomic elements underlying adaptive evolution”, National Institutes of Health R01 GM118652 (PI). Total costs over 5 years: $1,607,269 (6/6/2016 – 5/31/2021; no-cost extension until 5/31/2022).

Administrative Supplement for Workforce Development at the Interface of Information Sciences, Artificial Intelligence and Machine Learning (AI/ML), and Biomedical Sciences, as part of “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; co-I is Dr. Linda Clark). $86,400 (7/1/2021 – 6/30/2022).

Administrative Supplement to Enhance Program Evaluation Capacity, as part of “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; co-I is Dr. Judy Kimberly). $86,400 (7/1/2020 – 6/30/2021).

“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; no-cost extension until 1/31/2021).

“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

2024 – Abby Kuntzleman, National Science Foundation Graduate Research Fellowship

2023 – Abby Kuntzleman, NIH PREP Scholar

2022 – Cole Williams, National Science Foundation Graduate Research Fellowship

2021 – Cole Williams, trainee on NIH predoctoral training grant “Predoctoral Training Program in Biological Data Science at Brown University” (T32GM128596)

2020 – Selena Zhang '22, Karen T. Romer UTRA, Brown University; Greg Darnell, 2020 ASHG/Charles J. Epstein Award for Excellence in Human Genetics Research - Postdoctoral Semifinalist; Elizabeth (Elsie) Gibson, trainee on NIH predoctoral training grant "Predoctoral Training Program in Biological Data Science at Brown University" (T32GM128596)

2019 – Greg Darnell, Institute Postdoctoral Fellowship at the Institute for Computational and Experimental Research in Mathematics (ICERM) at Brown University

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

Invited faculty speaker, Biology Commencement, Brown University, 2023.

Moderator, "Our Data-Driven World: A Brunonian Vision for Data Science", 2023 Commencement Forum, Brown University (May 2023).

Search committee member, Provost, Brown University (convened by President Paxson); 2022

Member, Task Force on the Status of Women Faculty, Brown University (convened by President Paxson), 2021-2023

Search committee member, Dean of Biology and Medicine, Brown University; 2021

Question moderator, "Practices for addressing the underrepresentation of women in STEM", hosted by Carney Institute for Brain Science at Brown University with the National Academies of Sciences, Engineering, and Medicine (April 2020).

Faculty speaker, Responsible Conduct of Research course session on "Scientific Communication" for graduate students, Brown University Division of Biology and Medicine (October 2020).

Faculty peer reviewer, Peer Review Panel for Addressing Systemic Racism Seed Fund, Brown University, 2020-2021.

Member, Faculty Workgroup on the University's Response to the COVID-19 Pandemic, convened by the Faculty Executive Committee, Brown University, June 2020 - August 2020.

Life Sciences Research Ramp-up Subcommittee (COVID-19 pandemic) member, Brown University, April 2020 - August 2020.

Co-chairperson, Diversity and Inclusion Action Plan committee, Ecology and Evolutionary Biology, Brown University (January 2020 - May 2022).

Faculty speaker, Responsible Conduct of Research course session on "Mentoring" for graduate students, Brown University Division of Biology and Medicine (September 2019).

Library Advisory Board, Brown University, 2019-2021 (Chairperson: 2020-2021).

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.

Data Science Initiative Campus Advisory Board Member, July 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.

Data Science Initiative Executive Committee, July 2017 - present.

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 - July 2017. Led the design of the Bachelor of Arts in Computational Biology (approved December 2015). Concentration advisor in Computational Biology.

Member, Diversity Advisory Board, Brown University (2015-2017). 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 - 1/2021.

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, Spring 2020.

To the profession

International Advisory Board member, National Autonomous University of Mexico (UNAM) International Laboratory for Human Genome Research. 2024-present.

Organizing committee member; 2024 Population, Evolutionary and Quantitative Genetics meeting, Washington, DC.

Guest editor, with M. D. Edge and N. A. Rosenberg, of a 2022 special issue on 'Celebrating 50 years in Lewontin's apportionment of human diversity'.

Genetics Society of America, Publications Committee member (2021-)

Organizing committee member; 2021 Probabilistic Modeling in Genomics meeting, Cold Spring Harbor Laboratory

Session moderator, Machine Learning, American Society of Human Genetics 2020 annual meeting (held virtually due to COVID-19 pandemic).

Abstract reviewer, Evolution and Population Genetics topics, American Society of Human Genetics 2020 annual meeting.

Research Oversight Committee (ROC) member, Silent Genomes - Reducing health care disparities and improving diagnostic success for children with genetic diseases from Indigenous populations (September 2019 -). The ROC provides strategic advice to Genome BC/Genome Canada on approaches and directions to aid the project in achieving its short and long term objectives and maximizing the project's potential impacts.

Ad hoc reviewer for Biological Anthropology program, NSF (May 2020).

Ad hoc reviewer for Innovation for Biological Research Informatics program, NSF (May 2020).

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).

Ad hoc 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

Invited panelist, virtual discussion of *Ancestry Reimagined: Dismantling the Myth of Ethnicities* by Kostas Kampourakis, June 2023.

Invited distinguished keynote 2022 Youth Bioinformatics Symposium, International Society for Computational Biology.

Academic representative and speaker, meeting of the Bipartisan Commission on Biodefense, September 2020.

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

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)

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.

Selected 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

Finalist, Life Sciences, Blavatnik National Awards for Young Scientists, 2024. One of fifteen national finalists; includes an unrestricted gift of $15,000.

Brown University Presidential Faculty Award, 2022-2023; given to two members of the faculty each year for recognition of important and innovative scholarship. Includes a research stipend of $5,000 and a public lecture (Spring 2023).

Philip J. Bray Award winner for Excellence in Teaching in the Physical Sciences, 2021-2023. One of Brown University's Faculty Teaching Excellence Awards recognizing Brown faculty members for sustained and continued excellence in teaching. Includes annual research funds in the amount of $3,000.

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 semesters), Brown University. 70 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.

Scientific Communication: BIOL2150 (Fall semesters), Brown University. One section of 6 graduate students, including trainees from National Institutes of Health T32 GM128596 and second-year doctoral students in the Computational Biology Graduate Program. Course prepares students for developing and articulating thesis projects in written and oral presentations, as well as for critically reviewing scientific proposals.

Human Population Genomics: BIOL1465 (Fall semester, 2012, 2014), 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. Spring 2022 – Selena Zhang '22.

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, Jaison Jain '20 (co-advised)

Mentoring experience

Postdoctoral scholars: Dr. Julia Palacios (9/2013-9/2016; tenured Associate 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 (10/2017-9/2020; Senior Scientist, Statistical Genetics, Bristol Myers Squibb); Dr. Katherine Brunson (7/2018-12/2019; tenure-track Assistant Professor of Archaeology at Wesleyan University); Dr. Greg Darnell (9/2019-7/2020; Research Scientist in Health AI Division of AI/ML at Apple Inc.); Dr. Carlos Sarabia (1/2022-1/2024; postdoctoral fellow, University of Copenhagen); Dr. Xiran Liu (10/2023-present); Dr. Alex Diaz-Papkovich (10/2023-present).

Doctoral students: Priyanka Nakka (2013-2018; postdoctoral researcher with Joel Hirschhorn at The Broad Insitute, now Senior Statistical Geneticist at Regeneron); Stephen Rong (2014-2017; graduated from

William Fairbrother's lab at Brown University 1/2021); Wei Cheng (2017-2022; now Research Scientist at Meta/Facebook); Sahar Shahamatdar (2017-2021; MD/PhD student, now an internal medicine resident at Massachusetts General Hospital/Harvard Medical School); Samuel Smith (2017-2022; postdoctoral research associate with Arbel Harpak at the University of Texas at Austin, now Senior Scientist role at Genomics PLC); Kaileigh Ahlquist (2017-2022; now a Computational Scientist at the Samocha Lab, Broad Institute of Harvard/MIT); Elizabeth (Elsie) Chevy (2019-present); Cole Williams (2020-present); Brina Lopez Gfeller (2022-2024; completing MS in Fall 2024); Hannah Snell (2023-present); Shevaughn Holness (2023-present); Abigail Kuntzleman (postbacc researcher 2023-2024; doctoral student beginning Fall 2024)

Dissertation committees: Max Leiserson (Computer Science, Brown University; graduated 5/2016); Chris Graves (EEB, graduated 5/2017); Emily Hollenbeck (EEB, graduated 12/2018); Yinghong Lan (EEB, graduated 8/2018); Kim Cohen Neil (EEB, graduated 9/2020); Kealoha Kinney (EEB, graduated 5/2016); Adam Spierer (graduated 4/2020); William Jordan (Molecular Biology, Cell Biology, and Biochemistry, Brown University; graduated 5/2019); Joaquin Nunez (EEB, graduated 7/2020); Hannah Weller (EEB doctoral advisory committee); Patrick Freeman (EEB doctoral advisory committee; received MS 5/2020); John Burley (EEB); Gryte Satas (Computer Science, Brown University; graduated 10/2019); Alyssa Funk (Molecular Biology, Cell Biology, and Biochemistry, Brown University); Maya Weissman (EEB doctoral advisory committee); David Glidden (Computational Biology, MD/PhD student; completed doctorate 4/2020); Melissa McGuirl (Applied Mathematics, graduated 3/2020); MC Miles (EEB); Dana Udwin (Biostatistics); Patricia Vera-González (Biostatistics MS, second reader); Dafeng Zheng; David Peede; Audrey Dalgarno (Molecular Biology, Cell Biology, and Biochemistry, Brown University; served until 2024); Doudou Yu (Molecular Biology, Cell Biology, and Biochemistry, Brown University); Mayra Banuelos (Computational Biology); Peter Van Katwyk (Earth, Environmental, and Planetary Sciences doctoral advisory committee); Jazeps Medina Tretmanis (Computational Biology); Hannah Hoff.

External dissertation committee member: Natalie Swinford (PhD, University of California at Davis, graduated Fall 2022); Federica Sartori (thesis advisory committee, NYU); Nathan Nakatsuta (PhD, Harvard Medical School, 2020); Sophie Ran Wang (PhD, Harvard Medical School, 2014); Agnes Sjostrand (MS, École normale supérieure de Lyon, France, 2011); Alouette Zhang (McGill University, 2023)

Postbaccalaureate researchers: Abigail Kuntzleman (2023-2024; funded by NIH PREP program at Brown University).

High school researchers: Kathleen Lilla Hai-Salasz (summer 2012 - summer 2014; graduated from Emory University); Madalyn Redding (2015 - 2018; graduated from Cornell University).

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: Inference in Genomics and Molecular Biology (Brown University, Fall 2022); 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)