Noah A. Rosenberg

Department of Biology
327 Campus Drive
Stanford University
Stanford, CA 94305-5020 USA
Phone: 650-721-2599
Email: noahr@stanford.edu
Website: http://rosenberglab.stanford.edu/
July 10, 2023

Education

2001-2005	Postdoc, University of Southern California, Molecular and Computational Biology
1998-2001	PhD, Stanford University, Biological Sciences
1997-1999	MS, Stanford University, Mathematics
1993-1997	BA, Rice University, Mathematics and Russian Studies, *summa cum laude*

Academic appointments

2014-	Stanford Professor of Population Genetics and Society, Stanford University
School of Humanities and Sciences
2014-	Professor, Stanford University
Department of Biology
2011-2014	Associate Professor, Stanford University
Department of Biology
2009-2011	Associate Professor, University of Michigan
Depts. of Human Genetics, Ecology & Evolutionary Biology, and Biostatistics
Research Associate Professor, University of Michigan
Life Sciences Institute and Center for Computational Medicine & Bioinformatics
2005-2009	Assistant Professor, University of Michigan
Depts. of Human Genetics, Ecology & Evolutionary Biology (2006-2009), and Biostatistics
Research Assistant Professor, University of Michigan
Life Sciences Institute and Center for Computational Medicine & Bioinformatics

---

Recognition

2021	James F. Burgess Methods Article-of-the-Year in *Health Services Research*
2020	George C. Williams Prize, International Society for Evolution, Medicine & Public Health
2018	Elected Fellow, American Association for the Advancement of Science
2014	Stanford Professorship in Population Genetics and Society, Stanford University
2014	Stanford Prize in Population Genetics and Society, Stanford University
2010	Dean's Basic Science Research Award, University of Michigan Medical School
2007	Alumni Distinguished Leadership Award, Illinois Mathematics and Science Academy
2006-2010	Alfred P. Sloan Research Fellowship in Computational and Evolutionary Molecular Biology

2005	Biological Sciences Scholar, University of Michigan Medical School
2004-2014	Burroughs Wellcome Fund Career Award in the Biomedical Sciences
2003	*The Lancet* Biomedical Research Paper of the Year Award
2002-2004	National Science Foundation Postdoctoral Fellowship in Biological Informatics
2000-2001	Program in Mathematics and Molecular Biology Graduate Fellowship
1997-2000	National Defense Science and Engineering Graduate Fellowship
1997	National Science Foundation Graduate Research Fellowship Honorable Mention
1996-1997	Barry M. Goldwater Scholarship
1996	William Lowell Putnam Mathematical Competition top 100 students
1993-1997	Undergraduate Awards at Rice University
	-Phi Beta Kappa
	-Hubert E. Bray Prize in Mathematics
	-Dean's Profiles of Outstanding Undergraduates in the Humanities
	-Graham Stebbings College Service Award
	-Sallyport Award of the Association of Rice Alumni
	-Vice President of Student Affairs Appreciation Award

GRANT SUPPORT

CURRENT RESEARCH GRANTS

2021-2024	National Science Foundation BCS-2116322 *Genealogical ancestors, admixture, and population history.* Principal investigator 8/15/2021-7/31/2024.
2020-2023	National Science Foundation BCS-2017956. *Time transect of ancient genomes of Indigenous North Americans.* Principal investigator, 9/01/2020-8/31/2023.
2020-2023	France–Stanford Center for Interdisciplinary Studies. *Population genetics of cancer evolution.* Principal investigator, 9/01/2020-8/31/2023.
2018-2022	National Institutes of Health R01 GM131404. *Scalable coalescent inference for large data sets,* Co-investigator (J. Palacios, PI), 9/5/2018-6/30/2023.
2018-2022	United States–Israel Binational Science Foundation 2017024. *Theory of consanguinity and its effects on genomic sharing within and between individuals.* Principal investigator (multiple PI grant with S. Carmi), 10/1/2018-9/30/2023.
2010-2026	National Institutes of Health R01 HG005855. *Population genetics for large-scale sequencing studies of diverse populations,* 9/15/2017-7/31/2026. *Advanced strategies for genotype imputation,* 9/13/2010-6/30/2016. Principal investigator (administrative PI of multiple PI grant with P. Scheet, S. Zöllner).

COMPLETED RESEARCH GRANTS

2020-2021	Stanford RISE COVID-19 Crisis Response Faculty Seed Grand Program. *Minimizing effects of anti-vaccine sentiment on future COVID-19 dynamics.* Principal investigator, 8/15/2020-12/31/2021.
2015-2019	National Science Foundation DBI-1458059. *ABI innovation: computational population-genetic analysis for detection of soft selective sweeps.* Principal investigator, 8/1/2015-7/31/2019.

2015-2019　National Science Foundation BCS-1515127.
Using paleogenomic data to decipher genomic effects of European colonization on indigenous North Americans.
Principal investigator, 8/1/2015-7/31/2019.

2015-2019　National Institutes of Health R01 GM117590.
Mathematical and computational analysis for species tree inference.
Co-investigator (J. Rhodes, PI), 8/1/2015-4/30/2019.

2015-2018　National Institute of Justice 2014-DN-BX-K015.
Advanced statistical population genetics methods for forensic DNA identification.
Principal investigator, 1/1/2015-12/31/2018.

2014-2018　France–Stanford Center for Interdisciplinary Studies.
Inference of demographic history using joint genetic and linguistic analyses in Cape Verde.
Principal investigator, 9/1/2014-8/31/2018.

2014-2018　Stanford Center for Computational, Evolutionary, and Human Genomics.
Ancestry in forensic identification: a dual skeleton and genetic analysis.
Principal investigator (trainee-led research grant with trainee Bridget Algee-Hewitt), 9/1/2014-8/31/2018.

2013-2017　Stanford Center for Computational, Evolutionary, and Human Genomics.
Deleterious recessive variation and runs of homozygosity in Ashkenazi Jews.
Principal investigator (trainee-led research grant with trainees Doc Edge and Amy Goldberg), 10/1/2013-9/30/2017.

2011-2015　National Science Foundation DBI-1146722.
Novel methodologies for genome-scale evolutionary analysis of multi-locus data.
Principal investigator, 7/1/2011-6/30/2015.

2010-2014　National Science Foundation BCS-1147534.
Anthropological-genomic effects of European colonization on Native North Americans.
Principal investigator, 9/15/2010-8/31/2014.

2004-2014　Burroughs Wellcome Fund Career Award in the Biomedical Sciences.
Efficient genome-based inference of ancestry for use in genetic association studies.
Principal investigator, 9/1/2004-8/31/2014.

2007-2013　National Institutes of Health R01 GM081441.
Population-genetic studies for association mapping.
Principal investigator, 5/1/2007-4/30/2013.

2011　Stanford Center for Population Research.
Genetic and linguistic admixture in Cape Verdean populations.
Principal investigator, 9/1/2011-12/31/2011.

2009-2011　National Institutes of Health R01 GM081441.
American Recovery and Reinvestment Act administrative supplement to *Population-genetic studies for association mapping.*
Principal investigator, 8/31/2009-7/31/2011.

2007-2011　National Science Foundation DEB-0716904.
Theory of gene trees and species trees.
Principal investigator, 8/1/2007-7/31/2011.

2009-2011　University of Michigan/Israeli Universities Partnership.
Genetic relationships among Jewish populations.
Principal investigator, 2/1/2009-3/31/2011.

2006-2011　Horace H. Rackham Graduate School at the University of Michigan, Faculty Fellowship Enhancement Award.
Principal investigator, 9/1/2006-8/31/2011.

2007-2011	National Institutes of Health R01 HL090564. *Computational statistical approaches to gene-environment interaction.* Co-investigator (S. Zöllner, PI), 9/20/2007-6/30/2011.
2009-2010	Life Sciences Institute, University of Michigan. *Genetic diversity of human embryonic stem cell lines.* Principal investigator (multiple PI grant with S. Morrison), 9/1/2009-12/31/2010.
2007-2010	University of Michigan/Israeli Universities Partnership. *Genetic relationships among Jewish populations.* Principal investigator, 7/1/2007-6/30/2010.
2007	Horace H. Rackham Graduate School at the University of Michigan, Faculty Research Award. Principal investigator, 5/1/2007-12/31/2007.
2006-2010	Alfred P. Sloan Research Fellowship in Computational and Evolutionary Molecular Biology. Principal investigator, 9/16/2006-9/15/2010.
2009	National Institutes of Health U01 HL084729. *Integrated parametric and non-parametric mapping for genome-wide association studies.* Co-investigator (G. Abecasis, PI), 6/15/2006-5/31/2009.
2006-2007	National Science Foundation DEB-0609760. *A new approach to inference of sex-biased migration from X-chromosomal and autosomal population-genetic data.* Principal investigator, 4/15/2006-4/30/2007.
2004-2005	University of Southern California Center of Excellence in Genomic Science Pilot Project Grant in Human Genetic Variation. *Genetic structure of populations from India.* Principal investigator, 9/1/2004-8/31/2005.

GRANTS FOR EDUCATIONAL ACTIVITIES

2013-2014	Stanford Center for Computational, Evolutionary, and Human Genomics. *Genomics and philosophy of race.* Principal investigator, 9/1/2013-8/31/2014.
2012	Stanford Center for Population Research. *From generation to generation: the genetics of Jewish populations.* Principal investigator, 9/1/2012-12/31/2012.
2007-2009	Paul Goldstein and Lillian Goldstein Lande Scientific Exchange Fund. *Camp Evolution: a program for interaction between the Life Sciences Institute at the University of Michigan and the ecology and evolution community in Israel.* Principal investigator, 1/1/2007-12/31/2009.
2006-2009	Horace H. Rackham Graduate School at the University of Michigan. *Population genetics workshop.* Principal investigator, 9/1/2006-12/31/2009.

SCHOLARLY ACTIVITIES AND SERVICE

SELECTED MAJOR SERVICE ACTIVITIES.   Editor-in-Chief, *Theoretical Population Biology* (2013-); Editor of special issues (2013, 2020, 2022); Genome Research Review Committee study section standing member, National Human Genome Research Institute (2010-2014); Stanford Center for Computational, Evolutionary, and Human Genomics founding committee and ongoing committee service (2012-).

Editorial boards

    2014-   Associate Editor, *Evolution, Medicine, and Public Health*

    2013-   Editor-in-Chief, *Theoretical Population Biology* (Associate Editor, 2009-2012)

    2010-   Associate Editor, *Human Biology*

 2010-2018   Associate Editor, *Genetics*

 2011-2014   Associate Editor, *Molecular Biology and Evolution*

 2010-2014   Associate Editor, *BMC Bioinformatics*

 2008-2010   Associate Editor, *American Journal of Human Genetics*

Editorial coordination of thematic article collections

    2022   Celebrating 50 years since Lewontin's apportionment of human diversity, *Philosophical Transactions of the Royal Society of London B: Biological Sciences*

    2020   Fifty years of *Theoretical Population Biology*, *Theoretical Population Biology*

    2013   From generation to generation: the genetics of Jewish populations, *Human Biology*

    2013   Phylogenomics and population genomics: models, algorithms, and analytical tools, *Pacific Symposium on Biocomputing*

Advisory roles

    2018-   Advisory Board for "Humane Genetics" high school curriculum, BSCS Science Learning

    2021   George C. Williams Prize selection committee chair, International Society for Evolution, Medicine, and Public Health

 2020, 2021   Virtual roundtable panelist, British Academy

    2018   Bioinformatics & Systems Biology PhD program external review panelist, University of California, San Diego

    2015   Advisory Committee for the 100th Anniversary of *Genetics*, Genetics Society of America

    2015   Gilbert S. Omenn Prize selection committee, Evolution, Medicine, and Public Health Foundation

 2011-2013   Advisory Board for the Summer Internship for Native Americans in Genomics, University of Illinois at Urbana-Champaign

National Institutes of Health review panels

 2020, 2021   Genomic Innovator Special Emphasis Panel member, National Human Genome Research Institute

    2016   Genes, Genomes, and Genetics F08 Fellowships panelist, National Institutes of Health

    2015   Training Program Data Coordinating Center Special Emphasis Panel chair, National Human Genome Research Institute

    2013   Provocative Questions Initiative workshop panelist, National Cancer Institute

 2010-2014   Genome Research Review Committee study section standing member, National Human Genome Research Institute

    2009   1000 Genomes Project Dataset Analysis Special Emphasis Panel member, National Human Genome Research Institute

    2009   Genomes & Genetics American Recovery and Reinvestment Act Challenge Grants ad hoc reviewer, National Institutes of Health

2010-	PhD external examiner (National University of Singapore, University of Auckland)
2010-	External referee for appointments and promotions ($\sim$35; 6 countries)
2015-	External referee for international research agency evaluations of individuals ($\sim$10; 4 countries)
2006-	Guest Associate Editor; *PLoS Genetics* (2006, 2008, 2011), *Proceedings of the National Academy of Sciences USA* (2015)
2004-	National Science Foundation ad hoc grant reviewer (Biological Anthropology, Dimensions of Biodiversity, Evolutionary Ecology, Evolutionary Genetics, Phylogenetic Systematics, Plant Genome Research, Population and Evolutionary Processes, Systematic Biology and Biodiversity Inventories)
2005-	Ad hoc grant reviewer for $\sim$20 additional granting organizations (Austrian Science Fund, Banff International Research Station, Belgian National Fund for Scientific Research, Columbia University Research Initiatives in Science and Engineering, Chan-Zuckerberg Initiative, Estonian Science Fund, Finnish Academy, German Israeli Foundation, German Research Foundation, Human Frontier Science Foundation, Israel Science Foundation, Leakey Foundation, Netherlands Genomics Initiative, Oak Ridge Associated Universities, Royal Society of New Zealand, South Africa National Research Foundation, Swiss National Science Foundation, United Kingdom Biotechnology and Biological Sciences Research Council, United Kingdom Natural Environment Research Council, Wellcome Trust)
2004-	Book proposal reviewer (Elsevier, Roberts & Company, Springer)
1999-	Manuscript reviewer for >60 journals

CONFERENCE ORGANIZATION

2016	International scientific committee, "Founder populations and their contribution to biology and history: lessons from the Jewish genome," Haifa
2013	Organizing committee and local host, "Genomics and the philosophy of race" research cluster (Stanford University; University of California, Davis; University of California, Santa Cruz)
2013	Program committee, "Why we can't wait: conference to eliminate health disparities in genomic medicine," San Francisco
2008-2010	Program committee, Intelligent Systems for Molecular Biology conference (Evolution and Phylogeny 2008 & 2009, Population Genomics 2009 & 2010)
2009	Symposium organizer, "Evolutionary biology: 150 years after the *Origin*," Life Sciences Institute, University of Michigan
2008, 2012	Abstract review committee, Population and Evolutionary Genetics session, American Society of Human Genetics annual meeting (session moderator 2008)
2008	Program committee, Mathematics and Informatics in Evolution and Phylogeny conference, Montpellier
2006	Symposium organizer, "Gene trees and species trees" session, Society for Molecular Biology and Evolution annual meeting

UNIVERSITY AND DEPARTMENTAL SERVICE

STANFORD UNIVERSITY (2011-PRESENT)

2023	Selection Committee, Stanford Chapter of Phi Beta Kappa
2022	Biology Librarian Search Committee, Stanford University Libraries
2021-	Faculty Affiliate, Biomedical Informatics PhD program
2021-	Faculty Affiliate, Computational and Mathematical Engineering PhD program
2021	External Scientific Advisory Committee for Curricular Development, Dept. of Mathematics
2016	Fulbright Campus Committee, Overseas Research Center

2014-	Member, Bio-X
2013-	Fellowships Chair, Center for Computational, Evolutionary, and Human Genomics
2012-	Executive Committee, Center for Computational, Evolutionary, and Human Genomics
2012	Founding Committee, Center for Computational, Evolutionary, and Human Genomics
2012-	Member, Taube Center for Jewish Studies
2011-2016	Faculty Affiliate, Stanford Center for Population Research
2011-	Ecology & Evolution subdepartment (many committees)
2011-	Department of Biology (many committees)

UNIVERSITY OF MICHIGAN (2005-2011)

2010-2011	Executive Committee, Training Program in Genomic Science
2005-2011	Member, Training Program in Genomic Science
2005-2011	Bioinformatics Graduate Program, Center for Genetics in Health and Medicine, Department of Ecology & Evolutionary Biology, and Department of Human Genetics (many committees)
2005-2007	Organizer, Population Genetics Rackham Interdisciplinary Workshop

PROFESSIONAL SOCIETIES

American Association for the Advancement of Science
American Mathematical Society
American Society of Human Genetics
Genetics Society of America
International Society for Evolution, Medicine & Public Health
Society for Industrial and Applied Mathematics
Society for Mathematical Biology
Society for Molecular Biology and Evolution
Society for the Study of Evolution

MENTORSHIP

POSTDOCTORAL FELLOWS

2021-	LILY AGRANAT-TAMIR. PhD from Hebrew University of Jerusalem.
2020-2021	JAZLYN MOONEY. PhD from University of California, Los Angeles. Current position: Assistant Professor, Dept. of Quantitative & Computational Biology, University of Southern California
2019-2020	AIRAM BLANCAS. PhD from Centro de Investigación de Matemáticas in Guanajuato. Current position: Assistant Professor, Dept. of Statistics, Instituto Technológico Autónomo de México.
2017-2020	GILI GREENBAUM. PhD from Ben Gurion University. Current position: Assistant Professor, Dept. of Ecology, Evolution & Behavior, Hebrew University of Jerusalem.
2015-2021	JAEHEE KIM. PhD from Stanford University. Current position: Assistant Professor, Dept. of Computational Biology, Cornell University.
2015-2018	LAWRENCE URICCHIO. PhD from University of California, San Francisco. Current position: Assistant Professor, Dept. of Biology, Tufts University.
2013-2018	BRIDGET ALGEE-HEWITT. PhD from University of Tennessee. First position: Senior Research Scientist, Ctr. for Comparative Studies in Race & Ethnicity, Stanford University.

2014-2017   NICOLAS ALCALA. PhD from University of Lausanne.
             Current position: Scientist, International Agency for Cancer, Lyon.

2013-2017   FILIPPO DISANTO. PhD from University of Paris 7/University of Siena.
             Current position: Lecturer, Dept. of Mathematics, University of Pisa.

2013-2016   OLGA KAMNEVA. PhD from University of Wyoming.
             First position: Staff Scientist, Affymetrix.

2012-2013   LARS ANDERSEN. PhD from University of Aarhus.
             Current position: Associate Professor, Dept. of Mathematics, University of Aarhus.

2009-2012   CUONG THAN. PhD from Rice University.
             First position: Postdoc, University of Tubingen.

2009-2012   PAUL VERDU. PhD from University of Paris 6.
             Current position: CNRS Faculty, Muséum National de Histoire Naturelle, Paris.

2009-2012   ERKAN BUZBAS. PhD from University of Idaho.
             Current position: Associate Professor, Dept. of Statistical Science, University of Idaho.

2008-2012   TREVOR PEMBERTON. DPhil from University of Sussex.
             First position: Assistant Professor, Dept. of Biochemistry & Medical Genetics, University of
             Manitoba.

2007-2008   JAMES DEGNAN. PhD from University of New Mexico.
             Current position: Associate Professor, University of New Mexico.

2006-2008   PAUL SCHEET. PhD from University of Washington.
             Current position: Professor and Chair, Dept. of Epidemiology, M. D. Anderson Cancer Center.

2005-2008   MATTIAS JAKOBSSON. PhD from Lund University.
             Current position: Professor, Dept. of Evolutionary Biology, Uppsala University.

2005-2006   MICHAEL BLUM. PhD from Institut National Polytechnique de Grenoble.
             First position: CNRS Faculty, Laboratory on Techniques for Biomedical Engineering & Complexity Management, University of Grenoble.

PHD STUDENTS

2023-   JUAN ESTEBAN RODRIGUEZ. Ecology & Evolution, Stanford University.
             PhD major recognition: Stanford Graduate Fellowship.

2023-   CHLOE SHIFF. Computational & Mathematical Engineering, Stanford University.
             PhD major recognition: NSF Graduate Research Fellowship.

2022-   EGOR LAPPO. Ecology & Evolution, Stanford University.
             PhD major recognition: Stanford Graduate Fellowship.

2020-   MAIKE MORRISON. Ecology & Evolution, Stanford University.
             PhD major recognition: NSF Graduate Research Fellowship, Stanford Graduate Fellowship.

2019-   XIRAN LIU. Computational & Mathematical Engineering, Stanford University.
             Computational methods and mathematical measures for population relationships.
             PhD major recognition: Gene H. Golub Dissertation Award from Stanford Institute for Computational & Mathematical Engineering

2019-   DANIEL COTTER. Genetics, Stanford University.
             The effects of relatedness and sex-biased demographic processes on human genetic variation.
             PhD major recognition: NSF Graduate Research Fellowship.

2017-2021   ALISSA SEVERSON. Genetics, Stanford University.
             The effect of relatedness and population structure on patterns of genomic sharing.
             PhD major recognition: NSF Graduate Research Fellowship.
             Current position: D2G Oncology.

2014-2018   ILANA ARBISSER. Ecology & Evolution, Stanford University.
             Mathematical investigations into fundamental population genetics statistics and models.
             First position: Cruise Automation, Inc.

2013-2018   ROHAN MEHTA. Ecology & Evolution, Stanford University.
Mathematical modeling of genetic and cultural traits.
PhD major recognition: NSF Graduate Research Fellowship Honorable Mention, Samuel Karlin Prize in Mathematical Biology from Stanford Biology, Stanford Graduate Fellowship.
Current position: Postdoc, Emory University.

2013-2018   JONATHAN KANG. Ecology & Evolution, Stanford University.
Analysis and application of linkage disequilibrium in population and statistical genetics.
Current position: Lecturer, School of Mathematics and Science, Singapore Polytechnic.

2012-2017   AMY GOLDBERG. Ecology & Evolution, Stanford University.
Mathematical and statistical approaches to elucidate recent human evolutionary history.
PhD major recognition: Achievement Rewards for College Scientists Fellowship, American Association of Physical Anthropologists Sherwood Washburn Prize, Genetics Society of America James F. Crow Early Career Researcher Finalist, NSF Graduate Research Fellowship, Samuel Karlin Prize in Mathematical Biology from Stanford Biology.
Current position: Assistant Professor, Dept. of Evolutionary Anthropology, Duke University.

2012-2016   MICHAEL "DOC" EDGE. Ecology & Evolution, Stanford University.
Pick up the pieces: combining information from multiple genetic loci.
PhD major recognition: Samuel Karlin Prize in Mathematical Biology from Stanford Biology, Stanford Graduate Fellowship.
Current position: Assistant Professor, Dept. of Quantitative & Computational Biology, University of Southern California.

2010-2014   ETHAN JEWETT. Ecology & Evolution, Stanford University.
Models and tools for studying genetic and cultural variation.
PhD major recognition: Samuel Karlin Prize in Mathematical Biology from Stanford Biology.
Current position: 23andMe, Inc.

2007-2014   NAAMA KOPELMAN. Environmental Studies, Tel Aviv University (co-supervisor Lewi Stone).
The complex genealogy of Jewish populations.
Current position: Senior Lecturer, Faculty of Sciences, Holon Institute of Technology.

2009-2012   CHAOLONG WANG. Bioinformatics, University of Michhigan.
Statistical methods for analyzing human genetic variation in diverse populations.
PhD major recognition: HHMI International Student Research Fellowship, Rackham Graduate School Predoctoral Fellowship.
Current position: Professor, School of Public Health, Huazhong University of Science and Technology.

2008-2012   ZACHARY SZPIECH. Bioinformatics, University of Michigan.
Human migration, population divergence, and the accumulation of deleterious alleles: insights from private genetic variation and whole-exome sequencing.
Current position: Assistant Professor, Dept. of Biology, Penn State University

2006-2011   LUCY HUANG. Bioinformatics, University of Michigan.
Genotype imputation in diverse populations: empirical and theoretical approaches.
PhD major recognition: Rackham Graduate School Predoctoral Fellowship.
Current position: Google, Inc.

2007-2011   MICHAEL DEGIORGIO. Bioinformatics, University of Michigan. *Genetic variation and modern human origins.*
PhD major recognition: Ford Foundation Diversity Fellowship Honorable Mention, NSF Graduate Research Fellowship Honorable Mention, ProQuest Distinguished Dissertation Honorable Mention for best dissertation in the university.
Current position: Associate Professor, Dept. of Electrical & Computer Engineering and Computer Science, Florida Atlantic University

MASTER'S STUDENTS

2014-2016   BRIAN DONOVAN. Biology MS student and PhD student in Science Education, Stanford University.
MS major recognition: Stanford Interdisciplinary Graduate Fellowship.
Current position: Research Scientist, BSCS Science Learning.

2010-2011   LAURA HELMKAMP. Biostatistics MS student, University of Michigan.
Current position: Data science.

2006-2008   JENNA (VANLIERE) CANZONIERO. Bioinformatics MS student and Medical student, University of Michigan.
Current position: Assistant Professor, Dept. of Oncology, Johns Hopkins School of Medicine

2004-2005   SAURABH MAHAJAN. Computer Science MS student, University of Southern California (co-supervisor Pragna Patel).
Current position: Software industry.

UNDERGRADUATE RESEARCHERS

2023-   MICHAEL DOBOLI. Mathematics, Stanford University.

2023-   EMILY DICKEY. Mathematics, Stanford University.

2022-   BRADLEY MOON. Mathematics, Stanford University.

2022-   FRANCIS BECKERT. Mathematics, Stanford University.

2022-   ZARIF AHSAN. Mathematics, Stanford University.

2022-2023   THEODORE GRESS. Ecology & Evolution, Stanford University

2022-2023   ANDREW LEE. Mathematics, Stanford University.

2022   TARUN MARTHESWARAN. Biomedical Computation, Stanford University.

2021-2022   MATTHEW KING. Mathematics, Stanford University.

2021   ELYSSA HOFGARD. Physics, Stanford University.

2021   ALESSANDRA MARANCA. Mathematics, Stanford University.

2018-2022   EGOR ALIMPIEV. Mathematics, Stanford University.
Recognition for undergraduate research: Honorable Mention for the American Mathematical Society Frank and Brennie Morgan Prize for Outstanding Research in Mathematics by an Undergraduate Student.

2017-2019   ZOE HIMWICH. Mathematics, Stanford University.

2016-2018   HORMAZD GODREJ. Biology, Stanford University.
Thesis: *Detecting categories of consanguinity through X chromosomal runs of homozygosity.*

2015-2018   ALAN AW. Mathematical & Computational Science, Stanford University.
Thesis: *Mathematical and computational studies in human evolution and population genetics.*
Recognition for undergraduate research: Deans' Award for Academic Achievement.

2014-2015   LUCAS HANSEN. Mathematical & Computational Science, Stanford University.

2014   ANANYA RASTOGI. Biology/Mathematical Biology, Indian Institute of Science Education and Research, Mohali.

2011   AMY GOLDBERG. Biological Anthropology and Mathematics, University of Michigan.

2008-2010   SHASHIR REDDY. Mathematics, University of Michigan.

2008-2010   IVANA JANKOVIC. Molecular & Cellular Biology, University of Michigan.

2006   RANDA TAO. Ecology & Evolutionary Biology, University of Michigan.
Thesis: *Gene and species trees under the coalescent process: analysis of discordance within five taxa.*
Recognition for undergraduate research: High Honors in Biology.

2006-2007   ZACHARY SZPIECH. Mathematics, University of Michigan.

ADDITIONAL PHD ROTATION STUDENTS

2023   TAMI GJORGJIEVA. Genetics, Stanford University.

2022   HUISHENG JULIE ZHU. Ecology & Evolution, Stanford University.

2021   SHAILI MATHUR. Ecology & Evolution, Stanford University.

2019	ALYSSA FORTIER. Ecology & Evolution, Stanford University.
2018-2019	KALEDA DENTON. Ecology & Evolution, Stanford University.
2013-2014	ARBEL HARPAK. Ecology & Evolution, Stanford University.
2009	BRIAN METZGER. Ecology & Evolutionary Biology, University of Michigan.
2007	CONNER SANDEFUR. Bioinformatics, University of Michigan.
2005	JUSTIN VAN KLEIN. Bioinformatics, University of Michigan.

ADDITIONAL TRAINEE MENTORSHIP

2020-2021	RISHABH KAPOOR. Biology undergraduate, Stanford University (mentored teaching). Recognition: Lauren D. Weinstein Award in Science Education from Stanford Biology
2020-2021	YASH PERSHAD. Bioengineering undergraduate, Stanford University (mentored teaching).
2013	LUCIE GATTEPAILLE. Visiting Evolutionary Biology PhD student, Uppsala University.
2010	ANASTASIA WOLFF. Visiting Biology MS student, Ecole Normale Supériure, Paris.
2010	ERIC KALOSA-KENYON. High school student, Pioneer High School, Ann Arbor.
2007, 2008	SIMINA BOCA. Visiting Biostatistics PhD student, Johns Hopkins University.

PHD COMMITTEES

2022-	ANASTASIA LYULINA. Ecology & Evolution, Stanford University.
2020-	ROSHNI PATEL. Genetics, Stanford University.
2020-	RACHEL UNGAR. Genetics, Stanford University.
2020-2023	TALIA BOROFSKY. Ecology & Evolution, Stanford University.
2019-	JAVIER BLANCO. Ecology & Evolution, Stanford University.
2019-	MALLORY HARRIS. Ecology & Evolution, Stanford University.
2019-2023	SHA JIANG. Ecology & Evolution, Stanford University.
2018-2023	KALEDA DENTON. Ecology & Evolution, Stanford University.*
2018-2023	ALYSSA FORTIER. Ecology & Evolution, Stanford University.*
2020-2022	MARGARET ANTONIO. Biomedical Informatics, Stanford University.
2019-2022	HAO SHEN. Ecology & Evolution, Stanford University.
2016-2022	GRANT KINSLER. Ecology & Evolution, Stanford University.
2019-2021	ELLIE ARMSTRONG. Ecology & Evolution, Stanford University.*
2016-2021	ELORA LÓPEZ. Marine Biology, Stanford University.
2014-2019	DANIEL FRIEDMAN. Ecology & Evolution, Stanford University.
2013-2018	ALISON FEDER. Ecology & Evolution, Stanford University.*
2013-2018	ARBEL HARPAK. Ecology & Evolution, Stanford University.*
2016-2018	NATALIE TELIS. Biomedical Informatics, Stanford University.
2017	JULIAN HOMBURGER. Genetics, Stanford University.†
2014-2017	ALEXIS MYCHAJLIW. Ecology & Evolution, Stanford University.
2012-2017	LILY BLAIR. Ecology & Evolution, Stanford University.
2012-2016	MIKE BRAMSON. Ecology & Evolution, Stanford University.
2014-2016	BRIAN DONOVAN. Science Education, Stanford University.
2011-2016	JEREMY HSU. Ecology & Evolution, Stanford University.
2016	MICHAEL MACLAREN. Ecology & Evolution, Stanford University.
2012-2016	SIDDHARTHA KRISHNA KUMAR. Ecology & Evolution, Stanford University.
2013-2015	NANDITA GARUD. Genetics, Stanford University.*

2014	BRIAN MAPLES. Biomedical Informatics, Stanford University.[†]
2014	MARK LONGO. Ecology & Evolution, Stanford University.
2014	OANA CARJA. Ecology & Evolution, Stanford University.
2014	ROBERT FURROW. Ecology & Evolution, Stanford University.
2012-2014	PHILIP GREENSPOON. Ecology & Evolution, Stanford University.
2012-2013	ZHIYUAN SONG. Ecology & Evolution, Stanford University.
2011-2013	PENG ZHANG. Bioinformatics, University of Michigan.[*]
2010-2011	MATTHEW ZAWISTOWSKI. Biostatistics, University of Michigan.[*]
2010-2011	SHYAM GOPALAKRISHNAN. Biostatistics, University of Michigan.
2008-2011	RAQUEL ASSIS. Bioinformatics, University of Michigan.
2006-2011	ETHAN ROMERO-SEVERSON. Epidemiology, University of Michigan.
2007-2010	NICOLE SCOTT. Human Genetics, University of Michigan.
2009	LIMING LIANG, Biostatistics, University of Michigan.
2007-2009	YUN LI, Biostatistics, University of Michigan.
2006-2009	AMANDA ZELLMER, Ecology & Evolutionary Biology, University of Michigan.

[*]Committee service includes research collaboration, supervision of a project, or an informal co-mentor role.
[†]External chair.

NIH CAREER DEVELOPMENT MENTORING COMMITTEES

2010-2014	ERIK VOLZ, Department of Epidemiology, University of Michigan. NIH K01 AI091440: *Estimation of HIV transmission dynamics using genetic sequences of virus.*
2009-2014	CRISTEN WILLER, Department of Biostatistics, University of Michigan. NIH K99/R00 HL094535. *Genetic variants associated with HDL and LDL cholesterol, and triglyceride levels.*

UNDERGRADUATE ADVISING

2016-	Academic Advisor for 1-5 students annually in the Computational Biology track of the Biology major, Stanford University.

TEACHING

COURSES

STANFORD UNIVERSITY (2011-PRESENT)

2021-	Seminar in Computational, Evolutionary, and Human Genomics (Bio 388; 2021, 2022)
2018-2020	Evolution (Bio 85; 2019, 2020)
2015-2017	Evolution (Bio 143; 2015, 2016, 2017)
2021-	Mathematical Evolutionary Biology (Bio 187, CME 187; 2021, 2022)
2021	Evolutionary Medicine (Bio 89SI)
2016-	Advanced Topics in Mathematical Evolutionary Biology (Bio 287A; 2016, 2018, 2019)
2013-	Advanced Topics in Human Population Genetics (Bio 287B; 2013)
2012	From Generation to Generation: The Genetics of Jewish Populations (Bio 127)
2011-2016	Current Topics in Population Biology, Ecology, and Evolution (Bio 302, 303, 304)

2009	Ecology and Evolutionary Biology Capstone Seminar (EEB 410)
2006-2010	Introduction to Bioinformatics & Computational Biology (BI 527) (2-4 lectures)
2006-2011	Statistical Population Genetics (Biostat 664, Biostat 665/865; 2006, 2009, 2011)

Workshops and educational outreach

2021	"How biology is becoming more mathematical," The Future of Everything radio program (recorded podcast interview about the work of the lab)
2015	Human Population Genetics II, The Biomedical & Life Sciences Collection, Henry Stewart Talks, London, hstalks.com/?t=BL196 (co-editor of an online course, with R Nielsen)
2013	Copenhagen-BGI PhD Course in Human Population Genetic Analysis, Beijing Genomics Institute, Shenzhen (day of lectures)
2013	Okinawa Integrative Biology Course, Okinawa Institute of Science and Technology (day of lectures)
2012	Centro de Ciencias Genómicas, Universidad Nacional Autónoma de México, Cuernavaca (day of lectures)
2008	Huron Valley Archaeological Society, Ann Arbor, Michigan (guest lecture)
2007	Camp Evolution III—Human Evolutionary Genetics, Ben Gurion University, Israel (week of lectures and lab activities)
2007	Henry Stewart Publications series on Human Population Genetics (recorded lecture)
2006-2010	Mathematical and Theoretical Biology Institute, Arizona State University (2-3 days of lectures and lab activities)
2000	Workshop on the Analysis of Molecular Genetic Data in Population and Evolutionary Studies, Murdoch University (week of lectures and lab activities)

Research talks

Selected major lectures. International Meeting on Probabilistic, Combinatorial and Asymptotic Methods for the Analysis of Algorithms, Taipei (2023); International Society for Forensic Genetics, Washington, DC (2022); RECOMB-Genetics conference, University of California, Los Angeles (2017); Third International Conference on Mathematical and Computational Medicine, Nationwide Children's Hospital, Columbus, OH (2016); Mathematical and Computational Evolutionary Biology conference, Montpellier (2012); Future Directions in Phylogenetics: Methods and Models, Isaac Newton Institute for Mathematical Sciences, Cambridge, United Kingdom (2007).

Invited talks

2023	International Meeting on Probabilistic, Combinatorial and Asymptotic Methods for the Analysis of Algorithms, Taipei (keynote)
2022	International Society for Forensic Genetics, Washington, DC (keynote)
	40 Years of Computational Biology at USC, Los Angeles
2019	Department of Biostatistics, University of Washington
	International Society for Applied Biological Sciences, Split, Croatia
	Department of Biology, San Francisco State University
2018	Algorithmic Challenges in Protecting Privacy for Biomedical Data, University of California, Los Angeles
2017	RECOMB-Genetics conference, University of California, Los Angeles (keynote)
	Institute for Human Genetics, University of California, San Francisco
	Department of Biomolecular Engineering, University of California, Santa Cruz
	"Mathematical Approaches to Evolutionary Trees and Networks," Banff International Research Station, Banff, Canada

2016   Computational Genomics Summer Institute, University of California, Los Angeles

        "Founder populations and their contribution to biology and history: lessons from the Jewish genome" conference, Haifa

        Third International Conference on Mathematical and Computational Medicine, Nationwide Children's Hospital, Columbus, OH (keynote)

        Sackler Colloquium "In the Light of Evolution X: Phylogeography," National Academy of Sciences Beckman Center

2015   Bioinformatics Program, University of California, Los Angeles

        American Mathematical Society Central Fall Sectional meeting, Loyola University, Chicago

        Institute for Bioinformatics and Evolutionary Studies, University of Idaho

2014   Program in Interdisciplinary Biological and Biomedical Sciences, University of New Mexico

        "The Race Debates" conference, Department of Philosophy, University of San Francisco

        Department of Epidemiology & Biostatistics, University of California, San Francisco

        "Genomics and Philosophy of Race" conference, Institute for Humanities Research, University of California, Santa Cruz

        Department of Biology, San Francisco State University

        Institute for Genomic Medicine, University of California, San Diego

2013   Coalescent theory conference, Université de Montreal

        Society for Molecular Biology and Evolution Annual Meeting, Chicago

        "Why we can't wait" conference on health disparities in genomic medicine, San Francisco

        Department of Biological Statistics and Computational Biology, Cornell University

        Department of Mathematics, University of Alabama, Birmingham

        Section on Statistical Genetics, University of Alabama, Birmingham

        Bioinformatics and Systems Biology Graduate Program, University of California, San Diego

        Working Group on Gene Tree/Species Tree Reconciliation, National Institute for Mathematical and Biological Synthesis, University of Tennessee

        Centro de Ciencias Genómicas, Universidad Nacional Autónoma de México, Cuernavaca

        Mathematical and Computational Evolutionary Biology conference, Montpellier (keynote)

        23andMe, Inc., Mountain View, CA

2012   Genetics Graduate Group, University of California, Davis

        "30 Years of Molecular and Computational Biology at USC" conference, University of Southern California

        Royal Swedish Academy of Sciences Symposium on Modern Human Genetic Variation, Stockholm

        Symposium on Human Genome Variation, University of California, Berkeley

2011   Workshop on Coancestry, Association, and Population Genomics, Institute for Pure and Applied Mathematics, University of California, Los Angeles

        Global Health Equity Symposium, Novartis Institutes for BioMedical Research, Cambridge, MA

2010   Symposium on Human Variation, European Molecular Biology Laboratory, Heidelberg

        American Association of Physical Anthropologists Annual Meeting, Albuquerque

        Department of Biology, Stanford University

        Genetics Graduate Program, University of Iowa

        Genome Center of Wisconsin, University of Wisconsin (Genomics Seminar)

        Phyloseminar.org (live online seminar series)

        Computational Biology and Bioinformatics Program, Duke University

        Department of Biostatistics, Columbia University

2009   Health Disparities Research Collaborative Admixture Workshop, Henry Ford Health System

        Department of Bioengineering and Therapeutic Sciences, University of California, San Francisco

        Department of History, University of California, Los Angeles (DNA and History Seminar)

        DIMACS Conference on Algorithmics in Human Population Genomics, Rutgers University

        Institute for Human Genetics, University of California, San Francisco

        OCS Molecular Biology Seminar, The MITRE Corporation, McLean, VA

2008   Department of Mathematics, University of California, Berkeley (Mathematical and Computational Biology Seminar)

"Genome-wide Association: Analyze This" meeting of the Genes, Environment, and Health Initiative, National Institutes of Health, Bethesda

Society of Systematic Biologists Annual Meeting, University of Minnesota

Penn Bioinformatics Forum, University of Pennsylvania

Program in Ecology, Evolution, and Conservation Biology, University of Illinois, Urbana-Champaign

2007   Future Directions in Phylogenetics: Methods and Models, Isaac Newton Institute for Mathematical Sciences, Cambridge, United Kingdom (keynote)

Department of Anthropology, University of California, Davis

Institute for Mathematical Behavioral Sciences, University of California, Irvine

Santa Fe Institute, NM

Symposium on Trends in Human Genetics, Puri, India

National Center for Biological Sciences, Bangalore

Conférences Jacques Monod on Evolutionary Genomics, Roscoff, France

DNA Sampling: Strategies and Design, Musée de l'Homme, Paris

Department of Epidemiology and Biostatistics, Case Western Reserve University

Center for Clinical Epidemiology and Biostatistics, University of Pennsylvania

2006   Computational and Theoretical Biology Symposium, Department of Bioengineering, Rice University

Department of Ecology and Evolutionary Biology, Rice University

Department of Biology, York University, Toronto

Department of Statistics, Iowa State University (Mathematical Biology Seminar)

American Diabetes Association Annual Meeting, Washington, DC

Society for Molecular Biology and Evolution Annual Meeting, Arizona State University

2005   Workshop on Phylogenetics and Phylogeography, Mathematical Biosciences Institute, Ohio State University

Workshop on Recombination Hotspots and Haplotype Structure, Mathematical Biosciences Institute, Ohio State University

American Association of Physical Anthropologists Annual Meeting, Milwaukee

Department of Mathematics and Statistics, University of New Mexico

Center for Bioinformatics and Computational Biology, Duke University

Department of Ecology and Evolutionary Biology, University of California, Los Angeles

Department of Genetics, Stanford University

Department of Human Genetics, University of California, Los Angeles

Section of Evolution and Ecology, University of California, Davis

2004   Division of Human Biology, Fred Hutchinson Cancer Research Center, Seattle

Bioinformatics Graduate Program, University of Michigan

Department of Genetics, Stanford University (Annual Retreat)

London Mathematical Society Symposium on Mathematical Genetics, University of Durham, United Kingdom

Department of Genome Sciences, University of Washington

Department of Botany and Plant Biology, University of California, Riverside

2003   Department of Pharmaceutical Sciences, St. Jude Children's Research Hospital, Memphis

Department of Biomathematics, University of California, Los Angeles

Cambridge Healthtech Institute Molecular Medicine Marketplace, Santa Clara

American Association for the Advancement of Science Annual Meeting, Denver

The Center for the Advancement of Genomics, Rockville, MD

2001   Department of Ecology and Evolutionary Biology, University of California, Irvine

Center for Statistical Genetics, University of Michigan

Department of Mathematics, University of Southern California

2022	Data Science Initiative
2019	Center for Law and the Biosciences
2018	Biostatistics Workshop
2016	Bio X Undergraduate Summer Research Program
2014	Institute for Computational and Mathematical Engineering
	Stanford Center for Computational, Evolutionary, and Human Genomics
2013	Taube Center for Jewish Studies
	Biostatistics Workshop

University of Michigan (2005-2011)

2011	Undergraduate Research Opportunities Program Peer Group
2010	Center for Afroamerican and African Studies (Mellon Foundation Sawyer Seminar on Ethnicity in Africa)
	Center for Computational Medicine and Bioinformatics
	Training Program in Genomic Science
	Department of Molecular and Integrative Physiology
2009	Department of Internal Medicine (Grand Rounds)
2008	Department of Dermatology
	Center for Computational Medicine and Bioinformatics
2007	Department of Mathematics (Applied and Interdisciplinary Mathematics Seminar)
2006	Department of Ecology and Evolutionary Biology
	Life Sciences Institute (Colloquium)

Publications

Article collections edited

[C1] LK Nakhleh, **NA Rosenberg**, T Warnow (editors). Phylogenomics and population genomics: models, algorithms, and analytical tools. *Pacific Symposium on Biocomputing* 18: 247-306 (2013). [Link]

[C2] **NA Rosenberg**, SP Weitzman (editors). From generation to generation: the genetics of Jewish populations. *Human Biology* 85: 817-939 (2013). [Link]

[C3] **NA Rosenberg** (editor). Fifty years of *Theoretical Population Biology*. *Theoretical Population Biology* 133: 1-180 (2020). [Link]

[C4] MD Edge, S Ramachandran, **NA Rosenberg** (editors). Celebrating 50 years since Lewontin's apportionment of human diversity. *Philosophical Transactions of the Royal Society of London B: Biological Sciences* 377: 1852 (2022). [Link]

Peer-reviewed articles

[1] JK Pritchard, **NA Rosenberg**. Use of unlinked genetic markers to detect population stratification in association studies. *American Journal of Human Genetics* 65: 220-228 (1999). [Link]

[2] L Jin, ML Baskett, LL Cavalli-Sforza, LA Zhivotovsky, MW Feldman, **NA Rosenberg**. Microsatellite evolution in modern humans: a comparison of two data sets from the same populations. *Annals of Human Genetics* 64: 117-134 (2000). [Link]

[3] JK Pritchard, M Stephens, **NA Rosenberg**, P Donnelly. Association mapping in structured populations. *American Journal of Human Genetics* 67: 170-181 (2000). [Link]

[4] **NA Rosenberg**, E Woolf, JK Pritchard, T Schaap, D Gefel, I Shpirer, U Lavi, B Bonné-Tamir, J Hillel, MW Feldman. Distinctive genetic signatures in the Libyan Jews. *Proceedings of the National Academy of Sciences USA* 98: 858-863 (2001). [Link]

[5] MM Tanaka, **NA Rosenberg**. Optimal estimation of transposition rates of insertion sequences for molecular epidemiology. *Statistics in Medicine* 20: 2409-2420 (2001). [Link]

[6] **NA Rosenberg**, T Burke, K Elo, MW Feldman, PJ Freidlin, MAM Groenen, J Hillel, A Mäki-Tanila, M Tixier-Boichard, A Vignal, K Wimmers, S Weigend. Empirical evaluation of genetic clustering methods using multilocus genotypes from 20 chicken breeds. *Genetics* 159: 699-713 (2001). [Link]

[7] **NA Rosenberg**. The probability of topological concordance of gene trees and species trees. *Theoretical Population Biology* 61: 225-247 (2002). [Link]

[8] **NA Rosenberg**, M Nordborg. Genealogical trees, coalescent theory and the analysis of genetic polymorphisms. *Nature Reviews Genetics* 3: 380-390 (2002). [Link]

[9] **NA Rosenberg**, JK Pritchard, JL Weber, HM Cann, KK Kidd, LA Zhivotovsky, MW Feldman. Genetic structure of human populations. *Science* 298: 2381-2385 (2002). [Link]
    [*Current Biology* scientific commentary]
    [*Nature Genetics* scientific commentary]
    [*Science* scientific commentary]
    [*Lancet* Biomedical Research Paper of the Year Award]

[10] LA Zhivotovsky, **NA Rosenberg**, MW Feldman. Features of evolution and expansion of modern humans, inferred from genomewide microsatellite markers. *American Journal of Human Genetics* 72: 1171-1186 (2003). [Link]
    [*Discover* Top Science Stories of 2003]

[11] **NA Rosenberg**, JK Pritchard, JL Weber, HM Cann, KK Kidd, LA Zhivotovsky, MW Feldman. Response to comment on "Genetic structure of human populations." *Science* 300: 1877 (2003). [Link]

[12] **NA Rosenberg**, AG Tsolaki, MM Tanaka. Estimating change rates of genetic markers using serial samples: applications to the transposon IS*6110* in *Mycobacterium tuberculosis*. *Theoretical Population Biology* 63: 347-363 (2003). [Link]

[13] **NA Rosenberg**. The shapes of neutral gene genealogies in two species: probabilities of monophyly, paraphyly, and polyphyly in a coalescent model. *Evolution* 57: 1465-1477 (2003). [Link]

[14] **NA Rosenberg**, AE Hirsh. On the use of star-shaped genealogies in estimating coalescence times. *Genetics* 164: 1677-1682 (2003). [Link]

[15] **NA Rosenberg**, L Li, R Ward, JK Pritchard. Informativeness of genetic markers for inference of ancestry. *American Journal of Human Genetics* 73: 1402-1422 (2003). [Link]
    [*American Journal of Human Genetics* editorial highlight]

[16] S Ramachandran, **NA Rosenberg**, LA Zhivotovsky, MW Feldman. Robustness of the inference of human population structure: A comparison of X-chromosomal and autosomal microsatellites. *Human Genomics* 1: 87-97 (2004). [Link]

[17] **NA Rosenberg**. *Distruct*: a program for the graphical display of population structure. *Molecular Ecology Notes* 4: 137-138 (2004). [Link]

[18] MM Tanaka, **NA Rosenberg**, PM Small. The control of copy number of IS*6110* in *Mycobacterium tuberculosis*. *Molecular Biology and Evolution* 21: 2195-2201 (2004). [Link]

[19] **NA Rosenberg**, PP Calabrese. Polyploid and multilocus extensions of the Wahlund inequality. *Theoretical Population Biology* 66: 381-391 (2004). [Link]

[20] H Innan, K Zhang, P Marjoram, S Tavaré, **NA Rosenberg**. Statistical tests of the coalescent model based on the haplotype frequency distribution and the number of segregating sites. *Genetics* 169: 1763-1777 (2005). [Link]

[21] M Nordborg, TT Hu, Y Ishino, J Jhaveri, C Toomajian, H Zheng, E Bakker, P Calabrese, J Gladstone, R Goyal, M Jakobsson, S Kim, Y Morozov, B Padhukasahasram, V Plagnol, **NA Rosenberg**, C Shah, JD Wall, J Wang, K Zhao, T Kalbfleisch, V Schulz, M Kreitman, J Bergelson. The pattern of polymorphism in *Arabidopsis thaliana*. *PLoS Biology* 3: 1289-1299 (2005). [Link]

[22] **NA Rosenberg**. A sharp minimum on the mean number of steps taken in adaptive walks. *Journal of Theoretical Biology* 237: 17-22 (2005). [Link]

[23] S Ramachandran, O Deshpande, CC Roseman, **NA Rosenberg**, MW Feldman, LL Cavalli-Sforza. 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* 102: 15942-15947 (2005). [Link]

[24] **NA Rosenberg**. Algorithms for selecting informative marker panels for population assignment. *Journal of Computational Biology* 12: 1183-1201 (2005). [Link]

[25] **NA Rosenberg**, S Mahajan, S Ramachandran, C Zhao, JK Pritchard, MW Feldman. Clines, clusters, and the effect of study design on the inference of human population structure. *PLoS Genetics* 1: 660-671 (2005). [Link]

[26] **NA Rosenberg**. The mean and variance of the numbers of r-pronged nodes and r-caterpillars in Yule-generated genealogical trees. *Annals of Combinatorics* 10: 129-146 (2006). [Link]

[27] JH Degnan, **NA Rosenberg**. Discordance of species trees with their most likely gene trees. *PLoS Genetics* 2: 762-768 (2006). [Link]

[28] **NA Rosenberg**, M Nordborg. A general population-genetic model for the production by population structure of spurious genotype-phenotype associations in discrete, admixed or spatially distributed populations. *Genetics* 173: 1665-1678 (2006). [Link]

[29] **NA Rosenberg**. Standardized subsets of the HGDP-CEPH Human Genome Diversity Cell Line Panel, accounting for atypical and duplicated samples and pairs of close relatives. *Annals of Human Genetics* 70: 841-847 (2006). [Link]

[30] DF Conrad*, M Jakobsson*, G Coop*, X Wen, JD Wall, **NA Rosenberg**[†], JK Pritchard. A worldwide survey of haplotype variation and linkage disequilibrium in the human genome. *Nature Genetics* 38: 1251-1260 (2006). [Link]
    [*Nature Genetics* scientific commentary]
    [*Nature Genetics* cover article]
    [*Nature Reviews Genetics* editorial highlight]

[31] **NA Rosenberg**, S Mahajan, C Gonzales-Quevedo, MGB Blum, L Nino-Rosales, V Ninis, P Das, M Hegde, L Molinari, G Zapata, JL Weber, JW Belmont, PI Patel. Low levels of genetic divergence across geographically and linguistically diverse populations from India. *PLoS Genetics* 2: 2052-2061 (2006). [Link]

[32] **NA Rosenberg**. Statistical tests for taxonomic distinctiveness from observations of monophyly. *Evolution* 61: 317-323 (2007). [Link]

[33] KB Schroeder, TG Schurr, JC Long, **NA Rosenberg**, MH Crawford, LA Tarskaia, LP Osipova, SI Zhadanov, DG Smith. A private allele ubiquitous in the Americas. *Biology Letters* 3: 218-223 (2007). [Link]

[34] L David, **NA Rosenberg**, U Lavi, MW Feldman, J Hillel. Genetic diversity and population structure inferred from the partially duplicated genome of domesticated carp, *Cyprinus carpio* L. *Genetics Selection Evolution* 39: 319-340 (2007). [Link]

[35] M Jakobsson, **NA Rosenberg**. The probability distribution under a population-genetic model of the number of genetic founding lineages of a population or species. *Theoretical Population Biology* 71: 502-523 (2007). [Link]

[36] **NA Rosenberg**, MGB Blum. Sampling properties of homozygosity-based statistics for linkage disequilibrium. *Mathematical Biosciences* 208: 33-47 (2007). [Link]

[37] **NA Rosenberg**. Counting coalescent histories. *Journal of Computational Biology* 14: 360-377 (2007). [Link]

[38] MGB Blum, **NA Rosenberg**. Estimating the number of ancestral lineages using a maximum-likelihood method based on rejection sampling. *Genetics* 176: 1741-1757 (2007). [Link]
　　[*Genetics* editorial highlight]

[39] M Jakobsson, **NA Rosenberg**. CLUMPP: a cluster matching and permutation program for dealing with label switching and multimodality in analysis of population structure. *Bioinformatics* 23: 1801-1806 (2007). [Link]

[40] S Wang*, CM Lewis Jr*, M Jakobsson*, S Ramachandran, N Ray, G Bedoya, W Rojas, MV Parra, JA Molina, C Gallo, G Mazzotti, G Poletti, K Hill, AM Hurtado, D Labuda, W Klitz, R Barrantes, MC Bortolini, FM Salzano, ML Petzl-Erler, LT Tsuneto, E Llop, F Rothhammer, L Excoffier, MW Feldman, **NA Rosenberg**[†], A Ruiz-Linares. Genetic variation and population structure in Native Americans. *PLoS Genetics* 3: 2049-2067 (2007). [Link]
　　[2015 *PLoS Genetics* 10th Anniversary Collection]

[41] K Zhang, **NA Rosenberg**. On the genealogy of a duplicated microsatellite. *Genetics* 177: 2109-2122 (2007). [Link]

[42] M Jakobsson*, SW Scholz*, P Scheet*, JR Gibbs, JM VanLiere, H-C Fung, ZA Szpiech, JH Degnan, K Wang, R Guerreiro, JM Bras, JC Schymick, DG Hernandez, BJ Traynor, J Simon-Sanchez, M Matarin, A Britton, J van de Leemput, I Rafferty, M Bucan, HM Cann, JA Hardy, **NA Rosenberg**[†], AB Singleton. Genotype, haplotype, and copy-number in worldwide human populations. *Nature* 451: 998-1003 (2008). [Link]

[43] **NA Rosenberg**, R Tao. Discordance of species trees with their most likely gene trees: the case of five taxa. *Systematic Biology* 57: 131-140 (2008). [Link]

[44] JM Macpherson, J González, DM Witten, JC Davis, **NA Rosenberg**, AE Hirsh, DA Petrov. Nonadaptive explanations for signatures of partial selective sweeps in *Drosophila*. *Molecular Biology and Evolution* 25: 1025-1042 (2008). [Link]

[45] O François, MGB Blum, M Jakobsson, **NA Rosenberg**. Demographic history of European populations of *Arabidopsis thaliana*. *PLoS Genetics* 4: e1000075 (2008). [Link]

[46] TJ Pemberton*, M Jakobsson*, DF Conrad, G Coop, JD Wall, JK Pritchard, PI Patel, **NA Rosenberg**. Using population mixtures to optimize the utility of genomic databases: linkage disequilibrium and association study design in India. *Annals of Human Genetics* 72: 535-546 (2008). [Link]

[47] JM VanLiere, **NA Rosenberg**. Mathematical properties of the r^2 measure of linkage disequilibrium. *Theoretical Population Biology* 74: 130-137 (2008). [Link]

[48] **NA Rosenberg**, M Jakobsson. The relationship between homozygosity and the frequency of the most frequent allele. *Genetics* 179: 2027-2036 (2008). [Link]
　　[*Genetics* editorial highlight]

[49] ZA Szpiech, M Jakobsson, **NA Rosenberg**. ADZE: A rarefaction approach for counting alleles private to combinations of populations. *Bioinformatics* 24: 2498-2504 (2008). [Link]

[50] S Ramachandran, **NA Rosenberg**, MW Feldman, J Wakeley. Population differentiation and migration: coalescence times in a two-sex island model for autosomal and X-linked loci. *Theoretical Population Biology* 74: 291-301 (2008). [Link]

[51] L Huang, Y Li, AB Singleton, JA Hardy, G Abecasis, **NA Rosenberg**, P Scheet. Genotype-imputation accuracy across worldwide human populations. *American Journal of Human Genetics* 84: 235-250 (2009). [Link]

[52] M DeGiorgio, **NA Rosenberg**. An unbiased estimator of gene diversity in samples containing related individuals. *Molecular Biology and Evolution* 26: 501-512 (2009). [Link]

[53] KB Schroeder, M Jakobsson, MH Crawford, TG Schurr, SM Boca, DF Conrad, R Titotadeo, LP Osipova, LA Tarskaia, SI Zhadanov, JD Wall, JK Pritchard, RS Malhi, DG Smith, **NA Rosenberg**. Haplotypic background of a private allele in the Americas. *Molecular Biology and Evolution* 26: 995-1016 (2009). [Link]

[54] JH Degnan, **NA Rosenberg**. Gene tree discordance, phylogenetic inference and the multispecies coalescent. *Trends in Ecology and Evolution* 24: 332-340. [Link]

[55] JH Degnan, M DeGiorgio, D Bryant, **NA Rosenberg**. Properties of consensus methods for inferring species trees from gene trees. *Systematic Biology* 58: 35-54 (2009). [Link]

[56] **NA Rosenberg**, JM VanLiere. Replication of genetic associations as pseudoreplication due to shared genealogy. *Genetic Epidemiology* 33: 479-487 (2009). [Link]

[57] M DeGiorgio, M Jakobsson, **NA Rosenberg**. Explaining worldwide patterns of human genetic variation using a coalescent-based serial founder model of migration outward from Africa. *Proceedings of the National Academy of Sciences USA* 106: 16057-16062 (2009). [Link]

[58] L Huang, C Wang, **NA Rosenberg**. The relationship between imputation error and statistical power in genetic association studies in diverse populations. *American Journal of Human Genetics* 85: 692-698 (2009). [Link]
   [*American Journal of Human Genetics* editorial highlight]
   [*Nature Reviews Genetics* editorial highlight]

[59] NM Kopelman, L Stone, C Wang, D Gefel, MW Feldman, J Hillel, **NA Rosenberg**. Genomic microsatellites identify shared Jewish ancestry intermediate between Middle Eastern and European populations. *BMC Genetics* 10: 80 (2009). [Link]

[60] TJ Pemberton, CI Sandefur, M Jakobsson, **NA Rosenberg**. Sequence determinants of human microsatellite variability. *BMC Genomics* 10: 612 (2009). [Link]

[61] JT Mosher, TJ Pemberton, K Harter, C Wang, EO Buzbas, P Dvorak, C Simón, SJ Morrison, **NA Rosenberg**. Lack of population diversity in commonly used human embryonic stem-cell lines. *New England Journal of Medicine* 362: 183-185 (2010). [Link]
   [*Nature* editorial highlight]

[62] C Wang, ZA Szpiech, JH Degnan, M Jakobsson, TJ Pemberton, JA Hardy, AB Singleton, **NA Rosenberg**. Comparing spatial maps of human population-genetic variation using Procrustes analysis. *Statistical Applications in Genetics and Molecular Biology* 9: 13 (2010). [Link]

[63] **NA Rosenberg**, JH Degnan. Coalescent histories for discordant gene trees and species trees. *Theoretical Population Biology* 77: 145-151 (2010). [Link]

[64] **NA Rosenberg**, L Huang*, EM Jewett*, ZA Szpiech*, I Jankovic*, M Boehnke. Genome-wide association studies in diverse populations. *Nature Reviews Genetics* 11: 356-366 (2010). [Link]

[65] I Jankovic, BM vonHoldt, **NA Rosenberg**. Heterozygosity of the Yellowstone wolves. *Molecular Ecology* 19: 3246-3249 (2010). [Link]

[66] E Borràs*, M Pineda*, I Blanco, EM Jewett, F Wang, A Teulé, T Caldés, M Urioste, C Martínez-Bouzas, J Brunet, J Balmaña, A Torres, T Ramón y Cajal, J Sanz, L Pérez-Cabornero, S Castellví-Bel, A Alonso, A Lanas, S González, V Moreno, SB Gruber, **NA Rosenberg**, B Mukherjee, C Lázaro, G Capellá. *MLH1* founder mutations with moderate penetrance in Spanish Lynch syndrome families. *Cancer Research* 70: 7379-7391 (2010). [Link]

[67] TJ Pemberton, C Wang, JZ Li, **NA Rosenberg**. Inference of unexpected genetic relatedness among individuals in HapMap Phase III. *American Journal of Human Genetics* 87: 457-464 (2010). [Link]
   [*American Journal of Human Genetics* editorial highlight]
   [*Genetics* editorial highlight]

[68] M DeGiorgio*, I Jankovic*, **NA Rosenberg**. Unbiased estimation of gene diversity in samples containing relatives: exact variance and arbitrary ploidy. *Genetics* 186: 1367-1387 (2010). [Link]

[69] CV Than, **NA Rosenberg**. Consistency properties of species tree inference by minimizing deep coalescences. *Journal of Computational Biology* 18: 1-15 (2011). [Link]

[70] EO Buzbas, P Joyce, **NA Rosenberg**. Inference on the strength of balancing selection for epistatically interacting loci. *Theoretical Population Biology* 79: 102-113 (2011). [Link]

[71] Z Yang, M Rosenthal, **NA Rosenberg**, S Talarico, L Zhang, C Marrs, VO Thomsen, T Lillebaek, AB Andersen. How dormant is *Mycobacterium tuberculosis* during latency? A study integrating genomics and molecular epidemiology. *Infection, Genetics and Evolution* 11: 1164-1167 (2011). [Link]

[72] ZA Szpiech, **NA Rosenberg**. On the size distribution of private microsatellite alleles. *Theoretical Population Biology* 80: 100-113 (2011). [Link]

[73] SM Boca, **NA Rosenberg**. Mathematical properties of F_{st} between admixed populations and their parental source populations. *Theoretical Population Biology* 80: 208-216 (2011). [Link]

[74] M DeGiorgio, JH Degnan, **NA Rosenberg**. Coalescence time distributions in a serial founder model of human evolutionary history. *Genetics* 189: 579-593 (2011). [Link]
   [*Genetics* editorial highlight]

[75] S Ramachandran, **NA Rosenberg**. A test of the influence of continental axes of orientation on patterns of human gene flow. *American Journal of Physical Anthropology* 146: 515-529 (2011). [Link]
   [*American Journal of Physical Anthropology* cover article]

[76] P Verdu, **NA Rosenberg**. A general mechanistic model for admixture histories of hybrid populations. *Genetics* 189: 1413-1426 (2011). [Link]
   [*Genetics* editorial highlight]

[77] L Huang*, M Jakobsson*, TJ Pemberton, M Ibrahim, T Nyambo, S Omar, JK Pritchard, SA Tishkoff, **NA Rosenberg**. Haplotype variation and genotype imputation in African populations. *Genetic Epidemiology* 35: 766-780 (2011). [Link]

[78] **NA Rosenberg**. A population-genetic perspective on the similarities and differences among worldwide human populations. *Human Biology* 83: 659-684 (2011). [Link]
   [Re-published in a 2020 compilation]

[79] JH Degnan, **NA Rosenberg**‡, T Stadler. The probability distribution of ranked gene trees on a species tree. *Mathematical Biosciences* 235: 45-55 (2012). [Link]

[80] FA San Lucas, **NA Rosenberg**, P Scheet. Haploscope: a tool for the graphical display of haplotype structure in populations. *Genetic Epidemiology* 36: 17-21 (2012). [Link]

[81] SB Reddy, **NA Rosenberg**. Refining the relationship between homozygosity and the frequency of the most frequent allele. *Journal of Mathematical Biology* 64: 87-108 (2012). [Link]

[82] EM Jewett, **NA Rosenberg**. iGLASS: an improvement to the GLASS method for estimating species trees from gene trees. *Journal of Computational Biology* 19: 293-315 (2012). [Link]

[83] LJ Helmkamp, EM Jewett, **NA Rosenberg**. Improvements to a class of distance matrix methods for inferring species trees from gene trees. *Journal of Computational Biology* 19: 632-649 (2012). [Link]

[84] D Bryant, R Bouckaert, J Felsenstein, **NA Rosenberg**, A RoyChoudhury. Inferring species trees directly from biallelic genetic markers: bypassing gene trees in a full coalescent analysis. *Molecular Biology and Evolution* 29: 1917-1932 (2012). [Link]

[85] TJ Pemberton, D Absher, MW Feldman, RM Myers, **NA Rosenberg**, JZ Li. Genomic patterns of homozygosity in worldwide human populations. *American Journal of Human Genetics* 91: 275-292 (2012). [Link]

[86] EM Jewett*, M Zawistowski*, **NA Rosenberg**†, S Zöllner. A coalescent model for genotype imputation. *Genetics* 191: 1239-1255 (2012). [Link]

[87] TJ Pemberton, F-Y Li, EK Hanson, NU Mehta, S Choi, J Ballantyne, JW Belmont, **NA Rosenberg**, C Tyler-Smith, PI Patel. Impact of restricted marital practices on genetic variation in an endogamous Gujarati group. *American Journal of Physical Anthropology* 149: 92-103 (2012). [Link]

[88] C Wang, S Zöllner, **NA Rosenberg**. A quantitative comparison of the similarity between genes and geography in worldwide human populations. *PLoS Genetics* 8: e1002886 (2012). [Link]
[*Science* editorial highlight]

[89] C Wang, KB Schroeder, **NA Rosenberg**. A maximum-likelihood method to correct for allelic dropout in microsatellite data with no replicate genotypes. *Genetics* 192: 651-669 (2012). [Link]

[90] JH Degnan, **NA Rosenberg**[‡], T Stadler. A characterization of the set of species trees that produce anomalous ranked gene trees. *IEEE/ACM Transactions on Bioinformatics and Computational Biology* 9: 1558-1568 (2012). [Link]

[91] NM Kopelman, L Stone, O Gascuel, **NA Rosenberg**. The behavior of admixed populations in neighbor-joining inference of population trees. *Pacific Symposium on Biocomputing* 18: 273-284 (2013). [Link]

[92] M DeGiorgio, **NA Rosenberg**. Geographic sampling scheme as a determinant of the major axis of genetic variation in principal components analysis. *Molecular Biology and Evolution* 30: 480-488 (2013). [Link]

[93] M Jakobsson, MD Edge, **NA Rosenberg**. The relationship between F_{ST} and the frequency of the most frequent allele. *Genetics* 193: 515-528 (2013). [Link]
[*Genetics* scientific commentary]
[*Genetics* editorial highlight]

[94] CV Than, **NA Rosenberg**. Mathematical properties of the deep coalescence cost. *IEEE/ACM Transactions on Bioinformatics and Computational Biology* 10: 61-72 (2013). [Link]

[95] TJ Pemberton, M DeGiorgio, **NA Rosenberg**. Population structure in a comprehensive data set on human microsatellite variation. *G3: Genes, Genomes, Genetics* 3: 891-907 (2013). [Link]

[96] ZA Szpiech, J Xu, TJ Pemberton, W Peng, S Zöllner, **NA Rosenberg**[†], JZ Li. Long runs of homozygosity are enriched for deleterious variation. *American Journal of Human Genetics* 93: 90-102 (2013). [Link]
[*American Journal of Human Genetics* editorial highlight]

[97] L Huang, EO Buzbas, **NA Rosenberg**. Genotype imputation in a coalescent model with infinitely-many-sites mutation. *Theoretical Population Biology* 87: 62-74 (2013). [Link]

[98] **NA Rosenberg**, TJ Pemberton, JZ Li, JW Belmont. Runs of homozygosity and parental relatedness. *Genetics in Medicine* 15: 753-754 (2013). [Link]

[99] P Zhang, X Zhan, **NA Rosenberg**, S Zöllner. Genotype imputation reference panel selection using maximal phylogenetic diversity. *Genetics* 195: 319-330 (2013). [Link]

[100] **NA Rosenberg**. Discordance of species trees with their most likely gene trees: a unifying principle. *Molecular Biology and Evolution* 30: 2709-2713 (2013). [Link]

[101] MD Edge, P Gorroochurn, **NA Rosenberg**. Windfalls and pitfalls: applications of population genetics to the search for disease genes. *Evolution, Medicine, and Public Health* 2013: 254-272 (2013). [Link]

[102] **NA Rosenberg**. Coalescent histories for caterpillar-like families. *IEEE/ACM Transactions on Computational Biology and Bioinformatics* 10: 1253-1262 (2013). [Link]

[103] PJ Oefner, G Hölzl, P Shen, I Shpirer, D Gefel, T Lavi, E Woolf, J Cohen, C Cinnioglu, PA Underhill, **NA Rosenberg**, J Hochrein, JM Granka, J Hillel, MW Feldman. Genetics and the history of the Samaritans: Y-chromosomal microsatellites and genetic affinity between Samaritans and Cohanim. *Human Biology* 85: 825-857 (2013). [Link]

[104]   DM Behar*, M Metspalu*, Y Baran, NM Kopelman, B Yunusbayev, A Gladstein, S Tzur, H Sahakyan, A Bahmanimehr, L Yepiskoposyan, K Tambets, EK Khusnutdinova, A Kushniarevich, O Balanovsky, E Balanovsky, L Kovacevic, D Marjanovic, E Mihailov, A Kouvatsi, C Trianta-phyllidis, RJ King, O Semino, A Torroni, MF Hammer, E Metspalu, K Skorecki, S Rosset, E Halperin, R Villems, **NA Rosenberg**. No evidence from genome-wide data of a Khazar origin for the Ashkenazi Jews. *Human Biology* 85: 859-900 (2013). [Link]

[105]   EM Jewett, **NA Rosenberg**. Theory and applications of a deterministic approximation to the coalescent model. *Theoretical Population Biology* 93: 14-29 (2014). [Link]

[106]   M DeGiorgio, J Syring, AJ Eckert, A Liston, R Cronn, DB Neale, **NA Rosenberg**. An empirical evaluation of two-stage species tree inference strategies using a multilocus dataset from North American pines. *BMC Evolutionary Biology* 14: 67 (2014). [Link]

[107]   CV Than, **NA Rosenberg**. Mean deep coalescence cost under exchangeable probability distri-butions. *Discrete Applied Mathematics* 174: 11-26 (2014). [Link]

[108]   TJ Pemberton, **NA Rosenberg**. Population-genetic influences on genomic estimates of the in-breeding coefficient: a global perspective. *Human Heredity* 77: 37-48 (2014). [Link]

[109]   P Verdu, TJ Pemberton, R Laurent, BM Kemp, A Gonzalez-Oliver, C Gorodezky, CE Hughes, MR Shattuck, B Petzelt, J Mitchell, H Harry, T William, R Worl, JS Cybulski, **NA Rosenberg**[†], RS Malhi. Patterns of admixture and population structure in native populations of northwest North America. *PLoS Genetics* 10: e1004530 (2014). [Link]
    [2021 *PLoS Genetics* curated collection on Human Genetic Admixture]

[110]   MD Edge, **NA Rosenberg**. Upper bounds on F_{ST} in terms of the frequency of the most frequent allele and total homozygosity: the case of a specified number of alleles. *Theoretical Population Biology* 97: 20-34 (2014). [Link]

[111]   A Goldberg, P Verdu, **NA Rosenberg**. Autosomal admixture levels are informative about sex bias in admixed populations. *Genetics* 198: 1209-1229 (2014). [Link]

[112]   F Disanto, **NA Rosenberg**. On the number of ranked species trees producing anomalous ranked gene trees. *IEEE/ACM Transactions on Computational Biology and Bioinformatics* 11: 1229-1238 (2014). [Link]

[113]   EO Buzbas, **NA Rosenberg**. AABC: approximate approximate Bayesian computation for infer-ence in population-genetic models. *Theoretical Population Biology* 99: 31-42 (2015). [Link]

[114]   N Creanza, M Ruhlen, T Pemberton, **NA Rosenberg**, MW Feldman, S Ramachandran. Com-parison of worldwide phonemic and genetic variation in human populations. *Proceedings of the National Academy of Sciences USA* 112: 1265-1272 (2015). [Link]
    [*Proceedings of the National Academy USA* scientific commentary]
    [*Proceedings of the National Academy USA* editorial highlight]
    [*Nature Reviews Genetics* editorial highlight]

[115]   NR Garud, **NA Rosenberg**. Enhancing the mathematical properties of new haplotype homozy-gosity statistics for the detection of selective sweeps. *Theoretical Population Biology* 102: 94-101 (2015). [Link]

[116]   MD Edge, **NA Rosenberg**. Implications of the apportionment of human genetic diversity for the apportionment of human phenotypic diversity. *Studies in History and Philosophy of Biological and Biomedical Sciences* 52: 32-45 (2015). [Link]

[117]   NM Kopelman, J Mayzel, M Jakobsson, **NA Rosenberg**, I Mayrose. CLUMPAK: a program for identifying clustering modes and packaging population structure inferences across K. *Molecular Ecology Resources* 15: 1179-1191 (2015). [Link]

[118]   **NA Rosenberg**, JTL Kang. Genetic diversity and societally important disparities. *Genetics* 201: 1-12 (2015). [Link]
    [2015 "*Genetics* Spotlight" Collection of Research and Scholarship Excellence]
    [Genetics Society of America *Genes to Genomes* editorial highlight]

[119] A Goldberg, **NA Rosenberg**. Beyond 2/3 and 1/3: the complex signatures of sex-biased admixture on the X chromosome. *Genetics* 201: 263-279 (2015). [Link]

[120] R Ronen*, G Tesler*, A Akbari*, S Zakov, **NA Rosenberg**, V Bafna. Predicting carriers of ongoing selective sweeps without knowledge of the favored allele. *PLoS Genetics* 11: e1005527 (2015). [Link]

[121] F Disanto, **NA Rosenberg**. Coalescent histories for lodgepole species trees. *Journal of Computational Biology* 22: 918-929 (2015). [Link]

[122] JTL Kang, P Zhang, S Zöllner, **NA Rosenberg**. Choosing subsamples for sequencing studies by minimizing the average distance to the closest leaf. *Genetics* 201: 499-511 (2015). [Link]
       [*Genetics* editorial highlight]

[123] MD Edge, **NA Rosenberg**. A general model of the relationship between the apportionment of human genetic diversity and the apportionment of human phenotypic diversity. *Human Biology* 87: 313-337 (2015). [Link]

[124] BFB Algee-Hewitt*, MD Edge*, J Kim, JZ Li, **NA Rosenberg**. Individual identifiability predicts population identifiability in forensic microsatellite markers. *Current Biology* 26: 935-942 (2016). [Link]

[125] M DeGiorgio, **NA Rosenberg**. Consistency and inconsistency of consensus methods for inferring species trees from gene trees in the presence of ancestral population structure. *Theoretical Population Biology* 110: 12-24 (2016). [Link]

[126] T Stadler, JH Degnan, **NA Rosenberg**. Does gene tree discordance explain the mismatch between macroevolutionary models and empirical patterns of tree shape and branching times? *Systematic Biology* 65: 628-639 (2016). [Link]

[127] RS Mehta, D Bryant, **NA Rosenberg**. The probability of monophyly of a sample of gene lineages on a species tree. *Proceedings of the National Academy of Sciences USA* 113: 8002-8009 (2016). [Link]

[128] F Disanto, **NA Rosenberg**. Asymptotic properties of the number of matching coalescent histories for caterpillar-like families of species trees. *IEEE/ACM Transactions on Computational Biology and Bioinformatics* 13: 913-925 (2016). [Link]

[129] LH Uricchio, T Warnow, **NA Rosenberg**. An analytical upper bound on the number of loci required for all splits of a species tree to appear in a set of gene trees. *BMC Bioinformatics* 17: 1266 (2016). [Link]

[130] JTL Kang, A Goldberg, MD Edge, DM Behar, **NA Rosenberg**. Consanguinity rates predict long runs of homozygosity in Jewish populations. *Human Heredity* 82: 87-102 (2016). [Link]

[131] OK Kamneva, **NA Rosenberg**. Simulation-based evaluation of hybridization network reconstruction methods in the presence of incomplete lineage sorting. *Evolutionary Bioinformatics* 13: 1176934317691935 (2017). [Link]

[132] A Goldberg, T Günther, **NA Rosenberg**, M Jakobsson. Ancient X chromosomes reveal contrasting sex bias in Neolithic and Bronze Age Eurasian migrations. *Proceedings of the National Academy of Sciences USA* 114: 2657-2662 (2017). [Link]

[133] A Goldberg, T Günther, **NA Rosenberg**, M Jakobsson. Robust model-based inference of male-biased admixture during Bronze Age migration from the Pontic-Caspian Steppe. *Proceedings of the National Academy of Sciences USA* 114: E3875-E3877 (2017). [Link]

[134] MD Edge, BFB Algee-Hewitt, TJ Pemberton, JZ Li, **NA Rosenberg**. Linkage disequilibrium matches forensic genetic records to disjoint genomic marker sets. *Proceedings of the National Academy of Sciences USA* 114: 5671-5676 (2017). [Link]

[135] N Alcala, **NA Rosenberg**. Mathematical constraints on F_{ST}: biallelic markers in arbitrarily many populations. *Genetics* 206: 1581-1600 (2017). [Link]

[136] OK Kamneva, J Syring, A Liston, **NA Rosenberg**. Evaluating allopolyploid origins in strawberries (*Fragaria*) using haplotypes generated from target capture sequencing. *BMC Evolutionary Biology* 17: 180 (2017). [Link]

[137] P Verdu*, EM Jewett*, TJ Pemberton, **NA Rosenberg**†, M Baptista. Parallel trajectories of genetic and linguistic admixture in a genetically admixed creole population. *Current Biology* 27: 2529-2535 (2017). [Link]

[138] F Disanto, **NA Rosenberg**. Enumeration of ancestral configurations for matching gene trees and species trees. *Journal of Computational Biology* 24: 831-850 (2017). [Link]

[139] IM Arbisser, EM Jewett, **NA Rosenberg**. On the joint distribution of tree height and tree length under the coalescent. *Theoretical Population Biology* 122: 46-56 (2018). [Link]

[140] TJ Pemberton*, P Verdu*, NS Becker, CJ Willer, BS Hewlett, S Le Bomin, A Froment, **NA Rosenberg**†, E Heyer. A genome scan for genes underlying adult body size differences between Central African hunter-gatherers and farmers. *Human Genetics* 137: 487-509 (2018). [Link]

[141] A Goldberg, LH Uricchio, **NA Rosenberg**. Natural selection in human populations. *Oxford Bibliographies in Evolutionary Biology* doi:10.1093/OBO/9780199941728-0112 (2018). [Link]

[142] AJ Aw, **NA Rosenberg**. Bounding measures of genetic similarity and diversity using majorization. *Journal of Mathematical Biology* 77: 711-737 (2018). [Link]

[143] J Kim, MD Edge, BFB Algee-Hewitt, JZ Li, **NA Rosenberg**. Statistical detection of relatives typed with disjoint forensic and biomedical loci. *Cell* 175: 848-858 (2018). [Link]

[144] **NA Rosenberg**. Enumeration of lonely pairs of gene trees and species trees by means of antipodal cherries. *Advances in Applied Mathematics* 102: 1-19 (2019). [Link]

[145] F Disanto, **NA Rosenberg**. On the number of non-equivalent ancestral configurations for matching gene trees and species trees. *Bulletin of Mathematical Biology* 81: 384-407 (2019). [Link]

[146] J Kim, F Disanto, NM Kopelman, **NA Rosenberg**. Mathematical and simulation-based analysis of the behavior of admixed taxa in the neighbor-joining algorithm. *Bulletin of Mathematical Biology* 81: 452-493 (2019). [Link]

[147] **NA Rosenberg**, MD Edge, JK Pritchard, MW Feldman. Interpreting polygenic scores, polygenic adaptation, and human phenotypic differences. *Evolution, Medicine, and Public Health* 2019: 26-34 (2019). [Link]
        [George C. Williams Prize, International Society for Evolution, Medicine & Public Health]

[148] F Disanto, **NA Rosenberg**. Enumeration of compact coalescent histories for matching gene trees and species trees. *Journal of Mathematical Biology* 78: 155-188 (2019). [Link]

[149] N Alcala, **NA Rosenberg**. G'_{ST}, Jost's D, and F_{ST} are similarly constrained by allele frequencies: a mathematical, simulation, and empirical study. *Molecular Ecology* 28: 1624-1636 (2019). [Link]

[150] AL Severson, S Carmi, **NA Rosenberg**. The effect of consanguinity on between-individual identity-by-descent sharing. *Genetics* 212: 305-316 (2019). [Link]

[151] N Alcala, AE Launer, MF Westphal, R Seymour, EM Cole*, **NA Rosenberg***. Use of stochastic patch occupancy models in the California red-legged frog for Bayesian inference regarding past events and future persistence. *Conservation Biology* 33: 685-696 (2019). [Link]

[152] RS Mehta, AF Feder, SM Boca, **NA Rosenberg**. The relationship between haplotype-based F_{ST} and haplotype length. *Genetics* 213: 281-295 (2019). [Link]
        [*Genetics* editorial highlight]

[153] N Alcala, A Goldberg, U Ramakrishnan, **NA Rosenberg**. Coalescent theory of migration network motifs. *Molecular Biology and Evolution* 36: 2358-2374 (2019). [Link]

[154] RS Mehta, **NA Rosenberg**. The probability of reciprocal monophyly of gene lineages in three and four species. *Theoretical Population Biology* 129: 133-147 (2019). [Link]

[155] G Greenbaum, WM Getz, **NA Rosenberg**, MW Feldman, E Hovers, O Kolodny. Disease transmission and introgression can explain the long-lasting contact zone of modern humans and Neanderthals. *Nature Communications* 10: 5003 (2019). [Link]

[156] G Greenbaum, A Rubin, AR Templeton, **NA Rosenberg**. Network-based hierarchical population structure analysis for large genomic datasets. *Genome Research* 29: 2020-2033 (2019). [Link]

[157] JTL Kang, **NA Rosenberg**. Mathematical properties of linkage disequilibrium statistics defined by normalization of the coefficient $D = p_{AB} - p_A p_B$. *Human Heredity* 84: 127-143 (2019). [Link]

[158] ZM Himwich, **NA Rosenberg**. Roadblocked monotonic paths and the enumeration of coalescent histories for non-matching caterpillar gene trees and species trees. *Advances in Applied Mathematics* 113: 101939 (2020). [Link]

[159] **NA Rosenberg**, DM Zulman. Measures of care fragmentation: mathematical insights from population genetics. *Health Services Research* 55: 318-327 (2020). [Link]
    [James F. Burgess Methods Article-of-the-Year in *Health Services Research*]

[160] A Kim, **NA Rosenberg**, JH Degnan. Probabilities of unranked and ranked anomaly zones under birth–death models. *Molecular Biology and Evolution* 5: 1480-1494 (2020). [Link]

[161] NM Kopelman, L Stone, DG Hernandez, D Gefel, AB Singleton, E Heyer, MW Feldman, J Hillel, **NA Rosenberg**. High-resolution inference of genetic relationships among Jewish populations. *European Journal of Human Genetics* 28: 804-814 (2020). [Link]

[162] IM Arbisser, **NA Rosenberg**. F_{ST} and the triangle inequality for biallelic markers. *Theoretical Population Biology* 133: 117-129 (2020). [Link]

[163] RS Mehta, **NA Rosenberg**. Modelling anti-vaccination sentiment as a cultural pathogen. *Evolutionary Human Sciences* 2: e21. [Link]

[164] A Goldberg, A Rastogi, **NA Rosenberg**. Assortative mating by population of origin in a mechanistic model of admixture. *Theoretical Population Biology* 134: 129-146 (2020). [Link]

[165] AL Fortier, J Kim, **NA Rosenberg**. Human-genetic ancestry inference and false positives in forensic familial searching. *G3: Genes, Genomes, Genetics* 10: 2893-2902 (2020). [Link]

[166] J Kim, **NA Rosenberg**, JA Palacios. Distance metrics for ranked evolutionary trees. *Proceedings of the National Academy of Sciences USA* 117: 28876-28886 (2020). [Link]

[167] SM Boca, L Huang, **NA Rosenberg**. On the heterozygosity of an admixed population. *Journal of Mathematical Biology* 81: 1217-1250 (2020). [Link]

[168] **NA Rosenberg**. On the Colijn-Plazzotta numbering scheme for unlabeled binary rooted trees. *Discrete Applied Mathematics* 291: 88-98 (2021). [Link]

[169] A Harpak, N Garud, **NA Rosenberg**, DA Petrov, M Combs, PS Pennings, J Munshi-South. Genetic adaptation in New York City rats. *Genome Biology and Evolution* 13: evaa247 (2021). [Link]

[170] G Greenbaum, MW Feldman, **NA Rosenberg**, J Kim. Designing gene drives to limit spillover to non-target populations. *PLoS Genetics* 17: e1009278 (2021). [Link]

[171] J Kim, MD Edge, A Goldberg, **NA Rosenberg**. Skin deep: the decoupling of genetic admixture levels from phenotypes that differed between source populations. *American Journal of Physical Anthropology* 175: 406-421 (2021). [Link]

[172] AL Severson, S Carmi, **NA Rosenberg**. Variance and limiting distribution of coalescence times in a diploid model of a consanguineous population. *Theoretical Population Biology* 139: 50-65 (2021). [Link]

[173] DJ Cotter, AL Severson, **NA Rosenberg**. The effect of consanguinity on coalescence times on the X chromosome. *Theoretical Population Biology* 140: 32-43 (2021). [Link]

[174] E Alimpiev, **NA Rosenberg**. Enumeration of coalescent histories for caterpillar species trees and p-pseudocaterpillar gene trees. *Advances in Applied Mathematics* 131: 102265 (2021). [Link]

[175] MC King, **NA Rosenberg**. A simple derivation of the mean of the Sackin index of tree balance under the uniform model on rooted binary labeled trees. *Mathematical Biosciences* 342: 108688 (2021). [Link]

[176] E Alimpiev, **NA Rosenberg**. A compendium of covariances and correlation coefficients of coalescent tree properties. *Theoretical Population Biology* 143: 1-13 (2022). [Link]

[177] AL Severson, BF Byrd, EK Mallott, AC Owings, M DeGiorgio, A de Flamingh, C Nijmeh, MV Arellano, A Leventhal, **NA Rosenberg**†, RS Malhi. Ancient and modern genomics of the Ohlone Indigenous population of California. *Proceedings of the National Academy of Sciences USA* 119: e2111533119 (2022). [Link]

[178] N Alcala, **NA Rosenberg**. Mathematical constraints on F_{ST}: multiallelic markers in arbitrarily many populations. *Philosophical Transactions of the Royal Society of London B: Biological Sciences* 377: 20200414 (2022). [Link]

[179] JA Palacios, A Bhaskar, F Disanto, **NA Rosenberg**. Enumeration of binary trees compatible with a perfect phylogeny. *Journal of Mathematical Biology* 84: 54 (2022). [Link]

[180] X Liu, **NA Rosenberg**†, G Greenbaum. Extracting hierarchical features of cultural variation using network-based clustering. *Evolutionary Human Sciences* 4: e18 (2022). [Link]

[181] RS Mehta, M Steel, **NA Rosenberg**. The probability of joint monophyly of samples of gene lineages for all species in an arbitrary species tree. *Journal of Computational Biology* 29: 679-703 (2022). [Link]

[182] DJ Cotter, AL Severson, S Carmi, **NA Rosenberg**. Limiting distribution of X-chromosomal coalescence times under first-cousin consanguineous mating. *Theoretical Population Biology* 147: 1-15 (2022). [Link]

[183] ML Morrison, N Alcala, **NA Rosenberg**. FSTruct: an F_{ST}-based tool for measuring ancestry variation in inference of population structure. *Molecular Ecology Resources* 22: 2614-2626 (2022). [Link]

[184] E Lappo, **NA Rosenberg**. Approximations to the expectations and variances of ratios of tree properties under the coalescent. *G3: Genes, Genomes, Genetics* 12: jkac205 (2022). [Link]

[185] F Disanto, M Fuchs, A Paningbatan, **NA Rosenberg**‡. The distributions under two species-tree models of the number of root ancestral configurations for matching gene trees and species trees. *Annals of Applied Probability* 32: 4426-4458 (2022). [Link]

[186] S Mathur, **NA Rosenberg**. All galls are divided into three or more parts: recursive enumeration of labeled histories for galled trees. *Algorithms in Molecular Biology* 18: 1 (2023). [Link]

[187] DJ Cotter, EF Hofgard, J Novembre, ZA Szpiech, **NA Rosenberg**. A rarefaction approach for measuring population differences in rare and common variation. *Genetics* 2: iyad070 (2023). [Link]

[188] R Laurent, ZA Szpiech, SS da Costa, V Thouzeau, CA Fortes-Lima, F Dessarps-Freichey, L Lémée, J Utgé, **NA Rosenberg**, M Baptista, P Verdu. A genetic and linguistic analysis of the admixture histories of the islands of Cabo Verde. *eLife* 12: e79827 (2023). [Link]

[189] JA Mooney, L Agranat-Tamir, JK Pritchard, **NA Rosenberg**. On the number of genealogical ancestors tracing to the source groups of an admixed population. *Genetics* 224: iyad079 (2023). [Link]
    [Genetics Society of America *Genes to Genomes* editorial highlight]
    [*Genetics* cover article]

[190] X Liu, NM Kopelman, **NA Rosenberg**. A Dirichlet model of alignment cost in mixed-membership unsupervised clustering. *Journal of Computational and Graphical Statistics* in press (2023). [Link]

[191] MC King, **NA Rosenberg**. A mathematical connection between single-elimination sports tournaments and evolutionary trees. *Mathematics Magazine* in press (2023).

[192] J Kim, **NA Rosenberg**. Record-matching of STR profiles with fragmentary genomic SNP data. *European Journal of Human Genetics* in press (2023).

Author order follows the style of biosciences disciplines except where otherwise noted
*Equal authorship
†Corresponding author or joint senior author (only marked if not the first or last author)
‡Author order is alphabetical in accord with the convention of the associated discipline

PEER-REVIEWED BOOK CHAPTERS

[B1] **NA Rosenberg**, MW Feldman. The relationship between coalescence times and population divergence times. Chapter 9, pp. 130-164 in M Slatkin and M Veuille, eds. *Modern Developments in Theoretical Population Genetics*. Oxford: Oxford University Press (2002).

[B2] **NA Rosenberg**. Gene genealogies. Chapter 12, pp. 173-189 in CW Fox and JB Wolf, eds. *Evolutionary Genetics: Concepts and Case Studies*. Oxford: Oxford University Press (2006).

[B3] **NA Rosenberg**. Variance-partitioning and classification in human population genetics. Pp. 399-403 in RG Winther, ed. *Phylogenetic Inference, Selection Theory, and History of Science: Selected Papers of A. W. F. Edwards with Commentaries*. Cambridge: Cambridge University Press (2018).

SCIENTIFIC AND HISTORICAL COMMENTARIES

[H1] **NA Rosenberg**. Admixture models and the breeding systems of H. S. Jennings: a *Genetics* connection. *Genetics* 202: 9-13 (2016). [Peer-reviewed commentary] [Link]

[H2] L Altenberg, N Creanza, L Fogarty, L Hadany, O Kolodny, KN Laland, L Lehmann, SP Otto, **NA Rosenberg**, J Van Cleve, J Wakeley. Some topics in theoretical population genetics: editorial commentaries on a selection of Marc Feldman's *TPB* papers. *Theoretical Population Biology* 129: 4-8 (2019). [Peer-reviewed commentary] [Link]

[H3] **NA Rosenberg**. A population-genetic perspective on the similarities and differences among worldwide human populations. *Human Biology* 92: 135-152 (2020). [New foreword added to re-published article] [Link]

[H4] **NA Rosenberg**. Mendel of mathematics. *Notices of the American Mathematical Society* 69: 1564-1565 (2022). [Peer-reviewed commentary] [Link]

EDITORIALS

[E1] LK Nakhleh, **NA Rosenberg**, T Warnow. Phylogenomics and population genomics: models, algorithms, and analytical tools. *Pacific Symposium on Biocomputing* 18: 247-249 (2013). [Introduction to collection of articles] [Link]

[E2] **NA Rosenberg**. Editorial. *Theoretical Population Biology* 83: A2-A3 (2013). [Editorial] [Link]

[E3] **NA Rosenberg**, SP Weitzman. From generation to generation: the genetics of Jewish populations. *Human Biology* 85: 817-823 (2013). [Introduction to special issue] [Link]

[E4] **NA Rosenberg**. Core elements of a *TPB* paper. *Theoretical Population Biology* 92: 118-119 (2014). [Editorial] [Link]

[E5] **NA Rosenberg**. Theory in population biology, or biologically inspired mathematics? *Theoretical Population Biology* 102: 1-2 (2015). [Editorial] [Link]

[E6] L Lehmann, **NA Rosenberg**. Hamilton's rule: game theory meets coalescent theory. *Theoretical Population Biology* 103: 1 (2015). [Editorial] [Link]

[E7] **NA Rosenberg**. The 2018 Marcus W. Feldman prize in theoretical population biology. *Theoretical Population Biology* 119: 1-2 (2018). [Editorial] [Link]

[E8] AL Severson*, LH Uricchio*, IM Arbisser*, EC Glassberg, **NA Rosenberg**. Analysis of author gender in *TPB*, 1991-2018. *Theoretical Population Biology* 127: 1-6 (2019). [Editorial] [Link]

[E9] **NA Rosenberg**. Fifty years of *Theoretical Population Biology*. *Theoretical Population Biology* 133: 1-12 (2020). [Introduction to special issue] [Link]

[E10] **NA Rosenberg**. Population models, mathematical epidemiology, and the COVID-19 pandemic. *Theoretical Population Biology* 137: 1 (2021). [Editorial] [Link]

[E11] **NA Rosenberg**, MF Boni. Mathematical epidemiology for a later age. *Theoretical Population Biology* 144: 81-83 (2022). [Editorial] [Link]

[E12] MD Edge, S Ramachandran, **NA Rosenberg**. Celebrating 50 years since Lewontin's apportionment of human diversity. *Philosophical Transactions of the Royal Society of London B: Biological Sciences* 377: 20200405 (2022). [Introduction to special issue] [Link]

BOOK REVIEWS AND MEETING REPORTS

[R1] **NA Rosenberg**, D Nettle. Joining forces to infer human evolutionary history. *Trends in Ecology and Evolution* 17: 301-302 (2002). [Meeting report] [Link]

[R2] **NA Rosenberg**. Review of *Probability Models for DNA Sequence Evolution* by R Durrett. *Journal of the American Statistical Association* 99: 560-561 (2004). [Book review] [Link]

[R3] **NA Rosenberg**. Review of *First Peoples in a New World: Colonizing Ice Age America* by DJ Meltzer. *Quarterly Review of Biology* 85: 380-381 (2010). [Book review] [Link]

PROBLEMS AND SOLUTIONS

[P1] **N Rosenberg**. Solution to Problem 1445. *Mathematics Magazine* 68: 150 (1995). [Link]

[P2] **N Rosenberg**, R Stong. Problem 11039. *American Mathematical Monthly* 110: 743 (2003). [Link]

CONTRIBUTIONS TO THE ON-LINE ENCYCLOPEDIA OF INTEGER SEQUENCES OEIS.ORG

[O1] New sequences added (2019): [A306205], [A306266], [A306292], [A306295], [A306350], [A306364], [A306390], [A306391], [A306402], [A306422], [A306423]

[O2] New sequences added (2022): [A354468], [A354690], [A354970], [A355044], [A355108], [A355118]

[O3] Miscellaneous edits to ∼20 existing sequences (2019, 2022).

ABSTRACTS AND CONFERENCE PAPERS

[A1] DM Zulman, **NA Rosenberg**, ZH Cuevas, DM Yaurima. Prevalence of iron deficiency anemia in the state of Campeche, Mexico. *Journal of Investigative Medicine* 51: S92 (2003). [Published abstract for unpublished paper]

[A2] R Ronen, G Tesler, A Akbari, S Zakov, **NA Rosenberg**, V Bafna. Haplotype allele frequency (HAF) score: predicting carriers of ongoing selective sweeps without knowledge of the adaptive allele. *Lecture Notes in Computer Science* 9029: 276-280 (2015). [RECOMB conference paper superseded by article 120] [Link]

[A3] RS Mehta, D Bryant, **NA Rosenberg**. The probability of monophyly of a sample of gene lineages on a species tree. Chapter 6, pp. 113-135 in JC Avise and FJ Ayala, eds. *In the Light of Evolution, Volume X: Comparative Phylogeography*. Washington, DC: National Academies Press (2017). [Conference volume republishing article 127]

SELECTED INFORMATIONAL NOTES ON PUBLICATIONS

Undergraduate research: Articles 43, 49, 64, 65, 68, 81, 111, 142, 158, 164, 174, 175, 176, and 184 include the contributions of undergraduate researchers. Undergraduates are first author of articles 49, 65, 81, 111, 142, 158, 174, 175, 176, and 184.

Review articles: Articles 8, 54, 64, 78, 101, 118, 141, and 147 are articles that have a primary purpose of reviewing or synthesizing an area of the literature.

Software articles: Articles 17, 39, 49, 80, and 117 are articles that are structured as presentations of software packages.

Correspondence articles: Articles 65 and 98 are letters to the editor. Articles 11 and 133 are responses to letters to the editor.

Articles featured in special issues: Articles 26, 57, 75, 83, 91, 97, 103, 104, 108, 116, 123, 127, 139, 145, 146, 154, 162, 171, 178, and 181 and commentaries and editorials E1, E3, E9, E12, H1, H2, and H3 appear in thematic collections.
26: Phylogenetic combinatorics and its applications
57: Out of Africa: modern human origins
75: New developments in the origins and evolution of Native American populations
83: Birthdays of Mike Waterman and Simon Tavaré
91, E1: Phylogenomics and population genomics: models, algorithms, and analytical tools
97: Coalescent theory
103, 104, E3: From generation to generation: the genetics of Jewish populations
108: Consanguinity and genomics
116: Genomics and philosophy of race
123: The genetic anthropologist's contribution to understanding race and racial health disparities
H1: *Genetics* centennial
127: In the light of evolution X: comparative phylogeography
139: Paul Joyce
145, 146: Algebraic methods in phylogenetics
154, H2: Special issue in honor of Marcus Feldman's 75th birthday
162, E9: Fifty years of *Theoretical Population Biology*
H3: Race, racism, and the genetic structure of human populations
171: Race reconciled II: Interpreting and communicating biological variation and race in 2021
178, E12: Celebrating 50 years since Lewontin's apportionment of human diversity
181: Professor Michael Waterman's 80th birthday, part 1

SELECTED RECOGNITION FOR INDIVIDUAL ARTICLES

Commentaries: Articles 9, 30, 93, and 114 have been featured in scientific commentaries in *Current Biology* (9), *Genetics* (93), *Nature Genetics* (9, 30), *Proceedings of the National Academy of Sciences USA* (114), and *Science* (9).

Covers: Articles 30, 42, 68, 75, 189 are connected to journal covers. Journals include *Nature Genetics* (cover image associated with 30), *Studies in History and Philosophy of Biological and Biomedical Sciences* (cover image inspired by 42), *American Journal of Human Genetics* (cover image inspired by 68), *American Journal of Physical Anthropology* (cover image associated with 75), and *Genetics* (cover image associated with 189).

Editorial highlights: Articles 15, 30, 38, 48, 58, 61, 67, 74, 76, 88, 93, 96, 114, 122, and 152 have been featured in editor's highlights in *American Journal of Human Genetics* (15, 58, 67, 96), *Genetics* (38, 48, 67, 74, 76, 93, 122, 152), *Nature* (61), *Nature Reviews Genetics* (30, 58, 114), *Proceedings of the National Academy of Sciences USA* (114), and *Science* (88).

Research highlight services: Articles 21, 23, 36, 42, 45, 96, 146, 158, 168, 179, and 181 have been highlighted by research highlight services. Articles have been highlighted in curated comments by Mathematical Reviews (26, 36, 146, 158, 168, 179, 181) and Faculty of 1000 (21, 23, 42, 45, 96).

Special recognition: Articles 9, 10, 40, 78, 109, 118, 147, and 159 have received notable special recognition. Article 9 was named *The Lancet* Biomedical Research Paper of the Year (*Lancet* 362: 2101-2103, 2003); article 10 was listed in the *Discover* Top 100 Science Stories of 2003 (*Discover* 25: 56, 2004); article 40 was named by *PLoS Genetics* to the top ten research articles in the first ten years of the journal (*PLoS Genetics* 11: e1005557, 2015); article 78 was selected for republication in a special issue of *Human Biology*; article 109 was named to the 2021 *PLoS Genetics* collection on Human Genetic Admixture; article 118 was named to the 2015 *Genetics Spotlight* highlighting selected articles from the journal *Genetics* that were published in 2015; article 147 received the George C. Williams Prize for an outstanding paper in *Evolution, Medicine & Public Health*; article 159 was selected as the James F. Burgess Methods Article-of-the-Year in *Health Services Research*.

Media reports: Articles 9, 10, 23, 31, 33, 40, 42, 53, 61, 67, 75, 104, 114, 118, 124, 132, 134, 137, 143, 155, 169, 170, and 177 have appeared in news stories. Venues have included *Alaska Public Radio*, *CNN*, *Current World Archaeology*, *Discover*, *Genome Technology*, *Geotimes*, *National Geographic News*, *Nature*, *New Scientist*, *Science*, *Science News*, *Scientific American*, *StatNews*, *Vox*, *Wired*, and the *Detroit Free Press*, *Los Angeles Times*, *New York Times*, *Philadelphia Inquirer*, *San Francisco Chronicle*, *San Jose Mercury News*, *Wall Street Journal*, and *Washington Post*. Coverage has been extensive for articles 9, 40, 42, 75, 114, 143, and 177.