

# Noah A. Rosenberg

DEPARTMENT OF BIOLOGY  
STANFORD UNIVERSITY  
STANFORD, CA 94305-5020 USA  
(650) 721-2599 (PHONE)  
(650) 724-5114 (FAX)  
NOAHR@STANFORD.EDU  
[HTTP://ROSENBERGLAB.STANFORD.EDU/](http://ROSENBERGLAB.STANFORD.EDU/)  
July 17, 2013

## Academic appointments

- 2011- *Associate Professor*, Department of Biology, Stanford University
- 2009-2011 *Associate Professor*, Departments of Human Genetics, Ecology & Evolutionary Biology, and Biostatistics, University of Michigan; *Research Associate Professor*, Life Sciences Institute and Center for Computational Medicine & Bioinformatics, University of Michigan
- 2005-2009 *Assistant Professor*, Departments of Human Genetics, Ecology & Evolutionary Biology (2006-2009), and Biostatistics, University of Michigan; *Research Assistant Professor*, Life Sciences Institute and Center for Computational Medicine & Bioinformatics, University of Michigan

## Education

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

## Awards

### Fellowships

- 2007 Faculty Research Grant, University of Michigan Rackham Graduate School
- 2006 Faculty Fellowship Enhancement Award, University of Michigan Rackham Graduate School
- 2006-2010 Alfred P. Sloan Research Fellowship in Computational and Evolutionary Molecular Biology
- 2004-2014 Burroughs Wellcome Fund Career Award in the Biomedical Sciences
- 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
- 1996-1997 Barry M. Goldwater Scholarship

### Honors

- 2010 Dean's Basic Science Research Award, University of Michigan Medical School
- 2007 Alumni Distinguished Leadership Award, Illinois Mathematics and Science Academy
- 2005 Biological Sciences Scholar, University of Michigan Medical School

- 2003 *The Lancet* Biomedical Research Paper of the Year Award
- 1997 Phi Beta Kappa
- 1996 Hubert E. Bray Prize in Mathematics, Rice University

## Scholarly activities

### Editorial boards

- 2013- Editor-in-Chief, *Theoretical Population Biology*
- 2011- Associate Editor, *Molecular Biology and Evolution*
- 2010- Associate Editor, *BMC Bioinformatics*
- 2010- Editorial Board Member, *Human Biology*
- 2010- Associate Editor, *Genetics*
- 2009-2012 Associate Editor, *Theoretical Population Biology*
- 2008-2010 Associate Editor, *American Journal of Human Genetics*

### Editing of special collections of articles

- 2013 From generation to generation: the genetics of Jewish populations; issue of *Human Biology* in progress (with S. Weitzman)
- 2013 Phylogenomics and population genomics: models, algorithms, and analytical tools; section of *Pacific Symposium on Biocomputing* (with L. Nakhleh and T. Warnow)

### Reviewing activities

- 2013 Provocative Questions Initiative workshop panelist, National Cancer Institute
- 2010-2014 Genome Research Review Committee (GNOM-G) standing member, National Human Genome Research Institute, National Institutes of Health
- 2010- External examiner for PhD defenses (National University of Singapore, University of Auckland)
- 2010- External referee for appointments and promotions (various)
- 2009 National Human Genome Research Institute 1000 Genomes Project Dataset Analysis Special Emphasis Panel
- 2009 Ad hoc grant reviewer for National Institutes of Health (Genomes & Genetics American Recovery and Reinvestment Act challenge grants)
- 2006- Guest Associate Editor, *PLoS Genetics* (2006, 2008, 2011)
- 2004- Ad hoc grant reviewer for National Science Foundation (Dimensions of Biodiversity, Plant Genome Research, Population and Evolutionary Processes, Systematic Biology and Biodiversity Inventories)
- 2005- Ad hoc grant reviewer for ~10 additional organizations (Austrian Science Fund, Columbia University Research Initiatives in Science and Engineering, Estonian Science Fund, Finnish Academy, German Research Foundation, Israel Science Foundation, Netherlands Genomics Initiative, Royal Society of New Zealand Marsden Fund, United Kingdom Biotechnology and Biological Sciences Research Council, United Kingdom Natural Environment Research Council, Wellcome Trust)
- 2004- Book proposal reviewer (Elsevier, Roberts & Company)

- 1999- Manuscript reviewer for ~50 journals (*ACM Transactions on Algorithms*, *American Journal of Human Genetics*, *American Journal of Physical Anthropology*, *Annals of Combinatorics*, *Annals of Human Genetics*, *BioEssays*, *Bioinformatics*, *BMC Bioinformatics*, *BMC Evolutionary Biology*, *British Journal for the Philosophy of Science*, *Bulletin of the Institute of Combinatorics and its Applications*, *Conservation Genetics*, *Current Biology*, *DNA Repair*, *European Journal of Human Genetics*, *Evolution*, *G3: Genes, Genomes, Genetics*, *Genetic Epidemiology*, *Genetics*, *Genetics Research*, *Genome Research*, *Heredity*, *Human Genetics*, *Human Genomics*, *Human Heredity*, *Human Molecular Genetics*, *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, *Journal of the Association for Computing Machinery*, *Journal of Bioinformatics and Computational Biology*, *Journal of Mathematical Biology*, *Journal of Molecular Evolution*, *Journal of Theoretical Biology*, *Mathematical Population Studies*, *Molecular Biology and Evolution*, *Molecular Ecology*, *Molecular Phylogenetics and Evolution*, *Nature*, *Nature Genetics*, *Nature Reviews Genetics*, *New England Journal of Medicine*, *Pacific Symposium on Biocomputing*, *Pharmacogenomics Journal*, *PLoS Biology*, *PLoS Computational Biology*, *PLoS Genetics*, *PLoS One*, *Proceedings of the National Academy of Sciences USA*, *Proceedings of the Royal Society of London Series B: Biological Sciences*, *Science*, *Statistical Applications in Genetics and Molecular Biology*, *Statistics in Medicine*, *Theoretical Population Biology*, *Trends in Ecology and Evolution*, *Trends in Pharmacological Sciences*)

## Conference activities

- 2013 Program committee, “Why we can’t wait: conference to eliminate health disparities in genomic medicine”
- 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 service

### Stanford University (2011-present)

- 2013- Fellowships committee (Chair), Center for Computational, Evolutionary, and Human Genomics
- 2012- Executive committee, Center for Computational, Evolutionary, and Human Genomics
- 2012- New building committee, Department of Biology
- 2012- Graduate admissions committee, Department of Biology
- 2012- Member, Taube Center for Jewish Studies

### University of Michigan (2005-2011)

- 2010-2011 Faculty search committee, Department of Ecology & Evolutionary Biology
- 2010-2011 Executive committee, Training Program in Genomic Science
- 2008-2009 Faculty search committee, Department of Human Genetics
- 2006-2011 Graduate admissions committee (Chair, 2008-2009), Bioinformatics Graduate Program

- 2008-2011 Member, Center for Genetics in Health and Medicine  
 2008 Postdoctoral fellowship selection committee, Center for Genetics in Health and Medicine  
 2007-2009 Curriculum committee, Bioinformatics Graduate Program  
 2006 Faculty search committee, Ophthalmology/Human Genetics/Biostatistics  
 2005-2007 Organizer, Population Genetics Rackham Interdisciplinary Workshop  
 2005-2011 Member, Center for Statistical Genetics  
 2005-2011 Member, Training Program in Genomic Science

### Selected training activities

- 2003-2005 Guest lecturer, University of Southern California (Molecular Genetics & Biochemistry, Special Topics in Population Genetics & Molecular Evolution, Computational Biology Laboratory)  
 2000 Extended visit to the laboratory of Professor Jossi Hillel, Hebrew University of Jerusalem  
 1999 Complex Systems Summer School, Santa Fe Institute  
 1999 NATO-ASI Workshop on Mathematical Problems Arising from Biology, University of Toronto  
 1999-2000 Teaching assistant, Stanford University (Evolutionary Paleobiology, Advanced Genetics, Biostatistics)  
 1999-2000 Guest lecturer, Stanford University (Evolutionary Paleobiology, Biostatistics, Theoretical Population Genetics)  
 1998 Program in Mathematics & Molecular Biology Short Course, University of California, Berkeley  
 1997 Mathematics Student, United States Department of Defense, Fort Meade, MD  
 1996 William Lowell Putnam Mathematical Competition top 100 students  
 1995-1996 Undergraduate Research Fellow, Keck Center for Computational Biology, Rice University

## Grant support

### Research grants

- 2011-2014 National Science Foundation DBI-1146722. *Novel methodologies for genome-scale evolutionary analysis of multi-locus data*. Principal investigator, \$467,429 total costs, 7/1/2011-6/30/2014.  
 2010-2013 National Science Foundation BCS-1024627. *Anthropological-genomic effects of European colonization on Native North Americans*. Principal investigator, \$31,000 average annual direct costs, 9/15/2010-8/31/2013.  
 2010-2015 National Institutes of Health R01 HG005855. *Advanced strategies for genotype imputation*. Principal investigator (multiple PI grant with S. Zöllner), \$244,519 average annual direct costs, 9/13/2010-6/30/2015.  
 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, \$500,000 total costs, 9/1/2004-8/31/2014.  
 2007-2013 National Institutes of Health R01 GM081441. *Population-genetic studies for association mapping*. Principal investigator, \$1,422,981 total costs, 5/1/2007-4/30/2013.  
 2012 Stanford Center for Population Research. *Genetic and linguistic admixture in Cape Verdean populations*. Principal investigator, \$2,760 total direct costs, 2012.

- 2009-2011 National Institutes of Health R01 GM081441. American Recovery and Reinvestment Act administrative supplement to *Population-genetic studies for association mapping*. Principal investigator, \$321,124 total costs, 8/31/2009-7/31/2011.
- 2007-2011 National Science Foundation DEB-0716904. *Theory of gene trees and species trees*. Principal investigator, \$442,000 total costs, 8/1/2007-7/31/2011.
- 2009-2011 University of Michigan/Israeli Universities Partnership. *Genetic relationships among Jewish populations*. Principal investigator, \$200,000 total direct costs, 2/1/2009-3/31/2011.
- 2006-2011 Horace H. Rackham Graduate School at the University of Michigan, Faculty Fellowship Enhancement Award. Principal investigator, \$3,000 total direct costs, 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), \$54,873 total direct costs, 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), \$15,470 total direct costs, 9/1/2009-12/31/2010.
- 2008 National Institutes of Health R01 AI078752. *HIV risk dynamics, genetic patterns, and control*. Co-investigator (J. Koopman, PI), \$2,441 total direct costs, 7/2/2008-10/31/2008.
- 2007-2010 University of Michigan/Israeli Universities Partnership. *Genetic relationships among Jewish populations*. Principal investigator, \$25,000 total direct costs, 7/1/2007-6/30/2010.
- 2007 Horace H. Rackham Graduate School at the University of Michigan, Faculty Research Award. Principal investigator, \$22,419 total direct costs, 5/1/2007-12/31/2007.
- 2006-2010 Alfred P. Sloan Research Fellowship in Computational and Evolutionary Molecular Biology. Principal investigator, \$45,000 total direct costs, 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), \$79,755 total direct costs, 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, \$50,000 total direct costs, 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, \$25,000 total direct costs, 9/1/2004-8/31/2005.

## Grants for educational activities

- 2013 Stanford Center for Population Research. *From generation to generation: the genetics of Jewish populations*. Principal investigator, \$2,000 total direct costs, 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, \$9,000 total direct costs, 1/1/2007-12/31/2009.
- 2006-2009 Horace H. Rackham Graduate School at the University of Michigan. *Population genetics workshop*. Principal investigator, \$12,000 total direct costs, 9/1/2006-12/31/2009.

## Invited research talks

### External

- 2013 Society for Molecular Biology and Evolution Annual Meeting, Chicago  
Why we can't wait: conference to eliminate 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
- 2012 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.  
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
- 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

## Internal

### Stanford University (2011-present)

- 2013 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)

**Mentorship****Postdoctoral fellows**

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Dates	Name	Current position
2013-	Olga Kamneva	
2012-	Lars Andersen	
2009-2012	Cuong Than	Postdoc, University of Tübingen
2009-2012	Paul Verdu	CNRS Faculty, Muséum National de Histoire Naturelle, Paris
2009-2012	Erkan Buzbas	Assistant Professor, Department of Statistical Science, University of Idaho
2008-2012	Trevor Pemberton	Assistant Professor, Department of Biochemistry and Medical Genetics, University of Manitoba
2007-2008	James Degnan	Senior Lecturer, Department of Mathematics and Statistics, University of Canterbury
2006-2008	Paul Scheet	Assistant Professor, Department of Epidemiology, University of Texas M. D. Anderson Cancer Center
2005-2008	Mattias Jakobsson	Assistant Professor, Department of Evolutionary Biology, Uppsala University
2005-2006	Michael Blum	CNRS Faculty, Laboratory on Techniques for Biomedical Engineering and Complexity Management, University of Grenoble

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## PhD students

Dates	Name	Thesis	Current position
2012-	Amy Goldberg		
2012-	Michael “Doc” Edge		
2010-	Ethan Jewett		
2007-	Naama Kopelman*		
2009-2012	Chaolong Wang	Statistical methods for analyzing human genetic variation in diverse populations	Postdoc, Harvard University
2008-2012	Zachary Szpiech	Human migration, population divergence, and the accumulation of deleterious alleles: insights from private genetic variation and whole-exome sequencing	Postdoc, University of California, San Francisco
2006-2011	Lucy Huang	Genotype imputation in diverse populations: empirical and theoretical approaches	McKinsey & Company
2007-2011	Michael DeGiorgio	Genetic variation and modern human origins <sup>†</sup>	Postdoc, University of California, Berkeley (Starting January 2014 as Assistant Professor, Pennsylvania State University)

\*Student at Tel Aviv University, jointly supervised with Lewi Stone

<sup>†</sup>ProQuest Distinguished Dissertation Honorable Mention for best dissertation at the University of Michigan (one of 10 selected)

## Other supervision of lab members

2011	Amy Goldberg, Biological Anthropology undergraduate, University of Michigan
2010-2011	Laura Helmkamp, Biostatistics MS student, University of Michigan
2010-2011	Hanna Astephan, Mathematics undergraduate, University of Michigan
2010	Anastasia Wolff, Visiting Biology MS student, Ecole Normale Supérieure, Paris
2010	Eric Kalosa-Kenyon, High school student, Pioneer High School, Ann Arbor
2009	Brian Metzger, Ecology & Evolutionary Biology PhD rotation student, University of Michigan
2008-2010	Shashir Reddy, Mathematics undergraduate, University of Michigan
2008-2010	Ivana Jankovic, Molecular & Cellular Biology undergraduate, University of Michigan
2006-2008	Jenna VanLiere, Bioinformatics MS student, University of Michigan
2007	Conner Sandefur, Bioinformatics PhD rotation student, University of Michigan
2006-2007	Zachary Szpiech, Mathematics undergraduate, University of Michigan
2006	Randa Tao, Ecology & Evolutionary Biology undergraduate, University of Michigan (thesis: <i>Gene and species trees under the coalescent process: analysis of discordance within five taxa</i> , High Honors in Biology)
2005	Justin Van Klein, Bioinformatics PhD rotation student, University of Michigan
2004-2005	Saurabh Mahajan, Computer Science MS student, University of Southern California

## PhD committees

### Stanford University (2011-present)

<u>Dates</u>	<u>Name</u>	<u>PhD program</u>	<u>Primary advisor</u>
2012-	Mike Bramson	Biology (Eco/Evo)	Ward Watt
2012-	Philip Greenspoon	Biology (Eco/Evo)	Marc Feldman
2012-	Heather Machado	Biology (Eco/Evo)	Dmitri Petrov
2012-	Zhiyuan Song	Biology (Eco/Evo)	Marc Feldman
2012-	Ashley Tehranchi	Biology (Cell/Mol)	Hunter Fraser
2011-	Jeremy Hsu	Biology (Eco/Evo)	Liz Hadly

### University of Michigan (2005-2011)

<u>Dates</u>	<u>Name</u>	<u>PhD program</u>	<u>Thesis</u>
2011-2013	Peng Zhang	Bioinformatics	The road to identifying disease-causing genes: association tests, genotype imputations, and sampling strategies for sequencing studies
2010-2011	Matthew Zawistowski	Biostatistics	Statistical methods and models for modern genetic analysis
2010-2011	Shyam Gopalakrishnan	Biostatistics	Methods for statistical and population genetics analyses
2008-2011	Raquel Assis	Bioinformatics	Origin and evolution of novel sequences by gene duplication
2006-2011	Ethan Romero-Severson	Epidemiology	Sexual volatility and the spread of HIV
2007-2010	Nicole Scott	Human Genetics	Inferring biological population membership: an exploration of the continuum of genetic relationships
2009	Liming Liang	Biostatistics	Efficient methods for analysis of genome scale data
2007-2009	Yun Li	Biostatistics	In silico haplotyping, genotyping and analysis of resequencing data using Markov models
2006-2009	Amanda Zellmer	Ecology/Evolution	Ecological and evolutionary consequences of population connectivity in an amphibian with local adaptation

## 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”

## Teaching

### Courses

#### Stanford University (2011-present)

- 2013 Advanced Topics in Human Population Genetics (Bio 287)
- 2012 From Generation to Generation: The Genetics of Jewish Populations (Bio 127)

2011- Current Topics in Population Biology, Ecology, and Evolution (Bio 302, 303, 304)

### University of Michigan (2005-2011)

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

### Workshops and outreach

- 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 Genetic Ben Gurion University, Israel (week of lectures and lab activities)
- 2007 Henry Stewart Publications series on Human Population Genetics (recorded lecture)
- 2006-2009 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)

### Guest lectures in courses

#### Stanford University (2011-present)

- 2013 Principles of Biological Techniques (MI 215)

#### University of Michigan (2005-2011)

- 2008-2010 The Business of Biology
- 2007 Experimental Genetic Systems/Quantitative Genetics
- 2006 Basic Concepts in Population and Statistical Genetics
- 2006 Advanced Topics in Biostatistics: SNPs, Haplotypes, and Association Studies
- 2005 Fundamentals of Bioinformatics
- 2005, 2006 Molecular Genetics

## Publications

### 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).
- [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).

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- [3] JK Pritchard, M Stephens, **NA Rosenberg**, P Donnelly. Association mapping in structured populations. *American Journal of Human Genetics* 67: 170-181 (2000).
- [4] **NA Rosenberg**, E Woolf, JK Pritchard, T Schaap, D Gefel, I Shpirer, U Lavi, B Bonn -Tamir, J Hillel, MW Feldman. Distinctive genetic signatures in the Libyan Jews. *Proceedings of the National Academy of Sciences USA* 98: 858-863 (2001).
- [5] MM Tanaka, **NA Rosenberg**. Optimal estimation of transposition rates of insertion sequences for molecular epidemiology. *Statistics in Medicine* 20: 2409-2420 (2001).
- [6] **NA Rosenberg**, T Burke, K Elo, MW Feldman, PJ Freidlin, MAM Groenen, J Hillel, A Maki-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).
- [7] **NA Rosenberg**. The probability of topological concordance of gene trees and species trees. *Theoretical Population Biology* 61: 225-247 (2002).
- [8] **NA Rosenberg**, M Nordborg. Genealogical trees, coalescent theory and the analysis of genetic polymorphisms. *Nature Reviews Genetics* 3: 380-390 (2002). [Invited review]
- [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).
- [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).
- [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). [Correspondence]
- [12] **NA Rosenberg**, AG Tsolaki, MM Tanaka. Estimating change rates of genetic markers using serial samples: applications to the transposon IS6110 in *Mycobacterium tuberculosis*. *Theoretical Population Biology* 63: 347-363 (2003).
- [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).
- [14] **NA Rosenberg**, AE Hirsh. On the use of star-shaped genealogies in estimating coalescence times. *Genetics* 164: 1677-1682 (2003).
- [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).
- [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).
- [17] **NA Rosenberg**. *Distruct*: a program for the graphical display of population structure. *Molecular Ecology Notes* 4: 137-138 (2004). [Software note]
- [18] MM Tanaka, **NA Rosenberg**, PM Small. The control of copy number of IS6110 in *Mycobacterium tuberculosis*. *Molecular Biology and Evolution* 21: 2195-2201 (2004).
- [19] **NA Rosenberg**, PP Calabrese. Polyploid and multilocus extensions of the Wahlund inequality. *Theoretical Population Biology* 66: 381-391 (2004).
- [20] H Innan, K Zhang, P Marjoram, S Tavar , **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).

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

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## Selected reporting on research

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**Awards:** 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).

**Commentaries:** articles 9, 15, 21, 23, 30, 38, 42, 45, 48, 58, 59, 61, 67, 74, 76, 88, and 93 have been featured in Faculty of 1000 ratings (21, 23, 42, 45), scientific commentaries in *Current Biology* (9), *Genetics* (93), *Nature Genetics* (9, 30) and *Science* (9), BioMed Central “highly accessed” status (59), and editor’s highlights in *American Journal of Human Genetics* (15, 58, 67, 96), *Genetics* (38, 48, 67, 74, 76, 93), *Nature* (61), *Nature Reviews Genetics* (30, 58), and *Science* (88).

**Textbooks:** research has been featured in textbooks including *Human Evolutionary Genetics* by MA Jobling, ME Hurler, C Tyler-Smith (New York: Garland, 2004); *Statistical Methods in Genetic Epidemiology* by DC Thomas (New York: Oxford University Press, 2004); *Computational Genome Analysis* by RC Deonier, S Tavaré, MS Waterman (New York: Springer, 2005); *Evolutionary Analysis* 4th edition by S Freeman, JC Herron (Upper Saddle River, NJ: Prentice Hall, 2007); *Principles of Population Genetics* 4th edition by DL Hartl, AG Clark (Sunderland, MA: Sinauer, 2007).