



## Noah Rosenberg

Stanford Professor of Population Genetics and Society  
Biology

### Bio

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#### ACADEMIC APPOINTMENTS

- Professor, Biology
- Member, Bio-X
- Member, Institute for Computational and Mathematical Engineering (ICME)

#### HONORS AND AWARDS

- Career Award in the Biomedical Sciences, Burroughs Wellcome Fund (2004)
- Sloan Fellow in Computational and Evolutionary Molecular Biology, Alfred P. Sloan Foundation (2006)
- Dean's Basic Science Research Award, University of Michigan Medical School (2010)
- Stanford Professorship in Population Genetics & Society, Stanford University School of Humanities & Sciences (2014)
- Elected Fellow, American Association for the Advancement of Science (2018)
- George C. Williams Prize, International Society for Evolution, Medicine, & Public Health (2020)
- James V. Burgess Methods Article-of-the-Year Award, Health Services Research (2021)

#### BOARDS, ADVISORY COMMITTEES, PROFESSIONAL ORGANIZATIONS

- Associate Editor, PLoS Computational Biology (2025 - present)
- Founding Editor-in-Chief, Population Biology Modeling & Theory (2025 - present)
- Associate Editor, Evolution, Medicine, and Public Health (2014 - present)
- Editor-in-Chief, Theoretical Population Biology (2013 - 2024)
- Associate Editor, Molecular Biology and Evolution (2011 - 2014)
- Associate Editor, Human Biology (2010 - 2024)
- Associate Editor, Genetics (2010 - 2018)
- Associate Editor, BMC Bioinformatics (2010 - 2014)
- Associate Editor, Theoretical Population Biology (2009 - 2012)
- Associate Editor, American Journal of Human Genetics (2008 - 2010)

#### PROFESSIONAL EDUCATION

- BA, Rice University , Mathematics (1997)
- MS, Stanford University , Mathematics (1999)
- PhD, Stanford University , Biology (2001)

- Postdoc, University of Southern California , Molecular/Computational Biology (2005)

## LINKS

- Rosenberg Lab website: <https://web.stanford.edu/group/rosenberglab>

## Research & Scholarship

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### CURRENT RESEARCH AND SCHOLARLY INTERESTS

Research in the lab addresses problems in evolutionary biology and genetics through mathematical modeling, computer simulations, development of statistical methods, and inference from population-genetic data. Our current work covers topics such as combinatorics of evolutionary trees, inference of human evolutionary history, the role of population genetics in the search for disease-susceptibility genes, the relationship of gene trees and species trees, and mathematical properties of statistics used for analyzing genetic variability.

## Teaching

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### COURSES

#### 2025-26

- Fibonacci's Rabbits and Darwin's Elephants: Integer Sequences for Evolutionary Biology: BIO 22N (Win)
- Peregrinations With Trees: BIO 20N (Aut)

#### 2024-25

- Mathematical Population Biology: BIO 187, BIO 287, CME 187 (Win)
- Seminar on Statistical Methods in Ecology and Evolution: BIO 192, BIO 387 (Win)

#### 2023-24

- Advanced Topics in Mathematical Evolutionary Biology: BIO 287A (Aut)
- Seminar in Computational, Evolutionary, and Human Genomics: BIO 388 (Aut)

#### 2022-23

- Seminar in Computational, Evolutionary, and Human Genomics: BIO 388 (Aut)

### STANFORD ADVISEES

#### Doctoral Dissertation Reader (AC)

Javier Blanco, Tami Gjorgjieva, Julie Zhu

#### Postdoctoral Faculty Sponsor

Kennedy Agwamba, Lily Tamir

#### Doctoral Dissertation Advisor (AC)

Daniel Bauman, Egor Lappo, Chloe Shiff

### GRADUATE AND FELLOWSHIP PROGRAM AFFILIATIONS

- Biology (School of Humanities and Sciences) (Phd Program)

## Publications

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### PUBLICATIONS

- **Enumeration of rooted binary perfect phylogenies.** *Discrete applied mathematics (Amsterdam, Netherlands : 1988)*  
Shiff, C. E., Rosenberg, N. A.

2026; 380: 538-561

- **Enumeration of rooted binary perfect phylogenies** *DISCRETE APPLIED MATHEMATICS*  
Shiff, C. E., Rosenberg, N. A.  
2026; 380: 538-561
- **An  $n$ -Cousin Mating Model and the  $n$ -Anacci Numbers** *FIBONACCI QUARTERLY*  
Mora, E., Rosenberg, N. A.  
2026
- **Reflections on the Human Genome Diversity Project: a conversation with Marcus W. Feldman, Henry T. Greely, and Mary-Claire King.** *Genetics*  
Ramachandran, S., Rosenberg, N. A.  
2026
- **Shared Ancestors and the Birthday Problem** *AMERICAN STATISTICIAN*  
Agranat-Tamir, L., Agwamba, K. D., Mooney, J. A., Rosenberg, N. A.  
2026
- **Tree Height and the Asymptotic Mean of the Colijn-Plazzotta Rank of Unlabeled Binary Rooted Trees.** *Bulletin of mathematical biology*  
Devroye, L., Doboli, M. R., Rosenberg, N. A., Wagner, S.  
2025; 87 (12): 172
- **Toward minimal SNP sets for record-matching with CODIS STR profiles.** *European journal of human genetics : EJHG*  
Gjorgjieva, T., Rosenberg, N. A.  
2025
- **Coalescent theory of the  $\psi$  directionality index.** *G3 (Bethesda, Md.)*  
Lappo, E., Rosenberg, N. A.  
2025
- **Coalescent theory of the  $\psi$  directionality index.** *bioRxiv : the preprint server for biology*  
Lappo, E., Rosenberg, N. A.  
2025
- **Using mathematical constraints to explain narrow ranges for allele-sharing dissimilarities.** *Theoretical population biology*  
Liu, X., Ahsan, Z., Rosenberg, N. A.  
2025
- **Quantifying compositional variability in microbial communities with FAVA.** *Proceedings of the National Academy of Sciences of the United States of America*  
Morrison, M. L., Xue, K. S., Rosenberg, N. A.  
2025; 122 (11): e2413211122
- **Labelled histories with multifurcation and simultaneity.** *Philosophical transactions of the Royal Society of London. Series B, Biological sciences*  
Dickey, E. H., Rosenberg, N. A.  
2025; 380 (1919): 20230307
- **"A mathematical theory of evolution": phylogenetic models dating back 100 years.** *Philosophical transactions of the Royal Society of London. Series B, Biological sciences*  
Rosenberg, N. A., Stadler, T., Steel, M.  
2025; 380 (1919): 20230297
- **Using mathematical constraints to explain narrow ranges for allele-sharing dissimilarities.** *bioRxiv : the preprint server for biology*  
Liu, X., Ahsan, Z., Rosenberg, N. A.  
2024
- **Unraveling the genomic diversity and admixture history of captive tigers in the United States.** *Proceedings of the National Academy of Sciences of the United States of America*  
Armstrong, E. E., Mooney, J. A., Solari, K. A., Kim, B. Y., Barsh, G. S., Grant, V. B., Greenbaum, G., Kaelin, C. B., Panchenko, K., Pickrell, J. K., Rosenberg, N., Ryder, O. A., Yokoyama, et al

2024; 121 (39): e2402924121

- **Quantifying compositional variability in microbial communities with FAVA.** *bioRxiv : the preprint server for biology*  
Morrison, M. L., Xue, K. S., Rosenberg, N. A.  
2024
- **Enumeration of Rooted Binary Unlabeled Galled Trees.** *Bulletin of mathematical biology*  
Agranat-Tamir, L., Mathur, S., Rosenberg, N. A.  
2024; 86 (5): 45
- **Mathematical constraints on a family of biodiversity measures via connections with Rényi entropy.** *Bio Systems*  
Gress, T. D., Rosenberg, N. A.  
2024: 105153
- **Solving the Arizona search problem by imputation.** *iScience*  
Lappo, E., Rosenberg, N. A.  
2024; 27 (2): 108831
- **Bijections between the multifurcating unlabeled rooted trees and the positive integers** *ADVANCES IN APPLIED MATHEMATICS*  
Maranca, A., Rosenberg, N. A.  
2024; 153
- **A lattice structure for ancestral configurations arising from the relationship between gene trees and species trees.** *Discrete applied mathematics (Amsterdam, Netherlands : 1988)*  
Lappo, E., Rosenberg, N. A.  
2024; 343: 65-81
- **Counting the genetic ancestors from source populations in members of an admixed population.** *Genetics*  
Agranat-Tamir, L., Mooney, J. A., Rosenberg, N. A.  
2024
- **The distributions under two species-tree models of the total number of ancestral configurations for matching gene trees and species trees** *ADVANCES IN APPLIED MATHEMATICS*  
Disanto, F., Fuchs, M., Huang, C., Paningbatan, A. R., Rosenberg, N. A.  
2024; 152
- **Periodic Behavior of the Minimal Colijn-Plazzotta Rank for Trees with a Fixed Number of Leaves**  
Doboli, M. R., Hwang, H., Rosenberg, N. A.  
edited by Mailler, C., Wild, S.  
SCHLOSS DAGSTUHL, LEIBNIZ CENTER INFORMATICS.2024
- **Asymptotic Enumeration of Rooted Binary Unlabeled Galled Trees with a Fixed Number of Galls**  
Agranat-Tamir, L., Fuchs, M., Gittenberger, B., Rosenberg, N. A.  
edited by Mailler, C., Wild, S.  
SCHLOSS DAGSTUHL, LEIBNIZ CENTER INFORMATICS.2024
- **Tree Balance Indices: A Comprehensive Survey (Book Review)** *SIAM REVIEW*  
Book Review Authored by: Rosenberg, N. A.  
2024; 66 (2)
- **Clumpling: cluster matching and permutation program with integer linear programming.** *Bioinformatics (Oxford, England)*  
Liu, X., Kopelman, N. M., Rosenberg, N. A.  
2023
- **Cultural transmission of move choice in chess.** *Proceedings. Biological sciences*  
Lappo, E., Rosenberg, N. A., Feldman, M. W.  
2023; 290 (2011): 20231634
- **Modeling the effects of consanguinity on autosomal and X-chromosomal runs of homozygosity and identity-by-descent sharing.** *G3 (Bethesda, Md.)*  
Cotter, D. J., Severson, A. L., Kang, J. T., Godrej, H. N., Carmi, S., Rosenberg, N. A.

2023

- **A Dirichlet model of alignment cost in mixed-membership unsupervised clustering.** *Journal of computational and graphical statistics : a joint publication of American Statistical Association, Institute of Mathematical Statistics, Interface Foundation of North America*  
Liu, X., Kopelman, N. M., Rosenberg, N. A.  
2023; 32 (3): 1145-1159
- **Mathematical bounds on Shannon entropy given the abundance of the  $i$ th most abundant taxon.** *Journal of mathematical biology*  
Morrison, M. L., Rosenberg, N. A.  
2023; 87 (5): 76
- **Prolonged delays in human microbiota transmission after a controlled antibiotic perturbation.** *bioRxiv : the preprint server for biology*  
Xue, K. S., Walton, S. J., Goldman, D. A., Morrison, M. L., Verster, A. J., Parrott, A. B., Yu, F. B., Neff, N. F., Rosenberg, N. A., Ross, B. D., Petrov, D. A., Huang, K. C., Good, et al  
2023
- **The 2024 Feldman Prize.** *Theoretical population biology*  
Rosenberg, N. A.  
2023
- **Record-matching of STR profiles with fragmentary genomic SNP data.** *European journal of human genetics : EJHG*  
Kim, J., Rosenberg, N. A.  
2023
- **On the number of genealogical ancestors tracing to the source groups of an admixed population.** *Genetics*  
Mooney, J. A., Agranat-Tamir, L., Pritchard, J. K., Rosenberg, N. A.  
2023; 224 (3)
- **A genetic and linguistic analysis of the admixture histories of the islands of Cabo Verde.** *eLife*  
Laurent, R., Szpiech, Z. A., da Costa, S. S., Thouzeau, V., Fortes-Lima, C. A., Dessarps-Freichey, F., Lémée, L., Utgé, J., Rosenberg, N. A., Baptista, M., Verdu, P.  
2023; 12
- **A rarefaction approach for measuring population differences in rare and common variation.** *Genetics*  
Cotter, D. J., Hofgard, E. F., Novembre, J., Szpiech, Z. A., Rosenberg, N. A.  
2023
- **All galls are divided into three or more parts: recursive enumeration of labeled histories for galled trees.** *Algorithms for molecular biology : AMB*  
Mathur, S., Rosenberg, N. A.  
2023; 18 (1): 1
- **When is the allele-sharing dissimilarity between two populations exceeded by the allele-sharing dissimilarity of a population with itself?** *Statistical applications in genetics and molecular biology*  
Liu, X., Ahsan, Z., Martheswaran, T. K., Rosenberg, N. A.  
2023; 22 (1)
- **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*  
Disanto, F., Fuchs, M., Paningbatan, A. R., Rosenberg, N. A.  
2022; 32 (6): 4426-4458
- **A Dirichlet Model of Alignment Cost in Mixed-Membership Unsupervised Clustering** *JOURNAL OF COMPUTATIONAL AND GRAPHICAL STATISTICS*  
Liu, X., Kopelman, N. M., Rosenberg, N. A.  
2022
- **Limiting distribution of X-chromosomal coalescence times under first-cousin consanguineous mating.** *Theoretical population biology*  
Cotter, D. J., Severson, A. L., Carmi, S., Rosenberg, N. A.  
2022

- **Approximations to the expectations and variances of ratios of tree properties under the coalescent.** *G3 (Bethesda, Md.)*  
Lappo, E., Rosenberg, N. A.  
2022
- **Mathematical constraints on FST: multiallelic markers in arbitrarily many populations.** *Philosophical transactions of the Royal Society of London. Series B, Biological sciences*  
Alcala, N., Rosenberg, N. A.  
2022; 377 (1852): 20200414
- **Celebrating 50 years since Lewontin's apportionment of human diversity.** *Philosophical transactions of the Royal Society of London. Series B, Biological sciences*  
Edge, M. D., Ramachandran, S., Rosenberg, N. A.  
2022; 377 (1852): 20200405
- **FSTruct: an FST -based tool for measuring ancestry variation in inference of population structure.** *Molecular ecology resources*  
Morrison, M. L., Alcala, N., Rosenberg, N. A.  
2022
- **Enumeration of binary trees compatible with a perfect phylogeny.** *Journal of mathematical biology*  
Palacios, J. A., Bhaskar, A., Disanto, F., Rosenberg, N. A.  
2022; 84 (6): 54
- **The Probability of Joint Monophyly of Samples of Gene Lineages for All Species in an Arbitrary Species Tree.** *Journal of computational biology : a journal of computational molecular cell biology*  
Mehta, R. S., Steel, M., Rosenberg, N. A.  
2022
- **Extracting hierarchical features of cultural variation using network-based clustering** *EVOLUTIONARY HUMAN SCIENCES*  
Liu, X., Rosenberg, N. A., Greenbaum, G.  
2022; 4
- **Extracting hierarchical features of cultural variation using network-based clustering.** *Evolutionary human sciences*  
Liu, X., Rosenberg, N. A., Greenbaum, G.  
2022; 4
- **Ancient and modern genomics of the Ohlone Indigenous population of California.** *Proceedings of the National Academy of Sciences of the United States of America*  
Severson, A. L., Byrd, B. F., Mallott, E. K., Owings, A. C., DeGiorgio, M., de Flamingh, A., Nijmeh, C., Arellano, M. V., Leventhal, A., Rosenberg, N. A., Malhi, R. S.  
2022; 119 (13): e2111533119
- **Mathematical epidemiology for a later age.** *Theoretical population biology*  
Rosenberg, N. A., Boni, M. F.  
2022
- **The 2022 Feldman Prize.** *Theoretical population biology*  
Rosenberg, N. A.  
2021
- **A compendium of covariances and correlation coefficients of coalescent tree properties.** *Theoretical population biology*  
Alimpiev, E., Rosenberg, N. A.  
2021
- **Enumeration of coalescent histories for caterpillar species trees and p-pseudocaterpillar gene trees.** *Advances in applied mathematics*  
Alimpiev, E., Rosenberg, N. A.  
2021; 131
- **A simple derivation of the mean of the Sackin index of tree balance under the uniform model on rooted binary labeled trees.** *Mathematical biosciences*  
King, M. C., Rosenberg, N. A.

2021: 108688

- **A Population-Genetic Perspective on the Similarities and Differences among Worldwide Human Populations.** *Human biology*  
Rosenberg, N. A.  
2021; 92 (3): 135-152
- **The effect of consanguinity on coalescence times on the X chromosome.** *Theoretical population biology*  
Cotter, D. J., Severson, A. L., Rosenberg, N. A.  
2021
- **On the Colijn-Plazzotta numbering scheme for unlabeled binary rooted trees.** *Discrete applied mathematics (Amsterdam, Netherlands : 1988)*  
Rosenberg, N. A.  
2021; 291: 88–98
- **Variance and limiting distribution of coalescence times in a diploid model of a consanguineous population.** *Theoretical population biology*  
Severson, A. L., Carmi, S., Rosenberg, N. A.  
2021
- **Designing gene drives to limit spillover to non-target populations.** *PLoS genetics*  
Greenbaum, G., Feldman, M. W., Rosenberg, N. A., Kim, J.  
2021; 17 (2): e1009278
- **Population models, mathematical epidemiology, and the COVID-19 pandemic.** *Theoretical population biology*  
Rosenberg, N.  
2021
- **Skin deep: The decoupling of genetic admixture levels from phenotypes that differed between source populations.** *American journal of physical anthropology*  
Kim, J. n., Edge, M. D., Goldberg, A. n., Rosenberg, N. A.  
2021
- **Genetic Adaptation in New York City Rats.** *Genome biology and evolution*  
Harpak, A., Garud, N., Rosenberg, N. A., Petrov, D. A., Combs, M., Pennings, P. S., Munshi-South, J.  
2020
- **Distance metrics for ranked evolutionary trees.** *Proceedings of the National Academy of Sciences of the United States of America*  
Kim, J., Rosenberg, N. A., Palacios, J. A.  
2020
- **On the heterozygosity of an admixed population.** *Journal of mathematical biology*  
Boca, S. M., Huang, L., Rosenberg, N. A.  
2020
- **Human-Genetic Ancestry Inference and False Positives in Forensic Familial Searching.** *G3 (Bethesda, Md.)*  
Fortier, A. L., Kim, J., Rosenberg, N. A.  
2020
- **Modelling anti-vaccine sentiment as a cultural pathogen.** *Evolutionary human sciences*  
Mehta, R. S., Rosenberg, N. A.  
2020; 2: e21
- **Roadblocked monotonic paths and the enumeration of coalescent histories for non-matching caterpillar gene trees and species trees** *ADVANCES IN APPLIED MATHEMATICS*  
Himwich, Z. M., Rosenberg, N. A.  
2020; 113
- **Roadblocked monotonic paths and the enumeration of coalescent histories for non-matching caterpillar gene trees and species trees.** *Advances in applied mathematics*  
Himwich, Z. M., Rosenberg, N. A.  
2020; 113

- **Measures of care fragmentation: Mathematical insights from population genetics.** *Health services research*  
Rosenberg, N. A., Zulman, D. M.  
2020
- **High-resolution inference of genetic relationships among Jewish populations.** *European journal of human genetics : EJHG*  
Kopelman, N. M., Stone, L. n., Hernandez, D. G., Gefel, D. n., Singleton, A. B., Heyer, E. n., Feldman, M. W., Hillel, J. n., Rosenberg, N. A.  
2020
- **Mathematical Properties of Linkage Disequilibrium Statistics Defined by Normalization of the Coefficient  $D = pAB - pApB$ .** *Human heredity*  
Kang, J. T., Rosenberg, N. A.  
2020: 1–17
- **Fifty years of Theoretical Population Biology.** *Theoretical population biology*  
Rosenberg, N. A.  
2020
- **Assortative mating by population of origin in a mechanistic model of admixture.** *Theoretical population biology*  
Goldberg, A. n., Rastogi, A. n., Rosenberg, N. A.  
2020
- **The 2020 Feldman Prize.** *Theoretical population biology*  
Rosenberg, N. A.  
2019
- **Network-based hierarchical population structure analysis for large genomic datasets.** *Genome research*  
Greenbaum, G., Rubin, A., Templeton, A. R., Rosenberg, N. A.  
2019
- **Disease transmission and introgression can explain the long-lasting contact zone of modern humans and Neanderthals.** *Nature communications*  
Greenbaum, G., Getz, W. M., Rosenberg, N. A., Feldman, M. W., Hovers, E., Kolodny, O.  
2019; 10 (1): 5003
- **The probability of reciprocal monophyly of gene lineages in three and four species**  
Mehta, R. S., Rosenberg, N. A.  
ACADEMIC PRESS INC ELSEVIER SCIENCE.2019: 133–47
- **Some topics in theoretical population genetics: Editorial commentaries on a selection of Marc Feldman's TPB papers**  
Altenberg, L., Creanza, N., Fogarty, L., Hadany, L., Kolodny, O., Laland, K. N., Lehmann, L., Otto, S. P., Rosenberg, N. A., Van Cleve, J., Wakeley, J.  
ACADEMIC PRESS INC ELSEVIER SCIENCE.2019: 4–8
- **The Relationship Between Haplotype-Based FST and Haplotype Length.** *Genetics*  
Mehta, R. S., Feder, A. F., Boca, S. M., Rosenberg, N. A.  
2019; 213 (1): 281-295
- **The Relationship Between Haplotype-Based FST and Haplotype Length.** *Genetics*  
Mehta, R. S., Feder, A. F., Boca, S. M., Rosenberg, N. A.  
2019; 213 (1): 281-295
- **The Relationship Between Haplotype-Based FST and Haplotype Length.** *Genetics*  
Mehta, R. S., Feder, A. F., Boca, S. M., Rosenberg, N. A.  
2019
- **Analysis of author gender in TPB, 1991-2018** *THEORETICAL POPULATION BIOLOGY*  
Severson, A. L., Uricchio, L. H., Arbisser, I. M., Glassberg, E. C., Rosenberg, N. A.  
2019; 127: 1–6
- **Use of stochastic patch occupancy models in the California red-legged frog for Bayesian inference regarding past events and future persistence** *CONSERVATION BIOLOGY*  
Alcala, N., Launer, A. E., Westphal, M. F., Seymour, R., Cole, E. M., Rosenberg, N. A.

2019; 33 (3): 685–96

- **FST and the triangle inequality for biallelic markers.** *Theoretical population biology*  
Arbisser, I. M., Rosenberg, N. A.  
2019
- **The Effect of Consanguinity on Between-Individual Identity-by-Descent Sharing** *GENETICS*  
Severson, A. L., Carmi, S., Rosenberg, N. A.  
2019; 212 (1): 305–16
- **Analysis of author gender in TPB, 1991-2018.** *Theoretical population biology*  
Severson, A. L., Uricchio, L. H., Arbisser, I. M., Glassberg, E. C., Rosenberg, N. A.  
2019
- **The Effect of Consanguinity on Between-Individual Identity-By-Descent Sharing.** *Genetics*  
Severson, A. L., Carmi, S., Rosenberg, N. A.  
2019
- **Probabilities of unranked and ranked anomaly zones under birth-death models.** *Molecular biology and evolution*  
Kim, A. n., Rosenberg, N. A., Degnan, J. H.  
2019
- **Interpreting polygenic scores, polygenic adaptation, and human phenotypic differences** *EVOLUTION MEDICINE AND PUBLIC HEALTH*  
Rosenberg, N. A., Edge, M. D., Pritchard, J. K., Feldman, M. W.  
2019: 26–34
- **Interpreting polygenic scores, polygenic adaptation, and human phenotypic differences.** *Evolution, medicine, and public health*  
Rosenberg, N. A., Edge, M. D., Pritchard, J. K., Feldman, M. W.  
2019; 2019 (1): 26–34
- **Enumeration of lonely pairs of gene trees and species trees by means of antipodal cherries** *ADVANCES IN APPLIED MATHEMATICS*  
Rosenberg, N. A.  
2019; 102: 1–17
- **ENUMERATION OF LONELY PAIRS OF GENE TREES AND SPECIES TREES BY MEANS OF ANTIPODAL CHERRIES.** *Advances in applied mathematics*  
Rosenberg, N. A.  
2019; 102: 1-17
- **Coalescent theory of migration network motifs.** *Molecular biology and evolution*  
Alcala, N. n., Goldberg, A. n., Ramakrishnan, U. n., Rosenberg, N. A.  
2019
- **Enumeration of compact coalescent histories for matching gene trees and species trees** *JOURNAL OF MATHEMATICAL BIOLOGY*  
Disanto, F., Rosenberg, N. A.  
2019; 78 (1-2): 155–88
- **G'ST , Jost's D, and FST are similarly constrained by allele frequencies: a mathematical, simulation, and empirical study.** *Molecular ecology*  
Alcala, N., Rosenberg, N. A.  
2018
- **Some topics in theoretical population genetics: Editorial commentaries on a selection of Marc Feldman's TPB papers.** *Theoretical population biology*  
Altenberg, L., Creanza, N., Fogarty, L., Hadany, L., Kolodny, O., Laland, K. N., Lehmann, L., Otto, S. P., Rosenberg, N. A., Van Cleve, J., Wakeley, J.  
2018
- **Statistical Detection of Relatives Typed with Disjoint Forensic and Biomedical Loci.** *Cell*  
Kim, J., Edge, M. D., Algee-Hewitt, B. F., Li, J. Z., Rosenberg, N. A.  
2018

- **Use of stochastic patch-occupancy models in the California red-legged frog for Bayesian inference regarding past events and future persistence.** *Conservation biology : the journal of the Society for Conservation Biology*  
Alcala, N., Launer, A. E., Westphal, M. F., Seymour, R., Cole, E. M., Rosenberg, N. A.  
2018
- **A genome scan for genes underlying adult body size differences between Central African hunter-gatherers and farmers** *HUMAN GENETICS*  
Pemberton, T. J., Verdu, P., Becker, N. S., Willer, C. J., Hewlett, B. S., Le Bomin, S., Froment, A., Rosenberg, N. A., Heyer, E.  
2018; 137 (6-7): 487–509
- **Mathematical and Simulation-Based Analysis of the Behavior of Admixed Taxa in the Neighbor-Joining Algorithm.** *Bulletin of mathematical biology*  
Kim, J., Disanto, F., Kopelman, N. M., Rosenberg, N. A.  
2018
- **The probability of reciprocal monophyly of gene lineages in three and four species.** *Theoretical population biology*  
Mehta, R. S., Rosenberg, N. A.  
2018
- **Matching CODIS genotypes to SNP genotypes using linkage disequilibrium**  
Edge, M. D., Algee-Hewitt, B. F. B., Kim, J., Pemberton, T., Li, J. Z., Rosenberg, N. A.  
WILEY.2018: 75–76
- **Bounding measures of genetic similarity and diversity using majorization.** *Journal of mathematical biology*  
Aw, A. J., Rosenberg, N. A.  
2018
- **The 2018 Marcus W. Feldman Prize in Theoretical Population Biology** *THEORETICAL POPULATION BIOLOGY*  
Rosenberg, N. A.  
2018; 119: 1–2
- **On the joint distribution of tree height and tree length under the coalescent.** *Theoretical population biology*  
Arbisser, I. M., Jewett, E. M., Rosenberg, N. A.  
2017
- **On the Number of Non-equivalent Ancestral Configurations for Matching Gene Trees and Species Trees.** *Bulletin of mathematical biology*  
Disanto, F., Rosenberg, N. A.  
2017
- **Parallel Trajectories of Genetic and Linguistic Admixture in a Genetically Admixed Creole Population.** *Current biology : CB*  
Verdu, P., Jewett, E. M., Pemberton, T. J., Rosenberg, N. A., Baptista, M.  
2017; 27 (16): 2529-2535.e3
- **Evaluating allopolyploid origins in strawberries (Fragaria) using haplotypes generated from target capture sequencing** *BMC EVOLUTIONARY BIOLOGY*  
Kamneva, O. K., Syring, J., Liston, A., Rosenberg, N. A.  
2017; 17: 180
- **Linkage disequilibrium matches forensic genetic records to disjoint genomic marker sets.** *Proceedings of the National Academy of Sciences of the United States of America*  
Edge, M. D., Algee-Hewitt, B. F., Pemberton, T. J., Li, J. Z., Rosenberg, N. A.  
2017; 114 (22): 5671-5676
- **Reply to Lazaridis and Reich: Robust model-based inference of male-biased admixture during Bronze Age migration from the Pontic-Caspian Steppe.** *Proceedings of the National Academy of Sciences of the United States of America*  
Goldberg, A., Günther, T., Rosenberg, N. A., Jakobsson, M.  
2017; 114 (20): E3875-E3877
- **Mathematical Constraints on FST: Biallelic Markers in Arbitrarily Many Populations.** *Genetics*  
Alcala, N., Rosenberg, N. A.

2017

- **Enumeration of Ancestral Configurations for Matching Gene Trees and Species Trees.** *Journal of computational biology : a journal of computational molecular cell biology*  
Disanto, F., Rosenberg, N. A.  
2017
- **Neolithic familial migration contrasts Bronze Age male migration inferred from ancient X chromosomes**  
Goldberg, A., Gunter, T., Rosenberg, N. A., Jakobsson, M.  
WILEY.2017: 196
- **Simulation-Based Evaluation of Hybridization Network Reconstruction Methods in the Presence of Incomplete Lineage Sorting** *EVOLUTIONARY BIOINFORMATICS*  
Kamneva, O. K., Rosenberg, N. A.  
2017; 13
- **Ancient X chromosomes reveal contrasting sex bias in Neolithic and Bronze Age Eurasian migrations.** *Proceedings of the National Academy of Sciences of the United States of America*  
Goldberg, A., Günther, T., Rosenberg, N. A., Jakobsson, M.  
2017
- **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*  
Uricchio, L. H., Warnow, T., Rosenberg, N. A.  
2016; 17
- **Consanguinity Rates Predict Long Runs of Homozygosity in Jewish Populations.** *Human heredity*  
Kang, J. T., Goldberg, A., Edge, M. D., Behar, D. M., Rosenberg, N. A.  
2016; 82 (3-4): 87-102
- **Asymptotic Properties of the Number of Matching Coalescent Histories for Caterpillar-Like Families of Species Trees.** *IEEE/ACM transactions on computational biology and bioinformatics*  
Disanto, F., Rosenberg, N. A.  
2016; 13 (5): 913-925
- **Consistency and inconsistency of consensus methods for inferring species trees from gene trees in the presence of ancestral population structure.** *Theoretical population biology*  
DeGiorgio, M., Rosenberg, N. A.  
2016; 110: 12-24
- **The probability of monophyly of a sample of gene lineages on a species tree.** *Proceedings of the National Academy of Sciences of the United States of America*  
Mehta, R. S., Bryant, D., Rosenberg, N. A.  
2016; 113 (29): 8002-8009
- **Does Gene Tree Discordance Explain the Mismatch between Macroevolutionary Models and Empirical Patterns of Tree Shape and Branching Times?** *Systematic biology*  
Stadler, T., Degnan, J. H., Rosenberg, N. A.  
2016; 65 (4): 628-639
- **Individual Identifiability Predicts Population Identifiability in Forensic Microsatellite Markers.** *Current biology*  
Algee-Hewitt, B. F., Edge, M. D., Kim, J., Li, J. Z., Rosenberg, N. A.  
2016; 26 (7): 935-942
- **Individual Identifiability Predicts Population Identifiability in Forensic Microsatellite Markers** *CURRENT BIOLOGY*  
Algee-Hewitt, B. F., Edge, M. D., Kim, J., Li, J. Z., Rosenberg, N. A.  
2016; 26 (7): 935-942
- **Admixture Models and the Breeding Systems of H. S. Jennings: A GENETICS Connection.** *Genetics*  
Rosenberg, N. A.  
2016; 202 (1): 9-13

- **Choosing Subsamples for Sequencing Studies by Minimizing the Average Distance to the Closest Leaf** *GENETICS*  
Kang, J. T., Zhang, P., Zoellner, S., Rosenberg, N. A.  
2015; 201 (2): 499-511
- **A General Model of the Relationship between the Apportionment of Human Genetic Diversity and the Apportionment of Human Phenotypic Diversity** *HUMAN BIOLOGY*  
Edge, M. D., Rosenberg, N. A.  
2015; 87 (4): 313-337
- **A General Model of the Relationship between the Apportionment of Human Genetic Diversity and the Apportionment of Human Phenotypic Diversity.** *Human biology*  
Edge, M. D., Rosenberg, N. A.  
2015; 87 (4): 313-337
- **Coalescent Histories for Lodgepole Species Trees.** *Journal of computational biology*  
Disanto, F., Rosenberg, N. A.  
2015; 22 (10): 918-929
- **Clumpak: a program for identifying clustering modes and packaging population structure inferences across K** *MOLECULAR ECOLOGY RESOURCES*  
Kopelman, N. M., Mayzel, J., Jakobsson, M., Rosenberg, N. A., Mayrose, I.  
2015; 15 (5): 1179-1191
- **Genetic Diversity and Societally Important Disparities.** *Genetics*  
Rosenberg, N. A., Kang, J. T.  
2015; 201 (1): 1-12
- **Genetic Diversity and Societally Important Disparities.** *Genetics*  
Rosenberg, N. A., Kang, J. T.  
2015; 201 (1): 1-12
- **Beyond 2/3 and 1/3: The Complex Signatures of Sex-Biased Admixture on the X Chromosome.** *Genetics*  
Goldberg, A., Rosenberg, N. A.  
2015; 201 (1): 263-279
- **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*  
Edge, M. D., Rosenberg, N. A.  
2015; 52: 32-45
- **Hamilton's rule: Game theory meets coalescent theory.** *Theoretical population biology*  
Lehmann, L., Rosenberg, N. A.  
2015; 103: 1
- **Enhancing the mathematical properties of new haplotype homozygosity statistics for the detection of selective sweeps** *THEORETICAL POPULATION BIOLOGY*  
Garud, N. R., Rosenberg, N. A.  
2015; 102: 94-101
- **Theory in population biology, or biologically inspired mathematics?** *Theoretical population biology*  
Rosenberg, N. A.  
2015; 102: 1-2
- **A comparison of worldwide phonemic and genetic variation in human populations.** *Proceedings of the National Academy of Sciences of the United States of America*  
Creanza, N., Ruhlen, M., Pemberton, T. J., Rosenberg, N. A., Feldman, M. W., Ramachandran, S.  
2015; 112 (5): 1265-1272
- **AABC: Approximate approximate Bayesian computation for inference in population-genetic models.** *Theoretical population biology*  
Buzbas, E. O., Rosenberg, N. A.

2015; 99: 31-42

- **Predicting Carriers of Ongoing Selective Sweeps without Knowledge of the Favored Allele.** *PLoS genetics*  
Ronen, R. n., Tesler, G. n., Akbari, A. n., Zakov, S. n., Rosenberg, N. A., Bafna, V. n.  
2015; 11 (9): e1005527
- **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*  
Edge, M. D., Rosenberg, N. A.  
2014; 97: 20-34
- **Autosomal admixture levels are informative about sex bias in admixed populations.** *Genetics*  
Goldberg, A., Verdu, P., Rosenberg, N. A.  
2014; 198 (3): 1209-1229
- **Upper bounds on FST in terms of the frequency of the most frequent allele and total homozygosity: the case of a specified number of alleles.** *Theoretical population biology*  
Edge, M. D., Rosenberg, N. A.  
2014; 97: 20-34
- **On the Number of Ranked Species Trees Producing Anomalous Ranked Gene Trees** *IEEE-ACM TRANSACTIONS ON COMPUTATIONAL BIOLOGY AND BIOINFORMATICS*  
Disanto, F., Rosenberg, N. A.  
2014; 11 (6): 1229-1238
- **Autosomal Admixture Levels Are Informative About Sex Bias in Admixed Populations** *GENETICS*  
Goldberg, A., Verdu, P., Rosenberg, N. A.  
2014; 198 (3): 1209-1229
- **Mean deep coalescence cost under exchangeable probability distributions** *DISCRETE APPLIED MATHEMATICS*  
Than, C. V., Rosenberg, N. A.  
2014; 174: 11-26
- **Patterns of Admixture and Population Structure in Native Populations of Northwest North America** *PLOS GENETICS*  
Verdu, P., Pemberton, T. J., Laurent, R., Kemp, B. M., Gonzalez-Oliver, A., Gorodezky, C., Hughes, C. E., Shattuck, M. R., Petzelt, B., Mitchell, J., Harry, H., William, T., Worl, et al  
2014; 10 (8)
- **Theory and applications of a deterministic approximation to the coalescent model.** *Theoretical population biology*  
Jewett, E. M., Rosenberg, N. A.  
2014; 93: 14-29
- **An empirical evaluation of two-stage species tree inference strategies using a multilocus dataset from North American pines** *BMC EVOLUTIONARY BIOLOGY*  
DeGiorgio, M., Syring, J., Eckert, A. J., Liston, A., Cronn, R., Neale, D. B., Rosenberg, N. A.  
2014; 14
- **Core elements of a TPB paper.** *Theoretical population biology*  
Rosenberg, N. A.  
2014; 92: 118-9
- **Population-Genetic Influences on Genomic Estimates of the Inbreeding Coefficient: A Global Perspective** *HUMAN HEREDITY*  
Pemberton, T. J., Rosenberg, N. A.  
2014; 77 (1-4): 37-48
- **Discordance of Species Trees with Their Most Likely Gene Trees: A Unifying Principle** *MOLECULAR BIOLOGY AND EVOLUTION*  
Rosenberg, N. A.  
2013; 30 (12): 2709-2713
- **No Evidence from Genome-wide Data of a Khazar Origin for the Ashkenazi Jews.** *Human biology*

- Behar, D. M., Metspalu, M., Baran, Y., Kopelman, N. M., Yunusbayev, B., Gladstein, A., Tzur, S., Sahakyan, H., Bahmanimehr, A., Yepiskoposyan, L., Tambets, K., Khusnutdinova, E. K., Kushniarevich, et al  
2013; 85 (6): 859-900
- **Genetics and the History of the Samaritans: Y-Chromosomal Microsatellites and Genetic Affinity between Samaritans and Cohanim.** *Human biology*  
Oefner, P. J., Hölzi, G., Shen, P., Shpirer, I., Gefel, D., Lavi, T., Woolf, E., Cohen, J., Cinnioglu, C., Underhill, P. A., Rosenberg, N. A., Hochrein, J., Granka, et al  
2013; 85 (6): 825-858
  - **No Evidence from Genome-wide Data of a Khazar Origin for the Ashkenazi Jews** *HUMAN BIOLOGY*  
Behar, D. M., Metspalu, M., Baran, Y., Kopelman, N. M., Yunusbayev, B., Gladstein, A., Tzur, S., Sahakyan, H., Bahmanimehr, A., Yepiskoposyan, L., Tambets, K., Khusnutdinova, E. K., Kushniarevich, et al  
2013; 85 (6): 859-900
  - **Genetics and the History of the Samaritans: Y-Chromosomal Microsatellites and Genetic Affinity between Samaritans and Cohanim** *HUMAN BIOLOGY*  
Oefner, P. J., Hoelzi, G., Shen, P., Shpirer, I., Gefel, D., Lavi, T., Woolf, E., Cohen, J., Cinnioglu, C., Underhill, P. A., Rosenberg, N. A., Hochrein, J., Granka, et al  
2013; 85 (6): 825-857
  - **From generation to generation: the genetics of jewish populations.** *Human biology*  
Rosenberg, N. A., Weitzman, S. P.  
2013; 85 (6): 817-824
  - **Genotype Imputation Reference Panel Selection Using Maximal Phylogenetic Diversity** *GENETICS*  
Zhang, P., Zhan, X., Rosenberg, N. A., Zoellner, S.  
2013; 195 (2): 319-330
  - **Genotype imputation reference panel selection using maximal phylogenetic diversity.** *Genetics*  
Zhang, P., Zhan, X., Rosenberg, N. A., Zöllner, S.  
2013; 195 (2): 319-330
  - **Coalescent Histories for Caterpillar-Like Families** *IEEE-ACM TRANSACTIONS ON COMPUTATIONAL BIOLOGY AND BIOINFORMATICS*  
Rosenberg, N. A.  
2013; 10 (5): 1253-1262
  - **Runs of homozygosity and parental relatedness.** *Genetics in medicine*  
Rosenberg, N. A., Pemberton, T. J., Li, J. Z., Belmont, J. W.  
2013; 15 (9): 753-754
  - **Genotype imputation in a coalescent model with infinitely-many-sites mutation** *THEORETICAL POPULATION BIOLOGY*  
Huang, L., Buzbas, E. O., Rosenberg, N. A.  
2013; 87: 62-74
  - **Long Runs of Homozygosity Are Enriched for Deleterious Variation** *AMERICAN JOURNAL OF HUMAN GENETICS*  
Szpiech, Z. A., Xu, J., Pemberton, T. J., Peng, W., Zoellner, S., Rosenberg, N. A., Li, J. Z.  
2013; 93 (1): 90-102
  - **Population Structure in a Comprehensive Genomic Data Set on Human Microsatellite Variation** *G3-GENES GENOMES GENETICS*  
Pemberton, T. J., DeGiorgio, M., Rosenberg, N. A.  
2013; 3 (5): 891-907
  - **Geographic Sampling Scheme as a Determinant of the Major Axis of Genetic Variation in Principal Components Analysis** *MOLECULAR BIOLOGY AND EVOLUTION*  
DeGiorgio, M., Rosenberg, N. A.  
2013; 30 (2): 480-488
  - **The Relationship Between F-ST and the Frequency of the Most Frequent Allele** *GENETICS*  
Jakobsson, M., Edge, M. D., Rosenberg, N. A.  
2013; 193 (2): 515-528

- **Mathematical properties of the deep coalescence cost.** *IEEE/ACM transactions on computational biology and bioinformatics / IEEE, ACM*  
Than, C. V., Rosenberg, N. A.  
2013; 10 (1): 61-72
- **Windfalls and pitfalls: Applications of population genetics to the search for disease genes.** *Evolution, medicine, and public health*  
Edge, M. D., Gorroochurn, P., Rosenberg, N. A.  
2013; 2013 (1): 254-272
- **The behavior of admixed populations in neighbor-joining inference of population trees.** *Pacific Symposium on Biocomputing. Pacific Symposium on Biocomputing*  
Kopelman, N. M., Stone, L., Gascuel, O., Rosenberg, N. A.  
2013: 273-284
- **A Characterization of the Set of Species Trees that Produce Anomalous Ranked Gene Trees** *IEEE-ACM TRANSACTIONS ON COMPUTATIONAL BIOLOGY AND BIOINFORMATICS*  
Degnan, J. H., Rosenberg, N. A., Stadler, T.  
2012; 9 (6): 1558-1568
- **A maximum-likelihood method to correct for allelic dropout in microsatellite data with no replicate genotypes.** *Genetics*  
Wang, C., Schroeder, K. B., Rosenberg, N. A.  
2012; 192 (2): 651-669
- **Genomic Patterns of Homozygosity in Worldwide Human Populations** *AMERICAN JOURNAL OF HUMAN GENETICS*  
Pemberton, T. J., Absher, D., Feldman, M. W., Myers, R. M., Rosenberg, N. A., Li, J. Z.  
2012; 91 (2): 275-292
- **Inferring Species Trees Directly from Biallelic Genetic Markers: Bypassing Gene Trees in a Full Coalescent Analysis** *MOLECULAR BIOLOGY AND EVOLUTION*  
Bryant, D., Bouckaert, R., Felsenstein, J., Rosenberg, N. A., RoyChoudhury, A.  
2012; 29 (8): 1917-1932
- **A Quantitative Comparison of the Similarity between Genes and Geography in Worldwide Human Populations** *PLOS GENETICS*  
Wang, C., Zoellner, S., Rosenberg, N. A.  
2012; 8 (8)
- **Improvements to a Class of Distance Matrix Methods for Inferring Species Trees from Gene Trees** *JOURNAL OF COMPUTATIONAL BIOLOGY*  
Helmkamp, L. J., Jewett, E. M., Rosenberg, N. A.  
2012; 19 (6): 632-649
- **iGLASS: An Improvement to the GLASS Method for Estimating Species Trees from Gene Trees** *JOURNAL OF COMPUTATIONAL BIOLOGY*  
Jewett, E. M., Rosenberg, N. A.  
2012; 19 (3): 293-315
- **Refining the relationship between homozygosity and the frequency of the most frequent allele** *JOURNAL OF MATHEMATICAL BIOLOGY*  
Reddy, S. B., Rosenberg, N. A.  
2012; 64 (1-2): 87-108
- **The probability distribution of ranked gene trees on a species tree** *MATHEMATICAL BIOSCIENCES*  
Degnan, J. H., Rosenberg, N. A., Stadler, T.  
2012; 235 (1): 45-55
- **Haploscope: A Tool for the Graphical Display of Haplotype Structure in Populations** *GENETIC EPIDEMIOLOGY*  
San Lucas, F. A., Rosenberg, N. A., Scheet, P.  
2012; 36 (1): 17-21
- **A General Mechanistic Model for Admixture Histories of Hybrid Populations** *GENETICS*  
Verdu, P., Rosenberg, N. A.  
2011; 189 (4): 1413-?

- **A population-genetic perspective on the similarities and differences among worldwide human populations.** *Human biology*  
Rosenberg, N. A.  
2011; 83 (6): 659-84
- **A Test of the Influence of Continental Axes of Orientation on Patterns of Human Gene Flow** *AMERICAN JOURNAL OF PHYSICAL ANTHROPOLOGY*  
Ramachandran, S., Rosenberg, N. A.  
2011; 146 (4): 515-529
- **Haplotype variation and genotype imputation in African populations** *GENETIC EPIDEMIOLOGY*  
Huang, L., Jakobsson, M., Pemberton, T. J., Ibrahim, M., Nyambo, T., Omar, S., Pritchard, J. K., Tishkoff, S. A., Rosenberg, N. A.  
2011; 35 (8): 766-780
- **A Population-Genetic Perspective on the Similarities and Differences Among Worldwide Human Populations** *HUMAN BIOLOGY*  
Rosenberg, N. A.  
2011; 83 (6): 659-684
- **Mathematical properties of F<sub>st</sub> between admixed populations and their parental source populations** *THEORETICAL POPULATION BIOLOGY*  
Boca, S. M., Rosenberg, N. A.  
2011; 80 (3): 208-216
- **Coalescence-Time Distributions in a Serial Founder Model of Human Evolutionary History** *GENETICS*  
DeGiorgio, M., Degnan, J. H., Rosenberg, N. A.  
2011; 189 (2): 579-593
- **On the size distribution of private microsatellite alleles** *THEORETICAL POPULATION BIOLOGY*  
Szpiech, Z. A., Rosenberg, N. A.  
2011; 80 (2): 100-113
- **Inference on the strength of balancing selection for epistatically interacting loci** *THEORETICAL POPULATION BIOLOGY*  
Buzbas, E. O., Joyce, P., Rosenberg, N. A.  
2011; 79 (3): 102-113
- **Consistency Properties of Species Tree Inference by Minimizing Deep Coalescences** *JOURNAL OF COMPUTATIONAL BIOLOGY*  
Than, C. V., Rosenberg, N. A.  
2011; 18 (1): 1-15
- **Unbiased Estimation of Gene Diversity in Samples Containing Related Individuals: Exact Variance and Arbitrary Ploidy** *GENETICS*  
DeGiorgio, M., Jankovic, I., Rosenberg, N. A.  
2010; 186 (4): 1367-1387
- **Inference of Unexpected Genetic Relatedness among Individuals in HapMap Phase III** *AMERICAN JOURNAL OF HUMAN GENETICS*  
Pemberton, T. J., Wang, C., Li, J. Z., Rosenberg, N. A.  
2010; 87 (4): 457-464
- **MLH1 Founder Mutations with Moderate Penetrance in Spanish Lynch Syndrome Families** *CANCER RESEARCH*  
Borras, E., Pineda, M., Blanco, I., Jewett, E. M., Wang, F., Teule, A., Caldes, T., Urioste, M., Martinez-Bouzas, C., Brunet, J., Balmana, J., Torres, A., Ramon y Cajal, et al  
2010; 70 (19): 7379-7391
- **Coalescent histories for discordant gene trees and species trees** *THEORETICAL POPULATION BIOLOGY*  
Rosenberg, N. A., Degnan, J. H.  
2010; 77 (3): 145-151
- **Genome-wide association studies in diverse populations** *NATURE REVIEWS GENETICS*  
Rosenberg, N. A., Huang, L., Jewett, E. M., Szpiech, Z. A., Jankovic, I., Boehnke, M.  
2010; 11 (5): 356-366
- **Lack of Population Diversity in Commonly Used Human Embryonic Stem-Cell Lines** *NEW ENGLAND JOURNAL OF MEDICINE*

- Mosher, J. T., Pemberton, T. J., Harter, K., Wang, C., Buzbas, E. O., Dvorak, P., Simon, C., Morrison, S. J., Rosenberg, N. A.  
2010; 362 (2): 183-185
- **Comparing Spatial Maps of Human Population-Genetic Variation Using Procrustes Analysis** *STATISTICAL APPLICATIONS IN GENETICS AND MOLECULAR BIOLOGY*  
Wang, C., Szpiech, Z. A., Degnan, J. H., Jakobsson, M., Pemberton, T. J., Hardy, J. A., Singleton, A. B., Rosenberg, N. A.  
2010; 9 (1)
  - **Sequence determinants of human microsatellite variability** *BMC GENOMICS*  
Pemberton, T. J., Sandefur, C. I., Jakobsson, M., Rosenberg, N. A.  
2009; 10
  - **Genomic microsatellites identify shared Jewish ancestry intermediate between Middle Eastern and European populations** *BMC GENETICS*  
Kopelman, N. M., Stone, L., Wang, C., Gefel, D., Feldman, M. W., Hillel, J., Rosenberg, N. A.  
2009; 10
  - **The Relationship between Imputation Error and Statistical Power in Genetic Association Studies in Diverse Populations** *AMERICAN JOURNAL OF HUMAN GENETICS*  
Huang, L., Wang, C., Rosenberg, N. A.  
2009; 85 (5): 692-698
  - **Out of Africa: modern human origins special feature: 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 of the United States of America*  
DeGiorgio, M., Jakobsson, M., Rosenberg, N. A.  
2009; 106 (38): 16057-16062
  - **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 OF THE UNITED STATES OF AMERICA*  
DeGiorgio, M., Jakobsson, M., Rosenberg, N. A.  
2009; 106 (38): 16057-16062
  - **Replication of Genetic Associations as Pseudoreplication due to Shared Genealogy** *GENETIC EPIDEMIOLOGY*  
Rosenberg, N. A., VanLiere, J. M.  
2009; 33 (6): 479-487
  - **Gene tree discordance, phylogenetic inference and the multispecies coalescent** *TRENDS IN ECOLOGY & EVOLUTION*  
Degnan, J. H., Rosenberg, N. A.  
2009; 24 (6): 332-340
  - **Haplotypic Background of a Private Allele at High Frequency in the Americas** *MOLECULAR BIOLOGY AND EVOLUTION*  
Schroeder, K. B., Jakobsson, M., Crawford, M. H., Schurr, T. G., Boca, S. M., Conrad, D. F., Tito, R. Y., Osipova, L. P., Tarskaia, L. A., Zhadanov, S. I., Wall, J. D., Pritchard, J. K., Malhi, et al  
2009; 26 (5): 995-1016
  - **An Unbiased Estimator of Gene Diversity in Samples Containing Related Individuals** *MOLECULAR BIOLOGY AND EVOLUTION*  
DeGiorgio, M., Rosenberg, N. A.  
2009; 26 (3): 501-512
  - **Genotype-Imputation Accuracy across Worldwide Human Populations** *AMERICAN JOURNAL OF HUMAN GENETICS*  
Huang, L., Li, Y., Singleton, A. B., Hardy, J. A., Abecasis, G., Rosenberg, N. A., Scheet, P.  
2009; 84 (2): 235-250
  - **Properties of Consensus Methods for Inferring Species Trees from Gene Trees** *SYSTEMATIC BIOLOGY*  
Degnan, J. H., DeGiorgio, M., Bryant, D., Rosenberg, N. A.  
2009; 58 (1): 35-54
  - **Population differentiation and migration: Coalescence times in a two-sex island model for autosomal and X-linked loci** *THEORETICAL POPULATION BIOLOGY*  
Ramachandran, S., Rosenberg, N. A., Feldman, M. W., Wakeley, J.  
2008; 74 (4): 291-301

- **ADZE: a rarefaction approach for counting alleles private to combinations of populations** *BIOINFORMATICS*  
Szpiech, Z. A., Jakobsson, M., Rosenberg, N. A.  
2008; 24 (21): 2498-2504
- **Mathematical properties of the  $r(2)$  measure of linkage disequilibrium** *THEORETICAL POPULATION BIOLOGY*  
VanLiere, J. M., Rosenberg, N. A.  
2008; 74 (1): 130-137
- **The relationship between homozygosity and the frequency of the most frequent allele** *GENETICS*  
Rosenberg, N. A., Jakobsson, M.  
2008; 179 (4): 2027-2036
- **Using population mixtures to optimize the utility of genomic databases: Linkage disequilibrium and association study design in India** *ANNALS OF HUMAN GENETICS*  
Pemberton, T. J., Jakobsson, M., Conrad, D. F., Coop, G., Wall, J. D., Pritchard, J. K., Patel, P. I., Rosenberg, N. A.  
2008; 72: 535-546
- **Demographic history of European populations of *Arabidopsis thaliana*** *PLOS GENETICS*  
Francois, O., Blum, M. G., Jakobsson, M., Rosenberg, N. A.  
2008; 4 (5)
- **Genotype, haplotype and copy-number variation in worldwide human populations** *NATURE*  
Jakobsson, M., Scholz, S. W., Scheet, P., Gibbs, J. R., VanLiere, J. M., Fung, H., Szpiech, Z. A., Degnan, J. H., Wang, K., Guerreiro, R., Bras, J. M., Schymick, J. C., Hernandez, et al  
2008; 451 (7181): 998-1003
- **Genetic variation and population structure in Native Americans** *PLOS GENETICS*  
Wang, S., Lewis, C. M., Jakobsson, M., Ramachandran, S., Ray, N., Bedoya, G., Rojas, W., Parra, M. V., Molina, J. A., Gallo, C., Mazzotti, G., Poletti, G., Hill, et al  
2007; 3 (11): 2049-2067
- **CLUMPP: a cluster matching and permutation program for dealing with label switching and multimodality in analysis of population structure** *BIOINFORMATICS*  
Jakobsson, M., Rosenberg, N. A.  
2007; 23 (14): 1801-1806
- **Estimating the number of ancestral lineages using a maximum-likelihood method based on rejection sampling** *GENETICS*  
Blum, M. G., Rosenberg, N. A.  
2007; 176 (3): 1741-1757
- **Sampling properties of homozygosity-based statistics for linkage disequilibrium** *MATHEMATICAL BIOSCIENCES*  
Rosenberg, N. A., Blum, M. G.  
2007; 208 (1): 33-47
- **The probability distribution under a population divergence model of the number of genetic founding lineages of a population or species** *THEORETICAL POPULATION BIOLOGY*  
Jakobsson, M., Rosenberg, N. A.  
2007; 71 (4): 502-523
- **Genetic diversity and population structure inferred from the partially duplicated genome of domesticated carp, *Cyprinus carpio* L.** *GENETICS SELECTION EVOLUTION*  
David, L., Rosenberg, N. A., Lavi, U., Feldman, M. W., Hillel, J.  
2007; 39 (3): 319-340
- **A private allele ubiquitous in the Americas** *BIOLOGY LETTERS*  
Schroeder, K. B., Schurr, T. G., Long, J. C., Rosenberg, N. A., Crawford, M. H., Tarskaia, L. A., Osipova, L. P., Zhadanov, S. I., Smith, D. G.  
2007; 3 (2): 218-223
- **Low levels of genetic divergence across geographically and linguistically diverse populations from India** *PLOS GENETICS*  
Rosenberg, N. A., Mahajan, S., Gonzalez-Quevedo, C., Blum, M. G., Nino-Rosales, L., Ninis, V., Das, P., Hegde, M., Molinari, L., Zapata, G., Weber, J. L., Belmont, J. W., Patel, et al

2006; 2 (12): 2052-2061

- **A worldwide survey of haplotype variation and linkage disequilibrium in the human genome** *NATURE GENETICS*  
Conrad, D. F., Jakobsson, M., Coop, G., Wen, X., Wall, J. D., Rosenberg, N. A., Pritchard, J. K.  
2006; 38 (11): 1251-1260
- **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*  
Rosenberg, N. A.  
2006; 70: 841-847
- **A general population-genetic model for the production by population structure of spurious genotype-phenotype associations in discrete, admixed or spatially distributed populations** *GENETICS*  
Rosenberg, N. A., Nordborg, M.  
2006; 173 (3): 1665-1678
- **Discordance of species trees with their most likely gene trees** *PLOS GENETICS*  
Degnan, J. H., Rosenberg, N. A.  
2006; 2 (5): 762-768
- **Clines, clusters, and the effect of study design on the inference of human population structure** *PLOS GENETICS*  
Rosenberg, N. A., Mahajan, S., Ramachandran, S., Zhao, C. F., Pritchard, J. K., Feldman, M. W.  
2005; 1 (6): 660-671
- **The pattern of polymorphism in *Arabidopsis thaliana*** *PLOS BIOLOGY*  
Nordborg, M., Hu, T. T., Ishino, Y., Jhaveri, J., Toomajian, C., Zheng, H. G., Bakker, E., Calabrese, P., Gladstone, J., Goyal, R., Jakobsson, M., Kim, S., Morozov, et al  
2005; 3 (7): 1289-1299
- **Polypliod and multilocus extensions of the Wahlund inequality** *THEORETICAL POPULATION BIOLOGY*  
Rosenberg, N. A., Calabrese, P. P.  
2004; 66 (4): 381-391
- **Informativeness of genetic markers for inference of ancestry** *AMERICAN JOURNAL OF HUMAN GENETICS*  
Rosenberg, N. A., Li, L. M., Ward, R., Pritchard, J. K.  
2003; 73 (6): 1402-1422
- **Features of evolution and expansion of modern humans, inferred from genomewide microsatellite markers** *AMERICAN JOURNAL OF HUMAN GENETICS*  
Zhivotovsky, L. A., Rosenberg, N. A., Feldman, M. W.  
2003; 72 (5): 1171-1186
- **Genetic structure of human populations** *SCIENCE*  
Rosenberg, N. A., Pritchard, J. K., Weber, J. L., Cann, H. M., Kidd, K. K., Zhivotovsky, L. A., Feldman, M. W.  
2002; 298 (5602): 2381-2385
- **Genealogical trees, coalescent theory and the analysis of genetic polymorphisms** *NATURE REVIEWS GENETICS*  
Rosenberg, N. A., Nordborg, M.  
2002; 3 (5): 380-390
- **Association mapping in structured populations** *AMERICAN JOURNAL OF HUMAN GENETICS*  
Pritchard, J. K., Stephens, M., Rosenberg, N. A., Donnelly, P.  
2000; 67 (1): 170-181
- **Microsatellite evolution in modern humans: a comparison of two data sets from the same populations** *ANNALS OF HUMAN GENETICS*  
Jin, L., Baskett, M. L., Cavalli-Sforza, L. L., Zhivotovsky, L. A., Feldman, M. W., Rosenberg, N. A.  
2000; 64: 117-134
- **Use of unlinked genetic markers to detect population stratification in association studies** *AMERICAN JOURNAL OF HUMAN GENETICS*  
Pritchard, J. K., Rosenberg, N. A.  
1999; 65 (1): 220-228