

Stanford



Noah Rosenberg

Stanford Professor of Population Genetics and Society
Biology

Bio

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, *Evolution, Medicine, and Public Health* (2014 - present)
- Editor-in-Chief, *Theoretical Population Biology* (2013 - present)
- Associate Editor, *Molecular Biology and Evolution* (2011 - 2014)
- Associate Editor, *Human Biology* (2010 - present)
- Associate Editor, *Genetics* (2010 - 2018)
- Associate Editor, *BMC Bioinformatics* (2010 - 2014)
- 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

CURRENT RESEARCH AND SCHOLARLY INTERESTS

Research in the lab addresses problems in evolutionary biology and human genetics through a combination of mathematical modeling, computer simulations, development of statistical methods, and inference from population-genetic data. Our current work covers topics such as human genetic variation, 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

COURSES

2021-22

- Mathematical Population Biology: BIO 187 (Win)
- Seminar in Computational, Evolutionary, and Human Genomics: BIO 388 (Aut)

2020-21

- Evolutionary Medicine: BIO 89SI (Spr)
- Mathematical Population Biology: BIO 187, CME 187 (Win)

2019-20

- Advanced Topics in Mathematical Evolutionary Biology: BIO 287A (Aut)
- Evolution: BIO 85 (Win)

2018-19

- Advanced Topics in Mathematical Evolutionary Biology: BIO 287A (Win)
- Evolution: BIO 85 (Win)

STANFORD ADVISEES

Doctoral Dissertation Reader (AC)

Ellie Armstrong, Javier Blanco, Kaleda Denton, Alyssa Lyn Fortier, Roshni Patel, Hao Shen

Postdoctoral Faculty Sponsor

Jaehye Kim, Jazlyn Mooney, Lily Tamir

Doctoral Dissertation Advisor (AC)

Daniel Cotter, Xiran Liu

GRADUATE AND FELLOWSHIP PROGRAM AFFILIATIONS

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

Publications

PUBLICATIONS

- **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
- **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 core 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 $D = p_{AB} - p_A p_B$.** *Human heredity*
Kang, J. T., Rosenberg, N. A.
2020: 1–17
- **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
- **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 F_{ST} 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
- **F_{ST} 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
 - **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): 281–95
 - **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): 281–95
 - **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. 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
- **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
- **Parallel Trajectories of Genetic and Linguistic Admixture in a Genetically Admixed Creole Population.** *Current biology : CB*
Verdu, P. n., Jewett, E. M., Pemberton, T. J., Rosenberg, N. A., Baptista, M. n.
2017; 27 (16): 2529–35.e3
- **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
- **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
- **Consanguinity Rates Predict Long Runs of Homozygosity in Jewish Populations.** *Human heredity*
Kang, J. T., Goldberg, A. n., Edge, M. D., Behar, D. M., Rosenberg, N. A.
2016; 82 (3-4): 87–102
- **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
 - **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
 - **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
 - **Theory in population biology, or biologically inspired mathematics?** *Theoretical population biology*
Rosenberg, N. A.
2015; 102: 1-2
 - **Hamilton's rule: Game theory meets coalescent theory.** *Theoretical population biology*
-

- Lehmann, L. n., Rosenberg, N. A.
2015; 103: 1
- **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., Gorodetzky, 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
 - **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
 - **Core elements of a TPB paper.** *Theoretical population biology*
Rosenberg, N. A.
2014; 92: 118-19
 - **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., Hoelzl, 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*
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