

Stanford



Noah Rosenberg

Stanford Professor of Population Genetics and Society
Biology

Bio

ACADEMIC APPOINTMENTS

- Professor, Biology
- Member, Bio-X

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)

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: <http://www.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

2018-19

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

2017-18

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

2016-17

- Evolution: BIO 143 (Win)

2015-16

- Advanced topics in human population genetics: BIO 287 (Spr)
- Current Topics and Concepts in Population Biology, Ecology, and Evolution: BIO 302 (Aut)
- Current Topics and Concepts in Population Biology, Ecology, and Evolution: BIO 303 (Win)
- Current Topics and Concepts in Population Biology, Ecology, and Evolution: BIO 304 (Spr)
- Evolution: BIO 143 (Win)

STANFORD ADVISEES

Doctoral Dissertation Reader (AC)

Daniel Friedman, Elora López

Postdoctoral Faculty Sponsor

Gili Greenbaum, Jaehye Kim

GRADUATE AND FELLOWSHIP PROGRAM AFFILIATIONS

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

Publications

PUBLICATIONS

- **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
- **Coalescent Histories for Lodgepole Species Trees.** *Journal of computational biology*
Disanto, F., Rosenberg, N. A.
2015; 22 (10): 918-929

- **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
- **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
- **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
- **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
- **A Population-Genetic Perspective on the Similarities and Differences Among Worldwide Human Populations** *HUMAN BIOLOGY*
Rosenberg, N. A.
2011; 83 (6): 659-684
- **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
- **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
- **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
- **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
- **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*

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- 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
 - **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
 - **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
 - **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

- **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
- **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
- **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)
- **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
- **From generation to generation: the genetics of jewish populations.** *Human biology*
Rosenberg, N. A., Weitzman, S. P.
2013; 85 (6): 817-824
- **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
- **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 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
- **Mathematical properties of F_{st} 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*
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