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 Humanitites & 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

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)

2021-22

- Mathematical Population Biology: BIO 187, CME 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)

STANFORD ADVISEES

Doctoral Dissertation Reader (AC)

Javier Blanco, Mallory Harris, Roshni Patel, Rachel Ungar, Julie Zhang

Postdoctoral Faculty Sponsor

Lily Tamir

Doctoral Dissertation Advisor (AC)

Egor Lappo, Maike Morrison, Juan Esteban Rodriguez Rodriguez, Chloe Shiff

GRADUATE AND FELLOWSHIP PROGRAM AFFILIATIONS

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

Publications

PUBLICATIONS

- **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

- **Clumppling: 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 ith 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 frogfor Bayesian inference regardingpast 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
- **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.
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