

Noah A Rosenberg

List of Publications by Year in descending order

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199
papers

34,062
citations

34105

52
h-index

4117

175
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223
all docs

223
docs citations

223
times ranked

32844
citing authors

#	ARTICLE	IF	CITATIONS
1	CLUMPP: a cluster matching and permutation program for dealing with label switching and multimodality in analysis of population structure. <i>Bioinformatics</i> , 2007, 23, 1801-1806.	4.1	5,408
2	distruct: a program for the graphical display of population structure. <i>Molecular Ecology Notes</i> , 2003, 4, 137-138.	1.7	4,229
3	Genetic Structure of Human Populations. <i>Science</i> , 2002, 298, 2381-2385.	12.6	2,434
4	<scp>Clumpak</scp>: a program for identifying clustering modes and packaging population structure inferences across <i>K</i>. <i>Molecular Ecology Resources</i> , 2015, 15, 1179-1191.	4.8	2,411
5	Association Mapping in Structured Populations. <i>American Journal of Human Genetics</i> , 2000, 67, 170-181.	6.2	1,827
6	Gene tree discordance, phylogenetic inference and the multispecies coalescent. <i>Trends in Ecology and Evolution</i> , 2009, 24, 332-340.	8.7	1,500
7	Use of Unlinked Genetic Markers to Detect Population Stratification in Association Studies. <i>American Journal of Human Genetics</i> , 1999, 65, 220-228.	6.2	1,112
8	Support from the relationship of genetic and geographic distance in human populations for a serial founder effect originating in Africa. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 15942-15947.	7.1	957
9	The Pattern of Polymorphism in <i>Arabidopsis thaliana</i> . <i>PLoS Biology</i> , 2005, 3, e196.	5.6	895
10	Inferring Species Trees Directly from Biallelic Genetic Markers: Bypassing Gene Trees in a Full Coalescent Analysis. <i>Molecular Biology and Evolution</i> , 2012, 29, 1917-1932.	8.9	828
11	Genotype, haplotype and copy-number variation in worldwide human populations. <i>Nature</i> , 2008, 451, 998-1003.	27.8	780
12	Discordance of Species Trees with Their Most Likely Gene Trees. <i>PLoS Genetics</i> , 2006, 2, e68.	3.5	761
13	ADZE: a rarefaction approach for counting alleles private to combinations of populations. <i>Bioinformatics</i> , 2008, 24, 2498-2504.	4.1	666
14	Informativeness of Genetic Markers for Inference of Ancestry*. <i>American Journal of Human Genetics</i> , 2003, 73, 1402-1422.	6.2	600
15	Genealogical trees, coalescent theory and the analysis of genetic polymorphisms. <i>Nature Reviews Genetics</i> , 2002, 3, 380-390.	16.3	582
16	Genome-wide association studies in diverse populations. <i>Nature Reviews Genetics</i> , 2010, 11, 356-366.	16.3	518
17	A worldwide survey of haplotype variation and linkage disequilibrium in the human genome. <i>Nature Genetics</i> , 2006, 38, 1251-1260.	21.4	474
18	Clines, Clusters, and the Effect of Study Design on the Inference of Human Population Structure. <i>PLoS Genetics</i> , 2005, 1, e70.	3.5	473

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19	Genetic Variation and Population Structure in Native Americans. PLoS Genetics, 2007, 3, e185.	3.5	454
20	Genomic Patterns of Homozygosity in Worldwide Human Populations. American Journal of Human Genetics, 2012, 91, 275-292.	6.2	393
21	Empirical Evaluation of Genetic Clustering Methods Using Multilocus Genotypes From 20 Chicken Breeds. Genetics, 2001, 159, 699-713.	2.9	306
22	The Probability of Topological Concordance of Gene Trees and Species Trees. Theoretical Population Biology, 2002, 61, 225-247.	1.1	268
23	Features of Evolution and Expansion of Modern Humans, Inferred from Genomewide Microsatellite Markers. American Journal of Human Genetics, 2003, 72, 1171-1186.	6.2	233
24	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, 2006, 70, 841-847.	0.8	233
25	Genotype-Imputation Accuracy across Worldwide Human Populations. American Journal of Human Genetics, 2009, 84, 235-250.	6.2	231
26	Long Runs of Homozygosity Are Enriched for Deleterious Variation. American Journal of Human Genetics, 2013, 93, 90-102.	6.2	227
27	The Relationship Between F_{ST} and the Frequency of the Most Frequent Allele. Genetics, 2013, 193, 515-528.	2.9	212
28	THE SHAPES OF NEUTRAL GENE GENEALOGIES IN TWO SPECIES: PROBABILITIES OF MONOPHYLY, PARAPHYLY, AND POLYPHYLY IN A COALESCENT MODEL. Evolution; International Journal of Organic Evolution, 2003, 57, 1465-1477.	2.3	201
29	Demographic History of European Populations of Arabidopsis thaliana. PLoS Genetics, 2008, 4, e1000075.	3.5	182
30	STATISTICAL TESTS FOR TAXONOMIC DISTINCTIVENESS FROM OBSERVATIONS OF MONOPHYLY. Evolution; International Journal of Organic Evolution, 2007, 61, 317-323.	2.3	166
31	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, 2009, 106, 16057-16062.	7.1	161
32	Mathematical properties of the measure of linkage disequilibrium. Theoretical Population Biology, 2008, 74, 130-137.	1.1	152
33	Properties of Consensus Methods for Inferring Species Trees from Gene Trees. Systematic Biology, 2009, 58, 35-54.	5.6	135
34	Population Structure in a Comprehensive Genomic Data Set on Human Microsatellite Variation. G3: Genes, Genomes, Genetics, 2013, 3, 891-907.	1.8	123
35	A comparison of worldwide phonemic and genetic variation in human populations. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 1265-1272.	7.1	122
36	A Quantitative Comparison of the Similarity between Genes and Geography in Worldwide Human Populations. PLoS Genetics, 2012, 8, e1002886.	3.5	106

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37	Inference of Unexpected Genetic Relatedness among Individuals in HapMap Phase III. American Journal of Human Genetics, 2010, 87, 457-464.	6.2	104
38	Comparing Spatial Maps of Human Population-Genetic Variation Using Procrustes Analysis. Statistical Applications in Genetics and Molecular Biology, 2010, 9, Article 13.	0.6	103
39	Discordance of Species Trees with Their Most Likely Gene Trees: The Case of Five Taxa. Systematic Biology, 2008, 57, 131-140.	5.6	100
40	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, 2017, 114, 2657-2662.	7.1	94
41	Interpreting polygenic scores, polygenic adaptation, and human phenotypic differences. Evolution, Medicine and Public Health, 2019, 2019, 26-34.	2.5	90
42	Low Levels of Genetic Divergence across Geographically and Linguistically Diverse Populations from India. PLoS Genetics, 2006, 2, e215.	3.5	82
43	A Population-Genetic Perspective on the Similarities and Differences among Worldwide Human Populations. Human Biology, 2011, 83, 659-684.	0.2	82
44	Patterns of Admixture and Population Structure in Native Populations of Northwest North America. PLoS Genetics, 2014, 10, e1004530.	3.5	81
45	Discordance of Species Trees with Their Most Likely Gene Trees: A Unifying Principle. Molecular Biology and Evolution, 2013, 30, 2709-2713.	8.9	78
46	Haplotypic Background of a Private Allele at High Frequency in the Americas. Molecular Biology and Evolution, 2009, 26, 995-1016.	8.9	74
47	A General Mechanistic Model for Admixture Histories of Hybrid Populations. Genetics, 2011, 189, 1413-1426.	2.9	74
48	Beyond 2/3 and 1/3: The Complex Signatures of Sex-Biased Admixture on the X Chromosome. Genetics, 2015, 201, 263-279.	2.9	74
49	Consistency Properties of Species Tree Inference by Minimizing Deep Coalescences. Journal of Computational Biology, 2011, 18, 1-15.	1.6	71
50	Evaluating allopolyploid origins in strawberries (Fragaria) using haplotypes generated from target capture sequencing. BMC Evolutionary Biology, 2017, 17, 180.	3.2	69
51	The Relationship between Imputation Error and Statistical Power in Genetic Association Studies in Diverse Populations. American Journal of Human Genetics, 2009, 85, 692-698.	6.2	68
52	No Evidence from Genome-Wide Data of a Khazar Origin for the Ashkenazi Jews. Human Biology, 2013, 85, 859-900.	0.2	68
53	Algorithms for Selecting Informative Marker Panels for Population Assignment. Journal of Computational Biology, 2005, 12, 1183-1201.	1.6	67
54	The Mean and Variance of the Numbers of r-Pronged Nodes and r-Caterpillars in Yule-Generated Genealogical Trees. Annals of Combinatorics, 2006, 10, 129-146.	0.6	59

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55	Individual Identifiability Predicts Population Identifiability in Forensic Microsatellite Markers. <i>Current Biology</i> , 2016, 26, 935-942.	3.9	59
56	Robustness of the inference of human population structure: A comparison of X-chromosomal and autosomal microsatellites. <i>Human Genomics</i> , 2004, 1, 87-97.	2.9	56
57	Sequence determinants of human microsatellite variability. <i>BMC Genomics</i> , 2009, 10, 612.	2.8	56
58	A General Population-Genetic Model for the Production by Population Structure of Spurious Genotype-Phenotype Associations in Discrete, Admixed or Spatially Distributed Populations. <i>Genetics</i> , 2006, 173, 1665-1678.	2.9	55
59	A Maximum-Likelihood Method to Correct for Allelic Dropout in Microsatellite Data with No Replicate Genotypes. <i>Genetics</i> , 2012, 192, 651-669.	2.9	54
60	On the size distribution of private microsatellite alleles. <i>Theoretical Population Biology</i> , 2011, 80, 100-113.	1.1	50
61	Lack of Population Diversity in Commonly Used Human Embryonic Stem-Cell Lines. <i>New England Journal of Medicine</i> , 2010, 362, 183-185.	27.0	49
62	Linkage disequilibrium matches forensic genetic records to disjoint genomic marker sets. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 5671-5676.	7.1	49
63	Statistical Tests of the Coalescent Model Based on the Haplotype Frequency Distribution and the Number of Segregating Sites. <i>Genetics</i> , 2005, 169, 1763-1777.	2.9	46
64	Genomic microsatellites identify shared Jewish ancestry intermediate between Middle Eastern and European populations. <i>BMC Genetics</i> , 2009, 10, 80.	2.7	46
65	Counting Coalescent Histories. <i>Journal of Computational Biology</i> , 2007, 14, 360-377.	1.6	44
66	The probability distribution of ranked gene trees on a species tree. <i>Mathematical Biosciences</i> , 2012, 235, 45-55.	1.9	44
67	Coalescence-Time Distributions in a Serial Founder Model of Human Evolutionary History. <i>Genetics</i> , 2011, 189, 579-593.	2.9	41
68	Haplotype variation and genotype imputation in African populations. <i>Genetic Epidemiology</i> , 2011, 35, 766-780.	1.3	39
69	Statistical Detection of Relatives Typed with Disjoint Forensic and Biomedical Loci. <i>Cell</i> , 2018, 175, 848-858.e6.	28.9	37
70	Population differentiation and migration: Coalescence times in a two-sex island model for autosomal and X-linked loci. <i>Theoretical Population Biology</i> , 2008, 74, 291-301.	1.1	36
71	Population-Genetic Influences on Genomic Estimates of the Inbreeding Coefficient: A Global Perspective. <i>Human Heredity</i> , 2014, 77, 37-48.	0.8	35
72	Enhancing the mathematical properties of new haplotype homozygosity statistics for the detection of selective sweeps. <i>Theoretical Population Biology</i> , 2015, 102, 94-101.	1.1	35

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73	Disease transmission and introgression can explain the long-lasting contact zone of modern humans and Neanderthals. <i>Nature Communications</i> , 2019, 10, 5003.	12.8	30
74	<i>MLH1</i> Founder Mutations with Moderate Penetrance in Spanish Lynch Syndrome Families. <i>Cancer Research</i> , 2010, 70, 7379-7391.	0.9	29
75	Autosomal Admixture Levels Are Informative About Sex Bias in Admixed Populations. <i>Genetics</i> , 2014, 198, 1209-1229.	2.9	28
76	Genetic Diversity and Societally Important Disparities. <i>Genetics</i> , 2015, 201, 1-12.	2.9	28
77	An Unbiased Estimator of Gene Diversity in Samples Containing Related Individuals. <i>Molecular Biology and Evolution</i> , 2008, 26, 501-512.	8.9	26
78	iGLASS: An Improvement to the GLASS Method for Estimating Species Trees from Gene Trees. <i>Journal of Computational Biology</i> , 2012, 19, 293-315.	1.6	26
79	Implications of the apportionment of human genetic diversity for the apportionment of human phenotypic diversity. <i>Studies in History and Philosophy of Science Part C: Studies in History and Philosophy of Biological and Biomedical Sciences</i> , 2015, 52, 32-45.	1.3	26
80	Estimating change rates of genetic markers using serial samples: applications to the transposon IS6110 in <i>Mycobacterium tuberculosis</i> . <i>Theoretical Population Biology</i> , 2003, 63, 347-363.	1.1	25
81	Mathematical Constraints on <i>F_{ST}</i> : Biallelic Markers in Arbitrarily Many Populations. <i>Genetics</i> , 2017, 206, 1581-1600.	2.9	25
82	A test of the influence of continental axes of orientation on patterns of human gene flow. <i>American Journal of Physical Anthropology</i> , 2011, 146, 515-529.	2.1	24
83	A Coalescent Model for Genotype Imputation. <i>Genetics</i> , 2012, 191, 1239-1255.	2.9	24
84	Genotype Imputation Reference Panel Selection Using Maximal Phylogenetic Diversity. <i>Genetics</i> , 2013, 195, 319-330.	2.9	24
85	AABC: Approximate approximate Bayesian computation for inference in population-genetic models. <i>Theoretical Population Biology</i> , 2015, 99, 31-42.	1.1	24
86	Upper bounds on $\frac{1}{n} \sum_{i=1}^n \frac{f_i}{F} \geq \frac{1}{n} \sum_{i=1}^n \frac{f_i}{S} \geq \frac{1}{n} \sum_{i=1}^n \frac{f_i}{T}$ in terms of the frequency of the most frequent allele and total homozygosity: The case of a specified number of alleles. <i>Theoretical Population Biology</i> , 2014, 97, 20-34.	1.1	24
87	Consanguinity Rates Predict Long Runs of Homozygosity in Jewish Populations. <i>Human Heredity</i> , 2016, 82, 87-102.	0.8	22
88	Parallel Trajectories of Genetic and Linguistic Admixture in a Genetically Admixed Creole Population. <i>Current Biology</i> , 2017, 27, 2529-2535.e3.	3.9	22
89	The Control of Copy Number of IS6110 in <i>Mycobacterium tuberculosis</i> . <i>Molecular Biology and Evolution</i> , 2004, 21, 2195-2201.	8.9	21
90	Nonadaptive Explanations for Signatures of Partial Selective Sweeps in <i>Drosophila</i> . <i>Molecular Biology and Evolution</i> , 2008, 25, 1025-1042.	8.9	21

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91	An empirical evaluation of two-stage species tree inference strategies using a multilocus dataset from North American pines. BMC Evolutionary Biology, 2014, 14, 67.	3.2	21
92	On the Use of Star-Shaped Genealogies in Inference of Coalescence Times. Genetics, 2003, 164, 1677-1682.	2.9	21
93	THE SHAPES OF NEUTRAL GENE GENEALOGIES IN TWO SPECIES: PROBABILITIES OF MONOPHYLY, PARAPHYLY, AND POLYPHYLY IN A COALESCENT MODEL. Evolution; International Journal of Organic Evolution, 2003, 57, 1465.	2.3	20
94	Coalescent histories for discordant gene trees and species trees. Theoretical Population Biology, 2010, 77, 145-151.	1.1	20
95	Geographic Sampling Scheme as a Determinant of the Major Axis of Genetic Variation in Principal Components Analysis. Molecular Biology and Evolution, 2013, 30, 480-488.	8.9	20
96	Distance metrics for ranked evolutionary trees. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 28876-28886.	7.1	20
97	Genetic diversity and population structure inferred from the partially duplicated genome of domesticated carp, <i>Cyprinus carpio</i> L. Genetics Selection Evolution, 2007, 39, 319.	3.0	19
98	The Relationship Between Homozygosity and the Frequency of the Most Frequent Allele. Genetics, 2008, 179, 2027-2036.	2.9	19
99	Mathematical properties of $\sum_{i=1}^n \sum_{j=1}^n \frac{1}{n_i n_j} \frac{1}{n_i + n_j}$ for admixed populations and their parental source populations. Theoretical Population Biology, 2011, 80, 200-216.	1.1	19
100	A General Model of the Relationship between the Apportionment of Human Genetic Diversity and the Apportionment of Human Phenotypic Diversity. Human Biology, 2015, 87, 313.	0.2	19
101	Predicting Carriers of Ongoing Selective Sweeps without Knowledge of the Favored Allele. PLoS Genetics, 2015, 11, e1005527.	3.5	19
102	The Effect of Consanguinity on Between-Individual Identity-by-Descent Sharing. Genetics, 2019, 212, 305-316.	2.9	19
103	, Jost's D , and F_{ST} are similarly constrained by allele frequencies: A mathematical, simulation, and empirical study. Molecular Ecology, 2019, 28, 1624-1636.	3.9	19
104	Polyploid and multilocus extensions of the Wahlund inequality. Theoretical Population Biology, 2004, 66, 381-391.	1.1	18
105	Improvements to a Class of Distance Matrix Methods for Inferring Species Trees from Gene Trees. Journal of Computational Biology, 2012, 19, 632-649.	1.6	18
106	Impact of restricted marital practices on genetic variation in an endogamous Gujarati group. American Journal of Physical Anthropology, 2012, 149, 92-103.	2.1	18
107	Does Gene Tree Discordance Explain the Mismatch between Macroevolutionary Models and Empirical Patterns of Tree Shape and Branching Times?. Systematic Biology, 2016, 65, 628-639.	5.6	18
108	Optimal estimation of transposition rates of insertion sequences for molecular epidemiology. Statistics in Medicine, 2001, 20, 2409-2420.	1.6	17

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109	Mathematical Properties of the Deep Coalescence Cost. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2013, 10, 61-72.	3.0	17
110	Theory and applications of a deterministic approximation to the coalescent model. Theoretical Population Biology, 2014, 93, 14-29.	1.1	16
111	On the heterozygosity of an admixed population. Journal of Mathematical Biology, 2020, 81, 1217-1250.	1.9	16
112	A Characterization of the Set of Species Trees that Produce Anomalous Ranked Gene Trees. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2012, 9, 1558-1568.	3.0	15
113	Coalescent Histories for Lodgepole Species Trees. Journal of Computational Biology, 2015, 22, 918-929.	1.6	15
114	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, 2016, 113, 8002-8009.	7.1	15
115	Simulation-Based Evaluation of Hybridization Network Reconstruction Methods in the Presence of Incomplete Lineage Sorting. Evolutionary Bioinformatics, 2017, 13, 117693431769193.	1.2	15
116	A genome scan for genes underlying adult body size differences between Central African hunter-gatherers and farmers. Human Genetics, 2018, 137, 487-509.	3.8	15
117	Enumeration of Ancestral Configurations for Matching Gene Trees and Species Trees. Journal of Computational Biology, 2017, 24, 831-850.	1.6	14
118	Modelling anti-vaccine sentiment as a cultural pathogen. Evolutionary Human Sciences, 2020, 2, .	1.7	14
119	How dormant is Mycobacterium tuberculosis during latency? A study integrating genomics and molecular epidemiology. Infection, Genetics and Evolution, 2011, 11, 1164-1167.	2.3	13
120	Refining the relationship between homozygosity and the frequency of the most frequent allele. Journal of Mathematical Biology, 2012, 64, 87-108.	1.9	13
121	Coalescent Histories for Caterpillar-Like Families. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2013, 10, 1253-1262.	3.0	13
122	Consistency and inconsistency of consensus methods for inferring species trees from gene trees in the presence of ancestral population structure. Theoretical Population Biology, 2016, 110, 12-24.	1.1	13
123	Asymptotic Properties of the Number of Matching Coalescent Histories for Caterpillar-Like Families of Species Trees. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2016, 13, 913-925.	3.0	13
124	Assortative mating by population of origin in a mechanistic model of admixture. Theoretical Population Biology, 2020, 134, 129-146.	1.1	13
125	Genetic Adaptation in New York City Rats. Genome Biology and Evolution, 2021, 13, .	2.5	13
126	Designing gene drives to limit spillover to non-target populations. PLoS Genetics, 2021, 17, e1009278.	3.5	12

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127	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, 2017, 114, E3875-E3877.	7.1	11
128	A sharp minimum on the mean number of steps taken in adaptive walks. Journal of Theoretical Biology, 2005, 237, 17-22.	1.7	10
129	HaploScope: a tool for the graphical display of haplotype structure in populations. Genetic Epidemiology, 2012, 36, 17-21.	1.3	10
130	Admixture Models and the Breeding Systems of H. S. Jennings: A GENETICS Connection. Genetics, 2016, 202, 9-13.	2.9	10
131	Network-based hierarchical population structure analysis for large genomic data sets. Genome Research, 2019, 29, 2020-2033.	5.5	10
132	THE BEHAVIOR OF ADMIXED POPULATIONS IN NEIGHBOR-JOINING INFERENCE OF POPULATION TREES. , 2012, , .		10
133	Ancient and modern genomics of the Ohlone Indigenous population of California. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, e2111533119.	7.1	10
134	Read all about it: The Lancet 's Paper of the Year, 2003. Lancet, The, 2003, 362, 2101-2103.	13.7	9
135	Mathematical Properties of Linkage Disequilibrium Statistics Defined by Normalization of the Coefficient D' = $\frac{D}{\max(D , \frac{1}{2}(p_A - p_B)(p_A + p_B))}$ "Human Heredity, 2019, 84, 127-143.	0.8	9
136	Measures of care fragmentation: Mathematical insights from population genetics. Health Services Research, 2020, 55, 318-327.	2.0	9
137	Human-Genetic Ancestry Inference and False Positives in Forensic Familial Searching. G3: Genes, Genomes, Genetics, 2020, 10, 2893-2902.	1.8	9
138	Estimating the Number of Ancestral Lineages Using a Maximum-Likelihood Method Based on Rejection Sampling. Genetics, 2007, 176, 1741-1757.	2.9	8
139	On the Genealogy of a Duplicated Microsatellite. Genetics, 2007, 177, 2109-2122.	2.9	8
140	Sampling properties of homozygosity-based statistics for linkage disequilibrium. Mathematical Biosciences, 2007, 208, 33-47.	1.9	8
141	Heterozygosity of the Yellowstone wolves. Molecular Ecology, 2010, 19, 3246-3249.	3.9	8
142	Unbiased Estimation of Gene Diversity in Samples Containing Related Individuals: Exact Variance and Arbitrary Ploidy. Genetics, 2010, 186, 1367-1387.	2.9	8
143	Runs of homozygosity and parental relatedness. Genetics in Medicine, 2013, 15, 753-754.	2.4	8
144	Windfalls and pitfalls. Evolution, Medicine and Public Health, 2013, 2013, 254-272.	2.5	8

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145	Variance-Partitioning and Classification in Human Population Genetics. , 0, , 399-404.		8
146	Enumeration of compact coalescent histories for matching gene trees and species trees. Journal of Mathematical Biology, 2019, 78, 155-188.	1.9	8
147	Skin deep: The decoupling of genetic admixture levels from phenotypes that differed between source populations. American Journal of Physical Anthropology, 2021, 175, 406-421.	2.1	8
148	The behavior of admixed populations in neighbor-joining inference of population trees. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2013, , 273-84.	0.7	8
149	Replication of genetic associations as pseudoreplication due to shared genealogy. Genetic Epidemiology, 2009, 33, 479-487.	1.3	7
150	Inference on the strength of balancing selection for epistatically interacting loci. Theoretical Population Biology, 2011, 79, 102-113.	1.1	7
151	Genotype imputation in a coalescent model with infinitely-many-sites mutation. Theoretical Population Biology, 2013, 87, 62-74.	1.1	7
152	On the joint distribution of tree height and tree length under the coalescent. Theoretical Population Biology, 2018, 122, 46-56.	1.1	7
153	On the Number of Non-equivalent Ancestral Configurations for Matching Gene Trees and Species Trees. Bulletin of Mathematical Biology, 2019, 81, 384-407.	1.9	7
154	The probability of reciprocal monophyly of gene lineages in three and four species. Theoretical Population Biology, 2019, 129, 133-147.	1.1	7
155	Enumeration of lonely pairs of gene trees and species trees by means of antipodal cherries. Advances in Applied Mathematics, 2019, 102, 1-17.	0.7	7
156	Fifty years of Theoretical Population Biology. Theoretical Population Biology, 2020, 133, 1-12.	1.1	7
157	Variance and limiting distribution of coalescence times in a diploid model of a consanguineous population. Theoretical Population Biology, 2021, 139, 50-65.	1.1	7
158	Mathematical constraints on F_{ST} : multiallelic markers in arbitrarily many populations. Philosophical Transactions of the Royal Society B: Biological Sciences, 2022, 377, 20200414.	4.0	7
159	High-resolution inference of genetic relationships among Jewish populations. European Journal of Human Genetics, 2020, 28, 804-814.	2.8	6
160	The effect of consanguinity on coalescence times on the X chromosome. Theoretical Population Biology, 2021, 140, 32-43.	1.1	6
161	F_{ST} : An F_{ST} -based tool for measuring ancestry variation in inference of population structure. Molecular Ecology Resources, 2022, 22, 2614-2626.	4.8	6
162	The probability distribution under a population divergence model of the number of genetic founding lineages of a population or species. Theoretical Population Biology, 2007, 71, 502-523.	1.1	5

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163	On the Number of Ranked Species Trees Producing Anomalous Ranked Gene Trees. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2014, 11, 1229-1238.	3.0	5
164	Celebrating 50 years since Lewontin's apportionment of human diversity. Philosophical Transactions of the Royal Society B: Biological Sciences, 2022, 377, 20200405.	4.0	5
165	Genetics and the History of the Samaritans: Y-Chromosomal Microsatellites and Genetic Affinity between Samaritans and Cohanim. Human Biology, 2013, 85, 825-857.	0.2	4
166	Bounding measures of genetic similarity and diversity using majorization. Journal of Mathematical Biology, 2018, 77, 711-737.	1.9	4
167	The Relationship Between Haplotype-Based F_{ST} and Haplotype Length. Genetics, 2019, 213, 281-295.	2.9	4
168	Coalescent Theory of Migration Network Motifs. Molecular Biology and Evolution, 2019, 36, 2358-2374.	8.9	4
169	Roadblocked monotonic paths and the enumeration of coalescent histories for non-matching caterpillar gene trees and species trees. Advances in Applied Mathematics, 2020, 113, 101939.	0.7	4
170	On the Colijn-Plazzotta numbering scheme for unlabeled binary rooted trees. Discrete Applied Mathematics, 2021, 291, 88-98.	0.9	4
171	A simple derivation of the mean of the Sackin index of tree balance under the uniform model on rooted binary labeled trees. Mathematical Biosciences, 2021, 342, 108688.	1.9	4
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