

Noah A Rosenberg

List of Publications by Year in descending order

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Version: 2024-02-01

199
papers

34,062
citations

34105

52
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4117

175
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223
all docs

223
docs citations

223
times ranked

32844
citing authors

#	ARTICLE	IF	CITATIONS
1	A compendium of covariances and correlation coefficients of coalescent tree properties. Theoretical Population Biology, 2022, 143, 1-13.	1.1	4
2	The 2022 Feldman Prize. Theoretical Population Biology, 2022, 143, 105-106.	1.1	0
3	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
4	Mathematical epidemiology for a later age. Theoretical Population Biology, 2022, 144, 81-83.	1.1	0
5	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
6	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
7	The Probability of Joint Monophyly of Samples of Gene Lineages for All Species in an Arbitrary Species Tree. Journal of Computational Biology, 2022, , .	1.6	1
8	Enumeration of binary trees compatible with a perfect phylogeny. Journal of Mathematical Biology, 2022, 84, 54.	1.9	1
9	Extracting hierarchical features of cultural variation using network-based clustering. Evolutionary Human Sciences, 2022, 4, .	1.7	2
10	F_{ST} -based tool for measuring ancestry variation in inference of population structure. Molecular Ecology Resources, 2022, 22, 2614-2626.	4.8	6
11	Genetic Adaptation in New York City Rats. Genome Biology and Evolution, 2021, 13, .	2.5	13
12	Population models, mathematical epidemiology, and the COVID-19 pandemic. Theoretical Population Biology, 2021, 137, 1.	1.1	2
13	Designing gene drives to limit spillover to non-target populations. PLoS Genetics, 2021, 17, e1009278.	3.5	12
14	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
15	On the Colijn-Plazzotta numbering scheme for unlabeled binary rooted trees. Discrete Applied Mathematics, 2021, 291, 88-98.	0.9	4
16	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
17	The effect of consanguinity on coalescence times on the X chromosome. Theoretical Population Biology, 2021, 140, 32-43.	1.1	6
18	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

19	Enumeration of coalescent histories for caterpillar species trees and p-pseudocaterpillar gene trees. Advances in Applied Mathematics, 2021, 131, 102265.	0.7	3
20	$\sum_{i=1}^n \frac{1}{i}$ the triangle inequality for biallelic markers. Theoretical Population Biology, 2020, 133, 117-129.	0.8	3
21	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
22	Probabilities of Unranked and Ranked Anomaly Zones under Birth–Death Models. Molecular Biology and Evolution, 2020, 37, 1480-1494.	8.9	3
23	High-resolution inference of genetic relationships among Jewish populations. European Journal of Human Genetics, 2020, 28, 804-814.	2.8	6
24	The 2020 Feldman Prize. Theoretical Population Biology, 2020, 131, 1.	1.1	0
25	On the heterozygosity of an admixed population. Journal of Mathematical Biology, 2020, 81, 1217-1250.	1.9	16
26	Assortative mating by population of origin in a mechanistic model of admixture. Theoretical Population Biology, 2020, 134, 129-146.	1.1	13
27	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
28	Modelling anti-vaccine sentiment as a cultural pathogen. Evolutionary Human Sciences, 2020, 2, .	1.7	14
29	Measures of care fragmentation: Mathematical insights from population genetics. Health Services Research, 2020, 55, 318-327.	2.0	9
30	Fifty years of Theoretical Population Biology. Theoretical Population Biology, 2020, 133, 1-12.	1.1	7
31	A Population-Genetic Perspective on the Similarities and Differences among Worldwide Human Populations. Human Biology, 2020, 92, 135.	0.2	2
32	Human-Genetic Ancestry Inference and False Positives in Forensic Familial Searching. G3: Genes, Genomes, Genetics, 2020, 10, 2893-2902.	1.8	9
33	Mathematical and Simulation-Based Analysis of the Behavior of Admixed Taxa in the Neighbor-Joining Algorithm. Bulletin of Mathematical Biology, 2019, 81, 452-493.	1.9	2
34	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
35	The probability of reciprocal monophyly of gene lineages in three and four species. Theoretical Population Biology, 2019, 129, 133-147.	1.1	7

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37	Use of stochastic patch occupancy models in the California red-legged frog for Bayesian inference regarding past events and future persistence. <i>Conservation Biology</i> , 2019, 33, 685-696.	4.7	2
38	The Relationship Between Haplotype-Based F_{ST} and Haplotype Length. <i>Genetics</i> , 2019, 213, 281-295.	2.9	4
39	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
40	Network-based hierarchical population structure analysis for large genomic data sets. <i>Genome Research</i> , 2019, 29, 2020-2033.	5.5	10
41	Coalescent Theory of Migration Network Motifs. <i>Molecular Biology and Evolution</i> , 2019, 36, 2358-2374.	8.9	4
42	Analysis of author gender in TPB, 1991–2018. <i>Theoretical Population Biology</i> , 2019, 127, 1-6.	1.1	1
43	The Effect of Consanguinity on Between-Individual Identity-by-Descent Sharing. <i>Genetics</i> , 2019, 212, 305-316.	2.9	19
44	Mathematical Properties of Linkage Disequilibrium Statistics Defined by Normalization of the Coefficient D' : $D' = \frac{D}{\max(D , \frac{1}{2} \sum_{i \neq j} p_i p_j)}$ and D' for AB and ab are $D' = \frac{D}{\max(D , \frac{1}{2} \sum_{i \neq j} p_i p_j)}$. <i>Human Heredity</i> , 2019, 84, 127-143.	0.8	9
45	Jost's D' , and F_{ST} are similarly constrained by allele frequencies: A mathematical, simulation, and empirical study. <i>Molecular Ecology</i> , 2019, 28, 1624-1636.	3.9	19
46	Interpreting polygenic scores, polygenic adaptation, and human phenotypic differences. <i>Evolution, Medicine and Public Health</i> , 2019, 2019, 26-34.	2.5	90
47	Some topics in theoretical population genetics: Editorial commentaries on a selection of Marc Feldman's TPB papers. <i>Theoretical Population Biology</i> , 2019, 129, 4-8.	1.1	1
48	Enumeration of lonely pairs of gene trees and species trees by means of antipodal cherries. <i>Advances in Applied Mathematics</i> , 2019, 102, 1-17.	0.7	7
49	The 2018 Marcus W. Feldman Prize in Theoretical Population Biology. <i>Theoretical Population Biology</i> , 2018, 119, 1-2.	1.1	1
50	Bounding measures of genetic similarity and diversity using majorization. <i>Journal of Mathematical Biology</i> , 2018, 77, 711-737.	1.9	4
51	On the joint distribution of tree height and tree length under the coalescent. <i>Theoretical Population Biology</i> , 2018, 122, 46-56.	1.1	7
52	Statistical Detection of Relatives Typed with Disjoint Forensic and Biomedical Loci. <i>Cell</i> , 2018, 175, 848-858.e6.	28.9	37
53	A genome scan for genes underlying adult body size differences between Central African hunter-gatherers and farmers. <i>Human Genetics</i> , 2018, 137, 487-509.	3.8	15
54	Ancient X chromosomes reveal contrasting sex bias in Neolithic and Bronze Age Eurasian migrations. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 2657-2662.	7.1	94

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55	Mathematical Constraints on F_{ST} : Biallelic Markers in Arbitrarily Many Populations. <i>Genetics</i> , 2017, 206, 1581-1600.	2.9	25
56	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
57	Enumeration of Ancestral Configurations for Matching Gene Trees and Species Trees. <i>Journal of Computational Biology</i> , 2017, 24, 831-850.	1.6	14
58	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
59	Simulation-Based Evaluation of Hybridization Network Reconstruction Methods in the Presence of Incomplete Lineage Sorting. <i>Evolutionary Bioinformatics</i> , 2017, 13, 117693431769193.	1.2	15
60	Evaluating allopolyploid origins in strawberries (<i>Fragaria</i>) using haplotypes generated from target capture sequencing. <i>BMC Evolutionary Biology</i> , 2017, 17, 180.	3.2	69
61	Reply to Lazaridis and Reich: Robust model-based inference of male-biased admixture during Bronze Age migration from the Pontic-Caspian Steppe. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E3875-E3877.	7.1	11
62	Admixture Models and the Breeding Systems of H. S. Jennings: A GENETICS Connection. <i>Genetics</i> , 2016, 202, 9-13.	2.9	10
63	The probability of monophyly of a sample of gene lineages on a species tree. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 8002-8009.	7.1	15
64	Individual Identifiability Predicts Population Identifiability in Forensic Microsatellite Markers. <i>Current Biology</i> , 2016, 26, 935-942.	3.9	59
65	Consistency and inconsistency of consensus methods for inferring species trees from gene trees in the presence of ancestral population structure. <i>Theoretical Population Biology</i> , 2016, 110, 12-24.	1.1	13
66	Consanguinity Rates Predict Long Runs of Homozygosity in Jewish Populations. <i>Human Heredity</i> , 2016, 82, 87-102.	0.8	22
67	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. <i>BMC Bioinformatics</i> , 2016, 17, 417.	2.6	1
68	Does Gene Tree Discordance Explain the Mismatch between Macroevolutionary Models and Empirical Patterns of Tree Shape and Branching Times?. <i>Systematic Biology</i> , 2016, 65, 628-639.	5.6	18
69	Asymptotic Properties of the Number of Matching Coalescent Histories for Caterpillar-Like Families of Species Trees. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2016, 13, 913-925.	3.0	13
70	A General Model of the Relationship between the Apportionment of Human Genetic Diversity and the Apportionment of Human Phenotypic Diversity. <i>Human Biology</i> , 2015, 87, 313.	0.2	19
71	Predicting Carriers of Ongoing Selective Sweeps without Knowledge of the Favored Allele. <i>PLoS Genetics</i> , 2015, 11, e1005527.	3.5	19
72	Hamilton's rule: Game theory meets coalescent theory. <i>Theoretical Population Biology</i> , 2015, 103, 1.	1.1	0

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73	Choosing Subsamples for Sequencing Studies by Minimizing the Average Distance to the Closest Leaf. Genetics, 2015, 201, 499-511.	2.9	3
74	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
75	Coalescent Histories for Lodgepole Species Trees. Journal of Computational Biology, 2015, 22, 918-929.	1.6	15
76	Theory in population biology, or biologically inspired mathematics?. Theoretical Population Biology, 2015, 102, 1-2.	1.1	1
77	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
78	<scp>Clumpak</scp>: a program for identifying clustering modes and packaging population structure inferences across <i>K</i> . Molecular Ecology Resources, 2015, 15, 1179-1191.	4.8	2,411
79	Enhancing the mathematical properties of new haplotype homozygosity statistics for the detection of selective sweeps. Theoretical Population Biology, 2015, 102, 94-101.	1.1	35
80	Haplotype Allele Frequency (HAF) Score: Predicting Carriers of Ongoing Selective Sweeps Without Knowledge of the Adaptive Allele. Lecture Notes in Computer Science, 2015, , 276-280.	1.3	1
81	Implications of the apportionment of human genetic diversity for the apportionment of human phenotypic diversity. Studies in History and Philosophy of Science Part C: Studies in History and Philosophy of Biological and Biomedical Sciences, 2015, 52, 32-45.	1.3	26
82	Genetic Diversity and Societally Important Disparities. Genetics, 2015, 201, 1-12.	2.9	28
83	AABC: Approximate approximate Bayesian computation for inference in population-genetic models. Theoretical Population Biology, 2015, 99, 31-42.	1.1	24
84	Patterns of Admixture and Population Structure in Native Populations of Northwest North America. PLoS Genetics, 2014, 10, e1004530.	3.5	81
85	Autosomal Admixture Levels Are Informative About Sex Bias in Admixed Populations. Genetics, 2014, 198, 1209-1229.	2.9	28
86	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
87	Theory and applications of a deterministic approximation to the coalescent model. Theoretical Population Biology, 2014, 93, 14-29.	1.1	16
88	Upper bounds on $\frac{F_{ST}}{H_T}$ in terms of the frequency of the most frequent allele and total homozygosity: The case of a specified number of alleles. Theoretical Population Biology, 2014, 97, 20-34.	1.1	16
89	Population-Genetic Influences on Genomic Estimates of the Inbreeding Coefficient: A Global Perspective. Human Heredity, 2014, 77, 37-48.	0.8	35
90	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

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91	Core elements of a TPB paper. Theoretical Population Biology, 2014, 92, 118-119.	1.1	3
92	Genotype imputation in a coalescent model with infinitely-many-sites mutation. Theoretical Population Biology, 2013, 87, 62-74.	1.1	7
93	Runs of homozygosity and parental relatedness. Genetics in Medicine, 2013, 15, 753-754.	2.4	8
94	Long Runs of Homozygosity Are Enriched for Deleterious Variation. American Journal of Human Genetics, 2013, 93, 90-102.	6.2	227
95	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
96	From Generation to Generation: The Genetics of Jewish Populations. Human Biology, 2013, 85, 817-823.	0.2	1
97	Mathematical Properties of the Deep Coalescence Cost. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2013, 10, 61-72.	3.0	17
98	Coalescent Histories for Caterpillar-Like Families. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2013, 10, 1253-1262.	3.0	13
99	No Evidence from Genome-Wide Data of a Khazar Origin for the Ashkenazi Jews. Human Biology, 2013, 85, 859-900.	0.2	68
100	Population Structure in a Comprehensive Genomic Data Set on Human Microsatellite Variation. G3: Genes, Genomes, Genetics, 2013, 3, 891-907.	1.8	123
101	Genotype Imputation Reference Panel Selection Using Maximal Phylogenetic Diversity. Genetics, 2013, 195, 319-330.	2.9	24
102	Discordance of Species Trees with Their Most Likely Gene Trees: A Unifying Principle. Molecular Biology and Evolution, 2013, 30, 2709-2713.	8.9	78
103	Windfalls and pitfalls. Evolution, Medicine and Public Health, 2013, 2013, 254-272.	2.5	8
104	The Relationship Between F_{ST} and the Frequency of the Most Frequent Allele. Genetics, 2013, 193, 515-528.	2.9	212
105	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
106	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
107	A Quantitative Comparison of the Similarity between Genes and Geography in Worldwide Human Populations. PLoS Genetics, 2012, 8, e1002886.	3.5	106
108	A Coalescent Model for Genotype Imputation. Genetics, 2012, 191, 1239-1255.	2.9	24

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109	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
110	Improvements to a Class of Distance Matrix Methods for Inferring Species Trees from Gene Trees. <i>Journal of Computational Biology</i> , 2012, 19, 632-649.	1.6	18
111	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
112	A Characterization of the Set of Species Trees that Produce Anomalous Ranked Gene Trees. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2012, 9, 1558-1568.	3.0	15
113	The probability distribution of ranked gene trees on a species tree. <i>Mathematical Biosciences</i> , 2012, 235, 45-55.	1.9	44
114	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
115	Genomic Patterns of Homozygosity in Worldwide Human Populations. <i>American Journal of Human Genetics</i> , 2012, 91, 275-292.	6.2	393
116	Impact of restricted marital practices on genetic variation in an endogamous Gujarati group. <i>American Journal of Physical Anthropology</i> , 2012, 149, 92-103.	2.1	18
117	Haploscope: a tool for the graphical display of haplotype structure in populations. <i>Genetic Epidemiology</i> , 2012, 36, 17-21.	1.3	10
118	Refining the relationship between homozygosity and the frequency of the most frequent allele. <i>Journal of Mathematical Biology</i> , 2012, 64, 87-108.	1.9	13
119	THE BEHAVIOR OF ADMIXED POPULATIONS IN NEIGHBOR-JOINING INFERENCE OF POPULATION TREES. , 2012, , .		10
120	PHYLOGENOMICS AND POPULATION GENOMICS: MODELS, ALGORITHMS, AND ANALYTICAL TOOLS. , 2012, , .		0
121	A Population-Genetic Perspective on the Similarities and Differences among Worldwide Human Populations. <i>Human Biology</i> , 2011, 83, 659-684.	0.2	82
122	Consistency Properties of Species Tree Inference by Minimizing Deep Coalescences. <i>Journal of Computational Biology</i> , 2011, 18, 1-15.	1.6	71
123	Inference on the strength of balancing selection for epistatically interacting loci. <i>Theoretical Population Biology</i> , 2011, 79, 102-113.	1.1	7
124	On the size distribution of private microsatellite alleles. <i>Theoretical Population Biology</i> , 2011, 80, 100-113.	1.1	50
125	Mathematical properties of $\sum_{i=1}^n \frac{1}{i^2}$ and $\sum_{i=1}^n \frac{1}{i}$. <i>Mathematical Biosciences</i> , 2011, 240, 208-216.	1.1	19
126	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

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127	Haplotype variation and genotype imputation in African populations. Genetic Epidemiology, 2011, 35, 766-780.	1.3	39
128	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
129	Coalescence-Time Distributions in a Serial Founder Model of Human Evolutionary History. Genetics, 2011, 189, 579-593.	2.9	41
130	A General Mechanistic Model for Admixture Histories of Hybrid Populations. Genetics, 2011, 189, 1413-1426.	2.9	74
131	Inference of Unexpected Genetic Relatedness among Individuals in HapMap Phase III. American Journal of Human Genetics, 2010, 87, 457-464.	6.2	104
132	Coalescent histories for discordant gene trees and species trees. Theoretical Population Biology, 2010, 77, 145-151.	1.1	20
133	Heterozygosity of the Yellowstone wolves. Molecular Ecology, 2010, 19, 3246-3249.	3.9	8
134	Genome-wide association studies in diverse populations. Nature Reviews Genetics, 2010, 11, 356-366.	16.3	518
135	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
136	Unbiased Estimation of Gene Diversity in Samples Containing Related Individuals: Exact Variance and Arbitrary Ploidy. Genetics, 2010, 186, 1367-1387.	2.9	8
137	<i>MLH1</i> Founder Mutations with Moderate Penetrance in Spanish Lynch Syndrome Families. Cancer Research, 2010, 70, 7379-7391.	0.9	29
138	Lack of Population Diversity in Commonly Used Human Embryonic Stem-Cell Lines. New England Journal of Medicine, 2010, 362, 183-185.	27.0	49
139	Properties of Consensus Methods for Inferring Species Trees from Gene Trees. Systematic Biology, 2009, 58, 35-54.	5.6	135
140	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
141	Sequence determinants of human microsatellite variability. BMC Genomics, 2009, 10, 612.	2.8	56
142	Replication of genetic associations as pseudoreplication due to shared genealogy. Genetic Epidemiology, 2009, 33, 479-487.	1.3	7
143	Genomic microsatellites identify shared Jewish ancestry intermediate between Middle Eastern and European populations. BMC Genetics, 2009, 10, 80.	2.7	46
144	Genotype-Imputation Accuracy across Worldwide Human Populations. American Journal of Human Genetics, 2009, 84, 235-250.	6.2	231

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145	The Relationship between Imputation Error and Statistical Power in Genetic Association Studies in Diverse Populations. <i>American Journal of Human Genetics</i> , 2009, 85, 692-698.	6.2	68
146	Gene tree discordance, phylogenetic inference and the multispecies coalescent. <i>Trends in Ecology and Evolution</i> , 2009, 24, 332-340.	8.7	1,500
147	Haplotypic Background of a Private Allele at High Frequency in the Americas. <i>Molecular Biology and Evolution</i> , 2009, 26, 995-1016.	8.9	74
148	Genotype, haplotype and copy-number variation in worldwide human populations. <i>Nature</i> , 2008, 451, 998-1003.	27.8	780
149	Mathematical properties of the measure of linkage disequilibrium. <i>Theoretical Population Biology</i> , 2008, 74, 130-137.	1.1	152
150	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
151	Discordance of Species Trees with Their Most Likely Gene Trees: The Case of Five Taxa. <i>Systematic Biology</i> , 2008, 57, 131-140.	5.6	100
152	Demographic History of European Populations of <i>Arabidopsis thaliana</i> . <i>PLoS Genetics</i> , 2008, 4, e1000075.	3.5	182
153	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
154	ADZE: a rarefaction approach for counting alleles private to combinations of populations. <i>Bioinformatics</i> , 2008, 24, 2498-2504.	4.1	666
155	The Relationship Between Homozygosity and the Frequency of the Most Frequent Allele. <i>Genetics</i> , 2008, 179, 2027-2036.	2.9	19
156	An Unbiased Estimator of Gene Diversity in Samples Containing Related Individuals. <i>Molecular Biology and Evolution</i> , 2008, 26, 501-512.	8.9	26
157	Estimating the Number of Ancestral Lineages Using a Maximum-Likelihood Method Based on Rejection Sampling. <i>Genetics</i> , 2007, 176, 1741-1757.	2.9	8
158	Genetic Variation and Population Structure in Native Americans. <i>PLoS Genetics</i> , 2007, 3, e185.	3.5	454
159	On the Genealogy of a Duplicated Microsatellite. <i>Genetics</i> , 2007, 177, 2109-2122.	2.9	8
160	Counting Coalescent Histories. <i>Journal of Computational Biology</i> , 2007, 14, 360-377.	1.6	44
161	Sampling properties of homozygosity-based statistics for linkage disequilibrium. <i>Mathematical Biosciences</i> , 2007, 208, 33-47.	1.9	8
162	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

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163	The probability distribution under a population divergence model of the number of genetic founding lineages of a population or species. <i>Theoretical Population Biology</i> , 2007, 71, 502-523.	1.1	5
164	STATISTICAL TESTS FOR TAXONOMIC DISTINCTIVENESS FROM OBSERVATIONS OF MONOPHYLY. <i>Evolution; International Journal of Organic Evolution</i> , 2007, 61, 317-323.	2.3	166
165	Genetic diversity and population structure inferred from the partially duplicated genome of domesticated carp, <i>Cyprinus carpio</i> L.. <i>Genetics Selection Evolution</i> , 2007, 39, 319.	3.0	19
166	Genetic diversity and population structure inferred from the partially duplicated genome of domesticated carp, <i>Cyprinus carpio</i> L.. <i>Genetics Selection Evolution</i> , 2007, 39, 319-340.	3.0	1
167	Standardized Subsets of the HGDP-CEPH Human Genome Diversity Cell Line Panel, Accounting for Atypical and Duplicated Samples and Pairs of Close Relatives. <i>Annals of Human Genetics</i> , 2006, 70, 841-847.	0.8	233
168	A worldwide survey of haplotype variation and linkage disequilibrium in the human genome. <i>Nature Genetics</i> , 2006, 38, 1251-1260.	21.4	474
169	The Mean and Variance of the Numbers of r-Pronged Nodes and r-Caterpillars in Yule-Generated Genealogical Trees. <i>Annals of Combinatorics</i> , 2006, 10, 129-146.	0.6	59
170	Low Levels of Genetic Divergence across Geographically and Linguistically Diverse Populations from India. <i>PLoS Genetics</i> , 2006, 2, e215.	3.5	82
171	Discordance of Species Trees with Their Most Likely Gene Trees. <i>PLoS Genetics</i> , 2006, 2, e68.	3.5	761
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