

Noah A Rosenberg

List of Publications by Year in descending order

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Version: 2024-02-01

199
papers

34,062
citations

39113

52
h-index

4741

175
g-index

223
all docs

223
docs citations

223
times ranked

36585
citing authors

#	ARTICLE	IF	CITATIONS
1	A compendium of covariances and correlation coefficients of coalescent tree properties. <i>Theoretical Population Biology</i> , 2022, 143, 1-13.	0.5	4
2	The 2022 Feldman Prize. <i>Theoretical Population Biology</i> , 2022, 143, 105-106.	0.5	0
3	Ancient and modern genomics of the Ohlone Indigenous population of California. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, e2111533119.	3.3	10
4	Mathematical epidemiology for a later age. <i>Theoretical Population Biology</i> , 2022, 144, 81-83.	0.5	0
5	Celebrating 50 years since Lewontin's apportionment of human diversity. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2022, 377, 20200405.	1.8	5
6	Mathematical constraints on F_{ST} : multiallelic markers in arbitrarily many populations. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2022, 377, 20200414.	1.8	7
7	The Probability of Joint Monophyly of Samples of Gene Lineages for All Species in an Arbitrary Species Tree. <i>Journal of Computational Biology</i> , 2022, , .	0.8	1
8	Enumeration of binary trees compatible with a perfect phylogeny. <i>Journal of Mathematical Biology</i> , 2022, 84, 54.	0.8	1
9	Extracting hierarchical features of cultural variation using network-based clustering. <i>Evolutionary Human Sciences</i> , 2022, 4, .	0.9	2
10	F_{ST} : An F_{ST} -based tool for measuring ancestry variation in inference of population structure. <i>Molecular Ecology Resources</i> , 2022, 22, 2614-2626.	2.2	6
11	Genetic Adaptation in New York City Rats. <i>Genome Biology and Evolution</i> , 2021, 13, .	1.1	13
12	Population models, mathematical epidemiology, and the COVID-19 pandemic. <i>Theoretical Population Biology</i> , 2021, 137, 1.	0.5	2
13	Designing gene drives to limit spillover to non-target populations. <i>PLoS Genetics</i> , 2021, 17, e1009278.	1.5	12
14	Skin deep: The decoupling of genetic admixture levels from phenotypes that differed between source populations. <i>American Journal of Physical Anthropology</i> , 2021, 175, 406-421.	2.1	8
15	On the Colijn-Plazzotta numbering scheme for unlabeled binary rooted trees. <i>Discrete Applied Mathematics</i> , 2021, 291, 88-98.	0.5	4
16	Variance and limiting distribution of coalescence times in a diploid model of a consanguineous population. <i>Theoretical Population Biology</i> , 2021, 139, 50-65.	0.5	7
17	The effect of consanguinity on coalescence times on the X chromosome. <i>Theoretical Population Biology</i> , 2021, 140, 32-43.	0.5	6
18	A simple derivation of the mean of the Sackin index of tree balance under the uniform model on rooted binary labeled trees. <i>Mathematical Biosciences</i> , 2021, 342, 108688.	0.9	4

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19	Enumeration of coalescent histories for caterpillar species trees and p-pseudocaterpillar gene trees. <i>Advances in Applied Mathematics</i> , 2021, 131, 102265.	0.4	3
20	$\frac{F}{S} < \frac{T}{m}$ the triangle inequality for biallelic markers. <i>Theoretical Population Biology</i> , 2020, 133, 117-129.	0.5	0
21	Roadblocked monotonic paths and the enumeration of coalescent histories for non-matching caterpillar gene trees and species trees. <i>Advances in Applied Mathematics</i> , 2020, 113, 101939.	0.4	4
22	Probabilities of Unranked and Ranked Anomaly Zones under Birth-Death Models. <i>Molecular Biology and Evolution</i> , 2020, 37, 1480-1494.	3.5	3
23	High-resolution inference of genetic relationships among Jewish populations. <i>European Journal of Human Genetics</i> , 2020, 28, 804-814.	1.4	6
24	The 2020 Feldman Prize. <i>Theoretical Population Biology</i> , 2020, 131, 1.	0.5	0
25	On the heterozygosity of an admixed population. <i>Journal of Mathematical Biology</i> , 2020, 81, 1217-1250.	0.8	16
26	Assortative mating by population of origin in a mechanistic model of admixture. <i>Theoretical Population Biology</i> , 2020, 134, 129-146.	0.5	13
27	Distance metrics for ranked evolutionary trees. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 28876-28886.	3.3	20
28	Modelling anti-vaccine sentiment as a cultural pathogen. <i>Evolutionary Human Sciences</i> , 2020, 2, .	0.9	14
29	Measures of care fragmentation: Mathematical insights from population genetics. <i>Health Services Research</i> , 2020, 55, 318-327.	1.0	9
30	Fifty years of Theoretical Population Biology. <i>Theoretical Population Biology</i> , 2020, 133, 1-12.	0.5	7
31	A Population-Genetic Perspective on the Similarities and Differences among Worldwide Human Populations. <i>Human Biology</i> , 2020, 92, 135.	0.4	2
32	Human-Genetic Ancestry Inference and False Positives in Forensic Familial Searching. <i>G3: Genes, Genomes, Genetics</i> , 2020, 10, 2893-2902.	0.8	9
33	Mathematical and Simulation-Based Analysis of the Behavior of Admixed Taxa in the Neighbor-Joining Algorithm. <i>Bulletin of Mathematical Biology</i> , 2019, 81, 452-493.	0.9	2
34	On the Number of Non-equivalent Ancestral Configurations for Matching Gene Trees and Species Trees. <i>Bulletin of Mathematical Biology</i> , 2019, 81, 384-407.	0.9	7
35	The probability of reciprocal monophyly of gene lineages in three and four species. <i>Theoretical Population Biology</i> , 2019, 129, 133-147.	0.5	7
36	Enumeration of compact coalescent histories for matching gene trees and species trees. <i>Journal of Mathematical Biology</i> , 2019, 78, 155-188.	0.8	8

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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.	2.4	2
38	The Relationship Between Haplotype-Based F_{ST} and Haplotype Length. <i>Genetics</i> , 2019, 213, 281-295.	1.2	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.	5.8	30
40	Network-based hierarchical population structure analysis for large genomic data sets. <i>Genome Research</i> , 2019, 29, 2020-2033.	2.4	10
41	Coalescent Theory of Migration Network Motifs. <i>Molecular Biology and Evolution</i> , 2019, 36, 2358-2374.	3.5	4
42	Analysis of author gender in TPB, 1991–2018. <i>Theoretical Population Biology</i> , 2019, 127, 1-6.	0.5	1
43	The Effect of Consanguinity on Between-Individual Identity-by-Descent Sharing. <i>Genetics</i> , 2019, 212, 305-316.	1.2	19
44	Mathematical Properties of Linkage Disequilibrium Statistics Defined by Normalization of the Coefficient D' = $\frac{D}{\min(p_A, p_B)}$ Human Heredity, 2019, 84, 127-143.	0.4	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.	2.0	19
46	Interpreting polygenic scores, polygenic adaptation, and human phenotypic differences. <i>Evolution, Medicine and Public Health</i> , 2019, 2019, 26-34.	1.1	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.	0.5	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.	0.4	7
49	The 2018 Marcus W. Feldman Prize in Theoretical Population Biology. <i>Theoretical Population Biology</i> , 2018, 119, 1-2.	0.5	1
50	Bounding measures of genetic similarity and diversity using majorization. <i>Journal of Mathematical Biology</i> , 2018, 77, 711-737.	0.8	4
51	On the joint distribution of tree height and tree length under the coalescent. <i>Theoretical Population Biology</i> , 2018, 122, 46-56.	0.5	7
52	Statistical Detection of Relatives Typed with Disjoint Forensic and Biomedical Loci. <i>Cell</i> , 2018, 175, 848-858.e6.	13.5	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.	1.8	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.	3.3	94

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55	Mathematical Constraints on F_{ST} : Biallelic Markers in Arbitrarily Many Populations. <i>Genetics</i> , 2017, 206, 1581-1600.	1.2	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.	3.3	49
57	Enumeration of Ancestral Configurations for Matching Gene Trees and Species Trees. <i>Journal of Computational Biology</i> , 2017, 24, 831-850.	0.8	14
58	Parallel Trajectories of Genetic and Linguistic Admixture in a Genetically Admixed Creole Population. <i>Current Biology</i> , 2017, 27, 2529-2535.e3.	1.8	22
59	Simulation-Based Evaluation of Hybridization Network Reconstruction Methods in the Presence of Incomplete Lineage Sorting. <i>Evolutionary Bioinformatics</i> , 2017, 13, 117693431769193.	0.6	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.	3.3	11
62	Admixture Models and the Breeding Systems of H. S. Jennings: A GENETICS Connection. <i>Genetics</i> , 2016, 202, 9-13.	1.2	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.	3.3	15
64	Individual Identifiability Predicts Population Identifiability in Forensic Microsatellite Markers. <i>Current Biology</i> , 2016, 26, 935-942.	1.8	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.	0.5	13
66	Consanguinity Rates Predict Long Runs of Homozygosity in Jewish Populations. <i>Human Heredity</i> , 2016, 82, 87-102.	0.4	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.	1.2	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.	2.7	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.	1.9	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.	0.4	19
71	Predicting Carriers of Ongoing Selective Sweeps without Knowledge of the Favored Allele. <i>PLoS Genetics</i> , 2015, 11, e1005527.	1.5	19
72	Hamilton's rule: Game theory meets coalescent theory. <i>Theoretical Population Biology</i> , 2015, 103, 1.	0.5	0

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73	Choosing Subsamples for Sequencing Studies by Minimizing the Average Distance to the Closest Leaf. <i>Genetics</i> , 2015, 201, 499-511.	1.2	3
74	Beyond 2/3 and 1/3: The Complex Signatures of Sex-Biased Admixture on the X Chromosome. <i>Genetics</i> , 2015, 201, 263-279.	1.2	74
75	Coalescent Histories for Lodgepole Species Trees. <i>Journal of Computational Biology</i> , 2015, 22, 918-929.	0.8	15
76	Theory in population biology, or biologically inspired mathematics?. <i>Theoretical Population Biology</i> , 2015, 102, 1-2.	0.5	1
77	A comparison of worldwide phonemic and genetic variation in human populations. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 1265-1272.	3.3	122
78	<sc>Clumpak</sc>: a program for identifying clustering modes and packaging population structure inferences across <i>K</i>. <i>Molecular Ecology Resources</i> , 2015, 15, 1179-1191.	2.2	2,411
79	Enhancing the mathematical properties of new haplotype homozygosity statistics for the detection of selective sweeps. <i>Theoretical Population Biology</i> , 2015, 102, 94-101.	0.5	35
80	Haplotype Allele Frequency (HAF) Score: Predicting Carriers of Ongoing Selective Sweeps Without Knowledge of the Adaptive Allele. <i>Lecture Notes in Computer Science</i> , 2015, , 276-280.	1.0	1
81	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.	0.8	26
82	Genetic Diversity and Societally Important Disparities. <i>Genetics</i> , 2015, 201, 1-12.	1.2	28
83	AABC: Approximate approximate Bayesian computation for inference in population-genetic models. <i>Theoretical Population Biology</i> , 2015, 99, 31-42.	0.5	24
84	Patterns of Admixture and Population Structure in Native Populations of Northwest North America. <i>PLoS Genetics</i> , 2014, 10, e1004530.	1.5	81
85	Autosomal Admixture Levels Are Informative About Sex Bias in Admixed Populations. <i>Genetics</i> , 2014, 198, 1209-1229.	1.2	28
86	On the Number of Ranked Species Trees Producing Anomalous Ranked Gene Trees. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2014, 11, 1229-1238.	1.9	5
87	Theory and applications of a deterministic approximation to the coalescent model. <i>Theoretical Population Biology</i> , 2014, 93, 14-29.	0.5	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. <i>Theoretical Population Biology</i> , 2014, 97, 20-34.	0.5	23
89	Population-Genetic Influences on Genomic Estimates of the Inbreeding Coefficient: A Global Perspective. <i>Human Heredity</i> , 2014, 77, 37-48.	0.4	35
90	An empirical evaluation of two-stage species tree inference strategies using a multilocus dataset from North American pines. <i>BMC Evolutionary Biology</i> , 2014, 14, 67.	3.2	21

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91	Core elements of a TPB paper. <i>Theoretical Population Biology</i> , 2014, 92, 118-119.	0.5	3
92	Genotype imputation in a coalescent model with infinitely-many-sites mutation. <i>Theoretical Population Biology</i> , 2013, 87, 62-74.	0.5	7
93	Runs of homozygosity and parental relatedness. <i>Genetics in Medicine</i> , 2013, 15, 753-754.	1.1	8
94	Long Runs of Homozygosity Are Enriched for Deleterious Variation. <i>American Journal of Human Genetics</i> , 2013, 93, 90-102.	2.6	227
95	Genetics and the History of the Samaritans: Y-Chromosomal Microsatellites and Genetic Affinity between Samaritans and Cohanim. <i>Human Biology</i> , 2013, 85, 825-857.	0.4	4
96	From Generation to Generation: The Genetics of Jewish Populations. <i>Human Biology</i> , 2013, 85, 817-823.	0.4	1
97	Mathematical Properties of the Deep Coalescence Cost. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2013, 10, 61-72.	1.9	17
98	Coalescent Histories for Caterpillar-Like Families. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2013, 10, 1253-1262.	1.9	13
99	No Evidence from Genome-Wide Data of a Khazar Origin for the Ashkenazi Jews. <i>Human Biology</i> , 2013, 85, 859-900.	0.4	68
100	Population Structure in a Comprehensive Genomic Data Set on Human Microsatellite Variation. <i>G3: Genes, Genomes, Genetics</i> , 2013, 3, 891-907.	0.8	123
101	Genotype Imputation Reference Panel Selection Using Maximal Phylogenetic Diversity. <i>Genetics</i> , 2013, 195, 319-330.	1.2	24
102	Discordance of Species Trees with Their Most Likely Gene Trees: A Unifying Principle. <i>Molecular Biology and Evolution</i> , 2013, 30, 2709-2713.	3.5	78
103	Windfalls and pitfalls. <i>Evolution, Medicine and Public Health</i> , 2013, 2013, 254-272.	1.1	8
104	The Relationship Between F_{ST} and the Frequency of the Most Frequent Allele. <i>Genetics</i> , 2013, 193, 515-528.	1.2	212
105	Geographic Sampling Scheme as a Determinant of the Major Axis of Genetic Variation in Principal Components Analysis. <i>Molecular Biology and Evolution</i> , 2013, 30, 480-488.	3.5	20
106	The behavior of admixed populations in neighbor-joining inference of population trees. <i>Pacific Symposium on Biocomputing</i> 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. <i>PLoS Genetics</i> , 2012, 8, e1002886.	1.5	106
108	A Coalescent Model for Genotype Imputation. <i>Genetics</i> , 2012, 191, 1239-1255.	1.2	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.	1.2	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.	0.8	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.	0.8	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.	1.9	15
113	The probability distribution of ranked gene trees on a species tree. <i>Mathematical Biosciences</i> , 2012, 235, 45-55.	0.9	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.	3.5	828
115	Genomic Patterns of Homozygosity in Worldwide Human Populations. <i>American Journal of Human Genetics</i> , 2012, 91, 275-292.	2.6	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.	0.6	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.	0.8	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.	0.4	82
122	Consistency Properties of Species Tree Inference by Minimizing Deep Coalescences. <i>Journal of Computational Biology</i> , 2011, 18, 1-15.	0.8	71
123	Inference on the strength of balancing selection for epistatically interacting loci. <i>Theoretical Population Biology</i> , 2011, 79, 102-113.	0.5	7
124	On the size distribution of private microsatellite alleles. <i>Theoretical Population Biology</i> , 2011, 80, 100-113.	0.5	50
125	Mathematical properties of $\sum_{i=1}^n \frac{1}{i^2}$ admixed populations and their parental source populations. <i>Theoretical Population Biology</i> , 2011, 80, 208-216.	0.5	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. <i>Genetic Epidemiology</i> , 2011, 35, 766-780.	0.6	39
128	How dormant is <i>Mycobacterium tuberculosis</i> during latency? A study integrating genomics and molecular epidemiology. <i>Infection, Genetics and Evolution</i> , 2011, 11, 1164-1167.	1.0	13
129	Coalescence-Time Distributions in a Serial Founder Model of Human Evolutionary History. <i>Genetics</i> , 2011, 189, 579-593.	1.2	41
130	A General Mechanistic Model for Admixture Histories of Hybrid Populations. <i>Genetics</i> , 2011, 189, 1413-1426.	1.2	74
131	Inference of Unexpected Genetic Relatedness among Individuals in HapMap Phase III. <i>American Journal of Human Genetics</i> , 2010, 87, 457-464.	2.6	104
132	Coalescent histories for discordant gene trees and species trees. <i>Theoretical Population Biology</i> , 2010, 77, 145-151.	0.5	20
133	Heterozygosity of the Yellowstone wolves. <i>Molecular Ecology</i> , 2010, 19, 3246-3249.	2.0	8
134	Genome-wide association studies in diverse populations. <i>Nature Reviews Genetics</i> , 2010, 11, 356-366.	7.7	518
135	Comparing Spatial Maps of Human Population-Genetic Variation Using Procrustes Analysis. <i>Statistical Applications in Genetics and Molecular Biology</i> , 2010, 9, Article 13.	0.2	103
136	Unbiased Estimation of Gene Diversity in Samples Containing Related Individuals: Exact Variance and Arbitrary Ploidy. <i>Genetics</i> , 2010, 186, 1367-1387.	1.2	8
137	<i>MLH1</i> Founder Mutations with Moderate Penetrance in Spanish Lynch Syndrome Families. <i>Cancer Research</i> , 2010, 70, 7379-7391.	0.4	29
138	Lack of Population Diversity in Commonly Used Human Embryonic Stem-Cell Lines. <i>New England Journal of Medicine</i> , 2010, 362, 183-185.	13.9	49
139	Properties of Consensus Methods for Inferring Species Trees from Gene Trees. <i>Systematic Biology</i> , 2009, 58, 35-54.	2.7	135
140	Explaining worldwide patterns of human genetic variation using a coalescent-based serial founder model of migration outward from Africa. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 16057-16062.	3.3	161
141	Sequence determinants of human microsatellite variability. <i>BMC Genomics</i> , 2009, 10, 612.	1.2	56
142	Replication of genetic associations as pseudoreplication due to shared genealogy. <i>Genetic Epidemiology</i> , 2009, 33, 479-487.	0.6	7
143	Genomic microsatellites identify shared Jewish ancestry intermediate between Middle Eastern and European populations. <i>BMC Genetics</i> , 2009, 10, 80.	2.7	46
144	Genotype-Imputation Accuracy across Worldwide Human Populations. <i>American Journal of Human Genetics</i> , 2009, 84, 235-250.	2.6	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.	2.6	68
146	Gene tree discordance, phylogenetic inference and the multispecies coalescent. <i>Trends in Ecology and Evolution</i> , 2009, 24, 332-340.	4.2	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.	3.5	74
148	Genotype, haplotype and copy-number variation in worldwide human populations. <i>Nature</i> , 2008, 451, 998-1003.	13.7	780
149	Mathematical properties of the measure of linkage disequilibrium. <i>Theoretical Population Biology</i> , 2008, 74, 130-137.	0.5	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.	0.5	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.	2.7	100
152	Demographic History of European Populations of <i>Arabidopsis thaliana</i> . <i>PLoS Genetics</i> , 2008, 4, e1000075.	1.5	182
153	Nonadaptive Explanations for Signatures of Partial Selective Sweeps in <i>Drosophila</i> . <i>Molecular Biology and Evolution</i> , 2008, 25, 1025-1042.	3.5	21
154	ADZE: a rarefaction approach for counting alleles private to combinations of populations. <i>Bioinformatics</i> , 2008, 24, 2498-2504.	1.8	666
155	The Relationship Between Homozygosity and the Frequency of the Most Frequent Allele. <i>Genetics</i> , 2008, 179, 2027-2036.	1.2	19
156	An Unbiased Estimator of Gene Diversity in Samples Containing Related Individuals. <i>Molecular Biology and Evolution</i> , 2008, 26, 501-512.	3.5	26
157	Estimating the Number of Ancestral Lineages Using a Maximum-Likelihood Method Based on Rejection Sampling. <i>Genetics</i> , 2007, 176, 1741-1757.	1.2	8
158	Genetic Variation and Population Structure in Native Americans. <i>PLoS Genetics</i> , 2007, 3, e185.	1.5	454
159	On the Genealogy of a Duplicated Microsatellite. <i>Genetics</i> , 2007, 177, 2109-2122.	1.2	8
160	Counting Coalescent Histories. <i>Journal of Computational Biology</i> , 2007, 14, 360-377.	0.8	44
161	Sampling properties of homozygosity-based statistics for linkage disequilibrium. <i>Mathematical Biosciences</i> , 2007, 208, 33-47.	0.9	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.	1.8	5,408

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