

Noah A Rosenberg

List of Publications by Citations

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

188
papers

26,690
citations

49
h-index

163
g-index

223
ext. papers

31,292
ext. citations

5.7
avg, IF

7.61
L-index

#	Paper	IF	Citations
188	CLUMPP: a cluster matching and permutation program for dealing with label switching and multimodality in analysis of population structure. <i>Bioinformatics</i> , 2007 , 23, 1801-6	7.2	4312
187	distruct: a program for the graphical display of population structure. <i>Molecular Ecology Notes</i> , 2003 , 4, 137-138		3436
186	Genetic structure of human populations. <i>Science</i> , 2002 , 298, 2381-5	33.3	1995
185	Clumpak: a program for identifying clustering modes and packaging population structure inferences across K. <i>Molecular Ecology Resources</i> , 2015 , 15, 1179-91	8.4	1526
184	Association mapping in structured populations. <i>American Journal of Human Genetics</i> , 2000 , 67, 170-81	11	1472
183	Gene tree discordance, phylogenetic inference and the multispecies coalescent. <i>Trends in Ecology and Evolution</i> , 2009 , 24, 332-40	10.9	1166
182	Use of unlinked genetic markers to detect population stratification in association studies. <i>American Journal of Human Genetics</i> , 1999 , 65, 220-8	11	993
181	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, 15942-7	11.5	773
180	The pattern of polymorphism in <i>Arabidopsis thaliana</i> . <i>PLoS Biology</i> , 2005 , 3, e196	9.7	764
179	Genotype, haplotype and copy-number variation in worldwide human populations. <i>Nature</i> , 2008 , 451, 998-1003	50.4	662
178	Discordance of species trees with their most likely gene trees. <i>PLoS Genetics</i> , 2006 , 2, e68	6	590
177	Inferring species trees directly from biallelic genetic markers: bypassing gene trees in a full coalescent analysis. <i>Molecular Biology and Evolution</i> , 2012 , 29, 1917-32	8.3	553
176	ADZE: a rarefaction approach for counting alleles private to combinations of populations. <i>Bioinformatics</i> , 2008 , 24, 2498-504	7.2	505
175	Informativeness of genetic markers for inference of ancestry. <i>American Journal of Human Genetics</i> , 2003 , 73, 1402-22	11	495
174	Genealogical trees, coalescent theory and the analysis of genetic polymorphisms. <i>Nature Reviews Genetics</i> , 2002 , 3, 380-90	30.1	473
173	Genome-wide association studies in diverse populations. <i>Nature Reviews Genetics</i> , 2010 , 11, 356-66	30.1	422
172	Clines, clusters, and the effect of study design on the inference of human population structure. <i>PLoS Genetics</i> , 2005 , 1, e70	6	407

171	A worldwide survey of haplotype variation and linkage disequilibrium in the human genome. <i>Nature Genetics</i> , 2006 , 38, 1251-60	36.3	406
170	Genetic variation and population structure in native Americans. <i>PLoS Genetics</i> , 2007 , 3, e185	6	392
169	Genomic patterns of homozygosity in worldwide human populations. <i>American Journal of Human Genetics</i> , 2012 , 91, 275-92	11	281
168	Empirical evaluation of genetic clustering methods using multilocus genotypes from 20 chicken breeds. <i>Genetics</i> , 2001 , 159, 699-713	4	268
167	The probability of topological concordance of gene trees and species trees. <i>Theoretical Population Biology</i> , 2002 , 61, 225-47	1.2	236
166	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, 841-7	2.2	211
165	Features of evolution and expansion of modern humans, inferred from genomewide microsatellite markers. <i>American Journal of Human Genetics</i> , 2003 , 72, 1171-86	11	198
164	Genotype-imputation accuracy across worldwide human populations. <i>American Journal of Human Genetics</i> , 2009 , 84, 235-50	11	191
163	The shapes of neutral gene genealogies in two species: probabilities of monophyly, paraphyly, and polyphyly in a coalescent model. <i>Evolution; International Journal of Organic Evolution</i> , 2003 , 57, 1465-77	3.8	183
162	Long runs of homozygosity are enriched for deleterious variation. <i>American Journal of Human Genetics</i> , 2013 , 93, 90-102	11	153
161	Demographic history of european populations of <i>Arabidopsis thaliana</i> . <i>PLoS Genetics</i> , 2008 , 4, e10000756		150
160	The relationship between F_{ST} and the frequency of the most frequent allele. <i>Genetics</i> , 2013 , 193, 515-28		145
159	Statistical tests for taxonomic distinctiveness from observations of monophyly. <i>Evolution; International Journal of Organic Evolution</i> , 2007 , 61, 317-23	3.8	130
158	Out of Africa: modern human origins special feature: explaining worldwide patterns of human genetic variation using a coalescent-based serial founder model of migration outward from Africa. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009 , 106, 16057-62	11.5	124
157	Mathematical properties of the r^2 measure of linkage disequilibrium. <i>Theoretical Population Biology</i> , 2008 , 74, 130-7	1.2	119
156	Properties of consensus methods for inferring species trees from gene trees. <i>Systematic Biology</i> , 2009 , 58, 35-54	8.4	116
155	Inference of unexpected genetic relatedness among individuals in HapMap Phase III. <i>American Journal of Human Genetics</i> , 2010 , 87, 457-64	11	89
154	Discordance of species trees with their most likely gene trees: the case of five taxa. <i>Systematic Biology</i> , 2008 , 57, 131-40	8.4	87

153	Comparing spatial maps of human population-genetic variation using Procrustes analysis. <i>Statistical Applications in Genetics and Molecular Biology</i> , 2010 , 9, Article 13	1.2	84
152	A quantitative comparison of the similarity between genes and geography in worldwide human populations. <i>PLoS Genetics</i> , 2012 , 8, e1002886	6	83
151	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, 1265-72	11.5	77
150	Population structure in a comprehensive genomic data set on human microsatellite variation. <i>G3: Genes, Genomes, Genetics</i> , 2013 , 3, 891-907	3.2	73
149	Low levels of genetic divergence across geographically and linguistically diverse populations from India. <i>PLoS Genetics</i> , 2006 , 2, e215	6	70
148	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	11.5	69
147	Consistency properties of species tree inference by minimizing deep coalescences. <i>Journal of Computational Biology</i> , 2011 , 18, 1-15	1.7	66
146	Discordance of species trees with their most likely gene trees: a unifying principle. <i>Molecular Biology and Evolution</i> , 2013 , 30, 2709-13	8.3	64
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, 692-8	11	58
144	A population-genetic perspective on the similarities and differences among worldwide human populations. <i>Human Biology</i> , 2011 , 83, 659-84	1.2	57
143	A general mechanistic model for admixture histories of hybrid populations. <i>Genetics</i> , 2011 , 189, 1413-264		54
142	Interpreting polygenic scores, polygenic adaptation, and human phenotypic differences. <i>Evolution, Medicine and Public Health</i> , 2019 , 2019, 26-34	3	51
141	Patterns of admixture and population structure in native populations of Northwest North America. <i>PLoS Genetics</i> , 2014 , 10, e1004530	6	49
140	No evidence from genome-wide data of a Khazar origin for the Ashkenazi Jews. <i>Human Biology</i> , 2013 , 85, 859-900	1.2	49
139	Algorithms for selecting informative marker panels for population assignment. <i>Journal of Computational Biology</i> , 2005 , 12, 1183-201	1.7	49
138	Haplotypic background of a private allele at high frequency in the Americas. <i>Molecular Biology and Evolution</i> , 2009 , 26, 995-1016	8.3	48
137	Evaluating allopolyploid origins in strawberries (<i>Fragaria</i>) using haplotypes generated from target capture sequencing. <i>BMC Evolutionary Biology</i> , 2017 , 17, 180	3	47
136	Robustness of the inference of human population structure: a comparison of X-chromosomal and autosomal microsatellites. <i>Human Genomics</i> , 2004 , 1, 87-97	6.8	47

135	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, 1665-78	4	45
134	Lack of population diversity in commonly used human embryonic stem-cell lines. <i>New England Journal of Medicine</i> , 2010 , 362, 183-5	59.2	44
133	Beyond 2/3 and 1/3: The Complex Signatures of Sex-Biased Admixture on the X Chromosome. <i>Genetics</i> , 2015 , 201, 263-79	4	42
132	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	0.7	42
131	Genomic microsatellites identify shared Jewish ancestry intermediate between Middle Eastern and European populations. <i>BMC Genetics</i> , 2009 , 10, 80	2.6	41
130	A maximum-likelihood method to correct for allelic dropout in microsatellite data with no replicate genotypes. <i>Genetics</i> , 2012 , 192, 651-69	4	40
129	Statistical tests of the coalescent model based on the haplotype frequency distribution and the number of segregating sites. <i>Genetics</i> , 2005 , 169, 1763-77	4	39
128	On the size distribution of private microsatellite alleles. <i>Theoretical Population Biology</i> , 2011 , 80, 100-131.2	1.2	38
127	Individual Identifiability Predicts Population Identifiability in Forensic Microsatellite Markers. <i>Current Biology</i> , 2016 , 26, 935-42	6.3	38
126	Sequence determinants of human microsatellite variability. <i>BMC Genomics</i> , 2009 , 10, 612	4.5	36
125	Counting coalescent histories. <i>Journal of Computational Biology</i> , 2007 , 14, 360-77	1.7	36
124	Haplotype variation and genotype imputation in African populations. <i>Genetic Epidemiology</i> , 2011 , 35, 766-80	2.6	31
123	Coalescence-time distributions in a serial founder model of human evolutionary history. <i>Genetics</i> , 2011 , 189, 579-93	4	29
122	MLH1 founder mutations with moderate penetrance in Spanish Lynch syndrome families. <i>Cancer Research</i> , 2010 , 70, 7379-91	10.1	28
121	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	11.5	27
120	Population-genetic influences on genomic estimates of the inbreeding coefficient: a global perspective. <i>Human Heredity</i> , 2014 , 77, 37-48	1.1	27
119	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	1.2	24
118	iGLASS: an improvement to the GLASS method for estimating species trees from gene trees. <i>Journal of Computational Biology</i> , 2012 , 19, 293-315	1.7	23

117	The probability distribution of ranked gene trees on a species tree. <i>Mathematical Biosciences</i> , 2012 , 235, 45-55	3.9	23
116	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, 347-63	1.2	23
115	Nonadaptive explanations for signatures of partial selective sweeps in <i>Drosophila</i> . <i>Molecular Biology and Evolution</i> , 2008 , 25, 1025-42	8.3	21
114	Enhancing the mathematical properties of new haplotype homozygosity statistics for the detection of selective sweeps. <i>Theoretical Population Biology</i> , 2015 , 102, 94-101	1.2	20
113	Autosomal admixture levels are informative about sex bias in admixed populations. <i>Genetics</i> , 2014 , 198, 1209-29	4	19
112	Genotype imputation reference panel selection using maximal phylogenetic diversity. <i>Genetics</i> , 2013 , 195, 319-30	4	19
111	Statistical Detection of Relatives Typed with Disjoint Forensic and Biomedical Loci. <i>Cell</i> , 2018 , 175, 848-858	5.2	19
110	AABC: approximate approximate Bayesian computation for inference in population-genetic models. <i>Theoretical Population Biology</i> , 2015 , 99, 31-42	1.2	18
109	Upper bounds on F_{ST} in terms of the frequency of the most frequent allele and total homozygosity: the case of a specified number of alleles. <i>Theoretical Population Biology</i> , 2014 , 97, 20-34	1.2	18
108	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	18
107	A coalescent model for genotype imputation. <i>Genetics</i> , 2012 , 191, 1239-55	4	18
106	An unbiased estimator of gene diversity in samples containing related individuals. <i>Molecular Biology and Evolution</i> , 2009 , 26, 501-12	8.3	18
105	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, 319-40	4.9	18
104	Genetic Diversity and Societally Important Disparities. <i>Genetics</i> , 2015 , 201, 1-12	4	17
103	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, 515-29	2.5	17
102	Coalescent histories for discordant gene trees and species trees. <i>Theoretical Population Biology</i> , 2010 , 77, 145-51	1.2	17
101	The control of copy number of IS6110 in <i>Mycobacterium tuberculosis</i> . <i>Molecular Biology and Evolution</i> , 2004 , 21, 2195-201	8.3	17
100	On the use of star-shaped genealogies in inference of coalescence times. <i>Genetics</i> , 2003 , 164, 1677-82	4	17

99	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	0.6	16
98	Mathematical properties of the deep coalescence cost. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2013 , 10, 61-72	3	16
97	The relationship between homozygosity and the frequency of the most frequent allele. <i>Genetics</i> , 2008 , 179, 2027-36	4	16
96	Optimal estimation of transposition rates of insertion sequences for molecular epidemiology. <i>Statistics in Medicine</i> , 2001 , 20, 2409-20	2.3	16
95	Improvements to a class of distance matrix methods for inferring species trees from gene trees. <i>Journal of Computational Biology</i> , 2012 , 19, 632-49	1.7	15
94	THE SHAPES OF NEUTRAL GENE GENEALOGIES IN TWO SPECIES: PROBABILITIES OF MONOPHYLY, PARAPHYLY, AND POLYPHYLY IN A COALESCENT MODEL. <i>Evolution; International Journal of Organic Evolution</i> , 2003 , 57, 1465	3.8	15
93	Mathematical Constraints on : Biallelic Markers in Arbitrarily Many Populations. <i>Genetics</i> , 2017 , 206, 1581-1600	14	14
92	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	6.3	14
91	Disease transmission and introgression can explain the long-lasting contact zone of modern humans and Neanderthals. <i>Nature Communications</i> , 2019 , 10, 5003	17.4	14
90	Impact of restricted marital practices on genetic variation in an endogamous Gujarati group. <i>American Journal of Physical Anthropology</i> , 2012 , 149, 92-103	2.5	14
89	Mathematical properties of Fst between admixed populations and their parental source populations. <i>Theoretical Population Biology</i> , 2011 , 80, 208-16	1.2	14
88	Polyploid and multilocus extensions of the Wahlund inequality. <i>Theoretical Population Biology</i> , 2004 , 66, 381-91	1.2	14
87	Consanguinity Rates Predict Long Runs of Homozygosity in Jewish Populations. <i>Human Heredity</i> , 2016 , 82, 87-102	1.1	13
86	Predicting Carriers of Ongoing Selective Sweeps without Knowledge of the Favored Allele. <i>PLoS Genetics</i> , 2015 , 11, e1005527	6	13
85	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, 1558-68	3	13
84	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, 628-39	8.4	12
83	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, 313-337	1.2	12
82	Coalescent Histories for Lodgepole Species Trees. <i>Journal of Computational Biology</i> , 2015 , 22, 918-29	1.7	12

81	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, 8002-9	11.5	12
80	Theory and applications of a deterministic approximation to the coalescent model. <i>Theoretical Population Biology</i> , 2014 , 93, 14-29	1.2	11
79	Consistency and inconsistency of consensus methods for inferring species trees in the presence of ancestral population structure. <i>Theoretical Population Biology</i> , 2016 , 110, 12-24	1.2	11
78	The Effect of Consanguinity on Between-Individual Identity-by-Descent Sharing. <i>Genetics</i> , 2019 , 212, 305-316	4	10
77	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		10
76	Refining the relationship between homozygosity and the frequency of the most frequent allele. <i>Journal of Mathematical Biology</i> , 2012 , 64, 87-108	2	10
75	Coalescent histories for caterpillar-like families. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2013 , 10, 1253-62	3	10
74	How dormant is Mycobacterium tuberculosis during latency? A study integrating genomics and molecular epidemiology. <i>Infection, Genetics and Evolution</i> , 2011 , 11, 1164-7	4.5	10
73	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	11.5	10
72	, Jost S D, and F are similarly constrained by allele frequencies: A mathematical, simulation, and empirical study. <i>Molecular Ecology</i> , 2019 , 28, 1624-1636	5.7	10
71	Simulation-Based Evaluation of Hybridization Network Reconstruction Methods in the Presence of Incomplete Lineage Sorting. <i>Evolutionary Bioinformatics</i> , 2017 , 13, 1176934317691935	1.9	9
70	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, 480-8	8.3	9
69	Read all about it: The Lancet's Paper of the Year, 2003. <i>Lancet, The</i> , 2003 , 362, 2101-3	40	9
68	A sharp minimum on the mean number of steps taken in adaptive walks. <i>Journal of Theoretical Biology</i> , 2005 , 237, 17-22	2.3	9
67	Enumeration of Ancestral Configurations for Matching Gene Trees and Species Trees. <i>Journal of Computational Biology</i> , 2017 , 24, 831-850	1.7	8
66	Parallel Trajectories of Genetic and Linguistic Admixture in a Genetically Admixed Creole Population. <i>Current Biology</i> , 2017 , 27, 2529-2535.e3	6.3	8
65	On the genealogy of a duplicated microsatellite. <i>Genetics</i> , 2007 , 177, 2109-22	4	8
64	HaploScope: a tool for the graphical display of haplotype structure in populations. <i>Genetic Epidemiology</i> , 2012 , 36, 17-21	2.6	7

63	Inference on the strength of balancing selection for epistatically interacting loci. <i>Theoretical Population Biology</i> , 2011 , 79, 102-13	1.2	7
62	Estimating the number of ancestral lineages using a maximum-likelihood method based on rejection sampling. <i>Genetics</i> , 2007 , 176, 1741-57	4	7
61	The behavior of admixed populations in neighbor-joining inference of population trees. <i>Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing</i> , 2013 , 273-84	1.3	7
60	Enumeration of compact coalescent histories for matching gene trees and species trees. <i>Journal of Mathematical Biology</i> , 2019 , 78, 155-188	2	6
59	Runs of homozygosity and parental relatedness. <i>Genetics in Medicine</i> , 2013 , 15, 753-4	8.1	6
58	Heterozygosity of the Yellowstone wolves. <i>Molecular Ecology</i> , 2010 , 19, 3246-9	5.7	6
57	Replication of genetic associations as pseudoreplication due to shared genealogy. <i>Genetic Epidemiology</i> , 2009 , 33, 479-87	2.6	6
56	Genetic Adaptation in New York City Rats. <i>Genome Biology and Evolution</i> , 2021 , 13,	3.9	6
55	Variance-Partitioning and Classification in Human Population Genetics		399-404 6
54	Modelling anti-vaccine sentiment as a cultural pathogen. <i>Evolutionary Human Sciences</i> , 2020 , 2,	2.2	5
53	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	2.1	5
52	On the Number of Ranked Species Trees Producing Anomalous Ranked Gene Trees. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2014 , 11, 1229-38	3	5
51	Unbiased estimation of gene diversity in samples containing related individuals: exact variance and arbitrary ploidy. <i>Genetics</i> , 2010 , 186, 1367-87	4	5
50	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, 502-23	1.2	5
49	Sampling properties of homozygosity-based statistics for linkage disequilibrium. <i>Mathematical Biosciences</i> , 2007 , 208, 33-47	3.9	5
48	On the heterozygosity of an admixed population. <i>Journal of Mathematical Biology</i> , 2020 , 81, 1217-1250	2	5
47	Admixture Models and the Breeding Systems of H. S. Jennings: A GENETICS Connection. <i>Genetics</i> , 2016 , 202, 9-13	4	5
46	Genotype imputation in a coalescent model with infinitely-many-sites mutation. <i>Theoretical Population Biology</i> , 2013 , 87, 62-74	1.2	4

45	Windfalls and pitfalls: Applications of population genetics to the search for disease genes. <i>Evolution, Medicine and Public Health</i> , 2013 , 2013, 254-72	3	4
44	Human-Genetic Ancestry Inference and False Positives in Forensic Familial Searching. <i>G3: Genes, Genomes, Genetics</i> , 2020 , 10, 2893-2902	3.2	4
43	Assortative mating by population of origin in a mechanistic model of admixture. <i>Theoretical Population Biology</i> , 2020 , 134, 129-146	1.2	4
42	Designing gene drives to limit spillover to non-target populations. <i>PLoS Genetics</i> , 2021 , 17, e1009278	6	4
41	On the joint distribution of tree height and tree length under the coalescent. <i>Theoretical Population Biology</i> , 2018 , 122, 46-56	1.2	4
40	Coalescent Theory of Migration Network Motifs. <i>Molecular Biology and Evolution</i> , 2019 , 36, 2358-2374	8.3	3
39	Measures of care fragmentation: Mathematical insights from population genetics. <i>Health Services Research</i> , 2020 , 55, 318-327	3.4	3
38	The probability of reciprocal monophyly of gene lineages in three and four species. <i>Theoretical Population Biology</i> , 2019 , 129, 133-147	1.2	3
37	Familial migration of the Neolithic contrasts massive male migration during Bronze Age in Europe inferred from ancient X chromosomes		3
36	Genetic Adaptation in New York City Rats		3
35	Probabilities of Unranked and Ranked Anomaly Zones under Birth-Death Models. <i>Molecular Biology and Evolution</i> , 2020 , 37, 1480-1494	8.3	3
34	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	0.8	3
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	2.1	2
32	The Relationship Between Haplotype-Based and Haplotype Length. <i>Genetics</i> , 2019 , 213, 281-295	4	2
31	Network-based hierarchical population structure analysis for large genomic data sets. <i>Genome Research</i> , 2019 , 29, 2020-2033	9.7	2
30	Genetics and the history of the Samaritans: Y-chromosomal microsatellites and genetic affinity between Samaritans and Cohanim. <i>Human Biology</i> , 2013 , 85, 825-58	1.2	2
29	A Population-Genetic Perspective on the Similarities and Differences among Worldwide Human Populations. <i>Human Biology</i> , 2021 , 92, 135-152	1.2	2
28	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	11.5	2

27	Variance and limiting distribution of coalescence times in a diploid model of a consanguineous population. <i>Theoretical Population Biology</i> , 2021 , 139, 50-65	1.2	2
26	Mathematical Properties of Linkage Disequilibrium Statistics Defined by Normalization of the Coefficient $D = p_{AB} - p_A p_B$. <i>Human Heredity</i> , 2019 , 84, 127-143	1.1	2
25	Mathematical constraints on : multiallelic markers in arbitrarily many populations.. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2022 , 377, 20200414	5.8	2
24	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	0.9	1
23	Bounding measures of genetic similarity and diversity using majorization. <i>Journal of Mathematical Biology</i> , 2018 , 77, 711-737	2	1
22	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	3.6	1
21	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	6	1
20	From generation to generation: the genetics of Jewish populations. Introduction. <i>Human Biology</i> , 2013 , 85, 817-24	1.2	1
19	Choosing Subsamples for Sequencing Studies by Minimizing the Average Distance to the Closest Leaf. <i>Genetics</i> , 2015 , 201, 499-511	4	1
18	Variance and limiting distribution of coalescence times in a diploid model of a consanguineous population		1
17	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	4.9	1
16	Linkage disequilibrium connects genetic records of relatives typed with disjoint genomic marker sets		1
15	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, 101939-101939	0.8	1
14	High-resolution inference of genetic relationships among Jewish populations. <i>European Journal of Human Genetics</i> , 2020 , 28, 804-814	5.3	1
13	Mathematical constraints on FST: multiallelic markers in arbitrarily many populations		1
12	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	2.5	1
11	A compendium of covariances and correlation coefficients of coalescent tree properties. <i>Theoretical Population Biology</i> , 2021 , 143, 1-13	1.2	0
10	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	1.2	0

9	F and the triangle inequality for biallelic markers. <i>Theoretical Population Biology</i> , 2020 , 133, 117-129	1.2	0
8	The effect of consanguinity on coalescence times on the X chromosome. <i>Theoretical Population Biology</i> , 2021 , 140, 32-43	1.2	0
7	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	3.9	0
6	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	11.5	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	5.8	0
4	Extracting hierarchical features of cultural variation using network-based clustering. <i>Evolutionary Human Sciences</i> , 1-35	2.2	0
3	Joining forces to uncover human evolutionary history. <i>Trends in Ecology and Evolution</i> , 2002 , 17, 301-302	10.9	0
2	On the Colijn-Plazzotta numbering scheme for unlabeled binary rooted trees. <i>Discrete Applied Mathematics</i> , 2021 , 291, 88-98	1	0
1	Enumeration of binary trees compatible with a perfect phylogeny.. <i>Journal of Mathematical Biology</i> , 2022 , 84, 54	2	0