

Bruce Rannala

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.

87
papers

13,955
citations

42
h-index

92
g-index

92
ext. papers

16,073
ext. citations

7.4
avg, IF

7.05
L-index

#	Paper	IF	Citations
87	Detecting immigration by using multilocus genotypes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1997 , 94, 9197-201	11.5	1699
86	Bayesian inference of recent migration rates using multilocus genotypes. <i>Genetics</i> , 2003 , 163, 1177-91	4	1284
85	Probability distribution of molecular evolutionary trees: a new method of phylogenetic inference. <i>Journal of Molecular Evolution</i> , 1996 , 43, 304-11	3.1	1190
84	Bayesian phylogenetic inference using DNA sequences: a Markov Chain Monte Carlo Method. <i>Molecular Biology and Evolution</i> , 1997 , 14, 717-24	8.3	926
83	Bayesian species delimitation using multilocus sequence data. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010 , 107, 9264-9	11.5	918
82	Bayes estimation of species divergence times and ancestral population sizes using DNA sequences from multiple loci. <i>Genetics</i> , 2003 , 164, 1645-56	4	755
81	Phylogenetic methods come of age: testing hypotheses in an evolutionary context. <i>Science</i> , 1997 , 276, 227-32	33.3	696
80	Frequentist properties of Bayesian posterior probabilities of phylogenetic trees under simple and complex substitution models. <i>Systematic Biology</i> , 2004 , 53, 904-13	8.4	669
79	Bayesian estimation of species divergence times under a molecular clock using multiple fossil calibrations with soft bounds. <i>Molecular Biology and Evolution</i> , 2006 , 23, 212-26	8.3	559
78	Molecular phylogenetics: principles and practice. <i>Nature Reviews Genetics</i> , 2012 , 13, 303-14	30.1	403
77	Unguided species delimitation using DNA sequence data from multiple Loci. <i>Molecular Biology and Evolution</i> , 2014 , 31, 3125-35	8.3	337
76	The Bayesian revolution in genetics. <i>Nature Reviews Genetics</i> , 2004 , 5, 251-61	30.1	328
75	Inferring speciation times under an episodic molecular clock. <i>Systematic Biology</i> , 2007 , 56, 453-66	8.4	304
74	Accommodating phylogenetic uncertainty in evolutionary studies. <i>Science</i> , 2000 , 288, 2349-50	33.3	261
73	The influence of gene flow on species tree estimation: a simulation study. <i>Systematic Biology</i> , 2014 , 63, 17-30	8.4	210
72	The accuracy of species tree estimation under simulation: a comparison of methods. <i>Systematic Biology</i> , 2011 , 60, 126-37	8.4	190
71	Critically evaluating the theory and performance of Bayesian analysis of macroevolutionary mixtures. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016 , 113, 9569-74	11.5	190

70	Taxon sampling and the accuracy of large phylogenies. <i>Systematic Biology</i> , 1998 , 47, 702-10	8.4	184
69	Improved reversible jump algorithms for Bayesian species delimitation. <i>Genetics</i> , 2013 , 194, 245-53	4	178
68	Estimating allele age. <i>Annual Review of Genomics and Human Genetics</i> , 2000 , 1, 225-49	9.7	171
67	Branch-length prior influences Bayesian posterior probability of phylogeny. <i>Systematic Biology</i> , 2005 , 54, 455-70	8.4	155
66	Phylogenetic inference using whole genomes. <i>Annual Review of Genomics and Human Genetics</i> , 2008 , 9, 217-31	9.7	138
65	Species Tree Inference with BPP Using Genomic Sequences and the Multispecies Coalescent. <i>Molecular Biology and Evolution</i> , 2018 , 35, 2585-2593	8.3	132
64	Identifiability of parameters in MCMC Bayesian inference of phylogeny. <i>Systematic Biology</i> , 2002 , 51, 754-60	8.4	125
63	DMLE+: Bayesian linkage disequilibrium gene mapping. <i>Bioinformatics</i> , 2002 , 18, 894-5	7.2	108
62	The Spectre of Too Many Species. <i>Systematic Biology</i> , 2019 , 68, 168-181	8.4	105
61	High-resolution multipoint linkage-disequilibrium mapping in the context of a human genome sequence. <i>American Journal of Human Genetics</i> , 2001 , 69, 159-78	11	104
60	A Bayesian framework for the analysis of cospeciation. <i>Evolution; International Journal of Organic Evolution</i> , 2000 , 54, 352-64	3.8	98
59	The art and science of species delimitation. <i>Environmental Epigenetics</i> , 2015 , 61, 846-853	2.4	91
58	Efficient Bayesian Species Tree Inference under the Multispecies Coalescent. <i>Systematic Biology</i> , 2017 , 66, 823-842	8.4	84
57	Likelihood analysis of disequilibrium mapping, and related problems. <i>American Journal of Human Genetics</i> , 1998 , 62, 459-73	11	79
56	Maximum likelihood estimation of phylogeny using stratigraphic data. <i>Paleobiology</i> , 1997 , 23, 174-180	2.6	67
55	Tail paradox, partial identifiability, and influential priors in Bayesian branch length inference. <i>Molecular Biology and Evolution</i> , 2012 , 29, 325-35	8.3	63
54	Estimating gene flow in island populations. <i>Genetical Research</i> , 1996 , 67, 147-58	1.1	60
53	Finding genes influencing susceptibility to complex diseases in the post-genome era. <i>Molecular Diagnosis and Therapy</i> , 2001 , 1, 203-21		59

52	Using linked markers to infer the age of a mutation. <i>Human Mutation</i> , 2001 , 18, 87-100	4.7	57
51	Bayesian species identification under the multispecies coalescent provides significant improvements to DNA barcoding analyses. <i>Molecular Ecology</i> , 2017 , 26, 3028-3036	5.7	48
50	STATISTICAL TESTS OF HOST-PARASITE COSPECIATION. <i>Evolution; International Journal of Organic Evolution</i> , 1997 , 51, 410-419	3.8	47
49	Bayesian species delimitation can be robust to guide-tree inference errors. <i>Systematic Biology</i> , 2014 , 63, 993-1004	8.4	44
48	Statistical Tests of Host-Parasite Cospeciation. <i>Evolution; International Journal of Organic Evolution</i> , 1997 , 51, 410	3.8	44
47	Disease surveillance in recombining pathogens: multilocus genotypes identify sources of human <i>Coccidioides</i> infections. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002 , 99, 9067-71	11.5	43
46	Robustness of compound Dirichlet priors for Bayesian inference of branch lengths. <i>Systematic Biology</i> , 2012 , 61, 779-84	8.4	42
45	Methylation patterns and mathematical models reveal dynamics of stem cell turnover in the human colon. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2001 , 98, 10519-21 ^{1.5}	11.5	42
44	A stop-EGFP transgenic mouse to detect clonal cell lineages generated by mutation. <i>EMBO Reports</i> , 2004 , 5, 914-20	6.5	40
43	Bayesian inference of fine-scale recombination rates using population genomic data. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2008 , 363, 3921-30	5.8	36
42	INSIGHT INTO SPECIATION FROM HISTORICAL DEMOGRAPHY IN THE PHYTOPHAGOUS BEETLE GENUS OPHRAELLA. <i>Evolution; International Journal of Organic Evolution</i> , 1999 , 53, 1846-1856	3.8	36
41	The Sampling Theory of Neutral Alleles in an Island Population of Fluctuating Size. <i>Theoretical Population Biology</i> , 1996 , 50, 91-104	1.2	36
40	A Bayesian Implementation of the Multispecies Coalescent Model with Introgression for Phylogenomic Analysis. <i>Molecular Biology and Evolution</i> , 2020 , 37, 1211-1223	8.3	33
39	Colony choice in birds: models based on temporally invariant site quality. <i>Behavioral Ecology and Sociobiology</i> , 1995 , 36, 221-228	2.5	31
38	Likelihood models of somatic mutation and codon substitution in cancer genes. <i>Genetics</i> , 2003 , 165, 695-705	7.05	30
37	Inferring complex DNA substitution processes on phylogenies using uniformization and data augmentation. <i>Systematic Biology</i> , 2006 , 55, 259-69	8.4	29
36	TP53 gene mutations of lung cancer patients in upper northern Thailand and environmental risk factors. <i>Cancer Genetics and Cytogenetics</i> , 2008 , 185, 20-7		28
35	Relatedness and conflict over optimal group size. <i>Trends in Ecology and Evolution</i> , 1994 , 9, 117-9	10.9	28

34	Gene genealogy in a population of variable size. <i>Heredity</i> , 1997 , 78 (Pt 4), 417-23	3.6	27
33	Summarizing a posterior distribution of trees using agreement subtrees. <i>Systematic Biology</i> , 2007 , 56, 578-90	8.4	26
32	Evidence from the stop-EGFP mouse supports a niche-sharing model of epidermal proliferative units. <i>Experimental Dermatology</i> , 2005 , 14, 838-43	4	23
31	Population genomic inference of recombination rates and hotspots. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009 , 106, 6215-9	11.5	21
30	Probability distribution of molecular evolutionary trees: A new method of phylogenetic inference 1996 , 43, 304		21
29	Conceptual issues in Bayesian divergence time estimation. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2016 , 371,	5.8	20
28	Methods for multipoint disease mapping using linkage disequilibrium. <i>Genetic Epidemiology</i> , 2000 , 19 Suppl 1, S71-7	2.6	18
27	In silico analysis of disease-association mapping strategies using the coalescent process and incorporating ascertainment and selection. <i>American Journal of Human Genetics</i> , 2005 , 76, 1066-73	11	16
26	Meiotic gene-conversion rate and tract length variation in the human genome. <i>European Journal of Human Genetics</i> , 2013 ,	5.3	15
25	Comparative evolutionary genetics of trematode parasites (Plagiorchiidae) and their anuran hosts. <i>Canadian Journal of Zoology</i> , 1992 , 70, 993-1000	1.5	14
24	Identification and analysis of evolutionary selection pressures acting at the molecular level in five forkhead subfamilies. <i>BMC Evolutionary Biology</i> , 2008 , 8, 261	3	13
23	The Impact of Cross-Species Gene Flow on Species Tree Estimation. <i>Systematic Biology</i> , 2020 , 69, 830-848.	8.4	12
22	Methods for estimating gene frequencies and detecting selection in bacterial populations. <i>Genetics</i> , 2000 , 155, 499-508	4	12
21	A novel solution for the time-dependent probability of gene fixation or loss under natural selection. <i>Genetics</i> , 2004 , 168, 1081-4	4	11
20	Polymorphic Characters and Phylogenetic Analysis: A Statistical Perspective. <i>Systematic Biology</i> , 1995 , 44, 421-429	8.4	10
19	The sampling distribution of disease-associated alleles. <i>Genetics</i> , 1997 , 147, 1855-61	4	9
18	DETECTING CORRELATION BETWEEN CHARACTERS IN A COMPARATIVE ANALYSIS WITH UNCERTAIN PHYLOGENY. <i>Evolution; International Journal of Organic Evolution</i> , 2003 , 57, 1237	3.8	8
17	On the genealogy of a rare allele. <i>Theoretical Population Biology</i> , 1997 , 52, 216-23	1.2	7

16	The functional significance of common polymorphisms in zinc finger transcription factors. <i>G3: Genes, Genomes, Genetics</i> , 2014 , 4, 1647-55	3.2	6
15	Using rare mutations to estimate population divergence times: a maximum likelihood approach. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1998 , 95, 15452-7	11.5	6
14	The cost of ectoparasitism in Cliff Swallows declines over 35 years. <i>Ecological Monographs</i> , 2021 , 91, e01446	9	6
13	Bayesian inference of shared recombination hotspots between humans and chimpanzees. <i>Genetics</i> , 2014 , 198, 1621-8	4	5
12	Bayesian population genomic inference of crossing over and gene conversion. <i>Genetics</i> , 2011 , 189, 607-19	4	3
11	Inferring somatic mutation rates using the stop-enhanced green fluorescent protein mouse. <i>Genetics</i> , 2007 , 177, 9-16	4	3
10	Species Identification by Bayesian Fingerprinting: A Powerful Alternative to DNA Barcoding		3
9	The Spectre of Too Many Species		3
8	Methods for multipoint disease mapping using linkage disequilibrium. <i>Genetic Epidemiology</i> , 2000 , 19, S71-S77	2.6	3
7	Polymorphic Characters and Phylogenetic Analysis: A Statistical Perspective. <i>Systematic Biology</i> , 1995 , 44, 421	8.4	2
6	The Impact of Cross-Species Gene Flow on Species Tree Estimation		2
5	A Bayesian implementation of the multispecies coalescent model with introgression for comparative genomic analysis		1
4	Simulating a Coalescent Process with Recombination and Ascertainment. <i>Lecture Notes in Computer Science</i> , 2004 , 84-95	0.9	1
3	Gene genealogy in a population of variable size		1
2	Haplotype analysis of the internationally distributed BRCA1 c.3331_3334delCAAG founder mutation reveals a common ancestral origin in Iberia. <i>Breast Cancer Research</i> , 2020 , 22, 108	8.3	0
1	A Glance at Recombination Hotspots in the Domestic Cat. <i>PLoS ONE</i> , 2016 , 11, e0148710	3.7	