

Ziheng Yang

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128
papers

35,705
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65
h-index

145
g-index

145
ext. papers

43,176
ext. citations

7.6
avg, IF

8.31
L-index

#	Paper	IF	Citations
128	PAML 4: phylogenetic analysis by maximum likelihood. <i>Molecular Biology and Evolution</i> , 2007 , 24, 1586-98	9.3	7907
127	PAML: a program package for phylogenetic analysis by maximum likelihood. <i>Bioinformatics</i> , 1997 , 13, 555-6	7.2	2753
126	Maximum likelihood phylogenetic estimation from DNA sequences with variable rates over sites: approximate methods. <i>Journal of Molecular Evolution</i> , 1994 , 39, 306-14	3.1	2125
125	Codon-substitution models for heterogeneous selection pressure at amino acid sites. <i>Genetics</i> , 2000 , 155, 431-49	4	1740
124	Bayes empirical bayes inference of amino acid sites under positive selection. <i>Molecular Biology and Evolution</i> , 2005 , 22, 1107-18	8.3	1669
123	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
122	Likelihood models for detecting positively selected amino acid sites and applications to the HIV-1 envelope gene. <i>Genetics</i> , 1998 , 148, 929-36	4	1190
121	Codon-substitution models for detecting molecular adaptation at individual sites along specific lineages. <i>Molecular Biology and Evolution</i> , 2002 , 19, 908-17	8.3	993
120	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
119	Among-site rate variation and its impact on phylogenetic analyses. <i>Trends in Ecology and Evolution</i> , 1996 , 11, 367-72	10.9	902
118	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
117	Estimating the pattern of nucleotide substitution. <i>Journal of Molecular Evolution</i> , 1994 , 39, 105-11	3.1	673
116	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
115	Accuracy and power of the likelihood ratio test in detecting adaptive molecular evolution. <i>Molecular Biology and Evolution</i> , 2001 , 18, 1585-92	8.3	559
114	Computational Molecular Evolution 2006 ,		547
113	Synonymous and nonsynonymous rate variation in nuclear genes of mammals. <i>Journal of Molecular Evolution</i> , 1998 , 46, 409-18	3.1	463
112	Best practices for justifying fossil calibrations. <i>Systematic Biology</i> , 2012 , 61, 346-59	8.4	446

111	Molecular phylogenetics: principles and practice. <i>Nature Reviews Genetics</i> , 2012 , 13, 303-14	30.1	403
110	The timescale of early land plant evolution. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018 , 115, E2274-E2283	11.5	398
109	The BPP program for species tree estimation and species delimitation. <i>Environmental Epigenetics</i> , 2015 , 61, 854-865	2.4	378
108	Estimation of primate speciation dates using local molecular clocks. <i>Molecular Biology and Evolution</i> , 2000 , 17, 1081-90	8.3	361
107	Unguided species delimitation using DNA sequence data from multiple Loci. <i>Molecular Biology and Evolution</i> , 2014 , 31, 3125-35	8.3	337
106	Phylogenomic datasets provide both precision and accuracy in estimating the timescale of placental mammal phylogeny. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2012 , 279, 3491-5004	4.4	333
105	Maximum-Likelihood Models for Combined Analyses of Multiple Sequence Data. <i>Journal of Molecular Evolution</i> , 1996 , 42, 587-96	3.1	315
104	Inferring speciation times under an episodic molecular clock. <i>Systematic Biology</i> , 2007 , 56, 453-66	8.4	304
103	Codon-substitution models to detect adaptive evolution that account for heterogeneous selective pressures among site classes. <i>Molecular Biology and Evolution</i> , 2002 , 19, 49-57	8.3	282
102	Comparison of likelihood and Bayesian methods for estimating divergence times using multiple gene Loci and calibration points, with application to a radiation of cute-looking mouse lemur species. <i>Systematic Biology</i> , 2003 , 52, 705-16	8.4	269
101	Uncertainty in the Timing of Origin of Animals and the Limits of Precision in Molecular Timescales. <i>Current Biology</i> , 2015 , 25, 2939-50	6.3	241
100	Statistical properties of the branch-site test of positive selection. <i>Molecular Biology and Evolution</i> , 2011 , 28, 1217-28	8.3	221
99	Mutation-selection models of codon substitution and their use to estimate selective strengths on codon usage. <i>Molecular Biology and Evolution</i> , 2008 , 25, 568-79	8.3	220
98	The influence of gene flow on species tree estimation: a simulation study. <i>Systematic Biology</i> , 2014 , 63, 17-30	8.4	210
97	Phylogenetic analysis using parsimony and likelihood methods. <i>Journal of Molecular Evolution</i> , 1996 , 42, 294-307	3.1	206
96	On the best evolutionary rate for phylogenetic analysis. <i>Systematic Biology</i> , 1998 , 47, 125-33	8.4	204
95	Maximum Likelihood Trees from DNA Sequences: A Peculiar Statistical Estimation Problem. <i>Systematic Biology</i> , 1995 , 44, 384-399	8.4	198
94	Evaluation of a bayesian coalescent method of species delimitation. <i>Systematic Biology</i> , 2011 , 60, 747-618	18.4	195

93	The impact of the representation of fossil calibrations on Bayesian estimation of species divergence times. <i>Systematic Biology</i> , 2010 , 59, 74-89	8.4	190
92	The effect of insertions, deletions, and alignment errors on the branch-site test of positive selection. <i>Molecular Biology and Evolution</i> , 2010 , 27, 2257-67	8.3	189
91	Improved reversible jump algorithms for Bayesian species delimitation. <i>Genetics</i> , 2013 , 194, 245-53	4	178
90	Maximum likelihood estimation on large phylogenies and analysis of adaptive evolution in human influenza virus A. <i>Journal of Molecular Evolution</i> , 2000 , 51, 423-32	3.1	164
89	Exploring uncertainty in the calibration of the molecular clock. <i>Biology Letters</i> , 2012 , 8, 156-9	3.6	163
88	Bayesian molecular clock dating of species divergences in the genomics era. <i>Nature Reviews Genetics</i> , 2016 , 17, 71-80	30.1	158
87	Dating primate divergences through an integrated analysis of palaeontological and molecular data. <i>Systematic Biology</i> , 2011 , 60, 16-31	8.4	155
86	Branch-length prior influences Bayesian posterior probability of phylogeny. <i>Systematic Biology</i> , 2005 , 54, 455-70	8.4	155
85	Approximate likelihood calculation on a phylogeny for Bayesian estimation of divergence times. <i>Molecular Biology and Evolution</i> , 2011 , 28, 2161-72	8.3	153
84	Likelihood and Bayes estimation of ancestral population sizes in hominoids using data from multiple loci. <i>Genetics</i> , 2002 , 162, 1811-23	4	149
83	Estimation of the transition/transversion rate bias and species sampling. <i>Journal of Molecular Evolution</i> , 1999 , 48, 274-83	3.1	147
82	Molecular Evolution 2014 ,		146
81	Inference of selection from multiple species alignments. <i>Current Opinion in Genetics and Development</i> , 2002 , 12, 688-94	4.9	145
80	Phylogenetic inference using whole genomes. <i>Annual Review of Genomics and Human Genetics</i> , 2008 , 9, 217-31	9.7	138
79	Estimation of hominoid ancestral population sizes under bayesian coalescent models incorporating mutation rate variation and sequencing errors. <i>Molecular Biology and Evolution</i> , 2008 , 25, 1979-94	8.3	133
78	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
77	In defence of model-based inference in phylogeography. <i>Molecular Ecology</i> , 2010 , 19, 436-446	5.7	127
76	Maximum likelihood methods for detecting adaptive evolution after gene duplication. <i>Journal of Structural and Functional Genomics</i> , 2003 , 3, 201-212		115

75	The Spectre of Too Many Species. <i>Systematic Biology</i> , 2019 , 68, 168-181	8.4	105
74	An empirical examination of the utility of codon-substitution models in phylogeny reconstruction. <i>Systematic Biology</i> , 2005 , 54, 808-18	8.4	95
73	A biologist's guide to Bayesian phylogenetic analysis. <i>Nature Ecology and Evolution</i> , 2017 , 1, 1446-1454	12.3	93
72	Challenges in Species Tree Estimation Under the Multispecies Coalescent Model. <i>Genetics</i> , 2016 , 204, 1353-1368	4	89
71	Constraining uncertainty in the timescale of angiosperm evolution and the veracity of a Cretaceous Terrestrial Revolution. <i>New Phytologist</i> , 2018 , 218, 819-834	9.8	88
70	Efficient Bayesian Species Tree Inference under the Multispecies Coalescent. <i>Systematic Biology</i> , 2017 , 66, 823-842	8.4	84
69	Using Phylogenomic Data to Explore the Effects of Relaxed Clocks and Calibration Strategies on Divergence Time Estimation: Primates as a Test Case. <i>Systematic Biology</i> , 2018 , 67, 594-615	8.4	84
68	The unbearable uncertainty of Bayesian divergence time estimation. <i>Journal of Systematics and Evolution</i> , 2013 , 51, 30-43	2.9	83
67	The power of phylogenetic comparison in revealing protein function. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005 , 102, 3179-80	11.5	82
66	Neither phylogenomic nor palaeontological data support a Palaeogene origin of placental mammals. <i>Biology Letters</i> , 2014 , 10, 20131003	3.6	77
65	Phylogenetic tree building in the genomic age. <i>Nature Reviews Genetics</i> , 2020 , 21, 428-444	30.1	76
64	MtZoa: a general mitochondrial amino acid substitutions model for animal evolutionary studies. <i>Molecular Phylogenetics and Evolution</i> , 2009 , 52, 268-72	4.1	72
63	The impact of the rate prior on Bayesian estimation of divergence times with multiple Loci. <i>Systematic Biology</i> , 2014 , 63, 555-65	8.4	63
62	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
61	Substitution rates in Drosophila nuclear genes: implications for translational selection. <i>Genetics</i> , 2001 , 157, 295-305	4	58
60	The evolution of methods for establishing evolutionary timescales. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2016 , 371,	5.8	57
59	Rates of nucleotide substitution and mammalian nuclear gene evolution. Approximate and maximum-likelihood methods lead to different conclusions. <i>Genetics</i> , 2000 , 156, 1299-308	4	56
58	Characterization of the uncertainty of divergence time estimation under relaxed molecular clock models using multiple loci. <i>Systematic Biology</i> , 2015 , 64, 267-80	8.4	54

57	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
56	STATISTICAL TESTS OF HOST-PARASITE COSPECIATION. <i>Evolution; International Journal of Organic Evolution</i> , 1997 , 51, 410-419	3.8	47
55	Fair-balance paradox, star-tree paradox, and Bayesian phylogenetics. <i>Molecular Biology and Evolution</i> , 2007 , 24, 1639-55	8.3	46
54	A likelihood ratio test of speciation with gene flow using genomic sequence data. <i>Genome Biology and Evolution</i> , 2010 , 2, 200-11	3.9	45
53	On the estimation of ancestral population sizes of modern humans. <i>Genetical Research</i> , 1997 , 69, 111-6	1.1	45
52	Bayesian species delimitation can be robust to guide-tree inference errors. <i>Systematic Biology</i> , 2014 , 63, 993-1004	8.4	44
51	Maximum likelihood implementation of an isolation-with-migration model with three species for testing speciation with gene flow. <i>Molecular Biology and Evolution</i> , 2012 , 29, 3131-42	8.3	44
50	Dating phylogenies with sequentially sampled tips. <i>Systematic Biology</i> , 2013 , 62, 674-88	8.4	43
49	Complexity of the simplest phylogenetic estimation problem. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2000 , 267, 109-16	4.4	40
48	Coalescent-Based Analyses of Genomic Sequence Data Provide a Robust Resolution of Phylogenetic Relationships among Major Groups of Gibbons. <i>Molecular Biology and Evolution</i> , 2018 , 35, 159-179	8.3	39
47	Molecular and morphological evidence on the phylogeny of the Elephantidae. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2000 , 267, 2493-500	4.4	39
46	Coalescent Analysis of Phylogenomic Data Confidently Resolves the Species Relationships in the <i>Anopheles gambiae</i> Species Complex. <i>Molecular Biology and Evolution</i> , 2018 , 35, 2512-2527	8.3	38
45	Maximum Likelihood Trees from DNA Sequences: A Peculiar Statistical Estimation Problem. <i>Systematic Biology</i> , 1995 , 44, 384	8.4	37
44	Bayesian selection of misspecified models is overconfident and may cause spurious posterior probabilities for phylogenetic trees. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018 , 115, 1854-1859	11.5	34
43	Testing the molecular clock using mechanistic models of fossil preservation and molecular evolution. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2017 , 284,	4.4	33
42	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
41	Molecular evolution of the hepatitis B virus genome. <i>Journal of Molecular Evolution</i> , 1995 , 41, 587-96	3.1	32
40	Searching for efficient Markov chain Monte Carlo proposal kernels. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013 , 110, 19307-12	11.5	30

39	Prevalence of cryptic species in morphologically uniform taxa - Fast speciation and evolutionary radiation in Asian frogs. <i>Molecular Phylogenetics and Evolution</i> , 2018 , 127, 723-731	4.1	28
38	Comparison of different strategies for using fossil calibrations to generate the time prior in Bayesian molecular clock dating. <i>Molecular Phylogenetics and Evolution</i> , 2017 , 114, 386-400	4.1	28
37	Multilocus estimation of divergence times and ancestral effective population sizes of <i>Oryza</i> species and implications for the rapid diversification of the genus. <i>New Phytologist</i> , 2013 , 198, 1155-1164	9.8	28
36	Maximum Likelihood Implementation of an Isolation-with-Migration Model for Three Species. <i>Systematic Biology</i> , 2017 , 66, 379-398	8.4	28
35	Dog10K: an international sequencing effort to advance studies of canine domestication, phenotypes and health. <i>National Science Review</i> , 2019 , 6, 810-824	10.8	27
34	Evaluation of Ancestral Sequence Reconstruction Methods to Infer Nonstationary Patterns of Nucleotide Substitution. <i>Genetics</i> , 2015 , 200, 873-90	4	26
33	An Evaluation of Different Partitioning Strategies for Bayesian Estimation of Species Divergence Times. <i>Systematic Biology</i> , 2018 , 67, 61-77	8.4	23
32	Probability distribution of molecular evolutionary trees: A new method of phylogenetic inference 1996 , 43, 304		21
31	Rapid morphological evolution in placental mammals post-dates the origin of the crown group. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2019 , 286, 20182418	4.4	18
30	Bayesian Estimation of Species Divergence Times Using Correlated Quantitative Characters. <i>Systematic Biology</i> , 2019 , 68, 967-986	8.4	16
29	Bayesian Molecular Clock Dating Using Genome-Scale Datasets. <i>Methods in Molecular Biology</i> , 2019 , 1910, 309-330	1.4	16
28	Molecular Clocks without Rocks: New Solutions for Old Problems. <i>Trends in Genetics</i> , 2020 , 36, 845-856	8.5	15
27	Empirical evaluation of a prior for Bayesian phylogenetic inference. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2008 , 363, 4031-9	5.8	14
26	The Impact of Cross-Species Gene Flow on Species Tree Estimation. <i>Systematic Biology</i> , 2020 , 69, 830-848	8.4	12
25	Bayesian estimation of nonsynonymous/synonymous rate ratios for pairwise sequence comparisons. <i>Molecular Biology and Evolution</i> , 2014 , 31, 1902-13	8.3	12
24	Defining Species When There is Gene Flow. <i>Systematic Biology</i> , 2021 , 70, 108-119	8.4	11
23	Reply to Hedges et al.: Accurate timetrees do indeed require accurate calibrations. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018 , 115, E9512-E9513	11.5	9
22	Phylogeny and species delimitation of the C-genome diploid species in <i>Oryza</i> . <i>Journal of Systematics and Evolution</i> , 2011 , 49, 386-395	2.9	8

21	On the varied pattern of evolution of 2 fungal genomes: a critique of Hughes and Friedman. <i>Molecular Biology and Evolution</i> , 2006 , 23, 2279-82	8.3	8
20	SlimCodeML: An Optimized Version of CodeML for the Branch-Site Model 2012 ,		7
19	On the general reversible Markov process model of nucleotide substitution: A reply to Saccone et al.. <i>Journal of Molecular Evolution</i> , 1995 , 41, 254	3.1	6
18	Complexity of the simplest species tree problem. <i>Molecular Biology and Evolution</i> , 2021 , 38, 3993-4009	8.3	6
17	A Species-Level Timeline of Mammal Evolution Integrating Phylogenomic Data.. <i>Nature</i> , 2021 ,	50.4	6
16	Dating species divergences using rocks and clocks. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2016 , 371,	5.8	5
15	A Simulation Study to Examine the Information Content in Phylogenomic Data Sets under the Multispecies Coalescent Model. <i>Molecular Biology and Evolution</i> , 2020 , 37, 3211-3224	8.3	4
14	Species Identification by Bayesian Fingerprinting: A Powerful Alternative to DNA Barcoding		3
13	The Spectre of Too Many Species		3
12	Adaptive Molecular Evolution 2019 , 369-396		3
11	The Impact of Cross-Species Gene Flow on Species Tree Estimation		2
10	Phase Resolution of Heterozygous Sites in Diploid Genomes is Important to Phylogenomic Analysis under the Multispecies Coalescent Model. <i>Systematic Biology</i> , 2021 ,	8.4	2
9	Functional and Adaptive Significance of Promoter Mutations That Affect Divergent Myocardial Expressions of TRIM72 in Primates. <i>Molecular Biology and Evolution</i> , 2021 , 38, 2930-2945	8.3	2
8	Multispecies coalescent and its applications to infer species phylogenies and cross-species gene flow.. <i>National Science Review</i> , 2021 , 8, nwab127	10.8	2
7	A discrete-beta model for testing gene flow after speciation. <i>Methods in Ecology and Evolution</i> , 2015 , 6, 715-724	7.7	1
6	A Bayesian implementation of the multispecies coalescent model with introgression for comparative genomic analysis		1
5	The Asymptotic Behavior of Bootstrap Support Values in Molecular Phylogenetics. <i>Systematic Biology</i> , 2021 , 70, 774-785	8.4	1
4	Using Phylogenomic Data to Explore the Effects of Relaxed Clocks and Calibration Strategies on Divergence Time Estimation: Primates as a Test Case		1

- 3 RADseq data reveal a lack of admixture in a mouse lemur contact zone contrary to previous microsatellite results 1
- 2 Ambiguity Coding Allows Accurate Inference of Evolutionary Parameters from Alignments in an Aggregated State-Space. *Systematic Biology*, **2021**, 70, 21-32 8.4
- 1 A. W. F. Edwards and the Origin of Bayesian Phylogenetics 352-362