

List of Publications by Year in descending order

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52
papers

6,118
citations

126907

33
h-index

175258

52
g-index

60
all docs

60
docs citations

60
times ranked

7581
citing authors

#	ARTICLE	IF	CITATIONS
1	A Linear-Time Algorithm for Gaussian and Non-Gaussian Trait Evolution Models. <i>Systematic Biology</i> , 2014, 63, 397-408.	5.6	782
2	TESTING FOR DIFFERENT RATES OF CONTINUOUS TRAIT EVOLUTION USING LIKELIHOOD. <i>Evolution; International Journal of Organic Evolution</i> , 2006, 60, 922-933.	2.3	516
3	Bayesian Estimation of Concordance among Gene Trees. <i>Molecular Biology and Evolution</i> , 2006, 24, 412-426.	8.9	420
4	The iPlant Collaborative: Cyberinfrastructure for Plant Biology. <i>Frontiers in Plant Science</i> , 2011, 2, 34.	3.6	396
5	BUCKy: Gene tree/species tree reconciliation with Bayesian concordance analysis. <i>Bioinformatics</i> , 2010, 26, 2910-2911.	4.1	389
6	Inferring Phylogenetic Networks with Maximum Pseudolikelihood under Incomplete Lineage Sorting. <i>PLoS Genetics</i> , 2016, 12, e1005896.	3.5	348
7	PhyloNetworks: A Package for Phylogenetic Networks. <i>Molecular Biology and Evolution</i> , 2017, 34, 3292-3298.	8.9	250
8	Prospects for Building the Tree of Life from Large Sequence Databases. <i>Science</i> , 2004, 306, 1172-1174.	12.6	233
9	Fast and accurate detection of evolutionary shifts in Ornstein-Uhlenbeck models. <i>Methods in Ecology and Evolution</i> , 2016, 7, 811-824.	5.2	201
10	TESTING FOR DIFFERENT RATES OF CONTINUOUS TRAIT EVOLUTION USING LIKELIHOOD. <i>Evolution; International Journal of Organic Evolution</i> , 2006, 60, 922.	2.3	183
11	Rphylopars: fast multivariate phylogenetic comparative methods for missing data and within-species variation. <i>Methods in Ecology and Evolution</i> , 2017, 8, 22-27.	5.2	174
12	Monocot plastid phylogenomics, timeline, net rates of species diversification, the power of multi-gene analyses, and a functional model for the origin of monocots. <i>American Journal of Botany</i> , 2018, 105, 1888-1910.	1.7	161
13	Intrinsic inference difficulties for trait evolution with Ornstein-Uhlenbeck models. <i>Methods in Ecology and Evolution</i> , 2014, 5, 1133-1146.	5.2	154
14	Bayesian species delimitation combining multiple genes and traits in a unified framework. <i>Evolution; International Journal of Organic Evolution</i> , 2015, 69, 492-507.	2.3	152
15	Inconsistency of Species Tree Methods under Gene Flow. <i>Systematic Biology</i> , 2016, 65, 843-851.	5.6	146
16	THE ROLE OF POLLINATOR SHIFTS IN THE FLORAL DIVERSIFICATION OF <i>IOCHROMA</i> (SOLANACEAE). <i>Evolution; International Journal of Organic Evolution</i> , 2008, 62, 793-806.	2.3	142
17	Fine-Scale Phylogenetic Discordance across the House Mouse Genome. <i>PLoS Genetics</i> , 2009, 5, e1000729.	3.5	104
18	Comparing Two Bayesian Methods for Gene Tree/Species Tree Reconstruction: Simulations with Incomplete Lineage Sorting and Horizontal Gene Transfer. <i>Systematic Biology</i> , 2011, 60, 261-275.	5.6	103

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19	Do potatoes and tomatoes have a single evolutionary history, and what proportion of the genome supports this history?. BMC Evolutionary Biology, 2009, 9, 191.	3.2	89
20	Phylogenetic Comparative Methods on Phylogenetic Networks with Reticulations. Systematic Biology, 2018, 67, 800-820.	5.6	88
21	Inference of Adaptive Shifts for Multivariate Correlated Traits. Systematic Biology, 2018, 67, 662-680.	5.6	78
22	LOCATING EVOLUTIONARY PRECURSORS ON A PHYLOGENETIC TREE. Evolution; International Journal of Organic Evolution, 2012, 66, 3918-3930.	2.3	77
23	Using HSV-1 Genome Phylogenetics to Track Past Human Migrations. PLoS ONE, 2013, 8, e76267.	2.5	76
24	Detecting and Locating Whole Genome Duplications on a Phylogeny: A Probabilistic Approach. Molecular Biology and Evolution, 2014, 31, 750-762.	8.9	73
25	Phylogenetic Trees and Networks Can Serve as Powerful and Complementary Approaches for Analysis of Genomic Data. Systematic Biology, 2020, 69, 593-601.	5.6	72
26	Covariation Structure in Plastid Genome Evolution: A New Statistical Test. Molecular Biology and Evolution, 2005, 22, 914-924.	8.9	66
27	Identifiability of a Markovian model of molecular evolution with gamma-distributed rates. Advances in Applied Probability, 2008, 40, 229-249.	0.7	63
28	Exploring Tree-Like and Non-Tree-Like Patterns Using Genome Sequences: An Example Using the Inbreeding Plant Species <i>Arabidopsis thaliana</i> (L.) Heynh. Systematic Biology, 2015, 64, 809-823.	5.6	57
29	Evaluating and Characterizing Ancient Whole-Genome Duplications in Plants with Gene Count Data. Genome Biology and Evolution, 2016, 8, 1023-1037.	2.5	53
30	Analysis of comparative data with hierarchical autocorrelation. Annals of Applied Statistics, 2008, 2, .	1.1	48
31	Missing the Forest for the Trees: Phylogenetic Compression and Its Implications for Inferring Complex Evolutionary Histories. Systematic Biology, 2005, 54, 146-157.	5.6	47
32	Proteomic analysis of the winter-protected phenotype of hibernating ground squirrel intestine. American Journal of Physiology - Regulatory Integrative and Comparative Physiology, 2008, 295, R316-R328.	1.8	45
33	Asymptotic theory with hierarchical autocorrelation: Ornstein-Uhlenbeck tree models. Annals of Statistics, 2013, 41, .	2.6	45
34	Reticulate Evolution Helps Explain Apparent Homoplasy in Floral Biology and Pollination in Baobabs (<i>Adansonia</i> ; <i>Bombacoideae</i> ; <i>Malvaceae</i>). Systematic Biology, 2020, 69, 462-478.	5.6	32
35	A Bayesian Perspective on a Non-parsimonious Parsimony Model. Systematic Biology, 2008, 57, 406-419.	5.6	28
36	Detecting Phylogenetic Breakpoints and Discordance from Genome-Wide Alignments for Species Tree Reconstruction. Genome Biology and Evolution, 2011, 3, 246-258.	2.5	28

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37	Single copy nuclear gene analysis of polyploidy in wild potatoes (<i>Solanum</i> section <i>Petota</i>). <i>BMC Evolutionary Biology</i> , 2012, 12, 70.	3.2	28
38	A new carnivorous plant lineage (<i>Triantha</i>) with a unique sticky-inflorescence trap. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	7.1	26
39	A Malvaceae mystery: A mallow maelstrom of genome multiplications and maybe misleading methods?. <i>Journal of Integrative Plant Biology</i> , 2019, 61, 12-31.	8.5	25
40	THE EVOLUTION OF HYBRID INCOMPATIBILITIES ALONG A PHYLOGENY. <i>Evolution; International Journal of Organic Evolution</i> , 2013, 67, n/a-n/a.	2.3	21
41	Identifiability of a Markovian model of molecular evolution with gamma-distributed rates. <i>Advances in Applied Probability</i> , 2008, 40, 229-249.	0.7	17
42	Assessing the fit of the multi-species network coalescent to multi-locus data. <i>Bioinformatics</i> , 2021, 37, 634-641.	4.1	14
43	Phase transition on the convergence rate of parameter estimation under an Ornstein-Uhlenbeck diffusion on a tree. <i>Journal of Mathematical Biology</i> , 2017, 74, 355-385.	1.9	13
44	MACROEVOLUTIONARY TESTS OF POLLINATION SYNDROMES: A REPLY TO FENSTER ET AL.. <i>Evolution; International Journal of Organic Evolution</i> , 2009, 63, 2763-2767.	2.3	9
45	Groves of Phylogenetic Trees. <i>Annals of Combinatorics</i> , 2009, 13, 139-167.	0.6	8
46	Mapping Quantitative Trait Loci onto a Phylogenetic Tree. <i>Genetics</i> , 2012, 192, 267-279.	2.9	8
47	Statistical evidence for common ancestry: Application to primates. <i>Evolution; International Journal of Organic Evolution</i> , 2016, 70, 1354-1363.	2.3	8
48	KIMGENS: a novel method to estimate kinship in organisms with mixed haploid diploid genetic systems robust to population structure. <i>Bioinformatics</i> , 2022, 38, 3044-3050.	4.1	5
49	Population pharmacokinetics/pharmacodynamics relationships of an anticancer drug. <i>Statistics in Medicine</i> , 2003, 22, 833-846.	1.6	3
50	Computing the Joint Distribution of Tree Shape and Tree Distance for Gene Tree Inference and Recombination Detection. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2013, 10, 1-1.	3.0	3
51	Evidence for hawkmoth pollination in the chiropterophilous African baobab (<i>Adansonia</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 10 T 5	1.6	2
52	Dating with constraints. <i>Peer Community in Evolutionary Biology</i> , 0, , .	0.0	0