

Siavash Mirarab

List of Publications by Year in descending order

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Version: 2024-02-01

82
papers

13,834
citations

76326

40
h-index

74163

75
g-index

117
all docs

117
docs citations

117
times ranked

17011
citing authors

#	ARTICLE	IF	CITATIONS
1	DEPP: Deep Learning Enables Extending Species Trees using Single Genes. <i>Systematic Biology</i> , 2023, 72, 17-34.	5.6	11
2	Fast and accurate distance-based phylogenetic placement using divide and conquer. <i>Molecular Ecology Resources</i> , 2022, 22, 1213-1227.	4.8	25
3	Completing gene trees without species trees in sub-quadratic time. <i>Bioinformatics</i> , 2022, 38, 1532-1541.	4.1	9
4	QuCo: quartet-based co-estimation of species trees and gene trees. <i>Bioinformatics</i> , 2022, 38, i413-i421.	4.1	2
5	Log Transformation Improves Dating of Phylogenies. <i>Molecular Biology and Evolution</i> , 2021, 38, 1151-1167.	8.9	7
6	Multiple Sequence Alignment for Large Heterogeneous Datasets Using SATÁ©, PASTA, and UPP. <i>Methods in Molecular Biology</i> , 2021, 2231, 99-119.	0.9	1
7	HIV Care Prioritization Using Phylogenetic Branch Length. <i>Journal of Acquired Immune Deficiency Syndromes (1999)</i> , 2021, 86, 626-637.	2.1	5
8	CONSULT: accurate contamination removal using locality-sensitive hashing. <i>NAR Genomics and Bioinformatics</i> , 2021, 3, lqab071.	3.2	14
9	TAPER: Pinpointing errors in multiple sequence alignments despite varying rates of evolution. <i>Methods in Ecology and Evolution</i> , 2021, 12, 2145-2158.	5.2	13
10	Multispecies Coalescent: Theory and Applications in Phylogenetics. <i>Annual Review of Ecology, Evolution, and Systematics</i> , 2021, 52, 247-268.	8.3	28
11	SODA: multi-locus species delimitation using quartet frequencies. <i>Bioinformatics</i> , 2021, 36, 5623-5631.	4.1	21
12	Estimating repeat spectra and genome length from low-coverage genome skims with RESPECT. <i>PLoS Computational Biology</i> , 2021, 17, e1009449.	3.2	17
13	APPLES: Scalable Distance-Based Phylogenetic Placement with or without Alignments. <i>Systematic Biology</i> , 2020, 69, 566-578.	5.6	51
14	INSTRAL: Discordance-Aware Phylogenetic Placement Using Quartet Scores. <i>Systematic Biology</i> , 2020, 69, 384-391.	5.6	14
15	ASTRAL-Pro: Quartet-Based Species-Tree Inference despite Paralogy. <i>Molecular Biology and Evolution</i> , 2020, 37, 3292-3307.	8.9	116
16	Dense sampling of bird diversity increases power of comparative genomics. <i>Nature</i> , 2020, 587, 252-257.	27.8	251
17	Phylogenetic double placement of mixed samples. <i>Bioinformatics</i> , 2020, 36, i335-i343.	4.1	11
18	Precise phylogenetic analysis of microbial isolates and genomes from metagenomes using PhyloPhlAn 3.0. <i>Nature Communications</i> , 2020, 11, 2500.	12.8	368

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19	Beyond DNA barcoding: The unrealized potential of genome skim data in sample identification. <i>Molecular Ecology</i> , 2020, 29, 2521-2534.	3.9	58
20	More is needed—Thousands of loci are required to elucidate the relationships of the “flowers of the sea” (Sabellida, Annelida). <i>Molecular Phylogenetics and Evolution</i> , 2020, 151, 106892.	2.7	24
21	The impact of contaminants on the accuracy of genome skimming and the effectiveness of exclusion read filters. <i>Molecular Ecology Resources</i> , 2020, 20, 649-661.	4.8	16
22	Forcing external constraints on tree inference using ASTRAL. <i>BMC Genomics</i> , 2020, 21, 218.	2.8	19
23	TADA: phylogenetic augmentation of microbiome samples enhances phenotype classification. <i>Bioinformatics</i> , 2019, 35, i31-i40.	4.1	9
24	Phylogenetic Signal of Indels and the Neoavian Radiation. <i>Diversity</i> , 2019, 11, 108.	1.7	33
25	TreeCluster: Clustering biological sequences using phylogenetic trees. <i>PLoS ONE</i> , 2019, 14, e0221068.	2.5	99
26	Large-scale ruminant genome sequencing provides insights into their evolution and distinct traits. <i>Science</i> , 2019, 364, .	12.6	266
27	ASTRAL-MP: scaling ASTRAL to very large datasets using randomization and parallelization. <i>Bioinformatics</i> , 2019, 35, 3961-3969.	4.1	57
28	Skmer: assembly-free and alignment-free sample identification using genome skims. <i>Genome Biology</i> , 2019, 20, 34.	8.8	70
29	Phylogenomics of 10,575 genomes reveals evolutionary proximity between domains Bacteria and Archaea. <i>Nature Communications</i> , 2019, 10, 5477.	12.8	197
30	FAVITES: simultaneous simulation of transmission networks, phylogenetic trees and sequences. <i>Bioinformatics</i> , 2019, 35, 1852-1861.	4.1	45
31	Multi-allele species reconstruction using ASTRAL. <i>Molecular Phylogenetics and Evolution</i> , 2019, 130, 286-296.	2.7	106
32	TreeCluster: Clustering biological sequences using phylogenetic trees. , 2019, 14, e0221068.		0
33	TreeCluster: Clustering biological sequences using phylogenetic trees. , 2019, 14, e0221068.		0
34	TreeCluster: Clustering biological sequences using phylogenetic trees. , 2019, 14, e0221068.		0
35	Phylogenetic Placement of Exact Amplicon Sequences Improves Associations with Clinical Information. <i>MSystems</i> , 2018, 3, .	3.8	376
36	A roadmap for global synthesis of the plant tree of life. <i>American Journal of Botany</i> , 2018, 105, 614-622.	1.7	38

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37	Identifying the favored mutation in a positive selective sweep. <i>Nature Methods</i> , 2018, 15, 279-282.	19.0	56
38	A Two-State Model of Tree Evolution and Its Applications to Alu Retrotransposition. <i>Systematic Biology</i> , 2018, 67, 475-489.	5.6	5
39	DiscoVista: Interpretable visualizations of gene tree discordance. <i>Molecular Phylogenetics and Evolution</i> , 2018, 122, 110-115.	2.7	106
40	Species Tree Estimation Using ASTRAL: How Many Genes Are Enough?. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2018, 15, 1738-1747.	3.0	19
41	Interspecific Gene Flow Shaped the Evolution of the Genus <i>Canis</i> . <i>Current Biology</i> , 2018, 28, 3441-3449.e5.	3.9	110
42	TreeShrink: fast and accurate detection of outlier long branches in collections of phylogenetic trees. <i>BMC Genomics</i> , 2018, 19, 272.	2.8	225
43	Testing for Polytomies in Phylogenetic Species Trees Using Quartet Frequencies. <i>Genes</i> , 2018, 9, 132.	2.4	107
44	ASTRAL-III: polynomial time species tree reconstruction from partially resolved gene trees. <i>BMC Bioinformatics</i> , 2018, 19, 153.	2.6	1,451
45	A communal catalogue reveals Earth's multiscale microbial diversity. <i>Nature</i> , 2017, 551, 457-463.	27.8	1,942
46	TreeShrink: Efficient Detection of Outlier Tree Leaves. <i>Lecture Notes in Computer Science</i> , 2017, , 116-140.	1.3	7
47	ASTRAL-III: Increased Scalability and Impacts of Contracting Low Support Branches. <i>Lecture Notes in Computer Science</i> , 2017, , 53-75.	1.3	129
48	Fragmentary Gene Sequences Negatively Impact Gene Tree and Species Tree Reconstruction. <i>Molecular Biology and Evolution</i> , 2017, 34, 3279-3291.	8.9	73
49	Phylogenomics: Constrained gene tree inference. <i>Nature Ecology and Evolution</i> , 2017, 1, 56.	7.8	9
50	Minimum variance rooting of phylogenetic trees and implications for species tree reconstruction. <i>PLoS ONE</i> , 2017, 12, e0182238.	2.5	71
51	Evaluating Summary Methods for Multilocus Species Tree Estimation in the Presence of Incomplete Lineage Sorting. <i>Systematic Biology</i> , 2016, 65, 366-380.	5.6	242
52	HIPPI: highly accurate protein family classification with ensembles of HMMs. <i>BMC Genomics</i> , 2016, 17, 765.	2.8	17
53	Fast Coalescent-Based Computation of Local Branch Support from Quartet Frequencies. <i>Molecular Biology and Evolution</i> , 2016, 33, 1654-1668.	8.9	650
54	Anchoring quartet-based phylogenetic distances and applications to species tree reconstruction. <i>BMC Genomics</i> , 2016, 17, 783.	2.8	24

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55	The Interrelationships of Placental Mammals and the Limits of Phylogenetic Inference. <i>Genome Biology and Evolution</i> , 2016, 8, 330-344.	2.5	195
56	Phylogenomic species tree estimation in the presence of incomplete lineage sorting and horizontal gene transfer. <i>BMC Genomics</i> , 2015, 16, S1.	2.8	57
57	A comparative study of SVDquartets and other coalescent-based species tree estimation methods. <i>BMC Genomics</i> , 2015, 16, S2.	2.8	128
58	Ultra-large alignments using phylogeny-aware profiles. <i>Genome Biology</i> , 2015, 16, 124.	8.8	113
59	ASTRAL-II: coalescent-based species tree estimation with many hundreds of taxa and thousands of genes. <i>Bioinformatics</i> , 2015, 31, i44-i52.	4.1	822
60	PASTA: Ultra-Large Multiple Sequence Alignment for Nucleotide and Amino-Acid Sequences. <i>Journal of Computational Biology</i> , 2015, 22, 377-386.	1.6	360
61	Phylogenomic analyses data of the avian phylogenomics project. <i>GigaScience</i> , 2015, 4, 4.	6.4	72
62	Response to Comment on "Whole-genome analyses resolve early branches in the tree of life of modern birds". <i>Science</i> , 2015, 349, 1460-1460.	12.6	53
63	Response to Comment on "Statistical binning enables an accurate coalescent-based estimation of the avian tree". <i>Science</i> , 2015, 350, 171-171.	12.6	12
64	Weighted Statistical Binning: Enabling Statistically Consistent Genome-Scale Phylogenetic Analyses. <i>PLoS ONE</i> , 2015, 10, e0129183.	2.5	98
65	TIPP: taxonomic identification and phylogenetic profiling. <i>Bioinformatics</i> , 2014, 30, 3548-3555.	4.1	93
66	Statistical binning enables an accurate coalescent-based estimation of the avian tree. <i>Science</i> , 2014, 346, 1250463.	12.6	225
67	Whole-genome analyses resolve early branches in the tree of life of modern birds. <i>Science</i> , 2014, 346, 1320-1331.	12.6	1,583
68	PASTA: Ultra-Large Multiple Sequence Alignment. <i>Lecture Notes in Computer Science</i> , 2014, , 177-191.	1.3	48
69	Data access for the 1,000 Plants (1KP) project. <i>GigaScience</i> , 2014, 3, 17.	6.4	582
70	Phylotranscriptomic analysis of the origin and early diversification of land plants. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, E4859-68.	7.1	1,123
71	BBCA: Improving the scalability of *BEAST using random binning. <i>BMC Genomics</i> , 2014, 15, S11.	2.8	38
72	Phylotastic! Making tree-of-life knowledge accessible, reusable and convenient. <i>BMC Bioinformatics</i> , 2013, 14, 158.	2.6	33

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73	Size-Constrained Regression Test Case Selection Using Multicriteria Optimization. IEEE Transactions on Software Engineering, 2012, 38, 936-956.	5.6	63
74	MRL and SuperFine+MRL: new supertree methods. Algorithms for Molecular Biology, 2012, 7, 3.	1.2	62
75	F<sc>AST</sc>SP: linear time calculation of alignment accuracy. Bioinformatics, 2011, 27, 3250-3258.	4.1	56
76	The Effects of Time Constraints on Test Case Prioritization: A Series of Controlled Experiments. IEEE Transactions on Software Engineering, 2010, 36, 593-617.	5.6	126
77	A requirement-based software testing framework: An industrial practice. , 2008, , .		7
78	Adaptive Action Selection in Autonomic Software Using Reinforcement Learning. , 2008, , .		31
79	An empirical study of the effect of time constraints on the cost-benefits of regression testing. , 2008, , .		60
80	An Empirical Study on Bayesian Network-based Approach for Test Case Prioritization. , 2008, , .		37
81	Using Bayesian Belief Networks to Predict Change Propagation in Software Systems. , 2007, , .		27
82	A Prioritization Approach for Software Test Cases Based on Bayesian Networks. , 2007, , 276-290.		42