

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	A communal catalogue reveals Earth's multiscale microbial diversity. <i>Nature</i> , 2017, 551, 457-463.	27.8	1,942
2	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
3	ASTRAL-III: polynomial time species tree reconstruction from partially resolved gene trees. <i>BMC Bioinformatics</i> , 2018, 19, 153.	2.6	1,451
4	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
5	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
6	Fast Coalescent-Based Computation of Local Branch Support from Quartet Frequencies. <i>Molecular Biology and Evolution</i> , 2016, 33, 1654-1668.	8.9	650
7	Data access for the 1,000 Plants (1KP) project. <i>GigaScience</i> , 2014, 3, 17.	6.4	582
8	Phylogenetic Placement of Exact Amplicon Sequences Improves Associations with Clinical Information. <i>MSystems</i> , 2018, 3, .	3.8	376
9	Precise phylogenetic analysis of microbial isolates and genomes from metagenomes using PhyloPhlAn 3.0. <i>Nature Communications</i> , 2020, 11, 2500.	12.8	368
10	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
11	Large-scale ruminant genome sequencing provides insights into their evolution and distinct traits. <i>Science</i> , 2019, 364, .	12.6	266
12	Dense sampling of bird diversity increases power of comparative genomics. <i>Nature</i> , 2020, 587, 252-257.	27.8	251
13	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
14	Statistical binning enables an accurate coalescent-based estimation of the avian tree. <i>Science</i> , 2014, 346, 1250-1257.	12.6	225
15	TreeShrink: fast and accurate detection of outlier long branches in collections of phylogenetic trees. <i>BMC Genomics</i> , 2018, 19, 272.	2.8	225
16	Phylogenomics of 10,575 genomes reveals evolutionary proximity between domains Bacteria and Archaea. <i>Nature Communications</i> , 2019, 10, 5477.	12.8	197
17	The Interrelationships of Placental Mammals and the Limits of Phylogenetic Inference. <i>Genome Biology and Evolution</i> , 2016, 8, 330-344.	2.5	195
18	ASTRAL-III: Increased Scalability and Impacts of Contracting Low Support Branches. <i>Lecture Notes in Computer Science</i> , 2017, , 53-75.	1.3	129

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19	A comparative study of SVDquartets and other coalescent-based species tree estimation methods. BMC Genomics, 2015, 16, S2.	2.8	128
20	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
21	ASTRAL-Pro: Quartet-Based Species-Tree Inference despite Paralogy. Molecular Biology and Evolution, 2020, 37, 3292-3307.	8.9	116
22	Ultra-large alignments using phylogeny-aware profiles. Genome Biology, 2015, 16, 124.	8.8	113
23	Interspecific Gene Flow Shaped the Evolution of the Genus Canis. Current Biology, 2018, 28, 3441-3449.e5.	3.9	110
24	Testing for Polytomies in Phylogenetic Species Trees Using Quartet Frequencies. Genes, 2018, 9, 132.	2.4	107
25	DiscoVista: Interpretable visualizations of gene tree discordance. Molecular Phylogenetics and Evolution, 2018, 122, 110-115.	2.7	106
26	Multi-allele species reconstruction using ASTRAL. Molecular Phylogenetics and Evolution, 2019, 130, 286-296.	2.7	106
27	TreeCluster: Clustering biological sequences using phylogenetic trees. PLoS ONE, 2019, 14, e0221068.	2.5	99
28	Weighted Statistical Binning: Enabling Statistically Consistent Genome-Scale Phylogenetic Analyses. PLoS ONE, 2015, 10, e0129183.	2.5	98
29	TIPP: taxonomic identification and phylogenetic profiling. Bioinformatics, 2014, 30, 3548-3555.	4.1	93
30	Fragmentary Gene Sequences Negatively Impact Gene Tree and Species Tree Reconstruction. Molecular Biology and Evolution, 2017, 34, 3279-3291.	8.9	73
31	Phylogenomic analyses data of the avian phylogenomics project. GigaScience, 2015, 4, 4.	6.4	72
32	Minimum variance rooting of phylogenetic trees and implications for species tree reconstruction. PLoS ONE, 2017, 12, e0182238.	2.5	71
33	Skmer: assembly-free and alignment-free sample identification using genome skims. Genome Biology, 2019, 20, 34.	8.8	70
34	Size-Constrained Regression Test Case Selection Using Multicriteria Optimization. IEEE Transactions on Software Engineering, 2012, 38, 936-956.	5.6	63
35	MRL and SuperFine+MRL: new supertree methods. Algorithms for Molecular Biology, 2012, 7, 3.	1.2	62
36	An empirical study of the effect of time constraints on the cost-benefits of regression testing. , 2008, , .		60

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37	Beyond DNA barcoding: The unrealized potential of genome skim data in sample identification. <i>Molecular Ecology</i> , 2020, 29, 2521-2534.	3.9	58
38	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
39	ASTRAL-MP: scaling ASTRAL to very large datasets using randomization and parallelization. <i>Bioinformatics</i> , 2019, 35, 3961-3969.	4.1	57
40	F<sc>AST</sc>SP: linear time calculation of alignment accuracy. <i>Bioinformatics</i> , 2011, 27, 3250-3258.	4.1	56
41	Identifying the favored mutation in a positive selective sweep. <i>Nature Methods</i> , 2018, 15, 279-282.	19.0	56
42	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
43	APPLES: Scalable Distance-Based Phylogenetic Placement with or without Alignments. <i>Systematic Biology</i> , 2020, 69, 566-578.	5.6	51
44	PASTA: Ultra-Large Multiple Sequence Alignment. <i>Lecture Notes in Computer Science</i> , 2014, , 177-191.	1.3	48
45	FAVITES: simultaneous simulation of transmission networks, phylogenetic trees and sequences. <i>Bioinformatics</i> , 2019, 35, 1852-1861.	4.1	45
46	A Prioritization Approach for Software Test Cases Based on Bayesian Networks. , 2007, , 276-290.		42
47	BBCA: Improving the scalability of *BEAST using random binning. <i>BMC Genomics</i> , 2014, 15, S11.	2.8	38
48	A roadmap for global synthesis of the plant tree of life. <i>American Journal of Botany</i> , 2018, 105, 614-622.	1.7	38
49	An Empirical Study on Bayesian Network-based Approach for Test Case Prioritization. , 2008, , .		37
50	Phylotastic! Making tree-of-life knowledge accessible, reusable and convenient. <i>BMC Bioinformatics</i> , 2013, 14, 158.	2.6	33
51	Phylogenetic Signal of Indels and the Neoavian Radiation. <i>Diversity</i> , 2019, 11, 108.	1.7	33
52	Adaptive Action Selection in Autonomic Software Using Reinforcement Learning. , 2008, , .		31
53	Multispecies Coalescent: Theory and Applications in Phylogenetics. <i>Annual Review of Ecology, Evolution, and Systematics</i> , 2021, 52, 247-268.	8.3	28
54	Using Bayesian Belief Networks to Predict Change Propagation in Software Systems. , 2007, , .		27

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55	Fast and accurate distance-based phylogenetic placement using divide and conquer. <i>Molecular Ecology Resources</i> , 2022, 22, 1213-1227.	4.8	25
56	Anchoring quartet-based phylogenetic distances and applications to species tree reconstruction. <i>BMC Genomics</i> , 2016, 17, 783.	2.8	24
57	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
58	SODA: multi-locus species delimitation using quartet frequencies. <i>Bioinformatics</i> , 2021, 36, 5623-5631.	4.1	21
59	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
60	Forcing external constraints on tree inference using ASTRAL. <i>BMC Genomics</i> , 2020, 21, 218.	2.8	19
61	HIPPI: highly accurate protein family classification with ensembles of HMMs. <i>BMC Genomics</i> , 2016, 17, 765.	2.8	17
62	Estimating repeat spectra and genome length from low-coverage genome skims with RESPECT. <i>PLoS Computational Biology</i> , 2021, 17, e1009449.	3.2	17
63	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
64	INSTRAL: Discordance-Aware Phylogenetic Placement Using Quartet Scores. <i>Systematic Biology</i> , 2020, 69, 384-391.	5.6	14
65	CONSULT: accurate contamination removal using locality-sensitive hashing. <i>NAR Genomics and Bioinformatics</i> , 2021, 3, lqab071.	3.2	14
66	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
67	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
68	Phylogenetic double placement of mixed samples. <i>Bioinformatics</i> , 2020, 36, i335-i343.	4.1	11
69	DEPP: Deep Learning Enables Extending Species Trees using Single Genes. <i>Systematic Biology</i> , 2023, 72, 17-34.	5.6	11
70	TADA: phylogenetic augmentation of microbiome samples enhances phenotype classification. <i>Bioinformatics</i> , 2019, 35, i31-i40.	4.1	9
71	Phylogenomics: Constrained gene tree inference. <i>Nature Ecology and Evolution</i> , 2017, 1, 56.	7.8	9
72	Completing gene trees without species trees in sub-quadratic time. <i>Bioinformatics</i> , 2022, 38, 1532-1541.	4.1	9

#	ARTICLE	IF	CITATIONS
73	A requirement-based software testing framework: An industrial practice. , 2008, , .		7
74	TreeShrink: Efficient Detection of Outlier Tree Leaves. Lecture Notes in Computer Science, 2017, , 116-140.	1.3	7
75	Log Transformation Improves Dating of Phylogenies. Molecular Biology and Evolution, 2021, 38, 1151-1167.	8.9	7
76	A Two-State Model of Tree Evolution and Its Applications to Alu Retrotransposition. Systematic Biology, 2018, 67, 475-489.	5.6	5
77	HIV Care Prioritization Using Phylogenetic Branch Length. Journal of Acquired Immune Deficiency Syndromes (1999), 2021, 86, 626-637.	2.1	5
78	QuCo: quartet-based co-estimation of species trees and gene trees. Bioinformatics, 2022, 38, i413-i421.	4.1	2
79	Multiple Sequence Alignment for Large Heterogeneous Datasets Using SATĀ©, PASTA, and UPP. Methods in Molecular Biology, 2021, 2231, 99-119.	0.9	1
80	TreeCluster: Clustering biological sequences using phylogenetic trees. , 2019, 14, e0221068.		0
81	TreeCluster: Clustering biological sequences using phylogenetic trees. , 2019, 14, e0221068.		0
82	TreeCluster: Clustering biological sequences using phylogenetic trees. , 2019, 14, e0221068.		0