

Tandy Warnow

List of Publications by Year in descending order

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Version: 2024-02-01

128
papers

12,065
citations

70961

41
h-index

35952

97
g-index

157
all docs

157
docs citations

157
times ranked

13556
citing authors

#	ARTICLE	IF	CITATIONS
1	Whole-genome analyses resolve early branches in the tree of life of modern birds. <i>Science</i> , 2014, 346, 1320-1331.	6.0	1,583
2	Towards complete and error-free genome assemblies of all vertebrate species. <i>Nature</i> , 2021, 592, 737-746.	13.7	1,139
3	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.	3.3	1,123
4	ASTRAL-II: coalescent-based species tree estimation with many hundreds of taxa and thousands of genes. <i>Bioinformatics</i> , 2015, 31, i44-i52.	1.8	822
5	Chemical phylogenetics of histone deacetylases. <i>Nature Chemical Biology</i> , 2010, 6, 238-243.	3.9	646
6	Data access for the 1,000 Plants (1KP) project. <i>GigaScience</i> , 2014, 3, 17.	3.3	582
7	Rapid and Accurate Large-Scale Coestimation of Sequence Alignments and Phylogenetic Trees. <i>Science</i> , 2009, 324, 1561-1564.	6.0	468
8	PASTA: Ultra-Large Multiple Sequence Alignment for Nucleotide and Amino-Acid Sequences. <i>Journal of Computational Biology</i> , 2015, 22, 377-386.	0.8	360
9	Evaluating Summary Methods for Multilocus Species Tree Estimation in the Presence of Incomplete Lineage Sorting. <i>Systematic Biology</i> , 2016, 65, 366-380.	2.7	242
10	Statistical binning enables an accurate coalescent-based estimation of the avian tree. <i>Science</i> , 2014, 346, 1250463.	6.0	225
11	A perspective on 16S rRNA operational taxonomic unit clustering using sequence similarity. <i>Npj Biofilms and Microbiomes</i> , 2016, 2, 16004.	2.9	208
12	The Interrelationships of Placental Mammals and the Limits of Phylogenetic Inference. <i>Genome Biology and Evolution</i> , 2016, 8, 330-344.	1.1	195
13	To Include or Not to Include: The Impact of Gene Filtering on Species Tree Estimation Methods. <i>Systematic Biology</i> , 2018, 67, 285-303.	2.7	189
14	RAxML and FastTree: Comparing Two Methods for Large-Scale Maximum Likelihood Phylogeny Estimation. <i>PLoS ONE</i> , 2011, 6, e27731.	1.1	179
15	On the Robustness to Gene Tree Estimation Error (or lack thereof) of Coalescent-Based Species Tree Methods. <i>Systematic Biology</i> , 2015, 64, 663-676.	2.7	161
16	Naive binning improves phylogenomic analyses. <i>Bioinformatics</i> , 2013, 29, 2277-2284.	1.8	156
17	ASTRID: Accurate Species TREes from Internode Distances. <i>BMC Genomics</i> , 2015, 16, S3.	1.2	143
18	Phylogenetic networks: modeling, reconstructibility, and accuracy. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2004, 1, 13-23.	1.9	135

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19	A comparative study of SVDquartets and other coalescent-based species tree estimation methods. BMC Genomics, 2015, 16, S2.	1.2	128
20	Kaikoura tree theorems: Computing the maximum agreement subtree. Information Processing Letters, 1993, 48, 77-82.	0.4	115
21	Ultra-large alignments using phylogeny-aware profiles. Genome Biology, 2015, 16, 124.	3.8	113
22	Tutorial on Computational Linguistic Phylogeny. Language and Linguistics Compass, 2008, 2, 760-820.	1.3	98
23	Weighted Statistical Binning: Enabling Statistically Consistent Genome-Scale Phylogenetic Analyses. PLoS ONE, 2015, 10, e0129183.	1.1	98
24	TIPP: taxonomic identification and phylogenetic profiling. Bioinformatics, 2014, 30, 3548-3555.	1.8	93
25	Steps toward accurate reconstructions of phylogenies from gene-order data. Journal of Computer and System Sciences, 2002, 65, 508-525.	0.9	90
26	A New Implementation and Detailed Study of Breakpoint Analysis. , 2000, , 583-94.		84
27	The development and application of bioinformatics core competencies to improve bioinformatics training and education. PLoS Computational Biology, 2018, 14, e1005772.	1.5	84
28	Long-Branch Attraction in Species Tree Estimation: Inconsistency of Partitioned Likelihood and Topology-Based Summary Methods. Systematic Biology, 2019, 68, 281-297.	2.7	77
29	Taking the First Steps towards a Standard for Reporting on Phylogenies: Minimum Information about a Phylogenetic Analysis (MIAPA). OMICS A Journal of Integrative Biology, 2006, 10, 231-237.	1.0	76
30	A comparison of phylogenetic reconstruction methods on an Indo-European dataset. Transactions of the Philological Society, 2005, 103, 171-192.	0.4	73
31	Phylogenomic analyses data of the avian phylogenomics project. GigaScience, 2015, 4, 4.	3.3	72
32	Algorithms for MDC-Based Multi-Locus Phylogeny Inference: Beyond Rooted Binary Gene Trees on Single Alleles. Journal of Computational Biology, 2011, 18, 1543-1559.	0.8	68
33	Misunderstood parameter of NCBI BLAST impacts the correctness of bioinformatics workflows. Bioinformatics, 2019, 35, 1613-1614.	1.8	65
34	MRL and SuperFine+MRL: new supertree methods. Algorithms for Molecular Biology, 2012, 7, 3.	0.3	62
35	A Fast Algorithm for the Computation and Enumeration of Perfect Phylogenies. SIAM Journal on Computing, 1997, 26, 1749-1763.	0.8	60
36	The performance of coalescent-based species tree estimation methods under models of missing data. BMC Genomics, 2018, 19, 286.	1.2	60

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37	The Impact of Multiple Protein Sequence Alignment on Phylogenetic Estimation. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2011, 8, 1108-1119.	1.9	59
38	Phylogenomic species tree estimation in the presence of incomplete lineage sorting and horizontal gene transfer. BMC Genomics, 2015, 16, S1.	1.2	57
39	FAST: linear time calculation of alignment accuracy. Bioinformatics, 2011, 27, 3250-3258.	1.8	56
40	Response to Comment on "Whole-genome analyses resolve early branches in the tree of life of modern birds". Science, 2015, 349, 1460-1460.	6.0	53
41	Primates, Lice and Bacteria: Speciation and Genome Evolution in the Symbionts of Hominid Lice. Molecular Biology and Evolution, 2017, 34, 1743-1757.	3.5	51
42	Why sequence all eukaryotes?. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, .	3.3	51
43	SuperFine: Fast and Accurate Supertree Estimation. Systematic Biology, 2012, 61, 214.	2.7	50
44	PASTA: Ultra-Large Multiple Sequence Alignment. Lecture Notes in Computer Science, 2014, , 177-191.	1.0	48
45	Phylogenomics from Whole Genome Sequences Using aTRAM. Systematic Biology, 2017, 66, syw105.	2.7	47
46	Multiple sequence alignment: a major challenge to large-scale phylogenetics. PLOS Currents, 2010, 2, RRN1198.	1.4	47
47	Fast and accurate methods for phylogenomic analyses. BMC Bioinformatics, 2011, 12, S4.	1.2	42
48	Distance-Based Genome Rearrangement Phylogeny. Journal of Molecular Evolution, 2006, 63, 473-483.	0.8	41
49	DACTAL: divide-and-conquer trees (almost) without alignments. Bioinformatics, 2012, 28, i274-i282.	1.8	41
50	MAGUS: Multiple sequence Alignment using Graph clUstering. Bioinformatics, 2021, 37, 1666-1672.	1.8	39
51	An experimental study comparing linguistic phylogenetic reconstruction methods. Diachronica, 2013, 30, 143-170.	0.2	38
52	BBCA: Improving the scalability of *BEAST using random binning. BMC Genomics, 2014, 15, S11.	1.2	38
53	A roadmap for global synthesis of the plant tree of life. American Journal of Botany, 2018, 105, 614-622.	0.8	38
54	An experimental study of Quartets MaxCut and other supertree methods. Algorithms for Molecular Biology, 2011, 6, 7.	0.3	36

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73	Minimizing phylogenetic number to find good evolutionary trees. <i>Discrete Applied Mathematics</i> , 1996, 71, 111-136.	0.5	22
74	Phylogenomics using Target-restricted Assembly Resolves Intra-generic Relationships of Parasitic Lice (<i>Phthiraptera</i> : <i>Columbicola</i>). <i>Systematic Biology</i> , 2017, 66, syx027.	2.7	22
75	Computing the Local Consensus of Trees. <i>SIAM Journal on Computing</i> , 1998, 27, 1695-1724.	0.8	20
76	DISCO: Species Tree Inference using Multicopy Gene Family Tree Decomposition. <i>Systematic Biology</i> , 2022, 71, 610-629.	2.7	20
77	Hen's Teeth and Whale's Feet: Generalized Characters and Their Compatibility. <i>Journal of Computational Biology</i> , 1995, 2, 515-525.	0.8	19
78	Better Methods for Solving Parsimony and Compatibility. <i>Journal of Computational Biology</i> , 1998, 5, 391-407.	0.8	19
79	TIPP2: metagenomic taxonomic profiling using phylogenetic markers. <i>Bioinformatics</i> , 2021, 37, 1839-1845.	1.8	18
80	Large-Scale Multiple Sequence Alignment and Tree Estimation Using SATÅ©. <i>Methods in Molecular Biology</i> , 2014, 1079, 219-244.	0.4	18
81	HIPPI: highly accurate protein family classification with ensembles of HMMs. <i>BMC Genomics</i> , 2016, 17, 765.	1.2	17
82	Statistically consistent divide-and-conquer pipelines for phylogeny estimation using NJMerge. <i>Algorithms for Molecular Biology</i> , 2019, 14, 14.	0.3	16
83	TreeMerge: a new method for improving the scalability of species tree estimation methods. <i>Bioinformatics</i> , 2019, 35, i417-i426.	1.8	15
84	High diversity of picornaviruses in rats from different continents revealed by deep sequencing. <i>Emerging Microbes and Infections</i> , 2016, 5, 1-8.	3.0	14
85	Scaling statistical multiple sequence alignment to large datasets. <i>BMC Genomics</i> , 2016, 17, 764.	1.2	13
86	FASTRAL: improving scalability of phylogenomic analysis. <i>Bioinformatics</i> , 2021, 37, 2317-2324.	1.8	13
87	Response to Comment on "Statistical binning enables an accurate coalescent-based estimation of the avian tree". <i>Science</i> , 2015, 350, 171-171.	6.0	12
88	OCTAL: Optimal Completion of gene trees in polynomial time. <i>Algorithms for Molecular Biology</i> , 2018, 13, 6.	0.3	12
89	MAGUS+eHMMs: improved multiple sequence alignment accuracy for fragmentary sequences. <i>Bioinformatics</i> , 2022, 38, 918-924.	1.8	12
90	NJMerge: A Generic Technique for Scaling Phylogeny Estimation Methods and Its Application to Species Trees. <i>Lecture Notes in Computer Science</i> , 2018, , 260-276.	1.0	11

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91	Divide-and-Conquer Tree Estimation: Opportunities and Challenges. Computational Biology, 2019, , 121-150.	0.1	11
92	Non-parametric correction of estimated gene trees using TRACTION. Algorithms for Molecular Biology, 2020, 15, 1.	0.3	11
93	Analyzing the Order of Items in Manuscripts of The Canterbury Tales. Computers and the Humanities, 2003, 37, 97-109.	1.4	10
94	Unidentifiable divergence times in rates-across-sites models. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2004, 1, 130-134.	1.9	10
95	WITCH: Improved Multiple Sequence Alignment Through Weighted Consensus Hidden Markov Model Alignment. Journal of Computational Biology, 2022, , .	0.8	10
96	Constrained incremental tree building: new absolute fast converging phylogeny estimation methods with improved scalability and accuracy. Algorithms for Molecular Biology, 2019, 14, 2.	0.3	9
97	Re-evaluating Deep Neural Networks for Phylogeny Estimation: The Issue of Taxon Sampling. Journal of Computational Biology, 2022, , .	0.8	9
98	PASTA for proteins. Bioinformatics, 2018, 34, 3939-3941.	1.8	8
99	Viewing computer science through citation analysis: Salton and Bergmark Redux. Scientometrics, 2020, 125, 271-287.	1.6	7
100	Disjoint Tree Mergers for Large-Scale Maximum Likelihood Tree Estimation. Algorithms, 2021, 14, 148.	1.2	7
101	Scalable and Accurate Phylogenetic Placement Using pplacer-XR. Lecture Notes in Computer Science, 2021, , 94-105.	1.0	7
102	Constructing Evolutionary Trees in the Presence of Polymorphic Characters. SIAM Journal on Computing, 1999, 29, 103-131.	0.8	6
103	Treelength Optimization for Phylogeny Estimation. PLoS ONE, 2012, 7, e33104.	1.1	6
104	Unblended disjoint tree merging using GTM improves species tree estimation. BMC Genomics, 2020, 21, 235.	1.2	6
105	Revisiting Evaluation of Multiple Sequence Alignment Methods. Methods in Molecular Biology, 2021, 2231, 299-317.	0.4	6
106	Polynomial-Time Statistical Estimation of Species Trees Under Gene Duplication and Loss. Lecture Notes in Computer Science, 2020, , 120-135.	1.0	6
107	Quintet Rooting: rooting species trees under the multi-species coalescent model. Bioinformatics, 2022, 38, i109-i117.	1.8	6
108	Using INC Within Divide-and-Conquer Phylogeny Estimation. Lecture Notes in Computer Science, 2019, , 167-178.	1.0	5

#	ARTICLE	IF	CITATIONS
109	Co-citations in context: Disciplinary heterogeneity is relevant. <i>Quantitative Science Studies</i> , 2020, 1, 264-276.	1.6	5
110	Finding scientific communities in citation graphs: Articles and authors. <i>Quantitative Science Studies</i> , 2021, 2, 184-203.	1.6	5
111	SIESTA: enhancing searches for optimal supertrees and species trees. <i>BMC Genomics</i> , 2018, 19, 252.	1.2	4
112	The Maximum Weight Trace Alignment Merging Problem. <i>Lecture Notes in Computer Science</i> , 2021, , 159-171.	1.0	4
113	Centerâ€™periphery structure in research communities. <i>Quantitative Science Studies</i> , 2022, 3, 289-314.	1.6	4
114	Profile Hidden Markov Models Are Not Identifiable. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2021, 18, 162-172.	1.9	3
115	Reconstructing Chromosomal Evolution. <i>SIAM Journal on Computing</i> , 2006, 36, 99-131.	0.8	2
116	Using Constrained-INC for Large-scale Gene Tree and Species Tree Estimation. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2020, 18, 1-1.	1.9	2
117	Accurate large-scale phylogeny-aware alignment using BALi-Phy. <i>Bioinformatics</i> , 2021, 37, 4677-4683.	1.8	2
118	Frequently cocited publications: Features and kinetics. <i>Quantitative Science Studies</i> , 2020, 1, 1223-1241.	1.6	2
119	Large-Scale Multiple Sequence Alignment and the Maximum Weight Trace Alignment Merging Problem. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2022, , 1-13.	1.9	2
120	An analytical upper bound on the number of loci required for all splits of a species tree to appear in a set of gene trees. <i>BMC Bioinformatics</i> , 2016, 17, 417.	1.2	1
121	Multiple Sequence Alignment for Large Heterogeneous Datasets Using SATÃ©, PASTA, and UPP. <i>Methods in Molecular Biology</i> , 2021, 2231, 99-119.	0.4	1
122	pplacerDC. , 2021, , .		1
123	Are Profile Hidden Markov Models Identifiable?. , 2018, , .		1
124	Scalable Species Tree Inference with External Constraints. <i>Journal of Computational Biology</i> , 2022, 29, 664-678.	0.8	1
125	In Memoriam Eugene L. Lawler. <i>Journal of Computational Biology</i> , 1994, 1, 255-256.	0.8	0
126	New Divide-and-Conquer Techniques for Large-Scale Phylogenetic Estimation. <i>Lecture Notes in Computer Science</i> , 2019, , 3-21.	1.0	0

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127	Using Robinson-Foulds supertrees in divide-and-conquer phylogeny estimation. <i>Algorithms for Molecular Biology</i> , 2021, 16, 12.	0.3	0
128	PHYLOGENOMICS AND POPULATION GENOMICS: MODELS, ALGORITHMS, AND ANALYTICAL TOOLS. , 2012, , .		0