

# 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	DISCO: Species Tree Inference using Multicopy Gene Family Tree Decomposition. <i>Systematic Biology</i> , 2022, 71, 610-629.	2.7	20
2	MAGUS+eHMMs: improved multiple sequence alignment accuracy for fragmentary sequences. <i>Bioinformatics</i> , 2022, 38, 918-924.	1.8	12
3	Re-evaluating Deep Neural Networks for Phylogeny Estimation: The Issue of Taxon Sampling. <i>Journal of Computational Biology</i> , 2022, , .	0.8	9
4	Why sequence all eukaryotes?. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, .	3.3	51
5	Scalable Species Tree Inference with External Constraints. <i>Journal of Computational Biology</i> , 2022, 29, 664-678.	0.8	1
6	Centerâ€™periphery structure in research communities. <i>Quantitative Science Studies</i> , 2022, 3, 289-314.	1.6	4
7	Quintet Rooting: rooting species trees under the multi-species coalescent model. <i>Bioinformatics</i> , 2022, 38, i109-i117.	1.8	6
8	WITCH: Improved Multiple Sequence Alignment Through Weighted Consensus Hidden Markov Model Alignment. <i>Journal of Computational Biology</i> , 2022, , .	0.8	10
9	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
10	MAGUS: Multiple sequence Alignment using Graph clUstering. <i>Bioinformatics</i> , 2021, 37, 1666-1672.	1.8	39
11	Phylogeny Estimation Given Sequence Length Heterogeneity. <i>Systematic Biology</i> , 2021, 70, 268-282.	2.7	29
12	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
13	Profile Hidden Markov Models Are Not Identifiable. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2021, 18, 162-172.	1.9	3
14	The Maximum Weight Trace Alignment Merging Problem. <i>Lecture Notes in Computer Science</i> , 2021, , 159-171.	1.0	4
15	Finding scientific communities in citation graphs: Articles and authors. <i>Quantitative Science Studies</i> , 2021, 2, 184-203.	1.6	5
16	TIPP2: metagenomic taxonomic profiling using phylogenetic markers. <i>Bioinformatics</i> , 2021, 37, 1839-1845.	1.8	18
17	FASTRAL: improving scalability of phylogenomic analysis. <i>Bioinformatics</i> , 2021, 37, 2317-2324.	1.8	13
18	Towards complete and error-free genome assemblies of all vertebrate species. <i>Nature</i> , 2021, 592, 737-746.	13.7	1,139

#	ARTICLE	IF	CITATIONS
19	Disjoint Tree Mergers for Large-Scale Maximum Likelihood Tree Estimation. <i>Algorithms</i> , 2021, 14, 148.	1.2	7
20	Using Robinson-Foulds supertrees in divide-and-conquer phylogeny estimation. <i>Algorithms for Molecular Biology</i> , 2021, 16, 12.	0.3	0
21	Accurate large-scale phylogeny-aware alignment using BAli-Phy. <i>Bioinformatics</i> , 2021, 37, 4677-4683.	1.8	2
22	pplacerDC. , 2021, , .		1
23	Multispecies Coalescent: Theory and Applications in Phylogenetics. <i>Annual Review of Ecology, Evolution, and Systematics</i> , 2021, 52, 247-268.	3.8	28
24	Scalable and Accurate Phylogenetic Placement Using pplacer-XR. <i>Lecture Notes in Computer Science</i> , 2021, , 94-105.	1.0	7
25	Revisiting Evaluation of Multiple Sequence Alignment Methods. <i>Methods in Molecular Biology</i> , 2021, 2231, 299-317.	0.4	6
26	Polynomial-Time Statistical Estimation of Species Trees Under Gene Duplication and Loss. <i>Journal of Computational Biology</i> , 2021, 28, 452-468.	0.8	23
27	Non-parametric correction of estimated gene trees using TRACTION. <i>Algorithms for Molecular Biology</i> , 2020, 15, 1.	0.3	11
28	FastMulRFS: fast and accurate species tree estimation under generic gene duplication and loss models. <i>Bioinformatics</i> , 2020, 36, i57-i65.	1.8	28
29	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
30	Viewing computer science through citation analysis: Salton and Bergmark Redux. <i>Scientometrics</i> , 2020, 125, 271-287.	1.6	7
31	Co-citations in context: Disciplinary heterogeneity is relevant. <i>Quantitative Science Studies</i> , 2020, 1, 264-276.	1.6	5
32	Unblended disjoint tree merging using GTM improves species tree estimation. <i>BMC Genomics</i> , 2020, 21, 235.	1.2	6
33	Polynomial-Time Statistical Estimation of Species Trees Under Gene Duplication and Loss. <i>Lecture Notes in Computer Science</i> , 2020, , 120-135.	1.0	6
34	Frequently cocited publications: Features and kinetics. <i>Quantitative Science Studies</i> , 2020, 1, 1223-1241.	1.6	2
35	TreeMerge: a new method for improving the scalability of species tree estimation methods. <i>Bioinformatics</i> , 2019, 35, i417-i426.	1.8	15
36	Statistically consistent divide-and-conquer pipelines for phylogeny estimation using NJMerge. <i>Algorithms for Molecular Biology</i> , 2019, 14, 14.	0.3	16

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37	New Divide-and-Conquer Techniques for Large-Scale Phylogenetic Estimation. Lecture Notes in Computer Science, 2019, , 3-21.	1.0	0
38	Using INC Within Divide-and-Conquer Phylogeny Estimation. Lecture Notes in Computer Science, 2019, , 167-178.	1.0	5
39	Divide-and-Conquer Tree Estimation: Opportunities and Challenges. Computational Biology, 2019, , 121-150.	0.1	11
40	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
41	Evaluating Statistical Multiple Sequence Alignment in Comparison to Other Alignment Methods on Protein Data Sets. Systematic Biology, 2019, 68, 396-411.	2.7	23
42	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
43	Misunderstood parameter of NCBI BLAST impacts the correctness of bioinformatics workflows. Bioinformatics, 2019, 35, 1613-1614.	1.8	65
44	A roadmap for global synthesis of the plant tree of life. American Journal of Botany, 2018, 105, 614-622.	0.8	38
45	OCTAL: Optimal Completion of gene trees in polynomial time. Algorithms for Molecular Biology, 2018, 13, 6.	0.3	12
46	SVDquest: Improving SVDquartets species tree estimation using exact optimization within a constrained search space. Molecular Phylogenetics and Evolution, 2018, 124, 122-136.	1.2	32
47	To Include or Not to Include: The Impact of Gene Filtering on Species Tree Estimation Methods. Systematic Biology, 2018, 67, 285-303.	2.7	189
48	NJMerge: A Generic Technique for Scaling Phylogeny Estimation Methods and Its Application to Species Trees. Lecture Notes in Computer Science, 2018, , 260-276.	1.0	11
49	Simultaneous radiation of bird and mammal lice following the K-Pg boundary. Biology Letters, 2018, 14, 20180141.	1.0	33
50	The performance of coalescent-based species tree estimation methods under models of missing data. BMC Genomics, 2018, 19, 286.	1.2	60
51	SIESTA: enhancing searches for optimal supertrees and species trees. BMC Genomics, 2018, 19, 252.	1.2	4
52	Gene tree parsimony for incomplete gene trees: addressing true biological loss. Algorithms for Molecular Biology, 2018, 13, 1.	0.3	30
53	PASTA for proteins. Bioinformatics, 2018, 34, 3939-3941.	1.8	8
54	Are Profile Hidden Markov Models Identifiable?. , 2018, , .		1

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55	The development and application of bioinformatics core competencies to improve bioinformatics training and education. PLoS Computational Biology, 2018, 14, e1005772.	1.5	84
56	FastRFS: fast and accurate Robinson-Foulds Supertrees using constrained exact optimization. Bioinformatics, 2017, 33, 631-639.	1.8	29
57	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
58	Phylogenomics from Whole Genome Sequences Using aTRAM. Systematic Biology, 2017, 66, syw105.	2.7	47
59	Phylogenomics using Target-restricted Assembly Resolves Intra-generic Relationships of Parasitic Lice (Phthiraptera: <i>Columbicola</i> ). Systematic Biology, 2017, 66, syx027.	2.7	22
60	Evaluating Summary Methods for Multilocus Species Tree Estimation in the Presence of Incomplete Lineage Sorting. Systematic Biology, 2016, 65, 366-380.	2.7	242
61	Applying, Evaluating and Refining Bioinformatics Core Competencies (An Update from the Curriculum) Tj ETQq1 1 0.784314 rrgBT /Over	1.5	24
62	HIPPI: highly accurate protein family classification with ensembles of HMMs. BMC Genomics, 2016, 17, 765.	1.2	17
63	High diversity of picornaviruses in rats from different continents revealed by deep sequencing. Emerging Microbes and Infections, 2016, 5, 1-8.	3.0	14
64	A perspective on 16S rRNA operational taxonomic unit clustering using sequence similarity. Npj Biofilms and Microbiomes, 2016, 2, 16004.	2.9	208
65	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. BMC Bioinformatics, 2016, 17, 417.	1.2	1
66	Scaling statistical multiple sequence alignment to large datasets. BMC Genomics, 2016, 17, 764.	1.2	13
67	The Interrelationships of Placental Mammals and the Limits of Phylogenetic Inference. Genome Biology and Evolution, 2016, 8, 330-344.	1.1	195
68	Phylogenomic species tree estimation in the presence of incomplete lineage sorting and horizontal gene transfer. BMC Genomics, 2015, 16, S1.	1.2	57
69	A comparative study of SVDquartets and other coalescent-based species tree estimation methods. BMC Genomics, 2015, 16, S2.	1.2	128
70	ASTRID: Accurate Species TRees from Internode Distances. BMC Genomics, 2015, 16, S3.	1.2	143
71	Ultra-large alignments using phylogeny-aware profiles. Genome Biology, 2015, 16, 124.	3.8	113
72	ASTRAL-II: coalescent-based species tree estimation with many hundreds of taxa and thousands of genes. Bioinformatics, 2015, 31, i44-i52.	1.8	822

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73	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
74	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
75	Phylogenomic analyses data of the avian phylogenomics project. <i>GigaScience</i> , 2015, 4, 4.	3.3	72
76	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.	6.0	53
77	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
78	Concatenation Analyses in the Presence of Incomplete Lineage Sorting. <i>PLOS Currents</i> , 2015, 7, .	1.4	31
79	Weighted Statistical Binning: Enabling Statistically Consistent Genome-Scale Phylogenetic Analyses. <i>PLoS ONE</i> , 2015, 10, e0129183.	1.1	98
80	TIPP: taxonomic identification and phylogenetic profiling. <i>Bioinformatics</i> , 2014, 30, 3548-3555.	1.8	93
81	Statistical binning enables an accurate coalescent-based estimation of the avian tree. <i>Science</i> , 2014, 346, 1250463.	6.0	225
82	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
83	PASTA: Ultra-Large Multiple Sequence Alignment. <i>Lecture Notes in Computer Science</i> , 2014, , 177-191.	1.0	48
84	Data access for the 1,000 Plants (1KP) project. <i>GigaScience</i> , 2014, 3, 17.	3.3	582
85	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
86	BBCA: Improving the scalability of *BEAST using random binning. <i>BMC Genomics</i> , 2014, 15, S11.	1.2	38
87	Disk covering methods improve phylogenomic analyses. <i>BMC Genomics</i> , 2014, 15, S7.	1.2	24
88	Large-Scale Multiple Sequence Alignment and Tree Estimation Using SAT-Å. <i>Methods in Molecular Biology</i> , 2014, 1079, 219-244.	0.4	18
89	Naive binning improves phylogenomic analyses. <i>Bioinformatics</i> , 2013, 29, 2277-2284.	1.8	156
90	An experimental study comparing linguistic phylogenetic reconstruction methods. <i>Diachronica</i> , 2013, 30, 143-170.	0.2	38

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91	DACTAL: divide-and-conquer trees (almost) without alignments. <i>Bioinformatics</i> , 2012, 28, i274-i282.	1.8	41
92	Estimating Optimal Species Trees from Incomplete Gene Trees Under Deep Coalescence. <i>Journal of Computational Biology</i> , 2012, 19, 591-605.	0.8	36
93	SuperFine: Fast and Accurate Supertree Estimation. <i>Systematic Biology</i> , 2012, 61, 214.	2.7	50
94	Treelength Optimization for Phylogeny Estimation. <i>PLoS ONE</i> , 2012, 7, e33104.	1.1	6
95	MRL and SuperFine+MRL: new supertree methods. <i>Algorithms for Molecular Biology</i> , 2012, 7, 3.	0.3	62
96	PHYLOGENOMICS AND POPULATION GENOMICS: MODELS, ALGORITHMS, AND ANALYTICAL TOOLS. , 2012, , .		0
97	Algorithms for MDC-Based Multi-Locus Phylogeny Inference: Beyond Rooted Binary Gene Trees on Single Alleles. <i>Journal of Computational Biology</i> , 2011, 18, 1543-1559.	0.8	68
98	The Impact of Multiple Protein Sequence Alignment on Phylogenetic Estimation. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2011, 8, 1108-1119.	1.9	59
99	RAxML and FastTree: Comparing Two Methods for Large-Scale Maximum Likelihood Phylogeny Estimation. <i>PLoS ONE</i> , 2011, 6, e27731.	1.1	179
100	An experimental study of Quartets MaxCut and other supertree methods. <i>Algorithms for Molecular Biology</i> , 2011, 6, 7.	0.3	36
101	Fast and accurate methods for phylogenomic analyses. <i>BMC Bioinformatics</i> , 2011, 12, S4.	1.2	42
102	F<sc>AST</sc>SP: linear time calculation of alignment accuracy. <i>Bioinformatics</i> , 2011, 27, 3250-3258.	1.8	56
103	A simulation study comparing supertree and combined analysis methods using SMIDGen. <i>Algorithms for Molecular Biology</i> , 2010, 5, 8.	0.3	30
104	Chemical phylogenetics of histone deacetylases. <i>Nature Chemical Biology</i> , 2010, 6, 238-243.	3.9	646
105	Multiple sequence alignment: a major challenge to large-scale phylogenetics. <i>PLOS Currents</i> , 2010, 2, RRN1198.	1.4	47
106	Rapid and Accurate Large-Scale Coestimation of Sequence Alignments and Phylogenetic Trees. <i>Science</i> , 2009, 324, 1561-1564.	6.0	468
107	Tutorial on Computational Linguistic Phylogeny. <i>Language and Linguistics Compass</i> , 2008, 2, 760-820.	1.3	98
108	Short Quartet Puzzling: A New Quartet-Based Phylogeny Reconstruction Algorithm. <i>Journal of Computational Biology</i> , 2008, 15, 91-103.	0.8	33

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109	Pattern Identification in Biogeography. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2006, 3, 334-346.	1.9	25
110	Distance-Based Genome Rearrangement Phylogeny. Journal of Molecular Evolution, 2006, 63, 473-483.	0.8	41
111	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
112	Reconstructing Chromosomal Evolution. SIAM Journal on Computing, 2006, 36, 99-131.	0.8	2
113	A comparison of phylogenetic reconstruction methods on an Indo-European dataset. Transactions of the Philological Society, 2005, 103, 171-192.	0.4	73
114	Advances in Phylogeny Reconstruction from Gene Order and Content Data. Methods in Enzymology, 2005, 395, 673-700.	0.4	24
115	Unidentifiable divergence times in rates-across-sites models. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2004, 1, 130-134.	1.9	10
116	Phylogenetic networks: modeling, reconstructibility, and accuracy. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2004, 1, 13-23.	1.9	135
117	Analyzing the Order of Items in Manuscripts of The Canterbury Tales. Computers and the Humanities, 2003, 37, 97-109.	1.4	10
118	Performance study of phylogenetic methods: (unweighted) quartet methods and neighbor-joining. Journal of Algorithms, 2003, 48, 173-193.	0.9	31
119	Steps toward accurate reconstructions of phylogenies from gene-order data. Journal of Computer and System Sciences, 2002, 65, 508-525.	0.9	90
120	A New Implementation and Detailed Study of Breakpoint Analysis. , 2000, , 583-94.		84
121	Constructing Evolutionary Trees in the Presence of Polymorphic Characters. SIAM Journal on Computing, 1999, 29, 103-131.	0.8	6
122	Computing the Local Consensus of Trees. SIAM Journal on Computing, 1998, 27, 1695-1724.	0.8	20
123	Better Methods for Solving Parsimony and Compatibility. Journal of Computational Biology, 1998, 5, 391-407.	0.8	19
124	A Fast Algorithm for the Computation and Enumeration of Perfect Phylogenies. SIAM Journal on Computing, 1997, 26, 1749-1763.	0.8	60
125	Minimizing phylogenetic number to find good evolutionary trees. Discrete Applied Mathematics, 1996, 71, 111-136.	0.5	22
126	Hen's Teeth and Whale's Feet: Generalized Characters and Their Compatibility. Journal of Computational Biology, 1995, 2, 515-525.	0.8	19



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127	In Memoriam Eugene L. Lawler. <i>Journal of Computational Biology</i> , 1994, 1, 255-256.	0.8	0
128	Kaikoura tree theorems: Computing the maximum agreement subtree. <i>Information Processing Letters</i> , 1993, 48, 77-82.	0.4	115