

Tandy Warnow

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

124
papers

7,936
citations

38
h-index

88
g-index

157
ext. papers

10,330
ext. citations

5.7
avg, IF

6.43
L-index

| # | Paper | IF | Citations |
|-----|--|------|-----------|
| 124 | Why sequence all eukaryotes?. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022 , 119, | 11.5 | 6 |
| 123 | Re-evaluating Deep Neural Networks for Phylogeny Estimation: The Issue of Taxon Sampling.. <i>Journal of Computational Biology</i> , 2022 , | 1.7 | 2 |
| 122 | MAGUS: Multiple sequence Alignment using Graph clUStering. <i>Bioinformatics</i> , 2021 , 37, 1666-1672 | 7.2 | 11 |
| 121 | MAGUS+eHMMs: Improved Multiple Sequence Alignment Accuracy for Fragmentary Sequences. <i>Bioinformatics</i> , 2021 , | 7.2 | 4 |
| 120 | Polynomial-Time Statistical Estimation of Species Trees Under Gene Duplication and Loss. <i>Journal of Computational Biology</i> , 2021 , 28, 452-468 | 1.7 | 8 |
| 119 | Using Constrained-INC for Large-Scale Gene Tree and Species Tree Estimation. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2021 , 18, 2-15 | 3 | 1 |
| 118 | Towards complete and error-free genome assemblies of all vertebrate species. <i>Nature</i> , 2021 , 592, 737-746 | 36.4 | 161 |
| 117 | Disjoint Tree Mergers for Large-Scale Maximum Likelihood Tree Estimation. <i>Algorithms</i> , 2021 , 14, 148 | 1.8 | 1 |
| 116 | Using Robinson-Foulds supertrees in divide-and-conquer phylogeny estimation. <i>Algorithms for Molecular Biology</i> , 2021 , 16, 12 | 1.8 | |
| 115 | Phylogeny Estimation Given Sequence Length Heterogeneity. <i>Systematic Biology</i> , 2021 , 70, 268-282 | 8.4 | 11 |
| 114 | Multiple Sequence Alignment for Large Heterogeneous Datasets Using SAT[PASTA], and UPP. <i>Methods in Molecular Biology</i> , 2021 , 2231, 99-119 | 1.4 | 1 |
| 113 | Profile Hidden Markov Models Are Not Identifiable. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2021 , 18, 162-172 | 3 | 1 |
| 112 | The Maximum Weight Trace Alignment Merging Problem. <i>Lecture Notes in Computer Science</i> , 2021 , 159-174 | 1.4 | 0 |
| 111 | Finding scientific communities in citation graphs: Articles and authors. <i>Quantitative Science Studies</i> , 2021 , 2, 184-203 | 3.8 | 3 |
| 110 | TIPP2: metagenomic taxonomic profiling using phylogenetic markers. <i>Bioinformatics</i> , 2021 , | 7.2 | 7 |
| 109 | Comparing Methods for Species Tree Estimation with Gene Duplication and Loss. <i>Lecture Notes in Computer Science</i> , 2021 , 106-117 | 0.9 | 0 |
| 108 | FASTRAL: Improving scalability of phylogenomic analysis. <i>Bioinformatics</i> , 2021 , | 7.2 | 1 |

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| 107 | Multispecies Coalescent: Theory and Applications in Phylogenetics. <i>Annual Review of Ecology, Evolution, and Systematics</i> , 2021 , 52, | 13.5 | 2 |
| 106 | Scalable and Accurate Phylogenetic Placement Using pplacer-XR. <i>Lecture Notes in Computer Science</i> , 2021 , 94-105 | 0.9 | 2 |
| 105 | Revisiting Evaluation of Multiple Sequence Alignment Methods. <i>Methods in Molecular Biology</i> , 2021 , 2231, 299-317 | 1.4 | 1 |
| 104 | Co-citations in context: Disciplinary heterogeneity is relevant. <i>Quantitative Science Studies</i> , 2020 , 1, 264-276 | 3.8 | 4 |
| 103 | Frequently cocited publications: Features and kinetics. <i>Quantitative Science Studies</i> , 2020 , 1, 1223-1241 | 3.8 | 1 |
| 102 | Polynomial-Time Statistical Estimation of Species Trees Under Gene Duplication and Loss. <i>Lecture Notes in Computer Science</i> , 2020 , 120-135 | 0.9 | 5 |
| 101 | Non-parametric correction of estimated gene trees using TRACTION. <i>Algorithms for Molecular Biology</i> , 2020 , 15, 1 | 1.8 | 3 |
| 100 | FastMulRFS: fast and accurate species tree estimation under generic gene duplication and loss models. <i>Bioinformatics</i> , 2020 , 36, i57-i65 | 7.2 | 14 |
| 99 | Viewing Computer Science through Citation Analysis: Salton and Bergmark Redux. <i>Scientometrics</i> , 2020 , 125, 271-287 | 3 | 3 |
| 98 | Unblended disjoint tree merging using GTM improves species tree estimation. <i>BMC Genomics</i> , 2020 , 21, 235 | 4.5 | 3 |
| 97 | New Divide-and-Conquer Techniques for Large-Scale Phylogenetic Estimation. <i>Lecture Notes in Computer Science</i> , 2019 , 3-21 | 0.9 | |
| 96 | Using INC Within Divide-and-Conquer Phylogeny Estimation. <i>Lecture Notes in Computer Science</i> , 2019 , 167-178 | 0.9 | 4 |
| 95 | Divide-and-Conquer Tree Estimation: Opportunities and Challenges. <i>Computational Biology</i> , 2019 , 121-150 | 5.7 | 5 |
| 94 | Constrained incremental tree building: new absolute fast converging phylogeny estimation methods with improved scalability and accuracy. <i>Algorithms for Molecular Biology</i> , 2019 , 14, 2 | 1.8 | 7 |
| 93 | TreeMerge: a new method for improving the scalability of species tree estimation methods. <i>Bioinformatics</i> , 2019 , 35, i417-i426 | 7.2 | 8 |
| 92 | Statistically consistent divide-and-conquer pipelines for phylogeny estimation using NJMerge. <i>Algorithms for Molecular Biology</i> , 2019 , 14, 14 | 1.8 | 9 |
| 91 | Evaluating Statistical Multiple Sequence Alignment in Comparison to Other Alignment Methods on Protein Data Sets. <i>Systematic Biology</i> , 2019 , 68, 396-411 | 8.4 | 13 |
| 90 | Long-Branch Attraction in Species Tree Estimation: Inconsistency of Partitioned Likelihood and Topology-Based Summary Methods. <i>Systematic Biology</i> , 2019 , 68, 281-297 | 8.4 | 43 |

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|----|---|-----|-----|
| 89 | Misunderstood parameter of NCBI BLAST impacts the correctness of bioinformatics workflows. <i>Bioinformatics</i> , 2019 , 35, 1613-1614 | 7.2 | 37 |
| 88 | A roadmap for global synthesis of the plant tree of life. <i>American Journal of Botany</i> , 2018 , 105, 614-622 | 2.7 | 29 |
| 87 | OCTAL: Optimal Completion of gene trees in polynomial time. <i>Algorithms for Molecular Biology</i> , 2018 , 13, 6 | 1.8 | 6 |
| 86 | SVDquest: Improving SVDquartets species tree estimation using exact optimization within a constrained search space. <i>Molecular Phylogenetics and Evolution</i> , 2018 , 124, 122-136 | 4.1 | 22 |
| 85 | To Include or Not to Include: The Impact of Gene Filtering on Species Tree Estimation Methods. <i>Systematic Biology</i> , 2018 , 67, 285-303 | 8.4 | 105 |
| 84 | The performance of coalescent-based species tree estimation methods under models of missing data. <i>BMC Genomics</i> , 2018 , 19, 286 | 4.5 | 33 |
| 83 | SIESTA: enhancing searches for optimal supertrees and species trees. <i>BMC Genomics</i> , 2018 , 19, 252 | 4.5 | 2 |
| 82 | Gene tree parsimony for incomplete gene trees: addressing true biological loss. <i>Algorithms for Molecular Biology</i> , 2018 , 13, 1 | 1.8 | 13 |
| 81 | PASTA for proteins. <i>Bioinformatics</i> , 2018 , 34, 3939-3941 | 7.2 | 4 |
| 80 | The development and application of bioinformatics core competencies to improve bioinformatics training and education. <i>PLoS Computational Biology</i> , 2018 , 14, e1005772 | 5 | 37 |
| 79 | 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 | 0.9 | 7 |
| 78 | Simultaneous radiation of bird and mammal lice following the K-Pg boundary. <i>Biology Letters</i> , 2018 , 14, | 3.6 | 19 |
| 77 | Primates, Lice and Bacteria: Speciation and Genome Evolution in the Symbionts of Hominid Lice. <i>Molecular Biology and Evolution</i> , 2017 , 34, 1743-1757 | 8.3 | 31 |
| 76 | Phylogenomics from Whole Genome Sequences Using aTRAM. <i>Systematic Biology</i> , 2017 , 66, 786-798 | 8.4 | 35 |
| 75 | Phylogenomics using Target-Restricted Assembly Resolves Intrageneric Relationships of Parasitic Lice (Phthiraptera: Columbicola). <i>Systematic Biology</i> , 2017 , 66, 896-911 | 8.4 | 17 |
| 74 | Computational Phylogenetics: An Introduction to Designing Methods for Phylogeny Estimation 2017 , | | 67 |
| 73 | FastRFS: fast and accurate Robinson-Foulds Supertrees using constrained exact optimization. <i>Bioinformatics</i> , 2017 , 33, 631-639 | 7.2 | 14 |
| 72 | Evaluating Summary Methods for Multilocus Species Tree Estimation in the Presence of Incomplete Lineage Sorting. <i>Systematic Biology</i> , 2016 , 65, 366-80 | 8.4 | 156 |

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| 71 | High diversity of picornaviruses in rats from different continents revealed by deep sequencing. <i>Emerging Microbes and Infections</i> , 2016 , 5, e90 | 18.9 | 12 |
| 70 | 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 | 3.6 | 1 |
| 69 | Scaling statistical multiple sequence alignment to large datasets. <i>BMC Genomics</i> , 2016 , 17, 764 | 4.5 | 9 |
| 68 | The Interrelationships of Placental Mammals and the Limits of Phylogenetic Inference. <i>Genome Biology and Evolution</i> , 2016 , 8, 330-44 | 3.9 | 130 |
| 67 | Applying, Evaluating and Refining Bioinformatics Core Competencies (An Update from the Curriculum Task Force of ISCB@ Education Committee). <i>PLoS Computational Biology</i> , 2016 , 12, e1004943 ⁵ | | 15 |
| 66 | HIPPI: highly accurate protein family classification with ensembles of HMMs. <i>BMC Genomics</i> , 2016 , 17, 765 | 4.5 | 9 |
| 65 | On the Robustness to Gene Tree Estimation Error (or lack thereof) of Coalescent-Based Species Tree Methods. <i>Systematic Biology</i> , 2015 , 64, 663-76 | 8.4 | 103 |
| 64 | Phylogenomic analyses data of the avian phylogenomics project. <i>GigaScience</i> , 2015 , 4, 4 | 7.6 | 54 |
| 63 | Response to Comment on "Whole-genome analyses resolve early branches in the tree of life of modern birds". <i>Science</i> , 2015 , 349, 1460 | 33.3 | 37 |
| 62 | Response to Comment on "Statistical binning enables an accurate coalescent-based estimation of the avian tree". <i>Science</i> , 2015 , 350, 171 | 33.3 | 11 |
| 61 | Phylogenomic species tree estimation in the presence of incomplete lineage sorting and horizontal gene transfer. <i>BMC Genomics</i> , 2015 , 16 Suppl 10, S1 | 4.5 | 44 |
| 60 | A comparative study of SVDquartets and other coalescent-based species tree estimation methods. <i>BMC Genomics</i> , 2015 , 16 Suppl 10, S2 | 4.5 | 95 |
| 59 | ASTRID: Accurate Species TRees from Internode Distances. <i>BMC Genomics</i> , 2015 , 16 Suppl 10, S3 | 4.5 | 112 |
| 58 | Ultra-large alignments using phylogeny-aware profiles. <i>Genome Biology</i> , 2015 , 16, 124 | 18.3 | 73 |
| 57 | ASTRAL-II: coalescent-based species tree estimation with many hundreds of taxa and thousands of genes. <i>Bioinformatics</i> , 2015 , 31, i44-52 | 7.2 | 593 |
| 56 | PASTA: Ultra-Large Multiple Sequence Alignment for Nucleotide and Amino-Acid Sequences. <i>Journal of Computational Biology</i> , 2015 , 22, 377-86 | 1.7 | 237 |
| 55 | Concatenation Analyses in the Presence of Incomplete Lineage Sorting. <i>PLOS Currents</i> , 2015 , 7, | | 22 |
| 54 | Weighted Statistical Binning: Enabling Statistically Consistent Genome-Scale Phylogenetic Analyses. <i>PLoS ONE</i> , 2015 , 10, e0129183 | 3.7 | 76 |

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| 53 | 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 | 11.5 | 835 |
| 52 | BBCA: Improving the scalability of *BEAST using random binning. <i>BMC Genomics</i> , 2014 , 15 Suppl 6, S11 | 4.5 | 30 |
| 51 | Disk covering methods improve phylogenomic analyses. <i>BMC Genomics</i> , 2014 , 15 Suppl 6, S7 | 4.5 | 21 |
| 50 | TIPP: taxonomic identification and phylogenetic profiling. <i>Bioinformatics</i> , 2014 , 30, 3548-55 | 7.2 | 59 |
| 49 | Statistical binning enables an accurate coalescent-based estimation of the avian tree. <i>Science</i> , 2014 , 346, 1250463 | 33.3 | 166 |
| 48 | Whole-genome analyses resolve early branches in the tree of life of modern birds. <i>Science</i> , 2014 , 346, 1320-31 | 33.3 | 1182 |
| 47 | PASTA: Ultra-Large Multiple Sequence Alignment. <i>Lecture Notes in Computer Science</i> , 2014 , 177-191 | 0.9 | 37 |
| 46 | Data access for the 1,000 Plants (1KP) project. <i>GigaScience</i> , 2014 , 3, 17 | 7.6 | 403 |
| 45 | Large-scale multiple sequence alignment and tree estimation using SAT. <i>Methods in Molecular Biology</i> , 2014 , 1079, 219-44 | 1.4 | 12 |
| 44 | Naive binning improves phylogenomic analyses. <i>Bioinformatics</i> , 2013 , 29, 2277-84 | 7.2 | 111 |
| 43 | An experimental study comparing linguistic phylogenetic reconstruction methods. <i>Diachronica</i> , 2013 , 30, 143-170 | 0.9 | 25 |
| 42 | MRL and SuperFine+MRL: new supertree methods. <i>Algorithms for Molecular Biology</i> , 2012 , 7, 3 | 1.8 | 52 |
| 41 | Treelength optimization for phylogeny estimation. <i>PLoS ONE</i> , 2012 , 7, e33104 | 3.7 | 5 |
| 40 | DACTAL: divide-and-conquer trees (almost) without alignments. <i>Bioinformatics</i> , 2012 , 28, i274-82 | 7.2 | 31 |
| 39 | Estimating optimal species trees from incomplete gene trees under deep coalescence. <i>Journal of Computational Biology</i> , 2012 , 19, 591-605 | 1.7 | 25 |
| 38 | SuperFine: fast and accurate supertree estimation. <i>Systematic Biology</i> , 2012 , 61, 214-27 | 8.4 | 42 |
| 37 | The impact of multiple protein sequence alignment on phylogenetic estimation. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2011 , 8, 1108-19 | 3 | 51 |
| 36 | RAXML and FastTree: comparing two methods for large-scale maximum likelihood phylogeny estimation. <i>PLoS ONE</i> , 2011 , 6, e27731 | 3.7 | 124 |

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| 35 | An experimental study of Quartets MaxCut and other supertree methods. <i>Algorithms for Molecular Biology</i> , 2011 , 6, 7 | 1.8 | 28 |
| 34 | Fast and accurate methods for phylogenomic analyses. <i>BMC Bioinformatics</i> , 2011 , 12 Suppl 9, S4 | 3.6 | 28 |
| 33 | Algorithms for MDC-based multi-locus phylogeny inference: beyond rooted binary gene trees on single alleles. <i>Journal of Computational Biology</i> , 2011 , 18, 1543-59 | 1.7 | 54 |
| 32 | FastSP: linear time calculation of alignment accuracy. <i>Bioinformatics</i> , 2011 , 27, 3250-8 | 7.2 | 36 |
| 31 | Chemical phylogenetics of histone deacetylases. <i>Nature Chemical Biology</i> , 2010 , 6, 238-243 | 11.7 | 564 |
| 30 | A simulation study comparing supertree and combined analysis methods using SMIDGen. <i>Algorithms for Molecular Biology</i> , 2010 , 5, 8 | 1.8 | 27 |
| 29 | Multiple sequence alignment: a major challenge to large-scale phylogenetics. <i>PLOS Currents</i> , 2010 , 2, RRN1198 | | 37 |
| 28 | Rapid and accurate large-scale coestimation of sequence alignments and phylogenetic trees. <i>Science</i> , 2009 , 324, 1561-4 | 33.3 | 417 |
| 27 | Tutorial on Computational Linguistic Phylogeny. <i>Language and Linguistics Compass</i> , 2008 , 2, 760-820 | 2 | 47 |
| 26 | Short quartet puzzling: a new quartet-based phylogeny reconstruction algorithm. <i>Journal of Computational Biology</i> , 2008 , 15, 91-103 | 1.7 | 25 |
| 25 | Distance-based genome rearrangement phylogeny. <i>Journal of Molecular Evolution</i> , 2006 , 63, 473-83 | 3.1 | 30 |
| 24 | Taking the first steps towards a standard for reporting on phylogenies: Minimum Information About a Phylogenetic Analysis (MIAPA). <i>OMICS A Journal of Integrative Biology</i> , 2006 , 10, 231-7 | 3.8 | 54 |
| 23 | Reconstructing Chromosomal Evolution. <i>SIAM Journal on Computing</i> , 2006 , 36, 99-131 | 1.1 | 0 |
| 22 | Pattern identification in biogeography. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2006 , 3, 334-46 | 3 | 20 |
| 21 | Advances in phylogeny reconstruction from gene order and content data. <i>Methods in Enzymology</i> , 2005 , 395, 673-700 | 1.7 | 18 |
| 20 | A comparison of phylogenetic reconstruction methods on an Indo-European dataset. <i>Transactions of the Philological Society</i> , 2005 , 103, 171-192 | 0.3 | 46 |
| 19 | Unidentifiable divergence times in rates-across-sites models. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2004 , 1, 130-4 | 3 | 8 |
| 18 | Phylogenetic networks: modeling, reconstructibility, and accuracy. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2004 , 1, 13-23 | 3 | 121 |

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|----|---|-----|----|
| 17 | Analyzing the Order of Items in Manuscripts of The Canterbury Tales. <i>Computers and the Humanities</i> , 2003 , 37, 97-109 | | 7 |
| 16 | Performance study of phylogenetic methods: (unweighted) quartet methods and neighbor-joining. <i>Journal of Algorithms</i> , 2003 , 48, 173-193 | | 24 |
| 15 | Steps toward accurate reconstructions of phylogenies from gene-order data. <i>Journal of Computer and System Sciences</i> , 2002 , 65, 508-525 | 1 | 79 |
| 14 | A new implementation and detailed study of breakpoint analysis. <i>Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing</i> , 2001 , 583-94 | 1.3 | 54 |
| 13 | Constructing Evolutionary Trees in the Presence of Polymorphic Characters. <i>SIAM Journal on Computing</i> , 1999 , 29, 103-131 | 1.1 | 3 |
| 12 | Computing the Local Consensus of Trees. <i>SIAM Journal on Computing</i> , 1998 , 27, 1695-1724 | 1.1 | 16 |
| 11 | Better methods for solving parsimony and compatibility. <i>Journal of Computational Biology</i> , 1998 , 5, 391-407 | | 17 |
| 10 | A Fast Algorithm for the Computation and Enumeration of Perfect Phylogenies. <i>SIAM Journal on Computing</i> , 1997 , 26, 1749-1763 | 1.1 | 49 |
| 9 | Minimizing phylogenetic number to find good evolutionary trees. <i>Discrete Applied Mathematics</i> , 1996 , 71, 111-136 | 1 | 18 |
| 8 | Hen's teeth and whale's feet: generalized characters and their compatibility. <i>Journal of Computational Biology</i> , 1995 , 2, 515-25 | 1.7 | 16 |
| 7 | Kaikoura tree theorems: Computing the maximum agreement subtree. <i>Information Processing Letters</i> , 1993 , 48, 77-82 | 0.8 | 85 |
| 6 | Polynomial-Time Statistical Estimation of Species Trees under Gene Duplication and Loss | | 2 |
| 5 | Advancing Divide-and-Conquer Phylogeny Estimation using Robinson-Foulds Supertrees | | 1 |
| 4 | Towards complete and error-free genome assemblies of all vertebrate species | | 38 |
| 3 | Statistically consistent divide-and-conquer pipelines for phylogeny estimation using NJMerge | | 3 |
| 2 | FastMulRFS: Fast and accurate species tree estimation under generic gene duplication and loss models | | 4 |
| 1 | Center-periphery structure in research communities. <i>Quantitative Science Studies</i> , 1-26 | 3.8 | 1 |