

Yu Lin

List of Publications by Year in descending order

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Version: 2024-02-01

62
papers

4,130
citations

471061

17
h-index

161609

54
g-index

74
all docs

74
docs citations

74
times ranked

5185
citing authors

#	ARTICLE	IF	CITATIONS
1	Assembly of long, error-prone reads using repeat graphs. <i>Nature Biotechnology</i> , 2019, 37, 540-546.	9.4	2,730
2	Assembly of long error-prone reads using de Bruijn graphs. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, E8396-E8405.	3.3	230
3	In silico spectral libraries by deep learning facilitate data-independent acquisition proteomics. <i>Nature Communications</i> , 2020, 11, 146.	5.8	135
4	MLGO: phylogeny reconstruction and ancestral inference from gene-order data. <i>BMC Bioinformatics</i> , 2014, 15, 354.	1.2	92
5	An Exact Algorithm to Compute the Double-Cut-and-Join Distance for Genomes with Duplicate Genes. <i>Journal of Computational Biology</i> , 2015, 22, 425-435.	0.8	61
6	GraphBin: refined binning of metagenomic contigs using assembly graphs. <i>Bioinformatics</i> , 2020, 36, 3307-3313.	1.8	56
7	Direct MALDI-TOF MS Identification of Bacterial Mixtures. <i>Analytical Chemistry</i> , 2018, 90, 10400-10408.	3.2	55
8	A Metric for Phylogenetic Trees Based on Matching. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2012, 9, 1014-1022.	1.9	54
9	Estimating true evolutionary distances under the DCJ model. <i>Bioinformatics</i> , 2008, 24, i114-i122.	1.8	47
10	Morphological stasis masks ecologically divergent coral species on tropical reefs. <i>Current Biology</i> , 2021, 31, 2286-2298.e8.	1.8	39
11	Detection and analysis of ancient segmental duplications in mammalian genomes. <i>Genome Research</i> , 2018, 28, 901-909.	2.4	38
12	Approximating the edit distance for genomes with duplicate genes under DCJ, insertion and deletion. <i>BMC Bioinformatics</i> , 2012, 13, .	1.2	28
13	Bacterial Whole Cell Typing by Mass Spectra Pattern Matching with Bootstrapping Assessment. <i>Analytical Chemistry</i> , 2017, 89, 12556-12561.	3.2	28
14	Deriving the Probabilities of Water Loss and Ammonia Loss for Amino Acids from Tandem Mass Spectra. <i>Journal of Proteome Research</i> , 2008, 7, 202-208.	1.8	24
15	MetaBCC-LR: <i>meta</i> genomics <i>binning</i> by <i>coverage</i> and <i>composition</i> for <i>long reads</i> . <i>Bioinformatics</i> , 2020, 36, i3-i11.	1.8	23
16	MAXIMUM LIKELIHOOD PHYLOGENETIC RECONSTRUCTION FROM HIGH-RESOLUTION WHOLE-GENOME DATA AND A TREE OF 68 EUKARYOTES. , 2012, , .		22
17	An Exact Algorithm to Compute the DCJ Distance for Genomes with Duplicate Genes. <i>Lecture Notes in Computer Science</i> , 2014, , 280-292.	1.0	20
18	Maximum likelihood phylogenetic reconstruction from high-resolution whole-genome data and a tree of 68 eukaryotes. <i>Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing</i> , 2013, , 285-96.	0.7	20

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19	Fast and Accurate Phylogenetic Reconstruction from High-Resolution Whole-Genome Data and a Novel Robustness Estimator. <i>Journal of Computational Biology</i> , 2011, 18, 1131-1139.	0.8	16
20	Reconstructing Yeasts Phylogenies and Ancestors from Whole Genome Data. <i>Scientific Reports</i> , 2017, 7, 15209.	1.6	16
21	TIBA: a tool for phylogeny inference from rearrangement data with bootstrap analysis. <i>Bioinformatics</i> , 2012, 28, 3324-3325.	1.8	15
22	What is the difference between the breakpoint graph and the de Bruijn graph?. <i>BMC Genomics</i> , 2014, 15, S6.	1.2	14
23	Sorting Signed Permutations by Inversions in $O(n \log n)$ Time. <i>Lecture Notes in Computer Science</i> , 2009, , 386-399.	1.0	14
24	Heuristics for the inversion median problem. <i>BMC Bioinformatics</i> , 2010, 11, S30.	1.2	13
25	Sorting Signed Permutations by Inversions in $O(n \log n)$ Time. <i>Journal of Computational Biology</i> , 2010, 17, 489-501.	0.8	13
26	A New Genomic Evolutionary Model for Rearrangements, Duplications, and Losses that Applies across Eukaryotes and Prokaryotes. <i>Journal of Computational Biology</i> , 2011, 18, 1055-1064.	0.8	13
27	Bootstrapping phylogenies inferred from rearrangement data. <i>Algorithms for Molecular Biology</i> , 2012, 7, 21.	0.3	13
28	Sorting genomes with rearrangements and segmental duplications through trajectory graphs. <i>BMC Bioinformatics</i> , 2013, 14, S9.	1.2	13
29	Estimating true evolutionary distances under rearrangements, duplications, and losses. <i>BMC Bioinformatics</i> , 2010, 11, S54.	1.2	12
30	Study of cell differentiation by phylogenetic analysis using histone modification data. <i>BMC Bioinformatics</i> , 2014, 15, 269.	1.2	12
31	Multiplex Bipartite Network Embedding using Dual Hypergraph Convolutional Networks. , 2021, , .		12
32	Improving metagenomic binning results with overlapped bins using assembly graphs. <i>Algorithms for Molecular Biology</i> , 2021, 16, 3.	0.3	12
33	Rearrangements in Phylogenetic Inference: Compare, Model, or Encode?. <i>Computational Biology</i> , 2013, , 147-171.	0.1	10
34	Hurdles Hardly Have to Be Heeded. <i>Lecture Notes in Computer Science</i> , 2008, , 241-251.	1.0	9
35	Large-scale 3D chromatin reconstruction from chromosomal contacts. <i>BMC Genomics</i> , 2019, 20, 186.	1.2	8
36	Query-by-Sketch: Scaling Shortest Path Graph Queries on Very Large Networks. , 2021, , .		8

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37	dK-Microaggregation: Anonymizing Graphs with Differential Privacy Guarantees. Lecture Notes in Computer Science, 2020, , 191-203.	1.0	8
38	Binning long reads in metagenomics datasets using composition and coverage information. Algorithms for Molecular Biology, 2022, 17, .	0.3	8
39	Skyblocking for entity resolution. Information Systems, 2019, 85, 30-43.	2.4	7
40	AN ITERATIVE ALGORITHM TO QUANTIFY FACTORS INFLUENCING PEPTIDE FRAGMENTATION DURING TANDEM MASS SPECTROMETRY. Journal of Bioinformatics and Computational Biology, 2007, 05, 297-311.	0.3	6
41	A maximum-likelihood approach for building cell-type trees by lifting. BMC Genomics, 2016, 17, 14.	1.2	6
42	Analysis of gene copy number changes in tumor phylogenetics. Algorithms for Molecular Biology, 2016, 11, 26.	0.3	5
43	A Median Solver and Phylogenetic Inference Based on Double-Cut-and-Join Sorting. Journal of Computational Biology, 2018, 25, 302-312.	0.8	5
44	A Fragmentation Event Model for Peptide Identification by Mass Spectrometry. Lecture Notes in Computer Science, 2008, , 154-166.	1.0	5
45	MetaCoAG: Binning Metagenomic Contigs via Composition, Coverage and Assembly Graphs. Lecture Notes in Computer Science, 2022, , 70-85.	1.0	5
46	Approximation Algorithms for Biclustering Problems. SIAM Journal on Computing, 2008, 38, 1504-1518.	0.8	4
47	Phylogeny analysis from gene-order data with massive duplications. BMC Genomics, 2017, 18, 760.	1.2	4
48	GraphPlas: Refined Classification of Plasmid Sequences Using Assembly Graphs. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2022, 19, 57-67.	1.9	4
49	An Iterative Approach for Phylogenetic Analysis of Tumor Progression Using FISH Copy Number. Lecture Notes in Computer Science, 2015, , 402-412.	1.0	4
50	Fast and Accurate Phylogenetic Reconstruction from High-Resolution Whole-Genome Data and a Novel Robustness Estimator. Lecture Notes in Computer Science, 2010, , 137-148.	1.0	4
51	Hurdles and Sorting by Inversions: Combinatorial, Statistical, and Experimental Results. Journal of Computational Biology, 2009, 16, 1339-1351.	0.8	3
52	DCHap: A divide-and-conquer haplotype phasing algorithm for third-generation sequences. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2020, PP, 1-1.	1.9	3
53	HaploJuice : accurate haplotype assembly from a pool of sequences with known relative concentrations. BMC Bioinformatics, 2018, 19, 389.	1.2	2
54	Phylogenetic Reconstruction for Copy-Number Evolution Problems. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2019, 16, 694-699.	1.9	2

#	ARTICLE	IF	CITATIONS
55	Bootstrapping Phylogenies Inferred from Rearrangement Data. Lecture Notes in Computer Science, 2011, , 175-187.	1.0	2
56	Kmer2SNP: reference-free SNP calling from raw reads based on matching. , 2020, , .		2
57	Can a breakpoint graph be decomposed into none other than 2-cycles?. Theoretical Computer Science, 2018, 734, 38-45.	0.5	1
58	Phylogenetic Analysis of Cell Types Using Histone Modifications. Lecture Notes in Computer Science, 2013, , 326-337.	1.0	1
59	Approximation Algorithms for Bi-clustering Problems. Lecture Notes in Computer Science, 2006, , 310-320.	1.0	1
60	AN ITERATIVE ALGORITHM TO QUANTIFY THE FACTORS INFLUENCING PEPTIDE FRAGMENTATION FOR MS/MS SPECTRUM. , 2006, , .		0
61	A New Genomic Evolutionary Model for Rearrangements, Duplications, and Losses That Applies across Eukaryotes and Prokaryotes. Lecture Notes in Computer Science, 2010, , 228-239.	1.0	0
62	An Algorithm to Mine Therapeutic Motifs for Cancer from Networks of Genetic Interactions. IEEE Journal of Biomedical and Health Informatics, 2022, PP, 1-1.	3.9	0