Yu Lin

List of Publications by Year
in descending order

62 papers	4,130 citations	471509 17 h-index	161849 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. Nature Biotechnology, 2019, 37, 540-546.	17.5	2,730
2	Assembly of long error-prone reads using de Bruijn graphs. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, E8396-E8405.	7.1	230
3	In silico spectral libraries by deep learning facilitate data-independent acquisition proteomics. Nature Communications, 2020, 11, 146.	12.8	135
4	MLGO: phylogeny reconstruction and ancestral inference from gene-order data. BMC Bioinformatics, 2014, 15, 354.	2.6	92
5	An Exact Algorithm to Compute the Double-Cut-and-Join Distance for Genomes with Duplicate Genes. Journal of Computational Biology, 2015, 22, 425-435.	1.6	61
6	GraphBin: refined binning of metagenomic contigs using assembly graphs. Bioinformatics, 2020, 36, 3307-3313.	4.1	56
7	Direct MALDI-TOF MS Identification of Bacterial Mixtures. Analytical Chemistry, 2018, 90, 10400-10408.	6.5	55
8	A Metric for Phylogenetic Trees Based on Matching. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2012, 9, 1014-1022.	3.0	54
9	Estimating true evolutionary distances under the DCJ model. Bioinformatics, 2008, 24, i114-i122.	4.1	47
10	Morphological stasis masks ecologically divergent coral species on tropical reefs. Current Biology, 2021, 31, 2286-2298.e8.	3.9	39
11	Detection and analysis of ancient segmental duplications in mammalian genomes. Genome Research, 2018, 28, 901-909.	5.5	38
12	Approximating the edit distance for genomes with duplicate genes under DCJ, insertion and deletion. BMC Bioinformatics, 2012, 13, .	2.6	28
13	Bacterial Whole Cell Typing by Mass Spectra Pattern Matching with Bootstrapping Assessment. Analytical Chemistry, 2017, 89, 12556-12561.	6.5	28
14	Deriving the Probabilities of Water Loss and Ammonia Loss for Amino Acids from Tandem Mass Spectra. Journal of Proteome Research, 2008, 7, 202-208.	3.7	24
15	MetaBCC-LR: *meta*genomics *b*inning by *c*overage and *c*omposition for *l*ong *r*eads. Bioinformatics, 2020, 36, i3-i11.	4.1	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. Lecture Notes in Computer Science, 2014, , 280-292.	1.3	20
18	Maximum likelihood phylogenetic reconstruction from high-resolution whole-genome data and a tree of 68 eukaryotes. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 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. Journal of Computational Biology, 2011, 18, 1131-1139.	1.6	16
20	Reconstructing Yeasts Phylogenies and Ancestors from Whole Genome Data. Scientific Reports, 2017, 7, 15209.	3.3	16
21	TIBA: a tool for phylogeny inference from rearrangement data with bootstrap analysis. Bioinformatics, 2012, 28, 3324-3325.	4.1	15
22	What is the difference between the breakpoint graph and the de Bruijn graph?. BMC Genomics, 2014, 15, S6.	2.8	14
23	Sorting Signed Permutations by Inversions in O(nlogn) Time. Lecture Notes in Computer Science, 2009, , 386-399.	1.3	14
24	Heuristics for the inversion median problem. BMC Bioinformatics, 2010, 11, S30.	2.6	13
25	Sorting Signed Permutations by Inversions in $O(n \log n)$ Time. Journal of Computational Biology, 2010, 17, 489-501.	1.6	13
26	A New Genomic Evolutionary Model for Rearrangements, Duplications, and Losses that Applies across Eukaryotes and Prokaryotes. Journal of Computational Biology, 2011, 18, 1055-1064.	1.6	13
27	Bootstrapping phylogenies inferred from rearrangement data. Algorithms for Molecular Biology, 2012, 7, 21.	1.2	13
28	Sorting genomes with rearrangements and segmental duplications through trajectory graphs. BMC Bioinformatics, 2013, 14, S9.	2.6	13
29	Estimating true evolutionary distances under rearrangements, duplications, and losses. BMC Bioinformatics, 2010, 11, S54.	2.6	12
30	Study of cell differentiation by phylogenetic analysis using histone modification data. BMC Bioinformatics, 2014, 15, 269.	2.6	12
31	Multiplex Bipartite Network Embedding using Dual Hypergraph Convolutional Networks. , 2021, , .		12
32	Improving metagenomic binning results with overlapped bins using assembly graphs. Algorithms for Molecular Biology, 2021, 16, 3.	1.2	12
33	Rearrangements in Phylogenetic Inference: Compare, Model, or Encode?. Computational Biology, 2013, , 147-171.	0.2	10
34	Hurdles Hardly Have to Be Heeded. Lecture Notes in Computer Science, 2008, , 241-251.	1.3	9
35	Large-scale 3D chromatin reconstruction from chromosomal contacts. BMC Genomics, 2019, 20, 186.	2.8	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.	1.3	8
38	Binning long reads in metagenomics datasets using composition and coverage information. Algorithms for Molecular Biology, 2022, 17, .	1.2	8
39	Skyblocking for entity resolution. Information Systems, 2019, 85, 30-43.	3.6	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.	0.8	6
41	A maximum-likelihood approach for building cell-type trees by lifting. BMC Genomics, 2016, 17, 14.	2.8	6
42	Analysis of gene copy number changes in tumor phylogenetics. Algorithms for Molecular Biology, 2016, 11, 26.	1.2	5
43	A Median Solver and Phylogenetic Inference Based on Double-Cut-and-Join Sorting. Journal of Computational Biology, 2018, 25, 302-312.	1.6	5
44	A Fragmentation Event Model for Peptide Identification by Mass Spectrometry. Lecture Notes in Computer Science, 2008, , 154-166.	1.3	5
45	MetaCoAG: Binning Metagenomic Contigs viaÂComposition, Coverage andÂAssembly Graphs. Lecture Notes in Computer Science, 2022, , 70-85.	1.3	5
46	Approximation Algorithms for Biclustering Problems. SIAM Journal on Computing, 2008, 38, 1504-1518.	1.0	4
47	Phylogeny analysis from gene-order data with massive duplications. BMC Genomics, 2017, 18, 760.	2.8	4
48	GraphPlas: Refined Classification of Plasmid Sequences Using Assembly Graphs. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2022, 19, 57-67.	3.0	4
49	An Iterative Approach for Phylogenetic Analysis of Tumor Progression Using FISH Copy Number. Lecture Notes in Computer Science, 2015, , 402-412.	1.3	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.	1.3	4
51	Hurdles and Sorting by Inversions: Combinatorial, Statistical, and Experimental Results. Journal of Computational Biology, 2009, 16, 1339-1351.	1.6	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.	3.0	3
53	HaploJuice : accurate haplotype assembly from a pool of sequences with known relative concentrations. BMC Bioinformatics, 2018, 19, 389.	2.6	2
54	Phylogenetic Reconstruction for Copy-Number Evolution Problems. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2019, 16, 694-699.	3.0	2

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55	Bootstrapping Phylogenies Inferred from Rearrangement Data. Lecture Notes in Computer Science, 2011, , 175-187.	1.3	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.	0.9	1
58	Phylogenetic Analysis of Cell Types Using Histone Modifications. Lecture Notes in Computer Science, 2013, , 326-337.	1.3	1
59	Approximation Algorithms for Bi-clustering Problems. Lecture Notes in Computer Science, 2006, , 310-320.	1.3	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.	1.3	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.	6.3	0