Yu Lin

List of Publications by Year
in descending order

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	GraphPlas: Refined Classification of Plasmid Sequences Using Assembly Graphs. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2022, 19, 57-67.	1.9	4
2	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
3	MetaCoAG: Binning Metagenomic Contigs viaÂComposition, Coverage andÂAssembly Graphs. Lecture Notes in Computer Science, 2022, , 70-85.	1.0	5
4	Binning long reads in metagenomics datasets using composition and coverage information. Algorithms for Molecular Biology, 2022, 17, .	0.3	8
5	Multiplex Bipartite Network Embedding using Dual Hypergraph Convolutional Networks. , 2021, , .		12
6	Improving metagenomic binning results with overlapped bins using assembly graphs. Algorithms for Molecular Biology, 2021, 16, 3.	0.3	12
7	Morphological stasis masks ecologically divergent coral species on tropical reefs. Current Biology, 2021, 31, 2286-2298.e8.	1.8	39
8	Query-by-Sketch: Scaling Shortest Path Graph Queries on Very Large Networks. , 2021, , .		8
9	In silico spectral libraries by deep learning facilitate data-independent acquisition proteomics. Nature Communications, 2020, 11, 146.	5.8	135
10	MetaBCC-LR: *meta*genomics *b*inning by *c*overage and *c*omposition for *l*ong *r*eads. Bioinformatics, 2020, 36, i3-i11.	1.8	23
11	GraphBin: refined binning of metagenomic contigs using assembly graphs. Bioinformatics, 2020, 36, 3307-3313.	1.8	56
12	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
13	dK-Microaggregation: Anonymizing Graphs with Differential Privacy Guarantees. Lecture Notes in Computer Science, 2020, , 191-203.	1.0	8
14	Kmer2SNP: reference-free SNP calling from raw reads based on matching. , 2020, , .		2
15	Phylogenetic Reconstruction for Copy-Number Evolution Problems. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2019, 16, 694-699.	1.9	2
16	Skyblocking for entity resolution. Information Systems, 2019, 85, 30-43.	2.4	7
17	Large-scale 3D chromatin reconstruction from chromosomal contacts. BMC Genomics, 2019, 20, 186.	1.2	8
18	Assembly of long, error-prone reads using repeat graphs. Nature Biotechnology, 2019, 37, 540-546.	9.4	2,730

#	Article	IF	Citations
19	A Median Solver and Phylogenetic Inference Based on Double-Cut-and-Join Sorting. Journal of Computational Biology, 2018, 25, 302-312.	0.8	5
20	Can a breakpoint graph be decomposed into none other than 2-cycles?. Theoretical Computer Science, 2018, 734, 38-45.	0.5	1
21	HaploJuice : accurate haplotype assembly from a pool of sequences with known relative concentrations. BMC Bioinformatics, 2018, 19, 389.	1.2	2
22	Detection and analysis of ancient segmental duplications in mammalian genomes. Genome Research, 2018, 28, 901-909.	2.4	38
23	Direct MALDI-TOF MS Identification of Bacterial Mixtures. Analytical Chemistry, 2018, 90, 10400-10408.	3.2	55
24	Reconstructing Yeasts Phylogenies and Ancestors from Whole Genome Data. Scientific Reports, 2017, 7, 15209.	1.6	16
25	Bacterial Whole Cell Typing by Mass Spectra Pattern Matching with Bootstrapping Assessment. Analytical Chemistry, 2017, 89, 12556-12561.	3.2	28
26	Phylogeny analysis from gene-order data with massive duplications. BMC Genomics, 2017, 18, 760.	1.2	4
27	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.	3.3	230
28	Analysis of gene copy number changes in tumor phylogenetics. Algorithms for Molecular Biology, 2016, 11, 26.	0.3	5
29	A maximum-likelihood approach for building cell-type trees by lifting. BMC Genomics, 2016, 17, 14.	1.2	6
30	An Exact Algorithm to Compute the Double-Cut-and-Join Distance for Genomes with Duplicate Genes. Journal of Computational Biology, 2015, 22, 425-435.	0.8	61
31	An Iterative Approach for Phylogenetic Analysis of Tumor Progression Using FISH Copy Number. Lecture Notes in Computer Science, 2015, , 402-412.	1.0	4
32	MLGO: phylogeny reconstruction and ancestral inference from gene-order data. BMC Bioinformatics, 2014, 15, 354.	1.2	92
33	Study of cell differentiation by phylogenetic analysis using histone modification data. BMC Bioinformatics, 2014, 15, 269.	1.2	12
34	What is the difference between the breakpoint graph and the de Bruijn graph?. BMC Genomics, 2014, 15, S6.	1.2	14
35	An Exact Algorithm to Compute the DCJ Distance for Genomes with Duplicate Genes. Lecture Notes in Computer Science, 2014, , 280-292.	1.0	20
36	Sorting genomes with rearrangements and segmental duplications through trajectory graphs. BMC Bioinformatics, 2013, 14, S9.	1.2	13

#	Article	IF	Citations
37	Rearrangements in Phylogenetic Inference: Compare, Model, or Encode?. Computational Biology, 2013, , 147-171.	0.1	10
38	Phylogenetic Analysis of Cell Types Using Histone Modifications. Lecture Notes in Computer Science, 2013, , 326-337.	1.0	1
39	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
40	TIBA: a tool for phylogeny inference from rearrangement data with bootstrap analysis. Bioinformatics, 2012, 28, 3324-3325.	1.8	15
41	A Metric for Phylogenetic Trees Based on Matching. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2012, 9, 1014-1022.	1.9	54
42	MAXIMUM LIKELIHOOD PHYLOGENETIC RECONSTRUCTION FROM HIGH-RESOLUTION WHOLE-GENOME DATA AND A TREE OF 68 EUKARYOTES. , 2012, , .		22
43	Approximating the edit distance for genomes with duplicate genes under DCJ, insertion and deletion. BMC Bioinformatics, 2012, 13, .	1.2	28
44	Bootstrapping phylogenies inferred from rearrangement data. Algorithms for Molecular Biology, 2012, 7, 21.	0.3	13
45	Fast and Accurate Phylogenetic Reconstruction from High-Resolution Whole-Genome Data and a Novel Robustness Estimator. Journal of Computational Biology, 2011, 18, 1131-1139.	0.8	16
46	A New Genomic Evolutionary Model for Rearrangements, Duplications, and Losses that Applies across Eukaryotes and Prokaryotes. Journal of Computational Biology, 2011, 18, 1055-1064.	0.8	13
47	Bootstrapping Phylogenies Inferred from Rearrangement Data. Lecture Notes in Computer Science, 2011, , 175-187.	1.0	2
48	Heuristics for the inversion median problem. BMC Bioinformatics, 2010, 11, S30.	1.2	13
49	Estimating true evolutionary distances under rearrangements, duplications, and losses. BMC Bioinformatics, 2010, 11, S54.	1.2	12
50	Sorting Signed Permutations by Inversions in $O(n \log n)$ Time. Journal of Computational Biology, 2010, 17, 489-501.	0.8	13
51	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
52	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
53	Hurdles and Sorting by Inversions: Combinatorial, Statistical, and Experimental Results. Journal of Computational Biology, 2009, 16, 1339-1351.	0.8	3
54	Sorting Signed Permutations by Inversions in O(nlogn) Time. Lecture Notes in Computer Science, 2009, , 386-399.	1.0	14

#	Article	IF	Citations
55	Approximation Algorithms for Biclustering Problems. SIAM Journal on Computing, 2008, 38, 1504-1518.	0.8	4
56	Deriving the Probabilities of Water Loss and Ammonia Loss for Amino Acids from Tandem Mass Spectra. Journal of Proteome Research, 2008, 7, 202-208.	1.8	24
57	Estimating true evolutionary distances under the DCJ model. Bioinformatics, 2008, 24, i114-i122.	1.8	47
58	A Fragmentation Event Model for Peptide Identification by Mass Spectrometry. Lecture Notes in Computer Science, 2008, , 154-166.	1.0	5
59	Hurdles Hardly Have to Be Heeded. Lecture Notes in Computer Science, 2008, , 241-251.	1.0	9
60	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
61	Approximation Algorithms for Bi-clustering Problems. Lecture Notes in Computer Science, 2006, , 310-320.	1.0	1
62	AN ITERATIVE ALGORITHM TO QUANTIFY THE FACTORS INFLUENCING PEPTIDE FRAGMENTATION FOR MS/MS SPECTRUM. , 2006, , .		0