

Tao Jiang

List of Publications by Year in descending order

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Version: 2024-02-01

107
papers

5,465
citations

101535

36
h-index

91872

69
g-index

109
all docs

109
docs citations

109
times ranked

5752
citing authors

#	ARTICLE	IF	CITATIONS
1	Transcriptome Profiling of <i>Candidatus</i> <i>Liberibacter asiaticus</i> ™ in Citrus and Psyllids. <i>Phytopathology</i> , 2022, 112, 116-130.	2.2	10
2	A global analysis of alternative splicing of <i>Dichocarpum</i> medicinal plants, Ranunculales. <i>Current Genomics</i> , 2022, 23, .	1.6	0
3	DeepLPI: a multimodal deep learning method for predicting the interactions between lncRNAs and protein isoforms. <i>BMC Bioinformatics</i> , 2021, 22, 24.	2.6	13
4	Characterizing RNA Pseudouridylation by Convolutional Neural Networks. <i>Genomics, Proteomics and Bioinformatics</i> , 2021, 19, 815-833.	6.9	5
5	Modeling multi-species RNA modification through multi-task curriculum learning. <i>Nucleic Acids Research</i> , 2021, 49, 3719-3734.	14.5	23
6	Enhancement and Imputation of Peak Signal Enables Accurate Cell-Type Classification in scATAC-seq. <i>Frontiers in Genetics</i> , 2021, 12, 658352.	2.3	2
7	FINER: enhancing the prediction of tissue-specific functions of isoforms by refining isoform interaction networks. <i>NAR Genomics and Bioinformatics</i> , 2021, 3, lqab057.	3.2	3
8	SKSV: ultrafast structural variation detection from circular consensus sequencing reads. <i>Bioinformatics</i> , 2021, 37, 3647-3649.	4.1	10
9	PanSVR: Pan-Genome Augmented Short Read Realignment for Sensitive Detection of Structural Variations. <i>Frontiers in Genetics</i> , 2021, 12, 731515.	2.3	2
10	Psi-Caller: A Lightweight Short Read-Based Variant Caller With High Speed and Accuracy. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 731424.	3.7	5
11	Riboexp: an interpretable reinforcement learning framework for ribosome density modeling. <i>Briefings in Bioinformatics</i> , 2021, 22, .	6.5	2
12	Long-read sequencing settings for efficient structural variation detection based on comprehensive evaluation. <i>BMC Bioinformatics</i> , 2021, 22, 552.	2.6	14
13	Dysregulation of Hypothalamic Gene Expression and the Oxytocinergic System by Soybean Oil Diets in Male Mice. <i>Endocrinology</i> , 2020, 161, .	2.8	11
14	OMGS: Optical Map-Based Genome Scaffolding. <i>Journal of Computational Biology</i> , 2020, 27, 519-533.	1.6	14
15	Long-read-based human genomic structural variation detection with cuteSV. <i>Genome Biology</i> , 2020, 21, 189.	8.8	164
16	Somatic SF3B1 hotspot mutation in prolactinomas. <i>Nature Communications</i> , 2020, 11, 2506.	12.8	38
17	Assessment of Machine Learning Methods for Classification in Single Cell ATAC-seq. , 2020, , .		1
18	MONN: A Multi-objective Neural Network for Predicting Pairwise Non-covalent Interactions and Binding Affinities Between Compounds and Proteins. <i>Lecture Notes in Computer Science</i> , 2020, , 259-260.	1.3	2

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19	NeoDTI: neural integration of neighbor information from a heterogeneous network for discovering new drug-target interactions. Bioinformatics, 2019, 35, 104-111.	4.1	218
20	DIFFUSE: predicting isoform functions from sequences and expression profiles via deep learning. Bioinformatics, 2019, 35, i284-i294.	4.1	28
21	SCALE method for single-cell ATAC-seq analysis via latent feature extraction. Nature Communications, 2019, 10, 4576.	12.8	162
22	DeepPASTA: deep neural network based polyadenylation site analysis. Bioinformatics, 2019, 35, 4577-4585.	4.1	35
23	Long-Read Based Novel Sequence Insertion Detection With rCANID. IEEE Transactions on Nanobioscience, 2019, 18, 343-352.	3.3	6
24	rMETL: sensitive mobile element insertion detection with long read realignment. Bioinformatics, 2019, 35, 3484-3486.	4.1	10
25	DeepIsoFun: a deep domain adaptation approach to predict isoform functions. Bioinformatics, 2019, 35, 2535-2544.	4.1	20
26	DeepHINT: understanding HIV-1 integration via deep learning with attention. Bioinformatics, 2019, 35, 1660-1667.	4.1	41
27	TAPAS: tool for alternative polyadenylation site analysis. Bioinformatics, 2018, 34, 2521-2529.	4.1	62
28	FreePSI: an alignment-free approach to estimating exon-inclusion ratios without a reference transcriptome. Nucleic Acids Research, 2018, 46, e11-e11.	14.5	3
29	Improved Approximation Algorithms for the Maximum Happy Vertices and Edges Problems. Algorithmica, 2018, 80, 1412-1438.	1.3	19
30	rCANID: read Clustering and Assembly-based Novel Insertion Detection tool. , 2018, , .		0
31	Integrative Analysis of Zika Virus Genome RNA Structure Reveals Critical Determinants of Viral Infectivity. Cell Host and Microbe, 2018, 24, 875-886.e5.	11.0	89
32	Constructing tissue-specific transcriptional regulatory networks via a Markov random field. BMC Genomics, 2018, 19, 884.	2.8	6
33	rMFilter: acceleration of long read-based structure variation calling by chimeric read filtering. Bioinformatics, 2017, 33, 2750-2752.	4.1	0
34	A deep boosting based approach for capturing the sequence binding preferences of RNA-binding proteins from high-throughput CLIP-seq data. Nucleic Acids Research, 2017, 45, e129-e129.	14.5	19
35	Analysis of Ribosome Stalling and Translation Elongation Dynamics by Deep Learning. Cell Systems, 2017, 5, 212-220.e6.	6.2	58
36	TITER: predicting translation initiation sites by deep learning. Bioinformatics, 2017, 33, i234-i242.	4.1	83

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37	H-PoP and H-PoPG: heuristic partitioning algorithms for single individual haplotyping of polyploids. <i>Bioinformatics</i> , 2016, 32, 3735-3744.	4.1	54
38	SDEAP: a splice graph based differential transcript expression analysis tool for population data. <i>Bioinformatics</i> , 2016, 32, 3593-3602.	4.1	3
39	TransComb: genome-guided transcriptome assembly via combing junctions in splicing graphs. <i>Genome Biology</i> , 2016, 17, 213.	8.8	75
40	Sequencing of 15,622 gene-bearing BACs clarifies the gene-dense regions of the barley genome. <i>Plant Journal</i> , 2015, 84, 216-227.	5.7	36
41	Differential regulation enrichment analysis via the integration of transcriptional regulatory network and gene expression data. <i>Bioinformatics</i> , 2015, 31, 563-571.	4.1	19
42	Improved Approximation Algorithms for the Maximum Happy Vertices and Edges Problems. <i>Lecture Notes in Computer Science</i> , 2015, , 159-170.	1.3	13
43	AlignGraph: algorithm for secondary <i>de novo</i> genome assembly guided by closely related references. <i>Bioinformatics</i> , 2014, 30, i319-i328.	4.1	61
44	Novel core promoter elements in the oomycete pathogen <i>Phytophthora infestans</i> and their influence on expression detected by genome-wide analysis. <i>BMC Genomics</i> , 2013, 14, 106.	2.8	31
45	Differential gene expression analysis using coexpression and RNA-Seq data. <i>Bioinformatics</i> , 2013, 29, 2153-2161.	4.1	32
46	Identifying potential cancer driver genes by genomic data integration. <i>Scientific Reports</i> , 2013, 3, 3538.	3.3	60
47	Workshop: Transcriptome assembly and isoform expression level estimation from biased RNA-Seq reads. , 2012, , .		0
48	Transcriptome assembly and isoform expression level estimation from biased RNA-Seq reads. <i>Bioinformatics</i> , 2012, 28, 2914-2921.	4.1	87
49	Identification of a binding motif specific to HNF4 by comparative analysis of multiple nuclear receptors. <i>Nucleic Acids Research</i> , 2012, 40, 5343-5356.	14.5	93
50	An Efficient Algorithm for Haplotype Inference on Pedigrees with Recombinations and Mutations. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2012, 9, 12-25.	3.0	9
51	A linear-time algorithm for reconstructing zero-recombinant haplotype configuration on a pedigree. <i>BMC Bioinformatics</i> , 2012, 13, S19.	2.6	7
52	An Efficient Algorithm for Haplotype Inference on Pedigrees with a Small Number of Recombinants. <i>Algorithmica</i> , 2012, 62, 951-981.	1.3	2
53	IsoLasso: A LASSO Regression Approach to RNA-Seq Based Transcriptome Assembly. <i>Journal of Computational Biology</i> , 2011, 18, 1693-1707.	1.6	139
54	A cochlear neuron based robust feature for speaker recognition. , 2011, , .		0

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55	Inference of Isoforms from Short Sequence Reads. Journal of Computational Biology, 2011, 18, 305-321.	1.6	54
56	INFERRING HAPLOTYPES FROM GENOTYPES ON A PEDIGREE WITH MUTATIONS, GENOTYPING ERRORS AND MISSING ALLELES. Journal of Bioinformatics and Computational Biology, 2011, 09, 339-365.	0.8	5
57	Some Algorithmic Challenges in Genome-Wide Ortholog Assignment. Journal of Computer Science and Technology, 2010, 25, 42-52.	1.5	9
58	A linear-time algorithm for reconstructing zero-recombinant haplotype configuration on pedigrees without mating loops. Journal of Combinatorial Optimization, 2010, 19, 217-240.	1.3	7
59	Beyond evolutionary trees. Natural Computing, 2010, 9, 421-435.	3.0	2
60	MSOAR 2.0: Incorporating tandem duplications into ortholog assignment based on genome rearrangement. BMC Bioinformatics, 2010, 11, 10.	2.6	72
61	Integrated approach for the identification of human hepatocyte nuclear factor 4 β target genes using protein binding microarrays. Hepatology, 2010, 51, 642-653.	7.3	151
62	Speaker identification and verification from audio coded speech in matched and mismatched conditions. , 2009, , .		6
63	Efficient Algorithms for Reconstructing Zero-Recombinant Haplotypes on a Pedigree Based on Fast Elimination of Redundant Linear Equations. SIAM Journal on Computing, 2009, 38, 2198-2219.	1.0	9
64	A MAX-FLOW BASED APPROACH TO THE IDENTIFICATION OF PROTEIN COMPLEXES USING PROTEIN INTERACTION AND MICROARRAY DATA. , 2008, , .		11
65	Prevalence of the initiator over the TATA box in human and yeast genes and identification of DNA motifs enriched in human TATA-less core promoters. Gene, 2007, 389, 52-65.	2.2	329
66	Complexity and approximation of the minimum recombinant haplotype configuration problem. Theoretical Computer Science, 2007, 378, 316-330.	0.9	16
67	Average-case analysis of QuickSort and Binary Insertion Tree height using incompressibility. Information Processing Letters, 2007, 103, 45-51.	0.6	3
68	EFFICIENT ALGORITHMS FOR GENOME-WIDE TAGSNP SELECTION ACROSS POPULATIONS VIA THE LINKAGE DISEQUILIBRIUM CRITERION. , 2007, , .		5
69	Linear-Time Reconstruction of Zero-Recombinant Mendelian Inheritance on Pedigrees without Mating Loops. , 2007, , .		1
70	COMPUTING THE BREAKPOINT DISTANCE BETWEEN PARTIALLY ORDERED GENOMES. , 2007, , .		1
71	Development of a 9600-clone procedure for oligonucleotide fingerprinting of rRNA genes: Utilization to identify soil bacterial rRNA genes that correlate in abundance with the development of avocado root rot. Journal of Microbiological Methods, 2006, 67, 171-180.	1.6	15
72	A Class of Edit Kernels for SVMs to Predict Translation Initiation Sites in Eukaryotic mRNAs. Journal of Computational Biology, 2005, 12, 702-718.	1.6	52

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73	Computing the Minimum Recombinant Haplotype Configuration from Incomplete Genotype Data on a Pedigree by Integer Linear Programming. Journal of Computational Biology, 2005, 12, 719-739.	1.6	71
74	More Reliable Protein NMR Peak Assignment via Improved 2-Interval Scheduling. Journal of Computational Biology, 2005, 12, 129-146.	1.6	4
75	Assignment of Orthologous Genes via Genome Rearrangement. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2005, 2, 302-315.	3.0	120
76	Evolutionary Dynamics of the DNA-Binding Domains in Putative R2R3-MYB Genes Identified from Rice Subspecies indica and japonica Genomes. Plant Physiology, 2004, 134, 575-585.	4.8	157
77	A Further Improved Approximation Algorithm for Breakpoint Graph Decomposition. Journal of Combinatorial Optimization, 2004, 8, 183-194.	1.3	17
78	Approximation algorithms for NMR spectral peak assignment. Theoretical Computer Science, 2003, 299, 211-229.	0.9	19
79	Computational Assignment of Protein Backbone NMR Peaks by Efficient Bounding and Filtering. Journal of Bioinformatics and Computational Biology, 2003, 01, 387-409.	0.8	6
80	EFFICIENT INFERENCE OF HAPLOTYPES FROM GENOTYPES ON A PEDIGREE. Journal of Bioinformatics and Computational Biology, 2003, 01, 41-69.	0.8	71
81	Minimum Recombinant Haplotype Configuration on Tree Pedigrees. Lecture Notes in Computer Science, 2003, , 339-353.	1.3	22
82	Efficient rule-based haplotyping algorithms for pedigree data. , 2003, , .		35
83	Identifying transcription factor binding sites through Markov chain optimization. Bioinformatics, 2002, 18, S100-S109.	4.1	71
84	Oligonucleotide Fingerprinting of rRNA Genes for Analysis of Fungal Community Composition. Applied and Environmental Microbiology, 2002, 68, 5999-6004.	3.1	80
85	Analysis of Bacterial Community Composition by Oligonucleotide Fingerprinting of rRNA Genes. Applied and Environmental Microbiology, 2002, 68, 3243-3250.	3.1	116
86	Automated assignment of backbone NMR peaks using constrained bipartite matching. Computing in Science and Engineering, 2002, 4, 50-62.	1.2	20
87	A General Edit Distance between RNA Structures. Journal of Computational Biology, 2002, 9, 371-388.	1.6	175
88	The average-case area of Heilbronn-type triangles*. Random Structures and Algorithms, 2002, 20, 206-219.	1.1	19
89	The longest common subsequence problem for sequences with nested arc annotations. Journal of Computer and System Sciences, 2002, 65, 465-480.	1.2	61
90	Efficient algorithms for locating the length-constrained heaviest segments with applications to biomolecular sequence analysis. Journal of Computer and System Sciences, 2002, 65, 570-586.	1.2	78

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91	A Heuristic Algorithm for Multiple Sequence Alignment Based on Blocks. Journal of Combinatorial Optimization, 2001, 5, 95-115.	1.3	8
92	Some Open Problems in Computational Molecular Biology. Journal of Algorithms, 2000, 34, 194-201.	0.9	16
93	New applications of the incompressibility method: Part II. Theoretical Computer Science, 2000, 235, 59-70.	0.9	15
94	Average-case analysis of algorithms using Kolmogorov complexity. Journal of Computer Science and Technology, 2000, 15, 402-408.	1.5	9
95	A lower bound on the average-case complexity of shellsort. Journal of the ACM, 2000, 47, 905-911.	2.2	15
96	A More Efficient Approximation Scheme for Tree Alignment. SIAM Journal on Computing, 2000, 30, 283-299.	1.0	27
97	The Incompressibility Method. Lecture Notes in Computer Science, 2000, , 36-53.	1.3	0
98	Two heads are better than two tapes. Journal of the ACM, 1997, 44, 237-256.	2.2	6
99	Approximation algorithms for tree alignment with a given phylogeny. Algorithmica, 1996, 16, 302-315.	1.3	49
100	On the complexity of comparing evolutionary trees. Discrete Applied Mathematics, 1996, 71, 153-169.	0.9	188
101	On the Approximation of Shortest Common Supersequences and Longest Common Subsequences. SIAM Journal on Computing, 1995, 24, 1122-1139.	1.0	160
102	Some MAX SNP-hard results concerning unordered labeled trees. Information Processing Letters, 1994, 49, 249-254.	0.6	109
103	Linear approximation of shortest superstrings. Journal of the ACM, 1994, 41, 630-647.	2.2	110
104	On the Complexity of Multiple Sequence Alignment. Journal of Computational Biology, 1994, 1, 337-348.	1.6	719
105	Minimal NFA Problems are Hard. SIAM Journal on Computing, 1993, 22, 1117-1141.	1.0	185
106	THE STRUCTURE AND COMPLEXITY OF MINIMAL NFA'S OVER A UNARY ALPHABET. International Journal of Foundations of Computer Science, 1991, 02, 163-182.	1.1	36
107	An efficient branch-and-bound algorithm for the assignment of protein backbone NMR peaks. , 0, , .		11