

Tao Jiang

List of Publications by Year in descending order

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Version: 2024-02-01

80
papers

2,391
citations

257450

24
h-index

243625

44
g-index

81
all docs

81
docs citations

81
times ranked

2355
citing authors

#	ARTICLE	IF	CITATIONS
1	NeoDTI: neural integration of neighbor information from a heterogeneous network for discovering new drug-target interactions. <i>Bioinformatics</i> , 2019, 35, 104-111.	4.1	218
2	SCALE method for single-cell ATAC-seq analysis via latent feature extraction. <i>Nature Communications</i> , 2019, 10, 4576.	12.8	162
3	IsoLasso: A LASSO Regression Approach to RNA-Seq Based Transcriptome Assembly. <i>Journal of Computational Biology</i> , 2011, 18, 1693-1707.	1.6	139
4	Assignment of Orthologous Genes via Genome Rearrangement. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2005, 2, 302-315.	3.0	120
5	Transcriptome assembly and isoform expression level estimation from biased RNA-Seq reads. <i>Bioinformatics</i> , 2012, 28, 2914-2921.	4.1	87
6	TITER: predicting translation initiation sites by deep learning. <i>Bioinformatics</i> , 2017, 33, i234-i242.	4.1	83
7	TransComb: genome-guided transcriptome assembly via combing junctions in splicing graphs. <i>Genome Biology</i> , 2016, 17, 213.	8.8	75
8	MSOAR 2.0: Incorporating tandem duplications into ortholog assignment based on genome rearrangement. <i>BMC Bioinformatics</i> , 2010, 11, 10.	2.6	72
9	EFFICIENT INFERENCE OF HAPLOTYPES FROM GENOTYPES ON A PEDIGREE. <i>Journal of Bioinformatics and Computational Biology</i> , 2003, 01, 41-69.	0.8	71
10	Computing the Minimum Recombinant Haplotype Configuration from Incomplete Genotype Data on a Pedigree by Integer Linear Programming. <i>Journal of Computational Biology</i> , 2005, 12, 719-739.	1.6	71
11	MSOAR: A High-Throughput Ortholog Assignment System Based on Genome Rearrangement. <i>Journal of Computational Biology</i> , 2007, 14, 1160-1175.	1.6	67
12	TAPAS: tool for alternative polyadenylation site analysis. <i>Bioinformatics</i> , 2018, 34, 2521-2529.	4.1	62
13	The longest common subsequence problem for sequences with nested arc annotations. <i>Journal of Computer and System Sciences</i> , 2002, 65, 465-480.	1.2	61
14	Analysis of Ribosome Stalling and Translation Elongation Dynamics by Deep Learning. <i>Cell Systems</i> , 2017, 5, 212-220.e6.	6.2	58
15	Inference of Isoforms from Short Sequence Reads. <i>Journal of Computational Biology</i> , 2011, 18, 305-321.	1.6	54
16	The longest common subsequence problem for arc-annotated sequences. <i>Journal of Discrete Algorithms</i> , 2004, 2, 257-270.	0.7	53
17	A Class of Edit Kernels for SVMs to Predict Translation Initiation Sites in Eukaryotic mRNAs. <i>Journal of Computational Biology</i> , 2005, 12, 702-718.	1.6	52
18	Pattern languages with and without erasing. <i>International Journal of Computer Mathematics</i> , 1994, 50, 147-163.	1.8	49

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19	Approximation algorithms for tree alignment with a given phylogeny. <i>Algorithmica</i> , 1996, 16, 302-315.	1.3	49
20	DeepHINT: understanding HIV-1 integration via deep learning with attention. <i>Bioinformatics</i> , 2019, 35, 1660-1667.	4.1	41
21	A novel machine learning framework for automated biomedical relation extraction from large-scale literature repositories. <i>Nature Machine Intelligence</i> , 2020, 2, 347-355.	16.0	37
22	THE STRUCTURE AND COMPLEXITY OF MINIMAL NFA ^s OVER A UNARY ALPHABET. <i>International Journal of Foundations of Computer Science</i> , 1991, 02, 163-182.	1.1	36
23	DeepPASTA: deep neural network based polyadenylation site analysis. <i>Bioinformatics</i> , 2019, 35, 4577-4585.	4.1	35
24	Efficient rule-based haplotyping algorithms for pedigree data. , 2003, , .		35
25	Differential gene expression analysis using coexpression and RNA-Seq data. <i>Bioinformatics</i> , 2013, 29, 2153-2161.	4.1	32
26	DIFFUSE: predicting isoform functions from sequences and expression profiles via deep learning. <i>Bioinformatics</i> , 2019, 35, i284-i294.	4.1	28
27	Orchestrating quartets: approximation and data correction. , 0, , .		24
28	An exact solution for finding minimum recombinant haplotype configurations on pedigrees with missing data by integer linear programming. , 2004, , .		24
29	Modeling multi-species RNA modification through multi-task curriculum learning. <i>Nucleic Acids Research</i> , 2021, 49, 3719-3734.	14.5	23
30	Minimum Recombinant Haplotype Configuration on Tree Pedigrees. <i>Lecture Notes in Computer Science</i> , 2003, , 339-353.	1.3	22
31	Automated assignment of backbone NMR peaks using constrained bipartite matching. <i>Computing in Science and Engineering</i> , 2002, 4, 50-62.	1.2	20
32	DeepIsoFun: a deep domain adaptation approach to predict isoform functions. <i>Bioinformatics</i> , 2019, 35, 2535-2544.	4.1	20
33	The average-case area of Heilbronn-type triangles*. <i>Random Structures and Algorithms</i> , 2002, 20, 206-219.	1.1	19
34	Approximation algorithms for NMR spectral peak assignment. <i>Theoretical Computer Science</i> , 2003, 299, 211-229.	0.9	19
35	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
36	A deep boosting based approach for capturing the sequence binding preferences of RNA-binding proteins from high-throughput CLIP-seq data. <i>Nucleic Acids Research</i> , 2017, 45, e129-e129.	14.5	19

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37	Improved Approximation Algorithms for the Maximum Happy Vertices and Edges Problems. <i>Algorithmica</i> , 2018, 80, 1412-1438.	1.3	19
38	DNA sequencing and string learning. <i>Mathematical Systems Theory</i> , 1996, 29, 387-405.	0.5	18
39	A SURVEY ON HAPLOTYPING ALGORITHMS FOR TIGHTLY LINKED MARKERS. <i>Journal of Bioinformatics and Computational Biology</i> , 2008, 06, 241-259.	0.8	18
40	An approximation scheme for some Steiner tree problems in the plane. <i>Networks</i> , 1996, 28, 187-193.	2.7	17
41	A Further Improved Approximation Algorithm for Breakpoint Graph Decomposition. <i>Journal of Combinatorial Optimization</i> , 2004, 8, 183-194.	1.3	17
42	Complexity and approximation of the minimum recombinant haplotype configuration problem. <i>Theoretical Computer Science</i> , 2007, 378, 316-330.	0.9	16
43	New applications of the incompressibility method: Part II. <i>Theoretical Computer Science</i> , 2000, 235, 59-70.	0.9	15
44	A lower bound on the average-case complexity of shellsort. <i>Journal of the ACM</i> , 2000, 47, 905-911.	2.2	15
45	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
46	Improved Approximation Algorithms for the Maximum Happy Vertices and Edges Problems. <i>Lecture Notes in Computer Science</i> , 2015, , 159-170.	1.3	13
47	Dysregulation of Hypothalamic Gene Expression and the Oxytocinergic System by Soybean Oil Diets in Male Mice. <i>Endocrinology</i> , 2020, 161, .	2.8	11
48	A Parsimony Approach to Genome-Wide Ortholog Assignment. <i>Lecture Notes in Computer Science</i> , 2006, , 578-594.	1.3	11
49	CLUSTERING OF MAIN ORTHOLOGS FOR MULTIPLE GENOMES. <i>Journal of Bioinformatics and Computational Biology</i> , 2008, 06, 573-584.	0.8	10
50	Mapping Clones with a Given Ordering or Interleaving. <i>Algorithmica</i> , 1998, 21, 262-284.	1.3	9
51	Average-case analysis of algorithms using Kolmogorov complexity. <i>Journal of Computer Science and Technology</i> , 2000, 15, 402-408.	1.5	9
52	Efficient Algorithms for Reconstructing Zero-Recombinant Haplotypes on a Pedigree Based on Fast Elimination of Redundant Linear Equations. <i>SIAM Journal on Computing</i> , 2009, 38, 2198-2219.	1.0	9
53	Some Algorithmic Challenges in Genome-Wide Ortholog Assignment. <i>Journal of Computer Science and Technology</i> , 2010, 25, 42-52.	1.5	9
54	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

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55	A linear-time algorithm for reconstructing zero-recombinant haplotype configuration on pedigrees without mating loops. <i>Journal of Combinatorial Optimization</i> , 2010, 19, 217-240.	1.3	7
56	A linear-time algorithm for reconstructing zero-recombinant haplotype configuration on a pedigree. <i>BMC Bioinformatics</i> , 2012, 13, S19.	2.6	7
57	AN IMPROVED GIBBS SAMPLING METHOD FOR MOTIF DISCOVERY VIA SEQUENCE WEIGHTING. , 2006, , .		7
58	Two heads are better than two tapes. <i>Journal of the ACM</i> , 1997, 44, 237-256.	2.2	6
59	Computational Assignment of Protein Backbone NMR Peaks by Efficient Bounding and Filtering. <i>Journal of Bioinformatics and Computational Biology</i> , 2003, 01, 387-409.	0.8	6
60	Constructing tissue-specific transcriptional regulatory networks via a Markov random field. <i>BMC Genomics</i> , 2018, 19, 884.	2.8	6
61	LEARNING POSITION WEIGHT MATRICES FROM SEQUENCE AND EXPRESSION DATA. , 2007, , .		6
62	INFERRING HAPLOTYPES FROM GENOTYPES ON A PEDIGREE WITH MUTATIONS, GENOTYPING ERRORS AND MISSING ALLELES. <i>Journal of Bioinformatics and Computational Biology</i> , 2011, 09, 339-365.	0.8	5
63	A New Model of Multi-Marker Correlation for Genome-Wide Tag SNP Selection. , 2008, , .		5
64	Facile Fabrication of Multilayer Stretchable Electronics via a Two-mode Mechanical Cutting Process. <i>ACS Nano</i> , 2022, 16, 1533-1546.	14.6	5
65	More Reliable Protein NMR Peak Assignment via Improved 2-Interval Scheduling. <i>Journal of Computational Biology</i> , 2005, 12, 129-146.	1.6	4
66	Average-case analysis of QuickSort and Binary Insertion Tree height using incompressibility. <i>Information Processing Letters</i> , 2007, 103, 45-51.	0.6	3
67	Workshop: Transcriptome assembly from RNA-Seq data: Objectives, algorithms and challenges. , 2011, , .		3
68	SDEAP: a splice graph based differential transcript expression analysis tool for population data. <i>Bioinformatics</i> , 2016, 32, 3593-3602.	4.1	3
69	FreePSI: an alignment-free approach to estimating exon-inclusion ratios without a reference transcriptome. <i>Nucleic Acids Research</i> , 2018, 46, e11-e11.	14.5	3
70	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
71	CLUSTERING OF MAIN ORTHOLOGS FOR MULTIPLE GENOMES. , 2007, , .		3
72	Beyond evolutionary trees. <i>Natural Computing</i> , 2010, 9, 421-435.	3.0	2

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73	An Efficient Algorithm for Haplotype Inference on Pedigrees with a Small Number of Recombinants. <i>Algorithmica</i> , 2012, 62, 951-981.	1.3	2
74	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
75	Riboexp: an interpretable reinforcement learning framework for ribosome density modeling. <i>Briefings in Bioinformatics</i> , 2021, 22, .	6.5	2
76	More Reliable Protein NMR Peak Assignment via Improved 2-Interval Scheduling. <i>Lecture Notes in Computer Science</i> , 2003, , 580-592.	1.3	2
77	A simulated annealing approach for resolution guided homogeneous cryo-electron microscopy image selection. <i>Quantitative Biology</i> , 2020, 8, 51-63.	0.5	1
78	Linear-Time Reconstruction of Zero-Recombinant Mendelian Inheritance on Pedigrees without Mating Loops. , 2007, , .		1
79	Polony Identification Using the EM Algorithm Based on a Gaussian Mixture Model. , 2010, , .		0
80	The Incompressibility Method. <i>Lecture Notes in Computer Science</i> , 2000, , 36-53.	1.3	0