

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	Facile Fabrication of Multilayer Stretchable Electronics via a Two-mode Mechanical Cutting Process. ACS Nano, 2022, 16, 1533-1546.	14.6	5
2	DeepLPI: a multimodal deep learning method for predicting the interactions between lncRNAs and protein isoforms. BMC Bioinformatics, 2021, 22, 24.	2.6	13
3	Modeling multi-species RNA modification through multi-task curriculum learning. Nucleic Acids Research, 2021, 49, 3719-3734.	14.5	23
4	Enhancement and Imputation of Peak Signal Enables Accurate Cell-Type Classification in scATAC-seq. Frontiers in Genetics, 2021, 12, 658352.	2.3	2
5	FINER: enhancing the prediction of tissue-specific functions of isoforms by refining isoform interaction networks. NAR Genomics and Bioinformatics, 2021, 3, lqab057.	3.2	3
6	Riboexp: an interpretable reinforcement learning framework for ribosome density modeling. Briefings in Bioinformatics, 2021, 22, .	6.5	2
7	Dysregulation of Hypothalamic Gene Expression and the Oxytocinergic System by Soybean Oil Diets in Male Mice. Endocrinology, 2020, 161, .	2.8	11
8	A novel machine learning framework for automated biomedical relation extraction from large-scale literature repositories. Nature Machine Intelligence, 2020, 2, 347-355.	16.0	37
9	A simulated annealing approach for resolution guided homogeneous cryo-electron microscopy image selection. Quantitative Biology, 2020, 8, 51-63.	0.5	1
10	NeoDTI: neural integration of neighbor information from a heterogeneous network for discovering new drug-target interactions. Bioinformatics, 2019, 35, 104-111.	4.1	218
11	DIFFUSE: predicting isoform functions from sequences and expression profiles via deep learning. Bioinformatics, 2019, 35, i284-i294.	4.1	28
12	SCALE method for single-cell ATAC-seq analysis via latent feature extraction. Nature Communications, 2019, 10, 4576.	12.8	162
13	DeepPASTA: deep neural network based polyadenylation site analysis. Bioinformatics, 2019, 35, 4577-4585.	4.1	35
14	DeepIsoFun: a deep domain adaptation approach to predict isoform functions. Bioinformatics, 2019, 35, 2535-2544.	4.1	20
15	DeepHINT: understanding HIV-1 integration via deep learning with attention. Bioinformatics, 2019, 35, 1660-1667.	4.1	41
16	TAPAS: tool for alternative polyadenylation site analysis. Bioinformatics, 2018, 34, 2521-2529.	4.1	62
17	FreePSI: an alignment-free approach to estimating exon-inclusion ratios without a reference transcriptome. Nucleic Acids Research, 2018, 46, e11-e11.	14.5	3
18	Improved Approximation Algorithms for the Maximum Happy Vertices and Edges Problems. Algorithmica, 2018, 80, 1412-1438.	1.3	19

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19	Constructing tissue-specific transcriptional regulatory networks via a Markov random field. BMC Genomics, 2018, 19, 884.	2.8	6
20	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
21	Analysis of Ribosome Stalling and Translation Elongation Dynamics by Deep Learning. Cell Systems, 2017, 5, 212-220.e6.	6.2	58
22	TITER: predicting translation initiation sites by deep learning. Bioinformatics, 2017, 33, i234-i242.	4.1	83
23	SDEAP: a splice graph based differential transcript expression analysis tool for population data. Bioinformatics, 2016, 32, 3593-3602.	4.1	3
24	TransComb: genome-guided transcriptome assembly via combing junctions in splicing graphs. Genome Biology, 2016, 17, 213.	8.8	75
25	Differential regulation enrichment analysis via the integration of transcriptional regulatory network and gene expression data. Bioinformatics, 2015, 31, 563-571.	4.1	19
26	Improved Approximation Algorithms for the Maximum Happy Vertices and Edges Problems. Lecture Notes in Computer Science, 2015, , 159-170.	1.3	13
27	Differential gene expression analysis using coexpression and RNA-Seq data. Bioinformatics, 2013, 29, 2153-2161.	4.1	32
28	Transcriptome assembly and isoform expression level estimation from biased RNA-Seq reads. Bioinformatics, 2012, 28, 2914-2921.	4.1	87
29	An Efficient Algorithm for Haplotype Inference on Pedigrees with Recombinations and Mutations. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2012, 9, 12-25.	3.0	9
30	A linear-time algorithm for reconstructing zero-recombinant haplotype configuration on a pedigree. BMC Bioinformatics, 2012, 13, S19.	2.6	7
31	An Efficient Algorithm for Haplotype Inference on Pedigrees with a Small Number of Recombinants. Algorithmica, 2012, 62, 951-981.	1.3	2
32	Workshop: Transcriptome assembly from RNA-Seq data: Objectives, algorithms and challenges. , 2011, , .		3
33	IsoLasso: A LASSO Regression Approach to RNA-Seq Based Transcriptome Assembly. Journal of Computational Biology, 2011, 18, 1693-1707.	1.6	139
34	Inference of Isoforms from Short Sequence Reads. Journal of Computational Biology, 2011, 18, 305-321.	1.6	54
35	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
36	Some Algorithmic Challenges in Genome-Wide Ortholog Assignment. Journal of Computer Science and Technology, 2010, 25, 42-52.	1.5	9

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37	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
38	Beyond evolutionary trees. <i>Natural Computing</i> , 2010, 9, 421-435.	3.0	2
39	MSOAR 2.0: Incorporating tandem duplications into ortholog assignment based on genome rearrangement. <i>BMC Bioinformatics</i> , 2010, 11, 10.	2.6	72
40	Polony Identification Using the EM Algorithm Based on a Gaussian Mixture Model. , 2010, , .		0
41	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
42	A SURVEY ON HAPLOTYPING ALGORITHMS FOR TIGHTLY LINKED MARKERS. <i>Journal of Bioinformatics and Computational Biology</i> , 2008, 06, 241-259.	0.8	18
43	CLUSTERING OF MAIN ORTHOLOGS FOR MULTIPLE GENOMES. <i>Journal of Bioinformatics and Computational Biology</i> , 2008, 06, 573-584.	0.8	10
44	A New Model of Multi-Marker Correlation for Genome-Wide Tag SNP Selection. , 2008, , .		5
45	MSOAR: A High-Throughput Ortholog Assignment System Based on Genome Rearrangement. <i>Journal of Computational Biology</i> , 2007, 14, 1160-1175.	1.6	67
46	Complexity and approximation of the minimum recombinant haplotype configuration problem. <i>Theoretical Computer Science</i> , 2007, 378, 316-330.	0.9	16
47	Average-case analysis of QuickSort and Binary Insertion Tree height using incompressibility. <i>Information Processing Letters</i> , 2007, 103, 45-51.	0.6	3
48	CLUSTERING OF MAIN ORTHOLOGS FOR MULTIPLE GENOMES. , 2007, , .		3
49	LEARNING POSITION WEIGHT MATRICES FROM SEQUENCE AND EXPRESSION DATA. , 2007, , .		6
50	Linear-Time Reconstruction of Zero-Recombinant Mendelian Inheritance on Pedigrees without Mating Loops. , 2007, , .		1
51	A Parsimony Approach to Genome-Wide Ortholog Assignment. <i>Lecture Notes in Computer Science</i> , 2006, , 578-594.	1.3	11
52	AN IMPROVED GIBBS SAMPLING METHOD FOR MOTIF DISCOVERY VIA SEQUENCE WEIGHTING. , 2006, , .		7
53	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
54	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

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55	More Reliable Protein NMR Peak Assignment via Improved 2-Interval Scheduling. Journal of Computational Biology, 2005, 12, 129-146.	1.6	4
56	Assignment of Orthologous Genes via Genome Rearrangement. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2005, 2, 302-315.	3.0	120
57	An exact solution for finding minimum recombinant haplotype configurations on pedigrees with missing data by integer linear programming. , 2004, , .		24
58	A Further Improved Approximation Algorithm for Breakpoint Graph Decomposition. Journal of Combinatorial Optimization, 2004, 8, 183-194.	1.3	17
59	The longest common subsequence problem for arc-annotated sequences. Journal of Discrete Algorithms, 2004, 2, 257-270.	0.7	53
60	Approximation algorithms for NMR spectral peak assignment. Theoretical Computer Science, 2003, 299, 211-229.	0.9	19
61	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
62	EFFICIENT INFERENCE OF HAPLOTYPES FROM GENOTYPES ON A PEDIGREE. Journal of Bioinformatics and Computational Biology, 2003, 01, 41-69.	0.8	71
63	Minimum Recombinant Haplotype Configuration on Tree Pedigrees. Lecture Notes in Computer Science, 2003, , 339-353.	1.3	22
64	More Reliable Protein NMR Peak Assignment via Improved 2-Interval Scheduling. Lecture Notes in Computer Science, 2003, , 580-592.	1.3	2
65	Efficient rule-based haplotyping algorithms for pedigree data. , 2003, , .		35
66	Automated assignment of backbone NMR peaks using constrained bipartite matching. Computing in Science and Engineering, 2002, 4, 50-62.	1.2	20
67	The average-case area of Heilbronn-type triangles*. Random Structures and Algorithms, 2002, 20, 206-219.	1.1	19
68	The longest common subsequence problem for sequences with nested arc annotations. Journal of Computer and System Sciences, 2002, 65, 465-480.	1.2	61
69	New applications of the incompressibility method: Part II. Theoretical Computer Science, 2000, 235, 59-70.	0.9	15
70	Average-case analysis of algorithms using Kolmogorov complexity. Journal of Computer Science and Technology, 2000, 15, 402-408.	1.5	9
71	A lower bound on the average-case complexity of shellsort. Journal of the ACM, 2000, 47, 905-911.	2.2	15
72	The Incompressibility Method. Lecture Notes in Computer Science, 2000, , 36-53.	1.3	0

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73	Mapping Clones with a Given Ordering or Interleaving. <i>Algorithmica</i> , 1998, 21, 262-284.	1.3	9
74	Two heads are better than two tapes. <i>Journal of the ACM</i> , 1997, 44, 237-256.	2.2	6
75	Approximation algorithms for tree alignment with a given phylogeny. <i>Algorithmica</i> , 1996, 16, 302-315.	1.3	49
76	DNA sequencing and string learning. <i>Mathematical Systems Theory</i> , 1996, 29, 387-405.	0.5	18
77	An approximation scheme for some Steiner tree problems in the plane. <i>Networks</i> , 1996, 28, 187-193.	2.7	17
78	Pattern languages with and without erasing. <i>International Journal of Computer Mathematics</i> , 1994, 50, 147-163.	1.8	49
79	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
80	Orchestrating quartets: approximation and data correction. , 0, , .		24