

Jianxing Wang

List of Publications by Year in descending order

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588
papers

13,699
citations

30070

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43889

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g-index

599
all docs

599
docs citations

599
times ranked

9139
citing authors

#	ARTICLE	IF	CITATIONS
1	REN: Receiver-Driven Congestion Control Using Explicit Notification for Data Center. IEEE Transactions on Cloud Computing, 2023, 11, 1381-1394.	4.4	2
2	SACall: A Neural Network Basecaller for Oxford Nanopore Sequencing Data Based on Self-Attention Mechanism. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2022, 19, 614-623.	3.0	14
3	LDICDL: LncRNA-Disease Association Identification Based on Collaborative Deep Learning. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2022, 19, 1715-1723.	3.0	47
4	APS: Adaptive Packet Spraying to Isolate Mix-Flows in Data Center Network. IEEE Transactions on Cloud Computing, 2022, 10, 1038-1051.	4.4	13
5	Feature and Nuclear Norm Minimization for Matrix Completion. IEEE Transactions on Knowledge and Data Engineering, 2022, 34, 2190-2199.	5.7	10
6	Predicting Drug-Drug Interactions Based on Integrated Similarity and Semi-Supervised Learning. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2022, 19, 168-179.	3.0	30
7	Drug-Target Interaction Prediction Using Multi-Head Self-Attention and Graph Attention Network. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2022, 19, 2208-2218.	3.0	35
8	BlockPolish: accurate polishing of long-read assembly via block divide-and-conquer. Briefings in Bioinformatics, 2022, 23, .	6.5	2
9	Biomedical Data and Deep Learning Computational Models for Predicting Compound-Protein Relations. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2022, 19, 2092-2110.	3.0	11
10	Automated Diagnosis of COVID-19 Using Deep Supervised Autoencoder With Multi-View Features From CT Images. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2022, 19, 2723-2736.	3.0	11
11	Multimodal Disentangled Variational Autoencoder With Game Theoretic Interpretability for Glioma Grading. IEEE Journal of Biomedical and Health Informatics, 2022, 26, 673-684.	6.3	23
12	End vertices of graph searches on bipartite graphs. Information Processing Letters, 2022, 173, 106176.	0.6	2
13	msRepDB: a comprehensive repetitive sequence database of over 80 000 species. Nucleic Acids Research, 2022, 50, D236-D245.	14.5	8
14	HyperAttentionDTI: improving drug-protein interaction prediction by sequence-based deep learning with attention mechanism. Bioinformatics, 2022, 38, 655-662.	4.1	55
15	TissueNexus: a database of human tissue functional gene networks built with a large compendium of curated RNA-seq data. Nucleic Acids Research, 2022, 50, D710-D718.	14.5	11
16	VAMP: A Predictive Approach to Audio/Video Bitrate Adaptation Over Wireless Networks. IEEE Wireless Communications Letters, 2022, 11, 513-517.	5.0	3
17	An Improved Bound and Singleton-Optimal Constructions of Fractional Repetition Codes. IEEE Transactions on Communications, 2022, 70, 749-758.	7.8	0
18	IsoCell: An Approach to Enhance Single Cell Clustering by Integrating Isoform-level Expression through Orthogonal Projection. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2022, PP, 1-1.	3.0	1

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19	AlzCode: a platform for multiview analysis of genes related to Alzheimer's disease. <i>Bioinformatics</i> , 2022, 38, 2030-2032.	4.1	3
20	A comparison of topologically associating domain callers based on Hi-C data. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2022, PP, 1-1.	3.0	5
21	An automated COVID-19 triage pipeline using artificial intelligence based on chest radiographs and clinical data. <i>Npj Digital Medicine</i> , 2022, 5, 5.	10.9	22
22	On Some Capacity-Achieving Fractional Repetition Codes. <i>IEEE Transactions on Vehicular Technology</i> , 2022, 71, 3332-3337.	6.3	1
23	Drug repositioning based on multi-view learning with matrix completion. <i>Briefings in Bioinformatics</i> , 2022, 23, .	6.5	9
24	End-to-End Congestion Control to Provide Deterministic Latency Over Internet. <i>IEEE Communications Letters</i> , 2022, 26, 843-847.	4.1	5
25	A Fully Automated Multimodal MRI-Based Multi-Task Learning for Glioma Segmentation and IDH Genotyping. <i>IEEE Transactions on Medical Imaging</i> , 2022, 41, 1520-1532.	8.9	62
26	A Refined Branching Algorithm for the Maximum Satisfiability Problem. <i>Algorithmica</i> , 2022, 84, 982-1006.	1.3	2
27	PDMDA: predicting deep-level miRNA-disease associations with graph neural networks and sequence features. <i>Bioinformatics</i> , 2022, 38, 2226-2234.	4.1	18
28	TRScore: a 3D RepVGG-based scoring method for ranking protein docking models. <i>Bioinformatics</i> , 2022, 38, 2444-2451.	4.1	6
29	COVID-19 mortality prediction in the intensive care unit with deep learning based on longitudinal chest X-rays and clinical data. <i>European Radiology</i> , 2022, 32, 4446-4456.	4.5	19
30	MLDRL: Multi-loss disentangled representation learning for predicting esophageal cancer response to neoadjuvant chemoradiotherapy using longitudinal CT images. <i>Medical Image Analysis</i> , 2022, 79, 102423.	11.6	14
31	Achieving Per-Flow Fairness and High Utilization With Limited Priority Queues in Data Center. <i>IEEE/ACM Transactions on Networking</i> , 2022, 30, 2374-2387.	3.8	4
32	DARC: Deep adaptive regularized clustering for histopathological image classification. <i>Medical Image Analysis</i> , 2022, 80, 102521.	11.6	14
33	Identifying and ranking potential cancer drivers using representation learning on attributed network. <i>Methods</i> , 2021, 192, 13-24.	3.8	11
34	Drug-drug similarity measure and its applications. <i>Briefings in Bioinformatics</i> , 2021, 22, .	6.5	17
35	FUNMarker: Fusion Network-Based Method to Identify Prognostic and Heterogeneous Breast Cancer Biomarkers. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2021, 18, 2483-2491.	3.0	10
36	DMFLDA: A Deep Learning Framework for Predicting lncRNA-Disease Associations. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2021, 18, 2353-2363.	3.0	38

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37	Identifying the tissues-of-origin of circulating cell-free DNAs is a promising way in noninvasive diagnostics. Briefings in Bioinformatics, 2021, 22, .	6.5	15
38	Deep Matrix Factorization Improves Prediction of Human CircRNA-Disease Associations. IEEE Journal of Biomedical and Health Informatics, 2021, 25, 891-899.	6.3	43
39	An Ensemble Method to Reconstruct Gene Regulatory Networks Based on Multivariate Adaptive Regression Splines. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2021, 18, 347-354.	3.0	17
40	MMHGE: detecting mild cognitive impairment based on multi-atlas multi-view hybrid graph convolutional networks and ensemble learning. Cluster Computing, 2021, 24, 103-113.	5.0	22
41	A survey on predicting microbe-disease associations: biological data and computational methods. Briefings in Bioinformatics, 2021, 22, .	6.5	15
42	IsoResolve: predicting splice isoform functions by integrating gene and isoform-level features with domain adaptation. Bioinformatics, 2021, 37, 522-530.	4.1	7
43	Heterogeneous graph inference with matrix completion for computational drug repositioning. Bioinformatics, 2021, 36, 5456-5464.	4.1	13
44	A Secure Scheme Based on One-Way Associated Key Management Model in Wireless Sensor Networks. IEEE Internet of Things Journal, 2021, 8, 2920-2930.	8.7	7
45	Protein2Vec: Aligning Multiple PPI Networks with Representation Learning. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2021, 18, 240-249.	3.0	7
46	DeepDSC: A Deep Learning Method to Predict Drug Sensitivity of Cancer Cell Lines. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2021, 18, 575-582.	3.0	67
47	ILDMSF: Inferring Associations Between Long Non-Coding RNA and Disease Based on Multi-Similarity Fusion. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2021, 18, 1106-1112.	3.0	57
48	High-Risk Prediction of Cardiovascular Diseases via Attention-Based Deep Neural Networks. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2021, 18, 1093-1105.	3.0	31
49	A Gene Rank Based Approach for Single Cell Similarity Assessment and Clustering. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2021, 18, 431-442.	3.0	12
50	Deletion Detection Method Using the Distribution of Insert Size and a Precise Alignment Strategy. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2021, 18, 1070-1081.	3.0	0
51	A Novel Drug Repositioning Approach Based on Collaborative Metric Learning. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2021, 18, 463-471.	3.0	11
52	MCHMDA: Predicting Microbe-Disease Associations Based on Similarities and Low-Rank Matrix Completion. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2021, 18, 611-620.	3.0	21
53	In silico prediction of new mutations that can improve the binding abilities between 2019-nCoV coronavirus and human ACE2. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2021, PP, 1-1.	3.0	5
54	An ensemble hybrid feature selection method for neuropsychiatric disorder classification. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2021, PP, 1-1.	3.0	5

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55	RNPredATC: a deep residual learning-based model with applications to the prediction of drug-ATC code association. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2021, PP, 1-1.	3.0	1
56	Improved Fixed-parameter Algorithm for the Tree Containment Problem on Unrooted Phylogenetic Network. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2021, PP, 1-1.	3.0	0
57	Efficient assembly of nanopore reads via highly accurate and intact error correction. Nature Communications, 2021, 12, 60.	12.8	166
58	Predicting the Survival of Cancer Patients with Multimodal Graph Neural Network. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2021, PP, 1-1.	3.0	10
59	An improved FPT algorithm for the flip distance problem. Information and Computation, 2021, 281, 104708.	0.7	3
60	MultiNanopolish: refined grouping method for reducing redundant calculations in Nanopolish. Bioinformatics, 2021, 37, 2757-2760.	4.1	6
61	SSRE: Cell Type Detection Based on Sparse Subspace Representation and Similarity Enhancement. Genomics, Proteomics and Bioinformatics, 2021, 19, 282-291.	6.9	21
62	Collaborative Matrix Factorization with Soft Regularization for Drug-Target Interaction Prediction. Journal of Computer Science and Technology, 2021, 36, 310-322.	1.5	8
63	Reconstruction and verification of chordal graphs with a distance oracle. Theoretical Computer Science, 2021, 859, 48-56.	0.9	3
64	A convolutional neural network and graph convolutional network-based method for predicting the classification of anatomical therapeutic chemicals. Bioinformatics, 2021, 37, 2841-2847.	4.1	18
65	Parallel computing for genome sequence processing. Briefings in Bioinformatics, 2021, 22, .	6.5	7
66	Incremental algorithms for the maximum internal spanning tree problem. Science China Information Sciences, 2021, 64, 1.	4.3	1
67	NeuralPolish: a novel Nanopore polishing method based on alignment matrix construction and orthogonal Bi-GRU Networks. Bioinformatics, 2021, 37, 3120-3127.	4.1	13
68	Mitigating Packet Reordering for Random Packet Spraying in Data Center Networks. IEEE/ACM Transactions on Networking, 2021, 29, 1183-1196.	3.8	22
69	A sensitive repeat identification framework based on short and long reads. Nucleic Acids Research, 2021, 49, e100-e100.	14.5	10
70	The learning of the precipitates morphological parameters from the composition of nickel-based superalloys. Materials and Design, 2021, 206, 109747.	7.0	6
71	Fixed-parameter tractability for the Tree Assembly problem. Theoretical Computer Science, 2021, 886, 3-12.	0.9	0
72	Modeling and Analysis of Latency Distribution in the 40-100Gbps Dual-Mode Energy Efficient Ethernet. IEEE Transactions on Green Communications and Networking, 2021, 5, 1426-1437.	5.5	0

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73	A dynamic predictor selection algorithm for predicting stock market movement. Expert Systems With Applications, 2021, 186, 115836.	7.6	4
74	Higher-order Interaction Goes Neural: A Substructure Assembling Graph Attention Network for Graph Classification. IEEE Transactions on Knowledge and Data Engineering, 2021, , 1-1.	5.7	11
75	Key residues influencing binding affinities of 2019-nCoV with ACE2 in different species. Briefings in Bioinformatics, 2021, 22, 963-975.	6.5	14
76	Biomedical data and computational models for drug repositioning: a comprehensive review. Briefings in Bioinformatics, 2021, 22, 1604-1619.	6.5	110
77	Time-Aware Multi-Type Data Fusion Representation Learning Framework for Risk Prediction of Cardiovascular Diseases. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2021, PP, 1-1.	3.0	12
78	RMC: Reordering Marking and Coding for Fine-Grained Load Balancing in Data Centers. IEEE Transactions on Communications, 2021, 69, 8363-8374.	7.8	4
79	OUP accepted manuscript. Briefings in Bioinformatics, 2021, , .	6.5	1
80	Genome-wide detection of cytosine methylations in plant from Nanopore data using deep learning. Nature Communications, 2021, 12, 5976.	12.8	47
81	Improving circRNA disease association prediction by sequence and ontology representations with convolutional and recurrent neural networks. Bioinformatics, 2021, 36, 5656-5664.	4.1	21
82	MultiGuideScan: a multi-processing tool for designing CRISPR guide RNA libraries. Bioinformatics, 2020, 36, 920-921.	4.1	8
83	Protein protein interaction site prediction through combining local and global features with deep neural networks. Bioinformatics, 2020, 36, 1114-1120.	4.1	157
84	GapReduce: A Gap Filling Algorithm Based on Partitioned Read Sets. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2020, 17, 877-886.	3.0	11
85	Identification of Protein Complexes by Using a Spatial and Temporal Active Protein Interaction Network. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2020, 17, 817-827.	3.0	24
86	Constructing Disease Similarity Networks Based on Disease Module Theory. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2020, 17, 906-915.	3.0	29
87	MEC: Misassembly Error Correction in Contigs based on Distribution of Paired-End Reads and Statistics of GC-contents. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2020, 17, 847-857.	3.0	17
88	miRTRS: A Recommendation Algorithm for Predicting miRNA Targets. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2020, 17, 1032-1041.	3.0	10
89	Deep convolutional neural network for automatically segmenting acute ischemic stroke lesion in multi-modality MRI. Neural Computing and Applications, 2020, 32, 6545-6558.	5.6	53
90	An Efficient Trimming Algorithm based on Multi-Feature Fusion Scoring Model for NGS Data. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2020, 17, 728-738.	3.0	14

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91	Improving de novo Assembly Based on Read Classification. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2020, 17, 177-188.	3.0	19
92	MultiMotifMaker: A Multi-Thread Tool for Identifying DNA Methylation Motifs from Pacbio Reads. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2020, 17, 220-225.	3.0	12
93	An approximation algorithm for the l-pseudoforest deletion problem. Theoretical Computer Science, 2020, 806, 446-454.	0.9	1
94	Deep convolutional neural network for accurate segmentation and quantification of white matter hyperintensities. Neurocomputing, 2020, 384, 231-242.	5.9	24
95	NIMCE: a gene regulatory network inference approach based on multi time delays causal entropy. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2020, PP, 1-1.	3.0	2
96	Improved ASD classification using dynamic functional connectivity and multi-task feature selection. Pattern Recognition Letters, 2020, 138, 82-87.	4.2	37
97	Attention convolutional neural network for accurate segmentation and quantification of lesions in ischemic stroke disease. Medical Image Analysis, 2020, 65, 101791.	11.6	63
98	Identification of early mild cognitive impairment using multi-modal data and graph convolutional networks. BMC Bioinformatics, 2020, 21, 123.	2.6	17
99	ALMAFE: Autism spectrum disorder identification with multi-atlas deep feature representation and ensemble learning. Journal of Neuroscience Methods, 2020, 343, 108840.	2.5	44
100	Multi-Receptive-Field CNN for Semantic Segmentation of Medical Images. IEEE Journal of Biomedical and Health Informatics, 2020, 24, 3215-3225.	6.3	58
101	Rethinking Fast and Friendly Transport in Data Center Networks. IEEE/ACM Transactions on Networking, 2020, 28, 2364-2377.	3.8	21
102	Dynamic kidney paired exchange using modified multiverse optimization. Evolutionary Intelligence, 2020, , 1.	3.6	0
103	miRTMC: A miRNA Target Prediction Method Based on Matrix Completion Algorithm. IEEE Journal of Biomedical and Health Informatics, 2020, 24, 3630-3641.	6.3	8
104	An Effective Convolutional Neural Network for Classifying Red Blood Cells in Malaria Diseases. Interdisciplinary Sciences, Computational Life Sciences, 2020, 12, 217-225.	3.6	24
105	A survey on U-shaped networks in medical image segmentations. Neurocomputing, 2020, 409, 244-258.	5.9	157
106	Predicting Human lncRNA-Disease Associations Based on Geometric Matrix Completion. IEEE Journal of Biomedical and Health Informatics, 2020, 24, 2420-2429.	6.3	32
107	Enhancing the feature representation of multi-modal MRI data by combining multi-view information for MCI classification. Neurocomputing, 2020, 400, 322-332.	5.9	40
108	CLPred: a sequence-based protein crystallization predictor using BLSTM neural network. Bioinformatics, 2020, 36, i709-i717.	4.1	8

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109	Prediction of Glioma Grade using Intratumoral and Peritumoral Radiomic Features from Multiparametric MRI Images. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2020, PP, 1-1.	3.0	20
110	On Fixed-Order Book Thickness Parameterized by the Pathwidth of the Vertex Ordering. <i>Lecture Notes in Computer Science</i> , 2020, , 225-237.	1.3	1
111	Automatic ICD-9 coding via deep transfer learning. <i>Neurocomputing</i> , 2019, 324, 43-50.	5.9	79
112	A Novel Scaffolding Algorithm Based on Contig Error Correction and Path Extension. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2019, 16, 764-773.	3.0	8
113	Classification of autism spectrum disorder by combining brain connectivity and deep neural network classifier. <i>Neurocomputing</i> , 2019, 324, 63-68.	5.9	161
114	DNRLMF-MDA:Predicting microRNA-Disease Associations Based on Similarities of microRNAs and Diseases. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2019, 16, 233-243.	3.0	59
115	An improved linear kernel for complementary maximal strip recovery: Simpler and smaller. <i>Theoretical Computer Science</i> , 2019, 786, 55-66.	0.9	28
116	BridgeTaint: A Bi-Directional Dynamic Taint Tracking Method for JavaScript Bridges in Android Hybrid Applications. <i>IEEE Transactions on Information Forensics and Security</i> , 2019, 14, 677-692.	6.9	9
117	Combining static and dynamic features for real-time moving pedestrian detection. <i>Multimedia Tools and Applications</i> , 2019, 78, 3781-3795.	3.9	19
118	Targeting TRPV1 on cellular plasticity regulated by Ovol 2 and Zeb 1 in hepatocellular carcinoma. <i>Biomedicine and Pharmacotherapy</i> , 2019, 118, 109270.	5.6	16
119	A novel extended Pareto Optimality Consensus model for predicting essential proteins. <i>Journal of Theoretical Biology</i> , 2019, 480, 141-149.	1.7	9
120	Randomized Parameterized Algorithms for the Kidney Exchange Problem. <i>Algorithms</i> , 2019, 12, 50.	2.1	2
121	Drug repositioning based on bounded nuclear norm regularization. <i>Bioinformatics</i> , 2019, 35, i455-i463.	4.1	116
122	EPGA-SC : A framework for de novo assembly of single-cell sequencing reads. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2019, 18, 1-1.	3.0	3
123	A Sequence-Based Novel Approach for Quality Evaluation of Third-Generation Sequencing Reads. <i>Genes</i> , 2019, 10, 44.	2.4	3
124	A Novel Coreâ€Attachmentâ€Based Method to Identify Dynamic Protein Complexes Based on Gene Expression Profiles and PPI Networks. <i>Proteomics</i> , 2019, 19, e1800129.	2.2	9
125	Scheduling two-stage jobs on multiple flowshops. <i>Theoretical Computer Science</i> , 2019, 776, 117-124.	0.9	8
126	Task-Aware TCP in Data Center Networks. <i>IEEE/ACM Transactions on Networking</i> , 2019, 27, 389-404.	3.8	20

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127	Decoding the Structural Keywords in Protein Structure Universe. Journal of Computer Science and Technology, 2019, 34, 3-15.	1.5	4
128	Controllability and Its Applications to Biological Networks. Journal of Computer Science and Technology, 2019, 34, 16-34.	1.5	25
129	Receiver-driven fair congestion control for TCP outcast in data center networks. Journal of Network and Computer Applications, 2019, 131, 75-88.	9.1	20
130	A Hybrid Clustering Algorithm for Identifying Cell Types from Single-Cell RNA-Seq Data. Genes, 2019, 10, 98.	2.4	14
131	A deep learning framework for identifying essential proteins by integrating multiple types of biological information. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2019, 18, 1-1.	3.0	65
132	An improved algorithm for the $(n, 3)$ -MaxSAT problem: asking branchings to satisfy the clauses. Journal of Combinatorial Optimization, 2019, , 1.	1.3	1
133	Understanding and improvement of the selection of replica servers in key-value stores. Information Systems, 2019, 83, 218-228.	3.6	6
134	Efficient multi-kernel DCNN with pixel dropout for stroke MRI segmentation. Neurocomputing, 2019, 350, 117-127.	5.9	28
135	Identifying Interactions Between Kinases and Substrates Based on Protein-Protein Interaction Network. Journal of Computational Biology, 2019, 26, 836-845.	1.6	5
136	Haste makes waste: The On-Off algorithm for replica selection in key-value stores. Journal of Parallel and Distributed Computing, 2019, 130, 80-90.	4.1	6
137	DeepSignal: detecting DNA methylation state from Nanopore sequencing reads using deep-learning. Bioinformatics, 2019, 35, 4586-4595.	4.1	158
138	Page-sharing-based virtual machine packing with multi-resource constraints to reduce network traffic in migration for clouds. Future Generation Computer Systems, 2019, 96, 462-471.	7.5	20
139	SinNLRR: a robust subspace clustering method for cell type detection by non-negative and low-rank representation. Bioinformatics, 2019, 35, 3642-3650.	4.1	112
140	Nothing Blocks Me: Precise and Real-Time LOS/NLOS Path Recognition in RFID Systems. IEEE Internet of Things Journal, 2019, 6, 5814-5824.	8.7	19
141	A novel method of gene regulatory network structure inference from gene knock-out expression data. Tsinghua Science and Technology, 2019, 24, 446-455.	6.1	17
142	BRWMDA: Predicting microbe-disease associations based on similarities and bi-random walk on disease and microbe networks. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2019, 17, 1-1.	3.0	33
143	Automatic ICD code assignment of Chinese clinical notes based on multilayer attention BiRNN. Journal of Biomedical Informatics, 2019, 91, 103114.	4.3	47
144	CAPS: Coding-Based Adaptive Packet Spraying to Reduce Flow Completion Time in Data Center. IEEE/ACM Transactions on Networking, 2019, 27, 2338-2353.	3.8	36

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145	DDIGIP: predicting drug-drug interactions based on Gaussian interaction profile kernels. BMC Bioinformatics, 2019, 20, 538.	2.6	24
146	Overlap matrix completion for predicting drug-associated indications. PLoS Computational Biology, 2019, 15, e1007541.	3.2	35
147	SCOP: a novel scaffolding algorithm based on contig classification and optimization. Bioinformatics, 2019, 35, 1142-1150.	4.1	13
148	Improved PTAS for the constrained k-means problem. Journal of Combinatorial Optimization, 2019, 37, 1091-1110.	1.3	11
149	BiXGBoost: a scalable, flexible boosting-based method for reconstructing gene regulatory networks. Bioinformatics, 2019, 35, 1893-1900.	4.1	59
150	FPC: A new approach to firewall policies compression. Tsinghua Science and Technology, 2019, 24, 65-76.	6.1	11
151	Real-time wide-view eye tracking based on resolving the spatial depth. Multimedia Tools and Applications, 2019, 78, 14633-14655.	3.9	4
152	LSTM based reserve prediction for bank outlets. Tsinghua Science and Technology, 2019, 24, 77-85.	6.1	16
153	Automated ICD-9 Coding via A Deep Learning Approach. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2019, 16, 1193-1202.	3.0	78
154	Against Signed Graph Deanonimization Attacks on Social Networks. International Journal of Parallel Programming, 2019, 47, 725-739.	1.5	8
155	On scheduling inclined jobs on multiple two-stage flowshops. Theoretical Computer Science, 2019, 786, 67-77.	0.9	7
156	Computational Drug Repositioning with Random Walk on a Heterogeneous Network. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2019, 16, 1890-1900.	3.0	47
157	MGT-SM: A Method for Constructing Cellular Signal Transduction Networks. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2019, 16, 417-424.	3.0	16
158	Construction of Refined Protein Interaction Network for Predicting Essential Proteins. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2019, 16, 1386-1397.	3.0	44
159	Resolution and linear CNF formulas: Improved (n,3)-MaxSAT algorithms. Theoretical Computer Science, 2019, 774, 113-123.	0.9	5
160	Analysis of Single-Cell RNA-seq Data by Clustering Approaches. Current Bioinformatics, 2019, 14, 314-322.	1.5	21
161	Overlap matrix completion for predicting drug-associated indications. , 2019, 15, e1007541.		0
162	Overlap matrix completion for predicting drug-associated indications. , 2019, 15, e1007541.		0

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163	Overlap matrix completion for predicting drug-associated indications. , 2019, 15, e1007541.		0
164	Overlap matrix completion for predicting drug-associated indications. , 2019, 15, e1007541.		0
165	Secure fine-grained spatio-temporal Top- k queries in TMWSNs. Future Generation Computer Systems, 2018, 86, 174-184.	7.5	7
166	A fine-grained rule partition algorithm in cloud data centers. Journal of Network and Computer Applications, 2018, 113, 14-25.	9.1	5
167	Reducing transport latency for short flows with multipath TCP. Journal of Network and Computer Applications, 2018, 108, 20-36.	9.1	29
168	Resisting re-identification mining on social graph data. World Wide Web, 2018, 21, 1759-1771.	4.0	10
169	CytoCtrlAnalyser: a Cytoscape app for biomolecular network controllability analysis. Bioinformatics, 2018, 34, 1428-1430.	4.1	17
170	On Threshold-Free Error Detection for Industrial Wireless Sensor Networks. IEEE Transactions on Industrial Informatics, 2018, 14, 2199-2209.	11.3	27
171	Computational drug repositioning using low-rank matrix approximation and randomized algorithms. Bioinformatics, 2018, 34, 1904-1912.	4.1	183
172	MMM: classification of schizophrenia using multi-modality multi-atlas feature representation and multi-kernel learning. Multimedia Tools and Applications, 2018, 77, 29651-29667.	3.9	23
173	DyNetViewer: a Cytoscape app for dynamic network construction, analysis and visualization. Bioinformatics, 2018, 34, 1597-1599.	4.1	27
174	Prediction of lncRNA-disease associations based on inductive matrix completion. Bioinformatics, 2018, 34, 3357-3364.	4.1	227
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