

Shuigeng Zhou

List of Publications by Year in descending order

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256
papers

6,224
citations

68787

39
h-index

113702

59
g-index

263
all docs

263
docs citations

263
times ranked

5311
citing authors

#	ARTICLE	IF	CITATIONS
1	Focusing Attention: Towards Accurate Text Recognition in Natural Images. , 2017, , .		328
2	Cassava genome from a wild ancestor to cultivated varieties. Nature Communications, 2014, 5, 5110.	13.2	238
3	Improving compound-protein interaction prediction by building up highly credible negative samples. Bioinformatics, 2015, 31, i221-i229.	4.2	227
4	Single-cell trajectories reconstruction, exploration and mapping of omics data with STREAM. Nature Communications, 2019, 10, 1903.	13.2	215
5	AON: Towards Arbitrarily-Oriented Text Recognition. , 2018, , .		199
6	Boosting compound-protein interaction prediction by deep learning. Methods, 2016, 110, 64-72.	3.9	151
7	Edit Probability for Scene Text Recognition. , 2018, , .		113
8	Exact solution for mean first-passage time on a pseudofractal scale-free web. Physical Review E, 2009, 79, 021127.	2.2	108
9	GString: A Novel Approach for Efficient Search in Graph Databases. , 2007, , .		107
10	TEPITOPEpan: Extending TEPITOPE for Peptide Binding Prediction Covering over 700 HLA-DR Molecules. PLoS ONE, 2012, 7, e30483.	2.4	102
11	Distributed Localization Using a Moving Beacon in Wireless Sensor Networks. IEEE Transactions on Parallel and Distributed Systems, 2008, 19, 587-600.	6.1	98
12	Standard random walks and trapping on the Koch network with scale-free behavior and small-world effect. Physical Review E, 2009, 79, 061113.	2.2	88
13	Approaches for scaling DBSCAN algorithm to large spatial databases. Journal of Computer Science and Technology, 2000, 15, 509-526.	1.5	82
14	Maximal planar scale-free Sierpinski networks with small-world effect and power law strength-degree correlation. Europhysics Letters, 2007, 79, 38007.	2.1	82
15	MiRenSVM: towards better prediction of microRNA precursors using an ensemble SVM classifier with multi-loop features. BMC Bioinformatics, 2010, 11, S11.	2.7	80
16	Robust Median Reversion Strategy for Online Portfolio Selection. IEEE Transactions on Knowledge and Data Engineering, 2016, 28, 2480-2493.	6.2	77
17	Epidemic spreading with nonlinear infectivity in weighted scale-free networks. Physica A: Statistical Mechanics and Its Applications, 2011, 390, 471-481.	2.6	73
18	Prediction of protein-protein interaction sites using an ensemble method. BMC Bioinformatics, 2009, 10, 426.	2.7	69

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19	Determining global mean-first-passage time of random walks on Vicsek fractals using eigenvalues of Laplacian matrices. <i>Physical Review E</i> , 2010, 81, 031118.	2.2	69
20	Recursive mechanism. , 2013, , .		67
21	The exact solution of the mean geodesic distance for Vicsek fractals. <i>Journal of Physics A: Mathematical and Theoretical</i> , 2008, 41, 485102.	2.2	66
22	PredHS: a web server for predicting protein-protein interaction hot spots by using structural neighborhood properties. <i>Nucleic Acids Research</i> , 2014, 42, W290-W295.	14.2	63
23	A general geometric growth model for pseudofractal scale-free web. <i>Physica A: Statistical Mechanics and Its Applications</i> , 2007, 377, 329-339.	2.6	62
24	ANGEL: Enhancing the Utility of Generalization for Privacy Preserving Publication. <i>IEEE Transactions on Knowledge and Data Engineering</i> , 2009, 21, 1073-1087.	6.2	61
25	Enumeration of spanning trees in a pseudofractal scale-free web. <i>Europhysics Letters</i> , 2010, 90, 68002.	2.1	61
26	Evolving Apollonian networks with small-world scale-free topologies. <i>Physical Review E</i> , 2006, 74, 046105.	2.2	58
27	Non-Local ConvLSTM for Video Compression Artifact Reduction. , 2019, , .		57
28	Explicit determination of mean first-passage time for random walks on deterministic uniform recursive trees. <i>Physical Review E</i> , 2010, 81, 016114.	2.2	56
29	Finding MicroRNA Targets in Plants: Current Status and Perspectives. <i>Genomics, Proteomics and Bioinformatics</i> , 2012, 10, 264-275.	7.5	56
30	DPHL: A DIA Pan-Human Protein Mass Spectrometry Library for Robust Biomarker Discovery. <i>Genomics, Proteomics and Bioinformatics</i> , 2020, 18, 104-119.	7.5	55
31	Analytical solution of average path length for Apollonian networks. <i>Physical Review E</i> , 2008, 77, 017102.	2.2	53
32	Random walks on the Apollonian network with a single trap. <i>Europhysics Letters</i> , 2009, 86, 10006.	2.1	52
33	A new hybrid method for learning bayesian networks: Separation and reunion. <i>Knowledge-Based Systems</i> , 2017, 121, 185-197.	7.4	52
34	Towards effective document clustering: A constrained K-means based approach. <i>Information Processing and Management</i> , 2008, 44, 1397-1409.	9.0	51
35	A Novel Image Registration Algorithm for Remote Sensing Under Affine Transformation. <i>IEEE Transactions on Geoscience and Remote Sensing</i> , 2014, 52, 4895-4912.	6.4	50
36	DeepCluster: A General Clustering Framework Based on Deep Learning. <i>Lecture Notes in Computer Science</i> , 2017, , 809-825.	0.2	50

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37	Distributed Skyline Retrieval with Low Bandwidth Consumption. IEEE Transactions on Knowledge and Data Engineering, 2009, 21, 384-400.	6.2	49
38	Fusing multiple protein-protein similarity networks to effectively predict lncRNA-protein interactions. BMC Bioinformatics, 2017, 18, 420.	2.7	49
39	Random Sierpinski network with scale-free small-world and modular structure. European Physical Journal B, 2008, 65, 141-147.	1.6	48
40	A new method for enhancer prediction based on deep belief network. BMC Bioinformatics, 2017, 18, 418.	2.7	47
41	Mapping Koch curves into scale-free small-world networks. Journal of Physics A: Mathematical and Theoretical, 2010, 43, 395101.	2.2	46
42	Boosting Prediction Performance of Protein-Protein Interaction Hot Spots by Using Structural Neighborhood Properties. Journal of Computational Biology, 2013, 20, 878-891.	1.7	42
43	Trapping in scale-free networks with hierarchical organization of modularity. Physical Review E, 2009, 80, 051120.	2.2	41
44	Distinct scalings for mean first-passage time of random walks on scale-free networks with the same degree sequence. Physical Review E, 2009, 80, 061111.	2.2	41
45	Evolving pseudofractal networks. European Physical Journal B, 2007, 58, 337-344.	1.6	40
46	Mean first-passage time for random walks on the T-graph. New Journal of Physics, 2009, 11, 103043.	2.9	39
47	Epidemic spreading in weighted scale-free networks with community structure. Journal of Statistical Mechanics: Theory and Experiment, 2009, 2009, P07043.	2.3	39
48	FraGAT: a fragment-oriented multi-scale graph attention model for molecular property prediction. Bioinformatics, 2021, 37, 2981-2987.	4.2	38
49	Deep structural clustering for single-cell RNA-seq data jointly through autoencoder and graph neural network. Briefings in Bioinformatics, 2022, 23, .	6.6	38
50	An empirical study of Chinese language networks. Physica A: Statistical Mechanics and Its Applications, 2008, 387, 3039-3047.	2.6	36
51	CloudNMF: A MapReduce Implementation of Nonnegative Matrix Factorization for Large-Scale Biological Datasets. Genomics, Proteomics and Bioinformatics, 2014, 12, 48-51.	7.5	36
52	Rumor evolution in social networks. Physical Review E, 2013, 87, .	2.2	35
53	Computationally predicting protein-RNA interactions using only positive and unlabeled examples. Journal of Bioinformatics and Computational Biology, 2015, 13, 1541005.	0.8	35
54	Selecting high-quality negative samples for effectively predicting protein-RNA interactions. BMC Systems Biology, 2017, 11, 9.	2.9	35

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55	Effective drug-target interaction prediction with mutual interaction neural network. <i>Bioinformatics</i> , 2022, 38, 3582-3589.	4.2	35
56	MOBCdb: a comprehensive database integrating multi-omics data on breast cancer for precision medicine. <i>Breast Cancer Research and Treatment</i> , 2018, 169, 625-632.	2.6	34
57	Evolutionary method for finding communities in bipartite networks. <i>Physical Review E</i> , 2011, 83, 066120.	2.2	31
58	Accurate Few-shot Object Detection with Support-Query Mutual Guidance and Hybrid Loss. , 2021, , .		31
59	Anomalous behavior of trapping on a fractal scale-free network. <i>Europhysics Letters</i> , 2009, 88, 10001.	2.1	30
60	Detecting potential collusive cliques in futures markets based on trading behaviors from real data. <i>Neurocomputing</i> , 2012, 92, 44-53.	6.2	30
61	Deterministic identification of specific individuals from GWAS results. <i>Bioinformatics</i> , 2015, 31, 1701-1707.	4.2	30
62	Predicting Enhancers from Multiple Cell Lines and Tissues across Different Developmental Stages Based On SVM Method. <i>Current Bioinformatics</i> , 2018, 13, 655-660.	1.5	30
63	Efficient top-k processing in large-scaled distributed environments. <i>Data and Knowledge Engineering</i> , 2007, 63, 315-335.	3.7	29
64	Incompatibility networks as models of scale-free small-world graphs. <i>European Physical Journal B</i> , 2007, 60, 259-264.	1.6	29
65	LIGHT: A Query-Efficient Yet Low-Maintenance Indexing Scheme over DHTs. <i>IEEE Transactions on Knowledge and Data Engineering</i> , 2010, 22, 59-75.	6.2	29
66	miRFam: an effective automatic miRNA classification method based on n-grams and a multiclass SVM. <i>BMC Bioinformatics</i> , 2011, 12, 216.	2.7	29
67	A RAMCloud Storage System based on HDFS: Architecture, implementation and evaluation. <i>Journal of Systems and Software</i> , 2013, 86, 744-750.	4.8	29
68	D2CL: A Dense Dilated Convolutional LSTM Model for Sea Surface Temperature Prediction. <i>IEEE Journal of Selected Topics in Applied Earth Observations and Remote Sensing</i> , 2021, 14, 12514-12523.	4.9	28
69	Topologies and Laplacian spectra of a deterministic uniform recursive tree. <i>European Physical Journal B</i> , 2008, 63, 507-513.	1.6	27
70	A unified model for Sierpinski networks with scale-free scaling and small-world effect. <i>Physica A: Statistical Mechanics and Its Applications</i> , 2009, 388, 2571-2578.	2.6	27
71	PRAGUE: Towards Blending Practical Visual Subgraph Query Formulation and Query Processing. , 2012, , .		27
72	Genome-wide search for miRNA-target interactions in <i>Arabidopsis thaliana</i> with an integrated approach. <i>BMC Genomics</i> , 2012, 13, S3.	2.9	27

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73	Local-world evolving networks with tunable clustering. <i>Physica A: Statistical Mechanics and Its Applications</i> , 2007, 380, 639-650.	2.6	26
74	Fractal scale-free networks resistant to disease spread. <i>Journal of Statistical Mechanics: Theory and Experiment</i> , 2008, 2008, P09008.	2.3	26
75	Correlations in random Apollonian network. <i>Physica A: Statistical Mechanics and Its Applications</i> , 2007, 380, 621-628.	2.6	25
76	Average distance in a hierarchical scale-free network: an exact solution. <i>Journal of Statistical Mechanics: Theory and Experiment</i> , 2009, 2009, P10022.	2.3	25
77	A New Unsupervised Binning Approach for Metagenomic Sequences Based on N-grams and Automatic Feature Weighting. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2014, 11, 42-54.	3.2	25
78	A General Framework for Unmet Demand Prediction in On-Demand Transport Services. <i>IEEE Transactions on Intelligent Transportation Systems</i> , 2019, 20, 2820-2830.	8.4	25
79	Achieving optimal data storage position in wireless sensor networks. <i>Computer Communications</i> , 2010, 33, 92-102.	5.5	24
80	A comparative evaluation on prediction methods of nucleosome positioning. <i>Briefings in Bioinformatics</i> , 2014, 15, 1014-1027.	6.6	24
81	HNet-DNN: Inferring New Drug-Disease Associations with Deep Neural Network Based on Heterogeneous Network Features. <i>Journal of Chemical Information and Modeling</i> , 2020, 60, 2367-2376.	5.7	24
82	Different thresholds of bond percolation in scale-free networks with identical degree sequence. <i>Physical Review E</i> , 2009, 79, 031110.	2.2	23
83	TOP: A deep mixture representation learning method for boosting molecular toxicity prediction. <i>Methods</i> , 2020, 179, 55-64.	3.9	23
84	Recursive solutions for Laplacian spectra and eigenvectors of a class of growing treelike networks. <i>Physical Review E</i> , 2009, 80, 016104.	2.2	22
85	A new and effective hierarchical overlay structure for Peer-to-Peer networks. <i>Computer Communications</i> , 2011, 34, 862-874.	5.5	22
86	Recursive weighted treelike networks. <i>European Physical Journal B</i> , 2007, 59, 99-107.	1.6	21
87	Transition from fractal to non-fractal scalings in growing scale-free networks. <i>European Physical Journal B</i> , 2008, 64, 277-283.	1.6	21
88	QUBLE: towards blending interactive visual subgraph search queries on large networks. <i>VLDB Journal</i> , 2014, 23, 401-426.	4.2	21
89	Effectively Identifying Compound-Protein Interactions by Learning from Positive and Unlabeled Examples. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2018, 15, 1832-1843.	3.2	21
90	A geometric growth model interpolating between regular and small-world networks. <i>Journal of Physics A: Mathematical and Theoretical</i> , 2007, 40, 11863-11876.	2.2	20

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91	Effects of accelerating growth on the evolution of weighted complex networks. <i>Physica A: Statistical Mechanics and Its Applications</i> , 2009, 388, 225-232.	2.6	20
92	The prisoner's dilemma in structured scale-free networks. <i>Journal of Physics A: Mathematical and Theoretical</i> , 2009, 42, 245002.	2.2	19
93	Active learning for protein function prediction in protein-protein interaction networks. <i>Neurocomputing</i> , 2014, 145, 44-52.	6.2	19
94	An effective approach to detecting both small and large complexes from protein-protein interaction networks. <i>BMC Bioinformatics</i> , 2017, 18, 419.	2.7	19
95	You Only Recognize Once. , 2019, , .		19
96	A Chaotic Ant Colony Optimized Link Prediction Algorithm. <i>IEEE Transactions on Systems, Man, and Cybernetics: Systems</i> , 2021, 51, 5274-5288.	9.7	19
97	Scalable continual top-k keyword search in relational databases. <i>Data and Knowledge Engineering</i> , 2013, 86, 206-223.	3.7	18
98	Computationally identifying hot spots in protein-DNA binding interfaces using an ensemble approach. <i>BMC Bioinformatics</i> , 2020, 21, 384.	2.7	18
99	Influences of degree inhomogeneity on average path length and random walks in disassortative scale-free networks. <i>Journal of Mathematical Physics</i> , 2009, 50, 033514.	1.2	17
100	DISKs. <i>Proceedings of the VLDB Endowment</i> , 2012, 5, 1966-1969.	3.9	17
101	Knowledge diffusion in complex networks. <i>Concurrency Computation Practice and Experience</i> , 2017, 29, e3791.	2.2	17
102	FREE: A Fast and Robust End-to-End Video Text Spotter. <i>IEEE Transactions on Image Processing</i> , 2021, 30, 822-837.	10.2	17
103	Privacy and efficiency guaranteed social subgraph matching. <i>VLDB Journal</i> , 2022, 31, 581-602.	4.2	17
104	A path-traceable query routing mechanism for search in unstructured peer-to-peer networks. <i>Journal of Network and Computer Applications</i> , 2010, 33, 115-127.	9.7	16
105	Deterministic weighted scale-free small-world networks. <i>Physica A: Statistical Mechanics and Its Applications</i> , 2010, 389, 3316-3324.	2.6	16
106	Characteristics of real futures trading networks. <i>Physica A: Statistical Mechanics and Its Applications</i> , 2011, 390, 398-409.	2.6	16
107	Single-cell RNA-seq data clustering: A survey with performance comparison study. <i>Journal of Bioinformatics and Computational Biology</i> , 2020, 18, 2040005.	0.8	16
108	From regular to growing small-world networks. <i>Physica A: Statistical Mechanics and Its Applications</i> , 2007, 385, 765-772.	2.6	15

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109	Private search on key-value stores with hierarchical indexes. , 2014, , .		15
110	Choosing appropriate models for proteinâ€“protein interaction networks: a comparison study. Briefings in Bioinformatics, 2014, 15, 823-838.	6.6	15
111	CPredictor3.0: detecting protein complexes from PPI networks with expression data and functional annotations. BMC Systems Biology, 2017, 11, 135.	2.9	15
112	Group-sparse Modeling Drug-kinase Networks for Predicting Combinatorial Drug Sensitivity in Cancer Cells. Current Bioinformatics, 2018, 13, 437-443.	1.5	15
113	Compensatory ability to null mutation in metabolic networks. Biotechnology and Bioengineering, 2009, 103, 361-369.	3.5	14
114	Traffic Fluctuations on Weighted Networks. IEEE Circuits and Systems Magazine, 2012, 12, 33-44.	2.6	14
115	Square++: Making a connection game win-lose complementary and playing-fair. Entertainment Computing, 2013, 4, 105-113.	3.1	14
116	A Unified Framework for Predicting KPIs of On-Demand Transport Services. IEEE Access, 2018, 6, 32005-32014.	4.4	14
117	Recent Few-shot Object Detection Algorithms: A Survey with Performance Comparison. ACM Transactions on Intelligent Systems and Technology, 2023, 14, 1-36.	4.7	14
118	WHEN CLOUD COMPUTING MEETS BIOINFORMATICS: A REVIEW. Journal of Bioinformatics and Computational Biology, 2013, 11, 1330002.	0.8	13
119	Histone modifications involved in cassette exon inclusions: a quantitative and interpretable analysis. BMC Genomics, 2014, 15, 1148.	2.9	13
120	NEpiC: a network-assisted algorithm for epigenetic studies using mean and variance combined signals. Nucleic Acids Research, 2016, 44, e134-e134.	14.2	13
121	Classifying early and late mild cognitive impairment stages of Alzheimerâ€™s disease by fusing default mode networks extracted with multiple seeds. BMC Bioinformatics, 2018, 19, 523.	2.7	13
122	Learning Competitive and Discriminative Reconstructions for Anomaly Detection. Proceedings of the AAAI Conference on Artificial Intelligence, 2019, 33, 5167-5174.	5.1	13
123	DEEPPEN: a convolutional neural network based method for super-enhancer prediction. BMC Bioinformatics, 2019, 20, 598.	2.7	13
124	BatchServer: A Web Server for Batch Effect Evaluation, Visualization, and Correction. Journal of Proteome Research, 2021, 20, 1079-1086.	3.8	13
125	Fast text classification: a training-corpus pruning based approach. , 2003, , .		12
126	LHT: A Low-Maintenance Indexing Scheme over DHTs. , 2008, , .		12

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127	Prediction of protein protein interactions from primary sequences. International Journal of Data Mining and Bioinformatics, 2010, 4, 211.	0.2	12
128	Diffusionâ€“annihilation processes in weighted scale-free networks with an identical degree sequence. Journal of Statistical Mechanics: Theory and Experiment, 2011, 2011, P10001.	2.3	12
129	Knowledge-guided fuzzy logic modeling to infer cellular signaling networks from proteomic data. Scientific Reports, 2016, 6, 35652.	3.5	12
130	Efficient Retrieval of Bounded-Cost Informative Routes. IEEE Transactions on Knowledge and Data Engineering, 2017, 29, 2182-2196.	6.2	12
131	Boosting the Performance of Video Compression Artifact Reduction with Reference Frame Proposals and Frequency Domain Information. , 2021, , .		12
132	Contact graphs of disk packings as a model of spatial planar networks. New Journal of Physics, 2009, 11, 083007.	2.9	11
133	The centrality of cancer proteins in human protein-protein interaction network: a revisit. International Journal of Computational Biology and Drug Design, 2014, 7, 146.	0.3	11
134	BOOMER. , 2018, , .		11
135	Gaming Temporal Networks. IEEE Transactions on Circuits and Systems II: Express Briefs, 2019, 66, 672-676.	3.2	11
136	MIMO: A Unified Spatio-Temporal Model for Multi-Scale Sea Surface Temperature Prediction. Remote Sensing, 2022, 14, 2371.	4.1	11
137	Group properties of generalized quasi-linear wave equations. Journal of Mathematical Analysis and Applications, 2010, 366, 460-472.	1.1	10
138	Rainbow-Seq: Combining Cell Lineage Tracing with Single-Cell RNA Sequencing in Preimplantation Embryos. IScience, 2018, 7, 16-29.	4.1	10
139	Accurately Detecting Protein Complexes by Graph Embedding and Combining Functions with Interactions. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2020, 17, 777-787.	3.2	10
140	Enabling GIS services in a P2P environment. , 0, , .		9
141	A Lightweight Multidimensional Index for Complex Queries over DHTs. IEEE Transactions on Parallel and Distributed Systems, 2011, 22, 2046-2054.	6.1	9
142	Group-Theoretical Analysis of Variable Coefficient Nonlinear Telegraph Equations. Acta Applicandae Mathematicae, 2012, 117, 135-183.	1.1	9
143	QUBLE. , 2013, , .		9
144	Learning Causal Structures Based on Divide and Conquer. IEEE Transactions on Cybernetics, 2022, 52, 3232-3243.	10.1	9

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145	Link Weight Prediction Using Weight Perturbation and Latent Factor. IEEE Transactions on Cybernetics, 2022, 52, 1785-1797.	10.1	9
146	SIPPER: Selecting Informative Peers in Structured P2P Environment for Content-Based Retrieval. , 2006, , .		8
147	The rigorous solution for the average distance of a Sierpinski network. Journal of Statistical Mechanics: Theory and Experiment, 2009, 2009, P02034.	2.3	8
148	LAYER: A cost-efficient mechanism to support multi-tenant database as a service in cloud. Journal of Systems and Software, 2015, 101, 86-96.	4.8	8
149	TOP: Towards Better Toxicity Prediction by Deep Molecular Representation Learning. , 2019, , .		8
150	Effective and scalable causal partitioning based on low-order conditional independent tests. Neurocomputing, 2020, 389, 146-154.	6.2	8
151	GPress: Towards Effective GML Documents Compression. , 2007, , .		7
152	Structural and spectral properties of a family of deterministic recursive trees: rigorous solutions. Journal of Physics A: Mathematical and Theoretical, 2009, 42, 165103.	2.2	7
153	Symbolic analysis and exact travelling wave solutions to a new modified Novikov equation. Applied Mathematics and Computation, 2010, 217, 590-598.	2.3	7
154	Efficient Skyline Retrieval on Peer-to-Peer Networks. , 2007, , .		6
155	Vertex labeling and routing in expanded Apollonian networks. Journal of Physics A: Mathematical and Theoretical, 2008, 41, 035004.	2.2	6
156	Detecting microarray data supported microRNA-mRNA interactions. International Journal of Data Mining and Bioinformatics, 2010, 4, 639.	0.2	6
157	Mechanisms of Analgesic Action of Gln49-PLA2 from Gloydius ussurensis Snake Venom. Applied Biochemistry and Biotechnology, 2010, 160, 773-779.	3.0	6
158	iHMS: a database integrating human histone modification data across developmental stages and tissues. BMC Bioinformatics, 2017, 18, 103.	2.7	6
159	Efficient Bottom-Up Discovery of Multi-scale Time Series Correlations Using Mutual Information. , 2019, , .		6
160	Recursively Learning Causal Structures Using Regression-Based Conditional Independence Test. Proceedings of the AAAI Conference on Artificial Intelligence, 2019, 33, 3108-3115.	5.1	6
161	FERRARI: an efficient framework for visual exploratory subgraph search in graph databases. VLDB Journal, 2020, 29, 973-998.	4.2	6
162	TiC2D: Trajectory Inference From Single-Cell RNA-Seq Data Using Consensus Clustering. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2022, 19, 2512-2522.	3.2	6

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163	Degree and component size distributions in the generalized uniform recursive tree. <i>Journal of Physics A: Mathematical and Theoretical</i> , 2008, 41, 185101.	2.2	5
164	LESSON: A system for lecture notes searching and sharing over Internet. <i>Journal of Systems and Software</i> , 2010, 83, 1851-1863.	4.8	5
165	Different behaviors of epidemic spreading in scale-free networks with identical degree sequence. <i>Journal of Physics A: Mathematical and Theoretical</i> , 2010, 43, 065001.	2.2	5
166	Automatically clustering large-scale miRNA sequences: methods and experiments. <i>BMC Genomics</i> , 2012, 13, S15.	2.9	5
167	RMDB: An Integrated Database of Single-cytosine-resolution DNA Methylation in <i>Oryza Sativa</i> . <i>Current Bioinformatics</i> , 2019, 14, 524-531.	1.5	5
168	Molecular property prediction by contrastive learning with attention-guided positive sample selection. <i>Bioinformatics</i> , 2023, 39, .	4.2	5
169	An analytic derivation of clustering coefficients for weighted networks. <i>Journal of Statistical Mechanics: Theory and Experiment</i> , 2010, 2010, P03013.	2.3	4
170	A machine learning-based method for protein global model quality assessment. <i>International Journal of General Systems</i> , 2011, 40, 417-425.	2.6	4
171	Probabilistic Time-Constrained Paths Search over Uncertain Road Networks. <i>IEEE Transactions on Services Computing</i> , 2018, 11, 399-414.	5.0	4
172	Measuring Conditional Independence by Independent Residuals for Causal Discovery. <i>ACM Transactions on Intelligent Systems and Technology</i> , 2019, 10, 1-19.	4.7	4
173	Genome-wide analysis of epigenetic dynamics across human developmental stages and tissues. <i>BMC Genomics</i> , 2019, 20, 221.	2.9	4
174	Combined cause inference: Definition, model and performance. <i>Information Sciences</i> , 2021, 574, 431-443.	7.2	4
175	Learning Latent Semantic Attributes for Zero-Shot Object Detection. , 2020, , .		4
176	Identifying essential proteins from protein-protein interaction networks based on influence maximization. <i>BMC Bioinformatics</i> , 2022, 23, .	2.7	4
177	Data management in Peer-to-Peer environment: A perspective of BestPeer. <i>Journal of Computer Science and Technology</i> , 2003, 18, 452-461.	1.5	3
178	Supporting Ranked Join in Peer-to-Peer Networks. , 0, , .		3
179	Gene Ontology-Based Protein Function Prediction by Using Sequence Composition Information. <i>Protein and Peptide Letters</i> , 2010, 17, 789-795.	0.9	3
180	imiRTP: An Integrated Method to Identifying miRNA-target Interactions in <i>Arabidopsis thaliana</i> . , 2011, , .		3

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181	An improved genetic algorithm for statistical potential function design and protein structure prediction. <i>International Journal of Data Mining and Bioinformatics</i> , 2012, 6, 162.	0.2	3
182	MeioBase: a comprehensive database for meiosis. <i>Frontiers in Plant Science</i> , 2014, 5, 728.	3.8	3
183	Revisiting topological properties and models of protein-protein interaction networks from the perspective of dataset evolution. <i>IET Systems Biology</i> , 2015, 9, 113-119.	1.6	3
184	Unfavorable Individuals in Social Gaming Networks. <i>Scientific Reports</i> , 2015, 5, 17481.	3.5	3
185	Identifying TF-MiRNA Regulatory Relationships Using Multiple Features. <i>PLoS ONE</i> , 2015, 10, e0125156.	2.4	3
186	Boosting compound-protein interaction prediction by deep learning. , 2015, , .		3
187	JeCache: Just-Enough Data Caching with Just-in-Time Prefetching for Big Data Applications. , 2017, , .		3
188	Towards efficiently supporting database as a service with QoS guarantees. <i>Journal of Systems and Software</i> , 2018, 139, 51-63.	4.8	3
189	Fusion analysis of resting-state networks and its application to Alzheimer's disease. <i>Tsinghua Science and Technology</i> , 2019, 24, 456-467.	6.5	3
190	Network as Regularization for Training Deep Neural Networks: Framework, Model and Performance. <i>Proceedings of the AAAI Conference on Artificial Intelligence</i> , 2020, 34, 6013-6020.	5.1	3
191	Causal Gene Identification Using Non-linear Regression-based Independence Tests. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2022, PP, 1-1.	3.2	3
192	PCGAN: a generative approach for protein complex identification from protein interaction networks. <i>Bioinformatics</i> , 2023, 39, .	4.2	3
193	Incremental mining of the schema of semistructured data. <i>Journal of Computer Science and Technology</i> , 2000, 15, 241-248.	1.5	2
194	Mobile agent-based distributed geographic information systems under Internet environment. , 0, , .		2
195	Hierarchically distributed data warehouse. , 2000, , .		2
196	Effective clustering of microRNA sequences by N-grams and feature weighting. , 2012, , .		2
197	A new algorithm for automatic computation of solitary wave solutions to nonlinear partial differential equations based on the Exp-function method. <i>Applied Mathematics and Computation</i> , 2012, 219, 1890-1896.	2.3	2
198	Group properties and invariant solutions of a sixth-order thin film equation in viscous fluid. <i>Journal of Mathematical Physics</i> , 2013, 54, 013510.	1.2	2

#	ARTICLE	IF	CITATIONS
199	Mean first passage time for random walk on dual structure of dendrimer. <i>Physica A: Statistical Mechanics and Its Applications</i> , 2014, 415, 463-472.	2.6	2
200	Data mining in systems biology. <i>Neurocomputing</i> , 2016, 206, 1-2.	6.2	2
201	An Indexing Framework for Efficient Visual Exploratory Subgraph Search in Graph Databases. , 2019, , .		2
202	Statistical learning with group invariance: problem, method and consistency. <i>International Journal of Machine Learning and Cybernetics</i> , 2019, 10, 1503-1511.	3.7	2
203	A general framework for privacy-preserving of data publication based on randomized response techniques. <i>Information Systems</i> , 2021, 96, 101648.	3.9	2
204	Boosting scRNA-seq data clustering by cluster-aware feature weighting. <i>BMC Bioinformatics</i> , 2021, 22, 130.	2.7	2
205	Effectively Clustering Single Cell RNA Sequencing Data by Sparse Representation. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2021, PP, 1-1.	3.2	2
206	Robustly Recognizing Irregular Scene Text by Rectifying Principle Irregularities. , 2022, , .		2
207	Towards Cross-Lingual Multi-Modal Misinformation Detection for E-Commerce Management. <i>IEEE Transactions on Network and Service Management</i> , 2023, 20, 1040-1050.	5.4	2
208	HiGRN: A Hierarchical Graph Recurrent Network for Global Sea Surface Temperature Prediction. <i>ACM Transactions on Intelligent Systems and Technology</i> , 2023, 14, 1-19.	4.7	2
209	Molecular property prediction by semantic-invariant contrastive learning. <i>Bioinformatics</i> , 2023, 39, .	4.2	2
210	Generalized multidimensional association rules. <i>Journal of Computer Science and Technology</i> , 2000, 15, 388-392.	1.5	1
211	Distributed geo-referenced information accessing and integrating based on mobile agents and GML. , 0, , .		1
212	A new full-text indexing model with low space overhead for chinese text retrieval. <i>International Journal on Digital Libraries</i> , 2004, 4, 272-282.	1.6	1
213	Inferring Minimal Feasible Metabolic Networks of <i>Escherichia coli</i> . <i>Applied Biochemistry and Biotechnology</i> , 2010, 160, 222-231.	3.0	1
214	Effectively predicting protein functions by collective classification — An extended abstract. , 2012, , .		1
215	A comparison study on protein-protein interaction network models. , 2012, , .		1
216	Enhancing Routing Robustness of Unstructured Peer-to-Peer Networks Using Mobile Agents. <i>Journal of Network and Systems Management</i> , 2012, 20, 309-352.	5.3	1

#	ARTICLE	IF	CITATIONS
217	Network Parameter Generation for One-Shot Object Detection. , 2019, , .		1
218	The Complexities of Random-Turn Hex, Square, and Triangle Games. IEEE Transactions on Games, 2022, 14, 180-190.	1.7	1
219	Text Recognition in Real Scenarios with a Few Labeled Samples. , 2021, , .		1
220	Universal consistency of twin support vector machines. International Journal of Machine Learning and Cybernetics, 2021, 12, 1867-1877.	3.7	1
221	ICDAR 2021 Competition on Scene Video Text Spotting. Lecture Notes in Computer Science, 2021, , 650-662.	0.2	1
222	CPredictor 4.0: effectively detecting protein complexes in weighted dynamic PPI networks. International Journal of Data Mining and Bioinformatics, 2018, 20, 303.	0.2	1
223	Multi-Modal Learning with Text Merging for TEXTVQA. , 2022, , .		1
224	Keyword-Based Diverse Image Retrieval by Semantics-aware Contrastive Learning and Transformer. , 2023, , .		1
225	Zero-Shot Object Detection by Semantics-Aware DETR with Adaptive Contrastive Loss. , 2023, , .		1
226	STIRER: A Unified Model for Low-Resolution Scene Text Image Recovery and Recognition. , 2023, , .		1
227	Molecular property prediction based on graph structure learning. Bioinformatics, 2024, 40, .	4.2	1
228	STRUCTBASE: a structure based chinese text database system. , 0, , .		0
229	Complex networks and computing. Frontiers of Computer Science, 2009, 3, 322-323.	0.8	0
230	Towards Keyword Search over Relational Databases in DHT Networks. , 2009, , .		0
231	Protein Backbone Dihedral Angle Prediction Based on Probabilistic Models. International Conference on Bioinformatics and Biomedical Engineering: [proceedings] International Conference on Bioinformatics and Biomedical Engineering, 2010, , .	0.0	0
232	Building Resilient Unstructured Peer-to-Peer Networks Using Mobile Agents. , 2010, , .		0
233	Revisiting topological properties of protein-protein interaction networks from the perspective of dataset evolution. , 2014, , .		0
234	Instance-level worst-case query bounds on R-trees. VLDB Journal, 2014, 23, 591-607.	4.2	0

#	ARTICLE	IF	CITATIONS
235	Knowledge Diffusion in Complex Networks. , 2015, , .		0
236	Introduction to the special issue on GIW 2016. Journal of Bioinformatics and Computational Biology, 2016, 14, 1602004.	0.8	0
237	An integrative analysis of nucleosome occupancy and positioning using diverse sequence dependent properties. Neurocomputing, 2016, 206, 35-41.	6.2	0
238	Histone modification patterns in highly differentiation cells. Neurocomputing, 2016, 206, 42-49.	6.2	0
239	Divide-and-conquer Tournament on Social Networks. Scientific Reports, 2017, 7, 15484.	3.5	0
240	Semi-Group Range Sum Revisited: Query-Space Lower Bound Tightened. Algorithmica, 2018, 80, 1315-1329.	1.3	0
241	Efficient Retrieval of Bounded-Cost Informative Routes. , 2018, , .		0
242	ROAM: A Fundamental Routing Query on Road Networks with Efficiency. IEEE Transactions on Knowledge and Data Engineering, 2020, 32, 1595-1609.	6.2	0
243	Recognizing Multiple Text Sequences from an Image by Pure End-to-End Learning. , 2021, , .		0
244	EarnCache: Self-adaptive Incremental Caching for Big Data Applications. Lecture Notes in Computer Science, 2018, , 379-393.	0.2	0
245	Interactive map matching and its visualisation: techniques and system. International Journal of Embedded Systems, 2019, 11, 340.	0.3	0
246	Conditional Independence Test Based on Residual Similarity. ACM Transactions on Knowledge Discovery From Data, 2023, 17, 1-18.	3.7	0
247	HPC-Atlas: Computationally Constructing a Comprehensive Atlas of Human Protein Complexes. Genomics, Proteomics and Bioinformatics, 2023, 21, 976-990.	7.5	0
248	Incremental Maximal Clique Enumeration for Hybrid Edge Changes in Large Dynamic Graphs. IEEE Transactions on Knowledge and Data Engineering, 2024, 36, 1650-1666.	6.2	0
249	Incremental Graph Classification by Class Prototype Construction and Augmentation. , 2023, , .		0
250	A new and effective two-step clustering approach for single cell RNA sequencing data. BMC Genomics, 2022, 23, .	2.9	0
251	IDDR-NGP:Incorporating Detectors for Distractors Removal with Instant Neural Radiance Field. , 2023, , .		0
252	Weakly Correlated Multimodal Sentiment Analysis: New Dataset and Topic-Oriented Model. IEEE Transactions on Affective Computing, 2024, , 1-13.	8.9	0

#	ARTICLE	IF	CITATIONS
253	Variate Associated Domain Adaptation for Unsupervised Multivariate Time Series Anomaly Detection. ACM Transactions on Knowledge Discovery From Data, 0, , .	3.7	0
254	Comment on "Critical points of Potts and O(N) models from eigenvalue identities in periodic Temperley-Lieb algebras". Journal of Physics A: Mathematical and Theoretical, 2024, 57, 258001.	2.2	0
255	Hybrid Causal Feature Selection for Cancer Biomarker Identification from RNA-seq Data. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2024, , 1-19.	3.2	0
256	Self-Supervised Spatio-Temporal Imputation Model for Highly Sparse Chl-a Data via Fusing Multi-source Satellite Data. IEEE Transactions on Geoscience and Remote Sensing, 2024, , 1-1.	6.4	0