

Jihong Guan

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

155
papers

2,464
citations

28
h-index

43
g-index

183
ext. papers

3,056
ext. citations

3.6
avg, IF

5.21
L-index

#	Paper	IF	Citations
155	Improving compound-protein interaction prediction by building up highly credible negative samples. <i>Bioinformatics</i> , 2015 , 31, i221-9	7.2	109
154	Exact solution for mean first-passage time on a pseudofractal scale-free web. <i>Physical Review E</i> , 2009 , 79, 021127	2.4	103
153	Boosting compound-protein interaction prediction by deep learning. <i>Methods</i> , 2016 , 110, 64-72	4.6	102
152	Single-cell trajectories reconstruction, exploration and mapping of omics data with STREAM. <i>Nature Communications</i> , 2019 , 10, 1903	17.4	97
151	Standard random walks and trapping on the Koch network with scale-free behavior and small-world effect. <i>Physical Review E</i> , 2009 , 79, 061113	2.4	78
150	Epidemic spreading with nonlinear infectivity in weighted scale-free networks. <i>Physica A: Statistical Mechanics and Its Applications</i> , 2011 , 390, 471-481	3.3	63
149	Maximal planar scale-free Sierpinski networks with small-world effect and power law strength-degree correlation. <i>Europhysics Letters</i> , 2007 , 79, 38007	1.6	63
148	MiRenSVM: towards better prediction of microRNA precursors using an ensemble SVM classifier with multi-loop features. <i>BMC Bioinformatics</i> , 2010 , 11 Suppl 11, S11	3.6	62
147	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	2.4	57
146	Random walks on the Apollonian network with a single trap. <i>Europhysics Letters</i> , 2009 , 86, 10006	1.6	49
145	PredHS: a web server for predicting protein-protein interaction hot spots by using structural neighborhood properties. <i>Nucleic Acids Research</i> , 2014 , 42, W290-5	20.1	48
144	Inferring new indications for approved drugs via random walk on drug-disease heterogeneous networks. <i>BMC Bioinformatics</i> , 2016 , 17, 539	3.6	45
143	Explicit determination of mean first-passage time for random walks on deterministic uniform recursive trees. <i>Physical Review E</i> , 2010 , 81, 016114	2.4	43
142	The exact solution of the mean geodesic distance for Vicsek fractals. <i>Journal of Physics A: Mathematical and Theoretical</i> , 2008 , 41, 485102	2	42
141	Finding microRNA targets in plants: current status and perspectives. <i>Genomics, Proteomics and Bioinformatics</i> , 2012 , 10, 264-75	6.5	39
140	Trapping in scale-free networks with hierarchical organization of modularity. <i>Physical Review E</i> , 2009 , 80, 051120	2.4	39
139	Towards effective document clustering: A constrained K-means based approach. <i>Information Processing and Management</i> , 2008 , 44, 1397-1409	6.3	39

138	A Novel Image Registration Algorithm for Remote Sensing Under Affine Transformation. <i>IEEE Transactions on Geoscience and Remote Sensing</i> , 2014 , 52, 4895-4912	8.1	38
137	Mapping Koch curves into scale-free small-world networks. <i>Journal of Physics A: Mathematical and Theoretical</i> , 2010 , 43, 395101	2	38
136	Mean first-passage time for random walks on the T-graph. <i>New Journal of Physics</i> , 2009 , 11, 103043	2.9	34
135	A new method for enhancer prediction based on deep belief network. <i>BMC Bioinformatics</i> , 2017 , 18, 418	3.6	32
134	A new hybrid method for learning bayesian networks: Separation and reunion. <i>Knowledge-Based Systems</i> , 2017 , 121, 185-197	7.3	31
133	CloudNMF: a MapReduce implementation of nonnegative matrix factorization for large-scale biological datasets. <i>Genomics, Proteomics and Bioinformatics</i> , 2014 , 12, 48-51	6.5	30
132	Epidemic spreading in weighted scale-free networks with community structure. <i>Journal of Statistical Mechanics: Theory and Experiment</i> , 2009 , 2009, P07043	1.9	30
131	Random Sierpinski network with scale-free small-world and modular structure. <i>European Physical Journal B</i> , 2008 , 65, 141-147	1.2	30
130	Fusing multiple protein-protein similarity networks to effectively predict lncRNA-protein interactions. <i>BMC Bioinformatics</i> , 2017 , 18, 420	3.6	29
129	Boosting prediction performance of protein-protein interaction hot spots by using structural neighborhood properties. <i>Journal of Computational Biology</i> , 2013 , 20, 878-91	1.7	29
128	Anomalous behavior of trapping on a fractal scale-free network. <i>Europhysics Letters</i> , 2009 , 88, 10001	1.6	29
127	Evolutionary method for finding communities in bipartite networks. <i>Physical Review E</i> , 2011 , 83, 066120	2.4	28
126	An empirical study of Chinese language networks. <i>Physica A: Statistical Mechanics and Its Applications</i> , 2008 , 387, 3039-3047	3.3	27
125	Rumor evolution in social networks. <i>Physical Review E</i> , 2013 , 87,	2.4	26
124	Incompatibility networks as models of scale-free small-world graphs. <i>European Physical Journal B</i> , 2007 , 60, 259-264	1.2	26
123	miRFam: an effective automatic miRNA classification method based on n-grams and a multiclass SVM. <i>BMC Bioinformatics</i> , 2011 , 12, 216	3.6	25
122	Mining frequent closed itemsets from a landmark window over online data streams. <i>Computers and Mathematics With Applications</i> , 2009 , 57, 927-936	2.7	25
121	Genome-wide search for miRNA-target interactions in Arabidopsis thaliana with an integrated approach. <i>BMC Genomics</i> , 2012 , 13 Suppl 3, S3	4.5	23

120	Local-world evolving networks with tunable clustering. <i>Physica A: Statistical Mechanics and Its Applications</i> , 2007 , 380, 639-650	3.3	23
119	Computationally predicting protein-RNA interactions using only positive and unlabeled examples. <i>Journal of Bioinformatics and Computational Biology</i> , 2015 , 13, 1541005	1	22
118	Topologies and Laplacian spectra of a deterministic uniform recursive tree. <i>European Physical Journal B</i> , 2008 , 63, 507-513	1.2	22
117	Predicting Enhancers from Multiple Cell Lines and Tissues across Different Developmental Stages Based On SVM Method. <i>Current Bioinformatics</i> , 2018 , 13, 655-660	4.7	21
116	Recursive solutions for Laplacian spectra and eigenvectors of a class of growing treelike networks. <i>Physical Review E</i> , 2009 , 80, 016104	2.4	20
115	Average distance in a hierarchical scale-free network: an exact solution. <i>Journal of Statistical Mechanics: Theory and Experiment</i> , 2009 , 2009, P10022	1.9	20
114	Recursive weighted treelike networks. <i>European Physical Journal B</i> , 2007 , 59, 99-107	1.2	20
113	A comparative evaluation on prediction methods of nucleosome positioning. <i>Briefings in Bioinformatics</i> , 2014 , 15, 1014-27	13.4	19
112	Detecting potential collusive cliques in futures markets based on trading behaviors from real data. <i>Neurocomputing</i> , 2012 , 92, 44-53	5.4	19
111	A RAMCloud Storage System based on HDFS: Architecture, implementation and evaluation. <i>Journal of Systems and Software</i> , 2013 , 86, 744-750	3.3	19
110	Different thresholds of bond percolation in scale-free networks with identical degree sequence. <i>Physical Review E</i> , 2009 , 79, 031110	2.4	19
109	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	3.3	19
108	Selecting high-quality negative samples for effectively predicting protein-RNA interactions. <i>BMC Systems Biology</i> , 2017 , 11, 9	3.5	18
107	Transition from fractal to non-fractal scalings in growing scale-free networks. <i>European Physical Journal B</i> , 2008 , 64, 277-283	1.2	18
106	Identification of cancer subtypes from single-cell RNA-seq data using a consensus clustering method. <i>BMC Medical Genomics</i> , 2018 , 11, 117	3.7	18
105	Effects of accelerating growth on the evolution of weighted complex networks. <i>Physica A: Statistical Mechanics and Its Applications</i> , 2009 , 388, 225-232	3.3	17
104	A new and effective hierarchical overlay structure for Peer-to-Peer networks. <i>Computer Communications</i> , 2011 , 34, 862-874	5.1	17
103	Active learning for protein function prediction in protein-protein interaction networks. <i>Neurocomputing</i> , 2014 , 145, 44-52	5.4	16

102	Characteristics of real futures trading networks. <i>Physica A: Statistical Mechanics and Its Applications</i> , 2011 , 390, 398-409	3.3	16
101	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	16
100	GITAR: An Open Source Tool for Analysis and Visualization of Hi-C Data. <i>Genomics, Proteomics and Bioinformatics</i> , 2018 , 16, 365-372	6.5	15
99	Scalable continual top-k keyword search in relational databases. <i>Data and Knowledge Engineering</i> , 2013 , 86, 206-223	1.5	14
98	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	7.9	14
97	Deterministic weighted scale-free small-world networks. <i>Physica A: Statistical Mechanics and Its Applications</i> , 2010 , 389, 3316-3324	3.3	14
96	From regular to growing small-world networks. <i>Physica A: Statistical Mechanics and Its Applications</i> , 2007 , 385, 765-772	3.3	14
95	An effective approach to detecting both small and large complexes from protein-protein interaction networks. <i>BMC Bioinformatics</i> , 2017 , 18, 419	3.6	13
94	Discovering pattern-based subspace clusters by pattern tree. <i>Knowledge-Based Systems</i> , 2009 , 22, 569-579	7.9	13
93	Towards a Secure Medium Access Control Protocol for Cluster-Based Underwater Wireless Sensor Networks. <i>International Journal of Distributed Sensor Networks</i> , 2015 , 11, 325474	1.7	13
92	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	12
91	Choosing appropriate models for protein-protein interaction networks: a comparison study. <i>Briefings in Bioinformatics</i> , 2014 , 15, 823-38	13.4	12
90	Diffusion-Annihilation processes in weighted scale-free networks with an identical degree sequence. <i>Journal of Statistical Mechanics: Theory and Experiment</i> , 2011 , 2011, P10001	1.9	12
89	Screening lifespan-extending drugs in <i>Caenorhabditis elegans</i> via label propagation on drug-protein networks. <i>BMC Systems Biology</i> , 2016 , 10, 131	3.5	12
88	Essential Protein Detection by Random Walk on Weighted Protein-Protein Interaction Networks. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2019 , 16, 377-387	3	12
87	CPredictor3.0: detecting protein complexes from PPI networks with expression data and functional annotations. <i>BMC Systems Biology</i> , 2017 , 11, 135	3.5	11
86	Group-sparse Modeling Drug-kinase Networks for Predicting Combinatorial Drug Sensitivity in Cancer Cells. <i>Current Bioinformatics</i> , 2018 , 13, 437-443	4.7	11
85	When cloud computing meets bioinformatics: a review. <i>Journal of Bioinformatics and Computational Biology</i> , 2013 , 11, 1330002	1	10

84	Knowledge diffusion in complex networks. <i>Concurrency Computation Practice and Experience</i> , 2017 , 29, e3791	1.4	9
83	Local Nash equilibrium in social networks. <i>Scientific Reports</i> , 2014 , 4, 6224	4.9	9
82	Traffic Fluctuations on Weighted Networks. <i>IEEE Circuits and Systems Magazine</i> , 2012 , 12, 33-44	3.2	9
81	DEEPESEN: a convolutional neural network based method for super-enhancer prediction. <i>BMC Bioinformatics</i> , 2019 , 20, 598	3.6	9
80	A General Framework for Unmet Demand Prediction in On-Demand Transport Services. <i>IEEE Transactions on Intelligent Transportation Systems</i> , 2019 , 20, 2820-2830	6.1	9
79	Identifying overlapping communities in networks using evolutionary method. <i>Physica A: Statistical Mechanics and Its Applications</i> , 2016 , 442, 182-192	3.3	8
78	Gaming Temporal Networks. <i>IEEE Transactions on Circuits and Systems II: Express Briefs</i> , 2019 , 66, 672-676	6.5	8
77	Denosing Protein-Protein interaction network via variational graph auto-encoder for protein complex detection. <i>Journal of Bioinformatics and Computational Biology</i> , 2020 , 18, 2040010	1	7
76	The centrality of cancer proteins in human protein-protein interaction network: a revisit. <i>International Journal of Computational Biology and Drug Design</i> , 2014 , 7, 146-56	0.4	7
75	Efficient Retrieval of Bounded-Cost Informative Routes. <i>IEEE Transactions on Knowledge and Data Engineering</i> , 2017 , 29, 2182-2196	4.2	7
74	Structural and spectral properties of a family of deterministic recursive trees: rigorous solutions. <i>Journal of Physics A: Mathematical and Theoretical</i> , 2009 , 42, 165103	2	7
73	DISKs. <i>Proceedings of the VLDB Endowment</i> , 2012 , 5, 1966-1969	3.1	7
72	Towards More Effective Text Summarization Based on Textual Association Networks 2008 ,		7
71	TOP: A deep mixture representation learning method for boosting molecular toxicity prediction. <i>Methods</i> , 2020 , 179, 55-64	4.6	6
70	A Unified Framework for Predicting KPIs of On-Demand Transport Services. <i>IEEE Access</i> , 2018 , 6, 32005-32014	3.9	6
69	Efficient Skyline Retrieval on Peer-to-Peer Networks 2007 ,		6
68	Computationally identifying hot spots in protein-DNA binding interfaces using an ensemble approach. <i>BMC Bioinformatics</i> , 2020 , 21, 384	3.6	6
67	Accurately Detecting Protein Complexes by Graph Embedding and Combining Functions with Interactions. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2020 , 17, 777-787	3	6

66	Classifying early and late mild cognitive impairment stages of Alzheimer's disease by fusing default mode networks extracted with multiple seeds. <i>BMC Bioinformatics</i> , 2018 , 19, 523	3.6	6
65	Identifying mammalian MicroRNA targets based on supervised distance metric learning. <i>IEEE Journal of Biomedical and Health Informatics</i> , 2013 , 17, 427-35	7.2	5
64	The rigorous solution for the average distance of a Sierpinski network. <i>Journal of Statistical Mechanics: Theory and Experiment</i> , 2009 , 2009, P02034	1.9	5
63	Degree and component size distributions in the generalized uniform recursive tree. <i>Journal of Physics A: Mathematical and Theoretical</i> , 2008 , 41, 185101	2	5
62	RMDB: An Integrated Database of Single-cytosine-resolution DNA Methylation in <i>Oryza Sativa</i> . <i>Current Bioinformatics</i> , 2019 , 14, 524-531	4.7	5
61	A Chaotic Ant Colony Optimized Link Prediction Algorithm. <i>IEEE Transactions on Systems, Man, and Cybernetics: Systems</i> , 2020 , 1-15	7.3	5
60	FraGAT: a fragment-oriented multi-scale graph attention model for molecular property prediction. <i>Bioinformatics</i> , 2021 ,	7.2	5
59	Detecting microarray data supported microRNA-mRNA interactions. <i>International Journal of Data Mining and Bioinformatics</i> , 2010 , 4, 639-55	0.5	4
58	An empirical study of an agglomeration network. <i>Journal of Physics A: Mathematical and Theoretical</i> , 2007 , 40, 12365-12375	2	4
57	STREAM: Single-cell Trajectories Reconstruction, Exploration And Mapping of omics data		4
56	Dynamic epigenetic mode analysis using spatial temporal clustering. <i>BMC Bioinformatics</i> , 2016 , 17, 537	3.6	4
55	LAYER: A cost-efficient mechanism to support multi-tenant database as a service in cloud. <i>Journal of Systems and Software</i> , 2015 , 101, 86-96	3.3	3
54	Link Weight Prediction Using Weight Perturbation and Latent Factor. <i>IEEE Transactions on Cybernetics</i> , 2020 , PP,	10.2	3
53	Probabilistic Time-Constrained Paths Search over Uncertain Road Networks. <i>IEEE Transactions on Services Computing</i> , 2018 , 11, 399-414	4.8	3
52	Influence of weight heterogeneity on random walks in scale-free networks. <i>Journal of Physics A: Mathematical and Theoretical</i> , 2016 , 49, 275101	2	3
51	Revisiting topological properties and models of protein-protein interaction networks from the perspective of dataset evolution. <i>IET Systems Biology</i> , 2015 , 9, 113-9	1.4	3
50	Unfavorable Individuals in Social Gaming Networks. <i>Scientific Reports</i> , 2015 , 5, 17481	4.9	3
49	Boosting compound-protein interaction prediction by deep learning 2015 ,		3

48	imiRTP: An Integrated Method to Identifying miRNA-target Interactions in Arabidopsis thaliana 2011 ,		3
47	A new approach to building histogram for selectivity estimation in query processing optimization. <i>Computers and Mathematics With Applications</i> , 2009 , 57, 1037-1047	2.7	3
46	An improved genetic algorithm for statistical potential function design and protein structure prediction. <i>International Journal of Data Mining and Bioinformatics</i> , 2012 , 6, 162-77	0.5	3
45	Privacy and efficiency guaranteed social subgraph matching. <i>VLDB Journal</i> ,1	3.9	3
44	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	4.7	3
43	Protein-protein interaction prediction based on ordinal regression and recurrent convolutional neural networks. <i>BMC Bioinformatics</i> , 2021 , 22, 485	3.6	3
42	Single-cell RNA-seq data clustering: A survey with performance comparison study. <i>Journal of Bioinformatics and Computational Biology</i> , 2020 , 18, 2040005	1	3
41	Link Prediction based on Quantum-Inspired Ant Colony Optimization. <i>Scientific Reports</i> , 2018 , 8, 13389	4.9	3
40	Genome-wide analysis of epigenetic dynamics across human developmental stages and tissues. <i>BMC Genomics</i> , 2019 , 20, 221	4.5	2
39	. <i>Tsinghua Science and Technology</i> , 2019 , 24, 456-467	3.4	2
38	Towards efficiently supporting database as a service with QoS guarantees. <i>Journal of Systems and Software</i> , 2018 , 139, 51-63	3.3	2
37	iHMS: a database integrating human histone modification data across developmental stages and tissues. <i>BMC Bioinformatics</i> , 2017 , 18, 103	3.6	2
36	Role of Individual Activity in Rumor Spreading in Scale-free Networks 2017 ,		2
35	Gaussian Weighting Reversion Strategy for Accurate On-Line Portfolio Selection 2017 ,		2
34	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	3.3	2
33	Gene ontology-based protein function prediction by using sequence composition information. <i>Protein and Peptide Letters</i> , 2010 , 17, 789-95	1.9	2
32	LESSON: A system for lecture notes searching and sharing over Internet. <i>Journal of Systems and Software</i> , 2010 , 83, 1851-1863	3.3	2
31	Routing Based Load Balancing for Unstructured P2P Networks 2007 ,		2

30	Learning Competitive and Discriminative Reconstructions for Anomaly Detection. <i>Proceedings of the AAAI Conference on Artificial Intelligence</i> , 2019 , 33, 5167-5174	5	2
29	A general framework for privacy-preserving of data publication based on randomized response techniques. <i>Information Systems</i> , 2021 , 96, 101648	2.7	2
28	Side-chain dynamics analysis of KE07 series. <i>Computational Biology and Chemistry</i> , 2016 , 65, 148-153	3.6	1
27	Determining average path length and average trapping time on generalized dual dendrimer. <i>International Journal of Modern Physics B</i> , 2015 , 29, 1550072	1.1	1
26	GR-tree: An efficient index structure for GML 2014 ,		1
25	A comparison study on protein-protein interaction network models 2012 ,		1
24	An analytic derivation of clustering coefficients for weighted networks. <i>Journal of Statistical Mechanics: Theory and Experiment</i> , 2010 , 2010, P03013	1.9	1
23	Effectively predicting protein functions by collective classification [An extended abstract 2012 ,		1
22	Efficient Continual Top-k Keyword Search in Relational Databases. <i>Journal of Information Processing</i> , 2012 , 20, 114-127	0.2	1
21	DCAD: a dual clustering algorithm for distributed spatial databases. <i>Geo-Spatial Information Science</i> , 2007 , 10, 137-144	3.5	1
20	GPress: Towards Effective GML Documents Compression 2007 ,		1
19	Calculating the Crossing Probability on the Square Tessellation of a Connection Game with Random Move Order: The Algorithm and Its Complexity. <i>Lecture Notes in Computer Science</i> , 2014 , 288-297	0.9	1
18	Classifying Cognitive Normal and Early Mild Cognitive Impairment of Alzheimer's Disease by Applying Restricted Boltzmann Machine to fMRI Data. <i>Current Bioinformatics</i> , 2021 , 16, 252-260	4.7	1
17	Recursively Learning Causal Structures Using Regression-Based Conditional Independence Test. <i>Proceedings of the AAAI Conference on Artificial Intelligence</i> , 2019 , 33, 3108-3115	5	1
16	MIMO: A Unified Spatio-Temporal Model for Multi-Scale Sea Surface Temperature Prediction. <i>Remote Sensing</i> , 2022 , 14, 2371	5	1
15	Measuring Conditional Independence by Independent Residuals for Causal Discovery. <i>ACM Transactions on Intelligent Systems and Technology</i> , 2019 , 10, 1-19	8	0
14	Revealing dynamic communities in networks using genetic algorithm with merge and split operators. <i>Physica A: Statistical Mechanics and Its Applications</i> , 2020 , 558, 124897	3.3	0
13	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	1.4	0

12	. <i>IEEE Access</i> , 2020 , 8, 166730-166741	3.5	○
11	Classification of Marine Plankton Based on Few-shot Learning. <i>Arabian Journal for Science and Engineering</i> , 2021 , 46, 9253-9262	2.5	○
10	Boosting scRNA-seq data clustering by cluster-aware feature weighting. <i>BMC Bioinformatics</i> , 2021 , 22, 130	3.6	○
9	Combined cause inference: Definition, model and performance. <i>Information Sciences</i> , 2021 , 574, 431-443	7.7	○
8	Protein Function Prediction Based on PPI Networks: Network Reconstruction vs Edge Enrichment.. <i>Frontiers in Genetics</i> , 2021 , 12, 758131	4.5	○
7	A New Method for Extracting the Hierarchical Organization of Networks. <i>International Journal of Information Technology and Decision Making</i> , 2017 , 16, 1359-1385	2.8	
6	Divide-and-conquer Tournament on Social Networks. <i>Scientific Reports</i> , 2017 , 7, 15484	4.9	
5	Enhancing Routing Robustness of Unstructured Peer-to-Peer Networks Using Mobile Agents. <i>Journal of Network and Systems Management</i> , 2012 , 20, 309-352	2.1	
4	SWER: small world-based efficient routing for wireless sensor networks with mobile sinks. <i>Frontiers of Computer Science</i> , 2009 , 3, 427-434		
3	The Complexities of Random-turn Hex, Square and Triangle Games. <i>IEEE Transactions on Games</i> , 2020 , 1-1	1.2	
2	An integrative analysis of nucleosome occupancy and positioning using diverse sequence dependent properties. <i>Neurocomputing</i> , 2016 , 206, 35-41	5.4	
1	Histone modification patterns in highly differentiation cells. <i>Neurocomputing</i> , 2016 , 206, 42-49	5.4	