Jiawei Luo

List of Publications by Year
in descending order

127 papers	3,777 citations	201575 27 h-index
129 all docs	129 docs citations	129 times ranked

143943
57
g-index

2966
citing authors

#	Article	IF	Citations
1	A survey of circular RNAs in complex diseases: databases, tools and computational methods. Briefings in Bioinformatics, 2022, 23, .	3.2	9
2	Data Integration Using Tensor Decomposition for the Prediction of miRNA-Disease Associations. IEEE Journal of Biomedical and Health Informatics, 2022, 26, 2370-2378.	3.9	6
3	Using Graph Attention Network and Graph Convolutional Network to Explore Human CircRNAâ€"Disease Associations Based on Multi-Source Data. Frontiers in Genetics, 2022, 13, 829937.	1.1	4
4	Pre-training graph neural networks for link prediction in biomedical networks. Bioinformatics, 2022, 38, 2254-2262.	1.8	26
5	Inferring RNA-binding protein target preferences using adversarial domain adaptation. PLoS Computational Biology, 2022, 18, e1009863.	1.5	2
6	A knowledge-driven network for fine-grained relationship detection between miRNA and disease. Briefings in Bioinformatics, 2022, 23, .	3.2	8
7	Predicting miRNA-disease associations based on graph attention network with multi-source information. BMC Bioinformatics, 2022, 23, .	1.2	13
8	GGAECDA: Predicting circRNA-disease associations using graph autoencoder based on graph representation learning. Computational Biology and Chemistry, 2022, 99, 107722.	1.1	5
9	Incorporating Clinical, Chemical and Biological Information for Predicting Small Molecule-microRNA Associations Based on Non-Negative Matrix Factorization. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2021, 18, 2535-2545.	1.9	13
10	SG-LSTM-FRAME: a computational frame using sequence and geometrical information via LSTM to predict miRNAâ€"gene associations. Briefings in Bioinformatics, 2021, 22, 2032-2042.	3.2	15
11	Adaptive multi-source multi-view latent feature learning for inferring potential disease-associated miRNAs. Briefings in Bioinformatics, 2021, 22, 2043-2057.	3.2	25
12	Association Mining to Identify Microbe Drug Interactions Based on Heterogeneous Network Embedding Representation. IEEE Journal of Biomedical and Health Informatics, 2021, 25, 266-275.	3.9	23
13	Inferring MicroRNA-Disease Associations Based on the Identification of a Functional Module. Journal of Computational Biology, 2021, 28, 33-42.	0.8	6
14	Predicting human microbeâ€"disease associations via graph attention networks with inductive matrix completion. Briefings in Bioinformatics, 2021, 22, .	3.2	40
15	iCDA-CMG: identifying circRNA-disease associations by federating multi-similarity fusion and collective matrix completion. Molecular Genetics and Genomics, 2021, 296, 223-233.	1.0	14
16	miRNA-Disease Associations Prediction Based on Neural Tensor Decomposition. Lecture Notes in Computer Science, 2021, , 312-323.	1.0	3
17	Graph contextualized attention network for predicting synthetic lethality in human cancers. Bioinformatics, 2021, 37, 2432-2440.	1.8	25
18	An In Silico Method for Predicting Drug Synergy Based on Multitask Learning. Interdisciplinary Sciences, Computational Life Sciences, 2021, 13, 299-311.	2.2	4

#	Article	IF	Citations
19	Segmented Encryption: A Quality and Safety Supervisory Model for Herbal Medicine Based on Blockchain Technology. , 2021, , .		0
20	NSL2CD: identifying potential circRNAâ€"disease associations based on network embedding and subspace learning. Briefings in Bioinformatics, 2021, 22, .	3.2	11
21	Multi-view Multichannel Attention Graph Convolutional Network for miRNAâ€"disease association prediction. Briefings in Bioinformatics, 2021, 22, .	3.2	74
22	Metapath-Based Deep Convolutional Neural Network for Predicting miRNA-Target Association on Heterogeneous Network. Interdisciplinary Sciences, Computational Life Sciences, 2021, 13, 547-558.	2.2	3
23	Cancer subtype identification by consensus guided graph autoencoders. Bioinformatics, 2021, 37, 4779-4786.	1.8	16
24	Heterogeneous graph attention networks for drug virus association prediction. Methods, 2021, 198, 11-11.	1.9	8
25	IDDkin: network-based influence deep diffusion model for enhancing prediction of kinase inhibitors. Bioinformatics, 2021, 36, 5481-5491.	1.8	13
26	DFL-PiDA: Prediction of Piwi-interacting RNA-Disease Associations based on Deep Feature Learning. , 2021, , .		5
27	Graph Attention Mechanism-based Deep Tensor Factorization for Predicting disease-associated miRNA-miRNA pairs. , 2021, , .		1
28	Computational Identification of RNA-Seq Based miRNA-Mediated Prognostic Modules in Cancer. IEEE Journal of Biomedical and Health Informatics, 2020, 24, 626-633.	3.9	10
29	Heterogeneous information network and its application to human health and disease. Briefings in Bioinformatics, 2020, 21, 1327-1346.	3.2	17
30	Incorporating Multisource Knowledge To Predict Drug Synergy Based on Graph Co-regularization. Journal of Chemical Information and Modeling, 2020, 60, 37-46.	2.5	14
31	A Survey of Regulatory Interactions Among RNA Binding Proteins and MicroRNAs in Cancer. Frontiers in Genetics, 2020, 11, 515094.	1.1	1
32	Identification of Small Moleculeâ€"miRNA Associations with Graph Regularization Techniques in Heterogeneous Networks. Journal of Chemical Information and Modeling, 2020, 60, 6709-6721.	2.5	11
33	Potential circRNA-disease association prediction using DeepWalk and network consistency projection. Journal of Biomedical Informatics, 2020, 112, 103624.	2.5	32
34	Multiview Joint Learning-Based Method for Identifying Small-Molecule-Associated MiRNAs by Integrating Pharmacological, Genomics, and Network Knowledge. Journal of Chemical Information and Modeling, 2020, 60, 4085-4097.	2.5	13
35	An in-silico method with graph-based multi-label learning for large-scale prediction of circRNA-disease associations. Genomics, 2020, 112, 3407-3415.	1.3	14
36	Multiview Consensus Graph Learning for lncRNAâ€"Disease Association Prediction. Frontiers in Genetics, 2020, 11, 89.	1.1	12

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37	Predicting human microbe–drug associations via graph convolutional network with conditional random field. Bioinformatics, 2020, 36, 4918-4927.	1.8	82
38	Genome-wide analysis of the light-harvesting chlorophyll a/b-binding gene family in apple (Malus) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 7 osmotic stress. Plant Physiology and Biochemistry, 2020, 154, 517-529.	2.8	33
39	Ensembling graph attention networks for human microbe–drug association prediction. Bioinformatics, 2020, 36, i779-i786.	1.8	34
40	Predicting Drugs for COVID-19/SARS-CoV-2 via Heterogeneous Graph Attention Networks. , 2020, , .		2
41	A Graph Convolutional Matrix Completion Method for miRNA-Disease Association Prediction. Lecture Notes in Computer Science, 2020, , 201-215.	1.0	0
42	Identifying lncRNA and mRNA Co-expression Modules from Matched Expression Data in Ovarian Cancer. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2019, 17, 1-1.	1.9	12
43	Ensemble Prediction of Synergistic Drug Combinations Incorporating Biological, Chemical, Pharmacological, and Network Knowledge. IEEE Journal of Biomedical and Health Informatics, 2019, 23, 1336-1345.	3.9	39
44	A Novel Framework for Improving the Prediction of Disease-Associated MicroRNAs. Lecture Notes in Computer Science, 2019, , 127-137.	1.0	0
45	Self-Weighted Multi-Kernel Multi-Label Learning for Potential miRNA-Disease Association Prediction. Molecular Therapy - Nucleic Acids, 2019, 17, 414-423.	2.3	11
46	BiModule: biclique modularity strategy for identifying transcription factor and microRNA co-regulatory modules. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2019, , 1-1.	1.9	3
47	Prediction of LncRNA-Disease Associations Based on Network Consistency Projection. IEEE Access, 2019, 7, 58849-58856.	2.6	42
48	Adaptive multi-view multi-label learning for identifying disease-associated candidate miRNAs. PLoS Computational Biology, 2019, 15, e1006931.	1.5	75
49	Multi-view manifold regularized learning-based method for prioritizing candidate disease miRNAs. Knowledge-Based Systems, 2019, 175, 118-129.	4.0	77
50	CeModule: an integrative framework for discovering regulatory patterns from genomic data in cancer. BMC Bioinformatics, 2019, 20, 67.	1.2	19
51	A Full-chain Innovation Ecological Environment for Postgraduate Education. , 2019, , .		0
52	Inferring Synergistic Drug Combinations based on Symmetric Meta-Path in a Novel Heterogeneous Network. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2019, 18, 1-1.	1.9	1
53	Co-Regulatory Functional Module Detection Based on Affinity Propagation and Neighborhood Inflation. , 2019, , .		0
54	WMGHMDA: a novel weighted meta-graph-based model for predicting human microbe-disease association on heterogeneous information network. BMC Bioinformatics, 2019, 20, 541.	1.2	25

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55	NCPCDA: network consistency projection for circRNA–disease association prediction. RSC Advances, 2019, 9, 33222-33228.	1.7	39
56	Computational Prediction of Human Disease- Associated circRNAs Based on Manifold Regularization Learning Framework. IEEE Journal of Biomedical and Health Informatics, 2019, 23, 2661-2669.	3.9	61
57	Inferring MicroRNA Targets Based on Restricted Boltzmann Machines. IEEE Journal of Biomedical and Health Informatics, 2019, 23, 427-436.	3.9	26
58	A Novel Cluster-Based Computational Method to Identify miRNA Regulatory Modules. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2019, 16, 681-687.	1.9	15
59	Feature selection in machine learning: A new perspective. Neurocomputing, 2018, 300, 70-79.	3.5	1,194
60	Human disease MiRNA inference by combining target information based on heterogeneous manifolds. Journal of Biomedical Informatics, 2018, 80, 26-36.	2.5	23
61	An Efficient Network Motif Discovery Approach for Co-Regulatory Networks. IEEE Access, 2018, 6, 14151-14158.	2.6	18
62	Prediction of microRNA–disease associations with a Kronecker kernel matrix dimension reduction model. RSC Advances, 2018, 8, 4377-4385.	1.7	16
63	Identification of overlapping protein complexes by fuzzy K-medoids clustering algorithm in yeast protein-protein interaction networks. Journal of Intelligent and Fuzzy Systems, 2018, 34, 93-103.	0.8	3
64	Semi-supervised prediction of human miRNA-disease association based on graph regularization framework in heterogeneous networks. Neurocomputing, 2018, 294, 29-38.	3.5	30
65	Identifying Functional Modules in Co-Regulatory Networks Through Overlapping Spectral Clustering. IEEE Transactions on Nanobioscience, 2018, 17, 134-144.	2.2	5
66	A Novel Approach to Identify the miRNA-mRNA Causal Regulatory Modules in Cancer. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2018, 15, 309-315.	1.9	10
67	A graph regularized non-negative matrix factorization method for identifying microRNA-disease associations. Bioinformatics, 2018, 34, 239-248.	1.8	219
68	MTMO: an efficient network‐centric algorithm for subtree counting and enumeration. Quantitative Biology, 2018, 6, 142-154.	0.3	3
69	NTSHMDA: Prediction of Human Microbe-Disease Association based on Random Walk by Integrating Network Topological Similarity. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2018, 17, 1-1.	1.9	72
70	A novel semi-supervised model for miRNA-disease association prediction based on ℓ_{1} ‐ 1 -norm graph. Journal of Translational Medicine, 2018, 16, 357.	1.8	12
71	The "Chain Mode and Reverse Improving"Teaching Mechanism for the "Internet of Things"Major in Hunan University. , 2018, , .		0
72	Live Video System-A Lecturer Mobile Assistant. , 2018, , .		0

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73	SNMDA : A novel method for predicting micro RNA â€disease associations based on sparse neighbourhood. Journal of Cellular and Molecular Medicine, 2018, 22, 5109-5120.	1.6	12
74	Predicting microRNA-disease associations using label propagation based on linear neighborhood similarity. Journal of Biomedical Informatics, 2018, 82, 169-177.	2.5	63
75	GRTR: Drug-Disease Association Prediction Based on Graph Regularized Transductive Regression on Heterogeneous Network. Lecture Notes in Computer Science, 2018, , 13-25.	1.0	6
76	Genome-Wide Analysis and Cloning of the Apple Stress-Associated Protein Gene Family Reveals MdSAP15, Which Confers Tolerance to Drought and Osmotic Stresses in Transgenic Arabidopsis. International Journal of Molecular Sciences, 2018, 19, 2478.	1.8	40
77	Discovering Synergistic Drug Combination from a Computational Perspective. Current Topics in Medicinal Chemistry, 2018, 18, 965-974.	1.0	10
78	RMCL-ESA: A Novel Method to Detect Co-regulatory Functional Modules in Cancer. Lecture Notes in Computer Science, 2018, , 840-846.	1.0	0
79	Feature Selection Using Information Distance Measure for Gene Expression Data. Current Proteomics, 2018, 15, 352-362.	0.1	0
80	Genetic algorithm and tabu search algorithm for solving the static manycast RWA problem in optical networks. Journal of Combinatorial Optimization, 2017, 33, 726-741.	0.8	10
81	Discovery of microRNAs and Transcription Factors Co-Regulatory Modules by Integrating Multiple Types of Genomic Data. IEEE Transactions on Nanobioscience, 2017, 16, 51-59.	2.2	11
82	A novel approach for predicting microRNA-disease associations by unbalanced bi-random walk on heterogeneous network. Journal of Biomedical Informatics, 2017, 66, 194-203.	2.5	96
83	A Novel Group Wise-Based Method for Calculating Human miRNA Functional Similarity. IEEE Access, 2017, 5, 2364-2372.	2.6	8
84	Genome-wide predicting disease-related protein complexes by walking on the heterogeneous network based on data integration and laplacian normalization. Computational Biology and Chemistry, 2017, 69, 41-47.	1.1	3
85	Measuring Interobserver Disagreement in Rating Diagnostic Characteristics of Pulmonary Nodule Using the Lung Imaging Database Consortium and Image Database Resource Initiative. Academic Radiology, 2017, 24, 401-410.	1.3	8
86	Predicting MicroRNA-Disease Associations Using Kronecker Regularized Least Squares Based on Heterogeneous Omics Data. IEEE Access, 2017, 5, 2503-2513.	2.6	59
87	Collective Prediction of Disease-Associated miRNAs Based on Transduction Learning. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2017, 14, 1468-1475.	1.9	63
88	Predicting MicroRNA-Disease Associations Using Network Topological Similarity Based on DeepWalk. IEEE Access, 2017, 5, 24032-24039.	2.6	49
89	A Meta-Path-Based Prediction Method for Human miRNA-Target Association. BioMed Research International, 2016, 2016, 1-9.	0.9	10
90	Inferring human miRNA functional similarity based on gene ontology annotations. , 2016, , .		3

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91	A cell-core-attachment approach for identifying protein complexes in yeast protein-protein interaction network. Journal of Intelligent and Fuzzy Systems, 2016, 31, 967-978.	0.8	1
92	Random optimization algorithm for solving the static manycast RWA problem in optical WDM networks. , 2016, , .		2
93	Detecting overlapping protein complexes in weighted protein-protein interaction networks using pseudo-clique extension based on fuzzy relation. , 2016, , .		2
94	PCE-FR: A Novel Method for Identifying Overlapping Protein Complexes in Weighted Protein-Protein Interaction Networks Using Pseudo-Clique Extension Based on Fuzzy Relation. IEEE Transactions on Nanobioscience, 2016, 15, 728-738.	2.2	14
95	A path-based measurement for human miRNA functional similarities using miRNA-disease associations. Scientific Reports, 2016, 6, 32533.	1.6	29
96	Prediction of Essential Proteins Based on Local Interaction Density. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2016, 13, 1170-1182.	1.9	19
97	A Novel Method to Detect Functional microRNA Regulatory Modules by Bicliques Merging. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2016, 13, 549-556.	1.9	119
98	Identification of Essential Proteins Based on a New Combination of Local Interaction Density and Protein Complexes. PLoS ONE, 2015, 10, e0131418.	1.1	63
99	A cell-core-attachment approach for identifying protein complexes in PPI network. , 2015, , .		0
100	Data Analysis of the Lung Imaging Database Consortium and Image Database Resource Initiative. Academic Radiology, 2015, 22, 488-495.	1.3	17
101	A novel motif-discovery algorithm to identify co-regulatory motifs in large transcription factor and microRNA co-regulatory networks in human. Bioinformatics, 2015, 31, 2348-2355.	1.8	30
102	MOEPGA: A novel method to detect protein complexes in yeast protein–protein interaction networks based on MultiObjective Evolutionary Programming Genetic Algorithm. Computational Biology and Chemistry, 2015, 58, 173-181.	1.1	25
103	Prioritization of potential candidate disease genes by topological similarity of protein–protein interaction network and phenotype data. Journal of Biomedical Informatics, 2015, 53, 229-236.	2.5	43
104	PREDICTION OF ESSENTIAL PROTEINS BASED ON EDGE CLUSTERING COEFFICIENT AND GENE ONTOLOGY INFORMATION. Journal of Biological Systems, 2014, 22, 339-351.	0.5	4
105	Exploring the application of gene ontology semantic similarity measure for identifying protein complexes. , 2014, , .		1
106	An efficient method for mining non-redundant sequential rules using attributed prefix-trees. Engineering Applications of Artificial Intelligence, 2014, 32, 88-99.	4.3	28
107	An efficient approach to reduce alerts generated by multiple IDS products. International Journal of Network Management, 2014, 24, 153-180.	1.4	10
108	Development of a Personalized Training System Using the Lung Image Database Consortium and Image Database Resource Initiative Database. Academic Radiology, 2014, 21, 1614-1622.	1.3	6

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109	Network simulation reveals significant contribution of network motifs to the age-dependency of yeast protein–protein interaction networks. Molecular BioSystems, 2014, 10, 2277.	2.9	7
110	A new method for predicting essential proteins based on dynamic network topology and complex information. Computational Biology and Chemistry, 2014, 52, 34-42.	1.1	14
111	Mirsynergy: detecting synergistic miRNA regulatory modules by overlapping neighbourhood expansion. Bioinformatics, 2014, 30, 2627-2635.	1.8	79
112	A Performance Weighted Collaborative Filtering algorithm for personalized radiology education. Journal of Biomedical Informatics, 2014, 51, 107-113.	2.5	0
113	Integrating Functional and Topological Properties to Identify Biological Network Motif in Protein Interaction Networks. Journal of Computational and Theoretical Nanoscience, 2014, 11, 744-750.	0.4	6
114	Network specific vulnerability based alert reduction approach. Security and Communication Networks, 2013, 6, 15-27.	1.0	5
115	Model the evolution of protein interaction network assisted with protein age. Journal of Theoretical Biology, 2013, 333, 10-17.	0.8	4
116	A New Integration-Centric Algorithm of Identifying Essential Proteins Based on Topology Structure of Protein-Protein Interaction Network and Complex Information. Current Bioinformatics, 2013, 8, 380-385.	0.7	11
117	MSGPs: A Novel Algorithm for Mining Sequential Generator Patterns. Lecture Notes in Computer Science, 2012, , 393-401.	1.0	13
118	RNA secondary structure alignment based on an extended binary coding method. International Journal of Quantum Chemistry, 2011, 111, 978-982.	1.0	1
119	A novel method of recognizing short coding sequences of human genes. , 2010, , .		0
120	A New Graphical Representation and Its Application in Similarity/Dissimilarity Analysis of DNA Sequences. International Conference on Bioinformatics and Biomedical Engineering: [proceedings] International Conference on Bioinformatics and Biomedical Engineering, 2010, , .	0.0	5
121	New Method for Constructing Phylogenetic Tree Based on 3D Graphical Representation. , 2007, , .		3
122	New invariant of DNA sequence based on 3DD-curves and its application on phylogeny. Journal of Computational Chemistry, 2007, 28, 2342-2346.	1.5	15
123	Novel method for analyzing proteome. International Journal of Quantum Chemistry, 2007, 107, 1295-1300.	1.0	8
124	A Novel Method for Constructing Phylogenetic Tree Based on 3D Graphical Representation. , 2006, , .		0
125	RNA secondary structure 2D graphical representation without degeneracy. International Journal of Quantum Chemistry, 2006, 106, 1749-1755.	1.0	21
126	RNA Secondary Structure 3D Graphical Representation Without Degeneracy. Journal of Mathematical Chemistry, 2006, 39, 629-636.	0.7	10

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127	Missing value estimation for microarray data based on fuzzy C-means clustering. , 2005, , .		9