Guoxian Yu

List of Publications by Year
in descending order

118 papers	2,651 citations	236925 25 h-index	276875 41 g-index
121 all docs	121 docs citations	121 times ranked	2399 citing authors

#	Article	IF	Citations
1	Predicting protein functions using incomplete hierarchical labels. BMC Bioinformatics, 2015, 16, 1.	2.6	436
2	Matrix factorization-based data fusion for the prediction of lncRNAâ€"disease associations. Bioinformatics, 2018, 34, 1529-1537.	4.1	157
3	Proteinâ€"protein interactions prediction based on ensemble deep neural networks. Neurocomputing, 2019, 324, 10-19.	5.9	102
4	Semi-supervised classification based on random subspace dimensionality reduction. Pattern Recognition, 2012, 45, 1119-1135.	8.1	96
5	BRWLDA: bi-random walks for predicting lncRNA-disease associations. Oncotarget, 2017, 8, 60429-60446.	1.8	67
6	ActiveHNE: Active Heterogeneous Network Embedding. , 2019, , .		58
7	A Literature Review of Gene Function Prediction by Modeling Gene Ontology. Frontiers in Genetics, 2020, 11, 400.	2.3	53
8	Weighted-object ensemble clustering: methods and analysis. Knowledge and Information Systems, 2017, 51, 661-689.	3.2	47
9	Ranking-Based Deep Cross-Modal Hashing. Proceedings of the AAAI Conference on Artificial Intelligence, 2019, 33, 4400-4407.	4.9	47
10	Protein Function Prediction Using Multilabel Ensemble Classification. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2013, 10, 1045-1057.	3.0	46
11	Incomplete Multi-View Weak-Label Learning. , 2018, , .		44
12	BMC3C: binning metagenomic contigs using codon usage, sequence composition and read coverage. Bioinformatics, 2018, 34, 4172-4179.	4.1	40
13	Feature-Induced Partial Multi-label Learning. , 2018, , .		39
14	Semi-supervised ensemble classification in subspaces. Applied Soft Computing Journal, 2012, 12, 1511-1522.	7.2	38
15	Protein-Protein Interactions Prediction Using a Novel Local Conjoint Triad Descriptor of Amino Acid Sequences. International Journal of Molecular Sciences, 2017, 18, 2373.	4.1	38
16	Predicting Protein Function via Semantic Integration of Multiple Networks. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2016, 13, 220-232.	3.0	37
17	Weighted matrix factorization on multi-relational data for LncRNA-disease association prediction. Methods, 2020, 173, 32-43.	3.8	36
18	Transductive multi-label ensemble classification for protein function prediction. , 2012, , .		34

#	Article	IF	Citations
19	Semi-supervised multi-label classification using incomplete label information. Neurocomputing, 2017, 260, 192-202.	5.9	34
20	Clustering cancer gene expression data by projective clustering ensemble. PLoS ONE, 2017, 12, e0171429.	2.5	34
21	Gene function prediction based on Gene Ontology Hierarchy Preserving Hashing. Genomics, 2019, 111, 334-342.	2.9	34
22	NegGOA: negative GO annotations selection using ontology structure. Bioinformatics, 2016, 32, 2996-3004.	4.1	33
23	Semi-supervised classification based on subspace sparse representation. Knowledge and Information Systems, 2015, 43, 81-101.	3.2	32
24	Individuality- and Commonality-Based Multiview Multilabel Learning. IEEE Transactions on Cybernetics, 2021, 51, 1716-1727.	9.5	32
25	NewGOA: Predicting New GO Annotations of Proteins by Bi-Random Walks on a Hybrid Graph. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2018, 15, 1390-1402.	3.0	30
26	Multi-View Multiple Clusterings Using Deep Matrix Factorization. Proceedings of the AAAI Conference on Artificial Intelligence, 2020, 34, 6348-6355.	4.9	30
27	Multi-Label Co-Training. , 2018, , .		30
28	Predicting Protein Function Using Multiple Kernels. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2015, 12, 219-233.	3.0	27
29	Multi-Label Classiﬁcation Based on Low Rank Representation for Image Annotation. Remote Sensing, 2017, 9, 109.	4.0	27
30	Isoform function prediction based on bi-random walks on a heterogeneous network. Bioinformatics, 2020, 36, 303-310.	4.1	27
31	Protein Function Prediction with Incomplete Annotations. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2014, 11, 579-591.	3.0	25
32	HiSeeker: Detecting High-Order SNP Interactions Based on Pairwise SNP Combinations. Genes, 2017, 8, 153.	2.4	25
33	Differentiating isoform functions with collaborative matrix factorization. Bioinformatics, 2020, 36, 1864-1871.	4.1	24
34	Feature selection with missing labels based on label compression and local feature correlation. Neurocomputing, 2020, 395, 95-106.	5.9	24
35	Integrating multiple networks for protein function prediction. BMC Systems Biology, 2015, 9, S3.	3.0	23
36	Attributed heterogeneous network fusion via collaborative matrix tri-factorization. Information Fusion, 2020, 63, 153-165.	19.1	23

#	Article	IF	Citations
37	Predicting protein function via downward random walks on a gene ontology. BMC Bioinformatics, 2015, 16, 271.	2.6	22
38	Multi-label zero-shot learning with graph convolutional networks. Neural Networks, 2020, 132, 333-341.	5.9	22
39	Multi-View Multiple Clustering. , 2019, , .		22
40	Multi-view Weak-label Learning based on Matrix Completion. , 2018, , 450-458.		21
41	Protein Function Prediction Using Dependence Maximization. Lecture Notes in Computer Science, 2013, , 574-589.	1.3	21
42	Multi-label Answer Aggregation Based on Joint Matrix Factorization. , 2018, , .		20
43	Predicting protein-protein interactions using high-quality non-interacting pairs. BMC Bioinformatics, 2018, 19, 525.	2.6	20
44	Predicting functions of maize proteins using graph convolutional network. BMC Bioinformatics, 2020, 21, 420.	2.6	20
45	Enhanced locality preserving projections using robust path based similarity. Neurocomputing, 2011, 74, 598-605.	5.9	19
46	ClusterMI: Detecting High-Order SNP Interactions Based on Clustering and Mutual Information. International Journal of Molecular Sciences, 2018, 19, 2267.	4.1	18
47	Network-aided Bi-Clustering for discovering cancer subtypes. Scientific Reports, 2017, 7, 1046.	3.3	17
48	Weighted samples based semi-supervised classification. Applied Soft Computing Journal, 2019, 79, 46-58.	7.2	17
49	Multi-View Multi-Instance Multi-Label Learning Based on Collaborative Matrix Factorization. Proceedings of the AAAI Conference on Artificial Intelligence, 2019, 33, 5508-5515.	4.9	17
50	HashGO: hashing gene ontology for protein function prediction. Computational Biology and Chemistry, 2017, 71, 264-273.	2.3	15
51	DualWMDR: Detecting epistatic interaction with dual screening and multifactor dimensionality reduction. Human Mutation, 2020, 41, 719-734.	2.5	15
52	Co-clustering Ensembles based on Multiple Relevance Measures. IEEE Transactions on Knowledge and Data Engineering, 2019, , 1-1.	5.7	14
53	DeepGOA: Predicting Gene Ontology Annotations of Proteins via Graph Convolutional Network. , 2019, , .		14
54	Cost-effective Batch-mode Multi-label Active Learning. Neurocomputing, 2021, 463, 355-367.	5.9	14

#	Article	IF	Citations
55	Interspecies gene function prediction using semantic similarity. BMC Systems Biology, 2016, 10, 121.	3.0	13
56	EnSVMB: Metagenomics Fragments Classification using Ensemble SVM and BLAST. Scientific Reports, 2017, 7, 9440.	3.3	13
57	NoGOA: predicting noisy GO annotations using evidences and sparse representation. BMC Bioinformatics, 2017, 18, 350.	2.6	13
58	Active Multilabel Crowd Consensus. IEEE Transactions on Neural Networks and Learning Systems, 2021, 32, 1448-1459.	11.3	13
59	Cost Effective Multi-label Active Learning via Querying Subexamples. , 2018, , .		12
60	Discovering Multiple Co-Clusterings in Subspaces. , 2019, , 423-431.		12
61	NMFGO: Gene Function Prediction via Nonnegative Matrix Factorization with Gene Ontology. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2020, 17, 238-249.	3.0	12
62	CDPath: Cooperative Driver Pathways Discovery Using Integer Linear Programming and Markov Clustering. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2021, 18, 1384-1395.	3.0	11
63	Discovering Multiple Co-Clusterings With Matrix Factorization. IEEE Transactions on Cybernetics, 2021, 51, 3576-3587.	9.5	11
64	Deep Incomplete Multi-view Multiple Clusterings. , 2020, , .		11
65	Semi-supervised classification by discriminative regularization. Applied Soft Computing Journal, 2017, 58, 245-255.	7.2	10
66	Protein Function Prediction Using Deep Restricted Boltzmann Machines. BioMed Research International, 2017, 2017, 1-9.	1.9	10
67	Multiple Independent Subspace Clusterings. Proceedings of the AAAI Conference on Artificial Intelligence, 2019, 33, 5353-5360.	4.9	10
68	Multi-label crowd consensus via joint matrix factorization. Knowledge and Information Systems, 2020, 62, 1341-1369.	3.2	10
69	Selective Matrix Factorization for Multi-relational Data Fusion. Lecture Notes in Computer Science, 2019, , 313-329.	1.3	10
70	Partial Multi-label Learning using Label Compression. , 2020, , .		9
71	Protein function prediction using weak-label learning. , 2012, , .		8
72	NoisyGOA: Noisy GO annotations prediction using taxonomic and semantic similarity. Computational Biology and Chemistry, 2016, 65, 203-211.	2.3	8

#	Article	IF	Citations
73	Semi-Supervised Multi-Label Dimensionality Reduction Based on Dependence Maximization. IEEE Access, 2017, 5, 21927-21940.	4.2	8
74	Cross-Species Protein Function Prediction with Asynchronous-Random Walk. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2021, 18, 1439-1450.	3.0	8
75	Drug repositioning based on individual bi-random walks on a heterogeneous network. BMC Bioinformatics, 2019, 20, 547.	2.6	8
76	Weakly-supervised Cross-modal Hashing. IEEE Transactions on Big Data, 2019, , 1-1.	6.1	8
77	Cooperative driver pathway discovery via fusion of multi-relational data of genes, miRNAs and pathways. Briefings in Bioinformatics, 2021, 22, 1984-1999.	6.5	8
78	DeepIDA: Predicting Isoform-Disease Associations by Data Fusion and Deep Neural Networks. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2022, 19, 2166-2176.	3.0	8
79	Multiview Multi-Instance Multilabel Active Learning. IEEE Transactions on Neural Networks and Learning Systems, 2022, 33, 4311-4321.	11.3	8
80	Imbalance deep multiâ€instance learning for predicting isoformâ€"isoform interactions. International Journal of Intelligent Systems, 2021, 36, 2797-2824.	5.7	8
81	Multiple Co-clusterings. , 2018, , .		7
82	Cross-Modal Zero-Shot Hashing. , 2019, , .		7
83	Flexible Cross-Modal Hashing. IEEE Transactions on Neural Networks and Learning Systems, 2022, 33, 304-314.	11.3	7
84	CMAL: Cost-Effective Multi-Label Active Learning by Querying Subexamples. IEEE Transactions on Knowledge and Data Engineering, 2022, 34, 2091-2105.	5.7	7
85	DMIL-IsoFun: predicting isoform function using deep multi-instance learning. Bioinformatics, 2021, 37, 4818-4825.	4.1	7
86	Weighted matrix factorization based data fusion for predicting lncRNA-disease associations. , 2018, , .		6
87	Lung Cancer Subtype Diagnosis by Fusing Image-genomics Data and Hybrid Deep Networks. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2021, PP, 1-1.	3.0	6
88	DMIL-III: Isoform-isoform interaction prediction using deep multi-instance learning method. , 2019, , .		5
89	EpiMC: Detecting Epistatic Interactions Using Multiple Clusterings. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2022, 19, 243-254.	3.0	5
90	Semi-supervised Multi-label Linear Discriminant Analysis. Lecture Notes in Computer Science, 2017, , 688-698.	1.3	5

#	Article	IF	Citations
91	Predicting irrelevant functions of proteins based on dimensionality reduction. Scientia Sinica Informationis, 2017, 47, 1349-1368.	0.4	5
92	Protein Function Prediction by Random Walks on a Hybrid Graph. Current Proteomics, 2016, 13, 130-142.	0.3	5
93	Weakly-Supervised Multi-view Multi-instance Multi-label Learning. , 2020, , .		5
94	Partial Multi-label Learning with Label and Feature Collaboration. Lecture Notes in Computer Science, 2020, , 621-637.	1.3	5
95	ELSSI: parallel SNP–SNP interactions detection by ensemble multi-type detectors. Briefings in Bioinformatics, 2022, 23, .	6.5	5
96	CoDP: Cooperative Driver Pathways Discovery With Matrix Factorization and Tri-Random Walk. IEEE Access, 2019, 7, 77738-77749.	4.2	4
97	Multiple clusterings of heterogeneous information networks. Machine Learning, 2021, 110, 1505-1526.	5.4	4
98	Multi-typed Objects Multi-view Multi-instance Multi-label Learning. , 2020, , .		4
99	Semi-Supervised Multi-Label Feature Selection based on Sparsity Regularization and Dependence Maximization. , 2018, , .		3
100	DeepIII: Predicting Isoform-Isoform Interactions by Deep Neural Networks and Data Fusion. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2022, 19, 2177-2187.	3.0	3
101	Cost‐effective multi‐instance multilabel active learning. International Journal of Intelligent Systems, 2021, 36, 7177-7203.	5.7	3
102	EpiHNet: Detecting Epistasis by Heterogeneous Molecule Network. Methods, 2021, , .	3.8	3
103	Semi-Supervised Classification Based on Mixture Graph. Algorithms, 2015, 8, 1021-1034.	2.1	2
104	Affinity Propagation Clustering Using Path Based Similarity. Algorithms, 2016, 9, 46.	2.1	2
105	TrioMDR: Detecting SNP interactions in trio families with model-based multifactor dimensionality reduction. Genomics, 2019, 111, 1176-1182.	2.9	2
106	Isoform-Disease Association Prediction by Data Fusion. Lecture Notes in Computer Science, 2020, , 44-55.	1.3	2
107	Crowdsourcing with Self-paced Workers. , 2021, , .		2
108	Weighted deep factorizing heterogeneous molecular network for genome-phenome association prediction. Methods, 2022, 205, 18-28.	3.8	2

#	Article	IF	Citations
109	Semi-supervised classification based on clustering adjusted similarity. International Journal of Computers and Applications, 2017, 39, 210-219.	1.3	1
110	CoPath: discovering cooperative driver pathways using greedy mutual exclusivity and bi-clustering. , 2019, , .		1
111	IsoDA: Isoform–Disease Association Prediction by Multiomics Data Fusion. Journal of Computational Biology, 2021, 28, 804-819.	1.6	1
112	EpIntMC: Detecting Epistatic Interactions Using Multiple Clusterings. Lecture Notes in Computer Science, 2020, , 56-67.	1.3	1
113	Epistasis Detection using Heterogeneous Bio-molecular Network. , 2020, , .		1
114	Maize Epistasis Detection by Multi-class Quantitative Multifactor Dimensionality Reduction. , 2021, , .		1
115	Tissue Specificity Based Isoform Function Prediction. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2022, 19, 3048-3059.	3.0	0
116	Consistent and Specific Multi-view Relative-Transform Classification. Communications in Computer and Information Science, 2019, , 272-285.	0.5	0
117	Affinity Propagation Clustering Using Centroid-Deviation-Distance Based Similarity. Communications in Computer and Information Science, 2019, , 286-299.	0.5	0
118	Incomplete Multi-view Multi-label Active Learning. , 2021, , .		0