

Guoxian Yu

List of Publications by Year in descending order

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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	Flexible Cross-Modal Hashing. IEEE Transactions on Neural Networks and Learning Systems, 2022, 33, 304-314.	11.3	7
2	CMAL: Cost-Effective Multi-Label Active Learning by Querying Subexamples. IEEE Transactions on Knowledge and Data Engineering, 2022, 34, 2091-2105.	5.7	7
3	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
4	Multiview Multi-Instance Multilabel Active Learning. IEEE Transactions on Neural Networks and Learning Systems, 2022, 33, 4311-4321.	11.3	8
5	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
6	Tissue Specificity Based Isoform Function Prediction. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2022, 19, 3048-3059.	3.0	0
7	EpiMC: Detecting Epistatic Interactions Using Multiple Clusterings. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2022, 19, 243-254.	3.0	5
8	ELSSI: parallel SNP-SNP interactions detection by ensemble multi-type detectors. Briefings in Bioinformatics, 2022, 23, .	6.5	5
9	Weighted deep factorizing heterogeneous molecular network for genome-phenome association prediction. Methods, 2022, 205, 18-28.	3.8	2
10	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
11	Cross-Species Protein Function Prediction with Asynchronous-Random Walk. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2021, 18, 1439-1450.	3.0	8
12	Discovering Multiple Co-Clusterings With Matrix Factorization. IEEE Transactions on Cybernetics, 2021, 51, 3576-3587.	9.5	11
13	Active Multilabel Crowd Consensus. IEEE Transactions on Neural Networks and Learning Systems, 2021, 32, 1448-1459.	11.3	13
14	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
15	Individuality- and Commonality-Based Multiview Multilabel Learning. IEEE Transactions on Cybernetics, 2021, 51, 1716-1727.	9.5	32
16	Imbalance deep multi-instance learning for predicting isoform-isoform interactions. International Journal of Intelligent Systems, 2021, 36, 2797-2824.	5.7	8
17	Multiple clusterings of heterogeneous information networks. Machine Learning, 2021, 110, 1505-1526.	5.4	4
18	DMIL-IsoFun: predicting isoform function using deep multi-instance learning. Bioinformatics, 2021, 37, 4818-4825.	4.1	7

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19	IsoDA: Isoform-Disease Association Prediction by Multiomics Data Fusion. <i>Journal of Computational Biology</i> , 2021, 28, 804-819.	1.6	1
20	Cost-effective multi-instance multilabel active learning. <i>International Journal of Intelligent Systems</i> , 2021, 36, 7177-7203.	5.7	3
21	EpiHNet: Detecting Epistasis by Heterogeneous Molecule Network. <i>Methods</i> , 2021, , .	3.8	3
22	Cost-effective Batch-mode Multi-label Active Learning. <i>Neurocomputing</i> , 2021, 463, 355-367.	5.9	14
23	Lung Cancer Subtype Diagnosis by Fusing Image-genomics Data and Hybrid Deep Networks. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2021, PP, 1-1.	3.0	6
24	Maize Epistasis Detection by Multi-class Quantitative Multifactor Dimensionality Reduction. , 2021, , .		1
25	Crowdsourcing with Self-paced Workers. , 2021, , .		2
26	Incomplete Multi-view Multi-label Active Learning. , 2021, , .		0
27	Differentiating isoform functions with collaborative matrix factorization. <i>Bioinformatics</i> , 2020, 36, 1864-1871.	4.1	24
28	NMFGO: Gene Function Prediction via Nonnegative Matrix Factorization with Gene Ontology. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2020, 17, 238-249.	3.0	12
29	Weighted matrix factorization on multi-relational data for LncRNA-disease association prediction. <i>Methods</i> , 2020, 173, 32-43.	3.8	36
30	Isoform function prediction based on bi-random walks on a heterogeneous network. <i>Bioinformatics</i> , 2020, 36, 303-310.	4.1	27
31	Multi-label crowd consensus via joint matrix factorization. <i>Knowledge and Information Systems</i> , 2020, 62, 1341-1369.	3.2	10
32	DualWMDR: Detecting epistatic interaction with dual screening and multifactor dimensionality reduction. <i>Human Mutation</i> , 2020, 41, 719-734.	2.5	15
33	Multi-label zero-shot learning with graph convolutional networks. <i>Neural Networks</i> , 2020, 132, 333-341.	5.9	22
34	Multi-View Multiple Clusterings Using Deep Matrix Factorization. <i>Proceedings of the AAAI Conference on Artificial Intelligence</i> , 2020, 34, 6348-6355.	4.9	30
35	Predicting functions of maize proteins using graph convolutional network. <i>BMC Bioinformatics</i> , 2020, 21, 420.	2.6	20
36	Attributed heterogeneous network fusion via collaborative matrix tri-factorization. <i>Information Fusion</i> , 2020, 63, 153-165.	19.1	23

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37	A Literature Review of Gene Function Prediction by Modeling Gene Ontology. <i>Frontiers in Genetics</i> , 2020, 11, 400.	2.3	53
38	Feature selection with missing labels based on label compression and local feature correlation. <i>Neurocomputing</i> , 2020, 395, 95-106.	5.9	24
39	Isoform-Disease Association Prediction by Data Fusion. <i>Lecture Notes in Computer Science</i> , 2020, , 44-55.	1.3	2
40	Deep Incomplete Multi-view Multiple Clusterings. , 2020, , .		11
41	Partial Multi-label Learning using Label Compression. , 2020, , .		9
42	Multi-typed Objects Multi-view Multi-instance Multi-label Learning. , 2020, , .		4
43	Weakly-Supervised Multi-view Multi-instance Multi-label Learning. , 2020, , .		5
44	EpIntMC: Detecting Epistatic Interactions Using Multiple Clusterings. <i>Lecture Notes in Computer Science</i> , 2020, , 56-67.	1.3	1
45	Partial Multi-label Learning with Label and Feature Collaboration. <i>Lecture Notes in Computer Science</i> , 2020, , 621-637.	1.3	5
46	Epistasis Detection using Heterogeneous Bio-molecular Network. , 2020, , .		1
47	Proteinâ€“protein interactions prediction based on ensemble deep neural networks. <i>Neurocomputing</i> , 2019, 324, 10-19.	5.9	102
48	Co-clustering Ensembles based on Multiple Relevance Measures. <i>IEEE Transactions on Knowledge and Data Engineering</i> , 2019, , 1-1.	5.7	14
49	Multiple Independent Subspace Clusterings. <i>Proceedings of the AAAI Conference on Artificial Intelligence</i> , 2019, 33, 5353-5360.	4.9	10
50	CoDP: Cooperative Driver Pathways Discovery With Matrix Factorization and Tri-Random Walk. <i>IEEE Access</i> , 2019, 7, 77738-77749.	4.2	4
51	TrioMDR: Detecting SNP interactions in trio families with model-based multifactor dimensionality reduction. <i>Genomics</i> , 2019, 111, 1176-1182.	2.9	2
52	Discovering Multiple Co-Clusterings in Subspaces. , 2019, , 423-431.		12
53	Weighted samples based semi-supervised classification. <i>Applied Soft Computing Journal</i> , 2019, 79, 46-58.	7.2	17
54	Ranking-Based Deep Cross-Modal Hashing. <i>Proceedings of the AAAI Conference on Artificial Intelligence</i> , 2019, 33, 4400-4407.	4.9	47

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55	Cross-Modal Zero-Shot Hashing. , 2019, , .		7
56	DMIL-III: Isoform-isoform interaction prediction using deep multi-instance learning method. , 2019, , .		5
57	CoPath: discovering cooperative driver pathways using greedy mutual exclusivity and bi-clustering. , 2019, , .		1
58	DeepGOA: Predicting Gene Ontology Annotations of Proteins via Graph Convolutional Network. , 2019, , .		14
59	Drug repositioning based on individual bi-random walks on a heterogeneous network. BMC Bioinformatics, 2019, 20, 547.	2.6	8
60	Weakly-supervised Cross-modal Hashing. IEEE Transactions on Big Data, 2019, , 1-1.	6.1	8
61	Gene function prediction based on Gene Ontology Hierarchy Preserving Hashing. Genomics, 2019, 111, 334-342.	2.9	34
62	Selective Matrix Factorization for Multi-relational Data Fusion. Lecture Notes in Computer Science, 2019, , 313-329.	1.3	10
63	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
64	ActiveHNE: Active Heterogeneous Network Embedding. , 2019, , .		58
65	Multi-View Multiple Clustering. , 2019, , .		22
66	Consistent and Specific Multi-view Relative-Transform Classification. Communications in Computer and Information Science, 2019, , 272-285.	0.5	0
67	Affinity Propagation Clustering Using Centroid-Deviation-Distance Based Similarity. Communications in Computer and Information Science, 2019, , 286-299.	0.5	0
68	Matrix factorization-based data fusion for the prediction of lncRNA-disease associations. Bioinformatics, 2018, 34, 1529-1537.	4.1	157
69	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
70	Weighted matrix factorization based data fusion for predicting lncRNA-disease associations. , 2018, , .		6
71	Semi-Supervised Multi-Label Feature Selection based on Sparsity Regularization and Dependence Maximization. , 2018, , .		3
72	Feature-Induced Partial Multi-label Learning. , 2018, , .		39

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73	Multi-label Answer Aggregation Based on Joint Matrix Factorization. , 2018, , .		20
74	Cost Effective Multi-label Active Learning via Querying Subexamples. , 2018, , .		12
75	Multiple Co-clusterings. , 2018, , .		7
76	Predicting protein-protein interactions using high-quality non-interacting pairs. BMC Bioinformatics, 2018, 19, 525.	2.6	20
77	Multi-view Weak-label Learning based on Matrix Completion. , 2018, , 450-458.		21
78	BMC3C: binning metagenomic contigs using codon usage, sequence composition and read coverage. Bioinformatics, 2018, 34, 4172-4179.	4.1	40
79	ClusterMI: Detecting High-Order SNP Interactions Based on Clustering and Mutual Information. International Journal of Molecular Sciences, 2018, 19, 2267.	4.1	18
80	Incomplete Multi-View Weak-Label Learning. , 2018, , .		44
81	Multi-Label Co-Training. , 2018, , .		30
82	Network-aided Bi-Clustering for discovering cancer subtypes. Scientific Reports, 2017, 7, 1046.	3.3	17
83	Semi-supervised multi-label classification using incomplete label information. Neurocomputing, 2017, 260, 192-202.	5.9	34
84	Semi-supervised classification by discriminative regularization. Applied Soft Computing Journal, 2017, 58, 245-255.	7.2	10
85	Semi-supervised classification based on clustering adjusted similarity. International Journal of Computers and Applications, 2017, 39, 210-219.	1.3	1
86	HashGO: hashing gene ontology for protein function prediction. Computational Biology and Chemistry, 2017, 71, 264-273.	2.3	15
87	EnSVMB: Metagenomics Fragments Classification using Ensemble SVM and BLAST. Scientific Reports, 2017, 7, 9440.	3.3	13
88	Weighted-object ensemble clustering: methods and analysis. Knowledge and Information Systems, 2017, 51, 661-689.	3.2	47
89	Semi-Supervised Multi-Label Dimensionality Reduction Based on Dependence Maximization. IEEE Access, 2017, 5, 21927-21940.	4.2	8
90	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

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91	HiSeeker: Detecting High-Order SNP Interactions Based on Pairwise SNP Combinations. <i>Genes</i> , 2017, 8, 153.	2.4	25
92	Protein Function Prediction Using Deep Restricted Boltzmann Machines. <i>BioMed Research International</i> , 2017, 2017, 1-9.	1.9	10
93	NoGOA: predicting noisy GO annotations using evidences and sparse representation. <i>BMC Bioinformatics</i> , 2017, 18, 350.	2.6	13
94	Clustering cancer gene expression data by projective clustering ensemble. <i>PLoS ONE</i> , 2017, 12, e0171429.	2.5	34
95	Multi-Label Classification Based on Low Rank Representation for Image Annotation. <i>Remote Sensing</i> , 2017, 9, 109.	4.0	27
96	BRWLDA: bi-random walks for predicting lncRNA-disease associations. <i>Oncotarget</i> , 2017, 8, 60429-60446.	1.8	67
97	Semi-supervised Multi-label Linear Discriminant Analysis. <i>Lecture Notes in Computer Science</i> , 2017, , 688-698.	1.3	5
98	Predicting irrelevant functions of proteins based on dimensionality reduction. <i>Scientia Sinica Informationis</i> , 2017, 47, 1349-1368.	0.4	5
99	Affinity Propagation Clustering Using Path Based Similarity. <i>Algorithms</i> , 2016, 9, 46.	2.1	2
100	NoisyGOA: Noisy GO annotations prediction using taxonomic and semantic similarity. <i>Computational Biology and Chemistry</i> , 2016, 65, 203-211.	2.3	8
101	Interspecies gene function prediction using semantic similarity. <i>BMC Systems Biology</i> , 2016, 10, 121.	3.0	13
102	NegGOA: negative GO annotations selection using ontology structure. <i>Bioinformatics</i> , 2016, 32, 2996-3004.	4.1	33
103	Predicting Protein Function via Semantic Integration of Multiple Networks. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2016, 13, 220-232.	3.0	37
104	Protein Function Prediction by Random Walks on a Hybrid Graph. <i>Current Proteomics</i> , 2016, 13, 130-142.	0.3	5
105	Semi-Supervised Classification Based on Mixture Graph. <i>Algorithms</i> , 2015, 8, 1021-1034.	2.1	2
106	Predicting Protein Function Using Multiple Kernels. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2015, 12, 219-233.	3.0	27
107	Integrating multiple networks for protein function prediction. <i>BMC Systems Biology</i> , 2015, 9, S3.	3.0	23
108	Predicting protein functions using incomplete hierarchical labels. <i>BMC Bioinformatics</i> , 2015, 16, 1.	2.6	436

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109	Predicting protein function via downward random walks on a gene ontology. BMC Bioinformatics, 2015, 16, 271.	2.6	22
110	Semi-supervised classification based on subspace sparse representation. Knowledge and Information Systems, 2015, 43, 81-101.	3.2	32
111	Protein Function Prediction with Incomplete Annotations. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2014, 11, 579-591.	3.0	25
112	Protein Function Prediction Using Multilabel Ensemble Classification. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2013, 10, 1045-1057.	3.0	46
113	Protein Function Prediction Using Dependence Maximization. Lecture Notes in Computer Science, 2013, , 574-589.	1.3	21
114	Protein function prediction using weak-label learning. , 2012, , .		8
115	Transductive multi-label ensemble classification for protein function prediction. , 2012, , .		34
116	Semi-supervised ensemble classification in subspaces. Applied Soft Computing Journal, 2012, 12, 1511-1522.	7.2	38
117	Semi-supervised classification based on random subspace dimensionality reduction. Pattern Recognition, 2012, 45, 1119-1135.	8.1	96
118	Enhanced locality preserving projections using robust path based similarity. Neurocomputing, 2011, 74, 598-605.	5.9	19