Jiajie Peng

List of Publications by Year
in descending order

76	2,355	270111	263392
papers	citations	25 h-index	45 g-index

87	87	87	2096
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Enhancing discoveries of molecular QTL studies with small sample size using summary statistic imputation. Briefings in Bioinformatics, 2022, 23, .	3.2	15
2	A network-based method for brain disease gene prediction by integrating brain connectome and molecular network. Briefings in Bioinformatics, 2022, 23, .	3.2	7
3	Flexibility and rigidity index for chromosome packing, flexibility and dynamics analysis. Frontiers of Computer Science, 2022, 16, 1.	1.6	1
4	Explore potential disease related metabolites based on latent factor model. BMC Genomics, 2022, 23, 269.	1.2	5
5	Editorial: Data Mining and Statistical Methods for Knowledge Discovery in Diseases Based on Multimodal Omics. Frontiers in Genetics, 2022, 13, 895796.	1.1	4
6	Identifying Non-Math Students from Brain MRIs with an Ensemble Classifier Based on Subspace-Enhanced Contrastive Learning. Brain Sciences, 2022, 12, 908.	1.1	3
7	A novel subnetwork representation learning method for uncovering disease-disease relationships. Methods, 2021, 192, 77-84.	1.9	17
8	Integrating multi-network topology for gene function prediction using deep neural networks. Briefings in Bioinformatics, 2021, 22, 2096-2105.	3.2	73
9	Identifying drugâ€“target interactions based on graph convolutional network and deep neural network. Briefings in Bioinformatics, 2021, 22, 2141-2150.	3.2	172
10	SC2disease: a manually curated database of single-cell transcriptome for human diseases. Nucleic Acids Research, 2021, 49, D1413-D1419.	6.5	65
11	Prediction and collection of proteinâ€“metabolite interactions. Briefings in Bioinformatics, 2021, 22, .	3.2	52
12	An end-to-end heterogeneous graph representation learning-based framework for drugâ€“target interaction prediction. Briefings in Bioinformatics, 2021, 22, .	3.2	87
13	DeepLearnMOR: a deep-learning framework for fluorescence image-based classification of organelle morphology. Plant Physiology, 2021, 186, 1786-1799.	2.3	12
14	Genome-wide survival study identifies a novel synaptic locus and polygenic score for cognitive progression in Parkinsonâ€™s disease. Nature Genetics, 2021, 53, 787-793.	9.4	82
15	A novel method for predicting cell abundance based on single-cell RNA-seq data. BMC Bioinformatics, 2021, 22, 281.	1.2	7
16	Predicting Chromosome Flexibility from the Genomic Sequence Based on Deep Learning Neural Networks. Current Bioinformatics, 2021, 16, 1311-1319.	0.7	5
17	Benchmarked approaches for reconstruction of inÂvitro cell lineages and in silico models of C. elegans and M. musculus developmental trees. Cell Systems, 2021, 12, 810-826.e4.	2.9	36
18	A pipeline for RNA-seq based eQTL analysis with automated quality control procedures. BMC Bioinformatics, 2021, 22, 403.	1.2	27

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19	R-CRISPR: A Deep Learning Network to Predict Off-Target Activities with Mismatch, Insertion and Deletion in CRISPR-Cas9 System. Genes, 2021, 12, 1878.	1.0	8
20	Integrated proteogenomic analysis revealed the metabolic heterogeneity in noncancerous liver tissues of patients with hepatocellular carcinoma. Journal of Hematology and Oncology, 2021, 14, 205.	6.9	6
21	Predicting Hepatoma-Related Genes Based on Representation Learning of PPI network and Gene Ontology Annotations. , 2021, , .		4
22	DCAE: Selecting Discriminative Genes on Single-cell RNA-seq Data for Cell-type Quantification. , 2021, , .		1
23	Identifying emerging phenomenon in long temporal phenotyping experiments. Bioinformatics, 2020, 36, 568-577.	1.8	8
24	Mining Relationships among Multiple Entities in Biological Networks. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2020, 17, 769-776.	1.9	14
25	FSM: Fast and scalable network motif discovery for exploring higher-order network organizations. Methods, 2020, 173, 83-93.	1.9	26
26	Classification and Prognosis Prediction from Histopathological Images of Hepatocellular Carcinoma by a Fully Automated Pipeline Based on Machine Learning. Annals of Surgical Oncology, 2020, 27, 2359-2369.	0.7	33
27	A learning-based method for drug-target interaction prediction based on feature representation learning and deep neural network. BMC Bioinformatics, 2020, 21, 394.	1.2	54
28	Combining sequence and network information to enhance proteinâ€“protein interaction prediction. BMC Bioinformatics, 2020, 21, 537.	1.2	20
29	DeepLGP: a novel deep learning method for prioritizing lncRNA target genes. Bioinformatics, 2020, 36, 4466-4472.	1.8	106
30	Deep learningâ€based classification and mutation prediction from histopathological images of hepatocellular carcinoma. Clinical and Translational Medicine, 2020, 10, e102.	1.7	50
31	Reduction in TOM1 expression exacerbates Alzheimerâ€™s disease. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 3915-3916.	3.3	20
32	SpliVert: A Protein Multiple Sequence Alignment Refinement Method Based on Splitting-Splicing Vertically. Protein and Peptide Letters, 2020, 27, 295-302.	0.4	6
33	A Survey of Network Representation Learning Methods for Link Prediction in Biological Network. Current Pharmaceutical Design, 2020, 26, 3076-3084.	0.9	6
34	Automatic Term Name Generation for Gene Ontology: Task and Dataset. , 2020, , .		3
35	Efficient Deep Reinforcement Learning via Adaptive Policy Transfer. , 2020, , .		9
36	Towards Gene Function Prediction via Multi-Networks Representation Learning. Proceedings of the AAAI Conference on Artificial Intelligence, 2019, 33, 10069-10070.	3.6	3

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37	Combining gene ontology with deep neural networks to enhance the clustering of single cell RNA-Seq data. BMC Bioinformatics, 2019, 20, 284.	1.2	48
38	Predicting Parkinson's Disease Genes Based on Node2vec and Autoencoder. Frontiers in Genetics, 2019, 10, 226.	1.1	91
39	A learning-based framework for miRNA-disease association identification using neural networks. Bioinformatics, 2019, 35, 4364-4371.	1.8	142
40	Predicting disease-related phenotypes using an integrated phenotype similarity measurement based on HPO. BMC Systems Biology, 2019, 13, 34.	3.0	12
41	A deconvolution method for predicting cell abundance based on single cell RNA-seq data. , 2019, , .		0
42	Integrating Sequence and Network Information to Enhance Protein-Protein Interaction Prediction Using Graph Convolutional Networks. , 2019, , .		4
43	TS-GOEA: a web tool for tissue-specific gene set enrichment analysis based on gene ontology. BMC Bioinformatics, 2019, 20, 572.	1.2	7
44	Prioritizing candidate diseases-related metabolites based on literature and functional similarity. BMC Bioinformatics, 2019, 20, 574.	1.2	9
45	LncDisAP: a computation model for LncRNA-disease association prediction based on multiple biological datasets. BMC Bioinformatics, 2019, 20, 582.	1.2	11
46	eQTLMAPT: Fast and Accurate eQTL Mediation Analysis With Efficient Permutation Testing Approaches. Frontiers in Genetics, 2019, 10, 1309.	1.1	17
47	Integrating Multi-Network Topology via Deep Semi-supervised Node Embedding. , 2019, , .		3
48	Measuring phenotype-phenotype similarity through the interactome. BMC Bioinformatics, 2018, 19, 114.	1.2	32
49	TSGOE: A web tool for tissue-specific gene ontology enrichment. , 2018, , .		0
50	Identifying Representative Network Motifs for Inferring Higher-order Structure of Biological Networks. , 2018, , .		1
51	Predicting candidate disease-related lncRNAs based on network random walk. , 2018, , .		0
52	An online tool for measuring and visualizing phenotype similarities using HPO. BMC Genomics, 2018, 19, 571.	1.2	7
53	InfAcrOnt: calculating cross-ontology term similarities using information flow by a random walk. BMC Genomics, 2018, 19, 919.	1.2	98
54	Improving the measurement of semantic similarity by combining gene ontology and co-functional network: a random walk based approach. BMC Systems Biology, 2018, 12, 18.	3.0	52

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55	Predicting disease-related genes using integrated biomedical networks. BMC Genomics, 2017, 18, 1043.	1.2	46
56	A novel method to measure the semantic similarity of HPO terms. International Journal of Data Mining and Bioinformatics, 2017, 17, 173.	0.1	51
57	Identifying consistent disease subnetworks using DNet. Methods, 2017, 131, 104-110.	1.9	16
58	Measuring phenotype-phenotype similarity through the interactome. , 2017, , .		1
59	Investigations on factors influencing HPO-based semantic similarity calculation. Journal of Biomedical Semantics, 2017, 8, 34.	0.9	3
60	Identifying term relations cross different gene ontology categories. BMC Bioinformatics, 2017, 18, 573.	1.2	46
61	A novel method to measure the semantic similarity of HPO terms. International Journal of Data Mining and Bioinformatics, 2017, 17, 173.	0.1	1
62	Measuring phenotype semantic similarity using Human Phenotype Ontology. , 2016, , .		6
63	InteGO2: a web tool for measuring and visualizing gene semantic similarities using Gene Ontology. BMC Genomics, 2016, 17, 530.	1.2	26
64	Analyzing factors involved in the HPO-based semantic similarity calculation. , 2016, , .		0
65	Joint detection of copy number variations in parent-offspring trios. Bioinformatics, 2016, 32, 1130-1137.	1.8	18
66	Extending gene ontology with gene association networks. Bioinformatics, 2016, 32, 1185-1194.	1.8	42
67	Constructing Networks of Organelle Functional Modules in Arabidopsis. Current Genomics, 2016, 17, 427-438.	0.7	16
68	LncRNA2Function: a comprehensive resource for functional investigation of human lncRNAs based on RNA-seq data. BMC Genomics, 2015, 16, S2.	1.2	117
69	A web tool for measuring gene semantic similarities by combining gene ontology and gene co-function networks. , 2015, , .		0
70	Measuring semantic similarities by combining gene ontology annotations and gene co-function networks. BMC Bioinformatics, 2015, 16, 44.	1.2	39
71	LncRNA2Target: a database for differentially expressed genes after lncRNA knockdown or overexpression. Nucleic Acids Research, 2015, 43, D193-D196.	6.5	124
72	A Generalized Topological Entropy for Analyzing the Complexity of DNA Sequences. PLoS ONE, 2014, 9, e88519.	1.1	16

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73	SemFunSim: A New Method for Measuring Disease Similarity by Integrating Semantic and Gene Functional Association. PLoS ONE, 2014, 9, e99415.	1.1	117
74	Towards integrative gene functional similarity measurement. BMC Bioinformatics, 2014, 15, S5.	1.2	26
75	An integrative approach for measuring semantic similarities using gene ontology. BMC Systems Biology, 2014, 8, S8.	3.0	20
76	Identifying cross-category relations in gene ontology and constructing genome-specific term association networks. BMC Bioinformatics, 2013, 14, S15.	1.2	14