Qing Yan

List of Publications by Year
in descending order

105 papers	1,978 citations	304743 22 h-index	302126 39 g-index
107 all docs	107 docs citations	107 times ranked	1706 citing authors

#	Article	IF	Citations
1	Predicting miRNA–Disease Associations Through Deep Autoencoder With Multiple Kernel Learning. IEEE Transactions on Neural Networks and Learning Systems, 2023, 34, 5570-5579.	11.3	19
2	A New Method Based on Matrix Completion and Non-Negative Matrix Factorization for Predicting Disease-Associated miRNAs. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2022, 19, 763-772.	3.0	7
3	An Ensemble Framework for Improving the Prediction of Deleterious Synonymous Mutation. IEEE Transactions on Circuits and Systems for Video Technology, 2022, 32, 2603-2611.	8.3	6
4	Visualization and Analysis of Single Cell RNA-Seq Data by Maximizing Correntropy Based Non-Negative Low Rank Representation. IEEE Journal of Biomedical and Health Informatics, 2022, 26, 1872-1882.	6.3	4
5	HTRPCA: Hypergraph Regularized Tensor Robust Principal Component Analysis for Sample Clustering in Tumor Omics Data. Interdisciplinary Sciences, Computational Life Sciences, 2022, 14, 22-33.	3.6	7
6	Unsupervised Cluster Analysis and Gene Marker Extraction of scRNA-seq Data Based On Non-Negative Matrix Factorization. IEEE Journal of Biomedical and Health Informatics, 2022, 26, 458-467.	6.3	14
7	NCPLP: A Novel Approach for Predicting Microbe-Associated Diseases With Network Consistency Projection and Label Propagation. IEEE Transactions on Cybernetics, 2022, 52, 5079-5087.	9.5	24
8	A two-step ensemble learning for predicting protein hot spot residues from whole protein sequence. Amino Acids, 2022, 54, 765-776.	2.7	3
9	scHFC: a hybrid fuzzy clustering method for single-cell RNA-seq data optimized by natural computation. Briefings in Bioinformatics, 2022, 23, .	6.5	6
10	SLRRSC: Single-Cell Type Recognition Method Based on Similarity and Graph Regularization Constraints. IEEE Journal of Biomedical and Health Informatics, 2022, 26, 3556-3566.	6.3	8
11	Promoter prediction in nannochloropsis based on densely connected convolutional neural networks. Methods, 2022, 204, 38-46.	3.8	6
12	Nuclei-Guided Network for Breast Cancer Grading in HE-Stained Pathological Images. Sensors, 2022, 22, 4061.	3.8	8
13	scCNC: a method based on capsule network for clustering scRNA-seq data. Bioinformatics, 2022, 38, 3703-3709.	4.1	6
14	Correntropy-Based Hypergraph Regularized NMF for Clustering and Feature Selection on Multi-Cancer Integrated Data. IEEE Transactions on Cybernetics, 2021, 51, 3952-3963.	9.5	62
15	Potential Pathogenic Genes Prioritization Based on Protein Domain Interaction Network Analysis. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2021, 18, 1026-1034.	3.0	13
16	Imbalance Data Processing Strategy for Protein Interaction Sites Prediction. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2021, 18, 985-994.	3.0	25
17	GAERF: predicting lncRNA-disease associations by graph auto-encoder and random forest. Briefings in Bioinformatics, 2021, 22, .	6.5	51
18	Joint Lp-Norm and L2,1-Norm Constrained Graph Laplacian PCA for Robust Tumor Sample Clustering and Gene Network Module Discovery. Frontiers in Genetics, 2021, 12, 621317.	2.3	3

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19	usDSM: a novel method for deleterious synonymous mutation prediction using undersampling scheme. Briefings in Bioinformatics, 2021, 22, .	6.5	12
20	MiRNA-disease association prediction via hypergraph learning based on high-dimensionality features. BMC Medical Informatics and Decision Making, 2021, 21, 133.	3.0	11
21	Richer fusion network for breast cancer classification based on multimodal data. BMC Medical Informatics and Decision Making, 2021, 21, 134.	3.0	22
22	A Cascade Graph Convolutional Network for Predicting Protein–Ligand Binding Affinity. International Journal of Molecular Sciences, 2021, 22, 4023.	4.1	18
23	Identification of driver genes based on gene mutational effects and network centrality. BMC Bioinformatics, 2021, 22, 457.	2.6	3
24	Double matrix completion for circRNA-disease association prediction. BMC Bioinformatics, 2021, 22, 307.	2.6	10
25	SCDRHA: A scRNA-Seq Data Dimensionality Reduction Algorithm Based on Hierarchical Autoencoder. Frontiers in Genetics, 2021, 12, 733906.	2.3	8
26	Predicting miRNA-Disease Associations Based on Heterogeneous Graph Attention Networks. Frontiers in Genetics, 2021, 12, 727744.	2.3	7
27	GATNNCDA: A Method Based on Graph Attention Network and Multi-Layer Neural Network for Predicting circRNA-Disease Associations. International Journal of Molecular Sciences, 2021, 22, 8505.	4.1	7
28	DLFF-ACP: prediction of ACPs based on deep learning and multi-view features fusion. PeerJ, 2021, 9, e11906.	2.0	10
29	Kernel Risk-Sensitive Loss based Hyper-graph Regularized Robust Extreme Learning Machine and Its Semi-supervised Extension for Classification. Knowledge-Based Systems, 2021, 227, 107226.	7.1	7
30	ILPMDA: Predicting miRNA–Disease Association Based on Improved Label Propagation. Frontiers in Genetics, 2021, 12, 743665.	2.3	1
31	Sparse Hyper-graph Non-negative Matrix Factorization by Maximizing Correntropy. , 2021, , .		1
32	Breast cancer histopathological image classification using a hybrid deep neural network. Methods, 2020, 173, 52-60.	3.8	204
33	Comparison and integration of computational methods for deleterious synonymous mutation prediction. Briefings in Bioinformatics, 2020, 21, 970-981.	6.5	56
34	A Heuristic Algorithm for Identifying Molecular Signatures in Cancer. IEEE Transactions on Nanobioscience, 2020, 19, 132-141.	3.3	41
35	A feature-based approach to predict hot spots in protein–DNA binding interfaces. Briefings in Bioinformatics, 2020, 21, 1038-1046.	6.5	31
36	Integrative Hypergraph Regularization Principal Component Analysis for Sample Clustering and Co-Expression Genes Network Analysis on Multi-Omics Data. IEEE Journal of Biomedical and Health Informatics, 2020, 24, 1823-1834.	6.3	16

#	ARTICLE	IF	CITATIONS
37	Correntropy induced loss based sparse robust graph regularized extreme learning machine for cancer classification. BMC Bioinformatics, 2020, 21, 445.	2.6	8
38	Convolutional Residual-Attention: A Deep Learning Approach for Precipitation Nowcasting. Advances in Meteorology, 2020, 2020, 1-12.	1.6	24
39	Prioritizing Cancer Genes Based on an Improved Random Walk Method. Frontiers in Genetics, 2020, 11, 377.	2.3	22
40	Block-Constraint Laplacian-Regularized Low-Rank Representation and Its Application for Cancer Sample Clustering Based on Integrated TCGA Data. Complexity, 2020, 2020, 1-13.	1.6	6
41	Absolute radiometric calibration of Fengyun-3D Medium Resolution Spectral Imager-II and radiation characteristics analysis. Journal of Applied Remote Sensing, 2020, 14, .	1.3	5
42	Locally Manifold Non-negative Matrix Factorization Based on Centroid for scRNA-seq Data Analysis. , 2020, , .		0
43	NANet: Nuclei-Aware Network for Grading of Breast Cancer in HE Stained Pathological Images. , 2020, , .		8
44	A Mixed-Norm Laplacian Regularized Low-Rank Representation Method for Tumor Samples Clustering. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2019, 16, 172-182.	3.0	16
45	A Random Walk Based Cluster Ensemble Approach for Data Integration and Cancer Subtyping. Genes, 2019, 10, 66.	2.4	4
46	Supervised Discriminative Sparse PCA for Com-Characteristic Gene Selection and Tumor Classification on Multiview Biological Data. IEEE Transactions on Neural Networks and Learning Systems, 2019, 30, 2926-2937.	11.3	42
47	MECoRank: cancer driver genes discovery simultaneously evaluating the impact of SNVs and differential expression on transcriptional networks. BMC Medical Genomics, 2019, 12, 140.	1.5	3
48	Sparse Graph Regularization Non-Negative Matrix Factorization Based on Huber Loss Model for Cancer Data Analysis. Frontiers in Genetics, 2019, 10, 1054.	2.3	7
49	A convolutional neural network Cascade for plantar pressure images registration. Gait and Posture, 2019, 68, 403-408.	1.4	5
50	Integrative graph regularized matrix factorization for drug-pathway associations analysis. Computational Biology and Chemistry, 2019, 78, 474-480.	2.3	4
51	Introducing Heuristic Information into Ant Colony Optimization Algorithm for Identifying Epistasis. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2019, 17, 1-1.	3.0	10
52	A Dynamic Scale-Free Network Particle Swarm Optimization for Extracting Features on Multi-Omics Data. Journal of Computational Biology, 2019, 26, 769-781.	1.6	2
53	Non-Negative Symmetric Low-Rank Representation Graph Regularized Method for Cancer Clustering Based on Score Function. Frontiers in Genetics, 2019, 10, 1353.	2.3	2
54	Computational identification of deleterious synonymous variants in human genomes using a feature-based approach. BMC Medical Genomics, 2019, 12, 12.	1.5	47

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55	Regularized Non-Negative Matrix Factorization for Identifying Differentially Expressed Genes and Clustering Samples: A Survey. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2018, 15, 974-987.	3.0	52
56	Spectral and Multi-Spatial-Feature Based Deep Learning for Hyperspectral Remote Sensing Image Classification. , 2018, , .		1
57	A Hybrid Convolutional and Recurrent Deep Neural Network for Breast Cancer Pathological Image Classification. , 2018, , .		12
58	Semi-Supervised Subspace Clustering via Non-Negative Low-Rank Representation for Hyperspectral Images. , 2018, , .		2
59	Approximate sparse spectral clustering based on local information maintenance for hyperspectral image classification. PLoS ONE, 2018, 13, e0202161.	2.5	1
60	Protein fold recognition based on sparse representation based classification. Artificial Intelligence in Medicine, 2017, 79, 1-8.	6.5	36
61	Cancer Subtype Discovery Based on Integrative Model of Multigenomic Data. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2017, 14, 1115-1121.	3.0	32
62	Graph regularized robust non-negative matrix factorization for clustering and selecting differentially expressed genes. , 2017, , .		5
63	Robust graph regularized sparse orthogonal nonnegative matrix factorization for identifying differentially expressed genes. , 2017, , .		0
64	Low-rank representation regularized by $L_{2,1}$-norm for identifying differentially expressed genes. , 2017, , .		0
65	DriverFinder: A Gene Length-Based Network Method to Identify Cancer Driver Genes. Complexity, 2017, 2017, 1-10.	1.6	12
66	Class Probability Propagation of Supervised Information Based on Sparse Subspace Clustering for Hyperspectral Images. Remote Sensing, 2017, 9, 1017.	4.0	15
67	Prediction of Protein Hotspots from Whole Protein Sequences by a Random Projection Ensemble System. International Journal of Molecular Sciences, 2017, 18, 1543.	4.1	18
68	Robust Nonnegative Matrix Factorization via Joint Graph Laplacian and Discriminative Information for Identifying Differentially Expressed Genes. Complexity, 2017, 2017, 1-11.	1.6	16
69	Identifying drug-pathway association pairs based on L2,1-integrative penalized matrix decomposition. BMC Systems Biology, 2017, 11, 119.	3.0	11
70	epiACO - a method for identifying epistasis based on ant Colony optimization algorithm. BioData Mining, 2017, 10, 23.	4.0	51
71	Identifying drug-pathway association pairs based on L1L2,1-integrative penalized matrix decomposition. Oncotarget, 2017, 8, 48075-48085.	1.8	6
72	ndmaSNF: cancer subtype discovery based on integrative framework assisted by network diffusion model. Oncotarget, 2017, 8, 89021-89032.	1.8	15

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73	L<inf>21</inf>-iPaD: An efficient method for drug-pathway association pairs inference. , 2016, , .		0
74	Robust graph regularized discriminative nonnegative matrix factorization for characteristic gene selection. , 2016, , .		0
75	Cancer genes discovery based on integtating transcriptomic data and the impact of gene length. , 2016, , .		0
76	Differentially expressed genes selection via Truncated Nuclear Norm Regularization. , 2016, , .		0
77	LNDriver: identifying driver genes by integrating mutation and expression data based on gene-gene interaction network. BMC Bioinformatics, 2016, 17, 467.	2.6	28
78	A p-norm singular value decomposition method for robust tumor clustering. , 2016, , .		0
79	Concordance between somatic copy number loss and down-regulated expression: A pan-cancer study of cancer predisposition genes. Scientific Reports, 2016, 6, 37358.	3.3	13
80	Sparse singular value decomposition-based feature extraction for identifying differentially expressed genes. , 2016, , .		2
81	Differentially expressed genes selection via Laplacian regularized low-rank representation method. Computational Biology and Chemistry, 2016, 65, 185-192.	2.3	14
82	CINOEDV: a co-information based method for detecting and visualizing n-order epistatic interactions. BMC Bioinformatics, 2016, 17, 214.	2.6	27
83	Identification of mutated driver pathways in cancer using a multi-objective optimization model. Computers in Biology and Medicine, 2016, 72, 22-29.	7.0	18
84	Block-Constraint Robust Principal Component Analysis and its Application to Integrated Analysis of TCGA Data. IEEE Transactions on Nanobioscience, 2016, 15, 510-516.	3.3	17
85	An NMF-L2,1-Norm Constraint Method for Characteristic Gene Selection. PLoS ONE, 2016, 11, e0158494.	2.5	21
86	Predicting hot spots in protein interfaces based on protrusion index, pseudo hydrophobicity and electron-ion interaction pseudopotential features. Oncotarget, 2016, 7, 18065-18075.	1.8	21
87	Identification of breast cancer candidate genes using gene co-expression and protein-protein interaction information. Oncotarget, 2016, 7, 36092-36100.	1.8	19
88	dbCPG: A web resource for cancer predisposition genes. Oncotarget, 2016, 7, 37803-37811.	1.8	15
89	MGDB: a comprehensive database of genes involved in melanoma. Database: the Journal of Biological Databases and Curation, 2015, 2015, bav097.	3.0	11
90	An Improved Opposition-Based Learning Particle Swarm Optimization for the Detection of SNP-SNP Interactions. BioMed Research International, 2015, 2015, 1-12.	1.9	38

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91	Module Based Differential Coexpression Analysis Method for Type 2 Diabetes. BioMed Research International, 2015, 2015, 1-8.	1.9	12
92	*j*NMFMA: a joint non-negative matrix factorization meta-analysis of transcriptomics data. Bioinformatics, 2015, 31, 572-580.	4.1	46
93	A new pedestrian detection method based on combined HOG and LSS features. Neurocomputing, 2015, 151, 1006-1014.	5.9	49
94	Low-Rank and Eigenface Based Sparse Representation for Face Recognition. PLoS ONE, 2014, 9, e110318.	2.5	3
95	Sparse Representation for Tumor Classification Based on Feature Extraction Using Latent Low-Rank Representation. BioMed Research International, 2014, 2014, 1-7.	1.9	8
96	Simulated Annealing Based Algorithm for Identifying Mutated Driver Pathways in Cancer. BioMed Research International, 2014, 2014, 1-7.	1.9	6
97	A Class-information-based SNMF method for selecting characteristic genes. , 2014, , .		0
98	A survey of pattern classification-based methods for predicting survival time of lung cancer patients. , 2014, , .		4
99	MutualCascade method for pedestrian detection. Neurocomputing, 2014, 137, 127-135.	5.9	18
100	Differential coexpression analysis in gene modules level and its application to type 2 diabetes. , 2013, , .		1
101	Tumor Classification Using Eigengene-Based Classifier Committee Learning Algorithm. IEEE Signal Processing Letters, 2012, 19, 455-458.	3.6	8
102	A large scale test dataset to determine optimal retention index threshold based on three mass spectral similarity measures. Journal of Chromatography A, 2012, 1251, 188-193.	3.7	20
103	Molecular Pattern Discovery Based on Penalized Matrix Decomposition. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2011, 8, 1592-1603.	3.0	86
104	Tumor Classification Based on Non-Negative Matrix Factorization Using Gene Expression Data. IEEE Transactions on Nanobioscience, 2011, 10, 86-93.	3.3	49
105	Palmprint recognition using FastICA algorithm and radial basis probabilistic neural network. Neurocomputing, 2006, 69, 1782-1786.	5.9	185