

Qing Yan

List of Publications by Year in descending order

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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	Breast cancer histopathological image classification using a hybrid deep neural network. <i>Methods</i> , 2020, 173, 52-60.	3.8	204
2	Palmprint recognition using FastICA algorithm and radial basis probabilistic neural network. <i>Neurocomputing</i> , 2006, 69, 1782-1786.	5.9	185
3	Molecular Pattern Discovery Based on Penalized Matrix Decomposition. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2011, 8, 1592-1603.	3.0	86
4	Correntropy-Based Hypergraph Regularized NMF for Clustering and Feature Selection on Multi-Cancer Integrated Data. <i>IEEE Transactions on Cybernetics</i> , 2021, 51, 3952-3963.	9.5	62
5	Comparison and integration of computational methods for deleterious synonymous mutation prediction. <i>Briefings in Bioinformatics</i> , 2020, 21, 970-981.	6.5	56
6	Regularized Non-Negative Matrix Factorization for Identifying Differentially Expressed Genes and Clustering Samples: A Survey. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2018, 15, 974-987.	3.0	52
7	epiACO - a method for identifying epistasis based on ant Colony optimization algorithm. <i>BioData Mining</i> , 2017, 10, 23.	4.0	51
8	GAERF: predicting lncRNA-disease associations by graph auto-encoder and random forest. <i>Briefings in Bioinformatics</i> , 2021, 22, .	6.5	51
9	Tumor Classification Based on Non-Negative Matrix Factorization Using Gene Expression Data. <i>IEEE Transactions on Nanobioscience</i> , 2011, 10, 86-93.	3.3	49
10	A new pedestrian detection method based on combined HOG and LSS features. <i>Neurocomputing</i> , 2015, 151, 1006-1014.	5.9	49
11	Computational identification of deleterious synonymous variants in human genomes using a feature-based approach. <i>BMC Medical Genomics</i> , 2019, 12, 12.	1.5	47
12	<i>nmfma</i> : a joint non-negative matrix factorization meta-analysis of transcriptomics data. <i>Bioinformatics</i> , 2015, 31, 572-580.	4.1	46
13	Supervised Discriminative Sparse PCA for Com-Characteristic Gene Selection and Tumor Classification on Multiview Biological Data. <i>IEEE Transactions on Neural Networks and Learning Systems</i> , 2019, 30, 2926-2937.	11.3	42
14	A Heuristic Algorithm for Identifying Molecular Signatures in Cancer. <i>IEEE Transactions on Nanobioscience</i> , 2020, 19, 132-141.	3.3	41
15	An Improved Opposition-Based Learning Particle Swarm Optimization for the Detection of SNP-SNP Interactions. <i>BioMed Research International</i> , 2015, 2015, 1-12.	1.9	38
16	Protein fold recognition based on sparse representation based classification. <i>Artificial Intelligence in Medicine</i> , 2017, 79, 1-8.	6.5	36
17	Cancer Subtype Discovery Based on Integrative Model of Multigenomic Data. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2017, 14, 1115-1121.	3.0	32
18	A feature-based approach to predict hot spots in protein-DNA binding interfaces. <i>Briefings in Bioinformatics</i> , 2020, 21, 1038-1046.	6.5	31

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19	LNDriver: identifying driver genes by integrating mutation and expression data based on gene-gene interaction network. BMC Bioinformatics, 2016, 17, 467.	2.6	28
20	CINOEDV: a co-information based method for detecting and visualizing n-order epistatic interactions. BMC Bioinformatics, 2016, 17, 214.	2.6	27
21	Imbalance Data Processing Strategy for Protein Interaction Sites Prediction. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2021, 18, 985-994.	3.0	25
22	Convolutional Residual-Attention: A Deep Learning Approach for Precipitation Nowcasting. Advances in Meteorology, 2020, 2020, 1-12.	1.6	24
23	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
24	Prioritizing Cancer Genes Based on an Improved Random Walk Method. Frontiers in Genetics, 2020, 11, 377.	2.3	22
25	Richer fusion network for breast cancer classification based on multimodal data. BMC Medical Informatics and Decision Making, 2021, 21, 134.	3.0	22
26	An NMF-L2,1-Norm Constraint Method for Characteristic Gene Selection. PLoS ONE, 2016, 11, e0158494.	2.5	21
27	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
28	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
29	Identification of breast cancer candidate genes using gene co-expression and protein-protein interaction information. Oncotarget, 2016, 7, 36092-36100.	1.8	19
30	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
31	MutualCascade method for pedestrian detection. Neurocomputing, 2014, 137, 127-135.	5.9	18
32	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
33	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
34	A Cascade Graph Convolutional Network for Predicting Protein-Ligand Binding Affinity. International Journal of Molecular Sciences, 2021, 22, 4023.	4.1	18
35	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
36	Robust Nonnegative Matrix Factorization via Joint Graph Laplacian and Discriminative Information for Identifying Differentially Expressed Genes. Complexity, 2017, 2017, 1-11.	1.6	16

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37	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
38	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
39	Class Probability Propagation of Supervised Information Based on Sparse Subspace Clustering for Hyperspectral Images. Remote Sensing, 2017, 9, 1017.	4.0	15
40	ndmaSNF: cancer subtype discovery based on integrative framework assisted by network diffusion model. Oncotarget, 2017, 8, 89021-89032.	1.8	15
41	dbCPG: A web resource for cancer predisposition genes. Oncotarget, 2016, 7, 37803-37811.	1.8	15
42	Differentially expressed genes selection via Laplacian regularized low-rank representation method. Computational Biology and Chemistry, 2016, 65, 185-192.	2.3	14
43	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
44	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
45	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
46	Module Based Differential Coexpression Analysis Method for Type 2 Diabetes. BioMed Research International, 2015, 2015, 1-8.	1.9	12
47	DriverFinder: A Gene Length-Based Network Method to Identify Cancer Driver Genes. Complexity, 2017, 2017, 1-10.	1.6	12
48	A Hybrid Convolutional and Recurrent Deep Neural Network for Breast Cancer Pathological Image Classification. , 2018, , .		12
49	usDSM: a novel method for deleterious synonymous mutation prediction using undersampling scheme. Briefings in Bioinformatics, 2021, 22, .	6.5	12
50	MGDB: a comprehensive database of genes involved in melanoma. Database: the Journal of Biological Databases and Curation, 2015, 2015, bav097.	3.0	11
51	Identifying drug-pathway association pairs based on L2,1-integrative penalized matrix decomposition. BMC Systems Biology, 2017, 11, 119.	3.0	11
52	MiRNA-disease association prediction via hypergraph learning based on high-dimensionality features. BMC Medical Informatics and Decision Making, 2021, 21, 133.	3.0	11
53	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
54	Double matrix completion for circRNA-disease association prediction. BMC Bioinformatics, 2021, 22, 307.	2.6	10

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55	DLFF-ACP: prediction of ACPs based on deep learning and multi-view features fusion. PeerJ, 2021, 9, e11906.	2.0	10
56	Tumor Classification Using Eigengene-Based Classifier Committee Learning Algorithm. IEEE Signal Processing Letters, 2012, 19, 455-458.	3.6	8
57	Sparse Representation for Tumor Classification Based on Feature Extraction Using Latent Low-Rank Representation. BioMed Research International, 2014, 2014, 1-7.	1.9	8
58	Correntropy induced loss based sparse robust graph regularized extreme learning machine for cancer classification. BMC Bioinformatics, 2020, 21, 445.	2.6	8
59	SCDRHA: A scRNA-Seq Data Dimensionality Reduction Algorithm Based on Hierarchical Autoencoder. Frontiers in Genetics, 2021, 12, 733906.	2.3	8
60	NANet: Nuclei-Aware Network for Grading of Breast Cancer in HE Stained Pathological Images. , 2020, , .		8
61	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
62	Nuclei-Guided Network for Breast Cancer Grading in HE-Stained Pathological Images. Sensors, 2022, 22, 4061.	3.8	8
63	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
64	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
65	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
66	Predicting miRNA-Disease Associations Based on Heterogeneous Graph Attention Networks. Frontiers in Genetics, 2021, 12, 727744.	2.3	7
67	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
68	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
69	Simulated Annealing Based Algorithm for Identifying Mutated Driver Pathways in Cancer. BioMed Research International, 2014, 2014, 1-7.	1.9	6
70	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
71	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
72	Identifying drug-pathway association pairs based on L1L2,1-integrative penalized matrix decomposition. Oncotarget, 2017, 8, 48075-48085.	1.8	6

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73	scHFC: a hybrid fuzzy clustering method for single-cell RNA-seq data optimized by natural computation. <i>Briefings in Bioinformatics</i> , 2022, 23, .	6.5	6
74	Promoter prediction in nanochloropsis based on densely connected convolutional neural networks. <i>Methods</i> , 2022, 204, 38-46.	3.8	6
75	scCNC: a method based on capsule network for clustering scRNA-seq data. <i>Bioinformatics</i> , 2022, 38, 3703-3709.	4.1	6
76	Graph regularized robust non-negative matrix factorization for clustering and selecting differentially expressed genes. , 2017, , .		5
77	A convolutional neural network Cascade for plantar pressure images registration. <i>Gait and Posture</i> , 2019, 68, 403-408.	1.4	5
78	Absolute radiometric calibration of Fengyun-3D Medium Resolution Spectral Imager-II and radiation characteristics analysis. <i>Journal of Applied Remote Sensing</i> , 2020, 14, .	1.3	5
79	A survey of pattern classification-based methods for predicting survival time of lung cancer patients. , 2014, , .		4
80	A Random Walk Based Cluster Ensemble Approach for Data Integration and Cancer Subtyping. <i>Genes</i> , 2019, 10, 66.	2.4	4
81	Integrative graph regularized matrix factorization for drug-pathway associations analysis. <i>Computational Biology and Chemistry</i> , 2019, 78, 474-480.	2.3	4
82	Visualization and Analysis of Single Cell RNA-Seq Data by Maximizing Correntropy Based Non-Negative Low Rank Representation. <i>IEEE Journal of Biomedical and Health Informatics</i> , 2022, 26, 1872-1882.	6.3	4
83	Low-Rank and Eigenface Based Sparse Representation for Face Recognition. <i>PLoS ONE</i> , 2014, 9, e110318.	2.5	3
84	MECoRank: cancer driver genes discovery simultaneously evaluating the impact of SNVs and differential expression on transcriptional networks. <i>BMC Medical Genomics</i> , 2019, 12, 140.	1.5	3
85	Joint Lp-Norm and L2,1-Norm Constrained Graph Laplacian PCA for Robust Tumor Sample Clustering and Gene Network Module Discovery. <i>Frontiers in Genetics</i> , 2021, 12, 621317.	2.3	3
86	Identification of driver genes based on gene mutational effects and network centrality. <i>BMC Bioinformatics</i> , 2021, 22, 457.	2.6	3
87	A two-step ensemble learning for predicting protein hot spot residues from whole protein sequence. <i>Amino Acids</i> , 2022, 54, 765-776.	2.7	3
88	Sparse singular value decomposition-based feature extraction for identifying differentially expressed genes. , 2016, , .		2
89	Semi-Supervised Subspace Clustering via Non-Negative Low-Rank Representation for Hyperspectral Images. , 2018, , .		2
90	A Dynamic Scale-Free Network Particle Swarm Optimization for Extracting Features on Multi-Omics Data. <i>Journal of Computational Biology</i> , 2019, 26, 769-781.	1.6	2

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91	Non-Negative Symmetric Low-Rank Representation Graph Regularized Method for Cancer Clustering Based on Score Function. <i>Frontiers in Genetics</i> , 2019, 10, 1353.	2.3	2
92	Differential coexpression analysis in gene modules level and its application to type 2 diabetes. , 2013, , .		1
93	Spectral and Multi-Spatial-Feature Based Deep Learning for Hyperspectral Remote Sensing Image Classification. , 2018, , .		1
94	Approximate sparse spectral clustering based on local information maintenance for hyperspectral image classification. <i>PLoS ONE</i> , 2018, 13, e0202161.	2.5	1
95	ILPMDA: Predicting miRNA-Disease Association Based on Improved Label Propagation. <i>Frontiers in Genetics</i> , 2021, 12, 743665.	2.3	1
96	Sparse Hyper-graph Non-negative Matrix Factorization by Maximizing Correntropy. , 2021, , .		1
97	A Class-information-based SNMF method for selecting characteristic genes. , 2014, , .		0
98	L<inf>21</inf>-iPaD: An efficient method for drug-pathway association pairs inference. , 2016, , .		0
99	Robust graph regularized discriminative nonnegative matrix factorization for characteristic gene selection. , 2016, , .		0
100	Cancer genes discovery based on integtating transcriptomic data and the impact of gene length. , 2016, , .		0
101	Differentially expressed genes selection via Truncated Nuclear Norm Regularization. , 2016, , .		0
102	A p-norm singular value decomposition method for robust tumor clustering. , 2016, , .		0
103	Robust graph regularized sparse orthogonal nonnegative matrix factorization for identifying differentially expressed genes. , 2017, , .		0
104	Low-rank representation regularized by $L_{2,1}$ -norm for identifying differentially expressed genes. , 2017, , .		0
105	Locally Manifold Non-negative Matrix Factorization Based on Centroid for scRNA-seq Data Analysis. , 2020, , .		0