

# Jin-Xing Liu

## List of Publications by Year in descending order

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142  
papers

1,572  
citations

331259

21  
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433756

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151  
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151  
docs citations

151  
times ranked

1066  
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.	7.2	19
2	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.	3.9	4
3	Robust Principal Component Analysis Based On Hypergraph Regularization for Sample Clustering and Co-Characteristic Gene Selection. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2022, 19, 2420-2430.	1.9	1
4	HTRPCA: Hypergraph Regularized Tensor Robust Principal Component Analysis for Sample Clustering in Tumor Omics Data. Interdisciplinary Sciences, Computational Life Sciences, 2022, 14, 22-33.	2.2	7
5	Kernel risk-sensitive mean p-power error based robust extreme learning machine for classification. International Journal of Machine Learning and Cybernetics, 2022, 13, 199-216.	2.3	1
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.	3.9	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.	6.2	24
8	MSF-LRR: Multi-similarity Information Fusion through Low-Rank Representation to Predict Disease-associated Microbes. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2022, PP, 1-1.	1.9	2
9	SLRRSC: Single-Cell Type Recognition Method Based on Similarity and Graph Regularization Constraints. IEEE Journal of Biomedical and Health Informatics, 2022, 26, 3556-3566.	3.9	8
10	Multi-View Random-Walk Graph Regularization Low-Rank Representation for Cancer Clustering and Differentially Expressed Gene Selection. IEEE Journal of Biomedical and Health Informatics, 2022, 26, 3578-3589.	3.9	5
11	Tensor decomposition based on the potential low-rank and p-shrinkage generalized threshold algorithm for analyzing cancer multiomics data. Journal of Bioinformatics and Computational Biology, 2022, , 2250002.	0.3	0
12	Predicting miRNA-disease associations via layer attention graph convolutional network model. BMC Medical Informatics and Decision Making, 2022, 22, 69.	1.5	3
13	Effects of Multi-Omics Characteristics on Identification of Driver Genes Using Machine Learning Algorithms. Genes, 2022, 13, 716.	1.0	3
14	Tensor Decomposition Based on Global Features and Sparse Structure for Analyzing Cancer Multiomics Data. Current Bioinformatics, 2022, 17, 946-957.	0.7	1
15	Multi-Objective Artificial Bee Colony Algorithm Based on Scale-Free Network for Epistasis Detection. Genes, 2022, 13, 871.	1.0	3
16	DSTPCA: Double-Sparse Constrained Tensor Principal Component Analysis Method for Feature Selection. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2021, 18, 1481-1491.	1.9	12
17	Correntropy-Based Hypergraph Regularized NMF for Clustering and Feature Selection on Multi-Cancer Integrated Data. IEEE Transactions on Cybernetics, 2021, 51, 3952-3963.	6.2	62
18	Dual Hyper-Graph Regularized Supervised NMF for Selecting Differentially Expressed Genes and Tumor Classification. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2021, 18, 2375-2383.	1.9	12

#	ARTICLE	IF	CITATIONS
19	Protein Fold Recognition by Combining Support Vector Machines and Pairwise Sequence Similarity Scores. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2021, 18, 2008-2016.	1.9	13
20	WGRCMF: A Weighted Graph Regularized Collaborative Matrix Factorization Method for Predicting Novel LncRNA-Disease Associations. <i>IEEE Journal of Biomedical and Health Informatics</i> , 2021, 25, 257-265.	3.9	18
21	LWPCMF: Logistic Weighted Profile-Based Collaborative Matrix Factorization for Predicting MiRNA-Disease Associations. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2021, 18, 1122-1129.	1.9	17
22	The Automatic Detection of Seizure Based on Tensor Distance And Bayesian Linear Discriminant Analysis. <i>International Journal of Neural Systems</i> , 2021, 31, 2150006.	3.2	21
23	Sparse robust graph-regularized non-negative matrix factorization based on correntropy. <i>Journal of Bioinformatics and Computational Biology</i> , 2021, 19, 2050047.	0.3	3
24	Extreme Learning Machine Based on Double Kernel Risk-Sensitive Loss for Cancer Samples Classification. <i>Lecture Notes in Computer Science</i> , 2021, , 532-539.	1.0	0
25	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.	1.1	3
26	Logistic Weighted Profile-Based Bi-Random Walk for Exploring MiRNA-Disease Associations. <i>Journal of Computer Science and Technology</i> , 2021, 36, 276-287.	0.9	5
27	Multiscale part mutual information for quantifying nonlinear direct associations in networks. <i>Bioinformatics</i> , 2021, 37, 2920-2929.	1.8	0
28	Multi-Label Fusion Collaborative Matrix Factorization for Predicting LncRNA-Disease Associations. <i>IEEE Journal of Biomedical and Health Informatics</i> , 2021, 25, 881-890.	3.9	13
29	IPCARF: improving lncRNA-disease association prediction using incremental principal component analysis feature selection and a random forest classifier. <i>BMC Bioinformatics</i> , 2021, 22, 175.	1.2	34
30	DSCMF: prediction of lncRNA-disease associations based on dual sparse collaborative matrix factorization. <i>BMC Bioinformatics</i> , 2021, 22, 241.	1.2	16
31	Ensemble Adaptive Total Variation Graph Regularized NMF for Singlecell RNA-seq Data Analysis. <i>Current Bioinformatics</i> , 2021, 16, 1014-1023.	0.7	5
32	Adaptive Total-Variation Regularized Low-Rank Representation for Analyzing Single-Cell RNA-seq Data. <i>Interdisciplinary Sciences, Computational Life Sciences</i> , 2021, 13, 476-489.	2.2	7
33	NMFNA: A Non-negative Matrix Factorization Network Analysis Method for Identifying Modules and Characteristic Genes of Pancreatic Cancer. <i>Frontiers in Genetics</i> , 2021, 12, 678642.	1.1	4
34	Similarity and Dissimilarity Regularized Nonnegative Matrix Factorization for Single-Cell RNA-seq Analysis. <i>Interdisciplinary Sciences, Computational Life Sciences</i> , 2021, , 1.	2.2	1
35	Kernel Risk-Sensitive Loss based Hyper-graph Regularized Robust Extreme Learning Machine and Its Semi-supervised Extension for Classification. <i>Knowledge-Based Systems</i> , 2021, 227, 107226.	4.0	7
36	Automatic detection for epileptic seizure using graph-regularized nonnegative matrix factorization and Bayesian linear discriminate analysis. <i>Biocybernetics and Biomedical Engineering</i> , 2021, 41, 1258-1271.	3.3	7

#	ARTICLE	IF	CITATIONS
37	MOPIO: A Multi-Objective Pigeon-Inspired Optimization Algorithm for Community Detection. <i>Symmetry</i> , 2021, 13, 49.	1.1	5
38	Bipartite graph-based collaborative matrix factorization method for predicting miRNA-disease associations. <i>BMC Bioinformatics</i> , 2021, 22, 573.	1.2	2
39	Robust Tensor Method Based on Correntropy and Tensor Singular Value Decomposition for Cancer Genomics Data. , 2021, , .		2
40	Adaptive total-variation joint learning model for analyzing single cell RNA seq data. , 2021, , .		0
41	Sparse Hyper-graph Non-negative Matrix Factorization by Maximizing Correntropy. , 2021, , .		1
42	lncRNA-Disease Associations Prediction Using Bipartite Local Model With Nearest Profile-Based Association Inferring. <i>IEEE Journal of Biomedical and Health Informatics</i> , 2020, 24, 1519-1527.	3.9	21
43	Integrative Hypergraph Regularization Principal Component Analysis for Sample Clustering and Co-Expression Genes Network Analysis on Multi-Omics Data. <i>IEEE Journal of Biomedical and Health Informatics</i> , 2020, 24, 1823-1834.	3.9	16
44	Correntropy induced loss based sparse robust graph regularized extreme learning machine for cancer classification. <i>BMC Bioinformatics</i> , 2020, 21, 445.	1.2	8
45	L2,1-Extreme Learning Machine: An Efficient Robust Classifier for Tumor Classification. <i>Computational Biology and Chemistry</i> , 2020, 89, 107368.	1.1	9
46	IDSSIM: an lncRNA functional similarity calculation model based on an improved disease semantic similarity method. <i>BMC Bioinformatics</i> , 2020, 21, 339.	1.2	17
47	MCCMF: collaborative matrix factorization based on matrix completion for predicting miRNA-disease associations. <i>BMC Bioinformatics</i> , 2020, 21, 454.	1.2	12
48	Single-cell RNA Sequencing Data Clustering by Low-Rank Subspace Ensemble Framework. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2020, PP, 1-1.	1.9	10
49	Hyper-Graph Regularized Constrained NMF for Selecting Differentially Expressed Genes and Tumor Classification. <i>IEEE Journal of Biomedical and Health Informatics</i> , 2020, 24, 3002-3011.	3.9	37
50	Block-Constraint Laplacian-Regularized Low-Rank Representation and Its Application for Cancer Sample Clustering Based on Integrated TCGA Data. <i>Complexity</i> , 2020, 2020, 1-13.	0.9	6
51	Automatic Seizure Prediction based on Modified Stockwell Transform and Tensor Decomposition. , 2020, , .		4
52	Application of a Deep Matrix Factorization Model on Integrated Gene Expression Data. <i>Current Bioinformatics</i> , 2020, 15, 359-367.	0.7	4
53	Inferring Communities and Key Genes of Triple Negative Breast Cancer Based on Robust Principal Component Analysis and Network Analysis. <i>Communications in Computer and Information Science</i> , 2020, , 137-151.	0.4	0
54	Locally Manifold Non-negative Matrix Factorization Based on Centroid for scRNA-seq Data Analysis. , 2020, , .		0

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55	Tensor Robust Principal Component Analysis with Low-Rank Weight Constraints for Sample Clustering. , 2020, , .		1
56	Sparse Regularization Tensor Robust PCA Based on t-product and Its Application in Cancer Genomic Data. , 2020, , .		5
57	An Integrated Robust Graph Regularized Non-negative Matrix Factorization for Multi-dimensional Genomic Data Analysis. Communications in Computer and Information Science, 2020, , 97-111.	0.4	1
58	DSNPCMF: Predicting MiRNA-Disease Associations with Collaborative Matrix Factorization Based on Double Sparse and Nearest Profile. Communications in Computer and Information Science, 2020, , 196-208.	0.4	0
59	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.	1.9	16
60	Dual Sparse Collaborative Matrix Factorization Method Based on Gaussian Kernel Function for Predicting LncRNA-Disease Associations. Lecture Notes in Computer Science, 2019, , 318-326.	1.0	4
61	NPCMF: Nearest Profile-based Collaborative Matrix Factorization method for predicting miRNA-disease associations. BMC Bioinformatics, 2019, 20, 353.	1.2	27
62	HC-HDSD: A method of hypergraph construction and high-density subgraph detection for inferring high-order epistatic interactions. Computational Biology and Chemistry, 2019, 78, 440-447.	1.1	4
63	Principal Component Analysis Based on Graph Laplacian and Double Sparse Constraints for Feature Selection and Sample Clustering on Multi-View Data. Human Heredity, 2019, 84, 47-58.	0.4	2
64	An Integrated Graph Regularized Non-Negative Matrix Factorization Model for Gene Co-Expression Network Analysis. IEEE Access, 2019, 7, 126594-126602.	2.6	9
65	Dual Graph-Laplacian PCA: A Closed-Form Solution for Bi-Clustering to Find “Checkerboard” Structures on Gene Expression Data. IEEE Access, 2019, 7, 151329-151338.	2.6	8
66	Robust hypergraph regularized non-negative matrix factorization for sample clustering and feature selection in multi-view gene expression data. Human Genomics, 2019, 13, 46.	1.4	8
67	Hypergraph Regularized Discriminative Nonnegative Matrix Factorization on Sample Classification and Co-Differentially Expressed Gene Selection. Complexity, 2019, 2019, 1-12.	0.9	4
68	PSO-CFDP: A Particle Swarm Optimization-Based Automatic Density Peaks Clustering Method for Cancer Subtyping. Human Heredity, 2019, 84, 9-20.	0.4	3
69	A Low-Rank Representation Method Regularized by Dual-Hypergraph Laplacian for Selecting Differentially Expressed Genes. Human Heredity, 2019, 84, 21-33.	0.4	2
70	NIPMI: A Network Method Based on Interaction Part Mutual Information to Detect Characteristic Genes From Integrated Data on Multi-Cancers. IEEE Access, 2019, 7, 135845-135854.	2.6	2
71	Dual-network sparse graph regularized matrix factorization for predicting miRNA-disease associations. Molecular Omics, 2019, 15, 130-137.	1.4	20
72	L2,1-GRMF: an improved graph regularized matrix factorization method to predict drug-target interactions. BMC Bioinformatics, 2019, 20, 287.	1.2	17

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73	Differentially Expressed Genes Extracted by the Tensor Robust Principal Component Analysis (TRPCA) Method. <i>Complexity</i> , 2019, 2019, 1-13.	0.9	11
74	LJELSR: A Strengthened Version of JELSR for Feature Selection and Clustering. <i>International Journal of Molecular Sciences</i> , 2019, 20, 886.	1.8	1
75	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.	7.2	42
76	A Review of Ant Colony Optimization Based Methods for Detecting Epistatic Interactions. <i>IEEE Access</i> , 2019, 7, 13497-13509.	2.6	25
77	Multi-cancer samples clustering via graph regularized low-rank representation method under sparse and symmetric constraints. <i>BMC Bioinformatics</i> , 2019, 20, 718.	1.2	7
78	A new method for mining information of co-expression network based on multi-cancers integrated data. <i>BMC Medical Genomics</i> , 2019, 12, 155.	0.7	6
79	RCMF: a robust collaborative matrix factorization method to predict miRNA-disease associations. <i>BMC Bioinformatics</i> , 2019, 20, 686.	1.2	6
80	Sparse Graph Regularization Non-Negative Matrix Factorization Based on Huber Loss Model for Cancer Data Analysis. <i>Frontiers in Genetics</i> , 2019, 10, 1054.	1.1	7
81	Integrative graph regularized matrix factorization for drug-pathway associations analysis. <i>Computational Biology and Chemistry</i> , 2019, 78, 474-480.	1.1	4
82	Introducing Heuristic Information into Ant Colony Optimization Algorithm for Identifying Epistasis. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2019, 17, 1-1.	1.9	10
83	Laplacian regularized low-rank representation for cancer samples clustering. <i>Computational Biology and Chemistry</i> , 2019, 78, 504-509.	1.1	9
84	The computational prediction of drug-disease interactions using the dual-network L2,1-CMF method. <i>BMC Bioinformatics</i> , 2019, 20, 5.	1.2	30
85	Network Analyses of Integrated Differentially Expressed Genes in Papillary Thyroid Carcinoma to Identify Characteristic Genes. <i>Genes</i> , 2019, 10, 45.	1.0	8
86	ACCBN: ant-Colony-clustering-based bipartite network method for predicting long non-coding RNA-protein interactions. <i>BMC Bioinformatics</i> , 2019, 20, 16.	1.2	26
87	Network analysis based on low-rank method for mining information on integrated data of multi-cancers. <i>Computational Biology and Chemistry</i> , 2019, 78, 468-473.	1.1	5
88	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.	0.8	2
89	Non-Negative Symmetric Low-Rank Representation Graph Regularized Method for Cancer Clustering Based on Score Function. <i>Frontiers in Genetics</i> , 2019, 10, 1353.	1.1	2
90	A New Model of Identifying Differentially Expressed Genes via Weighted Network Analysis Based on Dimensionality Reduction Method. <i>Current Bioinformatics</i> , 2019, 14, 762-770.	0.7	1

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91	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.	1.9	52
92	Hypergraph regularized NMF by $L_{2,1}$ -norm for Clustering and Com-abnormal Expression Genes Selection. , 2018, , .		4
93	A Fast Quantum Clustering Approach for Cancer Gene Clustering. , 2018, , .		2
94	Sparse Orthogonal Nonnegative Matrix Factorization for Identifying Differentially Expressed Genes and Clustering Tumor Samples. , 2018, , .		0
95	Co-differential Gene Selection and Clustering Based on Graph Regularized Multi-View NMF in Cancer Genomic Data. Genes, 2018, 9, 586.	1.0	25
96	The earth mover's distance and Bayesian linear discriminant analysis for epileptic seizure detection in scalp EEG. Biomedical Engineering Letters, 2018, 8, 373-382.	2.1	22
97	Identifying Characteristic Genes and Clustering via an $L_p$ -Norm Robust Feature Selection Method for Integrated Data. Lecture Notes in Computer Science, 2018, , 419-431.	1.0	1
98	A joint- $L_{2,1}$ -norm-constraint-based semi-supervised feature extraction for RNA-Seq data analysis. Neurocomputing, 2017, 228, 263-269.	3.5	27
99	PCA Based on Graph Laplacian Regularization and P-Norm for Gene Selection and Clustering. IEEE Transactions on Nanobioscience, 2017, 16, 257-265.	2.2	34
100	Robust and Efficient Biomolecular Clustering of Tumor Based on $\{p\}$ -Norm Singular Value Decomposition. IEEE Transactions on Nanobioscience, 2017, 16, 341-348.	2.2	5
101	Robust Principal Component Analysis Regularized by Truncated Nuclear Norm for Identifying Differentially Expressed Genes. IEEE Transactions on Nanobioscience, 2017, 16, 447-454.	2.2	8
102	Graph regularized robust non-negative matrix factorization for clustering and selecting differentially expressed genes. , 2017, , .		5
103	Feature selection and clustering via robust graph-laplacian PCA based on capped $L_{1,1}$ -norm. , 2017, , .		7
104	Robust graph regularized sparse orthogonal nonnegative matrix factorization for identifying differentially expressed genes. , 2017, , .		0
105	A convex multi-view low-rank sparse regression for feature selection and clustering. , 2017, , .		0
106	Low-rank representation regularized by $L_{2,1}$ -norm for identifying differentially expressed genes. , 2017, , .		0
107	Robust Nonnegative Matrix Factorization via Joint Graph Laplacian and Discriminative Information for Identifying Differentially Expressed Genes. Complexity, 2017, 2017, 1-11.	0.9	16
108	Joint $L_{2,1}$ -Norm Constraint and Graph-Laplacian PCA Method for Feature Extraction. BioMed Research International, 2017, 2017, 1-14.	0.9	8

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109	Identifying drug-pathway association pairs based on L <sub>2,1</sub> -integrative penalized matrix decomposition. BMC Systems Biology, 2017, 11, 119.	3.0	11
110	epiACO - a method for identifying epistasis based on ant Colony optimization algorithm. BioData Mining, 2017, 10, 23.	2.2	51
111	A Robust Manifold Graph Regularized Nonnegative Matrix Factorization Algorithm for Cancer Gene Clustering. Molecules, 2017, 22, 2131.	1.7	14
112	Identifying drug-pathway association pairs based on L <sub>1L2,1</sub> -integrative penalized matrix decomposition. Oncotarget, 2017, 8, 48075-48085.	0.8	6
113	L <sub>1</sub> -iPaD: An efficient method for drug-pathway association pairs inference. , 2016, , .		0
114	Robust graph regularized discriminative nonnegative matrix factorization for characteristic gene selection. , 2016, , .		0
115	Differentially expressed genes selection via Truncated Nuclear Norm Regularization. , 2016, , .		0
116	A p-norm singular value decomposition method for robust tumor clustering. , 2016, , .		0
117	Characteristic gene selection via L <sub>2,1</sub> -norm Sparse Principal Component Analysis. , 2016, , .		1
118	Sparse singular value decomposition-based feature extraction for identifying differentially expressed genes. , 2016, , .		2
119	A graph-Laplacian PCA based on L <sub>1/2</sub> -norm constraint for characteristic gene selection. , 2016, , .		1
120	Differentially expressed genes selection via Laplacian regularized low-rank representation method. Computational Biology and Chemistry, 2016, 65, 185-192.	1.1	14
121	A Simple Review of Sparse Principal Components Analysis. Lecture Notes in Computer Science, 2016, , 374-383.	1.0	11
122	Coexpression Module Discovery Based on Gene Expression Data. , 2016, , .		0
123	CINOEDV: a co-information based method for detecting and visualizing n-order epistatic interactions. BMC Bioinformatics, 2016, 17, 214.	1.2	27
124	Block-Constraint Robust Principal Component Analysis and its Application to Integrated Analysis of TCGA Data. IEEE Transactions on Nanobioscience, 2016, 15, 510-516.	2.2	17
125	Characteristic Gene Selection Based on Robust Graph Regularized Non-Negative Matrix Factorization. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2016, 13, 1059-1067.	1.9	33
126	A Class-Information-Based Sparse Component Analysis Method to Identify Differentially Expressed Genes on RNA-Seq Data. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2016, 13, 392-398.	1.9	19

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127	An NMF-L2,1-Norm Constraint Method for Characteristic Gene Selection. PLoS ONE, 2016, 11, e0158494.	1.1	21
128	Gene Extraction Based on Sparse Singular Value Decomposition. Lecture Notes in Computer Science, 2016, , 285-293.	1.0	1
129	An Improved Opposition-Based Learning Particle Swarm Optimization for the Detection of SNP-SNP Interactions. BioMed Research International, 2015, 2015, 1-12.	0.9	38
130	RPCA-Based Tumor Classification Using Gene Expression Data. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2015, 12, 964-970.	1.9	75
131	A P-Norm Robust Feature Extraction Method for Identifying Differentially Expressed Genes. PLoS ONE, 2015, 10, e0133124.	1.1	11
132	Application of Graph Regularized Non-negative Matrix Factorization in Characteristic Gene Selection. Lecture Notes in Computer Science, 2015, , 601-611.	1.0	2
133	Graph Regularized Non-negative Matrix with L0-Constraints for Selecting Characteristic Genes. Lecture Notes in Computer Science, 2015, , 612-622.	1.0	0
134	A Class-Information-Based Penalized Matrix Decomposition for Identifying Plants Core Genes Responding to Abiotic Stresses. PLoS ONE, 2014, 9, e106097.	1.1	11
135	A Class-information-based SNMF method for selecting characteristic genes. , 2014, , .		0
136	Differential Expression Analysis on RNA-Seq Count Data Based on Penalized Matrix Decomposition. IEEE Transactions on Nanobioscience, 2014, 13, 12-18.	2.2	12
137	Robust PCA based method for discovering differentially expressed genes. BMC Bioinformatics, 2013, 14, S3.	1.2	46
138	Face Recognition Using Sparse Representation-Based Classification on K-Nearest Subspace. PLoS ONE, 2013, 8, e59430.	1.1	32
139	Extracting plants core genes responding to abiotic stresses by penalized matrix decomposition. Computers in Biology and Medicine, 2012, 42, 582-589.	3.9	28
140	Characteristic Gene Selection via Weighting Principal Components by Singular Values. PLoS ONE, 2012, 7, e38873.	1.1	17
141	Discovering the transcriptional modules using microarray data by penalized matrix decomposition. Computers in Biology and Medicine, 2011, 41, 1041-1050.	3.9	7
142	Kernel risk-sensitive mean p-power loss based hyper-graph regularized robust extreme learning machine and its semi-supervised extension for sample classification. Applied Intelligence, 0, , 1.	3.3	0