Jin-Xing Liu

List of Publications by Year
in descending order

142 papers	1,572 citations	331259 21 h-index	433756 31 g-index
151 all docs	151 docs citations	151 times ranked	1066 citing authors

#	Article	IF	Citations
1	RPCA-Based Tumor Classification Using Gene Expression Data. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2015, 12, 964-970.	1.9	75
2	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
3	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
4	epiACO - a method for identifying epistasis based on ant Colony optimization algorithm. BioData Mining, 2017, 10, 23.	2.2	51
5	Robust PCA based method for discovering differentially expressed genes. BMC Bioinformatics, 2013, 14, S3.	1.2	46
6	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.	7.2	42
7	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
8	Hyper-Graph Regularized Constrained NMF for Selecting Differentially Expressed Genes and Tumor Classification. IEEE Journal of Biomedical and Health Informatics, 2020, 24, 3002-3011.	3.9	37
9	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
10	IPCARF: improving lncRNA-disease association prediction using incremental principal component analysis feature selection and a random forest classifier. BMC Bioinformatics, 2021, 22, 175.	1.2	34
11	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
12	Face Recognition Using Sparse Representation-Based Classification on K-Nearest Subspace. PLoS ONE, 2013, 8, e59430.	1.1	32
13	The computational prediction of drug-disease interactions using the dual-network L2,1-CMF method. BMC Bioinformatics, 2019, 20, 5.	1.2	30
14	Extracting plants core genes responding to abiotic stresses by penalized matrix decomposition. Computers in Biology and Medicine, 2012, 42, 582-589.	3.9	28
15	CINOEDV: a co-information based method for detecting and visualizing n-order epistatic interactions. BMC Bioinformatics, 2016, 17, 214.	1.2	27
16	A joint-L2,1-norm-constraint-based semi-supervised feature extraction for RNA-Seq data analysis. Neurocomputing, 2017, 228, 263-269.	3.5	27
17	NPCMF: Nearest Profile-based Collaborative Matrix Factorization method for predicting miRNA-disease associations. BMC Bioinformatics, 2019, 20, 353.	1.2	27
18	ACCBN: ant-Colony-clustering-based bipartite network method for predicting long non-coding RNAâ€"protein interactions. BMC Bioinformatics, 2019, 20, 16.	1.2	26

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19	Co-differential Gene Selection and Clustering Based on Graph Regularized Multi-View NMF in Cancer Genomic Data. Genes, 2018, 9, 586.	1.0	25
20	A Review of Ant Colony Optimization Based Methods for Detecting Epistatic Interactions. IEEE Access, 2019, 7, 13497-13509.	2.6	25
21	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
22	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
23	LncRNA-Disease Associations Prediction Using Bipartite Local Model With Nearest Profile-Based Association Inferring. IEEE Journal of Biomedical and Health Informatics, 2020, 24, 1519-1527.	3.9	21
24	The Automatic Detection of Seizure Based on Tensor Distance And Bayesian Linear Discriminant Analysis. International Journal of Neural Systems, 2021, 31, 2150006.	3.2	21
25	An NMF-L2,1-Norm Constraint Method for Characteristic Gene Selection. PLoS ONE, 2016, 11, e0158494.	1.1	21
26	Dual-network sparse graph regularized matrix factorization for predicting miRNA-disease associations. Molecular Omics, 2019, 15, 130-137.	1.4	20
27	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
28	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
29	WGRCMF: A Weighted Graph Regularized Collaborative Matrix Factorization Method for Predicting Novel LncRNA-Disease Associations. IEEE Journal of Biomedical and Health Informatics, 2021, 25, 257-265.	3.9	18
30	Characteristic Gene Selection via Weighting Principal Components by Singular Values. PLoS ONE, 2012, 7, e38873.	1.1	17
31	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
32	L2,1-GRMF: an improved graph regularized matrix factorization method to predict drug-target interactions. BMC Bioinformatics, 2019, 20, 287.	1.2	17
33	IDSSIM: an lncRNA functional similarity calculation model based on an improved disease semantic similarity method. BMC Bioinformatics, 2020, 21, 339.	1.2	17
34	LWPCMF: Logistic Weighted Profile-Based Collaborative Matrix Factorization for Predicting MiRNA-Disease Associations. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2021, 18, 1122-1129.	1.9	17
35	Robust Nonnegative Matrix Factorization via Joint Graph Laplacian and Discriminative Information for Identifying Differentially Expressed Genes. Complexity, 2017, 2017, 1-11.	0.9	16
36	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

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37	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.	3.9	16
38	DSCMF: prediction of LncRNA-disease associations based on dual sparse collaborative matrix factorization. BMC Bioinformatics, 2021, 22, 241.	1.2	16
39	Differentially expressed genes selection via Laplacian regularized low-rank representation method. Computational Biology and Chemistry, 2016, 65, 185-192.	1.1	14
40	A Robust Manifold Graph Regularized Nonnegative Matrix Factorization Algorithm for Cancer Gene Clustering. Molecules, 2017, 22, 2131.	1.7	14
41	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
42	Protein Fold Recognition by Combining Support Vector Machines and Pairwise Sequence Similarity Scores. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2021, 18, 2008-2016.	1.9	13
43	Multi-Label Fusion Collaborative Matrix Factorization for Predicting LncRNA-Disease Associations. IEEE Journal of Biomedical and Health Informatics, 2021, 25, 881-890.	3.9	13
44	Differential Expression Analysis on RNA-Seq Count Data Based on Penalized Matrix Decomposition. IEEE Transactions on Nanobioscience, 2014, 13, 12-18.	2.2	12
45	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
46	MCCMF: collaborative matrix factorization based on matrix completion for predicting miRNA-disease associations. BMC Bioinformatics, 2020, 21, 454.	1.2	12
47	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
48	A Class-Information-Based Penalized Matrix Decomposition for Identifying Plants Core Genes Responding to Abiotic Stresses. PLoS ONE, 2014, 9, e106097.	1.1	11
49	A Simple Review of Sparse Principal Components Analysis. Lecture Notes in Computer Science, 2016, , 374-383.	1.0	11
50	Identifying drug-pathway association pairs based on L2,1-integrative penalized matrix decomposition. BMC Systems Biology, 2017, 11, 119.	3.0	11
51	Differentially Expressed Genes Extracted by the Tensor Robust Principal Component Analysis (TRPCA) Method. Complexity, 2019, 2019, 1-13.	0.9	11
52	A P-Norm Robust Feature Extraction Method for Identifying Differentially Expressed Genes. PLoS ONE, 2015, 10, e0133124.	1.1	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.	1.9	10
54	Single-cell RNA Sequencing Data Clustering by Low-Rank Subspace Ensemble Framework. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2020, PP, 1-1.	1.9	10

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55	An Integrated Graph Regularized Non-Negative Matrix Factorization Model for Gene Co-Expression Network Analysis. IEEE Access, 2019, 7, 126594-126602.	2.6	9
56	Laplacian regularized low-rank representation for cancer samples clustering. Computational Biology and Chemistry, 2019, 78, 504-509.	1.1	9
57	L2,1-Extreme Learning Machine: An Efficient Robust Classifier for Tumor Classification. Computational Biology and Chemistry, 2020, 89, 107368.	1.1	9
58	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
59	<math xmlns:mml="http://www.w3.org/1998/Math/MathML" id="M1"><mml:mrow><mml:msub><mml:mrow><mml:mi>L</mml:mi></mml:mrow><mml:mrow><mml:mn fontstyle="italic">1</mml:mn><mml:mo>/</mml:mo><mml:mn fontstyle="italic">2</mml:mn></mml:mrow></mml:msub></mml:mrow></mml:math>-Norm Constraint and Graph-Laplacian PCA Method for Feature Extraction. BioMed Research International, 2017, 2017, 1-14.	0.9	8
60	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
61	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
62	Network Analyses of Integrated Differentially Expressed Genes in Papillary Thyroid Carcinoma to Identify Characteristic Genes. Genes, 2019, 10, 45.	1.0	8
63	Correntropy induced loss based sparse robust graph regularized extreme learning machine for cancer classification. BMC Bioinformatics, 2020, 21, 445.	1.2	8
64	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
65	Discovering the transcriptional modules using microarray data by penalized matrix decomposition. Computers in Biology and Medicine, 2011, 41, 1041-1050.	3.9	7
66	Feature selection and clustering via robust graph-laplacian PCA based on capped L<inf>1</inf>-norm. , 2017, , .		7
67	Multi-cancer samples clustering via graph regularized low-rank representation method under sparse and symmetric constraints. BMC Bioinformatics, 2019, 20, 718.	1.2	7
68	Sparse Graph Regularization Non-Negative Matrix Factorization Based on Huber Loss Model for Cancer Data Analysis. Frontiers in Genetics, 2019, 10, 1054.	1.1	7
69	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
70	Adaptive Total-Variation Regularized Low-Rank Representation for Analyzing Single-Cell RNA-seq Data. Interdisciplinary Sciences, Computational Life Sciences, 2021, 13, 476-489.	2.2	7
71	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.	4.0	7
72	Automatic detection for epileptic seizure using graph-regularized nonnegative matrix factorization and Bayesian linear discriminate analysis. Biocybernetics and Biomedical Engineering, 2021, 41, 1258-1271.	3.3	7

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73	A new method for mining information of co-expression network based on multi-cancers integrated data. BMC Medical Genomics, 2019, 12, 155.	0.7	6
74	RCMF: a robust collaborative matrix factorization method to predict miRNA-disease associations. BMC Bioinformatics, 2019, 20, 686.	1.2	6
75	Block-Constraint Laplacian-Regularized Low-Rank Representation and Its Application for Cancer Sample Clustering Based on Integrated TCGA Data. Complexity, 2020, 2020, 1-13.	0.9	6
76	Identifying drug-pathway association pairs based on L1L2,1-integrative penalized matrix decomposition. Oncotarget, 2017, 8, 48075-48085.	0.8	6
77	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
78	Graph regularized robust non-negative matrix factorization for clustering and selecting differentially expressed genes. , 2017, , .		5
79	Network analysis based on low-rank method for mining information on integrated data of multi-cancers. Computational Biology and Chemistry, 2019, 78, 468-473.	1.1	5
80	Logistic Weighted Profile-Based Bi-Random Walk for Exploring MiRNA-Disease Associations. Journal of Computer Science and Technology, 2021, 36, 276-287.	0.9	5
81	Ensemble Adaptive Total Variation Graph Regularized NMF for Singlecell RNA-seq Data Analysis. Current Bioinformatics, 2021, 16, 1014-1023.	0.7	5
82	MOPIO: A Multi-Objective Pigeon-Inspired Optimization Algorithm for Community Detection. Symmetry, 2021, 13, 49.	1.1	5
83	Sparse Regularization Tensor Robust PCA Based on t-product and Its Application in Cancer Genomic Data. , 2020, , .		5
84	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
85	Hypergraph regularized NMF by L2,1-norm for Clustering and Com-abnormal Expression Genes Selection. , 2018, , .		4
86	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
87	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
88	Hypergraph Regularized Discriminative Nonnegative Matrix Factorization on Sample Classification and Co-Differentially Expressed Gene Selection. Complexity, 2019, 2019, 1-12.	0.9	4
89	Integrative graph regularized matrix factorization for drug-pathway associations analysis. Computational Biology and Chemistry, 2019, 78, 474-480.	1.1	4
90	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

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91	NMFNA: A Non-negative Matrix Factorization Network Analysis Method for Identifying Modules and Characteristic Genes of Pancreatic Cancer. Frontiers in Genetics, 2021, 12, 678642.	1.1	4
92	Automatic Seizure Prediction based on Modified Stockwell Transform and Tensor Decomposition. , 2020, , .		4
93	Application of a Deep Matrix Factorization Model on Integrated Gene Expression Data. Current Bioinformatics, 2020, 15, 359-367.	0.7	4
94	PSO-CFDP: A Particle Swarm Optimization-Based Automatic Density Peaks Clustering Method for Cancer Subtyping. Human Heredity, 2019, 84, 9-20.	0.4	3
95	Sparse robust graph-regularized non-negative matrix factorization based on correntropy. Journal of Bioinformatics and Computational Biology, 2021, 19, 2050047.	0.3	3
96	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.	1.1	3
97	Predicting miRNA-disease associations via layer attention graph convolutional network model. BMC Medical Informatics and Decision Making, 2022, 22, 69.	1.5	3
98	Effects of Multi-Omics Characteristics on Identification of Driver Genes Using Machine Learning Algorithms. Genes, 2022, 13, 716.	1.0	3
99	Multi-Objective Artificial Bee Colony Algorithm Based on Scale-Free Network for Epistasis Detection. Genes, 2022, 13, 871.	1.0	3
100	Sparse singular value decomposition-based feature extraction for identifying differentially expressed genes. , 2016, , .		2
101	A Fast Quantum Clustering Approach for Cancer Gene Clustering. , 2018, , .		2
102	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
103	A Low-Rank Representation Method Regularized by Dual-Hypergraph Laplacian for Selecting Differentially Expressed Genes. Human Heredity, 2019, 84, 21-33.	0.4	2
104	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
105	A Dynamic Scale-Free Network Particle Swarm Optimization for Extracting Features on Multi-Omics Data. Journal of Computational Biology, 2019, 26, 769-781.	0.8	2
106	Non-Negative Symmetric Low-Rank Representation Graph Regularized Method for Cancer Clustering Based on Score Function. Frontiers in Genetics, 2019, 10, 1353.	1.1	2
107	Application of Graph Regularized Non-negative Matrix Factorization in Characteristic Gene Selection. Lecture Notes in Computer Science, 2015, , 601-611.	1.0	2
108	Bipartite graph-based collaborative matrix factorization method for predicting miRNA-disease associations. BMC Bioinformatics, 2021, 22, 573.	1.2	2

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109	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
110	Robust Tensor Method Based on Correntropy and Tensor Singular Value Decomposition for Cancer Genomics Data. , 2021, , .		2
111	Characteristic gene selection via L$_{2,1}$-norm Sparse Principal Component Analysis. , 2016, , .		1
112	A graph-Laplacian PCA based on L$^{1/2}$-norm constraint for characteristic gene selection. , 2016, , .		1
113	LJELSR: A Strengthened Version of JELSR for Feature Selection and Clustering. International Journal of Molecular Sciences, 2019, 20, 886.	1.8	1
114	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
115	Similarity and Dissimilarity Regularized Nonnegative Matrix Factorization for Single-Cell RNA-seq Analysis. Interdisciplinary Sciences, Computational Life Sciences, 2021, , 1.	2.2	1
116	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
117	Identifying Characteristic Genes and Clustering via an Lp-Norm Robust Feature Selection Method for Integrated Data. Lecture Notes in Computer Science, 2018, , 419-431.	1.0	1
118	A New Model of Identifying Differentially Expressed Genes via Weighted Network Analysis Based on Dimensionality Reduction Method. Current Bioinformatics, 2019, 14, 762-770.	0.7	1
119	Gene Extraction Based on Sparse Singular Value Decomposition. Lecture Notes in Computer Science, 2016, , 285-293.	1.0	1
120	Tensor Robust Principal Component Analysis with Low-Rank Weight Constraints for Sample Clustering. , 2020, , .		1
121	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
122	Sparse Hyper-graph Non-negative Matrix Factorization by Maximizing Correntropy. , 2021, , .		1
123	Tensor Decomposition Based on Global Features and Sparse Structure for Analyzing Cancer Multiomics Data. Current Bioinformatics, 2022, 17, 946-957.	0.7	1
124	A Class-information-based SNMF method for selecting characteristic genes. , 2014, , .		0
125	L$_{21}$-iPaD: An efficient method for drug-pathway association pairs inference. , 2016, , .		0
126	Robust graph regularized discriminative nonnegative matrix factorization for characteristic gene selection. , 2016, , .		0

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127	Differentially expressed genes selection via Truncated Nuclear Norm Regularization. , 2016, , .		0
128	A p-norm singular value decomposition method for robust tumor clustering. , 2016, , .		0
129	Coexpression Module Discovery Based on Gene Expression Data. , 2016, , .		0
130	Robust graph regularized sparse orthogonal nonnegative matrix factorization for identifying differentially expressed genes. , 2017, , .		0
131	A convex multi-view low-rank sparse regression for feature selection and clustering. , 2017, , .		0
132	Low-rank representation regularized by L$_{2,1}$-norm for identifying differentially expressed genes. , 2017, , .		0
133	Sparse Orthogonal Nonnegative Matrix Factorization for Identifying Differentially Expressed Genes and Clustering Tumor Samples. , 2018, , .		0
134	Extreme Learning Machine Based on Double Kernel Risk-Sensitive Loss for Cancer Samples Classification. Lecture Notes in Computer Science, 2021, , 532-539.	1.0	0
135	Multiscale part mutual information for quantifying nonlinear direct associations in networks. Bioinformatics, 2021, 37, 2920-2929.	1.8	0
136	Graph Regularized Non-negative Matrix with L0-Constraints for Selecting Characteristic Genes. Lecture Notes in Computer Science, 2015, , 612-622.	1.0	0
137	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
138	Inferring Communities and Key Genes of Triple Negative Breast Cancer Based on Robust Principal Component Analysis and Network Analysis. Communications in Computer and Information Science, 2020, , 137-151.	0.4	0
139	Locally Manifold Non-negative Matrix Factorization Based on Centroid for scRNA-seq Data Analysis. , 2020, , .		0
140	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
141	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
142	Adaptive total-variation joint learning model for analyzing single cell RNA seq data. , 2021, , .		0