

Ling-Yun Dai

List of Publications by Year in descending order

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Version: 2024-02-01

23
papers

205
citations

1307594

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1058476

14
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all docs

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23
times ranked

221
citing authors

#	ARTICLE	IF	CITATIONS
1	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.	2.6	34
2	The computational prediction of drug-disease interactions using the dual-network L2,1-CMF method. <i>BMC Bioinformatics</i> , 2019, 20, 5.	2.6	30
3	ACCBN: ant-Colony-clustering-based bipartite network method for predicting long non-coding RNA-protein interactions. <i>BMC Bioinformatics</i> , 2019, 20, 16.	2.6	26
4	Co-differential Gene Selection and Clustering Based on Graph Regularized Multi-View NMF in Cancer Genomic Data. <i>Genes</i> , 2018, 9, 586.	2.4	25
5	L2,1-GRMF: an improved graph regularized matrix factorization method to predict drug-target interactions. <i>BMC Bioinformatics</i> , 2019, 20, 287.	2.6	17
6	Robust Nonnegative Matrix Factorization via Joint Graph Laplacian and Discriminative Information for Identifying Differentially Expressed Genes. <i>Complexity</i> , 2017, 2017, 1-11.	1.6	16
7	Laplacian regularized low-rank representation for cancer samples clustering. <i>Computational Biology and Chemistry</i> , 2019, 78, 504-509.	2.3	9
8	Multi-cancer samples clustering via graph regularized low-rank representation method under sparse and symmetric constraints. <i>BMC Bioinformatics</i> , 2019, 20, 718.	2.6	7
9	PCA via joint graph Laplacian and sparse constraint: Identification of differentially expressed genes and sample clustering on gene expression data. <i>BMC Bioinformatics</i> , 2019, 20, 716.	2.6	7
10	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.	2.3	5
11	Logistic Weighted Profile-Based Bi-Random Walk for Exploring miRNA-Disease Associations. <i>Journal of Computer Science and Technology</i> , 2021, 36, 276-287.	1.5	5
12	Hypergraph Regularized Discriminative Nonnegative Matrix Factorization on Sample Classification and Co-Differentially Expressed Gene Selection. <i>Complexity</i> , 2019, 2019, 1-12.	1.6	4
13	Integrative graph regularized matrix factorization for drug-pathway associations analysis. <i>Computational Biology and Chemistry</i> , 2019, 78, 474-480.	2.3	4
14	Joint Nonnegative Matrix Factorization Based on Sparse and Graph Laplacian Regularization for Clustering and Co-Differential Expression Genes Analysis. <i>Complexity</i> , 2020, 2020, 1-10.	1.6	3
15	Sparse robust graph-regularized non-negative matrix factorization based on correntropy. <i>Journal of Bioinformatics and Computational Biology</i> , 2021, 19, 2050047.	0.8	3
16	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
17	Predicting miRNA-disease associations via layer attention graph convolutional network model. <i>BMC Medical Informatics and Decision Making</i> , 2022, 22, 69.	3.0	3
18	A Low-Rank Representation Method Regularized by Dual-Hypergraph Laplacian for Selecting Differentially Expressed Genes. <i>Human Heredity</i> , 2019, 84, 21-33.	0.8	2

#	ARTICLE	IF	CITATIONS
19	Multi-view manifold regularized compact low-rank representation for cancer samples clustering on multi-omics data. BMC Bioinformatics, 2021, 22, 334.	2.6	2
20	Robust graph regularized discriminative nonnegative matrix factorization for characteristic gene selection. , 2016, , .		0
21	Robust graph regularized sparse orthogonal nonnegative matrix factorization for identifying differentially expressed genes. , 2017, , .		0
22	Low-rank representation regularized by $L_{2,1}$ -norm for identifying differentially expressed genes. , 2017, , .		0
23	Sparse Orthogonal Nonnegative Matrix Factorization for Identifying Differentially Expressed Genes and Clustering Tumor Samples. , 2018, , .		0