Xiao-Fei Zhang

List of Publications by Year
in descending order

49 papers	909 citations	430874 18 h-index	501196 28 g-index
51 all docs	51 docs citations	51 times ranked	966 citing authors

#	Article	IF	Citations
1	Identifying Gene Network Rewiring Based on Partial Correlation. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2022, 19, 513-521.	3.0	0
2	scDEA: differential expression analysis in single-cell RNA-sequencing data via ensemble learning. Briefings in Bioinformatics, 2022, 23, .	6.5	12
3	Inferring Gene Co-Expression Networks by Incorporating Prior Protein-Protein Interaction Networks. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2022, 19, 2894-2906.	3.0	1
4	Imputing dropouts for single-cell RNA sequencing based on multi-objective optimization. Bioinformatics, 2022, 38, 3222-3230.	4.1	5
5	Time-Varying Differential Network Analysis for Revealing Network Rewiring over Cancer Progression. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2021, 18, 1632-1642.	3.0	4
6	A Joint Graphical Model for Inferring Gene Networks Across Multiple Subpopulations and Data Types. IEEE Transactions on Cybernetics, 2021, 51, 1043-1055.	9.5	10
7	EnTSSR: A Weighted Ensemble Learning Method to Impute Single-Cell RNA Sequencing Data. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2021, 18, 2781-2787.	3.0	5
8	WDNE: an integrative graphical model for inferring differential networks from multi-platform gene expression data with missing values. Briefings in Bioinformatics, 2021, 22, .	6.5	2
9	Differential network analysis by simultaneously considering changes in gene interactions and gene expression. Bioinformatics, 2021, 37, 4414-4423.	4.1	10
10	Differential Network Analysis via Weighted Fused Conditional Gaussian Graphical Model. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2020, 17, 2162-2169.	3.0	2
11	EC-PGMGR: Ensemble Clustering Based on Probability Graphical Model With Graph Regularization for Single-Cell RNA-seq Data. Frontiers in Genetics, 2020, 11, 572242.	2.3	4
12	A graph regularized generalized matrix factorization model for predicting links in biomedical bipartite networks. Bioinformatics, 2020, 36, 3474-3481.	4.1	51
13	Sparse regularized low-rank tensor regression with applications in genomic data analysis. Pattern Recognition, 2020, 107, 107516.	8.1	6
14	scTSSR: gene expression recovery for single-cell RNA sequencing using two-side sparse self-representation. Bioinformatics, 2020, 36, 3131-3138.	4.1	22
15	Joint reconstruction of multiple gene networks by simultaneously capturing inter-tumor and intra-tumor heterogeneity. Bioinformatics, 2020, 36, 2755-2762.	4.1	4
16	Inferring Gene Network Rewiring by Combining Gene Expression and Gene Mutation Data. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2019, 16, 1042-1048.	3.0	6
17	Joint Learning of Multiple Differential Networks With Latent Variables. IEEE Transactions on Cybernetics, 2019, 49, 3494-3506.	9.5	10
18	Weighted Fused Pathway Graphical Lasso for Joint Estimation of Multiple Gene Networks. Frontiers in Genetics, 2019, 10, 623.	2.3	11

#	ARTICLE	IF	CITATIONS
19	DiffNetFDR: differential network analysis with false discovery rate control. Bioinformatics, 2019, 35, 3184-3186.	4.1	14
20	EnImpute: imputing dropout events in single-cell RNA-sequencing data via ensemble learning. Bioinformatics, 2019, 35, 4827-4829.	4.1	29
21	LncRNA-Disease Association Prediction Using Two-Side Sparse Self-Representation. Frontiers in Genetics, 2019, 10, 476.	2.3	17
22	Identifying gene network rewiring using robust differential graphical model with multivariate t-distribution. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2019, 17, 1-1.	3.0	3
23	Identifying Gene Network Rewiring by Integrating Gene Expression and Gene Network Data. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2018, 15, 2079-2085.	3.0	24
24	DiffGraph: an R package for identifying gene network rewiring using differential graphical models. Bioinformatics, 2018, 34, 1571-1573.	4.1	13
25	Subpixel three-dimensional laser imaging with a downscaled avalanche photodiode array using code division multiple access. Communications Physics, 2018, 2, 1-9.	5.3	46
26	Incorporating prior information into differential network analysis using non-paranormal graphical models. Bioinformatics, 2017, 33, 2436-2445.	4.1	40
27	Node-based learning of differential networks from multi-platform gene expression data. Methods, 2017, 129, 41-49.	3.8	16
28	Node-based differential network analysis in genomics. Computational Biology and Chemistry, 2017, 69, 194-201.	2.3	10
29	Identifying differential networks based on multi-platform gene expression data. Molecular BioSystems, 2017, 13, 183-192.	2.9	14
30	A multi-network clustering method for detecting protein complexes from multiple heterogeneous networks. BMC Bioinformatics, 2017, 18, 463.	2.6	21
31	Identifying protein complexes via multi-network clustering. , 2016, , .		1
32	Protein complex detection based on partially shared multi-view clustering. BMC Bioinformatics, 2016, 17, 371.	2.6	10
33	Comparative analysis of housekeeping and tissue-specific driver nodes in human protein interaction networks. BMC Bioinformatics, 2016, 17, 358.	2.6	14
34	Differential network analysis from cross-platform gene expression data. Scientific Reports, 2016, 6, 34112.	3.3	29
35	A two-layer integration framework for protein complex detection. BMC Bioinformatics, 2016, 17, 100.	2.6	17
36	Regularized logistic regression with network-based pairwise interaction for biomarker identification in breast cancer. BMC Bioinformatics, 2016, 17, 108.	2.6	18

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37	Determining minimum set of driver nodes in protein-protein interaction networks. BMC Bioinformatics, 2015, 16, 146.	2.6	51
38	Identifying binary protein-protein interactions from affinity purification mass spectrometry data. BMC Genomics, 2015, 16, 745.	2.8	11
39	Detecting Protein Complexes from Signed Protein-Protein Interaction Networks. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2015, 12, 1333-1344.	3.0	36
40	Detecting temporal protein complexes from dynamic protein-protein interaction networks. BMC Bioinformatics, 2014, 15, 335.	2.6	67
41	Detecting overlapping protein complexes based on a generative model with functional and topological properties. BMC Bioinformatics, 2014, 15, 186.	2.6	39
42	Identifying Spurious Interactions and Predicting Missing Interactions in the Protein-Protein Interaction Networks via a Generative Network Model. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2013, 10, 219-225.	3.0	16
43	Protein Complex Detection via Weighted Ensemble Clustering Based on Bayesian Nonnegative Matrix Factorization. PLoS ONE, 2013, 8, e62158.	2.5	28
44	Cancer Subtype Discovery and Biomarker Identification via a New Robust Network Clustering Algorithm. PLoS ONE, 2013, 8, e66256.	2.5	26
45	A Framework for Incorporating Functional Interrelationships into Protein Function Prediction Algorithms. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2012, 9, 740-753.	3.0	37
46	Protein Complexes Discovery Based on Protein-Protein Interaction Data via a Regularized Sparse Generative Network Model. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2012, 9, 857-870.	3.0	24
47	Exploring Overlapping Functional Units with Various Structure in Protein Interaction Networks. PLoS ONE, 2012, 7, e43092.	2.5	20
48	Protective effects of ion-imprinted chitooligosaccharides as uranium-specific chelating agents against the cytotoxicity of depleted uranium in human kidney cells. Toxicology, 2011, 286, 75-84.	4.2	52
49	Face recognition with continuous occlusion using partially iteratively reweighted sparse coding. , 2011, , .		0