

# Xiao-Fei Zhang

## List of Publications by Year in descending order

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Version: 2024-02-01

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	Detecting temporal protein complexes from dynamic protein-protein interaction networks. BMC Bioinformatics, 2014, 15, 335.	2.6	67
2	Protective effects of ion-imprinted chitoooligosaccharides as uranium-specific chelating agents against the cytotoxicity of depleted uranium in human kidney cells. Toxicology, 2011, 286, 75-84.	4.2	52
3	Determining minimum set of driver nodes in protein-protein interaction networks. BMC Bioinformatics, 2015, 16, 146.	2.6	51
4	A graph regularized generalized matrix factorization model for predicting links in biomedical bipartite networks. Bioinformatics, 2020, 36, 3474-3481.	4.1	51
5	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
6	Incorporating prior information into differential network analysis using non-paranormal graphical models. Bioinformatics, 2017, 33, 2436-2445.	4.1	40
7	Detecting overlapping protein complexes based on a generative model with functional and topological properties. BMC Bioinformatics, 2014, 15, 186.	2.6	39
8	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
9	Detecting Protein Complexes from Signed Protein-Protein Interaction Networks. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2015, 12, 1333-1344.	3.0	36
10	Differential network analysis from cross-platform gene expression data. Scientific Reports, 2016, 6, 34112.	3.3	29
11	EnImpute: imputing dropout events in single-cell RNA-sequencing data via ensemble learning. Bioinformatics, 2019, 35, 4827-4829.	4.1	29
12	Protein Complex Detection via Weighted Ensemble Clustering Based on Bayesian Nonnegative Matrix Factorization. PLoS ONE, 2013, 8, e62158.	2.5	28
13	Cancer Subtype Discovery and Biomarker Identification via a New Robust Network Clustering Algorithm. PLoS ONE, 2013, 8, e66256.	2.5	26
14	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
15	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
16	scTSSR: gene expression recovery for single-cell RNA sequencing using two-side sparse self-representation. Bioinformatics, 2020, 36, 3131-3138.	4.1	22
17	A multi-network clustering method for detecting protein complexes from multiple heterogeneous networks. BMC Bioinformatics, 2017, 18, 463.	2.6	21
18	Exploring Overlapping Functional Units with Various Structure in Protein Interaction Networks. PLoS ONE, 2012, 7, e43092.	2.5	20

#	ARTICLE	IF	CITATIONS
19	Regularized logistic regression with network-based pairwise interaction for biomarker identification in breast cancer. BMC Bioinformatics, 2016, 17, 108.	2.6	18
20	A two-layer integration framework for protein complex detection. BMC Bioinformatics, 2016, 17, 100.	2.6	17
21	LncRNA-Disease Association Prediction Using Two-Side Sparse Self-Representation. Frontiers in Genetics, 2019, 10, 476.	2.3	17
22	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
23	Node-based learning of differential networks from multi-platform gene expression data. Methods, 2017, 129, 41-49.	3.8	16
24	Comparative analysis of housekeeping and tissue-specific driver nodes in human protein interaction networks. BMC Bioinformatics, 2016, 17, 358.	2.6	14
25	Identifying differential networks based on multi-platform gene expression data. Molecular BioSystems, 2017, 13, 183-192.	2.9	14
26	DiffNetFDR: differential network analysis with false discovery rate control. Bioinformatics, 2019, 35, 3184-3186.	4.1	14
27	DiffGraph: an R package for identifying gene network rewiring using differential graphical models. Bioinformatics, 2018, 34, 1571-1573.	4.1	13
28	scDEA: differential expression analysis in single-cell RNA-sequencing data via ensemble learning. Briefings in Bioinformatics, 2022, 23, .	6.5	12
29	Identifying binary protein-protein interactions from affinity purification mass spectrometry data. BMC Genomics, 2015, 16, 745.	2.8	11
30	Weighted Fused Pathway Graphical Lasso for Joint Estimation of Multiple Gene Networks. Frontiers in Genetics, 2019, 10, 623.	2.3	11
31	Protein complex detection based on partially shared multi-view clustering. BMC Bioinformatics, 2016, 17, 371.	2.6	10
32	Node-based differential network analysis in genomics. Computational Biology and Chemistry, 2017, 69, 194-201.	2.3	10
33	Joint Learning of Multiple Differential Networks With Latent Variables. IEEE Transactions on Cybernetics, 2019, 49, 3494-3506.	9.5	10
34	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
35	Differential network analysis by simultaneously considering changes in gene interactions and gene expression. Bioinformatics, 2021, 37, 4414-4423.	4.1	10
36	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

#	ARTICLE	IF	CITATIONS
37	Sparse regularized low-rank tensor regression with applications in genomic data analysis. <i>Pattern Recognition</i> , 2020, 107, 107516.	8.1	6
38	EnTSSR: A Weighted Ensemble Learning Method to Impute Single-Cell RNA Sequencing Data. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2021, 18, 2781-2787.	3.0	5
39	Imputing dropouts for single-cell RNA sequencing based on multi-objective optimization. <i>Bioinformatics</i> , 2022, 38, 3222-3230.	4.1	5
40	Time-Varying Differential Network Analysis for Revealing Network Rewiring over Cancer Progression. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2021, 18, 1632-1642.	3.0	4
41	EC-PGMGR: Ensemble Clustering Based on Probability Graphical Model With Graph Regularization for Single-Cell RNA-seq Data. <i>Frontiers in Genetics</i> , 2020, 11, 572242.	2.3	4
42	Joint reconstruction of multiple gene networks by simultaneously capturing inter-tumor and intra-tumor heterogeneity. <i>Bioinformatics</i> , 2020, 36, 2755-2762.	4.1	4
43	Identifying gene network rewiring using robust differential graphical model with multivariate t-distribution. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2019, 17, 1-1.	3.0	3
44	Differential Network Analysis via Weighted Fused Conditional Gaussian Graphical Model. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2020, 17, 2162-2169.	3.0	2
45	WDNE: an integrative graphical model for inferring differential networks from multi-platform gene expression data with missing values. <i>Briefings in Bioinformatics</i> , 2021, 22, .	6.5	2
46	Identifying protein complexes via multi-network clustering. , 2016, , .		1
47	Inferring Gene Co-Expression Networks by Incorporating Prior Protein-Protein Interaction Networks. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2022, 19, 2894-2906.	3.0	1
48	Face recognition with continuous occlusion using partially iteratively reweighted sparse coding. , 2011, , .		0
49	Identifying Gene Network Rewiring Based on Partial Correlation. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2022, 19, 513-521.	3.0	0