

Le Ou-Yang

List of Publications by Year in descending order

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papers

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times ranked

721
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.	1.9	0
2	scDEA: differential expression analysis in single-cell RNA-sequencing data via ensemble learning. Briefings in Bioinformatics, 2022, 23, .	3.2	12
3	Matrix factorization for biomedical link prediction and scRNA-seq data imputation: an empirical survey. Briefings in Bioinformatics, 2022, 23, .	3.2	12
4	Anderson accelerating the preconditioned modulus approach for linear complementarity problems on second-order cones. Numerical Algorithms, 2022, 91, 803-839.	1.1	1
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.	1.9	4
6	Recent advances in network-based methods for disease gene prediction. Briefings in Bioinformatics, 2021, 22, .	3.2	42
7	A Joint Graphical Model for Inferring Gene Networks Across Multiple Subpopulations and Data Types. IEEE Transactions on Cybernetics, 2021, 51, 1043-1055.	6.2	10
8	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.	1.9	5
9	WMLRR: A Weighted Multi-View Low Rank Representation to Identify Cancer Subtypes From Multiple Types of Omics Data. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2021, 18, 2891-2897.	1.9	8
10	WDNE: an integrative graphical model for inferring differential networks from multi-platform gene expression data with missing values. Briefings in Bioinformatics, 2021, 22, .	3.2	2
11	Differential network analysis by simultaneously considering changes in gene interactions and gene expression. Bioinformatics, 2021, 37, 4414-4423.	1.8	10
12	The selection of the optimal parameter in the modulus-based matrix splitting algorithm for linear complementarity problems. Computational Optimization and Applications, 2021, 80, 617-638.	0.9	6
13	Differential Network Analysis via Weighted Fused Conditional Gaussian Graphical Model. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2020, 17, 2162-2169.	1.9	2
14	T3SEpp: an Integrated Prediction Pipeline for Bacterial Type III Secreted Effectors. MSystems, 2020, 5, .	1.7	23
15	A Machine Learning Approach to Blind Multi-Path Classification for Massive MIMO Systems. IEEE/ACM Transactions on Networking, 2020, 28, 2309-2322.	2.6	5
16	Predicting the impacts of mutations on protein-ligand binding affinity based on molecular dynamics simulations and machine learning methods. Computational and Structural Biotechnology Journal, 2020, 18, 439-454.	1.9	43
17	A graph regularized generalized matrix factorization model for predicting links in biomedical bipartite networks. Bioinformatics, 2020, 36, 3474-3481.	1.8	51
18	scTSSR: gene expression recovery for single-cell RNA sequencing using two-side sparse self-representation. Bioinformatics, 2020, 36, 3131-3138.	1.8	22

#	ARTICLE	IF	CITATIONS
19	Joint reconstruction of multiple gene networks by simultaneously capturing inter-tumor and intra-tumor heterogeneity. <i>Bioinformatics</i> , 2020, 36, 2755-2762.	1.8	4
20	A Machine Learning Approach to Phase Reference Estimation With Noise. <i>IEEE Transactions on Communications</i> , 2020, 68, 2579-2592.	4.9	4
21	Self-weighted adaptive structure learning for ASD diagnosis via multi-template multi-center representation. <i>Medical Image Analysis</i> , 2020, 63, 101662.	7.0	20
22	Spectrum Sharing in mmWave Cellular Networks Using Clustering Algorithms. <i>IEEE/ACM Transactions on Networking</i> , 2020, 28, 1378-1390.	2.6	2
23	Joint learning of multiple gene networks from single-cell gene expression data. <i>Computational and Structural Biotechnology Journal</i> , 2020, 18, 2583-2595.	1.9	10
24	Inferring Gene Network Rewiring by Combining Gene Expression and Gene Mutation Data. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2019, 16, 1042-1048.	1.9	6
25	Joint Learning of Multiple Differential Networks With Latent Variables. <i>IEEE Transactions on Cybernetics</i> , 2019, 49, 3494-3506.	6.2	10
26	Weighted Fused Pathway Graphical Lasso for Joint Estimation of Multiple Gene Networks. <i>Frontiers in Genetics</i> , 2019, 10, 623.	1.1	11
27	DiffNetFDR: differential network analysis with false discovery rate control. <i>Bioinformatics</i> , 2019, 35, 3184-3186.	1.8	14
28	EnImpute: imputing dropout events in single-cell RNA-sequencing data via ensemble learning. <i>Bioinformatics</i> , 2019, 35, 4827-4829.	1.8	29
29	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.	1.9	3
30	Predicting synthetic lethal interactions in human cancers using graph regularized self-representative matrix factorization. <i>BMC Bioinformatics</i> , 2019, 20, 657.	1.2	24
31	Identifying Gene Network Rewiring by Integrating Gene Expression and Gene Network Data. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2018, 15, 2079-2085.	1.9	24
32	DiffGraph: an R package for identifying gene network rewiring using differential graphical models. <i>Bioinformatics</i> , 2018, 34, 1571-1573.	1.8	13
33	Integrating node embeddings and biological annotations for genes to predict disease-gene associations. <i>BMC Systems Biology</i> , 2018, 12, 138.	3.0	29
34	Incorporating prior information into differential network analysis using non-paranormal graphical models. <i>Bioinformatics</i> , 2017, 33, 2436-2445.	1.8	40
35	Node-based learning of differential networks from multi-platform gene expression data. <i>Methods</i> , 2017, 129, 41-49.	1.9	16
36	Node-based differential network analysis in genomics. <i>Computational Biology and Chemistry</i> , 2017, 69, 194-201.	1.1	10

#	ARTICLE	IF	CITATIONS
37	Identifying differential networks based on multi-platform gene expression data. <i>Molecular BioSystems</i> , 2017, 13, 183-192.	2.9	14
38	A multi-network clustering method for detecting protein complexes from multiple heterogeneous networks. <i>BMC Bioinformatics</i> , 2017, 18, 463.	1.2	21
39	Identifying protein complexes via multi-network clustering. , 2016, , .		1
40	Protein complex detection based on partially shared multi-view clustering. <i>BMC Bioinformatics</i> , 2016, 17, 371.	1.2	10
41	Comparative analysis of housekeeping and tissue-specific driver nodes in human protein interaction networks. <i>BMC Bioinformatics</i> , 2016, 17, 358.	1.2	14
42	Differential network analysis from cross-platform gene expression data. <i>Scientific Reports</i> , 2016, 6, 34112.	1.6	29
43	A two-layer integration framework for protein complex detection. <i>BMC Bioinformatics</i> , 2016, 17, 100.	1.2	17
44	Regularized logistic regression with network-based pairwise interaction for biomarker identification in breast cancer. <i>BMC Bioinformatics</i> , 2016, 17, 108.	1.2	18
45	Determining minimum set of driver nodes in protein-protein interaction networks. <i>BMC Bioinformatics</i> , 2015, 16, 146.	1.2	51
46	Identifying binary protein-protein interactions from affinity purification mass spectrometry data. <i>BMC Genomics</i> , 2015, 16, 745.	1.2	11
47	Protein Complex Detection via Weighted Ensemble Clustering Based on Bayesian Nonnegative Matrix Factorization. <i>PLoS ONE</i> , 2013, 8, e62158.	1.1	28