Le Ou-Yang

List of Publications by Year
in descending order

47 papers	741 citations	516215 16 h-index	610482 24 g-index
47 all docs	47 docs citations	47 times ranked	721 citing authors

#	Article	IF	Citations
1	Determining minimum set of driver nodes in protein-protein interaction networks. BMC Bioinformatics, 2015, 16, 146.	1.2	51
2	A graph regularized generalized matrix factorization model for predicting links in biomedical bipartite networks. Bioinformatics, 2020, 36, 3474-3481.	1.8	51
3	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
4	Recent advances in network-based methods for disease gene prediction. Briefings in Bioinformatics, 2021, 22, .	3.2	42
5	Incorporating prior information into differential network analysis using non-paranormal graphical models. Bioinformatics, 2017, 33, 2436-2445.	1.8	40
6	Differential network analysis from cross-platform gene expression data. Scientific Reports, 2016, 6, 34112.	1.6	29
7	Integrating node embeddings and biological annotations for genes to predict disease-gene associations. BMC Systems Biology, 2018, 12, 138.	3.0	29
8	EnImpute: imputing dropout events in single-cell RNA-sequencing data via ensemble learning. Bioinformatics, 2019, 35, 4827-4829.	1.8	29
9	Protein Complex Detection via Weighted Ensemble Clustering Based on Bayesian Nonnegative Matrix Factorization. PLoS ONE, 2013, 8, e62158.	1.1	28
10	Identifying Gene Network Rewiring by Integrating Gene Expression and Gene Network Data. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2018, 15, 2079-2085.	1.9	24
11	Predicting synthetic lethal interactions in human cancers using graph regularized self-representative matrix factorization. BMC Bioinformatics, 2019, 20, 657.	1.2	24
12	T3SEpp: an Integrated Prediction Pipeline for Bacterial Type III Secreted Effectors. MSystems, 2020, 5, .	1.7	23
13	scTSSR: gene expression recovery for single-cell RNA sequencing using two-side sparse self-representation. Bioinformatics, 2020, 36, 3131-3138.	1.8	22
14	A multi-network clustering method for detecting protein complexes from multiple heterogeneous networks. BMC Bioinformatics, 2017, 18, 463.	1.2	21
15	Self-weighted adaptive structure learning for ASD diagnosis via multi-template multi-center representation. Medical Image Analysis, 2020, 63, 101662.	7.0	20
16	Regularized logistic regression with network-based pairwise interaction for biomarker identification in breast cancer. BMC Bioinformatics, 2016, 17, 108.	1.2	18
17	A two-layer integration framework for protein complex detection. BMC Bioinformatics, 2016, 17, 100.	1.2	17
18	Node-based learning of differential networks from multi-platform gene expression data. Methods, 2017, 129, 41-49.	1.9	16

#	Article	IF	Citations
19	Comparative analysis of housekeeping and tissue-specific driver nodes in human protein interaction networks. BMC Bioinformatics, 2016, 17, 358.	1.2	14
20	Identifying differential networks based on multi-platform gene expression data. Molecular BioSystems, 2017, 13, 183-192.	2.9	14
21	DiffNetFDR: differential network analysis with false discovery rate control. Bioinformatics, 2019, 35, 3184-3186.	1.8	14
22	DiffGraph: an R package for identifying gene network rewiring using differential graphical models. Bioinformatics, 2018, 34, 1571-1573.	1.8	13
23	scDEA: differential expression analysis in single-cell RNA-sequencing data via ensemble learning. Briefings in Bioinformatics, 2022, 23, .	3.2	12
24	Matrix factorization for biomedical link prediction and scRNA-seq data imputation: an empirical survey. Briefings in Bioinformatics, 2022, 23, .	3.2	12
25	Identifying binary protein-protein interactions from affinity purification mass spectrometry data. BMC Genomics, 2015, 16, 745.	1.2	11
26	Weighted Fused Pathway Graphical Lasso for Joint Estimation of Multiple Gene Networks. Frontiers in Genetics, 2019, 10, 623.	1.1	11
27	Protein complex detection based on partially shared multi-view clustering. BMC Bioinformatics, 2016, 17, 371.	1.2	10
28	Node-based differential network analysis in genomics. Computational Biology and Chemistry, 2017, 69, 194-201.	1.1	10
29	Joint Learning of Multiple Differential Networks With Latent Variables. IEEE Transactions on Cybernetics, 2019, 49, 3494-3506.	6.2	10
30	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
31	Differential network analysis by simultaneously considering changes in gene interactions and gene expression. Bioinformatics, 2021, 37, 4414-4423.	1.8	10
32	Joint learning of multiple gene networks from single-cell gene expression data. Computational and Structural Biotechnology Journal, 2020, 18, 2583-2595.	1.9	10
33	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
34	Inferring Gene Network Rewiring by Combining Gene Expression and Gene Mutation Data. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2019, 16, 1042-1048.	1.9	6
35	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
36	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

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37	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
38	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
39	Joint reconstruction of multiple gene networks by simultaneously capturing inter-tumor and intra-tumor heterogeneity. Bioinformatics, 2020, 36, 2755-2762.	1.8	4
40	A Machine Learning Approach to Phase Reference Estimation With Noise. IEEE Transactions on Communications, 2020, 68, 2579-2592.	4.9	4
41	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.	1.9	3
42	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
43	Spectrum Sharing in mmWave Cellular Networks Using Clustering Algorithms. IEEE/ACM Transactions on Networking, 2020, 28, 1378-1390.	2.6	2
44	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
45	Identifying protein complexes via multi-network clustering. , 2016, , .		1
46	Anderson accelerating the preconditioned modulus approach for linear complementarity problems on second-order cones. Numerical Algorithms, 2022, 91, 803-839.	1.1	1
47	Identifying Gene Network Rewiring Based on Partial Correlation. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2022, 19, 513-521.	1.9	0