

Jiadong Ji

List of Publications by Year in descending order

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Version: 2024-02-01

31
papers

609
citations

840776

11
h-index

677142

22
g-index

34
all docs

34
docs citations

34
times ranked

1052
citing authors

#	ARTICLE	IF	CITATIONS
1	Community assessment to advance computational prediction of cancer drug combinations in a pharmacogenomic screen. <i>Nature Communications</i> , 2019, 10, 2674.	12.8	240
2	Lung function and systemic inflammation associated with short-term air pollution exposure in chronic obstructive pulmonary disease patients in Beijing, China. <i>Environmental Health</i> , 2020, 19, 12.	4.0	58
3	<p>Short-term effects of ambient air pollution on chronic obstructive pulmonary disease admissions in Beijing, China (2013–2017)</p>. <i>International Journal of COPD</i> , 2019, Volume 14, 297-309.	2.3	40
4	JDINAC: joint density-based non-parametric differential interaction network analysis and classification using high-dimensional sparse omics data. <i>Bioinformatics</i> , 2017, 33, 3080-3087.	4.1	24
5	A Machine Learning Method for Identifying Critical Interactions Between Gene Pairs in Alzheimer's Disease Prediction. <i>Frontiers in Neurology</i> , 2019, 10, 1162.	2.4	23
6	<p>Risk Prediction of Dyslipidemia for Chinese Han Adults Using Random Forest Survival Model</p>. <i>Clinical Epidemiology</i> , 2019, Volume 11, 1047-1055.	3.0	21
7	Network or regression-based methods for disease discrimination: a comparison study. <i>BMC Medical Research Methodology</i> , 2016, 16, 100.	3.1	19
8	Dyslipidemia in rural areas of North China: prevalence, characteristics, and predictive value. <i>Lipids in Health and Disease</i> , 2016, 15, 154.	3.0	16
9	Prevalence of CHD-related metabolic comorbidity of diabetes mellitus in Northern Chinese adults: the REACTION study. <i>Journal of Diabetes and Its Complications</i> , 2016, 30, 199-205.	2.3	16
10	Molecular mechanisms involved in the side effects of fatty acid amide hydrolase inhibitors: a structural phenomics approach to proteome-wide cellular off-target deconvolution and disease association. <i>Npj Systems Biology and Applications</i> , 2016, 2, 16023.	3.0	14
11	A powerful score-based statistical test for group difference in weighted biological networks. <i>BMC Bioinformatics</i> , 2016, 17, 86.	2.6	14
12	A crowdsourced analysis to identify ab initio molecular signatures predictive of susceptibility to viral infection. <i>Nature Communications</i> , 2018, 9, 4418.	12.8	14
13	Detection for pathway effect contributing to disease in systems epidemiology with a case-control design. <i>BMJ Open</i> , 2015, 5, e006721-e006721.	1.9	13
14	A novel chi² square statistic for detecting group differences between pathways in systems epidemiology. <i>Statistics in Medicine</i> , 2016, 35, 5512-5524.	1.6	13
15	Integrated Multi-Omics Analysis Model to Identify Biomarkers Associated With Prognosis of Breast Cancer. <i>Frontiers in Oncology</i> , 0, 12, .	2.8	12
16	Robust feature screening for elliptical copula regression model. <i>Journal of Multivariate Analysis</i> , 2019, 173, 568-582.	1.0	11
17	A powerful weighted statistic for detecting group differences of directed biological networks. <i>Scientific Reports</i> , 2016, 6, 34159.	3.3	10
18	A powerful latent variable method for detecting and characterizing gene-based gene-gene interaction on multiple quantitative traits. <i>BMC Genetics</i> , 2013, 14, 89.	2.7	8

#	ARTICLE	IF	CITATIONS
19	The efficacy and adverse events of mTOR inhibitors in lymphangioleiomyomatosis: systematic review and meta-analysis. <i>Orphanet Journal of Rare Diseases</i> , 2018, 13, 134.	2.7	8
20	A new insight into underlying disease mechanism through semi-parametric latent differential network model. <i>BMC Bioinformatics</i> , 2018, 19, 493.	2.6	7
21	PMINR: Pointwise Mutual Information-Based Network Regression “ With Application to Studies of Lung Cancer and Alzheimer’s Disease. <i>Frontiers in Genetics</i> , 2020, 11, 556259.	2.3	6
22	Simultaneous differential network analysis and classification for matrix-variate data with application to brain connectivity. <i>Biostatistics</i> , 2022, 23, 967-989.	1.5	5
23	Joint estimation of multiple high-dimensional Gaussian copula graphical models. <i>Australian and New Zealand Journal of Statistics</i> , 2017, 59, 289-310.	0.9	4
24	Brain connectivity alteration detection via matrix-variate differential network model. <i>Biometrics</i> , 2021, 77, 1409-1421.	1.4	3
25	MCC-SP: a powerful integration method for identification of causal pathways from genetic variants to complex disease. <i>BMC Genetics</i> , 2020, 21, 90.	2.7	3
26	A novel Markov Blanket-based repeated-fishing strategy for capturing phenotype-related biomarkers in big omics data. <i>BMC Genetics</i> , 2016, 17, 51.	2.7	2
27	High-dimensional integrative copula discriminant analysis for multiomics data. <i>Statistics in Medicine</i> , 2020, 39, 4869-4884.	1.6	2
28	A powerful score-based test statistic for detecting gene-gene co-association. <i>BMC Genetics</i> , 2016, 17, 31.	2.7	1
29	Bidirectional association between serum carcinoembryonic antigen and metabolic syndrome among the Chinese male population: two cohort studies. <i>Lipids in Health and Disease</i> , 2020, 19, 233.	3.0	1
30	The sparse group lasso for high-dimensional integrative linear discriminant analysis with application to alzheimer’s disease prediction. <i>Journal of Statistical Computation and Simulation</i> , 2020, 90, 3218-3231.	1.2	1
31	Robust feature screening for multi-response trans-elliptical regression model with ultrahigh-dimensional covariates. <i>Random Matrices: Theory and Application</i> , 2020, 09, 2150001.	1.1	0