

Xingjie Shi

List of Publications by Year in descending order

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Version: 2024-02-01

22
papers

535
citations

687363

13
h-index

713466

21
g-index

22
all docs

22
docs citations

22
times ranked

640
citing authors

#	ARTICLE	IF	CITATIONS
1	Combining multidimensional genomic measurements for predicting cancer prognosis: observations from TCGA. <i>Briefings in Bioinformatics</i> , 2015, 16, 291-303.	6.5	122
2	Integrated analysis of multidimensional omics data on cutaneous melanoma prognosis. <i>Genomics</i> , 2016, 107, 223-230.	2.9	57
3	SC-MEB: spatial clustering with hidden Markov random field using empirical Bayes. <i>Briefings in Bioinformatics</i> , 2022, 23, .	6.5	44
4	Integrative analysis of omics data using penalty functions. <i>Wiley Interdisciplinary Reviews: Computational Statistics</i> , 2015, 7, 99-108.	3.9	34
5	CoMM-S2: a collaborative mixed model using summary statistics in transcriptome-wide association studies. <i>Bioinformatics</i> , 2020, 36, 2009-2016.	4.1	30
6	Deciphering the associations between gene expression and copy number alteration using a sparse double Laplacian shrinkage approach. <i>Bioinformatics</i> , 2015, 31, 3977-3983.	4.1	27
7	MR-LDP: a two-sample Mendelian randomization for GWAS summary statistics accounting for linkage disequilibrium and horizontal pleiotropy. <i>NAR Genomics and Bioinformatics</i> , 2020, 2, 1qaa028.	3.2	27
8	A penalized robust semiparametric approach for gene-environment interactions. <i>Statistics in Medicine</i> , 2015, 34, 4016-4030.	1.6	26
9	Joint dimension reduction and clustering analysis of single-cell RNA-seq and spatial transcriptomics data. <i>Nucleic Acids Research</i> , 2022, 50, e72-e72.	14.5	26
10	A Penalized Robust Method for Identifying Gene-Environment Interactions. <i>Genetic Epidemiology</i> , 2014, 38, 220-230.	1.3	24
11	Integrative Analysis of High-throughput Cancer Studies With Contrasted Penalization. <i>Genetic Epidemiology</i> , 2014, 38, 144-151.	1.3	17
12	Analysis of cancer gene expression data with an assisted robust marker identification approach. <i>Genetic Epidemiology</i> , 2017, 41, 779-789.	1.3	16
13	Measures for the degree of overlap of gene signatures and applications to TCGA. <i>Briefings in Bioinformatics</i> , 2015, 16, 735-744.	6.5	15
14	A tissue-specific collaborative mixed model for jointly analyzing multiple tissues in transcriptome-wide association studies. <i>Nucleic Acids Research</i> , 2020, 48, e109-e109.	14.5	15
15	Similarity of markers identified from cancer gene expression studies: observations from GEO. <i>Briefings in Bioinformatics</i> , 2014, 15, 671-684.	6.5	12
16	Analyzing Association Mapping in Pedigree-Based GWAS Using a Penalized Multitrait Mixed Model. <i>Genetic Epidemiology</i> , 2016, 40, 382-393.	1.3	11
17	MR-Corr2: a two-sample Mendelian randomization method that accounts for correlated horizontal pleiotropy using correlated instrumental variants. <i>Bioinformatics</i> , 2022, 38, 303-310.	4.1	10
18	VIMCO: variational inference for multiple correlated outcomes in genome-wide association studies. <i>Bioinformatics</i> , 2019, 35, 3693-3700.	4.1	9

#	ARTICLE	IF	CITATIONS
19	Promoting sign consistency in the cure model estimation and selection. <i>Statistical Methods in Medical Research</i> , 2020, 29, 15-28.	1.5	6
20	Horizontal and vertical integrative analysis methods for mental disorders omics data. <i>Scientific Reports</i> , 2019, 9, 13430.	3.3	5
21	Using Collaborative Mixed Models to Account for Imputation Uncertainty in Transcriptome-Wide Association Studies. <i>Methods in Molecular Biology</i> , 2021, 2212, 93-103.	0.9	2
22	Penalized Integrative Analysis of High-Dimensional Omics Data. , 0, , 174-204.		0