

Mengyun Wu

List of Publications by Year in descending order

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Version: 2024-02-01

25
papers

200
citations

1163117

8
h-index

1125743

13
g-index

25
all docs

25
docs citations

25
times ranked

154
citing authors

#	ARTICLE	IF	CITATIONS
1	Integrative functional linear model for genome-wide association studies with multiple traits. <i>Biostatistics</i> , 2022, 23, 574-590.	1.5	7
2	Multidimensional molecular measurementsâ€“environment interaction analysis for disease outcomes. <i>Biometrics</i> , 2022, 78, 1542-1554.	1.4	4
3	Analysis of cancer omics data: a selective review of statistical techniques. <i>Briefings in Bioinformatics</i> , 2022, 23, .	6.5	2
4	Network-based cancer heterogeneity analysis incorporating multi-view of prior information. <i>Bioinformatics</i> , 2022, 38, 2855-2862.	4.1	3
5	Vertical integration methods for gene expression data analysis. <i>Briefings in Bioinformatics</i> , 2021, 22, .	6.5	7
6	Integration of Proteomics and Other Omics Data. <i>Methods in Molecular Biology</i> , 2021, 2361, 307-324.	0.9	1
7	GEInter: an R package for robust geneâ€“environment interaction analysis. <i>Bioinformatics</i> , 2021, 37, 3691-3692.	4.1	4
8	Geneâ€“gene interaction analysis incorporating network information via a structured Bayesian approach. <i>Statistics in Medicine</i> , 2021, 40, 6619-6633.	1.6	1
9	Structured geneâ€“environment interaction analysis. <i>Biometrics</i> , 2020, 76, 23-35.	1.4	19
10	Identification of geneâ€“environment interactions with marginal penalization. <i>Genetic Epidemiology</i> , 2020, 44, 159-196.	1.3	6
11	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
12	Robust identification of gene-environment interactions for prognosis using a quantile partial correlation approach. <i>Genomics</i> , 2019, 111, 1115-1123.	2.9	21
13	Integrative interaction analysis using threshold gradient directed regularization. <i>Applied Stochastic Models in Business and Industry</i> , 2019, 35, 354-375.	1.5	5
14	Robust semiparametric geneâ€“environment interaction analysis using sparse boosting. <i>Statistics in Medicine</i> , 2019, 38, 4625-4641.	1.6	9
15	Integrative Analysis of Cancer Omics Data for Prognosis Modeling. <i>Genes</i> , 2019, 10, 604.	2.4	4
16	NCutYX: a package for clustering analysis of multilayer omics data. <i>Bioinformatics</i> , 2019, , .	4.1	0
17	Horizontal and vertical integrative analysis methods for mental disorders omics data. <i>Scientific Reports</i> , 2019, 9, 13430.	3.3	5
18	Histopathological Imagingâ€“Environment Interactions in Cancer Modeling. <i>Cancers</i> , 2019, 11, 579.	3.7	7

#	ARTICLE	IF	CITATIONS
19	Examination of Independent Prognostic Power of Gene Expressions and Histopathological Imaging Features in Cancer. <i>Cancers</i> , 2019, 11, 361.	3.7	20
20	Robust genetic interaction analysis. <i>Briefings in Bioinformatics</i> , 2019, 20, 624-637.	6.5	23
21	Identifying gene-gene interactions using penalized tensor regression. <i>Statistics in Medicine</i> , 2018, 37, 598-610.	1.6	22
22	Robust gene-environment interaction analysis using penalized trimmed regression. <i>Journal of Statistical Computation and Simulation</i> , 2018, 88, 3502-3528.	1.2	8
23	Assisted gene expression-based clustering with AWNCut. <i>Statistics in Medicine</i> , 2018, 37, 4386-4403.	1.6	8
24	A unified semi-empirical likelihood ratio confidence interval for treatment effects in the two sample problem with length-biased data. <i>Statistics and Its Interface</i> , 2018, 11, 531-540.	0.3	1
25	Accommodating missingness in environmental measurements in gene-environment interaction analysis. <i>Genetic Epidemiology</i> , 2017, 41, 523-554.	1.3	9