

Qingzhao Zhang

List of Publications by Year in descending order

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Version: 2024-02-01

49
papers

230
citations

1478505

6
h-index

1199594

12
g-index

49
all docs

49
docs citations

49
times ranked

163
citing authors

#	ARTICLE	IF	CITATIONS
1	Robust network-based analysis of the associations between (epi)genetic measurements. <i>Journal of Multivariate Analysis</i> , 2018, 168, 119-130.	1.0	28
2	Robust identification of gene-environment interactions for prognosis using a quantile partial correlation approach. <i>Genomics</i> , 2019, 111, 1115-1123.	2.9	21
3	Structured gene-environment interaction analysis. <i>Biometrics</i> , 2020, 76, 23-35.	1.4	19
4	Analysis of cancer gene expression data with an assisted robust marker identification approach. <i>Genetic Epidemiology</i> , 2017, 41, 779-789.	1.3	16
5	Integrative sparse principal component analysis. <i>Journal of Multivariate Analysis</i> , 2018, 166, 1-16.	1.0	11
6	Gaussian graphical model-based heterogeneity analysis via penalized fusion. <i>Biometrics</i> , 2022, 78, 524-535.	1.4	9
7	Inferring gene regulatory relationships with a high-dimensional robust approach. <i>Genetic Epidemiology</i> , 2017, 41, 437-454.	1.3	8
8	Improved model checking methods for parametric models with responses missing at random. <i>Journal of Multivariate Analysis</i> , 2017, 154, 147-161.	1.0	8
9	Histopathological imaging-based cancer heterogeneity analysis via penalized fusion with model averaging. <i>Biometrics</i> , 2021, 77, 1397-1408.	1.4	8
10	Efficient estimation for the heteroscedastic single-index varying coefficient models. <i>Statistics and Probability Letters</i> , 2016, 110, 84-93.	0.7	7
11	Focused information criterion and model averaging with generalized rank regression. <i>Statistics and Probability Letters</i> , 2017, 122, 11-19.	0.7	6
12	Probabilistic natural mapping of gene-level tests for genome-wide association studies. <i>Briefings in Bioinformatics</i> , 2018, 19, 545-553.	6.5	6
13	Identification of gene-environment interactions with marginal penalization. <i>Genetic Epidemiology</i> , 2020, 44, 159-196.	1.3	6
14	Information-incorporated Gaussian graphical model for gene expression data. <i>Biometrics</i> , 2022, 78, 512-523.	1.4	6
15	Jackknife empirical likelihood test for high-dimensional regression coefficients. <i>Computational Statistics and Data Analysis</i> , 2016, 94, 302-316.	1.2	5
16	Biclustering analysis of functionals via penalized fusion. <i>Journal of Multivariate Analysis</i> , 2021, 189, 104874.	1.0	5
17	Integrative sparse principal component analysis of gene expression data. <i>Genetic Epidemiology</i> , 2017, 41, 844-865.	1.3	4
18	Assisted graphical model for gene expression data analysis. <i>Statistics in Medicine</i> , 2019, 38, 2364-2380.	1.6	4

#	ARTICLE	IF	CITATIONS
19	Robust model-free feature screening for ultrahigh dimensional surrogate data. <i>Journal of Statistical Computation and Simulation</i> , 2020, 90, 550-569.	1.2	4
20	Structured sparse logistic regression with application to lung cancer prediction using breath volatile biomarkers. <i>Statistics in Medicine</i> , 2020, 39, 955-967.	1.6	4
21	HeteroGGM: an R package for Gaussian graphical model-based heterogeneity analysis. <i>Bioinformatics</i> , 2021, 37, 3073-3074.	4.1	4
22	Integrating approximate single factor graphical models. <i>Statistics in Medicine</i> , 2020, 39, 146-155.	1.6	3
23	Structured analysis of the high-dimensional FMR model. <i>Computational Statistics and Data Analysis</i> , 2020, 144, 106883.	1.2	3
24	Histopathological imaging features- versus molecular measurements-based cancer prognosis modeling. <i>Scientific Reports</i> , 2020, 10, 15030.	3.3	3
25	Tests for regression coefficients in high dimensional partially linear models. <i>Statistics and Probability Letters</i> , 2020, 163, 108772.	0.7	3
26	Integrative sparse partial least squares. <i>Statistics in Medicine</i> , 2021, 40, 2239-2256.	1.6	3
27	Promote sign consistency in the joint estimation of precision matrices. <i>Computational Statistics and Data Analysis</i> , 2021, 159, 107210.	1.2	3
28	Hierarchical cancer heterogeneity analysis based on histopathological imaging features. <i>Biometrics</i> , 2022, 78, 1579-1591.	1.4	3
29	A tree-based gene-environment interaction analysis with rare features. <i>Statistical Analysis and Data Mining</i> , 2022, 15, 648-674.	2.8	3
30	Least absolute relative error estimation for functional quadratic multiplicative model. <i>Communications in Statistics - Theory and Methods</i> , 2016, 45, 5802-5817.	1.0	2
31	Feature screening of quadratic inference functions for ultrahigh dimensional longitudinal data. <i>Journal of Statistical Computation and Simulation</i> , 2020, 90, 2614-2630.	1.2	2
32	Assisted estimation of gene expression graphical models. <i>Genetic Epidemiology</i> , 2021, 45, 372-385.	1.3	2
33	Gene-environment interaction identification via penalized robust divergence. <i>Biometrical Journal</i> , 2022, 64, 461-480.	1.0	2
34	Linear EV model with replicate observations on independent variables. <i>Science in China Series A: Mathematics</i> , 2006, 49, 752-769.	0.5	1
35	A note on the two-sample mean problem based on jackknife empirical likelihood. <i>Communications in Statistics - Theory and Methods</i> , 2017, 46, 7827-7836.	1.0	1
36	Joint detection for functional polynomial regression with autoregressive errors. <i>Communications in Statistics - Theory and Methods</i> , 2017, 46, 7837-7854.	1.0	1

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37	Smooth and locally sparse estimation for multiple-output functional linear regression. <i>Journal of Statistical Computation and Simulation</i> , 2020, 90, 341-354.	1.2	1
38	Structured sparse support vector machine with ordered features. <i>Journal of Applied Statistics</i> , 2022, 49, 1105-1120.	1.3	1
39	Estimation of partial derivative functionals with application to human mortality data analysis. <i>Science China Mathematics</i> , 2021, 64, 2117-2140.	1.7	1
40	Multivariate functional generalized additive models. <i>Journal of Statistical Computation and Simulation</i> , 2022, 92, 875-893.	1.2	1
41	Network-incorporated integrative sparse linear discriminant analysis. <i>Statistics and Its Interface</i> , 2019, 12, 149-166.	0.3	1
42	iSFun: an R package for integrative dimension reduction analysis. <i>Bioinformatics</i> , 2022, 38, 3134-3135.	4.1	1
43	A weighted Wilcoxon estimate for the covariate-specific ROC curve. <i>Science China Mathematics</i> , 2017, 60, 1705-1716.	1.7	0
44	Comparative studies on the adequacy check of parametric measurement error models with auxiliary variable. <i>Statistical Papers</i> , 2020, 62, 1723.	1.2	0
45	Model identification and selection for single-index varying-coefficient models. <i>Annals of the Institute of Statistical Mathematics</i> , 2021, 73, 457-480.	0.8	0
46	Robust high-dimensional regression for data with anomalous responses. <i>Annals of the Institute of Statistical Mathematics</i> , 2021, 73, 703-736.	0.8	0
47	Conditional score matching for high-dimensional partial graphical models. <i>Computational Statistics and Data Analysis</i> , 2021, 153, 107066.	1.2	0
48	Biomarker-guided heterogeneity analysis of genetic regulations via multivariate sparse fusion. <i>Statistics in Medicine</i> , 2021, 40, 3915-3936.	1.6	0
49	Network-adaptive robust penalized estimation of time-varying coefficient models with longitudinal data. <i>Journal of Statistical Computation and Simulation</i> , 0, , 1-21.	1.2	0