

# Shuangge

## List of Publications by Year in descending order

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Version: 2024-02-01

51  
papers

442  
citations

933447

10  
h-index

888059

17  
g-index

51  
all docs

51  
docs citations

51  
times ranked

464  
citing authors

#	ARTICLE	IF	CITATIONS
1	Kynurenic acid may underlie sex-specific immune responses to COVID-19. <i>Science Signaling</i> , 2021, 14, .	3.6	58
2	Robust network-based regularization and variable selection for high-dimensional genomic data in cancer prognosis. <i>Genetic Epidemiology</i> , 2019, 43, 276-291.	1.3	42
3	Dissecting gene-environment interactions: A penalized robust approach accounting for hierarchical structures. <i>Statistics in Medicine</i> , 2018, 37, 437-456.	1.6	30
4	Differences exist across insurance schemes in China post-consolidation. <i>PLoS ONE</i> , 2017, 12, e0187100.	2.5	23
5	Identifying gene-gene interactions using penalized tensor regression. <i>Statistics in Medicine</i> , 2018, 37, 598-610.	1.6	22
6	Structured gene-environment interaction analysis. <i>Biometrics</i> , 2020, 76, 23-35.	1.4	19
7	Semiparametric Bayesian variable selection for gene-environment interactions. <i>Statistics in Medicine</i> , 2020, 39, 617-638.	1.6	17
8	Analysis of cancer gene expression data with an assisted robust marker identification approach. <i>Genetic Epidemiology</i> , 2017, 41, 779-789.	1.3	16
9	Sparse boosting for high-dimensional survival data with varying coefficients. <i>Statistics in Medicine</i> , 2018, 37, 789-800.	1.6	14
10	Clustering multilayer omics data using MuNCut. <i>BMC Genomics</i> , 2018, 19, 198.	2.8	13
11	Assisted clustering of gene expression data using ANCut. <i>BMC Genomics</i> , 2017, 18, 623.	2.8	10
12	Identification of cancer omics commonality and difference via community fusion. <i>Statistics in Medicine</i> , 2019, 38, 1200-1212.	1.6	10
13	Accommodating missingness in environmental measurements in gene-environment interaction analysis. <i>Genetic Epidemiology</i> , 2017, 41, 523-554.	1.3	9
14	Robust semiparametric gene-environment interaction analysis using sparse boosting. <i>Statistics in Medicine</i> , 2019, 38, 4625-4641.	1.6	9
15	Identifying gene-environment interactions incorporating prior information. <i>Statistics in Medicine</i> , 2019, 38, 1620-1633.	1.6	9
16	Gaussian graphical model-based heterogeneity analysis via penalized fusion. <i>Biometrics</i> , 2022, 78, 524-535.	1.4	9
17	Inferring gene regulatory relationships with a high-dimensional robust approach. <i>Genetic Epidemiology</i> , 2017, 41, 437-454.	1.3	8
18	A Forward and Backward Stagewise algorithm for nonconvex loss functions with adaptive Lasso. <i>Computational Statistics and Data Analysis</i> , 2018, 124, 235-251.	1.2	8

#	ARTICLE	IF	CITATIONS
19	Assisted gene expression-based clustering with AWNCut. <i>Statistics in Medicine</i> , 2018, 37, 4386-4403.	1.6	8
20	Descriptions of self-treatment for the middle-aged and elderly in Shanxi, China. <i>PLoS ONE</i> , 2018, 13, e0198554.	2.5	8
21	Histopathological imaging-based cancer heterogeneity analysis via penalized fusion with model averaging. <i>Biometrics</i> , 2021, 77, 1397-1408.	1.4	8
22	Histopathological Imaging-Environment Interactions in Cancer Modeling. <i>Cancers</i> , 2019, 11, 579.	3.7	7
23	Identification of gene-environment interactions with marginal penalization. <i>Genetic Epidemiology</i> , 2020, 44, 159-196.	1.3	6
24	Information-incorporated Gaussian graphical model for gene expression data. <i>Biometrics</i> , 2022, 78, 512-523.	1.4	6
25	Overlapping clustering of gene expression data using penalized weighted normalized cut. <i>Genetic Epidemiology</i> , 2018, 42, 796-811.	1.3	5
26	Human disease cost network analysis. <i>Statistics in Medicine</i> , 2020, 39, 1237-1249.	1.6	5
27	Robust Bayesian Variable Selection for Gene-Environment Interactions. <i>Biometrics</i> , 2023, 79, 684-694.	1.4	5
28	Integrative sparse principal component analysis of gene expression data. <i>Genetic Epidemiology</i> , 2017, 41, 844-865.	1.3	4
29	Assisted graphical model for gene expression data analysis. <i>Statistics in Medicine</i> , 2019, 38, 2364-2380.	1.6	4
30	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
31	HeteroGGM: an R package for Gaussian graphical model-based heterogeneity analysis. <i>Bioinformatics</i> , 2021, 37, 3073-3074.	4.1	4
32	GEInter: an R package for robust gene-environment interaction analysis. <i>Bioinformatics</i> , 2021, 37, 3691-3692.	4.1	4
33	Multidimensional molecular measurements-environment interaction analysis for disease outcomes. <i>Biometrics</i> , 2022, 78, 1542-1554.	1.4	4
34	Penalized integrative semiparametric interaction analysis for multiple genetic datasets. <i>Statistics in Medicine</i> , 2019, 38, 3221-3242.	1.6	3
35	An integrative sparse boosting analysis of cancer genomic commonality and difference. <i>Statistical Methods in Medical Research</i> , 2020, 29, 1325-1337.	1.5	3
36	Integrating approximate single factor graphical models. <i>Statistics in Medicine</i> , 2020, 39, 146-155.	1.6	3

#	ARTICLE	IF	CITATIONS
37	Structured analysis of the high-dimensional FMR model. Computational Statistics and Data Analysis, 2020, 144, 106883.	1.2	3
38	Integrative sparse partial least squares. Statistics in Medicine, 2021, 40, 2239-2256.	1.6	3
39	Hierarchical cancer heterogeneity analysis based on histopathological imaging features. Biometrics, 2022, 78, 1579-1591.	1.4	3
40	Human disease clinical treatment network for the elderly: analysis of the medicare inpatient length of stay and readmission data. Biometrics, 2023, 79, 404-416.	1.4	3
41	Network-based cancer heterogeneity analysis incorporating multi-view of prior information. Bioinformatics, 2022, 38, 2855-2862.	4.1	3
42	A tree-based gene-environment interaction analysis with rare features. Statistical Analysis and Data Mining, 2022, 15, 648-674.	2.8	3
43	Assisted estimation of gene expression graphical models. Genetic Epidemiology, 2021, 45, 372-385.	1.3	2
44	Analysis of cancer omics data: a selective review of statistical techniques. Briefings in Bioinformatics, 2022, 23, .	6.5	2
45	A likelihood ratio test on temporal trends in age-period-cohort models with applications to the disparities of heart disease mortality among US populations and comparison with Japan. Statistics in Medicine, 2021, 40, 668-689.	1.6	1
46	Human disease clinical treatment network for the elderly: The analysis of medicare inpatient length of stay data. Statistics in Medicine, 2021, 40, 2083-2099.	1.6	1
47	Gene-gene interaction analysis incorporating network information via a structured Bayesian approach. Statistics in Medicine, 2021, 40, 6619-6633.	1.6	1
48	Conditional score matching for high-dimensional partial graphical models. Computational Statistics and Data Analysis, 2021, 153, 107066.	1.2	0
49	Biomarker-guided heterogeneity analysis of genetic regulations via multivariate sparse fusion. Statistics in Medicine, 2021, 40, 3915-3936.	1.6	0
50	Assisted differential network analysis for gene expression data. Genetic Epidemiology, 2021, 45, 604-620.	1.3	0
51	Bayesian hierarchical finite mixture of regression for histopathological imaging-based cancer data analysis. Statistics in Medicine, 2022, , .	1.6	0