

Jian Huang

List of Publications by Year in descending order

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145
papers

9,330
citations

76326

40
h-index

46799

89
g-index

147
all docs

147
docs citations

147
times ranked

8878
citing authors

#	ARTICLE	IF	CITATIONS
1	Linearized maximum rank correlation estimation. <i>Biometrika</i> , 2023, 110, 187-203.	2.4	4
2	Robust Signal Recovery for High-Dimensional Linear Log-Contrast Models with Compositional Covariates. <i>Journal of Business and Economic Statistics</i> , 2023, 41, 957-967.	2.9	0
3	GSDAR: a fast Newton algorithm for ℓ_0 regularized generalized linear models with statistical guarantee. <i>Computational Statistics</i> , 2022, 37, 507-533.	1.5	5
4	Robust post-selection inference of high-dimensional mean regression with heavy-tailed asymmetric or heteroskedastic errors. <i>Journal of Econometrics</i> , 2022, 230, 416-431.	6.5	3
5	Hierarchical cancer heterogeneity analysis based on histopathological imaging features. <i>Biometrics</i> , 2022, 78, 1579-1591.	1.4	3
6	PSNA: A pathwise semismooth Newton algorithm for sparse recovery with optimal local convergence and oracle properties. <i>Signal Processing</i> , 2022, 194, 108432.	3.7	0
7	Bayesian hierarchical finite mixture of regression for histopathological imaging-based cancer data analysis. <i>Statistics in Medicine</i> , 2022, , .	1.6	0
8	ℓ_0 -Regularized high-dimensional accelerated failure time model. <i>Computational Statistics and Data Analysis</i> , 2022, 170, 107430.	1.2	4
9	Histopathological imaging-based cancer heterogeneity analysis via penalized fusion with model averaging. <i>Biometrics</i> , 2021, 77, 1397-1408.	1.4	8
10	Subgroup analysis in the heterogeneous Cox model. <i>Statistics in Medicine</i> , 2021, 40, 739-757.	1.6	10
11	Fitting sparse linear models under the sufficient and necessary condition for model identification. <i>Statistics and Probability Letters</i> , 2021, 168, 108925.	0.7	4
12	Generalized Newton-Raphson algorithm for high dimensional LASSO regression. <i>Statistics and Its Interface</i> , 2021, 14, 339-350.	0.3	1
13	A Unified Primal Dual Active Set Algorithm for Nonconvex Sparse Recovery. <i>Statistical Science</i> , 2021, 36, .	2.8	17
14	A Semismooth Newton Algorithm for High-Dimensional Nonconvex Sparse Learning. <i>IEEE Transactions on Neural Networks and Learning Systems</i> , 2020, 31, 2993-3006.	11.3	10
15	Exploration of Heterogeneous Treatment Effects via Concave Fusion. <i>International Journal of Biostatistics</i> , 2020, 16, .	0.7	26
16	CoMM-S2: a collaborative mixed model using summary statistics in transcriptome-wide association studies. <i>Bioinformatics</i> , 2020, 36, 2009-2016.	4.1	30
17	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
18	Model pursuit and variable selection in the additive accelerated failure time model. <i>Statistical Papers</i> , 2020, , 1.	1.2	2

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19	A rank-based approach to estimating monotone individualized two treatment regimes. <i>Computational Statistics and Data Analysis</i> , 2020, 151, 107015.	1.2	0
20	High-dimensional integrative analysis with homogeneity and sparsity recovery. <i>Journal of Multivariate Analysis</i> , 2019, 174, 104529.	1.0	12
21	Inference for Low-Dimensional Covariates in a High-Dimensional Accelerated Failure Time Model. <i>Statistica Sinica</i> , 2019, 29, 877-894.	0.3	8
22	Oracle inequalities for sparse additive quantile regression in reproducing kernel Hilbert space. <i>Annals of Statistics</i> , 2018, 46, .	2.6	31
23	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
24	Identifying gene-gene interactions using penalized tensor regression. <i>Statistics in Medicine</i> , 2018, 37, 598-610.	1.6	22
25	A group adaptive elastic-net approach for variable selection in high-dimensional linear regression. <i>Science China Mathematics</i> , 2018, 61, 173-188.	1.7	7
26	LPG: A four-group probabilistic approach to leveraging pleiotropy in genome-wide association studies. <i>BMC Genomics</i> , 2018, 19, 503.	2.8	7
27	On the sign consistency of the Lasso for the high-dimensional Cox model. <i>Journal of Multivariate Analysis</i> , 2018, 167, 79-96.	1.0	3
28	Robust Decoding from 1-Bit Compressive Sampling with Ordinary and Regularized Least Squares. <i>SIAM Journal of Scientific Computing</i> , 2018, 40, A2062-A2086.	2.8	12
29	Estimating high-dimensional additive Cox model with time-dependent covariate processes. <i>Scandinavian Journal of Statistics</i> , 2018, 45, 900-922.	1.4	4
30	A lower bound based smoothed quasi-Newton algorithm for group bridge penalized regression. <i>Communications in Statistics Part B: Simulation and Computation</i> , 2017, 46, 4694-4707.	1.2	1
31	A Concave Pairwise Fusion Approach to Subgroup Analysis. <i>Journal of the American Statistical Association</i> , 2017, 112, 410-423.	3.1	126
32	Promoting Similarity of Sparsity Structures in Integrative Analysis With Penalization. <i>Journal of the American Statistical Association</i> , 2017, 112, 342-350.	3.1	20
33	Accommodating missingness in environmental measurements in gene-environment interaction analysis. <i>Genetic Epidemiology</i> , 2017, 41, 523-554.	1.3	9
34	Semismooth Newton Coordinate Descent Algorithm for Elastic-Net Penalized Huber Loss Regression and Quantile Regression. <i>Journal of Computational and Graphical Statistics</i> , 2017, 26, 547-557.	1.7	86
35	Analyzing Association Mapping in Pedigree-Based GWAS Using a Penalized Multitrait Mixed Model. <i>Genetic Epidemiology</i> , 2016, 40, 382-393.	1.3	11
36	Sieve Estimation of Cox Models with Latent Structures. <i>Biometrics</i> , 2016, 72, 1086-1097.	1.4	9

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37	Bayesian inference for high-dimensional linear regression under mnet priors. Canadian Journal of Statistics, 2016, 44, 180-197.	0.9	4
38	Statin Use and the Risk of Kidney Disease With Long-Term Follow-Up (8.4-Year Study). American Journal of Cardiology, 2016, 117, 647-655.	1.6	34
39	Asymptotic properties of Lasso in high-dimensional partially linear models. Science China Mathematics, 2016, 59, 769-788.	1.7	10
40	The Mnet method for variable selection. Statistica Sinica, 2016, , .	0.3	17
41	Concave 1-norm group selection. Biostatistics, 2015, 16, 252-267.	1.5	11
42	Deciphering the associations between gene expression and copy number alteration using a sparse double Laplacian shrinkage approach. Bioinformatics, 2015, 31, 3977-3983.	4.1	27
43	Integrative analysis of $\tilde{\text{omics}}^{\text{TM}}$ data using penalty functions. Wiley Interdisciplinary Reviews: Computational Statistics, 2015, 7, 99-108.	3.9	34
44	Group descent algorithms for nonconvex penalized linear and logistic regression models with grouped predictors. Statistics and Computing, 2015, 25, 173-187.	1.5	191
45	Combining multidimensional genomic measurements for predicting cancer prognosis: observations from TCGA. Briefings in Bioinformatics, 2015, 16, 291-303.	6.5	122
46	Integrative Analysis of High-throughput Cancer Studies With Contrasted Penalization. Genetic Epidemiology, 2014, 38, 144-151.	1.3	17
47	Integrative Analysis of Cancer Diagnosis Studies with Composite Penalization. Scandinavian Journal of Statistics, 2014, 41, 87-103.	1.4	31
48	A Penalized Robust Method for Identifying Gene-Environment Interactions. Genetic Epidemiology, 2014, 38, 220-230.	1.3	24
49	Integrative analysis of prognosis data on multiple cancer subtypes. Biometrics, 2014, 70, 480-488.	1.4	15
50	Majorization minimization by coordinate descent for concave penalized generalized linear models. Statistics and Computing, 2014, 24, 871-883.	1.5	9
51	Penalized multivariate linear mixed model for longitudinal genome-wide association studies. BMC Proceedings, 2014, 8, S73.	1.6	3
52	Similarity of markers identified from cancer gene expression studies: observations from GEO. Briefings in Bioinformatics, 2014, 15, 671-684.	6.5	12
53	Concave group methods for variable selection and estimation in high-dimensional varying coefficient models. Science China Mathematics, 2014, 57, 2073-2090.	1.7	4
54	Incorporating Network Structure in Integrative Analysis of Cancer Prognosis Data. Genetic Epidemiology, 2013, 37, 173-183.	1.3	18

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55	Identification of gene-environment interactions in cancer studies using penalization. <i>Genomics</i> , 2013, 102, 189-194.	2.9	47
56	Sparse group penalized integrative analysis of multiple cancer prognosis datasets. <i>Genetical Research</i> , 2013, 95, 68-77.	0.9	12
57	The cross-validated AUC for MCP-logistic regression with high-dimensional data. <i>Statistical Methods in Medical Research</i> , 2013, 22, 505-518.	1.5	15
58	Incorporating group correlations in genome-wide association studies using smoothed group Lasso. <i>Biostatistics</i> , 2013, 14, 205-219.	1.5	24
59	Integrative analysis of multiple cancer genomic datasets under the heterogeneity model. <i>Statistics in Medicine</i> , 2013, 32, 3509-3521.	1.6	13
60	Oracle inequalities for the lasso in the Cox model. <i>Annals of Statistics</i> , 2013, 41, 1142-1165.	2.6	75
61	Accounting for linkage disequilibrium in genome-wide association studies: a penalized regression method. <i>Statistics and Its Interface</i> , 2013, 6, 99-115.	0.3	22
62	MATS: a Bayesian framework for flexible detection of differential alternative splicing from RNA-Seq data. <i>Nucleic Acids Research</i> , 2012, 40, e61-e61.	14.5	330
63	Identification of cancer genomic markers via integrative sparse boosting. <i>Biostatistics</i> , 2012, 13, 509-522.	1.5	21
64	Gene network-based cancer prognosis analysis with sparse boosting. <i>Genetical Research</i> , 2012, 94, 205-221.	0.9	15
65	A Selective Review of Group Selection in High-Dimensional Models. <i>Statistical Science</i> , 2012, 27, .	2.8	254
66	Maintenance of hematopoietic stem cells through regulation of Wnt and mTOR pathways. <i>Nature Medicine</i> , 2012, 18, 1778-1785.	30.7	188
67	Integrative Analysis of Cancer Prognosis Data With Multiple Subtypes Using Regularized Gradient Descent. <i>Genetic Epidemiology</i> , 2012, 36, 829-838.	1.3	6
68	Integrative prescreening in analysis of multiple cancer genomic studies. <i>BMC Bioinformatics</i> , 2012, 13, 168.	2.6	8
69	Semiparametric Regression Pursuit. <i>Statistica Sinica</i> , 2012, 22, 1403-1426.	0.3	37
70	Identification of breast cancer prognosis markers via integrative analysis. <i>Computational Statistics and Data Analysis</i> , 2012, 56, 2718-2728.	1.2	4
71	Model Selection for Cox Models with Time-Varying Coefficients. <i>Biometrics</i> , 2012, 68, 419-428.	1.4	38
72	Analysis of Genome-Wide Association Studies with Multiple Outcomes Using Penalization. <i>PLoS ONE</i> , 2012, 7, e511198.	2.5	5

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73	Estimation and Selection via Absolute Penalized Convex Minimization And Its Multistage Adaptive Applications. <i>Journal of Machine Learning Research</i> , 2012, 13, 1839-1864.	62.4	24
74	Coordinate descent algorithms for nonconvex penalized regression, with applications to biological feature selection. <i>Annals of Applied Statistics</i> , 2011, 5, 232-253.	1.1	498
75	The sparse Laplacian shrinkage estimator for high-dimensional regression. <i>Annals of Statistics</i> , 2011, 39, 2021-2046.	2.6	72
76	Regularized regression method for genome-wide association studies. <i>BMC Proceedings</i> , 2011, 5, S67.	1.6	6
77	Incorporating higher-order representative features improves prediction in network-based cancer prognosis analysis. <i>BMC Medical Genomics</i> , 2011, 4, 5.	1.5	18
78	Integrative analysis of multiple cancer prognosis studies with gene expression measurements. <i>Statistics in Medicine</i> , 2011, 30, 3361-3371.	1.6	31
79	Variable selection and estimation in high-dimensional varying-coefficient models. <i>Statistica Sinica</i> , 2011, 21, 1515-1540.	0.3	98
80	Integrative analysis and variable selection with multiple high-dimensional data sets. <i>Biostatistics</i> , 2011, 12, 763-775.	1.5	39
81	Identification of Predictive Pathways for Non-Hodgkin Lymphoma Prognosis. <i>Cancer Informatics</i> , 2010, 9, CIN.S6315.	1.9	10
82	Variable selection in nonparametric additive models. <i>Annals of Statistics</i> , 2010, 38, 2282-2313.	2.6	357
83	Consistent group selection in high-dimensional linear regression. <i>Bernoulli</i> , 2010, 16, 1369-1384.	1.3	84
84	Variable selection in the accelerated failure time model via the bridge method. <i>Lifetime Data Analysis</i> , 2010, 16, 176-195.	0.9	84
85	A Spline-Based Semiparametric Maximum Likelihood Estimation Method for the Cox Model with Interval-Censored Data. <i>Scandinavian Journal of Statistics</i> , 2010, 37, 338-354.	1.4	109
86	Semiparametric prognosis models in genomic studies. <i>Briefings in Bioinformatics</i> , 2010, 11, 385-393.	6.5	7
87	Identification of non-Hodgkin's lymphoma prognosis signatures using the CTGDR method. <i>Bioinformatics</i> , 2010, 26, 15-21.	4.1	18
88	A group bridge approach for variable selection. <i>Biometrika</i> , 2009, 96, 339-355.	2.4	257
89	Regularized gene selection in cancer microarray meta-analysis. <i>BMC Bioinformatics</i> , 2009, 10, 1.	2.6	941
90	Identification of genes associated with multiple cancers via integrative analysis. <i>BMC Genomics</i> , 2009, 10, 535.	2.8	18

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91	Semiparametric Estimation Methods for Panel Count Data Using Monotone B -Splines. Journal of the American Statistical Association, 2009, 104, 1060-1070.	3.1	64
92	SCAD-penalized regression in high-dimensional partially linear models. Annals of Statistics, 2009, 37, .	2.6	145
93	Pivotal role for glycogen synthase kinase β 3 in hematopoietic stem cell homeostasis in mice. Journal of Clinical Investigation, 2009, 119, 3519-29.	8.2	109
94	Identification of cancer-associated gene clusters and genes via clustering penalization. Statistics and Its Interface, 2009, 2, 1-11.	0.3	8
95	Penalized methods for bi-level variable selection. Statistics and Its Interface, 2009, 2, 369-380.	0.3	180
96	Penalized feature selection and classification in bioinformatics. Briefings in Bioinformatics, 2008, 9, 392-403.	6.5	203
97	Asymptotic properties of bridge estimators in sparse high-dimensional regression models. Annals of Statistics, 2008, 36, .	2.6	337
98	The sparsity and bias of the Lasso selection in high-dimensional linear regression. Annals of Statistics, 2008, 36, .	2.6	488
99	Clustering threshold gradient descent regularization: with applications to microarray studies. Bioinformatics, 2007, 23, 466-472.	4.1	30
100	A semiparametric approach for the nonparametric transformation survival model with multiple covariates. Biostatistics, 2007, 8, 197-211.	1.5	37
101	Combining Clinical and Genomic Covariates via Cov-TGDR. Cancer Informatics, 2007, 3, 117693510700300.	1.9	4
102	Gene Expression Analysis of Photoreceptor Cell Loss in Bbs4-Knockout Mice Reveals an Early Stress Gene Response and Photoreceptor Cell Damage. , 2007, 48, 3329.		57
103	Combining Multiple Markers for Classification Using ROC. Biometrics, 2007, 63, 751-757.	1.4	63
104	Additive risk survival model with microarray data. BMC Bioinformatics, 2007, 8, 192.	2.6	34
105	Supervised group Lasso with applications to microarray data analysis. BMC Bioinformatics, 2007, 8, 60.	2.6	183
106	Combining clinical and genomic covariates via Cov-TGDR. Cancer Informatics, 2007, 3, 371-8.	1.9	6
107	Robust Semiparametric Microarray Normalization and Significance Analysis. Biometrics, 2006, 62, 555-561.	1.4	5
108	Regularized Estimation in the Accelerated Failure Time Model with High-Dimensional Covariates. Biometrics, 2006, 62, 813-820.	1.4	134

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109	Regularized binormal ROC method in disease classification using microarray data. BMC Bioinformatics, 2006, 7, 253.	2.6	18
110	Regulation of gene expression in the mammalian eye and its relevance to eye disease. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 14429-14434.	7.1	190
111	Homozygosity mapping with SNP arrays identifies <i>TRIM32</i> , an E3 ubiquitin ligase, as a Bardet-Biedl syndrome gene (<i>BBS11</i>). Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 6287-6292.	7.1	378
112	IL-21 Plus CpG ODN Induces Granzyme B-Dependent Induction of Apoptosis in CD5-Positive B Cells Including B-CLL Cells. Blood, 2006, 108, 2823-2823.	1.4	0
113	A robust two-way semi-linear model for normalization of cDNA microarray data. BMC Bioinformatics, 2005, 6, 14.	2.6	18
114	Regularized ROC method for disease classification and biomarker selection with microarray data. Bioinformatics, 2005, 21, 4356-4362.	4.1	152
115	A Two-Way Semilinear Model for Normalization and Analysis of cDNA Microarray Data. Journal of the American Statistical Association, 2005, 100, 814-829.	3.1	29
116	The Posterior Probability of Linkage Allowing for Linkage Disequilibrium and a New Estimate of Disequilibrium between a Trait and a Marker. Human Heredity, 2005, 59, 210-219.	0.8	25
117	Genome-wide linkage analysis of blood pressure under locus heterogeneity. BMC Genetics, 2003, 4, S78.	2.7	6
118	Genetic Linkage Analysis of a Dichotomous Trait Incorporating a Tightly Linked Quantitative Trait in Affected Sib Pairs. American Journal of Human Genetics, 2003, 72, 949-960.	6.2	16
119	Two-Locus Heterogeneity Cannot Be Distinguished from Two-Locus Epistasis on the Basis of Affected-Sib-Pair Data. American Journal of Human Genetics, 2003, 73, 223-232.	6.2	32
120	Reply to Cordell and Farrall. American Journal of Human Genetics, 2003, 73, 1471-1473.	6.2	12
121	A SEMIPARAMETRIC METHOD FOR MAPPING QUANTITATIVE TRAIT LOCI. , 2003, , 262-271.		0
122	Comparison of $\hat{\alpha}$ -Model-Free TM and $\hat{\alpha}$ -Model-Based TM Linkage Statistics in the Presence of Locus Heterogeneity: Single Data Set and Multiple Data Set Applications. Human Heredity, 2001, 51, 217-225.	0.8	45
123	Power to Detect Linkage Based on Multiple Sets of Data in the Presence of Locus Heterogeneity: Comparative Evaluation of Model-Based Linkage Methods for Affected Sib Pair Data. Human Heredity, 2001, 51, 199-208.	0.8	65
124	The Null Distribution of the Heterogeneity Lod Score Does Depend on the Assumed Genetic Model for the Trait. Human Heredity, 2001, 52, 217-222.	0.8	14
125	Genome Scan for Linkage to Asthma Using a Linkage Disequilibrium $\hat{\alpha}$ Lod Score Test. Genetic Epidemiology, 2001, 21, S303-7.	1.3	1
126	Combined Multipoint Analysis of Multiple Asthma Data Sets Based on the Posterior Probability of Linkage. Genetic Epidemiology, 2001, 21, S73-8.	1.3	11

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127	Evidence supporting WNT2 as an autism susceptibility gene. American Journal of Medical Genetics Part A, 2001, 105, 406-413.	2.4	188
128	The Score Statistic of the LD-Lod Analysis: Detecting Linkage Adaptive to Linkage Disequilibrium. Human Heredity, 2001, 52, 83-98.	0.8	3
129	Reply to Horvath et al.. American Journal of Human Genetics, 2000, 67, 534-535.	6.2	1
130	Genetic anticipation and breast cancer: a prospective follow-up study. Breast Cancer Research and Treatment, 1999, 55, 21-28.	2.5	14
131	Linkage Detection Adaptive to Linkage Disequilibrium: The Disequilibrium Maximum-Likelihood Binomial Test for Affected-Sibship Data. American Journal of Human Genetics, 1999, 65, 1741-1759.	6.2	26
132	A bayesian approach to replication of linkage findings. Genetic Epidemiology, 1999, 17, S749-54.	1.3	28
133	Efficient estimation of the partly linear additive Cox model. Annals of Statistics, 1999, 27, 1536.	2.6	122
134	Statistical Evaluation of Age-at-Onset Anticipation: A New Test and Evaluation of Its Behavior in Realistic Applications. American Journal of Human Genetics, 1998, 62, 1212-1227.	6.2	35
135	Sieve Estimation for the Proportional-Odds Failure-Time Regression Model with Interval Censoring. Journal of the American Statistical Association, 1997, 92, 960-967.	3.1	134
136	A new statistical test for age-of-onset anticipation: Application to bipolar disorder. Genetic Epidemiology, 1997, 14, 1091-1096.	1.3	31
137	A new statistical test for age-of-onset anticipation: Application to bipolar disorder. Genetic Epidemiology, 1997, 14, 1091-1096.	1.3	1
138	Interval Censored Survival Data: A Review of Recent Progress. Lecture Notes in Statistics, 1997, , 123-169.	0.2	128
139	Sieve Estimation for the Proportional-Odds Failure-Time Regression Model With Interval Censoring. Journal of the American Statistical Association, 1997, 92, 960.	3.1	93
140	Efficient estimation for the proportional hazards model with interval censoring. Annals of Statistics, 1996, 24, 540.	2.6	343
141	Immunohistochemical study of mucin carbohydrates and core proteins in human pancreatic tumors. Cancer, 1993, 71, 2191-2199.	4.1	170
142	Monoclonal antibody directed against colon cancer mucin has high specificity for malignancy. International Journal of Cancer, 1993, 54, 467-474.	5.1	22
143	Penalized Integrative Analysis of High-Dimensional Omics Data. , 0, , 174-204.		0
144	Projection-based and cross-validated estimation in high-dimensional Cox model. Scandinavian Journal of Statistics, 0, , .	1.4	1

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145	A Deep Generative Approach to Conditional Sampling. Journal of the American Statistical Association, 0, , 1-12.	3.1	4