Wei Pan

List of Publications by Year
in descending order

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185 papers	8,327 citations	66343 42 h-index	56724 83 g-index
190 all docs	190 docs citations	190 times ranked	10614 citing authors

#	Article	IF	Citations
1	Akaike's Information Criterion in Generalized Estimating Equations. Biometrics, 2001, 57, 120-125.	1.4	1,973
2	A comparative review of statistical methods for discovering differentially expressed genes in replicated microarray experiments. Bioinformatics, 2002, 18, 546-554.	4.1	456
3	A Data-Adaptive Sum Test for Disease Association with Multiple Common or Rare Variants. Human Heredity, 2010, 70, 42-54.	0.8	278
4	Asymptotic tests of association with multiple SNPs in linkage disequilibrium. Genetic Epidemiology, 2009, 33, 497-507.	1.3	208
5	Comparison of statistical tests for disease association with rare variants. Genetic Epidemiology, 2011, 35, 606-619.	1.3	205
6	Likelihood-Based Selection and Sharp Parameter Estimation. Journal of the American Statistical Association, 2012, 107, 223-232.	3.1	172
7	A Powerful and Adaptive Association Test for Rare Variants. Genetics, 2014, 197, 1081-1095.	2.9	150
8	Small-sample adjustments in using the sandwich variance estimator in generalized estimating equations. Statistics in Medicine, 2002, 21, 1429-1441.	1.6	138
9	A mixture model approach to detecting differentially expressed genes with microarray data. Functional and Integrative Genomics, 2003, 3, 117-124.	3.5	120
10	A Multiple Imputation Approach to Cox Regression with Interval-Censored Data. Biometrics, 2000, 56, 199-203.	1.4	116
11	A note on using permutation-based false discovery rate estimates to compare different analysis methods for microarray data. Bioinformatics, 2005, 21, 4280-4288.	4.1	104
12	Constrained maximum likelihood-based Mendelian randomization robust to both correlated and uncorrelated pleiotropic effects. American Journal of Human Genetics, 2021, 108, 1251-1269.	6.2	104
13	Incorporating biological knowledge into distance-based clustering analysis of microarray gene expression data. Bioinformatics, 2006, 22, 1259-1268.	4.1	103
14	How many replicates of arrays are required to detect gene expression changes in microarray experiments? A mixture model approach. Genome Biology, 2002, 3, research0022.1.	9.6	99
15	Linear regression and two-class classification with gene expression data. Bioinformatics, 2003, 19, 2072-2078.	4.1	97
16	Incorporating gene functions as priors in model-based clustering of microarray gene expression data. Bioinformatics, 2006, 22, 795-801.	4.1	91
17	Incorporating Predictor Network in Penalized Regression with Application to Microarray Data. Biometrics, 2010, 66, 474-484.	1.4	91
18	On the use of permutation in and the performance of a class of nonparametric methods to detect differential gene expression. Bioinformatics, 2003, 19, 1333-1340.	4.1	90

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19	Network-based support vector machine for classification of microarray samples. BMC Bioinformatics, 2009, 10, S21.	2.6	87
20	Extending the Iterative Convex Minorant Algorithm to the Cox Model for Interval-Censored Data. Journal of Computational and Graphical Statistics, 1999, 8, 109-120.	1.7	79
21	Sample Size and Power Calculations with Correlated Binary Data. Contemporary Clinical Trials, 2001, 22, 211-227.	1.9	76
22	Incorporating gene networks into statistical tests for genomic data via a spatially correlated mixture model. Bioinformatics, 2008, 24, 404-411.	4.1	75
23	Combining the strengths of inverse-variance weighting and Egger regression in Mendelian randomization using a mixture of regressions model. PLoS Genetics, 2021, 17, e1009922.	3.5	74
24	A Powerful Framework for Integrating eQTL and GWAS Summary Data. Genetics, 2017, 207, 893-902.	2.9	72
25	Model Selection in Estimating Equations. Biometrics, 2001, 57, 529-534.	1.4	71
26	An Adaptive Association Test for Multiple Phenotypes with GWAS Summary Statistics. Genetic Epidemiology, 2015, 39, 651-663.	1.3	71
27	Penalized model-based clustering with unconstrained covariance matrices. Electronic Journal of Statistics, 2009, 3, 1473-1496.	0.7	70
28	An adaptive association test for microbiome data. Genome Medicine, 2016, 8, 56.	8.2	69
29	Carotid Intimaâ€Media Thickness and Arterial Stiffness and the Risk of Atrial Fibrillation: The Atherosclerosis Risk in Communities (ARIC) Study, Multiâ€Ethnic Study of Atherosclerosis (MESA), and the Rotterdam Study. Journal of the American Heart Association, 2016, 5, .	3.7	66
30	Penalized model-based clustering with cluster-specific diagonal covariance matrices and grouped variables. Electronic Journal of Statistics, 2008, 2, 168-212.	0.7	65
31	Modified nonparametric approaches to detecting differentially expressed genes in replicated microarray experiments. Bioinformatics, 2003, 19, 1046-1054.	4.1	64
32	Incorporating prior knowledge of predictors into penalized classifiers with multiple penalty terms. Bioinformatics, 2007, 23, 1775-1782.	4.1	62
33	Relationship between genomic distanceâ€based regression and kernel machine regression for multiâ€marker association testing. Genetic Epidemiology, 2011, 35, 211-216.	1.3	62
34	A Powerful Pathway-Based Adaptive Test for Genetic Association with Common or Rare Variants. American Journal of Human Genetics, 2015, 97, 86-98.	6.2	61
35	Testing for association with multiple traits in generalized estimation equations, with application to neuroimaging data. NeuroImage, 2014, 96, 309-325.	4.2	60
36	Model-based cluster analysis of microarray gene-expression data. Genome Biology, 2002, 3, research0009.1.	9.6	58

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37	Incorporating prior knowledge of gene functional groups into regularized discriminant analysis of microarray data. Bioinformatics, 2007, 23, 3170-3177.	4.1	57
38	Imaging-wide association study: Integrating imaging endophenotypes in GWAS. NeuroImage, 2017, 159, 159-169.	4.2	57
39	An adaptive two-sample test for high-dimensional means. Biometrika, 2016, 103, 609-624.	2.4	55
40	Small-sample performance of the robust score test and its modifications in generalized estimating equations. Statistics in Medicine, 2005, 24, 3479-3495.	1.6	53
41	Adaptive gene- and pathway-trait association testing with GWAS summary statistics. Bioinformatics, 2016, 32, 1178-1184.	4.1	53
42	Estimation in the Cox Proportional Hazards Model with Left-Truncated and Interval-Censored Data. Biometrics, 2002, 58, 64-70.	1.4	51
43	A simple convolutional neural network for prediction of enhancerâ€“promoter interactions with DNA sequence data. Bioinformatics, 2019, 35, 2899-2906.	4.1	50
44	Adaptive tests for association analysis of rare variants. Genetic Epidemiology, 2011, 35, 381-388.	1.3	49
45	Comparison of statistical tests for group differences in brain functional networks. NeuroImage, 2014, 101, 681-694.	4.2	47
46	A two-sample test with interval censored data via multiple imputation. , 2000, 19, 1-11.		43
47	A comparative study of discriminating human heart failure etiology using gene expression profiles. BMC Bioinformatics, 2005, 6, 205.	2.6	43
48	On constrained and regularized high-dimensional regression. Annals of the Institute of Statistical Mathematics, 2013, 65, 807-832.	0.8	43
49	Longitudinal Analysis Is More Powerful than Cross-Sectional Analysis in Detecting Genetic Association with Neuroimaging Phenotypes. PLoS ONE, 2014, 9, e102312.	2.5	42
50	A Multiple Imputation Approach to Regression Analysis for Doubly Censored Data with Application to AIDS Studies. Biometrics, 2001, 57, 1245-1250.	1.4	41
51	Statistical significance analysis of longitudinal gene expression data. Bioinformatics, 2003, 19, 1628-1635.	4.1	40
52	Simultaneous Grouping Pursuit and Feature Selection Over an Undirected Graph. Journal of the American Statistical Association, 2013, 108, 713-725.	3.1	40
53	Adjustment for Population Stratification via Principal Components in Association Analysis of Rare Variants. Genetic Epidemiology, 2013, 37, 99-109.	1.3	38
54	Principal Component Regression and Linear Mixed Model in Association Analysis of Structured Samples: Competitors or Complements?. Genetic Epidemiology, 2015, 39, 149-155.	1.3	37

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55	Networkâ€Based Penalized Regression With Application to Genomic Data. Biometrics, 2013, 69, 582-593.	1.4	36
56	Integration of Enhancer-Promoter Interactions with GWAS Summary Results Identifies Novel Schizophrenia-Associated Genes and Pathways. Genetics, 2018, 209, 699-709.	2.9	34
57	Identification of gene expression profiles in rat ears with cDNA microarrays. Hearing Research, 2003, 175, 2-13.	2.0	33
58	Dpath software reveals hierarchical haemato-endothelial lineages of Etv2 progenitors based on single-cell transcriptome analysis. Nature Communications, 2017, 8, 14362.	12.8	33
59	Variable Selection in Penalized Modelâ€Based Clustering Via Regularization on Grouped Parameters. Biometrics, 2008, 64, 921-930.	1.4	32
60	A powerful fine-mapping method for transcriptome-wide association studies. Human Genetics, 2020, 139, 199-213.	3.8	32
61	Using frailties in the accelerated failure time model. Lifetime Data Analysis, 2001, 7, 55-64.	0.9	31
62	Cluster analysis using multivariate normal mixture models to detect differential gene expression with microarray data. Computational Statistics and Data Analysis, 2006, 51, 641-658.	1.2	31
63	Powerful and Adaptive Testing for Multi-trait and Multi-SNP Associations with GWAS and Sequencing Data. Genetics, 2016, 203, 715-731.	2.9	29
64	Conditional analysis of multiple quantitative traits based on marginal GWAS summary statistics. Genetic Epidemiology, 2017, 41, 427-436.	1.3	29
65	Network-based model weighting to detect multiple loci influencing complex diseases. Human Genetics, 2008, 124, 225-234.	3.8	28
66	Simultaneous supervised clustering and feature selection over a graph. Biometrika, 2012, 99, 899-914.	2.4	28
67	Penalized regression and model selection methods for polygenic scores on summary statistics. PLoS Computational Biology, 2020, 16, e1008271.	3.2	27
68	Implicating causal brain imaging endophenotypes in Alzheimerâ€™s disease using multivariable IWAS and GWAS summary data. NeuroImage, 2020, 223, 117347.	4.2	27
69	Cluster Analysis: Unsupervised Learning via Supervised Learning with a Non-convex Penalty. Journal of Machine Learning Research, 2013, 14, 1865.	62.4	27
70	Analysis by cDNA microarrays of altered gene expression in middle ears of rats following pneumococcal infection. International Journal of Pediatric Otorhinolaryngology, 2002, 65, 203-211.	1.0	26
71	Semi-supervised learning via penalized mixture model with application to microarray sample classification. Bioinformatics, 2006, 22, 2388-2395.	4.1	26
72	Penalized mixtures of factor analyzers with application to clustering high-dimensional microarray data. Bioinformatics, 2010, 26, 501-508.	4.1	26

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73	Gene- and pathway-based association tests for multiple traits with GWAS summary statistics. Bioinformatics, 2017, 33, 64-71.	4.1	26
74	Estimation of multiple networks in Gaussian mixture models. Electronic Journal of Statistics, 2016, 10, 1133-1154.	0.7	24
75	Comparing three methods for variance estimation with duplicated high density oligonucleotide arrays. Functional and Integrative Genomics, 2002, 2, 126-133.	3.5	23
76	Does it always help to adjust for misclassification of a binary outcome in logistic regression?. Statistics in Medicine, 2005, 24, 2221-2234.	1.6	23
77	Penalized regression and risk prediction in genomeâ€wide association studies. Statistical Analysis and Data Mining, 2013, 6, 315-328.	2.8	23
78	Smooth estimation of the survival function for interval censored data. Statistics in Medicine, 2000, 19, 2611-2624.	1.6	22
79	Bootstrapping Likelihood for Model Selection with Small Samples. Journal of Computational and Graphical Statistics, 1999, 8, 687-698.	1.7	21
80	Powerful multiâ€marker association tests: unifying genomic distanceâ€based regression and logistic regression. Genetic Epidemiology, 2010, 34, 680-688.	1.3	21
81	Adjusting for Population Stratification in a Fine Scale With Principal Components and Sequencing Data. Genetic Epidemiology, 2013, 37, 787-801.	1.3	21
82	Abnormal Endothelial Gene Expression Associated With Early Coronary Atherosclerosis. Journal of the American Heart Association, 2020, 9, e016134.	3.7	21
83	Integrating eQTL data with GWAS summary statistics in pathwayâ€based analysis with application to schizophrenia. Genetic Epidemiology, 2018, 42, 303-316.	1.3	20
84	A Linear Mixed-Effects Model for Multivariate Censored Data. Biometrics, 2000, 56, 160-166.	1.4	19
85	Incorporating Biological Information as a Prior in an Empirical Bayes Approach to Analyzing Microarray Data. Statistical Applications in Genetics and Molecular Biology, 2005, 4, Article12.	0.6	19
86	Network-based genomic discovery: application and comparison of Markov random-field models. Journal of the Royal Statistical Society Series C: Applied Statistics, 2010, 59, 105-125.	1.0	19
87	Test Selection with Application to Detecting Disease Association with Multiple SNPs. Human Heredity, 2010, 69, 120-130.	0.8	19
88	Testing Group Differences in Brain Functional Connectivity: Using Correlations or Partial Correlations?. Brain Connectivity, 2015, 5, 214-231.	1.7	19
89	Integration of methylation QTL and enhancerâ€“target gene maps with schizophrenia GWAS summary results identifies novel genes. Bioinformatics, 2019, 35, 3576-3583.	4.1	19
90	Some statistical consideration in transcriptomeâ€wide association studies. Genetic Epidemiology, 2020, 44, 221-232.	1.3	19

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91	Asymptotically independent U-statistics in high-dimensional testing. Annals of Statistics, 2021, 49, 154-181.	2.6	19
92	Extending the Iterative Convex Minorant Algorithm to the Cox Model for Interval-Censored Data. Journal of Computational and Graphical Statistics, 1999, 8, 109.	1.7	18
93	Approximate confidence intervals for one proportion and difference of two proportions. Computational Statistics and Data Analysis, 2002, 40, 143-157.	1.2	18
94	Highly adaptive tests for group differences in brain functional connectivity. NeuroImage: Clinical, 2015, 9, 625-639.	2.7	18
95	TCM visualizes trajectories and cell populations from single cell data. Nature Communications, 2018, 9, 2749.	12.8	18
96	Inferring causal direction between two traits in the presence of horizontal pleiotropy with GWAS summary data. PLoS Genetics, 2020, 16, e1009105.	3.5	18
97	Constrained likelihood for reconstructing a directed acyclic Gaussian graph. Biometrika, 2019, 106, 109-125.	2.4	17
98	Computation of the NPMLE of distribution functions for interval censored and truncated data with applications to the Cox model. Computational Statistics and Data Analysis, 1998, 28, 33-50.	1.2	15
99	Estimating Survival Curves with Left-Truncated and Interval-Censored Data under Monotone Hazards. Biometrics, 1998, 54, 1053.	1.4	15
100	A Note on the Use of Marginal Likelihood and Conditional Likelihood in Analyzing Clustered Data. American Statistician, 2002, 56, 171-174.	1.6	15
101	Combining Gene Annotations and Gene Expression Data in Model-Based Clustering: Weighted Method. OMICS A Journal of Integrative Biology, 2006, 10, 28.	2.0	15
102	Network-based multiple locus linkage analysis of expression traits. Bioinformatics, 2009, 25, 1390-1396.	4.1	15
103	Bayesian joint modeling of multiple gene networks and diverse genomic data to identify target genes of a transcription factor. Annals of Applied Statistics, 2012, 6, 334-355.	1.1	15
104	A note on inconsistency of NPMLE of the distribution function from left truncated and case I interval censored data. Lifetime Data Analysis, 1999, 5, 281-291.	0.9	14
105	Methods for Estimating and Interpreting Provider-Specific Standardized Mortality Ratios. Health Services and Outcomes Research Methodology, 2003, 4, 135-149.	1.8	14
106	A Case Study on Choosing Normalization Methods and Test Statistics for Two-Channel Microarray Data. Comparative and Functional Genomics, 2004, 5, 432-444.	2.0	14
107	Binomial Mixture Modelâ€based Association Tests under Genetic Heterogeneity. Annals of Human Genetics, 2009, 73, 614-630.	0.8	14
108	Multilocus association testing with penalized regression. Genetic Epidemiology, 2011, 35, 755-765.	1.3	14

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109	Testing for Polygenic Effects in Genomeâ€Wide Association Studies. Genetic Epidemiology, 2015, 39, 306-316.	1.3	14
110	GENE FUNCTION PREDICTION BY A COMBINED ANALYSIS OF GENE EXPRESSION DATA AND PROTEIN-PROTEIN INTERACTION DATA. Journal of Bioinformatics and Computational Biology, 2005, 03, 1371-1389.	0.8	13
111	Adaptive SNP-Set Association Testing in Generalized Linear Mixed Models with Application to Family Studies. Behavior Genetics, 2018, 48, 55-66.	2.1	13
112	Deep reinforcement learning for personalized treatment recommendation. Statistics in Medicine, 2022, 41, 4034-4056.	1.6	13
113	A Unified Framework for Detecting Genetic Association with Multiple SNPs in a Candidate Gene or Region: Contrasting Genotype Scores and LD Patterns between Cases and Controls. Human Heredity, 2010, 69, 1-13.	0.8	12
114	Testing Genetic Pleiotropy with GWAS Summary Statistics for Marginal and Conditional Analyses. Genetics, 2017, 207, 1285-1299.	2.9	12
115	Improved Use of Small Reference Panels for Conditional and Joint Analysis with GWAS Summary Statistics. Genetics, 2018, 209, 401-408.	2.9	12
116	Likelihood Ratio Tests for a Large Directed Acyclic Graph. Journal of the American Statistical Association, 2020, 115, 1304-1319.	3.1	12
117	On consistency of the monotone MLE of survival for left truncated and interval-censored data. Statistics and Probability Letters, 1998, 38, 49-57.	0.7	11
118	Statistical Tests of Genetic Association in the Presence of Gene-Gene and Gene-Environment Interactions. Human Heredity, 2010, 69, 131-142.	0.8	11
119	Adaptive Tests for Detecting Gene-Gene and Gene-Environment Interactions. Human Heredity, 2011, 72, 98-109.	0.8	11
120	Integrative and regularized principal component analysis of multiple sources of data. Statistics in Medicine, 2016, 35, 2235-2250.	1.6	11
121	On Robust Association Testing for Quantitative Traits and Rare Variants. G3: Genes, Genomes, Genetics, 2016, 6, 3941-3950.	1.8	11
122	Linear regression for bivariate censored data via multiple imputation. , 1999, 18, 3111-3121.		10
123	Bootstrap model selection in generalized linear models. Journal of Agricultural, Biological, and Environmental Statistics, 2001, 6, 49-61.	1.4	10
124	Operon information improves gene expression estimation for cDNA microarrays. BMC Genomics, 2006, 7, 87.	2.8	10
125	A powerful and versatile colocalization test. PLoS Computational Biology, 2020, 16, e1007778.	3.2	10
126	A multiple imputation approach to linear regression with clustered censored data. , 2001, 7, 111-123.		9

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127	A Bayesian approach to joint modeling of proteinâ€“DNA binding, gene expression and sequence data. Statistics in Medicine, 2010, 29, 489-503.	1.6	9
128	A Dimension Reduction Approach for Modeling Multi-Locus Interaction in Case-Control Studies. Human Heredity, 2011, 71, 234-245.	0.8	9
129	A Composite Likelihood Approach to Latent Multivariate Gaussian Modeling of SNP Data with Application to Genetic Association Testing. Biometrics, 2012, 68, 307-315.	1.4	9
130	Validation of genetic variants associated with early acute rejection in kidney allograft transplantation. Clinical Transplantation, 2012, 26, 418-423.	1.6	9
131	Adaptive testing for association between two random vectors in moderate to high dimensions. Genetic Epidemiology, 2017, 41, 599-609.	1.3	9
132	A comparison of some two-sample tests with interval censored data. Journal of Nonparametric Statistics, 1999, 12, 133-146.	0.9	8
133	Using Gene Expression to Improve the Power of Genome-Wide Association Analysis. Human Heredity, 2014, 78, 94-103.	0.8	8
134	Shrinking classification trees for bootstrap aggregation. Pattern Recognition Letters, 1999, 20, 961-965.	4.2	7
135	A cautionary note on using secondary phenotypes in neuroimaging genetic studies. NeuroImage, 2015, 121, 136-145.	4.2	7
136	Application of deep convolutional neural networks in classification of protein subcellular localization with microscopy images. Genetic Epidemiology, 2019, 43, 330-341.	1.3	7
137	Integrating DNA sequencing and transcriptomic data for association analyses of low-frequency variants and lipid traits. Human Molecular Genetics, 2020, 29, 515-526.	2.9	7
138	Incorporating gene functional annotations in detecting differential gene expression. Journal of the Royal Statistical Society Series C: Applied Statistics, 2006, 55, 301-316.	1.0	6
139	Approximate scoreâ€based testing with application to multivariate trait association analysis. Genetic Epidemiology, 2015, 39, 469-479.	1.3	6
140	On High-Dimensional Constrained Maximum Likelihood Inference. Journal of the American Statistical Association, 2020, 115, 217-230.	3.1	6
141	Integrating brain imaging endophenotypes with GWAS for Alzheimerâ€™s disease. Quantitative Biology, 2021, 9, 185-200.	0.5	6
142	Statistical power of transcriptomeâ€wide association studies. Genetic Epidemiology, 2022, 46, 572-588.	1.3	6
143	Graphical model checking with correlated response data. Statistics in Medicine, 2001, 20, 2935-2949.	1.6	5
144	Consensus Clustering of Gene Expression Data and its Application to Gene Function Prediction. Journal of Computational and Graphical Statistics, 2007, 16, 733-751.	1.7	5

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145	Incorporating Gene Functions into Regression Analysis of DNA-Protein Binding Data and Gene Expression Data to Construct Transcriptional Networks. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2008, 5, 401-415.	3.0	5
146	A Two-Step Penalized Regression Method with Networked Predictors. Statistics in Biosciences, 2012, 4, 27-46.	1.2	5
147	Local Epigenomic Data are more Informative than Local Genome Sequence Data in Predicting Enhancer-Promoter Interactions Using Neural Networks. Genes, 2020, 11, 41.	2.4	5
148	Support vector machines with disease-gene-centric network penalty for high dimensional microarray data. Statistics and Its Interface, 2009, 2, 257-269.	0.3	5
149	Robust inference of bi-directional causal relationships in presence of correlated pleiotropy with GWAS summary data. PLoS Genetics, 2022, 18, e1010205.	3.5	5
150	Significance Tests of Feature Relevance for a Black-Box Learner. IEEE Transactions on Neural Networks and Learning Systems, 2024, 35, 1898-1911.	11.3	5
151	Incorporating prior information via shrinkage: a combined analysis of genome-wide location data and gene expression data. Statistics in Medicine, 2007, 26, 2258-2275.	1.6	4
152	A Bayesian Partitioning Model for the Detection of Multilocus Effects in Case-Control Studies. Human Heredity, 2015, 79, 69-79.	0.8	4
153	Significance Testing for Allelic Heterogeneity. Genetics, 2018, 210, 25-32.	2.9	4
154	A graph convolutional neural network for gene expression data analysis with multiple gene networks. Statistics in Medicine, 2021, 40, 5547-5564.	1.6	4
155	Model checking via testing for direct effects in Mendelian Randomization and transcriptome-wide association studies. PLoS Computational Biology, 2021, 17, e1009266.	3.2	4
156	Bayesian Variable Selection in Regression with Networked Predictors. Frontiers of Statistics, 2010, , 147-165.	0.2	4
157	A New Algorithm and Theory for Penalized Regression-based Clustering. Journal of Machine Learning Research, 2016, 17, .	62.4	4
158	A parametric joint model of DNA-protein binding, gene expression and DNA sequence data to detect target genes of a transcription factor. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2008, , 465-76.	0.7	4
159	A practical problem with Egger regression in Mendelian randomization. PLoS Genetics, 2022, 18, e1010166.	3.5	4
160	Application of conditional moment tests to model checking for generalized linear models. Biostatistics, 2002, 3, 267-276.	1.5	3
161	Functional group-based linkage analysis of gene expression trait loci. BMC Proceedings, 2007, 1, S117.	1.6	3
162	Penalized regression approaches to testing for quantitative trait-rare variant association. Frontiers in Genetics, 2014, 5, 121.	2.3	3

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163	Adaptive testing for multiple traits in a proportional odds model with applications to detect SNP-brain network associations. Genetic Epidemiology, 2017, 41, 259-277.	1.3	3
164	Integrative analysis of multi-omics data for discovering low-frequency variants associated with low-density lipoprotein cholesterol levels. Bioinformatics, 2021, 36, 5223-5228.	4.1	3
165	Penalized model-based clustering of fMRI data. Biostatistics, 2022, 23, 825-843.	1.5	3
166	Accounting for nonlinear effects of gene expression identifies additional associated genes in transcriptomeÂwide association studies. Human Molecular Genetics, 2022, , .	2.9	3
167	Semi-supervised spectral clustering with application to detect population stratification. Frontiers in Genetics, 2013, 4, 215.	2.3	2
168	Adjusting for population stratification and relatedness with sequencing data. BMC Proceedings, 2014, 8, S42.	1.6	2
169	ADAPTIVE TESTING OF SNP-BRAIN FUNCTIONAL CONNECTIVITY ASSOCIATION VIA A MODULAR NETWORK ANALYSIS. , 2017, , .		2
170	An adaptive gene-based test for methylation data. BMC Proceedings, 2018, 12, 60.	1.6	2
171	An adaptive gene-level association test for pedigree data. BMC Genetics, 2018, 19, 68.	2.7	2
172	An adaptive test for metaâ€analysis of rare variant association studies. Genetic Epidemiology, 2020, 44, 104-116.	1.3	2
173	Integrating germline and somatic genetics to identify genes associated with lung cancer. Genetic Epidemiology, 2020, 44, 233-247.	1.3	2
174	Leveraging existing GWAS summary data of genetically correlated and uncorrelated traits to improve power for a new GWAS. Genetic Epidemiology, 2020, 44, 717-732.	1.3	2
175	Speeding up Monte Carlo simulations for the adaptive sum of powered score test with importance sampling. Biometrics, 2022, 78, 261-273.	1.4	2
176	A New Semiparametric Approach to Finite Mixture of Regressions using Penalized Regression via Fusion. Statistica Sinica, 2020, 30, 783-807.	0.3	2
177	ADAPTIVE TESTING OF SNP-BRAIN FUNCTIONAL CONNECTIVITY ASSOCIATION VIA A MODULAR NETWORK ANALYSIS. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2017, 22, 58-69.	0.7	2
178	Does the inclusion of rare variants improve risk prediction?. BMC Proceedings, 2014, 8, S94.	1.6	1
179	A Novel Statistic for Global Association Testing Based on Penalized Regression. Genetic Epidemiology, 2015, 39, 415-426.	1.3	1
180	Nonlinear joint latent variable models and integrative tumor subtype discovery. Statistical Analysis and Data Mining, 2016, 9, 106-116.	2.8	1

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181	Binomial Mixture Model Based Association Testing to Account for Genetic Heterogeneity for GWAS. Genetic Epidemiology, 2016, 40, 202-209.	1.3	1
182	A random covariance model for biâ€level graphical modeling with application to restingâ€state fMRI data. Biometrics, 2021, 77, 1385-1396.	1.4	1
183	Outcome weighted Ï^ â€learning for individualized treatment rules. Stat, 2021, 10, e343.	0.4	1
184	A PARAMETRIC JOINT MODEL OF DNA-PROTEIN BINDING, GENE EXPRESSION AND DNA SEQUENCE DATA TO DETECT TARGET GENES OF A TRANSCRIPTION FACTOR. , 2007, , .		1
185	A Regularization-Based Adaptive Test for High-Dimensional Generalized Linear Models. Journal of Machine Learning Research, 2020, 21, .	62.4	1