Wei Pan

List of Publications by Year
in descending order

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185	8,327	66234	56606
papers	citations	42 h-index	83 g-index

190	190	190	10614
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Significance Tests of Feature Relevance for a Black-Box Learner. IEEE Transactions on Neural Networks and Learning Systems, 2024, 35, 1898-1911.	7.2	5
2	Speeding up Monte Carlo simulations for the adaptive sum of powered score test with importance sampling. Biometrics, 2022, 78, 261-273.	0.8	2
3	Penalized model-based clustering of fMRI data. Biostatistics, 2022, 23, 825-843.	0.9	3
4	Accounting for nonlinear effects of gene expression identifies additional associated genes in transcriptomeÂwide association studies. Human Molecular Genetics, 2022, , .	1.4	3
5	A practical problem with Egger regression in Mendelian randomization. PLoS Genetics, 2022, 18, e1010166.	1.5	4
6	Robust inference of bi-directional causal relationships in presence of correlated pleiotropy with GWAS summary data. PLoS Genetics, 2022, 18, e1010205.	1.5	5
7	Deep reinforcement learning for personalized treatment recommendation. Statistics in Medicine, 2022, 41, 4034-4056.	0.8	13
8	Statistical power of transcriptomeâ€wide association studies. Genetic Epidemiology, 2022, 46, 572-588.	0.6	6
9	A random covariance model for biâ€level graphical modeling with application to restingâ€state fMRI data. Biometrics, 2021, 77, 1385-1396.	0.8	1
10	Integrating brain imaging endophenotypes with GWAS for Alzheimerâ€™s disease. Quantitative Biology, 2021, 9, 185-200.	0.3	6
11	Integrative analysis of multi-omics data for discovering low-frequency variants associated with low-density lipoprotein cholesterol levels. Bioinformatics, 2021, 36, 5223-5228.	1.8	3
12	Outcome weighted Ï^ â€learning for individualized treatment rules. Stat, 2021, 10, e343.	0.3	1
13	Asymptotically independent U-statistics in high-dimensional testing. Annals of Statistics, 2021, 49, 154-181.	1.4	19
14	Constrained maximum likelihood-based Mendelian randomization robust to both correlated and uncorrelated pleiotropic effects. American Journal of Human Genetics, 2021, 108, 1251-1269.	2.6	104
15	A graph convolutional neural network for gene expression data analysis with multiple gene networks. Statistics in Medicine, 2021, 40, 5547-5564.	0.8	4
16	Model checking via testing for direct effects in Mendelian Randomization and transcriptome-wide association studies. PLoS Computational Biology, 2021, 17, e1009266.	1.5	4
17	Combining the strengths of inverse-variance weighting and Egger regression in Mendelian randomization using a mixture of regressions model. PLoS Genetics, 2021, 17, e1009922.	1.5	74
18	On High-Dimensional Constrained Maximum Likelihood Inference. Journal of the American Statistical Association, 2020, 115, 217-230.	1.8	6

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19	Likelihood Ratio Tests for a Large Directed Acyclic Graph. Journal of the American Statistical Association, 2020, 115, 1304-1319.	1.8	12
20	An adaptive test for metaâ€analysis of rare variant association studies. Genetic Epidemiology, 2020, 44, 104-116.	0.6	2
21	A powerful fine-mapping method for transcriptome-wide association studies. Human Genetics, 2020, 139, 199-213.	1.8	32
22	Some statistical consideration in transcriptomeâ€wide association studies. Genetic Epidemiology, 2020, 44, 221-232.	0.6	19
23	Integrating germline and somatic genetics to identify genes associated with lung cancer. Genetic Epidemiology, 2020, 44, 233-247.	0.6	2
24	Penalized regression and model selection methods for polygenic scores on summary statistics. PLoS Computational Biology, 2020, 16, e1008271.	1.5	27
25	Abnormal Endothelial Gene Expression Associated With Early Coronary Atherosclerosis. Journal of the American Heart Association, 2020, 9, e016134.	1.6	21
26	Leveraging existing GWAS summary data of genetically correlated and uncorrelated traits to improve power for a new GWAS. Genetic Epidemiology, 2020, 44, 717-732.	0.6	2
27	Integrating DNA sequencing and transcriptomic data for association analyses of low-frequency variants and lipid traits. Human Molecular Genetics, 2020, 29, 515-526.	1.4	7
28	Local Epigenomic Data are more Informative than Local Genome Sequence Data in Predicting Enhancer-Promoter Interactions Using Neural Networks. Genes, 2020, 11, 41.	1.0	5
29	A powerful and versatile colocalization test. PLoS Computational Biology, 2020, 16, e1007778.	1.5	10
30	Implicating causal brain imaging endophenotypes in Alzheimerâ€™s disease using multivariable IWAS and GWAS summary data. NeuroImage, 2020, 223, 117347.	2.1	27
31	Inferring causal direction between two traits in the presence of horizontal pleiotropy with GWAS summary data. PLoS Genetics, 2020, 16, e1009105.	1.5	18
32	A New Semiparametric Approach to Finite Mixture of Regressions using Penalized Regression via Fusion. Statistica Sinica, 2020, 30, 783-807.	0.2	2
33	A Regularization-Based Adaptive Test for High-Dimensional Generalized Linear Models. Journal of Machine Learning Research, 2020, 21, .	62.4	1
34	Integration of methylation QTL and enhancerâ€“target gene maps with schizophrenia GWAS summary results identifies novel genes. Bioinformatics, 2019, 35, 3576-3583.	1.8	19
35	Constrained likelihood for reconstructing a directed acyclic Gaussian graph. Biometrika, 2019, 106, 109-125.	1.3	17
36	Application of deep convolutional neural networks in classification of protein subcellular localization with microscopy images. Genetic Epidemiology, 2019, 43, 330-341.	0.6	7

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37	A simple convolutional neural network for prediction of enhancerâ€“promoter interactions with DNA sequence data. Bioinformatics, 2019, 35, 2899-2906.	1.8	50
38	Improved Use of Small Reference Panels for Conditional and Joint Analysis with GWAS Summary Statistics. Genetics, 2018, 209, 401-408.	1.2	12
39	Integrating eQTL data with GWAS summary statistics in pathwayâ€based analysis with application to schizophrenia. Genetic Epidemiology, 2018, 42, 303-316.	0.6	20
40	Integration of Enhancer-Promoter Interactions with GWAS Summary Results Identifies Novel Schizophrenia-Associated Genes and Pathways. Genetics, 2018, 209, 699-709.	1.2	34
41	Adaptive SNP-Set Association Testing in Generalized Linear Mixed Models with Application to Family Studies. Behavior Genetics, 2018, 48, 55-66.	1.4	13
42	An adaptive gene-based test for methylation data. BMC Proceedings, 2018, 12, 60.	1.8	2
43	An adaptive gene-level association test for pedigree data. BMC Genetics, 2018, 19, 68.	2.7	2
44	Significance Testing for Allelic Heterogeneity. Genetics, 2018, 210, 25-32.	1.2	4
45	TCM visualizes trajectories and cell populations from single cell data. Nature Communications, 2018, 9, 2749.	5.8	18
46	Adaptive testing for multiple traits in a proportional odds model with applications to detect SNP-brain network associations. Genetic Epidemiology, 2017, 41, 259-277.	0.6	3
47	Dpath software reveals hierarchical haemato-endothelial lineages of Etv2 progenitors based on single-cell transcriptome analysis. Nature Communications, 2017, 8, 14362.	5.8	33
48	Conditional analysis of multiple quantitative traits based on marginal GWAS summary statistics. Genetic Epidemiology, 2017, 41, 427-436.	0.6	29
49	ADAPTIVE TESTING OF SNP-BRAIN FUNCTIONAL CONNECTIVITY ASSOCIATION VIA A MODULAR NETWORK ANALYSIS. , 2017, , .		2
50	Testing Genetic Pleiotropy with GWAS Summary Statistics for Marginal and Conditional Analyses. Genetics, 2017, 207, 1285-1299.	1.2	12
51	A Powerful Framework for Integrating eQTL and GWAS Summary Data. Genetics, 2017, 207, 893-902.	1.2	72
52	Imaging-wide association study: Integrating imaging endophenotypes in GWAS. NeuroImage, 2017, 159, 159-169.	2.1	57
53	Adaptive testing for association between two random vectors in moderate to high dimensions. Genetic Epidemiology, 2017, 41, 599-609.	0.6	9
54	Gene- and pathway-based association tests for multiple traits with GWAS summary statistics. Bioinformatics, 2017, 33, 64-71.	1.8	26

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55	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
56	An adaptive association test for microbiome data. Genome Medicine, 2016, 8, 56.	3.6	69
57	Integrative and regularized principal component analysis of multiple sources of data. Statistics in Medicine, 2016, 35, 2235-2250.	0.8	11
58	Nonlinear joint latent variable models and integrative tumor subtype discovery. Statistical Analysis and Data Mining, 2016, 9, 106-116.	1.4	1
59	Binomial Mixture Model Based Association Testing to Account for Genetic Heterogeneity for GWAS. Genetic Epidemiology, 2016, 40, 202-209.	0.6	1
60	An adaptive two-sample test for high-dimensional means. Biometrika, 2016, 103, 609-624.	1.3	55
61	On Robust Association Testing for Quantitative Traits and Rare Variants. G3: Genes, Genomes, Genetics, 2016, 6, 3941-3950.	0.8	11
62	Estimation of multiple networks in Gaussian mixture models. Electronic Journal of Statistics, 2016, 10, 1133-1154.	0.4	24
63	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, .	1.6	66
64	Powerful and Adaptive Testing for Multi-trait and Multi-SNP Associations with GWAS and Sequencing Data. Genetics, 2016, 203, 715-731.	1.2	29
65	Adaptive gene- and pathway-trait association testing with GWAS summary statistics. Bioinformatics, 2016, 32, 1178-1184.	1.8	53
66	A New Algorithm and Theory for Penalized Regression-based Clustering. Journal of Machine Learning Research, 2016, 17, .	62.4	4
67	Highly adaptive tests for group differences in brain functional connectivity. NeuroImage: Clinical, 2015, 9, 625-639.	1.4	18
68	A Novel Statistic for Global Association Testing Based on Penalized Regression. Genetic Epidemiology, 2015, 39, 415-426.	0.6	1
69	Approximate scoreâ€based testing with application to multivariate trait association analysis. Genetic Epidemiology, 2015, 39, 469-479.	0.6	6
70	An Adaptive Association Test for Multiple Phenotypes with GWAS Summary Statistics. Genetic Epidemiology, 2015, 39, 651-663.	0.6	71
71	A Bayesian Partitioning Model for the Detection of Multilocus Effects in Case-Control Studies. Human Heredity, 2015, 79, 69-79.	0.4	4
72	Principal Component Regression and Linear Mixed Model in Association Analysis of Structured Samples: Competitors or Complements?. Genetic Epidemiology, 2015, 39, 149-155.	0.6	37

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73	A cautionary note on using secondary phenotypes in neuroimaging genetic studies. NeuroImage, 2015, 121, 136-145.	2.1	7
74	A Powerful Pathway-Based Adaptive Test for Genetic Association with Common or Rare Variants. American Journal of Human Genetics, 2015, 97, 86-98.	2.6	61
75	Testing for Polygenic Effects in Genomeâ€Wide Association Studies. Genetic Epidemiology, 2015, 39, 306-316.	0.6	14
76	Testing Group Differences in Brain Functional Connectivity: Using Correlations or Partial Correlations?. Brain Connectivity, 2015, 5, 214-231.	0.8	19
77	Penalized regression approaches to testing for quantitative trait-rare variant association. Frontiers in Genetics, 2014, 5, 121.	1.1	3
78	Using Gene Expression to Improve the Power of Genome-Wide Association Analysis. Human Heredity, 2014, 78, 94-103.	0.4	8
79	Comparison of statistical tests for group differences in brain functional networks. NeuroImage, 2014, 101, 681-694.	2.1	47
80	A Powerful and Adaptive Association Test for Rare Variants. Genetics, 2014, 197, 1081-1095.	1.2	150
81	Adjusting for population stratification and relatedness with sequencing data. BMC Proceedings, 2014, 8, S42.	1.8	2
82	Does the inclusion of rare variants improve risk prediction?. BMC Proceedings, 2014, 8, S94.	1.8	1
83	Testing for association with multiple traits in generalized estimation equations, with application to neuroimaging data. NeuroImage, 2014, 96, 309-325.	2.1	60
84	Longitudinal Analysis Is More Powerful than Cross-Sectional Analysis in Detecting Genetic Association with Neuroimaging Phenotypes. PLoS ONE, 2014, 9, e102312.	1.1	42
85	Adjusting for Population Stratification in a Fine Scale With Principal Components and Sequencing Data. Genetic Epidemiology, 2013, 37, 787-801.	0.6	21
86	Simultaneous Grouping Pursuit and Feature Selection Over an Undirected Graph. Journal of the American Statistical Association, 2013, 108, 713-725.	1.8	40
87	Networkâ€Based Penalized Regression With Application to Genomic Data. Biometrics, 2013, 69, 582-593.	0.8	36
88	Adjustment for Population Stratification via Principal Components in Association Analysis of Rare Variants. Genetic Epidemiology, 2013, 37, 99-109.	0.6	38
89	On constrained and regularized high-dimensional regression. Annals of the Institute of Statistical Mathematics, 2013, 65, 807-832.	0.5	43
90	Penalized regression and risk prediction in genomeâ€wide association studies. Statistical Analysis and Data Mining, 2013, 6, 315-328.	1.4	23

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91	Semi-supervised spectral clustering with application to detect population stratification. Frontiers in Genetics, 2013, 4, 215.	1.1	2
92	Cluster Analysis: Unsupervised Learning via Supervised Learning with a Non-convex Penalty. Journal of Machine Learning Research, 2013, 14, 1865.	62.4	27
93	Likelihood-Based Selection and Sharp Parameter Estimation. Journal of the American Statistical Association, 2012, 107, 223-232.	1.8	172
94	Simultaneous supervised clustering and feature selection over a graph. Biometrika, 2012, 99, 899-914.	1.3	28
95	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.	0.5	15
96	A Composite Likelihood Approach to Latent Multivariate Gaussian Modeling of SNP Data with Application to Genetic Association Testing. Biometrics, 2012, 68, 307-315.	0.8	9
97	A Two-Step Penalized Regression Method with Networked Predictors. Statistics in Biosciences, 2012, 4, 27-46.	0.6	5
98	Validation of genetic variants associated with early acute rejection in kidney allograft transplantation. Clinical Transplantation, 2012, 26, 418-423.	0.8	9
99	Relationship between genomic distanceâ€based regression and kernel machine regression for multiâ€marker association testing. Genetic Epidemiology, 2011, 35, 211-216.	0.6	62
100	Adaptive tests for association analysis of rare variants. Genetic Epidemiology, 2011, 35, 381-388.	0.6	49
101	Comparison of statistical tests for disease association with rare variants. Genetic Epidemiology, 2011, 35, 606-619.	0.6	205
102	Multilocus association testing with penalized regression. Genetic Epidemiology, 2011, 35, 755-765.	0.6	14
103	A Dimension Reduction Approach for Modeling Multi-Locus Interaction in Case-Control Studies. Human Heredity, 2011, 71, 234-245.	0.4	9
104	Adaptive Tests for Detecting Gene-Gene and Gene-Environment Interactions. Human Heredity, 2011, 72, 98-109.	0.4	11
105	Powerful multiâ€marker association tests: unifying genomic distanceâ€based regression and logistic regression. Genetic Epidemiology, 2010, 34, 680-688.	0.6	21
106	A Bayesian approach to joint modeling of proteinâ€“DNA binding, gene expression and sequence data. Statistics in Medicine, 2010, 29, 489-503.	0.8	9
107	Incorporating Predictor Network in Penalized Regression with Application to Microarray Data. Biometrics, 2010, 66, 474-484.	0.8	91
108	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.	0.5	19

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109	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.	0.4	12
110	Test Selection with Application to Detecting Disease Association with Multiple SNPs. Human Heredity, 2010, 69, 120-130.	0.4	19
111	Statistical Tests of Genetic Association in the Presence of Gene-Gene and Gene-Environment Interactions. Human Heredity, 2010, 69, 131-142.	0.4	11
112	A Data-Adaptive Sum Test for Disease Association with Multiple Common or Rare Variants. Human Heredity, 2010, 70, 42-54.	0.4	278
113	Penalized mixtures of factor analyzers with application to clustering high-dimensional microarray data. Bioinformatics, 2010, 26, 501-508.	1.8	26
114	Bayesian Variable Selection in Regression with Networked Predictors. Frontiers of Statistics, 2010, , 147-165.	0.2	4
115	Network-based multiple locus linkage analysis of expression traits. Bioinformatics, 2009, 25, 1390-1396.	1.8	15
116	Network-based support vector machine for classification of microarray samples. BMC Bioinformatics, 2009, 10, S21.	1.2	87
117	Asymptotic tests of association with multiple SNPs in linkage disequilibrium. Genetic Epidemiology, 2009, 33, 497-507.	0.6	208
118	Binomial Mixture Modelâ€based Association Tests under Genetic Heterogeneity. Annals of Human Genetics, 2009, 73, 614-630.	0.3	14
119	Penalized model-based clustering with unconstrained covariance matrices. Electronic Journal of Statistics, 2009, 3, 1473-1496.	0.4	70
120	Support vector machines with disease-gene-centric network penalty for high dimensional microarray data. Statistics and Its Interface, 2009, 2, 257-269.	0.2	5
121	Network-based model weighting to detect multiple loci influencing complex diseases. Human Genetics, 2008, 124, 225-234.	1.8	28
122	Variable Selection in Penalized Modelâ€Based Clustering Via Regularization on Grouped Parameters. Biometrics, 2008, 64, 921-930.	0.8	32
123	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.	1.9	5
124	Incorporating gene networks into statistical tests for genomic data via a spatially correlated mixture model. Bioinformatics, 2008, 24, 404-411.	1.8	75
125	Penalized model-based clustering with cluster-specific diagonal covariance matrices and grouped variables. Electronic Journal of Statistics, 2008, 2, 168-212.	0.4	65
126	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

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127	Incorporating prior knowledge of predictors into penalized classifiers with multiple penalty terms. Bioinformatics, 2007, 23, 1775-1782.	1.8	62
128	Consensus Clustering of Gene Expression Data and its Application to Gene Function Prediction. Journal of Computational and Graphical Statistics, 2007, 16, 733-751.	0.9	5
129	Incorporating prior knowledge of gene functional groups into regularized discriminant analysis of microarray data. Bioinformatics, 2007, 23, 3170-3177.	1.8	57
130	Functional group-based linkage analysis of gene expression trait loci. BMC Proceedings, 2007, 1, S117.	1.8	3
131	Incorporating prior information via shrinkage: a combined analysis of genome-wide location data and gene expression data. Statistics in Medicine, 2007, 26, 2258-2275.	0.8	4
132	A PARAMETRIC JOINT MODEL OF DNA-PROTEIN BINDING, GENE EXPRESSION AND DNA SEQUENCE DATA TO DETECT TARGET GENES OF A TRANSCRIPTION FACTOR. , 2007, , .		1
133	Incorporating gene functional annotations in detecting differential gene expression. Journal of the Royal Statistical Society Series C: Applied Statistics, 2006, 55, 301-316.	0.5	6
134	Cluster analysis using multivariate normal mixture models to detect differential gene expression with microarray data. Computational Statistics and Data Analysis, 2006, 51, 641-658.	0.7	31
135	Operon information improves gene expression estimation for cDNA microarrays. BMC Genomics, 2006, 7, 87.	1.2	10
136	Incorporating biological knowledge into distance-based clustering analysis of microarray gene expression data. Bioinformatics, 2006, 22, 1259-1268.	1.8	103
137	Incorporating gene functions as priors in model-based clustering of microarray gene expression data. Bioinformatics, 2006, 22, 795-801.	1.8	91
138	Semi-supervised learning via penalized mixture model with application to microarray sample classification. Bioinformatics, 2006, 22, 2388-2395.	1.8	26
139	Combining Gene Annotations and Gene Expression Data in Model-Based Clustering: Weighted Method. OMICS A Journal of Integrative Biology, 2006, 10, 28.	1.0	15
140	A comparative study of discriminating human heart failure etiology using gene expression profiles. BMC Bioinformatics, 2005, 6, 205.	1.2	43
141	Does it always help to adjust for misclassification of a binary outcome in logistic regression?. Statistics in Medicine, 2005, 24, 2221-2234.	0.8	23
142	Small-sample performance of the robust score test and its modifications in generalized estimating equations. Statistics in Medicine, 2005, 24, 3479-3495.	0.8	53
143	A note on using permutation-based false discovery rate estimates to compare different analysis methods for microarray data. Bioinformatics, 2005, 21, 4280-4288.	1.8	104
144	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.	0.2	19

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145	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.	0.3	13
146	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
147	Methods for Estimating and Interpreting Provider-Specific Standardized Mortality Ratios. Health Services and Outcomes Research Methodology, 2003, 4, 135-149.	0.8	14
148	A mixture model approach to detecting differentially expressed genes with microarray data. Functional and Integrative Genomics, 2003, 3, 117-124.	1.4	120
149	Identification of gene expression profiles in rat ears with cDNA microarrays. Hearing Research, 2003, 175, 2-13.	0.9	33
150	Linear regression and two-class classification with gene expression data. Bioinformatics, 2003, 19, 2072-2078.	1.8	97
151	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.	1.8	90
152	Modified nonparametric approaches to detecting differentially expressed genes in replicated microarray experiments. Bioinformatics, 2003, 19, 1046-1054.	1.8	64
153	Statistical significance analysis of longitudinal gene expression data. Bioinformatics, 2003, 19, 1628-1635.	1.8	40
154	Application of conditional moment tests to model checking for generalized linear models. Biostatistics, 2002, 3, 267-276.	0.9	3
155	A comparative review of statistical methods for discovering differentially expressed genes in replicated microarray experiments. Bioinformatics, 2002, 18, 546-554.	1.8	456
156	A Note on the Use of Marginal Likelihood and Conditional Likelihood in Analyzing Clustered Data. American Statistician, 2002, 56, 171-174.	0.9	15
157	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.	13.9	99
158	Model-based cluster analysis of microarray gene-expression data. Genome Biology, 2002, 3, research0009.1.	13.9	58
159	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.	0.4	26
160	Comparing three methods for variance estimation with duplicated high density oligonucleotide arrays. Functional and Integrative Genomics, 2002, 2, 126-133.	1.4	23
161	Approximate confidence intervals for one proportion and difference of two proportions. Computational Statistics and Data Analysis, 2002, 40, 143-157.	0.7	18
162	Small-sample adjustments in using the sandwich variance estimator in generalized estimating equations. Statistics in Medicine, 2002, 21, 1429-1441.	0.8	138

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163	Estimation in the Cox Proportional Hazards Model with Left-Truncated and Interval-Censored Data. Biometrics, 2002, 58, 64-70.	0.8	51
164	Graphical model checking with correlated response data. Statistics in Medicine, 2001, 20, 2935-2949.	0.8	5
165	Using frailties in the accelerated failure time model. , 2001, 7, 55-64.		31
166	A multiple imputation approach to linear regression with clustered censored data. , 2001, 7, 111-123.		9
167	Bootstrap model selection in generalized linear models. Journal of Agricultural, Biological, and Environmental Statistics, 2001, 6, 49-61.	0.7	10
168	Akaike's Information Criterion in Generalized Estimating Equations. Biometrics, 2001, 57, 120-125.	0.8	1,973
169	Model Selection in Estimating Equations. Biometrics, 2001, 57, 529-534.	0.8	71
170	A Multiple Imputation Approach to Regression Analysis for Doubly Censored Data with Application to AIDS Studies. Biometrics, 2001, 57, 1245-1250.	0.8	41
171	Sample Size and Power Calculations with Correlated Binary Data. Contemporary Clinical Trials, 2001, 22, 211-227.	2.0	76
172	A two-sample test with interval censored data via multiple imputation. , 2000, 19, 1-11.		43
173	Smooth estimation of the survival function for interval censored data. Statistics in Medicine, 2000, 19, 2611-2624.	0.8	22
174	A Linear Mixed-Effects Model for Multivariate Censored Data. Biometrics, 2000, 56, 160-166.	0.8	19
175	A Multiple Imputation Approach to Cox Regression with Interval-Censored Data. Biometrics, 2000, 56, 199-203.	0.8	116
176	Extending the Iterative Convex Minorant Algorithm to the Cox Model for Interval-Censored Data. Journal of Computational and Graphical Statistics, 1999, 8, 109.	0.9	18
177	Shrinking classification trees for bootstrap aggregation. Pattern Recognition Letters, 1999, 20, 961-965.	2.6	7
178	A note on inconsistency of NPMLE of the distribution function from left truncated and case I interval censored data. , 1999, 5, 281-291.		14
179	Linear regression for bivariate censored data via multiple imputation. , 1999, 18, 3111-3121.		10
180	Bootstrapping Likelihood for Model Selection with Small Samples. Journal of Computational and Graphical Statistics, 1999, 8, 687-698.	0.9	21

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181	Extending the Iterative Convex Minorant Algorithm to the Cox Model for Interval-Censored Data. Journal of Computational and Graphical Statistics, 1999, 8, 109-120.	0.9	79
182	A comparison of some two-sample tests with interval censored data. Journal of Nonparametric Statistics, 1999, 12, 133-146.	0.4	8
183	On consistency of the monotone MLE of survival for left truncated and interval-censored data. Statistics and Probability Letters, 1998, 38, 49-57.	0.4	11
184	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.	0.7	15
185	Estimating Survival Curves with Left-Truncated and Interval-Censored Data under Monotone Hazards. Biometrics, 1998, 54, 1053.	0.8	15