Joseph G Ibrahim

List of Publications by Year
in descending order

292 papers	15,950 citations	26567 56 h-index	21474 114 g-index
297 all docs	297 docs citations	297 times ranked	13549 citing authors

#	Article	IF	Citations
1	Bayesian design of clinical trials using joint models for longitudinal and time-to-event data. Biostatistics, 2022, 23, 591-608.	0.9	3
2	Bayesian multivariate probability of success using historical data with type I error rate control. Biostatistics, 2022, 24, 17-31.	0.9	3
3	Large-scale GWAS reveals genetic architecture of brain white matter microstructure and genetic overlap with cognitive and mental health traits (nâ‰â‰17,706). Molecular Psychiatry, 2021, 26, 3943-3955.	4.1	100
4	Bayesian adaptive basket trial design using model averaging. Biostatistics, 2021, 22, 19-34.	0.9	27
5	Joint modelling of longitudinal and survival data in the presence of competing risks with applications to prostate cancer data. Statistical Modelling, 2021, 21, 72-94.	0.5	8
6	Model-based feature selection and clustering of RNA-seq data for unsupervised subtype discovery. Annals of Applied Statistics, 2021, 15, 481-508.	0.5	6
7	MRLocus: Identifying causal genes mediating a trait through Bayesian estimation of allelic heterogeneity. PLoS Genetics, 2021, 17, e1009455.	1.5	24
8	Inferring latent heterogeneity using many feature variables supervised by survival outcome. Statistics in Medicine, 2021, 40, 3181-3195.	0.8	0
9	Bayesian network metaâ€regression hierarchical models using heavyâ€tailed multivariate random effects with covariateâ€dependent variances. Statistics in Medicine, 2021, 40, 3582-3603.	0.8	1
10	Weighted functional linear Cox regression model. Statistical Methods in Medical Research, 2021, 30, 1917-1931.	0.7	3
11	On the normalized power prior. Statistics in Medicine, 2021, 40, 5251-5275.	0.8	7
12	BayesCTDesign: An R Package for Bayesian Trial Design Using Historical Control Data. Journal of Statistical Software, 2021, 100, .	1.8	0
13	ICeD-T Provides Accurate Estimates of Immune Cell Abundance in Tumor Samples by Allowing for Aberrant Gene Expression Patterns. Journal of the American Statistical Association, 2020, 115, 1055-1065.	1.8	18
14	Bayesian design of biosimilars clinical programs involving multiple therapeutic indications. Biometrics, 2020, 76, 630-642.	0.8	2
15	Global identifiability of latent class models with applications to diagnostic test accuracy studies: A GrÃ¶bner basis approach. Biometrics, 2020, 76, 98-108.	0.8	5
16	Modeling Between-Study Heterogeneity for Improved Replicability in Gene Signature Selection and Clinical Prediction. Journal of the American Statistical Association, 2020, 115, 1125-1138.	1.8	11
17	Joint analysis of singleâ€cell and bulk tissue sequencing data to infer intratumor heterogeneity. Biometrics, 2020, 76, 983-994.	0.8	2
18	Efficient Multiple Imputation for Sensitivity Analysis of Recurrent Events Data With Informative Censoring. Statistics in Biopharmaceutical Research, 2020, , 1-9.	0.6	1

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19	A marginal estimate for the overall treatment effect on a survival outcome within the joint modeling framework. Statistics in Medicine, 2020, 39, 4120-4132.	0.8	9
20	Network metaâ€regression for ordinal outcomes: Applications in comparing Crohn's disease treatments. Statistics in Medicine, 2020, 39, 1846-1870.	0.8	3
21	Partial least squares for functional joint models with applications to the Alzheimer's disease neuroimaging initiative study. Biometrics, 2020, 76, 1109-1119.	0.8	4
22	A hierarchical testing approach for detecting safety signals in clinical trials. Statistics in Medicine, 2020, 39, 1541-1557.	0.8	3
23	Bayesian Flexible Hierarchical Skew Heavy-Tailed Multivariate Meta Regression Models for Individual Patient Data with Applications. Statistics and Its Interface, 2020, 13, 485-500.	0.2	1
24	Penalized logistic regression using functional connectivity as covariates with an application to mild cognitive impairment. Communications for Statistical Applications and Methods, 2020, 27, 603-624.	0.1	0
25	Nonparametric expression analysis using inferential replicate counts. Nucleic Acids Research, 2019, 47, e105-e105.	6.5	54
26	Controlling false discovery proportion in identification of drugâ€related adverse events from multiple system organ classes. Statistics in Medicine, 2019, 38, 4378-4389.	0.8	3
27	A new Bayesian joint model for longitudinal count data with many zeros, intermittent missingness, and dropout with applications to HIV prevention trials. Statistics in Medicine, 2019, 38, 5565-5586.	0.8	3
28	Semiparametric Frailty Models for Zero-Inflated Event Count Data in the Presence of Informative Dropout. Biometrics, 2019, 75, 1168-1178.	0.8	2
29	Quantifying time-varying cause-specific hazard and subdistribution hazard ratios with competing risks data. Clinical Trials, 2019, 16, 363-374.	0.7	2
30	Improved Detection of Epigenomic Marks with Mixed-Effects Hidden Markov Models. Biometrics, 2019, 75, 1401-1413.	0.8	0
31	Efficient Methods for Signal Detection From Correlated Adverse Events in Clinical Trials. Biometrics, 2019, 75, 1000-1008.	0.8	3
32	A Powerful Global Test Statistic for Functional Statistical Inference. Proceedings of the AAAI Conference on Artificial Intelligence, 2019, 33, 5765-5772.	3.6	0
33	Bayesian multivariate skew meta-regression models for individual patient data. Statistical Methods in Medical Research, 2019, 28, 3415-3436.	0.7	3
34	Hard thresholding regression. Scandinavian Journal of Statistics, 2019, 46, 314-328.	0.9	6
35	Bayesian clinical trial design using historical data that inform the treatment effect. Biostatistics, 2019, 20, 400-415.	0.9	56
36	Bayesian inference for network meta-regression using multivariate random effects with applications to cholesterol lowering drugs. Biostatistics, 2019, 20, 499-516.	0.9	3

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37	MILFM: Multiple Index Latent Factor Model Based on High-Dimensional Features. Biometrics, 2018, 74, 834-844.	0.8	5
38	A Bayesian hierarchical model for network meta-analysis of multiple diagnostic tests. Biostatistics, 2018, 19, 87-102.	0.9	24
39	Biomarker threshold adaptive designs for survival endpoints. Journal of Biopharmaceutical Statistics, 2018, 28, 1038-1054.	0.4	8
40	Effect of grass sublingual tablet immunotherapy is similar in children and adults: A Bayesian approach to design pediatric sublingual immunotherapy trials. Journal of Allergy and Clinical Immunology, 2018, 141, 1744-1749.	1.5	10
41	FLCRM: Functional Linear Cox Regression Model. Biometrics, 2018, 74, 109-117.	0.8	42
42	Estimating Treatment Effects for Recurrent Events in the Presence of Rescue Medications: An Application to the Immune Thrombocytopenia Study. Statistics in Biosciences, 2018, 10, 473-489.	0.6	1
43	The effects of nonignorable missing data on label-free mass spectrometry proteomics experiments. Annals of Applied Statistics, 2018, 12, 2075-2095.	0.5	44
44	TPRM: Tensor partition regression models with applications in imaging biomarker detection. Annals of Applied Statistics, 2018, 12, 1422-1450.	0.5	12
45	A practical Bayesian adaptive design incorporating data from historical controls. Statistics in Medicine, 2018, 37, 4054-4070.	0.8	21
46	Bayesian design of a survival trial with a cured fraction using historical data. Statistics in Medicine, 2018, 37, 3814-3831.	0.8	8
47	Semiparametric regression analysis for composite endpoints subject to componentwise censoring. Biometrika, 2018, 105, 403-418.	1.3	5
48	Bayesian Modeling and Inference for Nonignorably Missing Longitudinal Binary Response Data with Applications to HIV Prevention Trials. Statistica Sinica, 2018, 28, 1929-1963.	0.2	3
49	Functional Linear Regression Model for Nonignorable Missing Scalar Responses. Statistica Sinica, 2018, 28, 1867-1886.	0.2	4
50	Bayesian Model Assessment in Joint Modeling of Longitudinal and Survival Data With Applications to Cancer Clinical Trials. Journal of Computational and Graphical Statistics, 2017, 26, 121-133.	0.9	28
51	Statistical design of noninferiority multiple region clinical trials to assess global and consistent treatment effects. Journal of Biopharmaceutical Statistics, 2017, 27, 933-944.	0.4	3
52	Bayesian longitudinal low-rank regression models for imaging genetic data from longitudinal studies. NeuroImage, 2017, 149, 305-322.	2.1	19
53	On inference of control-based imputation for analysis of repeated binary outcomes with missing data. Journal of Biopharmaceutical Statistics, 2017, 27, 358-372.	0.4	9
54	Pattern mixture models for clinical validation of biomarkers in the presence of missing data. Statistics in Medicine, 2017, 36, 2994-3004.	0.8	1

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55	Modeling event count data in the presence of informative dropout with application to bleeding and transfusion events in myelodysplastic syndrome. Statistics in Medicine, 2017, 36, 3475-3494.	0.8	3
56	Bayesian clinical trial design using Markov models with applications to autoimmune disease. Contemporary Clinical Trials, 2017, 63, 73-83.	0.8	1
57	Bayesian Sensitivity Analysis of a Nonlinear Dynamic Factor Analysis Model with Nonparametric Prior and Possible Nonignorable Missingness. Psychometrika, 2017, 82, 875-903.	1.2	9
58	Control€based imputation for sensitivity analyses in informative censoring for recurrent event data. Pharmaceutical Statistics, 2017, 16, 424-432.	0.7	11
59	Prediction of overall survival for patients with metastatic castration-resistant prostate cancer: development of a prognostic model through a crowdsourced challenge with open clinical trial data. Lancet Oncology, The, 2017, 18, 132-142.	5.1	124
60	LCN: a random graph mixture model for community detection in functional brain networks. Statistics and Its Interface, 2017, 10, 369-378.	0.2	5
61	Reply to Comments. Statistics in Medicine, 2016, 35, 1560-1560.	0.8	0
62	A statistical model to assess (allele-specific) associations between gene expression and epigenetic features using sequencing data. Annals of Applied Statistics, 2016, 10, 2254-2273.	0.5	2
63	Tamoxifen Dose Escalation in Patients With Diminished CYP2D6 Activity Normalizes Endoxifen Concentrations Without Increasing Toxicity. Oncologist, 2016, 21, 795-803.	1.9	42
64	SR-HARDI: Spatially Regularizing High Angular Resolution Diffusion Imaging. Journal of Computational and Graphical Statistics, 2016, 25, 1195-1211.	0.9	1
65	<tt>JMFit</tt>: A<i>SAS</i>Macro for Joint Models of Longitudinal and Survival Data. Journal of Statistical Software, 2016, 71, .	1.8	38
66	BFLCRM: A Bayesian functional linear Cox regression model for predicting time to conversion to Alzheimer€™s disease. Annals of Applied Statistics, 2015, 9, 2153-2178.	0.5	24
67	<i>In vivo</i> assessment of the metabolic activity of CYP2D6 diplotypes and alleles. British Journal of Clinical Pharmacology, 2015, 80, 1122-1130.	1.1	40
68	Hypothesis testing for two€stage designs with over or under enrollment. Statistics in Medicine, 2015, 34, 2417-2426.	0.8	5
69	The power prior: theory and applications. Statistics in Medicine, 2015, 34, 3724-3749.	0.8	178
70	Assessing temporal agreement between central and local progression€free survival times. Statistics in Medicine, 2015, 34, 844-858.	0.8	1
71	Responses to discussants of â€Joint modeling of survival and longitudinal non€survival data: current methods and issues. report of the DIA Bayesian joint modeling working groupâ€™. Statistics in Medicine, 2015, 34, 2202-2203.	0.8	6
72	The Use of Bayesian Hierarchical Models for Adaptive Randomization in Biomarker-Driven Phase II Studies. Journal of Biopharmaceutical Statistics, 2015, 25, 66-88.	0.4	9

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73	A CounterfactualP-Value Approach for Benefit-Risk Assessment in Clinical Trials. Journal of Biopharmaceutical Statistics, 2015, 25, 508-524.	0.4	1
74	SPReM: Sparse Projection Regression Model For High-Dimensional Linear Regression. Journal of the American Statistical Association, 2015, 110, 289-302.	1.8	10
75	Quantifying the average of the time-varying hazard ratio via a class of transformations. Lifetime Data Analysis, 2015, 21, 259-279.	0.4	6
76	Assessment of Fit in Longitudinal Data for Joint Models with Applications to Cancer Clinical Trials. ICSA Book Series in Statistics, 2015, , 347-365.	0.0	2
77	DNA Damage Checkpoint Responses in the S Phase of Synchronized Diploid Human Fibroblasts. Photochemistry and Photobiology, 2015, 91, 109-116.	1.3	9
78	Bayesian Inference for Multivariate Meta-Regression With a Partially Observed Within-Study Sample Covariance Matrix. Journal of the American Statistical Association, 2015, 110, 528-544.	1.8	9
79	Homology cluster differential expression analysis for interspecies mRNA-Seq experiments. Statistical Applications in Genetics and Molecular Biology, 2015, 14, 507-16.	0.2	1
80	Diagnostic measures for the Cox regression model with missing covariates. Biometrika, 2015, 102, 907-923.	1.3	9
81	Joint modeling of survival and longitudinal non–survival data: current methods and issues. Report of the DIA Bayesian joint modeling working group. Statistics in Medicine, 2015, 34, 2181-2195.	0.8	104
82	Bayesian probability of success for clinical trials using historical data. Statistics in Medicine, 2015, 34, 249-264.	0.8	18
83	Sample Size Determination in Shared Frailty Models for Multivariate Time-to-Event Data. Journal of Biopharmaceutical Statistics, 2014, 24, 908-923.	0.4	7
84	Flexible Stopping Boundaries When Changing Primary Endpoints After Unblinded Interim Analyses. Journal of Biopharmaceutical Statistics, 2014, 24, 817-833.	0.4	11
85	Use of historical control data for assessing treatment effects in clinical trials. Pharmaceutical Statistics, 2014, 13, 41-54.	0.7	340
86	Joint modeling of longitudinal and survival data with missing and left–censored time–varying covariates. Statistics in Medicine, 2014, 33, 4560-4576.	0.8	26
87	Effect of Cytotoxic Chemotherapy on Markers of Molecular Age in Patients With Breast Cancer. Journal of the National Cancer Institute, 2014, 106, dju057.	3.0	218
88	Development of DNA Damage Response Signaling Biomarkers using Automated, Quantitative Image Analysis. Journal of Histochemistry and Cytochemistry, 2014, 62, 185-196.	1.3	14
89	Bayesian design of superiority clinical trials for recurrent events data with applications to bleeding and transfusion events in myelodyplastic syndrome. Biometrics, 2014, 70, 1003-1013.	0.8	16
90	Bayesian gamma frailty models for survival data with semi-competing risks and treatment switching. Lifetime Data Analysis, 2014, 20, 76-105.	0.4	16

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91	Mechanisms of chromosomal instability in melanoma. Environmental and Molecular Mutagenesis, 2014, 55, 457-471.	0.9	16
92	Assessing model fit in joint models of longitudinal and survival data with applications to cancer clinical trials. Statistics in Medicine, 2014, 33, 4715-4733.	0.8	32
93	Bayesian Generalized Low Rank Regression Models for Neuroimaging Phenotypes and Genetic Markers. Journal of the American Statistical Association, 2014, 109, 977-990.	1.8	59
94	Bayesian Transformation Models for Multivariate Survival Data. Scandinavian Journal of Statistics, 2014, 41, 187-199.	0.9	2
95	Bayesian sequential meta‑analysis design in evaluating cardiovascular risk in a new antidiabetic drug development program. Statistics in Medicine, 2014, 33, 1600-1618.	0.8	13
96	A Community‑Based Multicenter Trial of Pharmacokinetically Guided 5‑Fluorouracil Dosing for Personalized Colorectal Cancer Therapy. Oncologist, 2014, 19, 959-965.	1.9	36
97	Multivariate Recurrent Events in the Presence of Multivariate Informative Censoring with Applications to Bleeding and Transfusion Events in Myelodysplastic Syndrome. Journal of Biopharmaceutical Statistics, 2014, 24, 429-442.	0.4	9
98	Cyclobutane Pyrimidine Dimer Density as a Predictive Biomarker of the Biological Effects of Ultraviolet Radiation in Normal Human Fibroblast. Photochemistry and Photobiology, 2014, 90, 145-154.	1.3	10
99	Post-diagnosis physical activity and survival after breast cancer diagnosis: the Long Island Breast Cancer Study. Breast Cancer Research and Treatment, 2014, 145, 735-742.	1.1	55
100	Some Statistical Strategies for DAE-seq Data Analysis: Variable Selection and Modeling Dependencies Among Observations. Journal of the American Statistical Association, 2014, 109, 78-94.	1.8	6
101	Functional-Mixed Effects Models for Candidate Genetic Mapping in Imaging Genetic Studies. Genetic Epidemiology, 2014, 38, 680-691.	0.6	6
102	Bayesian case-deletion model complexity and information criterion. Statistics and Its Interface, 2014, 7, 531-542.	0.2	3
103	Bayesian sensitivity analysis of statistical models with missing data. Statistica Sinica, 2014, 24, 871-896.	0.2	8
104	Change‑point models to estimate the limit of detection. Statistics in Medicine, 2013, 32, 4995-5007.	0.8	5
105	Pathologic and gene expression features of metastatic melanomas to the brain. Cancer, 2013, 119, 2737-2746.	2.0	42
106	Estimating time-varying effects for overdispersed recurrent events data with treatment switching. Biometrika, 2013, 100, 339-354.	1.3	9
107	Separation of intra-S checkpoint protein contributions to DNA replication fork protection and genomic stability in normal human fibroblasts. Cell Cycle, 2013, 12, 332-345.	1.3	19
108	Bayesian inference for multivariate meta‑analysis Box‑Cox transformation models for individual patient data with applications to evaluation of cholesterol‑lowering drugs. Statistics in Medicine, 2013, 32, 3972-3990.	0.8	10

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109	Bayesian modeling and inference for clinical trials with partial retrieved data following dropout. Statistics in Medicine, 2013, 32, 4180-4195.	0.8	3
110	Bayesian Spatial Transformation Models with Applications in Neuroimaging Data. Biometrics, 2013, 69, 1074-1083.	0.8	6
111	A prognostic signature of Gâ‚‚ checkpoint function in melanoma cell lines. Cell Cycle, 2013, 12, 1071-1082.	1.3	13
112	Is activation of the intra-S checkpoint in human fibroblasts an important factor in protection against UV-induced mutagenesis?. Cell Cycle, 2013, 12, 3555-3563.	1.3	3
113	Mapping the Genetic Variation of Regional Brain Volumes as Explained by All Common SNPs from the ADNI Study. PLoS ONE, 2013, 8, e71723.	1.1	23
114	The Bayesian covariance lasso. Statistics and Its Interface, 2013, 6, 243-259.	0.2	29
115	A note on the relationships between multiple imputation, maximum likelihood and fully Bayesian methods for missing responses in linear regression models. Statistics and Its Interface, 2013, 6, 315-324.	0.2	10
116	Bayesian Case Influence Measures for Statistical Models With Missing Data. Journal of Computational and Graphical Statistics, 2012, 21, 253-271.	0.9	9
117	Perturbation and scaled Cookâ€™s distance. Annals of Statistics, 2012, 40, 785-811.	1.4	23
118	Assessing Similarity to Existing Drugs to Decide Whether to Continue Drug Development. Statistics in Biopharmaceutical Research, 2012, 4, 293-300.	0.6	1
119	Estimating treatment effects with treatment switching via semicompeting risks models: an application to a colorectal cancer study. Biometrika, 2012, 99, 167-184.	1.3	25
120	Missing Data in Clinical Studies: Issues and Methods. Journal of Clinical Oncology, 2012, 30, 3297-3303.	0.8	145
121	Intrinsic Regression Models for Medial Representation of Subcortical Structures. Journal of the American Statistical Association, 2012, 107, 12-23.	1.8	5
122	Bayesian methods in clinical trials: a Bayesian analysis of ECOG trials E1684 and E1690. BMC Medical Research Methodology, 2012, 12, 183.	1.4	13
123	Metaâ€analysis methods and models with applications in evaluation of cholesterolâ€lowering drugs. Statistics in Medicine, 2012, 31, 3597-3616.	0.8	3
124	Projection Regression Models for Multivariate Imaging Phenotype. Genetic Epidemiology, 2012, 36, 631-641.	0.6	15
125	Bayesian Metaâ€Experimental Design: Evaluating Cardiovascular Risk in New Antidiabetic Therapies to Treat Type 2 Diabetes. Biometrics, 2012, 68, 578-586.	0.8	33
126	Bayesian Influence Measures for Joint Models for Longitudinal and Survival Data. Biometrics, 2012, 68, 954-964.	0.8	25

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127	Bayesian Lasso for Semiparametric Structural Equation Models. Biometrics, 2012, 68, 567-577.	0.8	38
128	Genotype-Guided Tamoxifen Dosing Increases Active Metabolite Exposure in Women With Reduced CYP2D6 Metabolism: A Multicenter Study. Journal of Clinical Oncology, 2011, 29, 3232-3239.	0.8	173
129	Timeless functions independently of the Tim-Tipin complex to promote sister chromatid cohesion in normal human fibroblasts. Cell Cycle, 2011, 10, 1618-1624.	1.3	41
130	Two-stage empirical likelihood for longitudinal neuroimaging data. Annals of Applied Statistics, 2011, 5, 1132-1158.	0.5	7
131	A generalized linear mixed model for longitudinal binary data with a marginal logit link function. Annals of Applied Statistics, 2011, 5, 449-467.	0.5	37
132	Fixed and Random Effects Selection in Mixed Effects Models. Biometrics, 2011, 67, 495-503.	0.8	103
133	A Bivariate Pseudolikelihood for Incomplete Longitudinal Binary Data with Nonignorable Nonmonotone Missingness. Biometrics, 2011, 67, 1119-1126.	0.8	4
134	Bayesian Design of Noninferiority Trials for Medical Devices Using Historical Data. Biometrics, 2011, 67, 1163-1170.	0.8	60
135	Bayesian local influence for survival models. Lifetime Data Analysis, 2011, 17, 43-70.	0.4	12
136	Rejoinder: Bayesian local influence for survival models. Lifetime Data Analysis, 2011, 17, 76-79.	0.4	0
137	Sample size and power determination in joint modeling of longitudinal and survival data. Statistics in Medicine, 2011, 30, 2295-2309.	0.8	48
138	Maximum likelihood estimation in generalized linear models with multiple covariates subject to detection limits. Statistics in Medicine, 2011, 30, 2551-2561.	0.8	32
139	Bayesian influence analysis: a geometric approach. Biometrika, 2011, 98, 307-323.	1.3	38
140	trans-Fatty acid consumption and its association with distal colorectal cancer in the North Carolina Colon Cancer Study II. Cancer Causes and Control, 2010, 21, 171-180.	0.8	34
141	On the estimation of disease prevalence by latent class models for screening studies using two screening tests with categorical disease status verified in test positives only. Statistics in Medicine, 2010, 29, 1206-1218.	0.8	11
142	A weighted combination of pseudo‐likelihood estimators for longitudinal binary data subject to non‐ignorable non‐monotone missingness. Statistics in Medicine, 2010, 29, 1511-1521.	0.8	5
143	A Bayesian proportional hazards regression model with non-ignorably missing time-varying covariates. Statistics in Medicine, 2010, 29, 3017-3029.	0.8	10
144	Variable Selection in the Cox Regression Model with Covariates Missing at Random. Biometrics, 2010, 66, 97-104.	0.8	23

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145	Basic Concepts and Methods for Joint Models of Longitudinal and Survival Data. Journal of Clinical Oncology, 2010, 28, 2796-2801.	0.8	298
146	Genomewide Multiple-Loci Mapping in Experimental Crosses by Iterative Adaptive Penalized Regression. Genetics, 2010, 185, 349-359.	1.2	67
147	Abasic sites preferentially form at regions undergoing DNA replication. FASEB Journal, 2010, 24, 3674-3680.	0.2	41
148	In Vitro Hepatic Metabolism Explains Higher Clearance of Voriconazole in Children versus Adults: Role of CYP2C19 and Flavin-Containing Monooxygenase 3. Drug Metabolism and Disposition, 2010, 38, 25-31.	1.7	115
149	A Semiparametric Bayesian Approach for Estimating the Gene Expression Distribution. Journal of Biopharmaceutical Statistics, 2010, 20, 267-280.	0.4	2
150	VARIABLE SELECTION FOR REGRESSION MODELS WITH MISSING DATA. Statistica Sinica, 2010, 20, 149-165.	0.2	32
151	INK4/ARF Transcript Expression Is Associated with Chromosome 9p21 Variants Linked to Atherosclerosis. PLoS ONE, 2009, 4, e5027.	1.1	217
152	Associations Between Trans Fatty Acid Consumption and Colon Cancer Among Whites and African Americans in the North Carolina Colon Cancer Study I. Nutrition and Cancer, 2009, 61, 427-436.	0.9	15
153	Estimation and inference for case-control studies with multiple non-gold standard exposure assessments: with an occupational health application. Biostatistics, 2009, 10, 591-602.	0.9	13
154	Gamma frailty transformation models for multivariate survival times. Biometrika, 2009, 96, 277-291.	1.3	33
155	Comment: Incomplete Data in Clinical Studies: Analysis, Sensitivity, and Sensitivity Analysis. Drug Information Journal, 2009, 43, 431-432.	0.5	2
156	InÂSilico Construction of a Protein Interaction Landscape for Nucleotide Excision Repair. Cell Biochemistry and Biophysics, 2009, 53, 101-114.	0.9	2
157	Missing data methods in longitudinal studies: a review. Test, 2009, 18, 1-43.	0.7	340
158	Rejoinder on: Missing data methods in longitudinal studies: a review. Test, 2009, 18, 68-75.	0.7	10
159	Bayesian Case Influence Diagnostics for Survival Models. Biometrics, 2009, 65, 116-124.	0.8	44
160	Local Influence for Generalized Linear Models with Missing Covariates. Biometrics, 2009, 65, 1164-1174.	0.8	21
161	A Bayesian Hidden Markov Model for Motif Discovery Through Joint Modeling of Genomic Sequence and ChIPâ€Chip Data. Biometrics, 2009, 65, 1087-1095.	0.8	10
162	Diagnostic Measures for Generalized Linear Models with Missing Covariates. Scandinavian Journal of Statistics, 2009, 36, 686-712.	0.9	14

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163	Expression of *p16*^{*INK4a*} in peripheral blood T‑cells is a biomarker of human aging. Aging Cell, 2009, 8, 439-448.	3.0	381
164	Maximum likelihood inference for the Cox regression model with applications to missing covariates. Journal of Multivariate Analysis, 2009, 100, 2018-2030.	0.5	25
165	Regression Models for Identifying Noise Sources in Magnetic Resonance Images. Journal of the American Statistical Association, 2009, 104, 623-637.	1.8	43
166	Intrinsic Regression Models for Positive-Definite Matrices With Applications to Diffusion Tensor Imaging. Journal of the American Statistical Association, 2009, 104, 1203-1212.	1.8	44
167	An Information Matrix Prior for Bayesian Analysis in Generalized Linear Models with High Dimensional Data. Statistica Sinica, 2009, 19, 1641-1663.	0.2	13
168	Bayesian variable selection for the Cox regression model with missing covariates. Lifetime Data Analysis, 2008, 14, 496-520.	0.4	15
169	A new class of mixture models for differential gene expression in DNA microarray data. Journal of Statistical Planning and Inference, 2008, 138, 387-404.	0.4	5
170	Theory and inference for regression models with missing responses and covariates. Journal of Multivariate Analysis, 2008, 99, 1302-1331.	0.5	34
171	Defective Cell Cycle Checkpoint Functions in Melanoma Are Associated with Altered Patterns of Gene Expression. Journal of Investigative Dermatology, 2008, 128, 175-187.	0.3	55
172	Model Selection Criteria for Missing-Data Problems Using the EM Algorithm. Journal of the American Statistical Association, 2008, 103, 1648-1658.	1.8	93
173	A Note on the Validity of Statistical Bootstrapping for Estimating the Uncertainty of Tensor Parameters in Diffusion Tensor Images. IEEE Transactions on Medical Imaging, 2008, 27, 1506-1514.	5.4	10
174	Consumption of trans-Fatty Acid and Its Association with Colorectal Adenomas. American Journal of Epidemiology, 2008, 168, 289-297.	1.6	36
175	Current Methods for Recurrent Events Data With Dependent Termination. Journal of the American Statistical Association, 2008, 103, 866-878.	1.8	26
176	Properties and Implementation of Jeffreys's Prior in Binomial Regression Models. Journal of the American Statistical Association, 2008, 103, 1659-1664.	1.8	35
177	*n*‑3 Fatty acids, hypertension and risk of cognitive decline among older adults in the Atherosclerosis Risk in Communities (ARIC) study. Public Health Nutrition, 2008, 11, 17-29.	1.1	50
178	Bayesian variable selection and computation for generalized linear models with conjugate priors. Bayesian Analysis, 2008, 3, 585-614.	1.6	33
179	Statistical Analysis of Diffusion Tensors in Diffusion-Weighted Magnetic Resonance Imaging Data. Journal of the American Statistical Association, 2007, 102, 1085-1102.	1.8	60
180	Structured Measurement Error in Nutritional Epidemiology. Journal of the American Statistical Association, 2007, 102, 856-866.	1.8	45

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181	A Statistical Analysis of Brain Morphology Using Wild Bootstrapping. IEEE Transactions on Medical Imaging, 2007, 26, 954-966.	5.4	39
182	Variable Selection in Regression Mixture Modeling for the Discovery of Gene Regulatory Networks. Journal of the American Statistical Association, 2007, 102, 867-880.	1.8	36
183	Sieve Maximum Likelihood Estimation for Regression Models With Covariates Missing at Random. Journal of the American Statistical Association, 2007, 102, 1309-1317.	1.8	8
184	Perturbation selection and influence measures in local influence analysis. Annals of Statistics, 2007, 35, .	1.4	79
185	Bayesian Hierarchical Modeling for Time Course Microarray Experiments. Biometrics, 2007, 63, 496-504.	0.8	5
186	A Note on Permutation Tests for Variance Components in Multilevel Generalized Linear Mixed Models. Biometrics, 2007, 63, 942-946.	0.8	48
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