

Sylvia T Richardson

List of Publications by Year in descending order

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Version: 2024-02-01

211
papers

16,544
citations

26567

56
h-index

18075

120
g-index

226
all docs

226
docs citations

226
times ranked

20373
citing authors

#	ARTICLE	IF	CITATIONS
1	Effect of frailty on 6-month outcome after traumatic brain injury: a multicentre cohort study with external validation. <i>Lancet Neurology</i> , The, 2022, 21, 153-162.	4.9	34
2	Time varying association between deprivation, ethnicity and SARS-CoV-2 infections in England: A population-based ecological study. <i>Lancet Regional Health - Europe</i> , The, 2022, 15, 100322.	3.0	14
3	Improving local prevalence estimates of SARS-CoV-2 infections using a causal debiasing framework. <i>Nature Microbiology</i> , 2022, 7, 97-107.	5.9	27
4	A genome-wide association study of outcome from traumatic brain injury. <i>EBioMedicine</i> , 2022, 77, 103933.	2.7	17
5	Interoperability of Statistical Models in Pandemic Preparedness: Principles and Reality. <i>Statistical Science</i> , 2022, 37, .	1.6	4
6	Imputation of Ordinal Outcomes: A Comparison of Approaches in Traumatic Brain Injury. <i>Journal of Neurotrauma</i> , 2021, 38, 455-463.	1.7	21
7	Drug sensitivity prediction with normal inverse Gaussian shrinkage informed by external data. <i>Biometrical Journal</i> , 2021, 63, 289-304.	0.6	3
8	A Computationally Efficient Bayesian Seemingly Unrelated Regressions Model for High-Dimensional Quantitative Trait Loci Discovery. <i>Journal of the Royal Statistical Society Series C: Applied Statistics</i> , 2021, 70, 886-908.	0.5	6
9	The RNA landscape of the human placenta in health and disease. <i>Nature Communications</i> , 2021, 12, 2639.	5.8	75
10	EPISPOT: An epigenome-driven approach for detecting and interpreting hotspots in molecular QTL studies. <i>American Journal of Human Genetics</i> , 2021, 108, 983-1000.	2.6	6
11	Fluid balance and outcome in critically ill patients with traumatic brain injury (CENTER-TBI and) Tj ETQq1 1 0.784314 rgBT /Overlock 10 20, 627-638.	4.9	40
12	Pathological Computed Tomography Features Associated With Adverse Outcomes After Mild Traumatic Brain Injury. <i>JAMA Neurology</i> , 2021, 78, 1137.	4.5	53
13	Protocol for the development of the Wales Multimorbidity e-Cohort (WMC): data sources and methods to construct a population-based research platform to investigate multimorbidity. <i>BMJ Open</i> , 2021, 11, e047101.	0.8	12
14	An informatics consult approach for generating clinical evidence for treatment decisions. <i>BMC Medical Informatics and Decision Making</i> , 2021, 21, 281.	1.5	8
15	Questionnaires vs Interviews for the Assessment of Global Functional Outcomes After Traumatic Brain Injury. <i>JAMA Network Open</i> , 2021, 4, e2134121.	2.8	5
16	Tracheal intubation in traumatic brain injury: a multicentre prospective observational study. <i>British Journal of Anaesthesia</i> , 2020, 125, 505-517.	1.5	19
17	Whole-genome sequencing of patients with rare diseases in a national health system. <i>Nature</i> , 2020, 583, 96-102.	13.7	338
18	Machine learning algorithms performed no better than regression models for prognostication in traumatic brain injury. <i>Journal of Clinical Epidemiology</i> , 2020, 122, 95-107.	2.4	117

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19	A flexible hierarchical framework for improving inference in area-referenced environmental health studies. <i>Biometrical Journal</i> , 2020, 62, 1650-1669.	0.6	2
20	Informed consent procedures in patients with an acute inability to provide informed consent: Policy and practice in the CENTER-TBI study. <i>Journal of Critical Care</i> , 2020, 59, 6-15.	1.0	8
21	A global-local approach for detecting hotspots in multiple-response regression. <i>Annals of Applied Statistics</i> , 2020, 14, 905-928.	0.5	8
22	Fast Bayesian Inference in Large Gaussian Graphical Models. <i>Biometrics</i> , 2019, 75, 1288-1298.	0.8	8
23	Case-mix, care pathways, and outcomes in patients with traumatic brain injury in CENTER-TBI: a European prospective, multicentre, longitudinal, cohort study. <i>Lancet Neurology</i> , The, 2019, 18, 923-934.	4.9	304
24	Discussion of "Gene hunting with hidden Markov model knockoffs". <i>Biometrika</i> , 2019, 106, 19-22.	1.3	3
25	Using ecological propensity score to adjust for missing confounders in small area studies. <i>Biostatistics</i> , 2019, 20, 1-16.	0.9	8
26	Age at menarche and the risk of operative delivery. <i>Journal of Maternal-Fetal and Neonatal Medicine</i> , 2019, 32, 411-418.	0.7	4
27	A two-step method for variable selection in the analysis of a case-cohort study. <i>International Journal of Epidemiology</i> , 2018, 47, 597-604.	0.9	6
28	Replicable and Coupled Changes in Innate and Adaptive Immune Gene Expression in Two Case-Control Studies of Blood Microarrays in Major Depressive Disorder. <i>Biological Psychiatry</i> , 2018, 83, 70-80.	0.7	158
29	Correcting the Mean-Variance Dependency for Differential Variability Testing Using Single-Cell RNA Sequencing Data. <i>Cell Systems</i> , 2018, 7, 284-294.e12.	2.9	71
30	De Novo Truncating Mutations in <i>WASF1</i> Cause Intellectual Disability with Seizures. <i>American Journal of Human Genetics</i> , 2018, 103, 144-153.	2.6	36
31	Comprehensive Cancer-Predisposition Gene Testing in an Adult Multiple Primary Tumor Series Shows a Broad Range of Deleterious Variants and Atypical Tumor Phenotypes. <i>American Journal of Human Genetics</i> , 2018, 103, 3-18.	2.6	46
32	Weibull regression with Bayesian variable selection to identify prognostic tumour markers of breast cancer survival. <i>Statistical Methods in Medical Research</i> , 2017, 26, 414-436.	0.7	20
33	ontologyX: a suite of R packages for working with ontological data. <i>Bioinformatics</i> , 2017, 33, 1104-1106.	1.8	86
34	Biallelic Mutation of <i>ARHGEF18</i> , Involved in the Determination of Epithelial Apicobasal Polarity, Causes Adult-Onset Retinal Degeneration. <i>American Journal of Human Genetics</i> , 2017, 100, 334-342.	2.6	26
35	Comprehensive Rare Variant Analysis via Whole-Genome Sequencing to Determine the Molecular Pathology of Inherited Retinal Disease. <i>American Journal of Human Genetics</i> , 2017, 100, 75-90.	2.6	343
36	Phenotypic Characterization of <i>EIF2AK4</i> Mutation Carriers in a Large Cohort of Patients Diagnosed Clinically With Pulmonary Arterial Hypertension. <i>Circulation</i> , 2017, 136, 2022-2033.	1.6	111

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37	Principles of Experimental Design for Big Data Analysis. <i>Statistical Science</i> , 2017, 32, 385-404.	1.6	24
38	Platelet function is modified by common sequence variation in megakaryocyte super enhancers. <i>Nature Communications</i> , 2017, 8, 16058.	5.8	50
39	A Fast Association Test for Identifying Pathogenic Variants Involved in Rare Diseases. <i>American Journal of Human Genetics</i> , 2017, 101, 104-114.	2.6	31
40	R2GUESS : A Graphics Processing Unit-Based <i>R</i> Package for Bayesian Variable Selection Regression of Multivariate Responses. <i>Journal of Statistical Software</i> , 2016, 69, .	1.8	21
41	A dominant gain-of-function mutation in universal tyrosine kinase <i>SRC</i> causes thrombocytopenia, myelofibrosis, bleeding, and bone pathologies. <i>Science Translational Medicine</i> , 2016, 8, 328ra30.	5.8	87
42	Age-related changes in murine myometrial transcript profile are mediated by exposure to the female sex hormones. <i>Aging Cell</i> , 2016, 15, 177-180.	3.0	6
43	JAM: A Scalable Bayesian Framework for Joint Analysis of Marginal SNP Effects. <i>Genetic Epidemiology</i> , 2016, 40, 188-201.	0.6	74
44	A gain-of-function variant in <i>DIAPH1</i> causes dominant macrothrombocytopenia and hearing loss. <i>Blood</i> , 2016, 127, 2903-2914.	0.6	121
45	Multidimensional analysis of the effect of occupational exposure to organic solvents on lung cancer risk: the ICARE study. <i>Occupational and Environmental Medicine</i> , 2016, 73, 368-377.	1.3	21
46	Beyond comparisons of means: understanding changes in gene expression at the single-cell level. <i>Genome Biology</i> , 2016, 17, 70.	3.8	90
47	Statistical Methods in Integrative Genomics. <i>Annual Review of Statistics and Its Application</i> , 2016, 3, 181-209.	4.1	75
48	Exploring dependence between categorical variables: Benefits and limitations of using variable selection within Bayesian clustering in relation to log-linear modelling with interaction terms. <i>Journal of Statistical Planning and Inference</i> , 2016, 173, 47-63.	0.4	4
49	Phenotype Similarity Regression for Identifying the Genetic Determinants of Rare Diseases. <i>American Journal of Human Genetics</i> , 2016, 98, 490-499.	2.6	49
50	MT-HESS: an efficient Bayesian approach for simultaneous association detection in OMICS datasets, with application to eQTL mapping in multiple tissues. <i>Bioinformatics</i> , 2016, 32, 523-532.	1.8	25
51	Insight into Genotype-Phenotype Associations through eQTL Mapping in Multiple Cell Types in Health and Immune-Mediated Disease. <i>PLoS Genetics</i> , 2016, 12, e1005908.	1.5	80
52	Bayesian regression discontinuity designs: incorporating clinical knowledge in the causal analysis of primary care data. <i>Statistics in Medicine</i> , 2015, 34, 2334-2352.	0.8	28
53	Dissection of a Complex Disease Susceptibility Region Using a Bayesian Stochastic Search Approach to Fine Mapping. <i>PLoS Genetics</i> , 2015, 11, e1005272.	1.5	55
54	BASiCS: Bayesian Analysis of Single-Cell Sequencing Data. <i>PLoS Computational Biology</i> , 2015, 11, e1004333.	1.5	264

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55	Human phenotype ontology annotation and cluster analysis to unravel genetic defects in 707 cases with unexplained bleeding and platelet disorders. <i>Genome Medicine</i> , 2015, 7, 36.	3.6	119
56	Bayesian Non-Parametric Models for Spatially Indexed Data of Mixed Type. <i>Journal of the Royal Statistical Society Series B: Statistical Methodology</i> , 2015, 77, 973-999.	1.1	14
57	Sampling from Dirichlet process mixture models with unknown concentration parameter: mixing issues in large data implementations. <i>Statistics and Computing</i> , 2015, 25, 1023-1037.	0.8	37
58	PRemiuM : An R Package for Profile Regression Mixture Models Using Dirichlet Processes. <i>Journal of Statistical Software</i> , 2015, 64, 1-30.	1.8	76
59	Identifying Cell Types from Spatially Referenced Single-Cell Expression Datasets. <i>PLoS Computational Biology</i> , 2014, 10, e1003824.	1.5	26
60	Dynamics of the Risk of Smoking-Induced Lung Cancer. <i>Epidemiology</i> , 2014, 25, 28-34.	1.2	9
61	Blood Pressure Differences Associated With Optimal Macronutrient Intake Trial for Heart Health (OMNIHEART)â€œLike Diet Compared With a Typical American Diet. <i>Hypertension</i> , 2014, 64, 1198-1204.	1.3	21
62	Breast cancer risk, nightwork, and circadian clock gene polymorphisms. <i>Endocrine-Related Cancer</i> , 2014, 21, 629-638.	1.6	71
63	Transcriptional diversity during lineage commitment of human blood progenitors. <i>Science</i> , 2014, 345, 1251033.	6.0	253
64	Spaceâ€œtime variability in burglary risk: A Bayesian spatio-temporal modelling approach. <i>Spatial Statistics</i> , 2014, 9, 180-191.	0.9	94
65	Online appendix for: Evaluating the No Cold Calling zones in Peterborough, England: application of a novel statistical method for evaluating neighbourhood policing policies. <i>Environment and Planning A</i> , 2014, .	2.1	1
66	Balancing the Robustness and Predictive Performance of Biomarkers. <i>Journal of Computational Biology</i> , 2013, 20, 979-989.	0.8	13
67	A semi-parametric approach to estimate risk functions associated with multi-dimensional exposure profiles: application to smoking and lung cancer. <i>BMC Medical Research Methodology</i> , 2013, 13, 129.	1.4	24
68	Evaluating the No Cold Calling Zones in Peterborough, England: Application of a Novel Statistical Method for Evaluating Neighbourhood Policing Policies. <i>Environment and Planning A</i> , 2013, 45, 2012-2026.	2.1	16
69	Aircraft noise and cardiovascular disease near Heathrow airport in London: small area study. <i>BMJ</i> , 2013, 347, f5432-f5432.	3.0	188
70	GUESS-ing Polygenic Associations with Multiple Phenotypes Using a GPU-Based Evolutionary Stochastic Search Algorithm. <i>PLoS Genetics</i> , 2013, 9, e1003657.	1.5	58
71	Uncovering selection bias in caseâ€œcontrol studies using Bayesian postâ€œstratification. <i>Statistics in Medicine</i> , 2013, 32, 2555-2570.	0.8	10
72	BaySTDetect: detecting unusual temporal patterns in small area data via Bayesian model choice. <i>Biostatistics</i> , 2012, 13, 695-710.	0.9	32

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73	Association of Environmental Insecticide Exposure and Fetal Growth With a Bayesian Model Including Multiple Exposure Sources: The PELAGIE Mother-Child Cohort. <i>American Journal of Epidemiology</i> , 2012, 175, 1182-1190.	1.6	29
74	Two-pronged Strategy for Using DIC to Compare Selection Models with Non-Ignorable Missing Responses. <i>Bayesian Analysis</i> , 2012, 7, .	1.6	15
75	Adjustment for Missing Confounders Using External Validation Data and Propensity Scores. <i>Journal of the American Statistical Association</i> , 2012, 107, 40-51.	1.8	30
76	A Bayesian Model of NMR Spectra for the Deconvolution and Quantification of Metabolites in Complex Biological Mixtures. <i>Journal of the American Statistical Association</i> , 2012, 107, 1259-1271.	1.8	41
77	Classification loss function for parameter ensembles in Bayesian hierarchical models. <i>Statistics and Probability Letters</i> , 2012, 82, 859-863.	0.4	1
78	Association of Sirtuin 1 (<i>SIRT1</i>) Gene SNPs and Transcript Expression Levels With Severe Obesity. <i>Obesity</i> , 2012, 20, 178-185.	1.5	68
79	Menarche, menopause, and breast cancer risk: individual participant meta-analysis, including 118,964 women with breast cancer from 117 epidemiological studies. <i>Lancet Oncology</i> , The, 2012, 13, 1141-1151.	5.1	753
80	Hierarchical priors for bias parameters in Bayesian sensitivity analysis for unmeasured confounding. <i>Statistics in Medicine</i> , 2012, 31, 383-396.	0.8	19
81	Exploring Data From Genetic Association Studies Using Bayesian Variable Selection and the Dirichlet Process: Application to Searching for Gene – Gene Patterns. <i>Genetic Epidemiology</i> , 2012, 36, 663-674.	0.6	32
82	Bayesian shared spatial component models to combine and borrow strength across sparse disease surveillance sources. <i>Biometrical Journal</i> , 2012, 54, 385-404.	0.6	20
83	Differential coexpression analysis of obesity-associated networks in human subcutaneous adipose tissue. <i>International Journal of Obesity</i> , 2012, 36, 137-147.	1.6	42
84	Identifying Vulnerable Populations through an Examination of the Association Between Multipollutant Profiles and Poverty. <i>Environmental Science & Technology</i> , 2011, 45, 7754-7760.	4.6	44
85	Data Mining Cancer Registries: Retrospective Surveillance of Small Area Time Trends in Cancer Incidence Using BaySTDetect. , 2011, , .		1
86	Haplotype and isoform specific expression estimation using multi-mapping RNA-seq reads. <i>Genome Biology</i> , 2011, 12, R13.	13.9	224
87	Application of the Lasso to Expression Quantitative Trait Loci Mapping. <i>Statistical Applications in Genetics and Molecular Biology</i> , 2011, 10, .	0.2	1
88	A Bayesian hierarchical analysis to compare classical and atypical scrapie surveillance data; Wales 2002–2006. <i>Preventive Veterinary Medicine</i> , 2011, 98, 29-38.	0.7	2
89	A Bayesian model of time activity data to investigate health effect of air pollution in time series studies. <i>Atmospheric Environment</i> , 2011, 45, 379-386.	1.9	25
90	Spatio-temporal patterns of bladder cancer incidence in Utah (1973-2004) and their association with the presence of toxic release inventory sites. <i>International Journal of Health Geographics</i> , 2011, 10, 16.	1.2	14

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91	Plasma proteome analysis in HTLV-1-associated myelopathy/tropical spastic paraparesis. <i>Retrovirology</i> , 2011, 8, 81.	0.9	17
92	A Bayesian analysis of the impact of air pollution episodes on cardio-respiratory hospital admissions in the Greater London area. <i>Statistical Methods in Medical Research</i> , 2011, 20, 69-80.	0.7	5
93	False Discovery Rate Estimation for Stability Selection: Application to Genome-Wide Association Studies. <i>Statistical Applications in Genetics and Molecular Biology</i> , 2011, 10, .	0.2	8
94	Bayesian Detection of Expression Quantitative Trait Loci Hot Spots. <i>Genetics</i> , 2011, 189, 1449-1459.	1.2	70
95	Examining the Joint Effect of Multiple Risk Factors Using Exposure Risk Profiles: Lung Cancer in Nonsmokers. <i>Environmental Health Perspectives</i> , 2011, 119, 84-91.	2.8	45
96	<i>ESS</i>: a C++ objected-oriented algorithm for Bayesian stochastic search model exploration. <i>Bioinformatics</i> , 2011, 27, 587-588.	1.8	29
97	Bayesian Models for Sparse Regression Analysis of High Dimensional Data*. , 2011, , 539-568.		20
98	Evolutionary stochastic search for Bayesian model exploration. <i>Bayesian Analysis</i> , 2010, 5, .	1.6	124
99	Inference from ecological models: Estimating the relative risk of stroke from air pollution exposure using small area data. <i>Spatial and Spatio-temporal Epidemiology</i> , 2010, 1, 123-131.	0.9	17
100	sdef: an R package to synthesize lists of significant features in related experiments. <i>BMC Bioinformatics</i> , 2010, 11, 270.	1.2	10
101	Simplified Bayesian Sensitivity Analysis for Mismeasured and Unobserved Confounders. <i>Biometrics</i> , 2010, 66, 1129-1137.	0.8	24
102	MMBGX: a method for estimating expression at the isoform level and detecting differential splicing using whole-transcript Affymetrix arrays. <i>Nucleic Acids Research</i> , 2010, 38, 1413-1413.	6.5	0
103	MMBGX: a method for estimating expression at the isoform level and detecting differential splicing using whole-transcript Affymetrix arrays. <i>Nucleic Acids Research</i> , 2010, 38, e4-e4.	6.5	22
104	Reply to Robert et al.: Model criticism informs model choice and model comparison. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, .	3.3	9
105	New Insights into the Genetic Control of Gene Expression using a Bayesian Multi-tissue Approach. <i>PLoS Computational Biology</i> , 2010, 6, e1000737.	1.5	55
106	Bayesian profile regression with an application to the National survey of children's health. <i>Biostatistics</i> , 2010, 11, 484-498.	0.9	118
107	WV0X tumour suppressor gene polymorphisms and ovarian cancer pathology and prognosis. <i>European Journal of Cancer</i> , 2010, 46, 818-825.	1.3	28
108	Model criticism based on likelihood-free inference, with an application to protein network evolution. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 10576-10581.	3.3	106

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109	Bayesian graphical models for regression on multiple data sets with different variables. <i>Biostatistics</i> , 2009, 10, 335-351.	0.9	40
110	Risk of cancer in the vicinity of municipal solid waste incinerators: importance of using a flexible modelling strategy. <i>International Journal of Health Geographics</i> , 2009, 8, 31.	1.2	18
111	Finding exclusively deleted or amplified genomic areas in lung adenocarcinomas using a novel chromosomal pattern analysis. <i>BMC Medical Genomics</i> , 2009, 2, 43.	0.7	6
112	Using Bayesian graphical models to model biases in observational studies and to combine multiple sources of data: application to low birth weight and water disinfection by-products. <i>Journal of the Royal Statistical Society Series A: Statistics in Society</i> , 2009, 172, 615-637.	0.6	20
113	Impact of Cliff and Ord (1969, 1981) on Spatial Epidemiology. <i>Geographical Analysis</i> , 2009, 41, 444-451.	1.9	3
114	Hierarchical Related Regression for Combining Aggregate and Individual Data in Studies of Socio-Economic Disease Risk Factors. <i>Journal of the Royal Statistical Society Series A: Statistics in Society</i> , 2008, 171, 159-178.	0.6	66
115	Bayesian Methods for Microarray Data. , 2008, , 267-295.		2
116	A Bayesian calibration model for combining different pre-processing methods in Affymetrix chips. <i>BMC Bioinformatics</i> , 2008, 9, 512.	1.2	4
117	Studying place effects on health by synthesising individual and area-level outcomes. <i>Social Science and Medicine</i> , 2008, 67, 1995-2006.	1.8	21
118	Geographic density of landfill sites and risk of congenital anomalies in England. <i>Occupational and Environmental Medicine</i> , 2008, 66, 81-89.	1.3	39
119	Comparing the Characteristics of Gene Expression Profiles Derived by Univariate and Multivariate Classification Methods. <i>Statistical Applications in Genetics and Molecular Biology</i> , 2008, 7, Article7.	0.2	45
120	Adjusting for selection bias in retrospective, case-control studies. <i>Biostatistics</i> , 2008, 10, 17-31.	0.9	106
121	Identifying cancer sites for human carcinogens in the IARC monographs. <i>Occupational and Environmental Medicine</i> , 2008, 66, 140-140.	1.3	3
122	Use of Space-Time Models to Investigate the Stability of Patterns of Disease. <i>Environmental Health Perspectives</i> , 2008, 116, 1111-1119.	2.8	85
123	Using Likelihood-Free Inference to Compare Evolutionary Dynamics of the Protein Networks of <i>H. pylori</i> and <i>P. falciparum</i> . <i>PLoS Computational Biology</i> , 2007, 3, e230.	1.5	69
124	Fully Bayesian Mixture Model for Differential Gene Expression: Simulations and Model Checks. <i>Statistical Applications in Genetics and Molecular Biology</i> , 2007, 6, Article36.	0.2	22
125	Statistical tools for synthesizing lists of differentially expressed features in related experiments. <i>Genome Biology</i> , 2007, 8, R54.	13.9	13
126	Using Statistical Models To Identify Factors That Have a Role in Defining the Abundance of Ions Produced by Tandem MS. <i>Analytical Chemistry</i> , 2007, 79, 5601-5607.	3.2	22

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127	Bayesian analysis of the multivariate geographical distribution of the socio-economic environment in England. <i>Environmetrics</i> , 2007, 18, 745-758.	0.6	12
128	Down syndrome in births near landfill sites. <i>Prenatal Diagnosis</i> , 2007, 27, 1191-1196.	1.1	19
129	Tail Posterior Probability for Inference in Pairwise and Multiclass Gene Expression Data. <i>Biometrics</i> , 2007, 63, 1117-1125.	0.8	21
130	BGX: a Bioconductor package for the Bayesian integrated analysis of Affymetrix GeneChips. <i>BMC Bioinformatics</i> , 2007, 8, 439.	1.2	19
131	Glycomics investigation into insulin action. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2006, 1760, 652-668.	1.1	17
132	Improving ecological inference using individual-level data. <i>Statistics in Medicine</i> , 2006, 25, 2136-2159.	0.8	121
133	Bayesian Modeling of Differential Gene Expression. <i>Biometrics</i> , 2006, 62, 10-18.	0.8	56
134	A powerful method for detecting differentially expressed genes from GeneChip arrays that does not require replicates. <i>BMC Bioinformatics</i> , 2006, 7, 353.	1.2	12
135	Detection of gene copy number changes in CGH microarrays using a spatially correlated mixture model. <i>Bioinformatics</i> , 2006, 22, 911-918.	1.8	63
136	Bayesian spatio-temporal analysis of joint patterns of male and female lung cancer risks in Yorkshire (UK). <i>Statistical Methods in Medical Research</i> , 2006, 15, 385-407.	0.7	105
137	“Equivalence of prospective and retrospective models in the Bayesian analysis of case-control studies”™. <i>Biometrika</i> , 2005, 92, 505-505.	1.3	1
138	BGX: a fully Bayesian integrated approach to the analysis of Affymetrix GeneChip data. <i>Biostatistics</i> , 2005, 6, 349-373.	0.9	48
139	A comparison of Bayesian spatial models for disease mapping. <i>Statistical Methods in Medical Research</i> , 2005, 14, 35-59.	0.7	403
140	Discussant: Sylvia Richardson. <i>International Statistical Review</i> , 2005, 73, 263-264.	1.1	0
141	Interpreting Posterior Relative Risk Estimates in Disease-Mapping Studies. <i>Environmental Health Perspectives</i> , 2004, 112, 1016-1025.	2.8	405
142	Equivalence of prospective and retrospective models in the Bayesian analysis of case-control studies. <i>Biometrika</i> , 2004, 91, 15-25.	1.3	57
143	A mixture model-based strategy for selecting sets of genes in multiclass response microarray experiments. <i>Bioinformatics</i> , 2004, 20, 2562-2571.	1.8	64
144	Ecological Bias: Use of Maximum-Entropy Approximations. <i>Australian and New Zealand Journal of Statistics</i> , 2004, 46, 233-255.	0.4	6

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145	Report of the Council for the session 2003-2004. Journal of the Royal Statistical Society Series A: Statistics in Society, 2004, 167, 669-756.	0.6	0
146	Flexible dose-response models for Japanese atomic bomb survivor data: Bayesian estimation and prediction of cancer risk. Radiation and Environmental Biophysics, 2004, 43, 233-245.	0.6	34
147	Medical event profiling of COPD patients. Pharmacoepidemiology and Drug Safety, 2004, 13, 547-555.	0.9	11
148	Bayesian hierarchical models in ecological studies of health-environment effects. Environmetrics, 2003, 14, 129-147.	0.6	40
149	A hierarchical model for space-time surveillance data on meningococcal disease incidence. Journal of the Royal Statistical Society Series C: Applied Statistics, 2003, 52, 169-183.	0.5	54
150	Bayesian Hierarchical Model for Identifying Changes in Gene Expression from Microarray Experiments. Journal of Computational Biology, 2002, 9, 671-683.	0.8	85
151	Hidden Markov Models and Disease Mapping. Journal of the American Statistical Association, 2002, 97, 1055-1070.	1.8	253
152	Bayesian Analysis of Poisson Mixtures. Journal of Nonparametric Statistics, 2002, 14, 181-202.	0.4	37
153	A Bayesian partition model for case-control studies on highly polymorphic candidate genes. Genetic Epidemiology, 2002, 22, 356-368.	0.6	12
154	Cancer risks in populations living near landfill sites in Great Britain. British Journal of Cancer, 2002, 86, 1732-1736.	2.9	61
155	Mixture models in measurement error problems, with reference to epidemiological studies. Journal of the Royal Statistical Society Series A: Statistics in Society, 2002, 165, 549-566.	0.6	47
156	Discussion on the meeting on 'Statistical modelling and analysis of genetic data'. Journal of the Royal Statistical Society Series B: Statistical Methodology, 2002, 64, 737-775.	1.1	11
157	Risk of adverse birth outcomes in populations living near landfill sites. BMJ: British Medical Journal, 2001, 323, 363-368.	2.4	235
158	Variable selection and Bayesian model averaging in case-control studies. Statistics in Medicine, 2001, 20, 3215-3230.	0.8	224
159	Modelling Heterogeneity With and Without the Dirichlet Process. Scandinavian Journal of Statistics, 2001, 28, 355-375.	0.9	199
160	Bayesian analysis of case-control studies with categorical covariates. Biometrika, 2001, 88, 1073-1088.	1.3	31
161	Biases in ecological studies: utility of including within-area distribution of confounders. , 2000, 19, 45-59.		41
162	Modeling Markers of Disease Progression by a Hidden Markov Process: Application to Characterizing CD4 Cell Decline. Biometrics, 2000, 56, 733-741.	0.8	58

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163	Projection of cancer risks from the Japanese atomic bomb survivors to the England and Wales population taking into account uncertainty in risk parameters. <i>Radiation and Environmental Biophysics</i> , 2000, 39, 241-252.	0.6	17
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