

David R Bickel

List of Publications by Year in descending order

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74
papers

1,049
citations

567281

15
h-index

501196

28
g-index

77
all docs

77
docs citations

77
times ranked

953
citing authors

#	ARTICLE	IF	CITATIONS
1	Genome-wide allele-specific expression analysis using Massively Parallel Signature Sequencing (MPSS [®]) Reveals cis- and trans-effects on gene expression in maize hybrid meristem tissue. <i>Plant Molecular Biology</i> , 2008, 66, 551-563.	3.9	110
2	On a fast, robust estimator of the mode: Comparisons to other robust estimators with applications. <i>Computational Statistics and Data Analysis</i> , 2006, 50, 3500-3530.	1.2	82
3	Robust cluster analysis of microarray gene expression data with the number of clusters determined biologically. <i>Bioinformatics</i> , 2003, 19, 818-824.	4.1	66
4	Robust estimators of the mode and skewness of continuous data. <i>Computational Statistics and Data Analysis</i> , 2002, 39, 153-163.	1.2	65
5	Degrees of differential gene expression: detecting biologically significant expression differences and estimating their magnitudes. <i>Bioinformatics</i> , 2004, 20, 682-688.	4.1	51
6	Muscle uncoupling protein 3 overexpression mimics endurance training and reduces circulating biomarkers of incomplete β -oxidation. <i>FASEB Journal</i> , 2013, 27, 4213-4225.	0.5	43
7	Robust and efficient estimation of the mode of continuous data: the mode as a viable measure of central tendency. <i>Journal of Statistical Computation and Simulation</i> , 2003, 73, 899-912.	1.2	35
8	Comparison of methods of temperature measurement in swine. <i>Laboratory Animals</i> , 2004, 38, 297-306.	1.0	26
9	Long-Chain Fatty Acid Combustion Rate Is Associated with Unique Metabolite Profiles in Skeletal Muscle Mitochondria. <i>PLoS ONE</i> , 2010, 5, e9834.	2.5	24
10	Probabilities of spurious connections in gene networks: application to expression time series. <i>Bioinformatics</i> , 2005, 21, 1121-1128.	4.1	22
11	Molecular evolution modeled as a fractal Poisson process in agreement with mammalian sequence comparisons. <i>Molecular Biology and Evolution</i> , 1998, 15, 967-977.	8.9	18
12	Error-Rate and Decision-Theoretic Methods of Multiple Testing: Which Genes Have High Objective Probabilities of Differential Expression?. <i>Statistical Applications in Genetics and Molecular Biology</i> , 2004, 3, 1-20.	0.6	18
13	Empirical Bayes estimation of posterior probabilities of enrichment: A comparative study of five estimators of the local false discovery rate. <i>BMC Bioinformatics</i> , 2013, 14, 87.	2.6	17
14	Estimating the intermittency of point processes with applications to human activity and viral DNA. <i>Physica A: Statistical Mechanics and Its Applications</i> , 1999, 265, 634-648.	2.6	16
15	Game-theoretic probability combination with applications to resolving conflicts between statistical methods. <i>International Journal of Approximate Reasoning</i> , 2012, 53, 880-891.	3.3	16
16	A prior-free framework of coherent inference and its derivation of simple shrinkage estimators. <i>Journal of Statistical Planning and Inference</i> , 2014, 145, 204-221.	0.6	16
17	Validation of differential gene expression algorithms: Application comparing fold-change estimation to hypothesis testing. <i>BMC Bioinformatics</i> , 2010, 11, 63.	2.6	15
18	Estimating the Null Distribution to Adjust Observed Confidence Levels for Genome-Scale Screening. <i>Biometrics</i> , 2011, 67, 363-370.	1.4	15

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19	Estimators of the local false discovery rate designed for small numbers of tests. <i>Statistical Applications in Genetics and Molecular Biology</i> , 2012, 11, 4.	0.6	15
20	Coherent Frequentism: A Decision Theory Based on Confidence Sets. <i>Communications in Statistics - Theory and Methods</i> , 2012, 41, 1478-1496.	1.0	15
21	Simple estimation of intermittency in multifractal stochastic processes: biomedical applications. <i>Physics Letters, Section A: General, Atomic and Solid State Physics</i> , 1999, 262, 251-256.	2.1	14
22	Implications of Fluctuations in Substitution Rates: Impact on the Uncertainty of Branch Lengths and on Relative-Rate Tests. <i>Journal of Molecular Evolution</i> , 2000, 50, 381-390.	1.8	14
23	Generalized entropy and multifractality of time-series: relationship between order and intermittency. <i>Chaos, Solitons and Fractals</i> , 2002, 13, 491-497.	5.1	13
24	A predictive approach to measuring the strength of statistical evidence for single and multiple comparisons. <i>Canadian Journal of Statistics</i> , 2011, 39, 610-631.	0.9	13
25	Simple estimators of false discovery rates given as few as one or two p-values without strong parametric assumptions. <i>Statistical Applications in Genetics and Molecular Biology</i> , 2013, 12, 529-43.	0.6	13
26	Molecular Evolution Modeled as a Fractal Renewal Point Process in Agreement with the Dispersion of Substitutions in Mammalian Genes. <i>Journal of Molecular Evolution</i> , 1998, 47, 551-556.	1.8	12
27	Inference after checking multiple Bayesian models for data conflict and applications to mitigating the influence of rejected priors. <i>International Journal of Approximate Reasoning</i> , 2015, 66, 53-72.	3.3	11
28	Self-consistent confidence sets and tests of composite hypotheses applicable to restricted parameters. <i>Bernoulli</i> , 2019, 25, .	1.3	11
29	Genomics Data Analysis. , 0, , .		11
30	Molecular evolution modeled as a fractal statistical process. <i>Physica A: Statistical Mechanics and Its Applications</i> , 1998, 249, 544-552.	2.6	10
31	Multiplicative and Fractal Process in DNA Evolution. <i>Fractals</i> , 1998, 06, 211-217.	3.7	10
32	Empirical Bayes Interval Estimates that are Conditionally Equal to Unadjusted Confidence Intervals or to Default Prior Credibility Intervals. <i>Statistical Applications in Genetics and Molecular Biology</i> , 2012, 11, Article 7.	0.6	10
33	Controlling the degree of caution in statistical inference with the Bayesian and frequentist approaches as opposite extremes. <i>Electronic Journal of Statistics</i> , 2012, 6, .	0.7	10
34	Parametric Estimation of the Local False Discovery Rate for Identifying Genetic Associations. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2013, 10, 98-108.	3.0	10
35	Sharpen statistical significance: Evidence thresholds and Bayes factors sharpened into Occam's razor. <i>Stat</i> , 2019, 8, e215.	0.4	10
36	Null Hypothesis Significance Testing Defended and Calibrated by Bayesian Model Checking. <i>American Statistician</i> , 2021, 75, 249-255.	1.6	10

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37	Detection of anomalous diffusion using confidence intervals of the scaling exponent with application to preterm neonatal heart rate variability. <i>Physical Review E</i> , 1998, 58, 6440-6448.	2.1	9
38	Minimax Optimal Strength of Statistical Evidence for a Composite Alternative Hypothesis. <i>International Statistical Review</i> , 2013, 81, 188-206.	1.9	9
39	Confidence distributions and empirical Bayes posterior distributions unified as distributions of evidential support. <i>Communications in Statistics - Theory and Methods</i> , 2022, 51, 3142-3163.	1.0	9
40	Small-scale Inference: Empirical Bayes and Confidence Methods for as Few as a Single Comparison. <i>International Statistical Review</i> , 2014, 82, 457-476.	1.9	8
41	Blending Bayesian and frequentist methods according to the precision of prior information with applications to hypothesis testing. <i>Statistical Methods and Applications</i> , 2015, 24, 523-546.	1.2	8
42	Correcting false discovery rates for their bias toward false positives. <i>Communications in Statistics Part B: Simulation and Computation</i> , 2021, 50, 3699-3713.	1.2	8
43	Shrinkage Estimation of Effect Sizes as an Alternative to Hypothesis Testing Followed by Estimation in High-Dimensional Biology: Applications to Differential Gene Expression. <i>Statistical Applications in Genetics and Molecular Biology</i> , 2010, 9, Article23.	0.6	7
44	A frequentist framework of inductive reasoning. <i>Sankhya A</i> , 2012, 74, 141-169.	0.8	7
45	Bayesian revision of a prior given prior-data conflict, expert opinion, or a similar insight: a large-deviation approach. <i>Statistics</i> , 2018, 52, 552-570.	0.6	7
46	Null Hypothesis Significance Testing Interpreted and Calibrated by Estimating Probabilities of Sign Errors: A Bayes-Frequentist Continuum. <i>American Statistician</i> , 2021, 75, 104-112.	1.6	7
47	Fractional-difference stochastic model of evolutionary substitutions in DNA sequences. <i>Physics Letters, Section A: General, Atomic and Solid State Physics</i> , 1999, 256, 188-196.	2.1	6
48	Confidence distributions applied to propagating uncertainty to inference based on estimating the local false discovery rate: A fiducial continuum from confidence sets to empirical Bayes set estimates as the number of comparisons increases. <i>Communications in Statistics - Theory and Methods</i> , 2017, 46, 10788-10799.	1.0	6
49	A note on fiducial model averaging as an alternative to checking Bayesian and frequentist models. <i>Communications in Statistics - Theory and Methods</i> , 2018, 47, 3125-3137.	1.0	6
50	Confidence intervals, significance values, maximum likelihood estimates, etc. sharpened into Occam's razors. <i>Communications in Statistics - Theory and Methods</i> , 2020, 49, 2703-2712.	1.0	6
51	Propagating clade and model uncertainty to confidence intervals of divergence times and branch lengths. <i>Molecular Phylogenetics and Evolution</i> , 2022, 167, 107357.	2.7	6
52	Asymptotic distribution of time-series intermittency estimates: applications to economic and clinical data. <i>Computational Statistics and Data Analysis</i> , 2001, 37, 419-431.	1.2	5
53	Gene network reconstruction from transcriptional dynamics under kinetic model uncertainty: a case for the second derivative. <i>Bioinformatics</i> , 2009, 25, 772-779.	4.1	5
54	Incorporating prior knowledge about genetic variants into the analysis of genetic association data: An empirical Bayes approach. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2019, 17, 1-1.	3.0	5

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55	Reporting Bayes factors or probabilities to decision makers of unknown loss functions. <i>Communications in Statistics - Theory and Methods</i> , 2019, 48, 2163-2174.	1.0	5
56	Testing prediction algorithms as null hypotheses: Application to assessing the performance of deep neural networks. <i>Stat</i> , 2020, 9, e270.	0.4	5
57	The performance of a new local false discovery rate method on tests of association between coronary artery disease (CAD) and genome-wide genetic variants. <i>PLoS ONE</i> , 2017, 12, e0185174.	2.5	5
58	Coherent checking and updating of Bayesian models without specifying the model space: A decision-theoretic semantics for possibility theory. <i>International Journal of Approximate Reasoning</i> , 2022, 142, 81-93.	3.3	5
59	Pseudo-Likelihood, Explanatory Power, and Bayes's Theorem [Comment on "A Likelihood Paradigm for Clinical Trials"]. <i>Journal of Statistical Theory and Practice</i> , 2013, 7, 178-182.	0.5	4
60	Departing from Bayesian inference toward minimaxity to the extent that the posterior distribution is unreliable. <i>Statistics and Probability Letters</i> , 2020, 164, 108802.	0.7	4
61	Interval estimation, point estimation, and null hypothesis significance testing calibrated by an estimated posterior probability of the null hypothesis. <i>Communications in Statistics - Theory and Methods</i> , 2023, 52, 763-787.	1.0	4
62	An Explanatory Rationale for Priors Sharpened Into Occam's Razors. <i>Bayesian Analysis</i> , 2020, 15, .	3.0	4
63	REST QUANTIFIED BY A FRACTAL DIMENSION OF MOVEMENT EVENTS: A BIOMEDICAL APPLICATION OF INTERMITTENCY ESTIMATION. <i>Fractals</i> , 2000, 08, 1-6.	3.7	3
64	Correcting the Estimated Level of Differential Expression for Gene Selection Bias: Application to a Microarray Study. <i>Statistical Applications in Genetics and Molecular Biology</i> , 2008, 7, Article10.	0.6	3
65	Model fusion and multiple testing in the likelihood paradigm: shrinkage and evidence supporting a point null hypothesis. <i>Statistics</i> , 2019, 53, 1187-1209.	0.6	3
66	Moderating probability distributions for unrepresented uncertainty: Application to sentiment analysis via deep learning. <i>Communications in Statistics - Theory and Methods</i> , 0, , 1-15.	1.0	3
67	Estimating the local false discovery rate via a bootstrap solution to the reference class problem. <i>PLoS ONE</i> , 2018, 13, e0206902.	2.5	2
68	Maximum entropy derived and generalized under idempotent probability to address Bayes-frequentist uncertainty and model revision uncertainty: An information-theoretic semantics for possibility theory. <i>Fuzzy Sets and Systems</i> , 2023, 453, 192-212.	2.7	2
69	Heart rate variability of preterm neonates quantified by energy entropy. <i>Australian Journal of Cancer Nursing</i> , 1999, 1, 103-111.	1.6	1
70	Electronic ion energy loss calculations on the basis of the binary encounter approximation. <i>Journal of Nuclear Materials</i> , 1999, 264, 133-140.	2.7	1
71	The sufficiency of the evidence, the relevancy of the evidence, and quantifying both with a single number. <i>Statistical Methods and Applications</i> , 2021, 30, 1157.	1.2	1
72	Smoothing Before Estimating Uncertainty, Scaling and Intermittency: Application to Short Heart Rate Signals. <i>Fractals</i> , 2003, 11, 245-252.	3.7	0

#	ARTICLE	IF	CITATIONS
73	Cluster and Classification Techniques for the Biosciences. By Alan Fielding. Cambridge and New York: Cambridge University Press. \$120.00 (hardcover); \$55.00 (paper). xii + 246 p; ill.; index. ISBN: 0-521-85281-1 (hc); 0-521-61800-2 (pb). 2007.. Quarterly Review of Biology, 2007, 82, 410-410.	0.1	0
74	Model averages sharpened into Occam's razors: Deep learning enhanced by Rényi entropy. Communications in Statistics - Theory and Methods, 0, , 1-13.	1.0	0