Ping

List of Publications by Year
in descending order

47	1,728	331670	302126
papers	citations	21	39
		h-index	g-index

47	47	47	2062
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Projectionâ€based techniques for highâ€dimensional optimal transport problems. Wiley Interdisciplinary Reviews: Computational Statistics, 2023, 15, .	3.9	4
2	Smoothing Splines Approximation Using Hilbert Curve Basis Selection. Journal of Computational and Graphical Statistics, 2022, 31, 802-812.	1.7	8
3	Online Distributed IoT Security Monitoring With Multidimensional Streaming Big Data. IEEE Internet of Things Journal, 2020, 7, 4387-4394.	8.7	41
4	More efficient approximation of smoothing splines via space-filling basis selection. Biometrika, 2020, 107, 723-735.	2.4	18
5	Normalization of large-scale behavioural data collected from zebrafish. PLoS ONE, 2019, 14, e0212234.	2.5	6
6	Genomic Characterization of the Zinc Transcriptional Regulatory Element Reveals Potential Functional Roles of ZNF658. Biological Trace Element Research, 2019, 192, 83-90.	3.5	3
7	Mini review: Revisiting mobile RNA silencing in plants. Plant Science, 2019, 278, 113-117.	3.6	43
8	Optimal Subsampling for Large Sample Logistic Regression. Journal of the American Statistical Association, 2018, 113, 829-844.	3.1	149
9	Optimal Penalized Function-on-Function Regression Under a Reproducing Kernel Hilbert Space Framework. Journal of the American Statistical Association, 2018, 113, 1601-1611.	3.1	30
10	Statistical Leveraging Methods in Big Data. Springer Handbooks of Computational Statistics, 2018, , 51-74.	0.2	4
11	Adaptive Basis Selection for Exponential Family Smoothing Splines with Application in Joint Modeling of Multiple Sequencing Samples. Statistica Sinica, 2018, , .	0.3	3
12	Statistical Analysis of Zebrafish Locomotor Behaviour by Generalized Linear Mixed Models. Scientific Reports, 2017, 7, 2937.	3.3	29
13	The Helicase Aquarius/EMB-4 Is Required to Overcome Intronic Barriers to Allow Nuclear RNAi Pathways to Heritably Silence Transcription. Developmental Cell, 2017, 42, 241-255.e6.	7.0	61
14	Statistical inference for time course RNA-Seq data using a negative binomial mixed-effect model. BMC Bioinformatics, 2016, 17, 324.	2.6	21
15	A Naturally-Derived Compound Schisandrin B Enhanced Light Sensation in the pde6c Zebrafish Model of Retinal Degeneration. PLoS ONE, 2016, 11, e0149663.	2.5	27
16	Smoothing spline analysis of variance models: A new tool for the analysis of cyclic biomechanical data. Journal of Biomechanics, 2016, 49, 3216-3222.	2.1	18
17	Smoothing spline ANOVA for super-large samples: scalable computation via rounding parameters. Statistics and Its Interface, 2016, 9, 433-444.	0.3	14
18	Statistical Analysis of Zebrafish Locomotor Response. PLoS ONE, 2015, 10, e0139521.	2.5	40

#	Article	IF	Citations
19	A parameter estimation method for fluorescence lifetime data. BMC Research Notes, 2015, 8, 230.	1.4	1
20	Efficient computation of smoothing splines via adaptive basis sampling. Biometrika, 2015, 102, 631-645.	2.4	20
21	Fast and Stable Multiple Smoothing Parameter Selection in Smoothing Spline Analysis of Variance Models With Large Samples. Journal of Computational and Graphical Statistics, 2015, 24, 715-732.	1.7	22
22	Analyzing spatiotemporal trends in social media data via smoothing spline analysis of variance. Spatial Statistics, 2015, 14, 491-504.	1.9	12
23	A dysregulated acetyl/ <scp>SUMO</scp> switch of <scp>FXR</scp> promotes hepatic inflammation in obesity. EMBO Journal, 2015, 34, 184-199.	7.8	106
24	Leveraging for big data regression. Wiley Interdisciplinary Reviews: Computational Statistics, 2015, 7, 70-76.	3.9	69
25	Methylated DNA is over-represented in whole-genome bisulfite sequencing data. Frontiers in Genetics, 2014, 5, 341.	2.3	64
26	Bias Correction in RNA-Seq Short-Read Counts Using Penalized Regression. Statistics in Biosciences, 2013, 5, 88-99.	1.2	1
27	Nonparametric Method for Genomics-Based Prediction of Performance of Quantitative Traits Involving Epistasis in Plant Breeding. PLoS ONE, 2012, 7, e50604.	2.5	20
28	Data analysis tools for uncertainty quantification of inverse problems. Inverse Problems, 2011, 27, 045001.	2.0	16
29	Nonparametric regression with cross-classified responses. Canadian Journal of Statistics, 2011, 39, 591-609.	0.9	11
30	Inner core rotation and its variability from nonparametric modeling. Journal of Geophysical Research, 2010, 115, .	3.3	26
31	Discovery of protein-DNA interactions by penalized multivariate regression. Nucleic Acids Research, 2009, 37, 5246-5254.	14.5	13
32	Identifying Differentially Expressed Genes in Time Course Microarray Data. Statistics in Biosciences, 2009, 1, 144-159.	1.2	19
33	Penalized Clustering of Large-Scale Functional Data With Multiple Covariates. Journal of the American Statistical Association, 2008, 103, 625-636.	3.1	37
34	Bayesian Functional Data Clustering for Temporal Microarray Data. International Journal of Plant Genomics, 2008, 2008, 1-4.	2.2	8
35	Factorial microarray analysis of zebrafish retinal development. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 12909-12914.	7.1	41
36	Global Assessment of Combinatorial Post-translational Modification of Core Histones in Yeast Using Contemporary Mass Spectrometry. Journal of Biological Chemistry, 2007, 282, 27923-27934.	3.4	77

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37	Gene Expression Profiling of Zebrafish Embryonic Retinal Pigment Epithelium In Vivo. , 2007, 48, 881.		28
38	Seismostratigraphy and Thermal Structure of Earth's Core-Mantle Boundary Region. Science, 2007, 315, 1813-1817.	12.6	238
39	Imaging of structure at and near the core–mantle boundary using a generalized radon transform: 2. Statistical inference of singularities. Journal of Geophysical Research, 2007, 112, .	3.3	11
40	Statistical assessment of the global regulatory role of histone acetylation in Saccharomyces cerevisiae. Genome Biology, 2006, 7, R70.	9.6	24
41	Imaging of structure at and near the core mantle boundary using a generalized radon transform: 1. Construction of image gathers. Journal of Geophysical Research, 2006, 111, n/a-n/a.	3.3	25
42	A data-driven clustering method for time course gene expression data. Nucleic Acids Research, 2006, 34, 1261-1269.	14.5	156
43	Generalized Nonparametric Mixed-Effect Models: Computation and Smoothing Parameter Selection. Journal of Computational and Graphical Statistics, 2005, 14, 485-504.	1.7	33
44	Optimal smoothing in nonparametric mixed-effect models. Annals of Statistics, 2005, 33, 1357.	2.6	55
45	RSIR: regularized sliced inverse regression for motif discovery. Bioinformatics, 2005, 21, 4169-4175.	4.1	61
46	Estimation of regularization parameters in multiple-image deblurring. Astronomy and Astrophysics, 2004, 423, 1179-1186.	5.1	13
47	Bayesian spline smoothing with ambiguous penalties. Canadian Journal of Statistics, 0, , .	0.9	2