

Robert Tibshirani

List of Publications by Year in descending order

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Version: 2024-02-01

76
papers

68,314
citations

32410

55
h-index

87275

74
g-index

77
all docs

77
docs citations

77
times ranked

82110
citing authors

#	ARTICLE	IF	CITATIONS
1	Regression Shrinkage and Selection Via the Lasso. Journal of the Royal Statistical Society Series B: Methodological, 1996, 58, 267-288.	0.8	14,507
2	Distinct types of diffuse large B-cell lymphoma identified by gene expression profiling. Nature, 2000, 403, 503-511.	13.7	8,977
3	Statistical significance for genomewide studies. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 9440-9445.	3.3	8,800
4	Least angle regression. Annals of Statistics, 2004, 32, 407.	1.4	6,530
5	Additive logistic regression: a statistical view of boosting (With discussion and a rejoinder by the) Tj ETQq1 1 0.784314 rgBT /Overlock	1.4	4,905
6	Repeated observation of breast tumor subtypes in independent gene expression data sets. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 8418-8423.	3.3	4,849
7	Sparse inverse covariance estimation with the graphical lasso. Biostatistics, 2008, 9, 432-441.	0.9	3,943
8	Empirical Bayes Analysis of a Microarray Experiment. Journal of the American Statistical Association, 2001, 96, 1151-1160.	1.8	1,420
9	Gene expression profiling identifies clinically relevant subtypes of prostate cancer. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 811-816.	3.3	1,175
10	Improvements on Cross-Validation: The 632+ Bootstrap Method. Journal of the American Statistical Association, 1997, 92, 548-560.	1.8	949
11	From The Cover: Robustness, scalability, and integration of a wound-response gene expression signature in predicting breast cancer survival. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 3738-3743.	3.3	934
12	Use of Gene-Expression Profiling to Identify Prognostic Subclasses in Adult Acute Myeloid Leukemia. New England Journal of Medicine, 2004, 350, 1605-1616.	13.9	915
13	Classification by pairwise coupling. Annals of Statistics, 1998, 26, 451.	1.4	845
14	On the "degrees of freedom" of the lasso. Annals of Statistics, 2007, 35, 2173.	1.4	655
15	Flexible Discriminant Analysis by Optimal Scoring. Journal of the American Statistical Association, 1994, 89, 1255-1270.	1.8	588
16	Empirical bayes methods and false discovery rates for microarrays. Genetic Epidemiology, 2002, 23, 70-86.	0.6	569
17	Semi-Supervised Methods to Predict Patient Survival from Gene Expression Data. PLoS Biology, 2004, 2, e108.	2.6	563
18	Regularized linear discriminant analysis and its application in microarrays. Biostatistics, 2007, 8, 86-100.	0.9	474

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19	Finding consistent patterns: A nonparametric approach for identifying differential expression in RNA-Seq data. <i>Statistical Methods in Medical Research</i> , 2013, 22, 519-536.	0.7	393
20	'Gene shaving' as a method for identifying distinct sets of genes with similar expression patterns. <i>Genome Biology</i> , 2000, 1, research0003.1.	13.9	392
21	Strong Rules for Discarding Predictors in Lasso-Type Problems. <i>Journal of the Royal Statistical Society Series B: Statistical Methodology</i> , 2012, 74, 245-266.	1.1	387
22	Class Prediction by Nearest Shrunken Centroids, with Applications to DNA Microarrays. <i>Statistical Science</i> , 2003, 18, 104.	1.6	321
23	Circulating Tumor DNA Measurements As Early Outcome Predictors in Diffuse Large B-Cell Lymphoma. <i>Journal of Clinical Oncology</i> , 2018, 36, 2845-2853.	0.8	313
24	Normalization, testing, and false discovery rate estimation for RNA-sequencing data. <i>Biostatistics</i> , 2012, 13, 523-538.	0.9	308
25	Gene Expression Patterns in Ovarian Carcinomas. <i>Molecular Biology of the Cell</i> , 2003, 14, 4376-4386.	0.9	302
26	Differentiation stage-specific expression of microRNAs in B lymphocytes and diffuse large B-cell lymphomas. <i>Blood</i> , 2009, 113, 3754-3764.	0.6	226
27	Transcriptional profiling of long non-coding RNAs and novel transcribed regions across a diverse panel of archived human cancers. <i>Genome Biology</i> , 2012, 13, R75.	13.9	221
28	Exact Post-Selection Inference for Sequential Regression Procedures. <i>Journal of the American Statistical Association</i> , 2016, 111, 600-620.	1.8	208
29	A Network Model of a Cooperative Genetic Landscape in Brain Tumors. <i>JAMA - Journal of the American Medical Association</i> , 2009, 302, 261.	3.8	180
30	Risk Factors of Delayed Extubation, Prolonged Length of Stay in the Intensive Care Unit, and Mortality in Patients Undergoing Coronary Artery Bypass Graft with Fast-track Cardiac Anesthesia. <i>Anesthesiology</i> , 1999, 91, 936-936.	1.3	178
31	Covariance-Regularized Regression and Classification for high Dimensional Problems. <i>Journal of the Royal Statistical Society Series B: Statistical Methodology</i> , 2009, 71, 615-636.	1.1	160
32	LMO2 Protein Expression Predicts Survival in Patients With Diffuse Large B-Cell Lymphoma Treated With Anthracycline-Based Chemotherapy With and Without Rituximab. <i>Journal of Clinical Oncology</i> , 2008, 26, 447-454.	0.8	159
33	Flexible Discriminant Analysis by Optimal Scoring. , 0, .		150
34	Supervised harvesting of expression trees. <i>Genome Biology</i> , 2001, 2, research0003.1.	13.9	148
35	Dynamic Risk Profiling Using Serial Tumor Biomarkers for Personalized Outcome Prediction. <i>Cell</i> , 2019, 178, 699-713.e19.	13.5	138
36	Averaged gene expressions for regression. <i>Biostatistics</i> , 2007, 8, 212-227.	0.9	123

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37	3â€²-End Sequencing for Expression Quantification (3SEQ) from Archival Tumor Samples. PLoS ONE, 2010, 5, e8768.	1.1	123
38	Survival analysis with high-dimensional covariates. Statistical Methods in Medical Research, 2010, 19, 29-51.	0.7	122
39	Human transcriptome array for high-throughput clinical studies. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 3707-3712.	3.3	122
40	Quantitative SD-OCT Imaging Biomarkers as Indicators of Age-Related Macular Degeneration Progression. , 2014, 55, 7093.		118
41	Gene expression profiles at diagnosis in de novo childhood AML patients identify FLT3 mutations with good clinical outcomes. Blood, 2004, 104, 2646-2654.	0.6	116
42	Single-cell developmental classification of B cell precursor acute lymphoblastic leukemia at diagnosis reveals predictors of relapse. Nature Medicine, 2018, 24, 474-483.	15.2	112
43	Expression and Prognostic Significance of a Panel of Tissue Hypoxia Markers in Head-and-Neck Squamous Cell Carcinomas. International Journal of Radiation Oncology Biology Physics, 2007, 69, 167-175.	0.4	111
44	Boolean implication networks derived from large scale, whole genome microarray datasets. Genome Biology, 2008, 9, R157.	13.9	108
45	Disease signatures are robust across tissues and experiments. Molecular Systems Biology, 2009, 5, 307.	3.2	101
46	Postâ€selection inference for â€penalized likelihood models. Canadian Journal of Statistics, 2018, 46, 41-61.	0.6	95
47	A multicentre study of primary breast diffuse large <scp>B</scp>â€cell lymphoma in the rituximab era. British Journal of Haematology, 2014, 165, 358-363.	1.2	91
48	HGAL is a novel interleukin-4â€inducible gene that strongly predicts survival in diffuse large B-cell lymphoma. Blood, 2003, 101, 433-440.	0.6	84
49	â€Preconditioningâ€for feature selection and regression in high-dimensional problems. Annals of Statistics, 2008, 36, .	1.4	82
50	Transposable regularized covariance models with an application to missing data imputation. Annals of Applied Statistics, 2010, 4, 764-790.	0.5	82
51	Childhood leukemia and personal monitoring of residential exposures to electric and magnetic fields in Ontario, Canada. Cancer Causes and Control, 1999, 10, 233-243.	0.8	77
52	Sequential Selection Procedures and False Discovery Rate Control. Journal of the Royal Statistical Society Series B: Statistical Methodology, 2016, 78, 423-444.	1.1	77
53	Landscape of monoallelic DNA accessibility in mouse embryonic stem cells and neural progenitor cells. Nature Genetics, 2017, 49, 377-386.	9.4	76
54	Active Idiotypic Vaccination Versus Control Immunotherapy for Follicular Lymphoma. Journal of Clinical Oncology, 2014, 32, 1797-1803.	0.8	75

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55	The Use of Plasma Surface-Enhanced Laser Desorption/Ionization Time-of-Flight Mass Spectrometry Proteomic Patterns for Detection of Head and Neck Squamous Cell Cancers. <i>Clinical Cancer Research</i> , 2004, 10, 4806-4812.	3.2	72
56	A tail strength measure for assessing the overall univariate significance in a dataset. <i>Biostatistics</i> , 2005, 7, 167-181.	0.9	68
57	Cardiolipins Are Biomarkers of Mitochondria-Rich Thyroid Oncocytic Tumors. <i>Cancer Research</i> , 2016, 76, 6588-6597.	0.4	63
58	The 'miss rate' for the analysis of gene expression data. <i>Biostatistics</i> , 2005, 6, 111-117.	0.9	56
59	Estimation of Sparse Binary Pairwise Markov Networks using Pseudo-likelihoods. <i>Journal of Machine Learning Research</i> , 2009, 10, 883-906.	62.4	47
60	Adaptive index models for marker-based risk stratification. <i>Biostatistics</i> , 2011, 12, 68-86.	0.9	37
61	Best Subset, Forward Stepwise or Lasso? Analysis and Recommendations Based on Extensive Comparisons. <i>Statistical Science</i> , 2020, 35, .	1.6	36
62	DR-Integrator: a new analytic tool for integrating DNA copy number and gene expression data. <i>Bioinformatics</i> , 2010, 26, 414-416.	1.8	32
63	CD81 protein is expressed at high levels in normal germinal center B cells and in subtypes of human lymphomas. <i>Human Pathology</i> , 2010, 41, 271-280.	1.1	31
64	Inference with Transposable Data: Modelling the Effects of Row and Column Correlations. <i>Journal of the Royal Statistical Society Series B: Statistical Methodology</i> , 2012, 74, 721-743.	1.1	25
65	C-C Chemokine Receptor 1 Expression in Human Hematolymphoid Neoplasia. <i>American Journal of Clinical Pathology</i> , 2010, 133, 473-483.	0.4	23
66	Machine learning methods applied to DNA microarray data can improve the diagnosis of cancer. <i>SIGKDD Explorations: Newsletter of the Special Interest Group (SIG) on Knowledge Discovery & Data Mining</i> , 2003, 5, 48-55.	3.2	22
67	A study of pre-validation. <i>Annals of Applied Statistics</i> , 2008, 2, .	0.5	21
68	A Pliable Lasso. <i>Journal of Computational and Graphical Statistics</i> , 2020, 29, 215-225.	0.9	18
69	Pathophysiological significance and therapeutic targeting of germinal center kinase in diffuse large B-cell lymphoma. <i>Blood</i> , 2016, 128, 239-248.	0.6	17
70	Rejoinder: Linear Smoothers and Additive Models. <i>Annals of Statistics</i> , 1989, 17, 543.	1.4	15
71	Monotone Shrinkage of Trees. <i>Journal of Computational and Graphical Statistics</i> , 1998, 7, 417-433.	0.9	15
72	Alteration of Gene Expression Signatures of Cortical Differentiation and Wound Response in Lethal Clear Cell Renal Cell Carcinomas. <i>PLoS ONE</i> , 2009, 4, e6039.	1.1	15

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73	Coaching variables for regression and classification. <i>Statistics and Computing</i> , 1998, 8, 25-33.	0.8	11
74	Local false discovery rate facilitates comparison of different microarray experiments. <i>Nucleic Acids Research</i> , 2009, 37, 7483-7497.	6.5	11
75	Genomic feature selection by coverage design optimization. <i>Journal of Applied Statistics</i> , 2018, 45, 2658-2676.	0.6	1
76	Noninvasive Cancer Classification Using Diverse Genomic Features in Circulating Tumor DNA. , 2016, , .		0