

Richard Simon

List of Publications by Year in descending order

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Version: 2024-02-01

81
papers

26,264
citations

41258

49
h-index

79541

73
g-index

88
all docs

88
docs citations

88
times ranked

27410
citing authors

#	ARTICLE	IF	CITATIONS
1	The Use of Molecular Profiling to Predict Survival after Chemotherapy for Diffuse Large-B-Cell Lymphoma. <i>New England Journal of Medicine</i> , 2002, 346, 1937-1947.	13.9	3,474
2	Optimal two-stage designs for phase II clinical trials. <i>Contemporary Clinical Trials</i> , 1989, 10, 1-10.	2.0	3,264
3	Flexible regression models with cubic splines. <i>Statistics in Medicine</i> , 1989, 8, 551-561.	0.8	2,142
4	Gene-Expression Profiles in Hereditary Breast Cancer. <i>New England Journal of Medicine</i> , 2001, 344, 539-548.	13.9	1,669
5	Prediction of Survival in Follicular Lymphoma Based on Molecular Features of Tumor-Infiltrating Immune Cells. <i>New England Journal of Medicine</i> , 2004, 351, 2159-2169.	13.9	1,293
6	Bias in error estimation when using cross-validation for model selection. <i>BMC Bioinformatics</i> , 2006, 7, 91.	1.2	1,174
7	Prediction error estimation: a comparison of resampling methods. <i>Bioinformatics</i> , 2005, 21, 3301-3307.	1.8	1,045
8	Molecular Diagnosis of Primary Mediastinal B Cell Lymphoma Identifies a Clinically Favorable Subgroup of Diffuse Large B Cell Lymphoma Related to Hodgkin Lymphoma. <i>Journal of Experimental Medicine</i> , 2003, 198, 851-862.	4.2	1,002
9	Relation of Gene Expression Phenotype to Immunoglobulin Mutation Genotype in B Cell Chronic Lymphocytic Leukemia. <i>Journal of Experimental Medicine</i> , 2001, 194, 1639-1648.	4.2	978
10	Pitfalls in the Use of DNA Microarray Data for Diagnostic and Prognostic Classification. <i>Journal of the National Cancer Institute</i> , 2003, 95, 14-18.	3.0	943
11	The proliferation gene expression signature is a quantitative integrator of oncogenic events that predicts survival in mantle cell lymphoma. <i>Cancer Cell</i> , 2003, 3, 185-197.	7.7	848
12	Molecular Diagnosis of Burkitt's Lymphoma. <i>New England Journal of Medicine</i> , 2006, 354, 2431-2442.	13.9	824
13	Predicting hepatitis B virus-“positive metastatic hepatocellular carcinomas using gene expression profiling and supervised machine learning. <i>Nature Medicine</i> , 2003, 9, 416-423.	15.2	805
14	Analysis of Gene Expression Data Using BRB-Array Tools. <i>Cancer Informatics</i> , 2007, 3, 117693510700300.	0.9	470
15	Analysis of gene expression data using BRB-ArrayTools. <i>Cancer Informatics</i> , 2007, 3, 11-7.	0.9	461
16	Roadmap for Developing and Validating Therapeutically Relevant Genomic Classifiers. <i>Journal of Clinical Oncology</i> , 2005, 23, 7332-7341.	0.8	361
17	Diffuse large B-cell lymphoma subgroups have distinct genetic profiles that influence tumor biology and improve gene-expression-based survival prediction. <i>Blood</i> , 2005, 106, 3183-3190.	0.6	348
18	Twenty Years of Phase III Trials for Patients With Extensive-Stage Small-Cell Lung Cancer: Perceptible Progress. <i>Journal of Clinical Oncology</i> , 1999, 17, 1794-1794.	0.8	340

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19	Effectiveness of Gene Expression Profiling for Response Prediction of Rectal Adenocarcinomas to Preoperative Chemoradiotherapy. <i>Journal of Clinical Oncology</i> , 2005, 23, 1826-1838.	0.8	325
20	Clinical Trial Designs for Cytostatic Agents: Are New Approaches Needed?. <i>Journal of Clinical Oncology</i> , 2001, 19, 265-272.	0.8	324
21	Gene Expression-Based Prognostic Signatures in Lung Cancer: Ready for Clinical Use?. <i>Journal of the National Cancer Institute</i> , 2010, 102, 464-474.	3.0	324
22	Evaluating the Efficiency of Targeted Designs for Randomized Clinical Trials. <i>Clinical Cancer Research</i> , 2004, 10, 6759-6763.	3.2	308
23	A Paradigm for Class Prediction Using Gene Expression Profiles. <i>Journal of Computational Biology</i> , 2002, 9, 505-511.	0.8	268
24	Practical Bayesian Guidelines for Phase II/III Clinical Trials. <i>Biometrics</i> , 1994, 50, 337.	0.8	197
25	Initiating oncogenic event determines gene-expression patterns of human breast cancer models. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002, 99, 6967-6972.	3.3	192
26	Design of studies using DNA microarrays. <i>Genetic Epidemiology</i> , 2002, 23, 21-36.	0.6	183
27	The Cross-Validated Adaptive Signature Design. <i>Clinical Cancer Research</i> , 2010, 16, 691-698.	3.2	182
28	The Use of Genomics in Clinical Trial Design. <i>Clinical Cancer Research</i> , 2008, 14, 5984-5993.	3.2	166
29	Clinical trial designs for evaluating the medical utility of prognostic and predictive biomarkers in oncology. <i>Personalized Medicine</i> , 2010, 7, 33-47.	0.8	155
30	Sample size determination in microarray experiments for class comparison and prognostic classification. <i>Biostatistics</i> , 2005, 6, 27-38.	0.9	151
31	Overfitting in prediction models – Is it a problem only in high dimensions?. <i>Contemporary Clinical Trials</i> , 2013, 36, 636-641.	0.8	122
32	Prognostic factors in Burkitt's lymphoma importance of total tumor burden. <i>Cancer</i> , 1980, 45, 1507-1515.	2.0	112
33	Gene Expression Profiling Reveals a Massive, Aneuploidy-Dependent Transcriptional Deregulation and Distinct Differences between Lymph Node–Negative and Lymph Node–Positive Colon Carcinomas. <i>Cancer Research</i> , 2007, 67, 41-56.	0.4	108
34	What should physicians look for in evaluating prognostic gene-expression signatures?. <i>Nature Reviews Clinical Oncology</i> , 2010, 7, 327-334.	12.5	104
35	Development and Validation of Therapeutically Relevant Multi-Gene Biomarker Classifiers. <i>Journal of the National Cancer Institute</i> , 2005, 97, 866-867.	3.0	95
36	A staging system for hepatocellular carcinoma: Prognostic factors in Ugandan patients. <i>Cancer</i> , 1975, 35, 1357-1364.	2.0	92

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37	Combination chemotherapy of advanced lung cancer. A randomized trial. <i>Cancer</i> , 1976, 38, 2201-2207.	2.0	85
38	Questions and Answers on Design of Dual-Label Microarrays for Identifying Differentially Expressed Genes. <i>Journal of the National Cancer Institute</i> , 2003, 95, 1362-1369.	3.0	81
39	A comparison of bootstrap methods and an adjusted bootstrap approach for estimating the prediction error in microarray classification. <i>Statistics in Medicine</i> , 2007, 26, 5320-5334.	0.8	81
40	The Bayesian basket design for genomic variant-driven phase II trials. <i>Seminars in Oncology</i> , 2016, 43, 13-18.	0.8	81
41	Development and Evaluation of Therapeutically Relevant Predictive Classifiers Using Gene Expression Profiling. <i>Journal of the National Cancer Institute</i> , 2006, 98, 1169-1171.	3.0	76
42	Critical Review of Umbrella, Basket, and Platform Designs for Oncology Clinical Trials. <i>Clinical Pharmacology and Therapeutics</i> , 2017, 102, 934-941.	2.3	71
43	A Bayesian approach to establishing sample size and monitoring criteria for phase II clinical trials. <i>Contemporary Clinical Trials</i> , 1994, 15, 463-481.	2.0	66
44	Development and validation of biomarker classifiers for treatment selection. <i>Journal of Statistical Planning and Inference</i> , 2008, 138, 308-320.	0.4	64
45	Supervised analysis when the number of candidate features (p) greatly exceeds the number of cases (n). <i>SICKDD Explorations: Newsletter of the Special Interest Group (SIG) on Knowledge Discovery & Data Mining</i> , 2003, 5, 31-36.	3.2	63
46	A decade of progress in statistical methodology for clinical trials. <i>Statistics in Medicine</i> , 1991, 10, 1789-1817.	0.8	60
47	Using single cell sequencing data to model the evolutionary history of a tumor. <i>BMC Bioinformatics</i> , 2014, 15, 27.	1.2	58
48	Lost in translation: Problems and pitfalls in translating laboratory observations to clinical utility. <i>European Journal of Cancer</i> , 2008, 44, 2707-2713.	1.3	57
49	Developing and Validating Continuous Genomic Signatures in Randomized Clinical Trials for Predictive Medicine. <i>Clinical Cancer Research</i> , 2012, 18, 6065-6073.	3.2	54
50	Microarray-based cancer prediction using single genes. <i>BMC Bioinformatics</i> , 2011, 12, 391.	1.2	50
51	Microarray-based expression profiling and informatics. <i>Current Opinion in Biotechnology</i> , 2008, 19, 26-29.	3.3	42
52	Analysis of DNA microarray expression data. <i>Best Practice and Research in Clinical Haematology</i> , 2009, 22, 271-282.	0.7	37
53	Using DNA microarrays for diagnostic and prognostic prediction. <i>Expert Review of Molecular Diagnostics</i> , 2003, 3, 587-595.	1.5	36
54	Calculating Confidence Intervals for Prediction Error in Microarray Classification Using Resampling. <i>Statistical Applications in Genetics and Molecular Biology</i> , 2008, 7, Article 8.	0.2	33

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55	An evaluation of resampling methods for assessment of survival risk prediction in high-dimensional settings. <i>Statistics in Medicine</i> , 2011, 30, 642-653.	0.8	33
56	An investigation of two multivariate permutation methods for controlling the false discovery proportion. <i>Statistics in Medicine</i> , 2007, 26, 4428-4440.	0.8	32
57	Iterative class discovery and feature selection using Minimal Spanning Trees. <i>BMC Bioinformatics</i> , 2004, 5, 126.	1.2	23
58	New designs for basket clinical trials in oncology. <i>Journal of Biopharmaceutical Statistics</i> , 2018, 28, 245-255.	0.4	23
59	When is a genomic classifier ready for prime time?. <i>Nature Clinical Practice Oncology</i> , 2004, 1, 4-5.	4.3	21
60	Validation of pharmacogenomic biomarker classifiers for treatment selection. <i>Cancer Biomarkers</i> , 2006, 2, 89-96.	0.8	21
61	Clinical trials for precision oncology using next-generation sequencing. <i>Personalized Medicine</i> , 2013, 10, 485-495.	0.8	21
62	Concerted changes in transcriptional regulation of genes involved in DNA methylation, demethylation, and folate-mediated one-carbon metabolism pathways in the NCI-60 cancer cell line panel in response to cancer drug treatment. <i>Clinical Epigenetics</i> , 2016, 8, 73.	1.8	21
63	Resampling Strategies for Model Assessment and Selection. , 2007, , 173-186.		18
64	Appropriateness of some resampling-based inference procedures for assessing performance of prognostic classifiers derived from microarray data. <i>Statistics in Medicine</i> , 2007, 26, 1102-1113.	0.8	15
65	Development and Validation of Predictive Indices for a Continuous Outcome Using Gene Expression Profiles. <i>Cancer Informatics</i> , 2010, 9, CIN.S3805.	0.9	13
66	Challenges of Microarray Data and the Evaluation of Gene Expression Profile Signatures. <i>Cancer Investigation</i> , 2008, 26, 327-332.	0.6	12
67	Class probability estimation for medical studies. <i>Biometrical Journal</i> , 2014, 56, 597-600.	0.6	12
68	Interpretation of Genomic Data: Questions and Answers. <i>Seminars in Hematology</i> , 2008, 45, 196-204.	1.8	11
69	Correlation of gene expression and associated mutation profiles of APOBEC3A, APOBEC3B, REV1, UNG, and FHIT with chemosensitivity of cancer cell lines to drug treatment. <i>Human Genomics</i> , 2018, 12, 20.	1.4	11
70	A computational study of the inhibition mechanisms of P-glycoprotein mediated paclitaxel efflux by kinase inhibitors. <i>BMC Systems Biology</i> , 2017, 11, 108.	3.0	10
71	Clinical Trial Designs for Therapeutic Cancer Vaccines. <i>Cancer Treatment and Research</i> , 2005, 123, 339-350.	0.2	8
72	Two-stage adaptive cutoff design for building and validating a prognostic biomarker signature. <i>Statistics in Medicine</i> , 2014, 33, 5097-5110.	0.8	5

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73	Moving from correlative science to predictive oncology. EPMA Journal, 2010, 1, 377-387.	3.3	4
74	Review of Statistical Methods for Biomarker-Driven Clinical Trials. JCO Precision Oncology, 2019, 3, 1-9.	1.5	3
75	Clinical Trial Designs for Therapeutic Vaccine Studies. , 2004, , 519-525.		1
76	Identification of Pharmacogenomic Biomarker Classifiers in Cancer Drug Development. , 2008, , 327-338.		1
77	Predictive Biomarker Classifiers in the Design of Pivotal Clinical Trials. Methods in Pharmacology and Toxicology, 2008, , 229-238.	0.1	0
78	Development of Prognostic Biomarker Signatures for Survival Using High-Dimensional Data. ICSA Book Series in Statistics, 2018, , 339-351.	0.0	0
79	Challenges of Microarray Data and the Evaluation of Gene Expression Profile Signatures. Translational Medicine Series, 2007, , 27-36.	0.0	0
80	Drug and Pharmacodiagnostic Co-Development. , 2010, , 185-205.		0
81	Integration of Predictive Biomarker Diagnostics into Clinical Trials for New Drug Development. , 2010, , 18-1-18-14.		0