Giovanni Parmigiani

List of Publications by Year
in descending order

176	16,421	57681	19470
papers	citations	46 h-index	122 g-index

192	192	192	27128
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Prediction of hereditary cancers using neural networks. Annals of Applied Statistics, 2022, 16, .	0.5	0
2	Validation of Breast Cancer Risk Models by Race/Ethnicity, Family History and Molecular Subtypes. Cancers, 2022, 14, 45.	1.7	11
3	Statistical methods for Mendelian models with multiple genes and cancers. Genetic Epidemiology, 2022, 46, 395-414.	0.6	3
4	Robustifying genomic classifiers to batch effects via ensemble learning. Bioinformatics, 2021, 37, 1521-1527.	1.8	13
5	Statistical approaches for metaâ€analysis of genetic mutation prevalence. Genetic Epidemiology, 2021, 45, 154-170.	0.6	1
6	Variation in cancer risk among families with genetic susceptibility. Genetic Epidemiology, 2021, 45, 209-221.	0.6	2
7	Extending models via gradient boosting: An application to Mendelian models. Annals of Applied Statistics, 2021, 15, .	0.5	1
8	covid19census: U.S. and Italy COVID-19 metrics and other epidemiological data. Database: the Journal of Biological Databases and Curation, 2021, 2021, .	1.4	0
9	Gene Expression Pathways in Prostate Tissue Associated with Vigorous Physical Activity in Prostate Cancer. Cancer Epidemiology Biomarkers and Prevention, 2021, 30, 751-756.	1.1	1
10	A risk prediction tool for individuals with a family history of breast, ovarian, or pancreatic cancer: BRCAPANCPRO. British Journal of Cancer, 2021, 125, 1712-1717.	2.9	4
11	IgM-MM is predominantly a preâ€“germinal center disorder and has a distinct genomic and transcriptomic signature from WM. Blood, 2021, 138, 1980-1985.	0.6	11
12	Inadequate Sars-Cov-2 Vaccine Effectiveness in Patients with Multiple Myeloma: A Large Nationwide Veterans Affairs Study. Blood, 2021, 138, 400-400.	0.6	1
13	The impact of different sources of heterogeneity on loss of accuracy from genomic prediction models. Biostatistics, 2020, 21, 253-268.	0.9	15
14	Performance of Breast Cancer Risk-Assessment Models in a Large Mammography Cohort. Journal of the National Cancer Institute, 2020, 112, 489-497.	3.0	59
15	Family history of prostate cancer and the incidence of ERGâ€•and phosphatase and tensin homologâ€defined prostate cancer. International Journal of Cancer, 2020, 146, 2694-2702.	2.3	3
16	Clinical Factors Associated With Gastric Cancer in Individuals With Lynch Syndrome. Clinical Gastroenterology and Hepatology, 2020, 18, 830-837.e1.	2.4	38
17	The Impact of Stroma Admixture on Molecular Subtypes and Prognostic Gene Signatures in Serous Ovarian Cancer. Cancer Epidemiology Biomarkers and Prevention, 2020, 29, 509-519.	1.1	34
18	ComBat-seq: batch effect adjustment for RNA-seq count data. NAR Genomics and Bioinformatics, 2020, 2, lqaa078.	1.5	591

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19	Multiomic Analysis of Subtype Evolution and Heterogeneity in High-Grade Serous Ovarian Carcinoma. Cancer Research, 2020, 80, 4335-4345.	0.4	57
20	Multiplex Immunofluorescence in Formalin-Fixed Paraffin-Embedded Tumor Tissue to Identify Single-Cellâ€“Level PI3K Pathway Activation. Clinical Cancer Research, 2020, 26, 5903-5913.	3.2	8
21	Legacy Genetic Testing Results for Cancer Susceptibility: How Common are Conflicting Classifications in a Large Variant Dataset from Multiple Practices?. Annals of Surgical Oncology, 2020, 27, 2212-2220.	0.7	1
22	Practical implementation of frailty models in Mendelian risk prediction. Genetic Epidemiology, 2020, 44, 564-578.	0.6	2
23	Penetrance of Colorectal Cancer Among Mismatch Repair Gene Mutation Carriers: A Meta-Analysis. JNCI Cancer Spectrum, 2020, 4, pkaa027.	1.4	17
24	Receiver operating characteristic curves with an indeterminacy zone. Pattern Recognition Letters, 2020, 136, 94-100.	2.6	3
25	Estimating the Effects of Fine Particulate Matter on 432 Cardiovascular Diseases Using Multi-Outcome Regression With Tree-Structured Shrinkage. Journal of the American Statistical Association, 2020, 115, 1689-1699.	1.8	3
26	Pathologic Complete Response after Neoadjuvant Chemotherapy and Impact on Breast Cancer Recurrence and Survival: A Comprehensive Meta-analysis. Clinical Cancer Research, 2020, 26, 2838-2848.	3.2	403
27	Penetrance of Breast and Ovarian Cancer in Women Who Carry a BRCA1/2 Mutation and Do Not Use Risk-Reducing Salpingo-Oophorectomy: An Updated Meta-Analysis. JNCI Cancer Spectrum, 2020, 4, pkaa029.	1.4	41
28	High-Dose Melphalan Significantly Increases Mutational Burden in Multiple Myeloma Cells at Relapse: Results from a Randomized Study in Multiple Myeloma. Blood, 2020, 136, 4-5.	0.6	11
29	Tree-Weighting for Multi-Study Ensemble Learners. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2020, 25, 451-462.	0.7	2
30	High-Dimensional Confounding Adjustment Using Continuous Spike and Slab Priors. Bayesian Analysis, 2019, 14, 805-828.	1.6	24
31	Using Machine Learning and Natural Language Processing to Review and Classify the Medical Literature on Cancer Susceptibility Genes. JCO Clinical Cancer Informatics, 2019, 3, 1-9.	1.0	37
32	Frequentist operating characteristics of Bayesian optimal designs via simulation. Statistics in Medicine, 2019, 38, 4026-4039.	0.8	5
33	Deciphering the chronology of copy number alterations in Multiple Myeloma. Blood Cancer Journal, 2019, 9, 39.	2.8	38
34	Validation of a Semiautomated Natural Language Processingâ€“Based Procedure for Meta-Analysis of Cancer Susceptibility Gene Penetrance. JCO Clinical Cancer Informatics, 2019, 3, 1-9.	1.0	21
35	A Prospective Study of the Association between Physical Activity and Risk of Prostate Cancer Defined by Clinical Features and TMPRSS2:ERG. European Urology, 2019, 76, 33-40.	0.9	26
36	Multi-Study Factor Analysis. Biometrics, 2019, 75, 337-346.	0.8	33

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37	Dysregulated Mirnas after Uniform Treatment Predict Outcome of Newly-Diagnosed Multiple Myeloma. Blood, 2019, 134, 4348-4348.	0.6	1
38	Tree-Weighting for Multi-Study Ensemble Learners. , 2019, , .		2
39	The Landscape of Genome Wide Somatic Alterations Identifies a Good-Risk Group in Newly Diagnosed Multiple Myeloma. Blood, 2019, 134, 3055-3055.	0.6	0
40	The clinical trials landscape for glioblastoma: is it adequate to develop new treatments?. Neuro-Oncology, 2018, 20, 1034-1043.	0.6	100
41	A Clinical Decision Support Tool to Predict Cancer Risk for Commonly Tested Cancerâ€Related Germline Mutations. Journal of Genetic Counseling, 2018, 27, 1187-1199.	0.9	38
42	Adding experimental arms to platform clinical trials: randomization procedures and interim analyses. Biostatistics, 2018, 19, 199-215.	0.9	19
43	Long intergenic non-coding RNAs have an independent impact on survival in multiple myeloma. Leukemia, 2018, 32, 2626-2635.	3.3	48
44	Training replicable predictors in multiple studies. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 2578-2583.	3.3	34
45	Nonparametric Adjustment for Measurement Error in Time-to-Event Data: Application to Risk Prediction Models. Journal of the American Statistical Association, 2018, 113, 14-25.	1.8	4
46	Integrative factor analysis â€" An unsupervised method for quantifying cross-study consistency of gene expression data. Genomics, 2018, 110, 80-88.	1.3	0
47	Transcriptome Deconvolution of Heterogeneous Tumor Samples with Immune Infiltration. IScience, 2018, 9, 451-460.	1.9	69
48	Continuity of transcriptomes among colorectal cancer subtypes based on meta-analysis. Genome Biology, 2018, 19, 142.	3.8	20
49	Efficient computation of the joint probability of multiple inherited risk alleles from pedigree data. Genetic Epidemiology, 2018, 42, 528-538.	0.6	3
50	Family History of Breast or Prostate Cancer and Prostate Cancer Risk. Clinical Cancer Research, 2018, 24, 5910-5917.	3.2	52
51	Consensus on Molecular Subtypes of High-Grade Serous Ovarian Carcinoma. Clinical Cancer Research, 2018, 24, 5037-5047.	3.2	93
52	Precision Prevention and Early Detection of Cancer: Fundamental Principles. Cancer Discovery, 2018, 8, 803-811.	7.7	62
53	Model Averaged Double Robust Estimation. Biometrics, 2017, 73, 410-421.	0.8	23
54	Reassessing risk models for atypical hyperplasia: age may not matter. Breast Cancer Research and Treatment, 2017, 165, 285-291.	1.1	14

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55	Combinatorial Mixtures of Multiparameter Distributions: An Application to Bivariate Data. International Journal of Biostatistics, 2017, 13, .	0.4	0
56	Leveraging molecular datasets for biomarker-based clinical trial design in glioblastoma. Neuro-Oncology, 2017, 19, 908-917.	0.6	23
57	Bayesian Response-Adaptive Designs for Basket Trials. Biometrics, 2017, 73, 905-915.	0.8	38
58	Propensity scores with misclassified treatment assignment: a likelihood-based adjustment. Biostatistics, 2017, 18, 695-710.	0.9	9
59	Stromal and epithelial transcriptional map of initiation progression and metastatic potential of human prostate cancer. Nature Communications, 2017, 8, 420.	5.8	91
60	Combining Bayesian experimental designs and frequentist data analyses: motivations and examples. Applied Stochastic Models in Business and Industry, 2017, 33, 302-313.	0.9	11
61	Designing Clinical Trials That Accept New Arms: An Example in Metastatic Breast Cancer. Journal of Clinical Oncology, 2017, 35, 3160-3168.	0.8	28
62	The DoppelgÃnger Effect: Hidden Duplicates in Databases of Transcriptome Profiles. Journal of the National Cancer Institute, 2016, 108, djw146.	3.0	18
63	I-SPY 2 â€" A Glimpse of the Future of Phase 2 Drug Development?. New England Journal of Medicine, 2016, 375, 7-9.	13.9	46
64	Penetrance of ATM Gene Mutations in Breast Cancer: A Metaâ€Analysis of Different Measures of Risk. Genetic Epidemiology, 2016, 40, 425-431.	0.6	98
65	Optimal Bayesian Adaptive Trials When Treatment Efficacy Depends on Biomarkers. Biometrics, 2016, 72, 414-421.	0.8	6
66	A two-stage approach to genetic risk assessment in primary care. Breast Cancer Research and Treatment, 2016, 155, 375-383.	1.1	13
67	Familial Risk and Heritability of Cancer Among Twins in Nordic Countries. JAMA - Journal of the American Medical Association, 2016, 315, 68.	3.8	648
68	A Detailed Alternate Splicing Landscape in Multiple Myeloma with Significant Potential Biological and Clinical Implications. Blood, 2016, 128, 356-356.	0.6	1
69	3' Untranslated Region (UTR) Alterations Are Frequently Targeted By MM-Related Mirnas and Affects the Clinical Outcome. Blood, 2016, 128, 4447-4447.	0.6	0
70	The Multiple Myeloma Genome Project: Development of a Molecular Segmentation Strategy for the Clinical Classification of Multiple Myeloma. Blood, 2016, 128, 196-196.	0.6	2
71	RNA-Seq De Novo Assembly of Clonal Immunoglobulin Rearrangements Identifies Interesting Biology and Uncovers Prognostic Features in Multiple Myeloma. Blood, 2016, 128, 195-195.	0.6	10
72	Generalized Quantile Treatment Effect: A Flexible Bayesian Approach Using Quantile Ratio Smoothing. Bayesian Analysis, 2015, 10, .	1.6	2

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73	Recent Enhancements to the Genetic Risk Prediction Model BRCAPRO. Cancer Informatics, 2015, 14s2, CIN.S17292.	0.9	34
74	Accounting for uncertainty in confounder and effect modifier selection when estimating average causal effects in generalized linear models. Biometrics, 2015, 71, 654-665.	0.8	33
75	Evaluating a 4-marker signature of aggressive prostate cancer using time-dependent AUC. Prostate, 2015, 75, 1926-1933.	1.2	8
76	BRCA1 Recruitment to Transcriptional Pause Sites Is Required for R-Loop-Driven DNA Damage Repair. Molecular Cell, 2015, 57, 636-647.	4.5	363
77	Combining progression-free survival and overall survival as a novel composite endpoint for glioblastoma trials. Neuro-Oncology, 2015, 17, 1106-1113.	0.6	21
78	Bayesian nonparametric cross-study validation of prediction methods. Annals of Applied Statistics, 2015, 9, .	0.5	24
79	Comparing Platforms for Messenger RNA Expression Profiling of Archival Formalin-Fixed, Paraffin-Embedded Tissues. Journal of Molecular Diagnostics, 2015, 17, 374-381.	1.2	22
80	Only three driver gene mutations are required for the development of lung and colorectal cancers. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 118-123.	3.3	325
81	Nuclease Activity Is Associated with Genomic Instability As Well As Survival in Myeloma; Underlying Mechanisms and Significance. Blood, 2015, 126, 2420-2420.	0.6	2
82	Differentially Expressed and Prognostically Significant Lincrnas May Impact Immune System and Tumor Progression in Multiple Myeloma (MM). Blood, 2015, 126, 2989-2989.	0.6	3
83	Identification of a Novel Long Intergenic Noncoding RNA - Linc00936, with Significant Impact on Multiple Myeloma Cell Growth Via mTOR Pathway Inhibition. Blood, 2015, 126, 504-504.	0.6	4
84	Functional and Clinical Impact of Splicing Factor Dysregulation in Multiple Myeloma. Blood, 2015, 126, 726-726.	0.6	1
85	The Fusion Gene Landscape in Multiple Myeloma, with Clinical Impact. Blood, 2015, 126, 835-835.	0.6	1
86	Redefining Mutational Profiling Using RNA-Seq: Insight into the Functional Mutational Landscape of Multiple Myeloma. Blood, 2015, 126, 837-837.	0.6	2
87	Genomic Landscape Predictive of Minimal Residual Disease (MRD) in Multiple Myeloma (MM). Blood, 2015, 126, 4212-4212.	0.6	0
88	Modular network construction using eQTL data: an analysis of computational costs and benefits. Frontiers in Genetics, 2014, 5, 40.	1.1	12
89	Misreported Family Histories and Underestimation of Risk. Journal of Clinical Oncology, 2014, 32, 3682-3683.	0.8	3
90	Cross-study validation for the assessment of prediction algorithms. Bioinformatics, 2014, 30, i105-i112.	1.8	75

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91	MÃ¡s-o-menos: a simple sign averaging method for discrimination in genomic data analysis. Bioinformatics, 2014, 30, 3062-3069.	1.8	34
92	Calibrated predictions for multivariate competing risks models. Lifetime Data Analysis, 2014, 20, 234-251.	0.4	10
93	Risk Prediction for Late-Stage Ovarian Cancer by Meta-analysis of 1525 Patient Samples. Journal of the National Cancer Institute, 2014, 106, .	3.0	184
94	Reclassification of predictions for uncovering subgroup specific improvement. Statistics in Medicine, 2014, 33, 1914-1927.	0.8	4
95	Comparative Meta-analysis of Prognostic Gene Signatures for Late-Stage Ovarian Cancer. Journal of the National Cancer Institute, 2014, 106, .	3.0	110
96	Heterogeneity of genomic evolution and mutational profiles in multiple myeloma. Nature Communications, 2014, 5, 2997.	5.8	741
97	Recent BRCAPRO Upgrades Significantly Improve Calibration. Cancer Epidemiology Biomarkers and Prevention, 2014, 23, 1689-1695.	1.1	20
98	Integrative correlation: Properties and relation to canonical correlations. Journal of Multivariate Analysis, 2014, 123, 270-280.	0.5	8
99	Differential and limited expression of mutant alleles in multiple myeloma. Blood, 2014, 124, 3110-3117.	0.6	54
100	Alternative Splicing Is a Frequent Event and Impacts Clinical Outcome in Myeloma: A Large RNA-Seq Data Analysis of Newly-Diagnosed Myeloma Patients. Blood, 2014, 124, 638-638.	0.6	25
101	Frequent Igh Fusion Transcripts with Clinical Impact in Multiple Myeloma. Blood, 2014, 124, 721-721.	0.6	1
102	Completing the Results of the 2013 Boston Marathon. PLoS ONE, 2014, 9, e93800.	1.1	3
103	Statistical Tools and R Software for Cancer Driver Probabilities. Methods in Molecular Biology, 2014, 1101, 113-134.	0.4	0
104	Bone Marrow Microenvironment Regulates Alternative Splicing Events in Myeloma Cells through Downregulation of RNA Binding Protein Fox2. Blood, 2014, 124, 4714-4714.	0.6	0
105	Providing access to risk prediction tools via the HL7 XML-formatted risk web service. Breast Cancer Research and Treatment, 2013, 140, 187-193.	1.1	13
106	Whole-genome sequencing identifies a recurrent functional synonymous mutation in melanoma. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 13481-13486.	3.3	147
107	A Decisionâ€Theory Approach to Interpretable Set Analysis for Highâ€Dimensional Data. Biometrics, 2013, 69, 614-623.	0.8	5
108	Frailty Models for Familial Risk With Application to Breast Cancer. Journal of the American Statistical Association, 2013, 108, 1205-1215.	1.8	16

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109	The penetrance of ductal carcinoma in situ among BRCA1 and BRCA2 mutation carriers. Breast Cancer Research and Treatment, 2013, 137, 315-318.	1.1	6
110	<scp>SNP</scp> Prioritization Using a <scp>B</scp>ayesian Probability of Association. Genetic Epidemiology, 2013, 37, 214-221.	0.6	13
111	Importance of Different Types of Prior Knowledge in Selecting Genomeâ€Wide Findings for Followâ€Up. Genetic Epidemiology, 2013, 37, 205-213.	0.6	14
112	Integrated genomic analyses identify ARID1A and ARID1B alterations in the childhood cancer neuroblastoma. Nature Genetics, 2013, 45, 12-17.	9.4	374
113	Simplifying clinical use of the genetic risk prediction model BRCAPRO. Breast Cancer Research and Treatment, 2013, 139, 571-579.	1.1	24
114	DeMix: deconvolution for mixed cancer transcriptomes using raw measured data. Bioinformatics, 2013, 29, 1865-1871.	1.8	97
115	curatedOvarianData: clinically annotated data for the ovarian cancer transcriptome. Database: the Journal of Biological Databases and Curation, 2013, 2013, bat013.	1.4	165
116	Reply to B. Freidlin et al. Journal of Clinical Oncology, 2013, 31, 970-971.	0.8	3
117	Biomarker-based adaptive trials for patients with glioblastoma--lessons from I-SPY 2. Neuro-Oncology, 2013, 15, 972-978.	0.6	37
118	Hierarchical Bayesian analysis of somatic mutation data in cancer. Annals of Applied Statistics, 2013, 7, .	0.5	4
119	Half or more of the somatic mutations in cancers of self-renewing tissues originate prior to tumor initiation. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 1999-2004.	3.3	348
120	Why tyrosine kinase inhibitor resistance is common in advanced gastrointestinal stromal tumors. F1000Research, 2013, 2, 152.	0.8	2
121	Bayesian Adaptive Randomized Trial Design for Patients With Recurrent Glioblastoma. Journal of Clinical Oncology, 2012, 30, 3258-3263.	0.8	104
122	Opportunities for the Primary Prevention of Colorectal Cancer in the United States. Cancer Prevention Research, 2012, 5, 138-145.	0.7	24
123	Response to Comments on â€œThe Predictive Capacity of Personal Genome Sequencingâ€• Science Translational Medicine, 2012, 4, .	5.8	1
124	Modeling dependent gene expression. Annals of Applied Statistics, 2012, 6, 542-560.	0.5	14
125	Detection of Chromosomal Alterations in the Circulation of Cancer Patients with Whole-Genome Sequencing. Science Translational Medicine, 2012, 4, 162ra154.	5.8	557
126	Expression Profiling of Archival Tumors for Long-term Health Studies. Clinical Cancer Research, 2012, 18, 6136-6146.	3.2	32

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127	The role of chemoprevention in modifying the risk of breast cancer in women with atypical breast lesions. Breast Cancer Research and Treatment, 2012, 136, 627-633.	1.1	115
128	Estimation of sequencing error rates in short reads. BMC Bioinformatics, 2012, 13, 185.	1.2	61
129	The Predictive Capacity of Personal Genome Sequencing. Science Translational Medicine, 2012, 4, 133ra58.	5.8	168
130	Assessing the added value of breast tumor markers in genetic risk prediction model BRCAPRO. Breast Cancer Research and Treatment, 2012, 133, 347-355.	1.1	21
131	Bayesian Effect Estimation Accounting for Adjustment Uncertainty. Biometrics, 2012, 68, 661-671.	0.8	84
132	Rejoinder: Bayesian Effect Estimation Accounting for Adjustment Uncertainty. Biometrics, 2012, 68, 680-686.	0.8	3
133	The Average Baseline BCR-ABL Levels Are Significantly Higher in Patients with Resistance to Dasatinib As First-Line Treatment for Early Chronic Phase Chronic Myeloid Leukemia. Blood, 2012, 120, 4436-4436.	0.6	0
134	The Genetic Landscape of the Childhood Cancer Medulloblastoma. Science, 2011, 331, 435-439.	6.0	652
135	Integrating diverse genomic data using gene sets. Genome Biology, 2011, 12, R105.	13.9	52
136	False discovery rates in somatic mutation studies of cancer. Annals of Applied Statistics, 2011, 5, .	0.5	6
137	Modeling Liquid Association. Biometrics, 2011, 67, 133-141.	0.8	26
138	OnionTree XML: A Format to Exchange Gene-Related Probabilities. Journal of Biomolecular Structure and Dynamics, 2011, 29, 417-423.	2.0	0
139	Multiple diseases in carrier probability estimation: Accounting for surviving all cancers other than breast and ovary in BRCAPRO. Statistics in Medicine, 2008, 27, 4532-4548.	0.8	16
140	Adjustment uncertainty in effect estimation. Biometrika, 2008, 95, 635-651.	1.3	42
141	Multiple Model Evaluation Absent the Gold Standard Through Model Combination. Journal of the American Statistical Association, 2008, 103, 897-909.	1.8	4
142	Systematic Review: Gene Expression Profiling Assays in Early-Stage Breast Cancer. Annals of Internal Medicine, 2008, 148, 358.	2.0	135
143	Cross-study validation and combined analysis of gene expression microarray data. Biostatistics, 2007, 9, 333-354.	0.9	46
144	Validity of Models for Predicting BRCA1 and BRCA2 Mutations. Annals of Internal Medicine, 2007, 147, 441.	2.0	106

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145	Meta-Analysis ofBRCA1andBRCA2Penetrance. Journal of Clinical Oncology, 2007, 25, 1329-1333.	0.8	1,560
146	The Genomic Landscapes of Human Breast and Colorectal Cancers. Science, 2007, 318, 1108-1113.	6.0	3,049
147	Prediction of Germline Mutations and Cancer Risk in the Lynch Syndrome. JAMA - Journal of the American Medical Association, 2006, 296, 1479.	3.8	328
148	Gene Expression Profiling Reveals Reproducible Human Lung Adenocarcinoma Subtypes in Multiple Independent Patient Cohorts. Journal of Clinical Oncology, 2006, 24, 5079-5090.	0.8	263
149	Relationship Between Bayesian and Frequentist Sample Size Determination. American Statistician, 2005, 59, 79-87.	0.9	43
150	BayesMendel: an R Environment for Mendelian Risk Prediction. Statistical Applications in Genetics and Molecular Biology, 2004, 3, 1-19.	0.2	74
151	MergeMaid: R Tools for Merging and Cross-Study Validation of Gene Expression Data. Statistical Applications in Genetics and Molecular Biology, 2004, 3, 1-13.	0.2	24
152	A Cross-Study Comparison of Gene Expression Studies for the Molecular Classification of Lung Cancer. Clinical Cancer Research, 2004, 10, 2922-2927.	3.2	196
153	Optimal Sample Size for Multiple Testing. Journal of the American Statistical Association, 2004, 99, 990-1001.	1.8	198
154	Cross-Calibration of Stroke Disability Measures. Journal of the American Statistical Association, 2003, 98, 273-281.	1.8	7
155	Designing Follow-Up Times. Journal of the American Statistical Association, 2002, 97, 847-858.	1.8	8
156	Modeling and Optimization in Early Detection Programs with a Single Exam. Biometrics, 2002, 58, 30-36.	0.8	18
157	Bayesian Semiparametric Analysis of Developmental Toxicology Data. Biometrics, 2001, 57, 150-157.	0.8	20
158	Conjugate analysis of multivariate normal data with incomplete observations. Canadian Journal of Statistics, 2000, 28, 533-550.	0.6	10
159	Genetic Susceptibility and Survival: Application to Breast Cancer. Journal of the American Statistical Association, 2000, 95, 28-42.	1.8	17
160	Is Axillary Lymph Node Dissection Indicated for Early-Stage Breast Cancer? A Decision Analysis. Journal of Clinical Oncology, 1999, 17, 1465-1465.	0.8	41
161	A Bayesian Hierarchical Approach for Combining Case-Control and Prospective Studies. Biometrics, 1999, 55, 858-866.	0.8	20
162	A dirichlet process elaboration diagnostic for binomial goodness of fit. Test, 1998, 7, 133-145.	0.7	3

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163	Determining Carrier Probabilities for Breast Cancerâ€“Susceptibility Genes BRCA1 and BRCA2. American Journal of Human Genetics, 1998, 62, 145-158.	2.6	690
164	Effect of BRCA1 and BRCA2 on the Association Between Breast Cancer Risk and Family History. Journal of the National Cancer Institute, 1998, 90, 1824-1829.	3.0	102
165	Assessing the Benefits of Testing for Breast Cancer Susceptibility Genes: A Decision Analysis. Breast Disease, 1998, 10, 115-125.	0.4	6
166	Probability of Carrying a Mutation of Breast-Ovarian Cancer Gene BRCA1 Based on Family History. Journal of the National Cancer Institute, 1997, 89, 227-237.	3.0	344
167	Diagnostic Measures for Model Criticism. Journal of the American Statistical Association, 1996, 91, 753-762.	1.8	45
168	Prediction via Orthogonalized Model Mixing. Journal of the American Statistical Association, 1996, 91, 1197-1208.	1.8	94
169	Optimal Design via Curve Fitting of Monte Carlo Experiments. Journal of the American Statistical Association, 1995, 90, 1322-1330.	1.8	76
170	On Optimal Screening Ages. Journal of the American Statistical Association, 1993, 88, 622-628.	1.8	55
171	A Note on the Residual Entropy Function. Probability in the Engineering and Informational Sciences, 1993, 7, 413-420.	0.6	19
172	Minimax, information and ultrapessimism. Theory and Decision, 1992, 33, 241-252.	0.5	11
173	On Optimal Screening Ages. , 0, .		8
174	Diagnostic Measures for Model Criticism. , 0, .		15
175	Prediction via Orthogonalized Model Mixing. , 0, .		21
176	Genetic Susceptibility and Survival: Application to Breast Cancer. , 0, .		4