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List of Publications by Citations

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

109 papers	15,396 citations	39 h-index	118 g-index
118 ext. papers	20,337 ext. citations	8.8 avg, IF	6.42 L-index

#	Paper	IF	Citations
109	Topological domains in mammalian genomes identified by analysis of chromatin interactions. *Nature*, **2012**, 485, 376-80	50.4	4098
108	TIMER: A Web Server for Comprehensive Analysis of Tumor-Infiltrating Immune Cells. *Cancer Research*, **2017**, 77, e108-e110	10.1	1919
107	Genetics of rheumatoid arthritis contributes to biology and drug discovery. *Nature*, **2014**, 506, 376-81	50.4	1426
106	Comprehensive analyses of tumor immunity: implications for cancer immunotherapy. *Genome Biology*, **2016**, 17, 174	18.3	942
105	Sequential Monte Carlo Methods for Dynamic Systems. *Journal of the American Statistical Association*, **1998**, 93, 1032-1044	2.8	927
104	Sequential Monte Carlo Methods for Dynamic Systems		538
103	Sequential Imputations and Bayesian Missing Data Problems. *Journal of the American Statistical Association*, **1994**, 89, 278-288	2.8	502
102	The Collapsed Gibbs Sampler in Bayesian Computations with Applications to a Gene Regulation Problem. *Journal of the American Statistical Association*, **1994**, 89, 958-966	2.8	372
101	Sequence determinants of improved CRISPR sgRNA design. *Genome Research*, **2015**, 25, 1147-57	9.7	335
100	Gibbs motif sampling: detection of bacterial outer membrane protein repeats. *Protein Science*, **1995** , 4, 1618-32	6.3	333
99	Metropolized independent sampling with comparisons to rejection sampling and importance sampling. *Statistics and Computing*, **1996**, 6, 113-119	1.8	297
98	Sequential Imputations and Bayesian Missing Data Problems		201
97	Landscape of tumor-infiltrating T cell repertoire of human cancers. *Nature Genetics*, **2016**, 48, 725-32	36.3	193
96	The Multiple-Try Method and Local Optimization in Metropolis Sampling. *Journal of the American Statistical Association*, **2000**, 95, 121-134	2.8	193
95	Bayesian Models for Multiple Local Sequence Alignment and Gibbs Sampling Strategies. *Journal of the American Statistical Association*, **1995**, 90, 1156-1170	2.8	193
94	Linear Combinations of Multiple Diagnostic Markers. *Journal of the American Statistical Association*, **1993**, 88, 1350-1355	2.8	184
93	Parameter Expansion for Data Augmentation. *Journal of the American Statistical Association*, **1999**, 94, 1264-1274	2.8	182

92	Blind Deconvolution via Sequential Imputations. *Journal of the American Statistical Association*, **1995**, 90, 567-576	2.8	182
91	Extracting protein alignment models from the sequence database. *Nucleic Acids Research*, **1997**, 25, 1665-77	20.1	178
90	Quality control, modeling, and visualization of CRISPR screens with MAGeCK-VISPR. *Genome Biology*, **2015**, 16, 281	18.3	171
89	Sequential Monte Carlo Methods for Statistical Analysis of Tables. *Journal of the American Statistical Association*, **2005**, 100, 109-120	2.8	152
88	Bayesian inference of spatial organizations of chromosomes. *PLoS Computational Biology*, **2013**, 9, e1002893	5	140
87	Convergent regulatory evolution and loss of flight in paleognathous birds. *Science*, **2019**, 364, 74-78	33.3	103
86	Blind Deconvolution via Sequential Imputations		81
85	Expansion of biological pathways based on evolutionary inference. *Cell*, **2014**, 158, 213-25	56.2	75
84	Rejection Control and Sequential Importance Sampling. *Journal of the American Statistical Association*, **1998**, 93, 1022-1031	2.8	75
83	A Theoretical Framework for Sequential Importance Sampling with Resampling **2001**, 225-246		74
82	Bayesian Models for Multiple Local Sequence Alignment and Gibbs Sampling Strategies		67
81	Inference of transcriptional regulation in cancers. *Proceedings of the National Academy of Sciences of the United States of America*, **2015**, 112, 7731-6	11.5	59
80	The Collapsed Gibbs Sampler in Bayesian Computations with Applications to a Gene Regulation Problem		58
79	Landscape of B cell immunity and related immune evasion in human cancers. *Nature Genetics*, **2019**, 51, 560-567	36.3	56
78	Quantitative and functional interrogation of parent-of-origin allelic expression biases in the brain. *ELife*, **2015**, 4, e07860	8.9	53
77	A new sequential importance sampling method and its application to the two-dimensional hydrophobic–hydrophilic model. *Journal of Chemical Physics*, **2002**, 117, 3492-3498	3.9	53
76	Markovian Structures in Biological Sequence Alignments. *Journal of the American Statistical Association*, **1999**, 94, 1-15	2.8	50
75	Peskun's theorem and a modified discrete-state Gibbs sampler. *Biometrika*, **1996**, 83, 681-682	2	48

74	Discovery of Conserved Sequence Patterns Using a Stochastic Dictionary Model. *Journal of the American Statistical Association*, **2003**, 98, 55-66	2.8	42
73	Ultrasensitive detection of TCR hypervariable-region sequences in solid-tissue RNA-seq data. *Nature Genetics*, **2017**, 49, 482-483	36.3	41
72	Network analysis of gene essentiality in functional genomics experiments. *Genome Biology*, **2015**, 16, 239	18.3	41
71	Parameter Expansion for Data Augmentation		39
70	The Multiple-Try Method and Local Optimization in Metropolis Sampling		38
69	Exploring genetic associations with ceRNA regulation in the human genome. *Nucleic Acids Research*, **2017**, 45, 5653-5665	20.1	30
68	Revisit linear regression-based deconvolution methods for tumor gene expression data. *Genome Biology*, **2017**, 18, 127	18.3	30
67	Predicting regulatory variants with composite statistic. *Bioinformatics*, **2016**, 32, 2729-36	7.2	30
66	Linear Combinations of Multiple Diagnostic Markers		29
65	Bayesian Aggregation of Order-Based Rank Data. *Journal of the American Statistical Association*, **2014**, 109, 1023-1039	2.8	28
64	Monte Carlo Bayesian Signal Processing for Wireless Communications. *Journal of Signal Processing Systems*, **2002**, 30, 89-105		28
63	High-dimensional genomic data bias correction and data integration using MANCIE. *Nature Communications*, **2016**, 7, 11305	17.4	28
62	cepip: context-dependent epigenomic weighting for prioritization of regulatory variants and disease-associated genes. *Genome Biology*, **2017**, 18, 52	18.3	27
61	Genome-Scale Signatures of Gene Interaction from Compound Screens Predict Clinical Efficacy of Targeted Cancer Therapies. *Cell Systems*, **2018**, 6, 343-354.e5	10.6	23
60	Understanding spatial organizations of chromosomes via statistical analysis of Hi-C data. *Quantitative Biology*, **2013**, 1, 156-174	3.9	22
59	The distribution of genomic variations in human iPSCs is related to replication-timing reorganization during reprogramming. *Cell Reports*, **2014**, 7, 70-8	10.6	21
58	On learning strategies for evolutionary Monte Carlo. *Statistics and Computing*, **2007**, 17, 23-38	1.8	21
57	A Theory for Dynamic Weighting in Monte Carlo Computation. *Journal of the American Statistical Association*, **2001**, 96, 561-573	2.8	20

56	CLIC, a tool for expanding biological pathways based on co-expression across thousands of datasets. *PLoS Computational Biology*, **2017**, 13, e1005653	5	20
55	Markovian Structures in Biological Sequence Alignments		20
54	Rejection Control and Sequential Importance Sampling		18
53	Bayesian Detection of Convergent Rate Changes of Conserved Noncoding Elements on Phylogenetic Trees. *Molecular Biology and Evolution*, **2019**, 36, 1086-1100	8.3	17
52	Identifying Differentially Expressed Genes in Time Course Microarray Data. *Statistics in Biosciences*, **2009**, 1, 144-159	1.5	17
51	Risk Classification with an Adaptive Naive Bayes Kernel Machine Model. *Journal of the American Statistical Association*, **2015**, 110, 393-404	2.8	16
50	Statistical inference for time course RNA-Seq data using a negative binomial mixed-effect model. *BMC Bioinformatics*, **2016**, 17, 324	3.6	16
49	Bayesian Clustering of Transcription Factor Binding Motifs. *Journal of the American Statistical Association*, **2008**, 103, 188-200	2.8	14
48	Implementation of Estimating Function-Based Inference Procedures With Markov Chain Monte Carlo Samplers. *Journal of the American Statistical Association*, **2007**, 102, 881-888	2.8	14
47	Conformational sampling and structure prediction of multiple interacting loops in soluble and βbarrel membrane proteins using multi-loop distance-guided chain-growth Monte Carlo method. *Bioinformatics*, **2015**, 31, 2646-52	7.2	13
46	Determinants of transcription factor regulatory range. *Nature Communications*, **2020**, 11, 2472	17.4	13
45	A Multiresolution Method for Parameter Estimation of Diffusion Processes. *Journal of the American Statistical Association*, **2012**, 107, 1558-1574	2.8	12
44	On the unsupervised analysis of domain-specific Chinese texts. *Proceedings of the National Academy of Sciences of the United States of America*, **2016**, 113, 6154-9	11.5	12
43	Bayesian Inference for Assessing Effects of Email Marketing Campaigns. *Journal of Business and Economic Statistics*, **2018**, 36, 253-266	3.8	11
42	Personalized chemotherapy selection for breast cancer using gene expression profiles. *Scientific Reports*, **2017**, 7, 43294	4.9	10
41	A RIPK1-regulated inflammatory microglial state in amyotrophic lateral sclerosis. *Proceedings of the National Academy of Sciences of the United States of America*, **2021**, 118,	11.5	10
40	Convergent regulatory evolution and the origin of flightlessness in palaeognathous birds		9
39	MetaGen: reference-free learning with multiple metagenomic samples. *Genome Biology*, **2017**, 18, 187	18.3	8

38	On Delay Tomography: Fast Algorithms and Spatially Dependent Models. *IEEE Transactions on Signal Processing*, **2012**, 60, 5685-5697	4.8	8
37	Robust Variable and Interaction Selection for Logistic Regression and General Index Models. *Journal of the American Statistical Association*, **2019**, 114, 271-286	2.8	8
36	Fast de novo discovery of low-energy protein loop conformations. *Proteins: Structure, Function and Bioinformatics*, **2017**, 85, 1402-1412	4.2	7
35	Reduction of mNAT1/hNAT2 Contributes to Cerebral Endothelial Necroptosis and Aβ Accumulation in Alzheimer's Disease. *Cell Reports*, **2020**, 33, 108447	10.6	7
34	Signed support recovery for single index models in high-dimensions. *Annals of Mathematical Sciences and Applications*, **2016**, 1, 379-426	1.3	7
33	Text Summarization Using FrameNet-Based Semantic Graph Model. *Scientific Programming*, **2016**, 2016, 1-10	1.4	6
32	Evaluation of immune repertoire inference methods from RNA-seq data. *Nature Biotechnology*, **2018**, 36, 1034	44.5	5
31	Evolutionary Monte Carlo Methods for Clustering. *Journal of Computational and Graphical Statistics*, **2007**, 16, 855-876	1.4	4
30	A hotspots analysis-relation discovery representation model for revealing diabetes mellitus and obesity. *BMC Systems Biology*, **2018**, 12, 116	3.5	4
29	Rasch Model and Its Extensions for Analysis of Aphasic Deficits in Syntactic Comprehension. *Journal of the American Statistical Association*, **2011**, 106, 1304-1316	2.8	3
28	SIMPLEs: a single-cell RNA sequencing imputation strategy preserving gene modules and cell clusters variation. *NAR Genomics and Bioinformatics*, **2020**, 2, lqaa077	3.7	3
27	An Extended Mallows Model for Ranked Data Aggregation. *Journal of the American Statistical Association*, **2020**, 115, 730-746	2.8	3
26	Wang-Landau algorithm as stochastic optimization and its acceleration. *Physical Review E*, **2020**, 101, 033301	2.4	2
25	On parallelizable Markov chain Monte Carlo algorithms with waste-recycling. *Statistics and Computing*, **2018**, 28, 1073-1081	1.8	2
24	Randomization Inference for Peer Effects. *Journal of the American Statistical Association*, **2019**, 114, 1651-1664	2.8	2
23	Bayesian Partition Models for Identifying Expression Quantitative Trait Loci. *Journal of the American Statistical Association*, **2015**, 110, 1350-1361	2.8	2
22	NGM: Neural Gaussian Mirror for Controlled Feature Selection in Neural Networks **2020**,		2
21	Monte Carlo Approximation of Bayes Factors via Mixing With Surrogate Distributions. *Journal of the American Statistical Association*, **2020**, 1-16	2.8	2

20	Systems biology analysis reveals new insights into invasive lung cancer. *BMC Systems Biology*, **2018**, 12, 117	3.5	2
19	Neuronized Priors for Bayesian Sparse Linear Regression. *Journal of the American Statistical Association*,1-16	2.8	2
18	False Discovery Rate Control via Data Splitting. *Journal of the American Statistical Association*,1-38	2.8	2
17	Inferring Spatial Organization of Individual Topologically Associated Domains via Piecewise Helical Model. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, **2020**, 17, 647-656	3	1
16	Long-term drug costs per life-month gained associated with first-line treatments for unresectable or metastatic melanoma. *Experimental Hematology and Oncology*, **2015**, 5, 9	7.8	1
15	Relation discovery and hotspots analysis on diabetes mellitus and obesity with representation model **2017**,		1
14	dslice: an R package for nonparametric testing of associations with application in QTL and gene set analysis. *Bioinformatics*, **2015**, 31, 1842-4	7.2	1
13	Discussions on A Bayesian Approach to DNA Sequence Segmentation *Biometrics*, **2004**, 60, 582-583	1.8	1
12	A data-adaptive Bayesian regression approach for polygenic risk prediction.. *Bioinformatics*, **2022**,	7.2	1
11	-Regularized Least Squares for Support Recovery of High Dimensional Single Index Models with Gaussian Designs. *Journal of Machine Learning Research*, **2016**, 17, 2976-3012	28.6	1
10	Interpretable selection and visualization of features and interactions using Bayesian forests. *Statistics and Its Interface*, **2018**, 11, 503-513	0.4	1
9	Controlling False Discovery Rate Using Gaussian Mirrors. *Journal of the American Statistical Association*,1-20	2.8	1
8	MiRACLe: an individual-specific approach to improve microRNA-target prediction based on a random contact model. *Briefings in Bioinformatics*, **2021**, 22,	13.4	1
7	Stratification and optimal resampling for sequential Monte Carlo. *Biometrika*,	2	1
6	Limited memory optimizes cooperation in social dilemma experiments. *Royal Society Open Science*, **2021**, 8, 210653	3.3	1
5	New Algorithms in RNA Structure Prediction Based on BHG. *International Journal of Pattern Recognition and Artificial Intelligence*, **2020**, 34, 2050031	1.1	0
4	Partition Mallows Model and Its Inference for Rank Aggregation. *Journal of the American Statistical Association*,1-17	2.8	0
3	Bayesian Methods in Biological Sequence Analysis **2008**, 67-96		

2	Kernel-based Partial Permutation Test for Detecting Heterogeneous Functional Relationship. *Journal of the American Statistical Association*,1-50	2.8
1	Analysis of ChIP-chip Data on Genome Tiling Microarrays. *Frontiers of Statistics*, **2009**, 239-257	