

Jun S Liu

List of Publications by Year in descending order

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Version: 2024-02-01

114
papers

23,295
citations

109137

35
h-index

40881

93
g-index

118
all docs

118
docs citations

118
times ranked

29169
citing authors

#	ARTICLE	IF	CITATIONS
1	Topological domains in mammalian genomes identified by analysis of chromatin interactions. <i>Nature</i> , 2012, 485, 376-380.	13.7	5,786
2	TIMER: A Web Server for Comprehensive Analysis of Tumor-Infiltrating Immune Cells. <i>Cancer Research</i> , 2017, 77, e108-e110.	0.4	4,049
3	Genetics of rheumatoid arthritis contributes to biology and drug discovery. <i>Nature</i> , 2014, 506, 376-381.	13.7	1,974
4	Comprehensive analyses of tumor immunity: implications for cancer immunotherapy. <i>Genome Biology</i> , 2016, 17, 174.	3.8	1,768
5	Sequential Monte Carlo Methods for Dynamic Systems. <i>Journal of the American Statistical Association</i> , 1998, 93, 1032-1044.	1.8	1,140
6	Sequential Monte Carlo Methods for Dynamic Systems. , 0, .		920
7	Sequential Imputations and Bayesian Missing Data Problems. <i>Journal of the American Statistical Association</i> , 1994, 89, 278-288.	1.8	665
8	Sequence determinants of improved CRISPR sgRNA design. <i>Genome Research</i> , 2015, 25, 1147-1157.	2.4	514
9	The Collapsed Gibbs Sampler in Bayesian Computations with Applications to a Gene Regulation Problem. <i>Journal of the American Statistical Association</i> , 1994, 89, 958-966.	1.8	504
10	Metropolized independent sampling with comparisons to rejection sampling and importance sampling. <i>Statistics and Computing</i> , 1996, 6, 113-119.	0.8	381
11	Gibbs motif sampling: Detection of bacterial outer membrane protein repeats. <i>Protein Science</i> , 1995, 4, 1618-1632.	3.1	371
12	Quality control, modeling, and visualization of CRISPR screens with MAGeCK-VISPR. <i>Genome Biology</i> , 2015, 16, 281.	3.8	330
13	Landscape of tumor-infiltrating T cell repertoire of human cancers. <i>Nature Genetics</i> , 2016, 48, 725-732.	9.4	288
14	Sequential Imputations and Bayesian Missing Data Problems. , 0, .		262
15	Blind Deconvolution via Sequential Imputations. <i>Journal of the American Statistical Association</i> , 1995, 90, 567-576.	1.8	252
16	The Multiple-Try Method and Local Optimization in Metropolis Sampling. <i>Journal of the American Statistical Association</i> , 2000, 95, 121-134.	1.8	245
17	Parameter Expansion for Data Augmentation. <i>Journal of the American Statistical Association</i> , 1999, 94, 1264-1274.	1.8	236
18	Bayesian Models for Multiple Local Sequence Alignment and Gibbs Sampling Strategies. <i>Journal of the American Statistical Association</i> , 1995, 90, 1156-1170.	1.8	235

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19	Sequential Monte Carlo Methods for Statistical Analysis of Tables. Journal of the American Statistical Association, 2005, 100, 109-120.	1.8	231
20	Linear Combinations of Multiple Diagnostic Markers. Journal of the American Statistical Association, 1993, 88, 1350-1355.	1.8	224
21	Extracting protein alignment models from the sequence database. Nucleic Acids Research, 1997, 25, 1665-1677.	6.5	206
22	Convergent regulatory evolution and loss of flight in paleognathous birds. Science, 2019, 364, 74-78.	6.0	189
23	Bayesian Inference of Spatial Organizations of Chromosomes. PLoS Computational Biology, 2013, 9, e1002893.	1.5	188
24	Landscape of B cell immunity and related immune evasion in human cancers. Nature Genetics, 2019, 51, 560-567.	9.4	115
25	Expansion of Biological Pathways Based on Evolutionary Inference. Cell, 2014, 158, 213-225.	13.5	107
26	A Theoretical Framework for Sequential Importance Sampling with Resampling. , 2001, , 225-246.		106
27	Blind Deconvolution via Sequential Imputations. , 0, .		103
28	Rejection Control and Sequential Importance Sampling. Journal of the American Statistical Association, 1998, 93, 1022-1031.	1.8	99
29	Inference of transcriptional regulation in cancers. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 7731-7736.	3.3	84
30	Bayesian Models for Multiple Local Sequence Alignment and Gibbs Sampling Strategies. , 0, .		77
31	Quantitative and functional interrogation of parent-of-origin allelic expression biases in the brain. ELife, 2015, 4, e07860.	2.8	75
32	Ultrasensitive detection of TCR hypervariable-region sequences in solid-tissue RNA-seq data. Nature Genetics, 2017, 49, 482-483.	9.4	66
33	The Collapsed Gibbs Sampler in Bayesian Computations with Applications to a Gene Regulation Problem. , 0, .		64
34	Miscellanea. Peskun's theorem and a modified discrete-state Gibbs sampler. Biometrika, 1996, 83, 681-682.	1.3	60
35	Markovian Structures in Biological Sequence Alignments. Journal of the American Statistical Association, 1999, 94, 1-15.	1.8	60
36	A new sequential importance sampling method and its application to the two-dimensional hydrophobic-hydrophilic model. Journal of Chemical Physics, 2002, 117, 3492-3498.	1.2	58

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37	High-dimensional genomic data bias correction and data integration using MANCIE. <i>Nature Communications</i> , 2016, 7, 11305.	5.8	52
38	Discovery of Conserved Sequence Patterns Using a Stochastic Dictionary Model. <i>Journal of the American Statistical Association</i> , 2003, 98, 55-66.	1.8	51
39	Parameter Expansion for Data Augmentation. , 0, .		51
40	Network analysis of gene essentiality in functional genomics experiments. <i>Genome Biology</i> , 2015, 16, 239.	3.8	50
41	Monte Carlo Bayesian Signal Processing for Wireless Communications. <i>Journal of Signal Processing Systems</i> , 2002, 30, 89-105.	1.0	46
42	Revisit linear regression-based deconvolution methods for tumor gene expression data. <i>Genome Biology</i> , 2017, 18, 127.	3.8	45
43	The Multiple-Try Method and Local Optimization in Metropolis Sampling. , 0, .		42
44	Bayesian Aggregation of Order-Based Rank Data. <i>Journal of the American Statistical Association</i> , 2014, 109, 1023-1039.	1.8	40
45	Predicting regulatory variants with composite statistic. <i>Bioinformatics</i> , 2016, 32, 2729-2736.	1.8	40
46	Genome-Scale Signatures of Gene Interaction from Compound Screens Predict Clinical Efficacy of Targeted Cancer Therapies. <i>Cell Systems</i> , 2018, 6, 343-354.e5.	2.9	40
47	Exploring genetic associations with ceRNA regulation in the human genome. <i>Nucleic Acids Research</i> , 2017, 45, 5653-5665.	6.5	39
48	Bayesian Detection of Convergent Rate Changes of Conserved Noncoding Elements on Phylogenetic Trees. <i>Molecular Biology and Evolution</i> , 2019, 36, 1086-1100.	3.5	39
49	A RIPK1-regulated inflammatory microglial state in amyotrophic lateral sclerosis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	36
50	Linear Combinations of Multiple Diagnostic Markers. , 0, .		36
51	cepip: context-dependent epigenomic weighting for prioritization of regulatory variants and disease-associated genes. <i>Genome Biology</i> , 2017, 18, 52.	3.8	33
52	CLIC, a tool for expanding biological pathways based on co-expression across thousands of datasets. <i>PLoS Computational Biology</i> , 2017, 13, e1005653.	1.5	30
53	Understanding spatial organizations of chromosomes via statistical analysis of Hi-C data. <i>Quantitative Biology</i> , 2013, 1, 156-174.	0.3	29
54	Determinants of transcription factor regulatory range. <i>Nature Communications</i> , 2020, 11, 2472.	5.8	28

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55	A Theory for Dynamic Weighting in Monte Carlo Computation. <i>Journal of the American Statistical Association</i> , 2001, 96, 561-573.	1.8	26
56	Reduction of mNAT1/hNAT2 Contributes to Cerebral Endothelial Necroptosis and A β Accumulation in Alzheimer's Disease. <i>Cell Reports</i> , 2020, 33, 108447.	2.9	26
57	On learning strategies for evolutionary Monte Carlo. <i>Statistics and Computing</i> , 2007, 17, 23-38.	0.8	24
58	The Distribution of Genomic Variations in Human iPSCs Is Related to Replication-Timing Reorganization during Reprogramming. <i>Cell Reports</i> , 2014, 7, 70-78.	2.9	24
59	Implementation of Estimating Function-Based Inference Procedures With Markov Chain Monte Carlo Samplers. <i>Journal of the American Statistical Association</i> , 2007, 102, 881-888.	1.8	21
60	Statistical inference for time course RNA-Seq data using a negative binomial mixed-effect model. <i>BMC Bioinformatics</i> , 2016, 17, 324.	1.2	21
61	On the unsupervised analysis of domain-specific Chinese texts. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 6154-6159.	3.3	21
62	Markovian Structures in Biological Sequence Alignments. , 0, .		21
63	Risk Classification With an Adaptive Naive Bayes Kernel Machine Model. <i>Journal of the American Statistical Association</i> , 2015, 110, 393-404.	1.8	20
64	Rejection Control and Sequential Importance Sampling. , 0, .		20
65	Identifying Differentially Expressed Genes in Time Course Microarray Data. <i>Statistics in Biosciences</i> , 2009, 1, 144-159.	0.6	19
66	Robust Variable and Interaction Selection for Logistic Regression and General Index Models. <i>Journal of the American Statistical Association</i> , 2019, 114, 271-286.	1.8	19
67	Bayesian Clustering of Transcription Factor Binding Motifs. <i>Journal of the American Statistical Association</i> , 2008, 103, 188-200.	1.8	17
68	False Discovery Rate Control via Data Splitting. <i>Journal of the American Statistical Association</i> , 2023, 118, 2503-2520.	1.8	17
69	Conformational sampling and structure prediction of multiple interacting loops in soluble and α -barrel membrane proteins using multi-loop distance-guided chain-growth Monte Carlo method. <i>Bioinformatics</i> , 2015, 31, 2646-2652.	1.8	16
70	Bayesian Inference for Assessing Effects of Email Marketing Campaigns. <i>Journal of Business and Economic Statistics</i> , 2018, 36, 253-266.	1.8	16
71	A Multiresolution Method for Parameter Estimation of Diffusion Processes. <i>Journal of the American Statistical Association</i> , 2012, 107, 1558-1574.	1.8	14
72	Personalized chemotherapy selection for breast cancer using gene expression profiles. <i>Scientific Reports</i> , 2017, 7, 43294.	1.6	13

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73	Controlling False Discovery Rate Using Gaussian Mirrors. <i>Journal of the American Statistical Association</i> , 2023, 118, 222-241.	1.8	13
74	MetaGen: reference-free learning with multiple metagenomic samples. <i>Genome Biology</i> , 2017, 18, 187.	3.8	12
75	On Delay Tomography: Fast Algorithms and Spatially Dependent Models. <i>IEEE Transactions on Signal Processing</i> , 2012, 60, 5685-5697.	3.2	11
76	Fast de novo discovery of low-energy protein loop conformations. <i>Proteins: Structure, Function and Bioinformatics</i> , 2017, 85, 1402-1412.	1.5	10
77	Randomization Inference for Peer Effects. <i>Journal of the American Statistical Association</i> , 2019, 114, 1651-1664.	1.8	9
78	Text Summarization Using FrameNet-Based Semantic Graph Model. <i>Scientific Programming</i> , 2016, 2016, 1-10.	0.5	8
79	An Extended Mallows Model for Ranked Data Aggregation. <i>Journal of the American Statistical Association</i> , 2020, 115, 730-746.	1.8	8
80	Signed support recovery for single index models in high-dimensions. <i>Annals of Mathematical Sciences and Applications</i> , 2016, 1, 379-426.	0.2	8
81	Evaluation of immune repertoire inference methods from RNA-seq data. <i>Nature Biotechnology</i> , 2018, 36, 1034-1034.	9.4	7
82	Neuronized Priors for Bayesian Sparse Linear Regression. <i>Journal of the American Statistical Association</i> , 2022, 117, 1695-1710.	1.8	7
83	Evolutionary Monte Carlo Methods for Clustering. <i>Journal of Computational and Graphical Statistics</i> , 2007, 16, 855-876.	0.9	6
84	On parallelizable Markov chain Monte Carlo algorithms with waste-recycling. <i>Statistics and Computing</i> , 2018, 28, 1073-1081.	0.8	6
85	A hotspots analysis-relation discovery representation model for revealing diabetes mellitus and obesity. <i>BMC Systems Biology</i> , 2018, 12, 116.	3.0	6
86	SIMPLEs: a single-cell RNA sequencing imputation strategy preserving gene modules and cell clusters variation. <i>NAR Genomics and Bioinformatics</i> , 2020, 2, lqaa077.	1.5	6
87	Monte Carlo Approximation of Bayes Factors via Mixing With Surrogate Distributions. <i>Journal of the American Statistical Association</i> , 2020, , 1-16.	1.8	5
88	NGM: Neural Gaussian Mirror for Controlled Feature Selection in Neural Networks. , 2020, , .		5
89	Limited memory optimizes cooperation in social dilemma experiments. <i>Royal Society Open Science</i> , 2021, 8, 210653.	1.1	4
90	Rasch Model and Its Extensions for Analysis of Aphasic Deficits in Syntactic Comprehension. <i>Journal of the American Statistical Association</i> , 2011, 106, 1304-1316.	1.8	3

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91	Stratification and optimal resampling for sequential Monte Carlo. <i>Biometrika</i> , 2022, 109, 181-194.	1.3	3
92	Openness weighted association studies: leveraging personal genome information to prioritize non-coding variants. <i>Bioinformatics</i> , 2021, 37, 4737-4743.	1.8	3
93	Bayesian Partition Models for Identifying Expression Quantitative Trait Loci. <i>Journal of the American Statistical Association</i> , 2015, 110, 1350-1361.	1.8	2
94	Systems biology analysis reveals new insights into invasive lung cancer. <i>BMC Systems Biology</i> , 2018, 12, 117.	3.0	2
95	Wang-Landau algorithm as stochastic optimization and its acceleration. <i>Physical Review E</i> , 2020, 101, 033301.	0.8	2
96	Partitioning Mallows Model and Its Inference for Rank Aggregation. <i>Journal of the American Statistical Association</i> , 2023, 118, 343-359.	1.8	2
97	Interpretable selection and visualization of features and interactions using Bayesian forests. <i>Statistics and Its Interface</i> , 2018, 11, 503-513.	0.2	2
98	-Regularized Least Squares for Support Recovery of High Dimensional Single Index Models with Gaussian Designs. <i>Journal of Machine Learning Research</i> , 2016, 17, 2976-3012.	62.4	2
99	Bayesian Analysis of Rank Data with Covariates and Heterogeneous Rankers. <i>Statistical Science</i> , 2022, 37, .	1.6	2
100	Discussions on a Bayesian Approach to DNA Sequence Segmentation. <i>Biometrics</i> , 2004, 60, 582-583.	0.8	1
101	Long-term drug costs per life-month gained associated with first-line treatments for unresectable or metastatic melanoma. <i>Experimental Hematology and Oncology</i> , 2015, 5, 9.	2.0	1
102	dslice: an R package for nonparametric testing of associations with application in QTL and gene set analysis. <i>Bioinformatics</i> , 2015, 31, 1842-1844.	1.8	1
103	Relation discovery and hotspots analysis on diabetes mellitus and obesity with representation model. , 2017, , .		1
104	Inferring Spatial Organization of Individual Topologically Associated Domains via Piecewise Helical Model. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2019, 17, 1-1.	1.9	1
105	MiRACLE: an individual-specific approach to improve microRNA-target prediction based on a random contact model. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	1
106	On Posterior Consistency of Bayesian Factor Models in High Dimensions. <i>Bayesian Analysis</i> , 2021, -1, .	1.6	1
107	New Algorithms in RNA Structure Prediction Based on BHG. <i>International Journal of Pattern Recognition and Artificial Intelligence</i> , 2020, 34, 2050031.	0.7	1
108	A data-adaptive Bayesian regression approach for polygenic risk prediction. <i>Bioinformatics</i> , 2022, 38, 1938-1946.	1.8	1

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109	Bayesian Methods in Biological Sequence Analysis. , 2008, , 67-96.		0
110	An Integrating Analysis Reveals Key Regulatory Networks in Breast Cancer. , 2019, , .		0
111	IMMIGRATE: A Margin-Based Feature Selection Method with Interaction Terms. Entropy, 2020, 22, 291.	1.1	0
112	Analysis of ChIP-chip Data on Genome Tiling Microarrays. Frontiers of Statistics, 2009, , 239-257.	0.2	0
113	Kernel-Based Partial Permutation Test for Detecting Heterogeneous Functional Relationship. Journal of the American Statistical Association, 2023, 118, 1429-1447.	1.8	0
114	Multi-Cell-Type Openness-Weighted Association Studies for Trait-Associated Genomic Segments Prioritization. Genes, 2022, 13, 1220.	1.0	0