

Jun S Liu

List of Publications by Year in descending order

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Version: 2024-02-01

83
papers

25,563
citations

61857

43
h-index

69108

77
g-index

85
all docs

85
docs citations

85
times ranked

33213
citing authors

#	ARTICLE	IF	CITATIONS
1	Stratification and optimal resampling for sequential Monte Carlo. <i>Biometrika</i> , 2022, 109, 181-194.	1.3	3
2	Neuronized Priors for Bayesian Sparse Linear Regression. <i>Journal of the American Statistical Association</i> , 2022, 117, 1695-1710.	1.8	7
3	Bayesian Analysis of Rank Data with Covariates and Heterogeneous Rankers. <i>Statistical Science</i> , 2022, 37, .	1.6	2
4	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
5	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
6	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
7	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
8	Determinants of transcription factor regulatory range. <i>Nature Communications</i> , 2020, 11, 2472.	5.8	28
9	Computational Deconvolution of Tumor-Infiltrating Immune Components with Bulk Tumor Gene Expression Data. <i>Methods in Molecular Biology</i> , 2020, 2120, 249-262.	0.4	18
10	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
11	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
12	Bayesian hidden Markov tree models for clustering genes with shared evolutionary history. <i>Annals of Applied Statistics</i> , 2019, 13, .	0.5	6
13	Convergent regulatory evolution and loss of flight in paleognathous birds. <i>Science</i> , 2019, 364, 74-78.	6.0	189
14	Landscape of B cell immunity and related immune evasion in human cancers. <i>Nature Genetics</i> , 2019, 51, 560-567.	9.4	115
15	Exploring the conformational space for protein folding with sequential Monte Carlo. <i>Annals of Applied Statistics</i> , 2018, 12, .	0.5	3
16	cepip: context-dependent epigenomic weighting for prioritization of regulatory variants and disease-associated genes. <i>Genome Biology</i> , 2017, 18, 52.	3.8	33
17	TIMER: A Web Server for Comprehensive Analysis of Tumor-Infiltrating Immune Cells. <i>Cancer Research</i> , 2017, 77, e108-e110.	0.4	4,049
18	Revisit linear regression-based deconvolution methods for tumor gene expression data. <i>Genome Biology</i> , 2017, 18, 127.	3.8	45

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19	Comprehensive analyses of tumor immunity: implications for cancer immunotherapy. <i>Genome Biology</i> , 2016, 17, 174.	3.8	1,768
20	Landscape of tumor-infiltrating T cell repertoire of human cancers. <i>Nature Genetics</i> , 2016, 48, 725-732.	9.4	288
21	Quality control, modeling, and visualization of CRISPR screens with MAGeCK-VISPR. <i>Genome Biology</i> , 2015, 16, 281.	3.8	330
22	Network analysis of gene essentiality in functional genomics experiments. <i>Genome Biology</i> , 2015, 16, 239.	3.8	50
23	MAGeCK enables robust identification of essential genes from genome-scale CRISPR/Cas9 knockout screens. <i>Genome Biology</i> , 2014, 15, 554.	3.8	1,614
24	Genetics of rheumatoid arthritis contributes to biology and drug discovery. <i>Nature</i> , 2014, 506, 376-381.	13.7	1,974
25	Association Pattern Discovery Via Theme Dictionary Models. <i>Journal of the Royal Statistical Society Series B: Statistical Methodology</i> , 2014, 76, 319-347.	1.1	7
26	Expansion of Biological Pathways Based on Evolutionary Inference. <i>Cell</i> , 2014, 158, 213-225.	13.5	107
27	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
28	Understanding spatial organizations of chromosomes via statistical analysis of Hi-C data. <i>Quantitative Biology</i> , 2013, 1, 156-174.	0.3	29
29	Bayesian hierarchical model of protein-binding microarray k-mer data reduces noise and identifies transcription factor subclasses and preferred k-mers. <i>Bioinformatics</i> , 2013, 29, 1390-1398.	1.8	16
30	Lookahead Strategies for Sequential Monte Carlo. <i>Statistical Science</i> , 2013, 28, .	1.6	35
31	Bayesian Inference of Spatial Organizations of Chromosomes. <i>PLoS Computational Biology</i> , 2013, 9, e1002893.	1.5	188
32	Statistical Methods in Bioinformatics. , 2013, , 101-149.		0
33	Cooperation between Polycomb and androgen receptor during oncogenic transformation. <i>Genome Research</i> , 2012, 22, 322-331.	2.4	122
34	Topological domains in mammalian genomes identified by analysis of chromatin interactions. <i>Nature</i> , 2012, 485, 376-380.	13.7	5,786
35	Nonparametric hierarchical Bayes analysis of binomial data via Bernstein polynomial priors. <i>Canadian Journal of Statistics</i> , 2012, 40, 328-344.	0.6	3
36	Statistical Learning and Modeling of TF-DNA Binding. , 2011, , 55-72.		0

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37	The EM Algorithm and the Rise of Computational Biology. <i>Statistical Science</i> , 2010, 25, .	1.6	7
38	Tmod: toolbox of motif discovery. <i>Bioinformatics</i> , 2010, 26, 405-407.	1.8	18
39	Bayesian Methods in Biological Sequence Analysis. , 2008, , 67-96.		0
40	Extracting sequence features to predict proteinâ€“DNA interactions: a comparative study. <i>Nucleic Acids Research</i> , 2008, 36, 4137-4148.	6.5	40
41	Genomic Sequence Is Highly Predictive of Local Nucleosome Depletion. <i>PLoS Computational Biology</i> , 2008, 4, e13.	1.5	156
42	On learning strategies for evolutionary Monte Carlo. <i>Statistics and Computing</i> , 2007, 17, 23-38.	0.8	24
43	Statistical assessment of the global regulatory role of histone acetylation in <i>Saccharomyces cerevisiae</i> . <i>Genome Biology</i> , 2006, 7, R70.	13.9	24
44	A Coalescence-Guided Hierarchical Bayesian Method for Haplotype Inference. <i>American Journal of Human Genetics</i> , 2006, 79, 313-322.	2.6	26
45	Monte Carlo sampling of near-native structures of proteins with applications. <i>Proteins: Structure, Function and Bioinformatics</i> , 2006, 66, 61-68.	1.5	20
46	On Side-Chain Conformational Entropy of Proteins. <i>PLoS Computational Biology</i> , 2006, 2, e168.	1.5	51
47	Stopping-time resampling for sequential Monte Carlo methods. <i>Journal of the Royal Statistical Society Series B: Statistical Methodology</i> , 2005, 67, 199-217.	1.1	23
48	BEST: Binding-site Estimation Suite of Tools. <i>Bioinformatics</i> , 2005, 21, 2909-2911.	1.8	46
49	A boosting approach for motif modeling using ChIP-chip data. <i>Bioinformatics</i> , 2005, 21, 2636-2643.	1.8	54
50	Sequential Monte Carlo Methods for Statistical Analysis of Tables. <i>Journal of the American Statistical Association</i> , 2005, 100, 109-120.	1.8	231
51	Defining a Centromere-like Element in <i>Bacillus subtilis</i> by Identifying the Binding Sites for the Chromosome-Anchoring Protein RacA. <i>Molecular Cell</i> , 2005, 17, 773-782.	4.5	93
52	Computational Discovery of Gene Regulatory Binding Motifs: A Bayesian Perspective. <i>Statistical Science</i> , 2004, 19, 188.	1.6	62
53	BioOptimizer: a Bayesian scoring function approach to motif discovery. <i>Bioinformatics</i> , 2004, 20, 1557-1564.	1.8	88
54	Modeling within-motif dependence for transcription factor binding site predictions. <i>Bioinformatics</i> , 2004, 20, 909-916.	1.8	129

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55	A suite of web-based programs to search for transcriptional regulatory motifs. <i>Nucleic Acids Research</i> , 2004, 32, W204-W207.	6.5	30
56	Haplotype Block Partitioning and Tag SNP Selection Using Genotype Data and Their Applications to Association Studies. <i>Genome Research</i> , 2004, 14, 908-916.	2.4	143
57	Monte Carlo Strategies in Scientific Computing. Springer Series in Statistics, 2004, , .	0.9	531
58	The Program of Gene Transcription for a Single Differentiating Cell Type during Sporulation in <i>Bacillus subtilis</i> . <i>PLoS Biology</i> , 2004, 2, e328.	2.6	308
59	Incorporating Genotyping Uncertainty in Haplotype Inference for Single-Nucleotide Polymorphisms. <i>American Journal of Human Genetics</i> , 2004, 74, 495-510.	2.6	45
60	Haplotype Inference and Its Application in Linkage Disequilibrium Mapping. <i>Lecture Notes in Computer Science</i> , 2004, , 48-61.	1.0	2
61	Dynamic Programming Algorithms for Haplotype Block Partitioning and Tag SNP Selection Using Haplotype Data or Genotype Data. <i>Lecture Notes in Computer Science</i> , 2004, , 96-112.	1.0	0
62	The Spo0A regulon of <i>Bacillus subtilis</i> . <i>Molecular Microbiology</i> , 2003, 50, 1683-1701.	1.2	466
63	Haplotype Information and Linkage Disequilibrium Mapping for Single Nucleotide Polymorphisms. <i>Genome Research</i> , 2003, 13, 2112-2117.	2.4	34
64	Integrating regulatory motif discovery and genome-wide expression analysis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 3339-3344.	3.3	319
65	A new sequential importance sampling method and its application to the two-dimensional hydrophobic-hydrophilic model. <i>Journal of Chemical Physics</i> , 2002, 117, 3492-3498.	1.2	58
66	Monte Carlo Bayesian Signal Processing for Wireless Communications. , 2002, , 89-105.		4
67	Bayesian Haplotype Inference for Multiple Linked Single-Nucleotide Polymorphisms. <i>American Journal of Human Genetics</i> , 2002, 70, 157-169.	2.6	591
68	Partition-Ligation-Expectation-Maximization Algorithm for Haplotype Inference with Single-Nucleotide Polymorphisms. <i>American Journal of Human Genetics</i> , 2002, 71, 1242-1247.	2.6	458
69	An algorithm for finding protein-DNA binding sites with applications to chromatin-immunoprecipitation microarray experiments. <i>Nature Biotechnology</i> , 2002, 20, 835-839.	9.4	617
70	Monte Carlo Bayesian Signal Processing for Wireless Communications. <i>Journal of Signal Processing Systems</i> , 2002, 30, 89-105.	1.0	46
71	Sequential importance sampling for nonparametric Bayes models: The next generation. <i>Canadian Journal of Statistics</i> , 1999, 27, 251-267.	0.6	128
72	Parameter Expansion for Data Augmentation. <i>Journal of the American Statistical Association</i> , 1999, 94, 1264-1274.	1.8	236

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73	Markovian Structures in Biological Sequence Alignments. Journal of the American Statistical Association, 1999, 94, 1-15.	1.8	60
74	Sequential Monte Carlo Methods for Dynamic Systems. Journal of the American Statistical Association, 1998, 93, 1032-1044.	1.8	1,140
75	Rejection Control and Sequential Importance Sampling. Journal of the American Statistical Association, 1998, 93, 1022-1031.	1.8	99
76	Predictive Updating Methods with Application to Bayesian Classification. Journal of the Royal Statistical Society Series B: Methodological, 1996, 58, 397-415.	0.8	12
77	Nonparametric hierarchical Bayes via sequential imputations. Annals of Statistics, 1996, 24, 911.	1.4	125
78	Statistical inference and Monte Carlo algorithms. Test, 1996, 5, 249-344.	0.7	29
79	Metropolized independent sampling with comparisons to rejection sampling and importance sampling. Statistics and Computing, 1996, 6, 113-119.	0.8	381
80	Bayesian Models for Multiple Local Sequence Alignment and Gibbs Sampling Strategies. Journal of the American Statistical Association, 1995, 90, 1156-1170.	1.8	235
81	Blind Deconvolution via Sequential Imputations. Journal of the American Statistical Association, 1995, 90, 567-576.	1.8	252
82	Sequential Imputations and Bayesian Missing Data Problems. Journal of the American Statistical Association, 1994, 89, 278-288.	1.8	665
83	The Collapsed Gibbs Sampler in Bayesian Computations with Applications to a Gene Regulation Problem. Journal of the American Statistical Association, 1994, 89, 958-966.	1.8	504