

Jun S Liu

List of Publications by Year in descending order

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Version: 2024-02-01

83
papers

25,563
citations

61984

43
h-index

66911

78
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.	2.4	3
2	Neuronized Priors for Bayesian Sparse Linear Regression. <i>Journal of the American Statistical Association</i> , 2022, 117, 1695-1710.	3.1	7
3	Bayesian Analysis of Rank Data with Covariates and Heterogeneous Rankers. <i>Statistical Science</i> , 2022, 37, .	2.8	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, .	7.1	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.	3.2	6
6	Monte Carlo Approximation of Bayes Factors via Mixing With Surrogate Distributions. <i>Journal of the American Statistical Association</i> , 2020, , 1-16.	3.1	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.	6.4	26
8	Determinants of transcription factor regulatory range. <i>Nature Communications</i> , 2020, 11, 2472.	12.8	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.	0.9	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.	3.0	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.	8.9	39
12	Bayesian hidden Markov tree models for clustering genes with shared evolutionary history. <i>Annals of Applied Statistics</i> , 2019, 13, .	1.1	6
13	Convergent regulatory evolution and loss of flight in paleognathous birds. <i>Science</i> , 2019, 364, 74-78.	12.6	189
14	Landscape of B cell immunity and related immune evasion in human cancers. <i>Nature Genetics</i> , 2019, 51, 560-567.	21.4	115
15	Exploring the conformational space for protein folding with sequential Monte Carlo. <i>Annals of Applied Statistics</i> , 2018, 12, .	1.1	3
16	cepip: context-dependent epigenomic weighting for prioritization of regulatory variants and disease-associated genes. <i>Genome Biology</i> , 2017, 18, 52.	8.8	33
17	TIMER: A Web Server for Comprehensive Analysis of Tumor-Infiltrating Immune Cells. <i>Cancer Research</i> , 2017, 77, e108-e110.	0.9	4,049
18	Revisit linear regression-based deconvolution methods for tumor gene expression data. <i>Genome Biology</i> , 2017, 18, 127.	8.8	45

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19	Comprehensive analyses of tumor immunity: implications for cancer immunotherapy. <i>Genome Biology</i> , 2016, 17, 174.	8.8	1,768
20	Landscape of tumor-infiltrating T cell repertoire of human cancers. <i>Nature Genetics</i> , 2016, 48, 725-732.	21.4	288
21	Quality control, modeling, and visualization of CRISPR screens with MAGECK-VISPR. <i>Genome Biology</i> , 2015, 16, 281.	8.8	330
22	Network analysis of gene essentiality in functional genomics experiments. <i>Genome Biology</i> , 2015, 16, 239.	8.8	50
23	MAGECK enables robust identification of essential genes from genome-scale CRISPR/Cas9 knockout screens. <i>Genome Biology</i> , 2014, 15, 554.	8.8	1,614
24	Genetics of rheumatoid arthritis contributes to biology and drug discovery. <i>Nature</i> , 2014, 506, 376-381.	27.8	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.	2.2	7
26	Expansion of Biological Pathways Based on Evolutionary Inference. <i>Cell</i> , 2014, 158, 213-225.	28.9	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.	6.4	24
28	Understanding spatial organizations of chromosomes via statistical analysis of Hi-C data. <i>Quantitative Biology</i> , 2013, 1, 156-174.	0.5	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.	4.1	16
30	Lookahead Strategies for Sequential Monte Carlo. <i>Statistical Science</i> , 2013, 28, .	2.8	35
31	Bayesian Inference of Spatial Organizations of Chromosomes. <i>PLoS Computational Biology</i> , 2013, 9, e1002893.	3.2	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.	5.5	122
34	Topological domains in mammalian genomes identified by analysis of chromatin interactions. <i>Nature</i> , 2012, 485, 376-380.	27.8	5,786
35	Nonparametric hierarchical Bayes analysis of binomial data via Bernstein polynomial priors. <i>Canadian Journal of Statistics</i> , 2012, 40, 328-344.	0.9	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. Statistical Science, 2010, 25, .	2.8	7
38	Tmod: toolbox of motif discovery. Bioinformatics, 2010, 26, 405-407.	4.1	18
39	Bayesian Methods in Biological Sequence Analysis. , 2008, , 67-96.		0
40	Extracting sequence features to predict proteinâ€“DNA interactions: a comparative study. Nucleic Acids Research, 2008, 36, 4137-4148.	14.5	40
41	Genomic Sequence Is Highly Predictive of Local Nucleosome Depletion. PLoS Computational Biology, 2008, 4, e13.	3.2	156
42	On learning strategies for evolutionary Monte Carlo. Statistics and Computing, 2007, 17, 23-38.	1.5	24
43	Statistical assessment of the global regulatory role of histone acetylation in Saccharomyces cerevisiae. Genome Biology, 2006, 7, R70.	9.6	24
44	A Coalescence-Guided Hierarchical Bayesian Method for Haplotype Inference. American Journal of Human Genetics, 2006, 79, 313-322.	6.2	26
45	Monte Carlo sampling of near-native structures of proteins with applications. Proteins: Structure, Function and Bioinformatics, 2006, 66, 61-68.	2.6	20
46	On Side-Chain Conformational Entropy of Proteins. PLoS Computational Biology, 2006, 2, e168.	3.2	51
47	Stopping-time resampling for sequential Monte Carlo methods. Journal of the Royal Statistical Society Series B: Statistical Methodology, 2005, 67, 199-217.	2.2	23
48	BEST: Binding-site Estimation Suite of Tools. Bioinformatics, 2005, 21, 2909-2911.	4.1	46
49	A boosting approach for motif modeling using ChIP-chip data. Bioinformatics, 2005, 21, 2636-2643.	4.1	54
50	Sequential Monte Carlo Methods for Statistical Analysis of Tables. Journal of the American Statistical Association, 2005, 100, 109-120.	3.1	231
51	Defining a Centromere-like Element in Bacillus subtilis by Identifying the Binding Sites for the Chromosome-Anchoring Protein RacA. Molecular Cell, 2005, 17, 773-782.	9.7	93
52	Computational Discovery of Gene Regulatory Binding Motifs: A Bayesian Perspective. Statistical Science, 2004, 19, 188.	2.8	62
53	BioOptimizer: a Bayesian scoring function approach to motif discovery. Bioinformatics, 2004, 20, 1557-1564.	4.1	88
54	Modeling within-motif dependence for transcription factor binding site predictions. Bioinformatics, 2004, 20, 909-916.	4.1	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.	14.5	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.	5.5	143
57	Monte Carlo Strategies in Scientific Computing. <i>Springer Series in Statistics</i> , 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.	5.6	308
59	Incorporating Genotyping Uncertainty in Haplotype Inference for Single-Nucleotide Polymorphisms. <i>American Journal of Human Genetics</i> , 2004, 74, 495-510.	6.2	45
60	Haplotype Inference and Its Application in Linkage Disequilibrium Mapping. <i>Lecture Notes in Computer Science</i> , 2004, , 48-61.	1.3	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.	1.3	0
62	The Spo0A regulon of <i>Bacillus subtilis</i> . <i>Molecular Microbiology</i> , 2003, 50, 1683-1701.	2.5	466
63	Haplotype Information and Linkage Disequilibrium Mapping for Single Nucleotide Polymorphisms. <i>Genome Research</i> , 2003, 13, 2112-2117.	5.5	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.	7.1	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.	3.0	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.	6.2	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.	6.2	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.	17.5	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.	0.9	128
72	Parameter Expansion for Data Augmentation. <i>Journal of the American Statistical Association</i> , 1999, 94, 1264-1274.	3.1	236

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73	Markovian Structures in Biological Sequence Alignments. Journal of the American Statistical Association, 1999, 94, 1-15.	3.1	60
74	Sequential Monte Carlo Methods for Dynamic Systems. Journal of the American Statistical Association, 1998, 93, 1032-1044.	3.1	1,140
75	Rejection Control and Sequential Importance Sampling. Journal of the American Statistical Association, 1998, 93, 1022-1031.	3.1	99
76	Predictive Updating Methods with Application to Bayesian Classification. Journal of the Royal Statistical Society Series B: Methodological, 1996, 58, 397-415.	0.7	12
77	Nonparametric hierarchical Bayes via sequential imputations. Annals of Statistics, 1996, 24, 911.	2.6	125
78	Statistical inference and Monte Carlo algorithms. Test, 1996, 5, 249-344.	1.1	29
79	Metropolized independent sampling with comparisons to rejection sampling and importance sampling. Statistics and Computing, 1996, 6, 113-119.	1.5	381
80	Bayesian Models for Multiple Local Sequence Alignment and Gibbs Sampling Strategies. Journal of the American Statistical Association, 1995, 90, 1156-1170.	3.1	235
81	Blind Deconvolution via Sequential Imputations. Journal of the American Statistical Association, 1995, 90, 567-576.	3.1	252
82	Sequential Imputations and Bayesian Missing Data Problems. Journal of the American Statistical Association, 1994, 89, 278-288.	3.1	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.	3.1	504