

Jun S Liu

List of Publications by Year in Descending Order

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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	A data-adaptive Bayesian regression approach for polygenic risk prediction.. <i>Bioinformatics</i> , 2022 ,	7.2	1
108	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,	11.5	10
107	MiRACLE: an individual-specific approach to improve microRNA-target prediction based on a random contact model. <i>Briefings in Bioinformatics</i> , 2021 , 22,	13.4	1
106	Limited memory optimizes cooperation in social dilemma experiments. <i>Royal Society Open Science</i> , 2021 , 8, 210653	3.3	1
105	Reduction of mNAT1/hNAT2 Contributes to Cerebral Endothelial Necroptosis and A β Accumulation in Alzheimer's Disease. <i>Cell Reports</i> , 2020 , 33, 108447	10.6	7
104	Determinants of transcription factor regulatory range. <i>Nature Communications</i> , 2020 , 11, 2472	17.4	13
103	Wang-Landau algorithm as stochastic optimization and its acceleration. <i>Physical Review E</i> , 2020 , 101, 033301	2.4	2
102	Inferring Spatial Organization of Individual Topologically Associated Domains via Piecewise Helical Model. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2020 , 17, 647-656	3	1
101	NGM: Neural Gaussian Mirror for Controlled Feature Selection in Neural Networks 2020 ,		2
100	New Algorithms in RNA Structure Prediction Based on BHG. <i>International Journal of Pattern Recognition and Artificial Intelligence</i> , 2020 , 34, 2050031	1.1	0
99	SIMPLEs: a single-cell RNA sequencing imputation strategy preserving gene modules and cell clusters variation. <i>NAR Genomics and Bioinformatics</i> , 2020 , 2, lqaa077	3.7	3
98	Monte Carlo Approximation of Bayes Factors via Mixing With Surrogate Distributions. <i>Journal of the American Statistical Association</i> , 2020 , 1-16	2.8	2
97	An Extended Mallows Model for Ranked Data Aggregation. <i>Journal of the American Statistical Association</i> , 2020 , 115, 730-746	2.8	3
96	Bayesian Detection of Convergent Rate Changes of Conserved Noncoding Elements on Phylogenetic Trees. <i>Molecular Biology and Evolution</i> , 2019 , 36, 1086-1100	8.3	17
95	Convergent regulatory evolution and loss of flight in paleognathous birds. <i>Science</i> , 2019 , 364, 74-78	33.3	103
94	Landscape of B cell immunity and related immune evasion in human cancers. <i>Nature Genetics</i> , 2019 , 51, 560-567	36.3	56
93	Randomization Inference for Peer Effects. <i>Journal of the American Statistical Association</i> , 2019 , 114, 1651-1664	13.6	2

92	Robust Variable and Interaction Selection for Logistic Regression and General Index Models. <i>Journal of the American Statistical Association</i> , 2019 , 114, 271-286	2.8	8
91	Bayesian Inference for Assessing Effects of Email Marketing Campaigns. <i>Journal of Business and Economic Statistics</i> , 2018 , 36, 253-266	3.8	11
90	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	10.6	23
89	On parallelizable Markov chain Monte Carlo algorithms with waste-recycling. <i>Statistics and Computing</i> , 2018 , 28, 1073-1081	1.8	2
88	Interpretable selection and visualization of features and interactions using Bayesian forests. <i>Statistics and Its Interface</i> , 2018 , 11, 503-513	0.4	1
87	Evaluation of immune repertoire inference methods from RNA-seq data. <i>Nature Biotechnology</i> , 2018 , 36, 1034	44.5	5
86	Systems biology analysis reveals new insights into invasive lung cancer. <i>BMC Systems Biology</i> , 2018 , 12, 117	3.5	2
85	A hotspots analysis-relation discovery representation model for revealing diabetes mellitus and obesity. <i>BMC Systems Biology</i> , 2018 , 12, 116	3.5	4
84	Personalized chemotherapy selection for breast cancer using gene expression profiles. <i>Scientific Reports</i> , 2017 , 7, 43294	4.9	10
83	Fast de novo discovery of low-energy protein loop conformations. <i>Proteins: Structure, Function and Bioinformatics</i> , 2017 , 85, 1402-1412	4.2	7
82	Exploring genetic associations with ceRNA regulation in the human genome. <i>Nucleic Acids Research</i> , 2017 , 45, 5653-5665	20.1	30
81	Ultrasensitive detection of TCR hypervariable-region sequences in solid-tissue RNA-seq data. <i>Nature Genetics</i> , 2017 , 49, 482-483	36.3	41
80	cepip: context-dependent epigenomic weighting for prioritization of regulatory variants and disease-associated genes. <i>Genome Biology</i> , 2017 , 18, 52	18.3	27
79	Revisit linear regression-based deconvolution methods for tumor gene expression data. <i>Genome Biology</i> , 2017 , 18, 127	18.3	30
78	MetaGen: reference-free learning with multiple metagenomic samples. <i>Genome Biology</i> , 2017 , 18, 187	18.3	8
77	TIMER: A Web Server for Comprehensive Analysis of Tumor-Infiltrating Immune Cells. <i>Cancer Research</i> , 2017 , 77, e108-e110	10.1	1919
76	Relation discovery and hotspots analysis on diabetes mellitus and obesity with representation model 2017 ,		1
75	CLIC, a tool for expanding biological pathways based on co-expression across thousands of datasets. <i>PLoS Computational Biology</i> , 2017 , 13, e1005653	5	20

74	Comprehensive analyses of tumor immunity: implications for cancer immunotherapy. <i>Genome Biology</i> , 2016 , 17, 174	18.3	942
73	Predicting regulatory variants with composite statistic. <i>Bioinformatics</i> , 2016 , 32, 2729-36	7.2	30
72	Landscape of tumor-infiltrating T cell repertoire of human cancers. <i>Nature Genetics</i> , 2016 , 48, 725-32	36.3	193
71	-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	28.6	1
70	Signed support recovery for single index models in high-dimensions. <i>Annals of Mathematical Sciences and Applications</i> , 2016 , 1, 379-426	1.3	7
69	Text Summarization Using FrameNet-Based Semantic Graph Model. <i>Scientific Programming</i> , 2016 , 2016, 1-10	1.4	6
68	Statistical inference for time course RNA-Seq data using a negative binomial mixed-effect model. <i>BMC Bioinformatics</i> , 2016 , 17, 324	3.6	16
67	High-dimensional genomic data bias correction and data integration using MANCIE. <i>Nature Communications</i> , 2016 , 7, 11305	17.4	28
66	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, 6154-9	11.5	12
65	Conformational sampling and structure prediction of multiple interacting loops in soluble and E-barrel membrane proteins using multi-loop distance-guided chain-growth Monte Carlo method. <i>Bioinformatics</i> , 2015 , 31, 2646-52	7.2	13
64	Network analysis of gene essentiality in functional genomics experiments. <i>Genome Biology</i> , 2015 , 16, 239	18.3	41
63	Risk Classification with an Adaptive Naive Bayes Kernel Machine Model. <i>Journal of the American Statistical Association</i> , 2015 , 110, 393-404	2.8	16
62	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	7.8	1
61	Quantitative and functional interrogation of parent-of-origin allelic expression biases in the brain. <i>ELife</i> , 2015 , 4, e07860	8.9	53
60	Inference of transcriptional regulation in cancers. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015 , 112, 7731-6	11.5	59
59	Sequence determinants of improved CRISPR sgRNA design. <i>Genome Research</i> , 2015 , 25, 1147-57	9.7	335
58	Quality control, modeling, and visualization of CRISPR screens with MAGeCK-VISPR. <i>Genome Biology</i> , 2015 , 16, 281	18.3	171
57	Bayesian Partition Models for Identifying Expression Quantitative Trait Loci. <i>Journal of the American Statistical Association</i> , 2015 , 110, 1350-1361	2.8	2

56	dslice: an R package for nonparametric testing of associations with application in QTL and gene set analysis. <i>Bioinformatics</i> , 2015 , 31, 1842-4	7.2	1
55	Genetics of rheumatoid arthritis contributes to biology and drug discovery. <i>Nature</i> , 2014 , 506, 376-81	50.4	1426
54	Bayesian Aggregation of Order-Based Rank Data. <i>Journal of the American Statistical Association</i> , 2014 , 109, 1023-1039	2.8	28
53	Expansion of biological pathways based on evolutionary inference. <i>Cell</i> , 2014 , 158, 213-25	56.2	75
52	The distribution of genomic variations in human iPSCs is related to replication-timing reorganization during reprogramming. <i>Cell Reports</i> , 2014 , 7, 70-8	10.6	21
51	Understanding spatial organizations of chromosomes via statistical analysis of Hi-C data. <i>Quantitative Biology</i> , 2013 , 1, 156-174	3.9	22
50	Bayesian inference of spatial organizations of chromosomes. <i>PLoS Computational Biology</i> , 2013 , 9, e1002893	3.9	140
49	A Multiresolution Method for Parameter Estimation of Diffusion Processes. <i>Journal of the American Statistical Association</i> , 2012 , 107, 1558-1574	2.8	12
48	Topological domains in mammalian genomes identified by analysis of chromatin interactions. <i>Nature</i> , 2012 , 485, 376-80	50.4	4098
47	On Delay Tomography: Fast Algorithms and Spatially Dependent Models. <i>IEEE Transactions on Signal Processing</i> , 2012 , 60, 5685-5697	4.8	8
46	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	2.8	3
45	Identifying Differentially Expressed Genes in Time Course Microarray Data. <i>Statistics in Biosciences</i> , 2009 , 1, 144-159	1.5	17
44	Analysis of CHIP-chip Data on Genome Tiling Microarrays. <i>Frontiers of Statistics</i> , 2009 , 239-257		
43	Bayesian Clustering of Transcription Factor Binding Motifs. <i>Journal of the American Statistical Association</i> , 2008 , 103, 188-200	2.8	14
42	Bayesian Methods in Biological Sequence Analysis 2008 , 67-96		
41	On learning strategies for evolutionary Monte Carlo. <i>Statistics and Computing</i> , 2007 , 17, 23-38	1.8	21
40	Evolutionary Monte Carlo Methods for Clustering. <i>Journal of Computational and Graphical Statistics</i> , 2007 , 16, 855-876	1.4	4
39	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	2.8	14

38	Sequential Monte Carlo Methods for Statistical Analysis of Tables. <i>Journal of the American Statistical Association</i> , 2005 , 100, 109-120	2.8	152
37	Discussions on "A Bayesian Approach to DNA Sequence Segmentation" <i>Biometrics</i> , 2004 , 60, 582-583	1.8	1
36	Discovery of Conserved Sequence Patterns Using a Stochastic Dictionary Model. <i>Journal of the American Statistical Association</i> , 2003 , 98, 55-66	2.8	42
35	Monte Carlo Bayesian Signal Processing for Wireless Communications. <i>Journal of Signal Processing Systems</i> , 2002 , 30, 89-105		28
34	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	3.9	53
33	A Theory for Dynamic Weighting in Monte Carlo Computation. <i>Journal of the American Statistical Association</i> , 2001 , 96, 561-573	2.8	20
32	A Theoretical Framework for Sequential Importance Sampling with Resampling 2001 , 225-246		74
31	The Multiple-Try Method and Local Optimization in Metropolis Sampling. <i>Journal of the American Statistical Association</i> , 2000 , 95, 121-134	2.8	193
30	Parameter Expansion for Data Augmentation. <i>Journal of the American Statistical Association</i> , 1999 , 94, 1264-1274	2.8	182
29	Markovian Structures in Biological Sequence Alignments. <i>Journal of the American Statistical Association</i> , 1999 , 94, 1-15	2.8	50
28	Sequential Monte Carlo Methods for Dynamic Systems. <i>Journal of the American Statistical Association</i> , 1998 , 93, 1032-1044	2.8	927
27	Rejection Control and Sequential Importance Sampling. <i>Journal of the American Statistical Association</i> , 1998 , 93, 1022-1031	2.8	75
26	Extracting protein alignment models from the sequence database. <i>Nucleic Acids Research</i> , 1997 , 25, 1665-1671	2.7	178
25	Peskun's theorem and a modified discrete-state Gibbs sampler. <i>Biometrika</i> , 1996 , 83, 681-682	2	48
24	Metropolized independent sampling with comparisons to rejection sampling and importance sampling. <i>Statistics and Computing</i> , 1996 , 6, 113-119	1.8	297
23	Gibbs motif sampling: detection of bacterial outer membrane protein repeats. <i>Protein Science</i> , 1995 , 4, 1618-32	6.3	333
22	Bayesian Models for Multiple Local Sequence Alignment and Gibbs Sampling Strategies. <i>Journal of the American Statistical Association</i> , 1995 , 90, 1156-1170	2.8	193
21	Blind Deconvolution via Sequential Imputations. <i>Journal of the American Statistical Association</i> , 1995 , 90, 567-576	2.8	182

20	Sequential Imputations and Bayesian Missing Data Problems. <i>Journal of the American Statistical Association</i> , 1994 , 89, 278-288	2.8	502
19	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	2.8	372
18	Linear Combinations of Multiple Diagnostic Markers. <i>Journal of the American Statistical Association</i> , 1993 , 88, 1350-1355	2.8	184
17	Kernel-based Partial Permutation Test for Detecting Heterogeneous Functional Relationship. <i>Journal of the American Statistical Association</i> , 1-50	2.8	
16	The Collapsed Gibbs Sampler in Bayesian Computations with Applications to a Gene Regulation Problem		58
15	Blind Deconvolution via Sequential Imputations		81
14	Sequential Imputations and Bayesian Missing Data Problems		201
13	Linear Combinations of Multiple Diagnostic Markers		29
12	Bayesian Models for Multiple Local Sequence Alignment and Gibbs Sampling Strategies		67
11	The Multiple-Try Method and Local Optimization in Metropolis Sampling		38
10	Markovian Structures in Biological Sequence Alignments		20
9	Rejection Control and Sequential Importance Sampling		18
8	Sequential Monte Carlo Methods for Dynamic Systems		538
7	Parameter Expansion for Data Augmentation		39
6	Convergent regulatory evolution and the origin of flightlessness in palaeognathous birds		9
5	Controlling False Discovery Rate Using Gaussian Mirrors. <i>Journal of the American Statistical Association</i> , 1-20	2.8	1
4	Stratification and optimal resampling for sequential Monte Carlo. <i>Biometrika</i> ,	2	1
3	Neuronized Priors for Bayesian Sparse Linear Regression. <i>Journal of the American Statistical Association</i> , 1-16	2.8	2

2	Partition-Mallows Model and Its Inference for Rank Aggregation. <i>Journal of the American Statistical Association</i> ,1-17	2.8	0
1	False Discovery Rate Control via Data Splitting. <i>Journal of the American Statistical Association</i> ,1-38	2.8	2