

Qing Zhou

List of Publications by Year in descending order

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Version: 2024-02-01

30
papers

1,713
citations

623734

14
h-index

526287

27
g-index

30
all docs

30
docs citations

30
times ranked

2646
citing authors

#	ARTICLE	IF	CITATIONS
1	Honest Confidence Sets for High-Dimensional Regression by Projection and Shrinkage. <i>Journal of the American Statistical Association</i> , 2023, 118, 469-488.	3.1	0
2	Partitioned hybrid learning of Bayesian network structures. <i>Machine Learning</i> , 2022, 111, 1695-1738.	5.4	1
3	Optimizing Regularized Cholesky Score for Order-Based Learning of Bayesian Networks. <i>IEEE Transactions on Pattern Analysis and Machine Intelligence</i> , 2021, 43, 3555-3572.	13.9	13
4	Causal network learning with non-invertible functional relationships. <i>Computational Statistics and Data Analysis</i> , 2021, 156, 107141.	1.2	1
5	Penalized estimation of directed acyclic graphs from discrete data. <i>Statistics and Computing</i> , 2019, 29, 161-176.	1.5	18
6	Learning Large-Scale Bayesian Networks with the <code>sparsebn</code> Package. <i>Journal of Statistical Software</i> , 2019, 91, .	3.7	21
7	Smaller desert dust cooling effect estimated from analysis of dust size and abundance. <i>Nature Geoscience</i> , 2017, 10, 274-278.	12.9	306
8	A penalized Bayesian approach to predicting sparse protein-DNA binding landscapes. <i>Bioinformatics</i> , 2014, 30, 636-643.	4.1	4
9	Detecting clustering and ordering binding patterns among transcription factors via point process models. <i>Bioinformatics</i> , 2014, 30, 2263-2271.	4.1	9
10	Learning Sparse Causal Gaussian Networks With Experimental Intervention: Regularization and Coordinate Descent. <i>Journal of the American Statistical Association</i> , 2013, 108, 288-300.	3.1	49
11	Finding multiple minimum-energy conformations of the hydrophobic-polar protein model via multidomain sampling. <i>Physical Review E</i> , 2012, 86, 031909.	2.1	13
12	Multi-Domain Sampling With Applications to Structural Inference of Bayesian Networks. <i>Journal of the American Statistical Association</i> , 2011, 106, 1317-1330.	3.1	20
13	Searching ChIP-seq genomic islands for combinatorial regulatory codes in mouse embryonic stem cells. <i>BMC Genomics</i> , 2011, 12, 515.	2.8	6
14	Random Walk over Basins of Attraction to Construct Ising Energy Landscapes. <i>Physical Review Letters</i> , 2011, 106, 180602.	7.8	14
15	Identification of Context-Dependent Motifs by Contrasting ChIP Binding Data. <i>Bioinformatics</i> , 2010, 26, 2826-2832.	4.1	36
16	Heterogeneity in DNA Multiple Alignments: Modeling, Inference, and Applications in Motif Finding. <i>Biometrics</i> , 2010, 66, 694-704.	1.4	3
17	On Weight Matrix and Free Energy Models for Sequence Motif Detection. <i>Journal of Computational Biology</i> , 2010, 17, 1621-1638.	1.6	3
18	Energy landscape of a spin-glass model: Exploration and characterization. <i>Physical Review E</i> , 2009, 79, 051117.	2.1	11

#	ARTICLE	IF	CITATIONS
19	ChIP-Seq of transcription factors predicts absolute and differential gene expression in embryonic stem cells. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 21521-21526.	7.1	312
20	Defining the Mechanism of Transcription Factor-Induced Epigenetic Reprogramming.. Blood, 2009, 114, SCI-41-SCI-41.	1.4	0
21	Extracting sequence features to predict protein-DNA interactions: a comparative study. Nucleic Acids Research, 2008, 36, 4137-4148.	14.5	40
22	Reconstructing the energy landscape of a distribution from Monte Carlo samples. Annals of Applied Statistics, 2008, 2, .	1.1	9
23	A gene regulatory network in mouse embryonic stem cells. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 16438-16443.	7.1	246
24	Coupling hidden Markov models for the discovery of Cis-regulatory modules in multiple species. Annals of Applied Statistics, 2007, 1, .	1.1	15
25	Equi-energy sampler with applications in statistical inference and statistical mechanics. Annals of Statistics, 2006, 34, 1581.	2.6	129
26	A boosting approach for motif modeling using ChIP-chip data. Bioinformatics, 2005, 21, 2636-2643.	4.1	54
27	Computational Discovery of Gene Regulatory Binding Motifs: A Bayesian Perspective. Statistical Science, 2004, 19, 188.	2.8	62
28	Modeling within-motif dependence for transcription factor binding site predictions. Bioinformatics, 2004, 20, 909-916.	4.1	129
29	CisModule: De novo discovery of cis-regulatory modules by hierarchical mixture modeling. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 12114-12119.	7.1	189
30	In silico prediction of transcription factors that interact with the E2F family of transcription factors. , 0, , .		0