Hua Zhou

List of Publications by Year
in descending order

71 papers	2,009 citations	361045 20 h-index	276539 41 g-index
77 all docs	77 docs citations	77 times ranked	2804 citing authors

#	ARTICLE	IF	CITATIONS
1	Tensor Regression with Applications in Neuroimaging Data Analysis. Journal of the American Statistical Association, 2013, 108, 540-552.	1.8	303
2	Testing in Microbiome-Profiling Studies with MiRKAT, the Microbiome Regression-Based Kernel Association Test. American Journal of Human Genetics, 2015, 96, 797-807.	2.6	248
3	A quasi-Newton acceleration for high-dimensional optimization algorithms. Statistics and Computing, 2011, 21, 261-273.	0.8	127
4	Regularized Matrix Regression. Journal of the Royal Statistical Society Series B: Statistical Methodology, 2014, 76, 463-483.	1.1	122
5	Association screening of common and rare genetic variants by penalized regression. Bioinformatics, 2010, 26, 2375-2382.	1.8	120
6	Mendel: the Swiss army knife of genetic analysis programs. Bioinformatics, 2013, 29, 1568-1570.	1.8	104
7	Algorithms for Fitting the Constrained Lasso. Journal of Computational and Graphical Statistics, 2018, 27, 861-871.	0.9	76
8	Tucker Tensor Regression and Neuroimaging Analysis. Statistics in Biosciences, 2018, 10, 520-545.	0.6	71
9	Regression Models for Multivariate Count Data. Journal of Computational and Graphical Statistics, 2017, 26, 1-13.	0.9	51
10	Genotype imputation via matrix completion. Genome Research, 2013, 23, 509-518.	2.4	50
11	MM Algorithms for Some Discrete Multivariate Distributions. Journal of Computational and Graphical Statistics, 2010, 19, 645-665.	0.9	48
12	Imaging genetics via sparse canonical correlation analysis. , 2013, 2013, 740-743.		40
13	Ordered multinomial regression for genetic association analysis of ordinal phenotypes at Biobank scale. Genetic Epidemiology, 2020, 44, 248-260.	0.6	37
14	Differential Destruction of Stem Cells: Implications for Targeted Cancer Stem Cell Therapy. Cancer Research, 2009, 69, 9481-9489.	0.4	35
15	MM algorithms for geometric and signomial programming. Mathematical Programming, 2014, 143, 339-356.	1.6	35
16	Graphics Processing Units and High-Dimensional Optimization. Statistical Science, 2010, 25, 311-324.	1.6	31
17	A Brief Survey of Modern Optimization for Statisticians. International Statistical Review, 2014, 82, 46-70.	1.1	31
18	On the Bumpy Road to the Dominant Mode. Scandinavian Journal of Statistics, 2010, 37, 612-631.	0.9	30

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19	OpenMendel: a cooperative programming project for statistical genetics. Human Genetics, 2020, 139, 61-71.	1.8	29
20	Fitting analysis and research of measured data of SAW micro-pressure sensor based on BP neural network. Measurement: Journal of the International Measurement Confederation, 2020, 155, 107533.	2.5	28
21	Rates of convergence of some multivariate Markov chains with polynomial eigenfunctions. Annals of Applied Probability, 2009, 19, .	0.6	27
22	Extinction models for cancer stem cell therapy. Mathematical Biosciences, 2011, 234, 132-146.	0.9	25
23	Distance majorization and its applications. Mathematical Programming, 2014, 146, 409-436.	1.6	22
24	A Path Algorithm for Constrained Estimation. Journal of Computational and Graphical Statistics, 2013, 22, 261-283.	0.9	20
25	Heritability of interpack aggression in a wild pedigreed population of North American grey wolves. Molecular Ecology, 2020, 29, 1764-1775.	2.0	19
26	Composition Markov chains of multinomial type. Advances in Applied Probability, 2009, 41, 270-291.	0.4	16
27	A Generic Path Algorithm for Regularized Statistical Estimation. Journal of the American Statistical Association, 2014, 109, 686-699.	1.8	15
28	EM vs MM: A case study. Computational Statistics and Data Analysis, 2012, 56, 3909-3920.	0.7	14
29	Boosting Gene Mapping Power and Efficiency with Efficient Exact Variance Component Tests of Single Nucleotide Polymorphism Sets. Genetics, 2016, 204, 921-931.	1.2	13
30	An Algorithm for Generating Individualized Treatment Decision Trees and Random Forests. Journal of Computational and Graphical Statistics, 2018, 27, 849-860.	0.9	13
31	MM Algorithms for Variance Components Models. Journal of Computational and Graphical Statistics, 2019, 28, 350-361.	0.9	13
32	GWAS of longitudinal trajectories at biobank scale. American Journal of Human Genetics, 2022, 109, 433-445.	2.6	13
33	Rating Movies and Rating the Raters Who Rate Them. American Statistician, 2009, 63, 297-307.	0.9	12
34	ConvexLAR: An Extension of Least Angle Regression. Journal of Computational and Graphical Statistics, 2015, 24, 603-626.	0.9	11
35	MGLM: An R Package for Multivariate Categorical Data Analysis. R Journal, 2018, 10, 73.	0.7	11
36	IsoDOT Detects Differential RNA-Isoform Expression/Usage With Respect to a Categorical or Continuous Covariate With High Sensitivity and Specificity. Journal of the American Statistical Association, 2015, 110, 975-986.	1.8	10

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37	Fast Genome‐Wide QTL Association Mapping on Pedigree and Population Data. Genetic Epidemiology, 2017, 41, 174-186.	0.6	10
38	Variance Component Selection With Applications to Microbiome Taxonomic Data. Frontiers in Microbiology, 2018, 9, 509.	1.5	10
39	Probabilistic Error Analysis for Inner Products. SIAM Journal on Matrix Analysis and Applications, 2020, 41, 1726-1741.	0.7	10
40	Iterative hard thresholding in genome-wide association studies: Generalized linear models, prior weights, and double sparsity. GigaScience, 2020, 9, .	3.3	10
41	Matrix Linear Discriminant Analysis. Technometrics, 2020, 62, 196-205.	1.3	8
42	Tensor canonical correlation analysis. Stat, 2019, 8, e253.	0.3	7
43	Risk controlled decision trees and random forests for precision Medicine. Statistics in Medicine, 2022, 41, 719-735.	0.8	6
44	Fast genome-wide pedigree quantitative trait loci analysis using MENDEL. BMC Proceedings, 2014, 8, S93.	1.8	5
45	Exact variance component tests for longitudinal microbiome studies. Genetic Epidemiology, 2019, 43, 250-262.	0.6	5
46	<tt>svt</tt>: Singular Value Thresholding in <i>MATLAB</i>. Journal of Statistical Software, 2017, 81, .	1.8	5
47	Path following in the exact penalty method of convex programming. Computational Optimization and Applications, 2015, 61, 609-634.	0.9	4
48	Classification based on neuroimaging data by tensor boosting. , 2017, 2017, 1174-1179.		4
49	Supraglottic Lung Microbiome Taxa Are Associated with Pulmonary Abnormalities in an HIV Longitudinal Cohort. American Journal of Respiratory and Critical Care Medicine, 2020, 202, 1727-1731.	2.5	4
50	A fast data-driven method for genotype imputation, phasing and local ancestry inference: MendelImpute.jl. Bioinformatics, 2021, 37, 4756-4763.	1.8	4
51	WiSER: Robust and scalable estimation and inference of within‐subject variances from intensive longitudinal data. Biometrics, 2022, 78, 1313-1327.	0.8	4
52	Tensor Generalized Estimating Equations for Longitudinal Imaging Analysis. Statistica Sinica, 2019, 29, 1977-2005.	0.2	4
53	Nonlinear dimension reduction with Wright-Fisher kernel for genotype aggregation and association mapping. Bioinformatics, 2012, 28, i375-i381.	1.8	3
54	End‐to‐end domain knowledge‐assisted automatic diagnosis of idiopathic pulmonary fibrosis (IPF) using computed tomography (CT). Medical Physics, 2021, 48, 2458-2467.	1.6	3

#	Article	IF	Citations
55	Modern simulation utilities for genetic analysis. BMC Bioinformatics, 2021, 22, 228.	1.2	3
56	Interactions Between Adiponectin-Pathway Polymorphisms and Obesity on Postmenopausal Breast Cancer Risk Among African American Women: The WHI SHARe Study. Frontiers in Oncology, 2021, 11, 698198.	1.3	3
57	OnlineStats.jl: A Julia package for statistics on data streams. Journal of Open Source Software, 2020, 5, 1816.	2.0	3
58	A fast procedure for calculating importance weights in bootstrap sampling. Computational Statistics and Data Analysis, 2011, 55, 26-33.	0.7	2
59	Determining Duration of HER2-Targeted Therapy Using Stem Cell Extinction Models. PLoS ONE, 2012, 7, e46613.	1.1	2
60	Orthogonal Trace-Sum Maximization: Applications, Local Algorithms, and Global Optimality. SIAM Journal on Matrix Analysis and Applications, 2021, 42, 859-882.	0.7	2
61	An automatic diagnosis of idiopathic pulmonary fibrosis (IPF) using domain knowledge-guided attention models in HRCT images. , 2021, , .		2
62	Mga-Net: Multi-Scale Guided Attention Models for an Automated Diagnosis of Idiopathic Pulmonary Fibrosis (IPF). , 2021, , .		2
63	Efficient Algorithms and Implementation of a Semiparametric Joint Model for Longitudinal and Competing Risk Data: With Applications to Massive Biobank Data. Computational and Mathematical Methods in Medicine, 2022, 2022, 1-12.	0.7	2
64	VCSEL: Prioritizing SNP-set by penalized variance component selection. Annals of Applied Statistics, 2021, 15, 1652-1672.	0.5	2
65	A novel nonlinear dimension reduction approach to infer population structure for low-coverage sequencing data. BMC Bioinformatics, 2021, 22, 348.	1.2	1
66	Matrix Linear Discriminant Analysis. Technometrics, 2020, 62, 196-205.	1.3	1
67	Provable Convex Co-clustering of Tensors. Journal of Machine Learning Research, 2020, 21, .	62.4	1
68	Genome-wide QTL and eQTL analyses using Mendel. BMC Proceedings, 2016, 10, 239-244.	1.8	0
69	MM ALGORITHMS FOR VARIANCE COMPONENT ESTIMATION AND SELECTION IN LOGISTIC LINEAR MIXED MODEL. Statistica Sinica, 2019, 29, 1585-1605.	0.2	0
70	Proximal Distance Algorithms: Theory and Practice. Journal of Machine Learning Research, 2019, 20, .	62.4	0
71	Bag of little bootstraps for massive and distributed longitudinal data. Statistical Analysis and Data Mining, 0, , .	1.4	0