

Hongzhe Li

List of Publications by Year in descending order

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Version: 2024-02-01

118
papers

14,036
citations

70961

41
h-index

24915

109
g-index

126
all docs

126
docs citations

126
times ranked

20905
citing authors

#	ARTICLE	IF	CITATIONS
1	Transfer Learning in Large-Scale Gaussian Graphical Models with False Discovery Rate Control. Journal of the American Statistical Association, 2023, 118, 2171-2183.	1.8	6
2	Inference for High-Dimensional Linear Mixed-Effects Models: A Quasi-Likelihood Approach. Journal of the American Statistical Association, 2022, 117, 1835-1846.	1.8	7
3	Estimation of genetic correlation with summary association statistics. Biometrika, 2022, 109, 421-438.	1.3	2
4	Transfer Learning for High-Dimensional Linear Regression: Prediction, Estimation and Minimax Optimality. Journal of the Royal Statistical Society Series B: Statistical Methodology, 2022, 84, 149-173.	1.1	29
5	The Macronutrient Composition of Infant Formula Produces Differences in Gut Microbiota Maturation That Associate with Weight Gain Velocity and Weight Status. Nutrients, 2022, 14, 1241.	1.7	8
6	Deep Learning to Predict the Biosynthetic Gene Clusters in Bacterial Genomes. Journal of Molecular Biology, 2022, 434, 167597.	2.0	6
7	Sparse block signal detection and identification for shared cross-trait association analysis. Annals of Applied Statistics, 2022, 16, .	0.5	0
8	Editorial: Artificial Intelligence, machine learning and the changing landscape of molecular biology. Journal of Molecular Biology, 2022, , 167712.	2.0	0
9	Optimal Estimation of Wasserstein Distance on a Tree With an Application to Microbiome Studies. Journal of the American Statistical Association, 2021, 116, 1237-1253.	1.8	2
10	MiRKAT: kernel machine regression-based global association tests for the microbiome. Bioinformatics, 2021, 37, 1595-1597.	1.8	18
11	Optimal Permutation Recovery in Permuted Monotone Matrix Model. Journal of the American Statistical Association, 2021, 116, 1358-1372.	1.8	8
12	Hypothesis testing for phylogenetic composition: a minimum-cost flow perspective. Biometrika, 2021, 108, 17-36.	1.3	6
13	Optimal estimation of bacterial growth rates based on a permuted monotone matrix. Biometrika, 2021, 108, 693-708.	1.3	4
14	IFAA: Robust Association Identification and Inference for Absolute Abundance in Microbiome Analyses. Journal of the American Statistical Association, 2021, 116, 1595-1608.	1.8	2
15	Global and Simultaneous Hypothesis Testing for High-Dimensional Logistic Regression Models. Journal of the American Statistical Association, 2021, 116, 984-998.	1.8	25
16	Maternal gut microbiota reflecting poor diet quality is associated with spontaneous preterm birth in a prospective cohort study. American Journal of Clinical Nutrition, 2021, 113, 602-611.	2.2	19
17	The Microbiome and p-Inulin in Hemodialysis: A Feasibility Study. Kidney360, 2021, 2, 445-455.	0.9	3
18	Role of dietary fiber in the recovery of the human gut microbiome and its metabolome. Cell Host and Microbe, 2021, 29, 394-407.e5.	5.1	137

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19	Meninâ€regulated Pbk controls high fat dietâ€induced compensatory beta cell proliferation. EMBO Molecular Medicine, 2021, 13, e13524.	3.3	5
20	Dietary Patterns and Growth From 12 to 24 Months of Age in African American Infants. Current Developments in Nutrition, 2021, 5, 454.	0.1	0
21	A compositional mediation model for a binary outcome: Application to microbiome studies. Bioinformatics, 2021, 38, 16-21.	1.8	3
22	A Randomized Trial Comparing the Specific Carbohydrate Diet to a Mediterranean Diet in Adults With Crohnâ€™s Disease. Gastroenterology, 2021, 161, 837-852.e9.	0.6	113
23	Mitochondrial dysfunction in inflammatory bowel disease alters intestinal epithelial metabolism of hepatic acylcarnitines. Journal of Clinical Investigation, 2021, 131, .	3.9	49
24	Bayesian Balance-Regression in Microbiome Studies Using Stochastic Search. , 2021, , 347-362.		2
25	Information content of high-order associations of the human gut microbiota network. Annals of Applied Statistics, 2021, 15, 1788-1807.	0.5	0
26	Multisample estimation of bacterial composition matrices in metagenomics data. Biometrika, 2020, 107, 75-92.	1.3	21
27	Multi-omic Analysis of the Interaction between Clostridioides difficile Infection and Pediatric Inflammatory Bowel Disease. Cell Host and Microbe, 2020, 28, 422-433.e7.	5.1	45
28	Emerging Priorities for Microbiome Research. Frontiers in Microbiology, 2020, 11, 136.	1.5	113
29	Bacterial colonization reprograms the neonatal gut metabolome. Nature Microbiology, 2020, 5, 838-847.	5.9	70
30	A Zero-Inflated Latent Dirichlet Allocation Model for Microbiome Studies. Frontiers in Genetics, 2020, 11, 602594.	1.1	10
31	Estimation of Heterogeneous Restricted Mean Survival Time Using Random Forest. Frontiers in Genetics, 2020, 11, 587378.	1.1	2
32	Systematic integrated analysis of genetic and epigenetic variation in diabetic kidney disease. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 29013-29024.	3.3	46
33	Castleman disease spectrum.. Journal of Clinical Oncology, 2020, 38, 8548-8548.	0.8	0
34	Generalized Linear Models With Linear Constraints for Microbiome Compositional Data. Biometrics, 2019, 75, 235-244.	0.8	40
35	Molecular analysis of the endobronchial stent microbial biofilm reveals bacterial communities that associate with stent material and frequent fungal constituents. PLoS ONE, 2019, 14, e0217306.	1.1	16
36	An Integrated Gaussian Graphical Model to evaluate the impact of exposures on metabolic networks. Computers in Biology and Medicine, 2019, 114, 103417.	3.9	5

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37	Pathologic gene network rewiring implicates PPP1R3A as a central regulator in pressure overload heart failure. <i>Nature Communications</i> , 2019, 10, 2760.	5.8	22
38	Kidney cytosine methylation changes improve renal function decline estimation in patients with diabetic kidney disease. <i>Nature Communications</i> , 2019, 10, 2461.	5.8	59
39	Integrative Analysis of Genetical Genomics Data Incorporating Network Structures. <i>Biometrics</i> , 2019, 75, 1063-1075.	0.8	5
40	Large Covariance Estimation for Compositional Data Via Composition-Adjusted Thresholding. <i>Journal of the American Statistical Association</i> , 2019, 114, 759-772.	1.8	33
41	Optimal Estimation of Genetic Relatedness in High-Dimensional Linear Models. <i>Journal of the American Statistical Association</i> , 2019, 114, 358-369.	1.8	21
42	Joint testing and false discovery rate control in high-dimensional multivariate regression. <i>Biometrika</i> , 2018, 105, 249-269.	1.3	10
43	Two-sample tests of high-dimensional means for compositional data. <i>Biometrika</i> , 2018, 105, 115-132.	1.3	25
44	Medication class enrichment analysis: a novel algorithm to analyze multiple pharmacologic exposures simultaneously using electronic health record data. <i>Journal of the American Medical Informatics Association: JAMIA</i> , 2018, 25, 780-789.	2.2	3
45	Comparative analyses of fecal microbiota in Chinese isolated Yao population, minority Zhuang and rural Han by 16sRNA sequencing. <i>Scientific Reports</i> , 2018, 8, 1142.	1.6	32
46	A GLM-based Latent Variable Ordination Method for Microbiome Samples. <i>Biometrics</i> , 2018, 74, 448-457.	0.8	27
47	Quantifying and comparing bacterial growth dynamics in multiple metagenomic samples. <i>Nature Methods</i> , 2018, 15, 1041-1044.	9.0	40
48	FXR-Dependent Modulation of the Human Small Intestinal Microbiome by the Bile Acid Derivative Obeticholic Acid. <i>Gastroenterology</i> , 2018, 155, 1741-1752.e5.	0.6	82
49	Conditional Regression Based on a Multivariate Zero-Inflated Logistic-Normal Model for Microbiome Relative Abundance Data. <i>Statistics in Biosciences</i> , 2018, 10, 587-608.	0.6	22
50	Reframing the Biological Basis of Neuroprotection Using Functional Genomics: Differentially Weighted, Time-Dependent Multifactor Pathogenesis of Human Ischemic Brain Damage. <i>Frontiers in Neurology</i> , 2018, 9, 497.	1.1	6
51	A general framework for association analysis of microbial communities on a taxonomic tree. <i>Bioinformatics</i> , 2017, 33, 1278-1285.	1.8	41
52	Sociability Deficits and Altered Amygdala Circuits in Mice Lacking Pcdh10, an Autism Associated Gene. <i>Biological Psychiatry</i> , 2017, 81, 193-202.	0.7	51
53	A Model-Based Approach for Species Abundance Quantification Based on Shotgun Metagenomic Data. <i>Statistics in Biosciences</i> , 2017, 9, 13-27.	0.6	8
54	Sparse Simultaneous Signal Detection for Identifying Genetically Controlled Disease Genes. <i>Journal of the American Statistical Association</i> , 2017, 112, 1032-1046.	1.8	9

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55	Genetic-Variation-Driven Gene-Expression Changes Highlight Genes with Important Functions for Kidney Disease. <i>American Journal of Human Genetics</i> , 2017, 100, 940-953.	2.6	81
56	A Model for Paired-Multinomial Data and Its Application to Analysis of Data on a Taxonomic Tree. <i>Biometrics</i> , 2017, 73, 1266-1278.	0.8	17
57	Optimal detection of weak positive latent dependence between two sequences of multiple tests. <i>Journal of Multivariate Analysis</i> , 2017, 160, 169-184.	0.5	5
58	A role for bacterial urease in gut dysbiosis and Crohn's disease. <i>Science Translational Medicine</i> , 2017, 9, .	5.8	171
59	A two-part mixed-effects model for analyzing longitudinal microbiome compositional data. <i>Bioinformatics</i> , 2016, 32, 2611-2617.	1.8	184
60	Activation of basolateral amygdala in juvenile C57BL/6J mice during social approach behavior. <i>Neuroscience</i> , 2016, 335, 184-194.	1.1	23
61	Regression analysis for microbiome compositional data. <i>Annals of Applied Statistics</i> , 2016, 10, .	0.5	87
62	Comparative metabolomics in vegans and omnivores reveal constraints on diet-dependent gut microbiota metabolite production. <i>Gut</i> , 2016, 65, 63-72.	6.1	428
63	Association of Cesarean Delivery and Formula Supplementation With the Intestinal Microbiome of 6-Week-Old Infants. <i>JAMA Pediatrics</i> , 2016, 170, 212.	3.3	238
64	Correction to the paper "Optimal False Discovery Rate Control for Dependent Data". <i>Statistics and Its Interface</i> , 2016, 9, 33-35.	0.2	2
65	Joint estimation of multiple high-dimensional precision matrices. <i>Statistica Sinica</i> , 2016, 26, 445-464.	0.2	34
66	Comparative Effectiveness of Nutritional and Biological Therapy in North American Children with Active Crohn's Disease. <i>Inflammatory Bowel Diseases</i> , 2015, 21, 1786-1793.	0.9	141
67	Nonparametric Tests for Differential Histone Enrichment with ChIP-Seq Data. <i>Cancer Informatics</i> , 2015, 14s1, CIN.S13972.	0.9	2
68	Genome Wide Nucleosome Mapping for HSV-1 Shows Nucleosomes Are Deposited at Preferred Positions during Lytic Infection. <i>PLoS ONE</i> , 2015, 10, e0117471.	1.1	21
69	SPARSE SEGMENT IDENTIFICATIONS WITH APPLICATIONS TO DNA COPY NUMBER VARIATION ANALYSIS. , 2015, , 863-887.		0
70	Microbiome, Metagenomics, and High-Dimensional Compositional Data Analysis. <i>Annual Review of Statistics and Its Application</i> , 2015, 2, 73-94.	4.1	226
71	The Ovarian Cancer Chemokine Landscape Is Conducive to Homing of Vaccine-Primed and CD3/CD28-Costimulated T Cells Prepared for Adoptive Therapy. <i>Clinical Cancer Research</i> , 2015, 21, 2840-2850.	3.2	52
72	Regularization Methods for High-Dimensional Instrumental Variables Regression With an Application to Genetical Genomics. <i>Journal of the American Statistical Association</i> , 2015, 110, 270-288.	1.8	57

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73	Testing in Microbiome-Profiling Studies with MiRKAT, the Microbiome Regression-Based Kernel Association Test. <i>American Journal of Human Genetics</i> , 2015, 96, 797-807.	2.6	248
74	Power and sample-size estimation for microbiome studies using pairwise distances and PERMANOVA. <i>Bioinformatics</i> , 2015, 31, 2461-2468.	1.8	326
75	Genetic sharing and heritability of paediatric age of onset autoimmune diseases. <i>Nature Communications</i> , 2015, 6, 8442.	5.8	58
76	Inflammation, Antibiotics, and Diet as Environmental Stressors of the Gut Microbiome in Pediatric Crohn's Disease. <i>Cell Host and Microbe</i> , 2015, 18, 489-500.	5.1	646
77	glmgraph: an R package for variable selection and predictive modeling of structured genomic data. <i>Bioinformatics</i> , 2015, 31, 3991-3993.	1.8	23
78	Meta-analysis of shared genetic architecture across ten pediatric autoimmune diseases. <i>Nature Medicine</i> , 2015, 21, 1018-1027.	15.2	212
79	Isoform Expression Analysis Based on RNA-seq Data. , 2014, , 247-259.		0
80	Direct estimation of differential networks. <i>Biometrika</i> , 2014, 101, 253-268.	1.3	88
81	Variable selection in regression with compositional covariates. <i>Biometrika</i> , 2014, 101, 785-797.	1.3	158
82	Parametric modeling of whole-genome sequencing data for CNV identification. <i>Biostatistics</i> , 2014, 15, 427-441.	0.9	6
83	More powerful genetic association testing via a new statistical framework for integrative genomics. <i>Biometrics</i> , 2014, 70, 881-890.	0.8	28
84	A change-point model for identifying 3' UTR switching by next-generation RNA sequencing. <i>Bioinformatics</i> , 2014, 30, 2162-2170.	1.8	43
85	Correlation Between Intraluminal Oxygen Gradient and Radial Partitioning of Intestinal Microbiota. <i>Gastroenterology</i> , 2014, 147, 1055-1063.e8.	0.6	658
86	A Functional Genomic Approach Identifies FAL1 as an Oncogenic Long Noncoding RNA that Associates with BMI1 and Represses p21 Expression in Cancer. <i>Cancer Cell</i> , 2014, 26, 344-357.	7.7	361
87	A Hierarchical Bayesian Model for Estimating and Inferring Differential Isoform Expression for Multi-sample RNA-Seq Data. <i>Statistics in Biosciences</i> , 2013, 5, 119-137.	0.6	8
88	A Logistic Normal Multinomial Regression Model for Microbiome Compositional Data Analysis. <i>Biometrics</i> , 2013, 69, 1053-1063.	0.8	95
89	Systems biology approaches to epidemiological studies of complex diseases. <i>Wiley Interdisciplinary Reviews: Systems Biology and Medicine</i> , 2013, 5, 677-686.	6.6	9
90	Covariate-adjusted precision matrix estimation with an application in genetical genomics. <i>Biometrika</i> , 2013, 100, 139-156.	1.3	74

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91	Adjusting for high-dimensional covariates in sparse precision matrix estimation by $\frac{1}{n} \sum_{i=1}^n \mathbf{X}_i \mathbf{X}_i^T$ Journal of Multivariate Analysis, 2013, 116, 365-381.	0.5	22
92	Learning local directed acyclic graphs based on multivariate time series data. Annals of Applied Statistics, 2013, 7, 1249-1835.	0.5	2
93	Variable selection for sparse Dirichlet-multinomial regression with an application to microbiome data analysis. Annals of Applied Statistics, 2013, 7, .	0.5	163
94	MATCHCLIP: locate precise breakpoints for copy number variation using CIGAR string by matching soft clipped reads. Frontiers in Genetics, 2013, 4, 157.	1.1	16
95	U-statistics in genetic association studies. Human Genetics, 2012, 131, 1395-1401.	1.8	12
96	High-Dimensional Heteroscedastic Regression with an Application to eQTL Data Analysis. Biometrics, 2012, 68, 316-326.	0.8	30
97	Robust Gaussian Graphical Modeling Via l_1 Penalization. Biometrics, 2012, 68, 1197-1206.	0.8	21
98	Introduction to Special Issue "Methods for Analysis of Graphs and Networks and Their Applications in Biosciences" Statistics in Biosciences, 2012, 4, 1-2.	0.6	5
99	Robust Detection and Identification of Sparse Segments in Ultrahigh Dimensional Data Analysis. Journal of the Royal Statistical Society Series B: Statistical Methodology, 2012, 74, 773-797.	1.1	21
100	Hidden Markov Random Field Models for Network-Based Analysis of Genomic Data. , 2011, , 353-368.		0
101	Linking Long-Term Dietary Patterns with Gut Microbial Enterotypes. Science, 2011, 334, 105-108.	6.0	5,253
102	A sparse conditional Gaussian graphical model for analysis of genetical genomics data. Annals of Applied Statistics, 2011, 5, 2630-2650.	0.5	115
103	The sparse Laplacian shrinkage estimator for high-dimensional regression. Annals of Statistics, 2011, 39, 2021-2046.	1.4	72
104	A Penalized Likelihood Approach for Bivariate Conditional Normal Models for Dynamic Co-expression Analysis. Biometrics, 2011, 67, 299-308.	0.8	11
105	Variable selection and regression analysis for graph-structured covariates with an application to genomics. Annals of Applied Statistics, 2010, 4, 1498-1516.	0.5	102
106	Network-Based Empirical Bayes Methods for Linear Models with Applications to Genomic Data. Journal of Biopharmaceutical Statistics, 2010, 20, 209-222.	0.4	8
107	Optimal Sparse Segment Identification With Application in Copy Number Variation Analysis. Journal of the American Statistical Association, 2010, 105, 1156-1166.	1.8	55
108	A hidden Markov random field model for genome-wide association studies. Biostatistics, 2010, 11, 139-150.	0.9	41

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109	Disordered Microbial Communities in the Upper Respiratory Tract of Cigarette Smokers. <i>PLoS ONE</i> , 2010, 5, e15216.	1.1	350
110	A Bayesian Approach for Graph-constrained Estimation for High-dimensional Regression. <i>International Journal of Systems and Synthetic Biology</i> , 2010, 1, 255-272.	0.0	0
111	Copy number variation at 1q21.1 associated with neuroblastoma. <i>Nature</i> , 2009, 459, 987-991.	13.7	329
112	UAE Statistics-based Tests for Multiple Genes in Genetic Association Studies. <i>Annals of Human Genetics</i> , 2008, 72, 821-833.	0.3	32
113	Vertex Clustering in Random Graphs via Reversible Jump Markov Chain Monte Carlo. <i>Journal of Computational and Graphical Statistics</i> , 2008, 17, 388-409.	0.9	3
114	Network-constrained regularization and variable selection for analysis of genomic data. <i>Bioinformatics</i> , 2008, 24, 1175-1182.	1.8	537
115	Chromosome 6p22 Locus Associated with Clinically Aggressive Neuroblastoma. <i>New England Journal of Medicine</i> , 2008, 358, 2585-2593.	13.9	271
116	A hidden spatial-temporal Markov random field model for network-based analysis of time course gene expression data. <i>Annals of Applied Statistics</i> , 2008, 2, .	0.5	51
117	A Markov random field model for network-based analysis of genomic data. <i>Bioinformatics</i> , 2007, 23, 1537-1544.	1.8	222
118	Gradient directed regularization for sparse Gaussian concentration graphs, with applications to inference of genetic networks. <i>Biostatistics</i> , 2006, 7, 302-317.	0.9	131