Can Yang

List of Publications by Year
in descending order

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79 papers	3,363 citations	279487 23 h-index	161609 54 g-index
86 all docs	86 docs citations	86 times ranked	4560 citing authors

#	Article	IF	Citations
1	XPXP: improving polygenic prediction by cross-population and cross-phenotype analysis. Bioinformatics, 2022, 38, 1947-1955.	1.8	16
2	FIRM: Flexible integration of single-cell RNA-sequencing data for large-scale multi-tissue cell atlas datasets. Briefings in Bioinformatics, 2022, 23, .	3.2	10
3	Editorial: Genetic Pleiotropy in Complex Traits and Diseases. Frontiers in Genetics, 2022, 13, 897383.	1.1	1
4	Adversarial domain translation networks for integrating large-scale atlas-level single-cell datasets. Nature Computational Science, 2022, 2, 317-330.	3.8	13
5	Leveraging the local genetic structure for trans-ancestry association mapping. American Journal of Human Genetics, 2022, 109, 1317-1337.	2.6	10
6	Mendelian randomization for causal inference accounting for pleiotropy and sample structure using genome-wide summary statistics. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, .	3.3	32
7	Accurate genetic and environmental covariance estimation with composite likelihood in genome-wide association studies. PLoS Genetics, 2021, 17, e1009293.	1.5	12
8	A unified framework for cross-population trait prediction by leveraging the genetic correlation of polygenic traits. American Journal of Human Genetics, 2021, 108, 632-655.	2.6	73
9	A Unified Primal Dual Active Set Algorithm for Nonconvex Sparse Recovery. Statistical Science, 2021, 36, .	1.6	17
10	Using Collaborative Mixed Models to Account for Imputation Uncertainty in Transcriptome-Wide Association Studies. Methods in Molecular Biology, 2021, 2212, 93-103.	0.4	2
11	Title is missing!. , 2021, 17, e1009293.		0
12	Title is missing!. , 2021, 17, e1009293.		0
13	Title is missing!. , 2021, 17, e1009293.		0
14	Title is missing!. , 2021, 17, e1009293.		0
15	Bayesian weighted Mendelian randomization for causal inference based on summary statistics. Bioinformatics, 2020, 36, 1501-1508.	1.8	39
16	BIVAS: A Scalable Bayesian Method for Bi-Level Variable Selection With Applications. Journal of Computational and Graphical Statistics, 2020, 29, 40-52.	0.9	6
17	LPM: a latent probit model to characterize the relationship among complex traits using summary statistics from multiple GWASs and functional annotations. Bioinformatics, 2020, 36, 2506-2514.	1.8	11
18	CoMM-S2: a collaborative mixed model using summary statistics in transcriptome-wide association studies. Bioinformatics, 2020, 36, 2009-2016.	1.8	30

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19	A tissue-specific collaborative mixed model for jointly analyzing multiple tissues in transcriptome-wide association studies. Nucleic Acids Research, 2020, 48, e109-e109.	6.5	15
20	MR-LDP: a two-sample Mendelian randomization for GWAS summary statistics accounting for linkage disequilibrium and horizontal pleiotropy. NAR Genomics and Bioinformatics, 2020, 2, lqaa028.	1.5	27
21	Testing and controlling for horizontal pleiotropy with probabilistic Mendelian randomization in transcriptome-wide association studies. Nature Communications, 2020, 11, 3861.	5.8	79
22	IGREX for quantifying the impact of genetically regulated expression on phenotypes. NAR Genomics and Bioinformatics, 2020, 2, lqaa010.	1.5	15
23	Exploring the Relationship Between Psychiatric Traits and the Risk of Mouth Ulcers Using Bi-Directional Mendelian Randomization. Frontiers in Genetics, 2020, 11, 608630.	1.1	10
24	Detection of cell-type-specific risk-CpG sites in epigenome-wide association studies. Nature Communications, 2019, 10, 3113.	5.8	19
25	CoMM: A Collaborative Mixed Model That Integrates GWAS and eQTL Data Sets to Investigate the Genetic Architecture of Complex Traits. Bioinformatics and Biology Insights, 2019, 13, 117793221988143.	1.0	5
26	Prediction Analysis for Microbiome Sequencing Data. Biometrics, 2019, 75, 875-884.	0.8	10
27	VIMCO: variational inference for multiple correlated outcomes in genome-wide association studies. Bioinformatics, 2019, 35, 3693-3700.	1.8	9
28	LEP: A Statistical Method Integrating Individual-Level and Summary-Level Data of the Same Trait From Different Populations. Biomedical Informatics Insights, 2019, 11, 117822261988162.	4.6	0
29	Joint analysis of individual-level and summary-level GWAS data by leveraging pleiotropy. Bioinformatics, 2019, 35, 1729-1736.	1.8	3
30	CoMM: a collaborative mixed model to dissecting genetic contributions to complex traits by leveraging regulatory information. Bioinformatics, 2019, 35, 1644-1652.	1.8	36
31	LSMM: a statistical approach to integrating functional annotations with genome-wide association studies. Bioinformatics, 2018, 34, 2788-2796.	1.8	18
32	LPG: A four-group probabilistic approach to leveraging pleiotropy in genome-wide association studies. BMC Genomics, 2018, 19, 503.	1.2	7
33	On Joint Estimation of Gaussian Graphical Models for Spatial and Temporal Data. Biometrics, 2017, 73, 769-779.	0.8	30
34	IGESS: a statistical approach to integrating individual-level genotype data and summary statistics in genome-wide association studies. Bioinformatics, 2017, 33, 2882-2889.	1.8	12
35	LLR: a latent low-rank approach to colocalizing genetic risk variants in multiple GWAS. Bioinformatics, 2017, 33, 3878-3886.	1.8	6
36	Leveraging functional annotations in genetic risk prediction for human complex diseases. PLoS Computational Biology, 2017, 13, e1005589.	1.5	134

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37	Analyzing Association Mapping in Pedigreeâ€Based GWAS Using a Penalized Multitrait Mixed Model. Genetic Epidemiology, 2016, 40, 382-393.	0.6	11
38	On high-dimensional misspecified mixed model analysis in genome-wide association study. Annals of Statistics, 2016, 44, .	1.4	38
39	Simultaneous dimension reduction and adjustment for confounding variation. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 14662-14667.	3.3	42
40	Computing exact permutation p-values for association rules. Information Sciences, 2016, 346-347, 146-162.	4.0	15
41	Introduction to Statistical Methods for Integrative Data Analysis in Genome-Wide Association Studies. , 2016, , 3-23.		3
42	Total Variation Regularized Tensor RPCA for Background Subtraction From Compressive Measurements. IEEE Transactions on Image Processing, 2016, 25, 4075-4090.	6.0	135
43	EPS: an empirical Bayes approach to integrating pleiotropy and tissue-specific information for prioritizing risk genes. Bioinformatics, 2016, 32, 1856-1864.	1.8	19
44	Dissecting ancestry genomic background in substance dependence genome-wide association studies. Pharmacogenomics, 2015, 16, 1487-1498.	0.6	22
45	Implications of pleiotropy: challenges and opportunities for mining Big Data in biomedicine. Frontiers in Genetics, 2015, 6, 229.	1.1	41
46	Low-Rank Modeling and Its Applications in Image Analysis. ACM Computing Surveys, 2015, 47, 1-33.	16.1	102
47	Pervasive pleiotropy between psychiatric disorders and immune disorders revealed by integrative analysis of multiple GWAS. Human Genetics, 2015, 134, 1195-1209.	1.8	72
48	GPA: A Statistical Approach to Prioritizing GWAS Results by Integrating Pleiotropy and Annotation. PLoS Genetics, 2014, 10, e1004787.	1.5	189
49	Improving genetic risk prediction by leveraging pleiotropy. Human Genetics, 2014, 133, 639-650.	1.8	71
50	Exploring the genetic architecture of alcohol dependence in African-Americans via analysis of a genomewide set of common variants. Human Genetics, 2014, 133, 617-624.	1.8	15
51	Admixture mapping analysis in the context of GWAS with GAW18 data. BMC Proceedings, 2014, 8, S3.	1.8	12
52	Adjustment of familial relatedness in association test for rare variants. BMC Proceedings, 2014, 8, S39.	1.8	1
53	A penalized linear mixed model for genomic prediction using pedigree structures. BMC Proceedings, 2014, 8, S67.	1.8	2
54	Moving Object Detection by Detecting Contiguous Outliers in the Low-Rank Representation. IEEE Transactions on Pattern Analysis and Machine Intelligence, 2013, 35, 597-610.	9.7	623

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55	The complete compositional epistasis detection in genome-wide association studies. BMC Genetics, 2013, 14, 7.	2.7	18
56	ProteinLasso: A Lasso regression approach to protein inference problem in shotgun proteomics. Computational Biology and Chemistry, 2013, 43, 46-54.	1.1	18
57	Empirical Bayes Correction for the Winner's Curse in Genetic Association Studies. Genetic Epidemiology, 2013, 37, 60-68.	0.6	32
58	Accounting for non-genetic factors by low-rank representation and sparse regression for eQTL mapping. Bioinformatics, 2013, 29, 1026-1034.	1.8	37
59	Peptide Reranking with Protein-Peptide Correspondence and Precursor Peak Intensity Information. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2012, 9, 1212-1219.	1.9	1
60	Automatic mitral leaflet tracking in echocardiography by outlier detection in the low-rank representation. , 2012, , .		7
61	Comments on â€˜An empirical comparison of several recent epistatic interaction detection methodsâ€™. Bioinformatics, 2012, 28, 145-146.	1.8	3
62	A hidden two-locus disease association pattern in genome-wide association studies. BMC Bioinformatics, 2011, 12, 156.	1.2	2
63	The choice of null distributions for detecting gene-gene interactions in genome-wide association studies. BMC Bioinformatics, 2011, 12, S26.	1.2	6
64	A Partial Set Covering Model for Protein Mixture Identification Using Mass Spectrometry Data. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2011, 8, 368-380.	1.9	13
65	GBOOST: a GPU-based tool for detecting geneâ€“gene interactions in genomeâ€“wide case control studies. Bioinformatics, 2011, 27, 1309-1310.	1.8	137
66	Identifying disease-associated SNP clusters via contiguous outlier detection. Bioinformatics, 2011, 27, 2578-2585.	1.8	6
67	BOOST: A Fast Approach to Detecting Gene-Gene Interactions in Genome-wide Case-Control Studies. American Journal of Human Genetics, 2010, 87, 325-340.	2.6	452
68	Identifying main effects and epistatic interactions from large-scale SNP data via adaptive group Lasso. BMC Bioinformatics, 2010, 11, S18.	1.2	33
69	Predictive rule inference for epistatic interaction detection in genome-wide association studies. Bioinformatics, 2010, 26, 30-37.	1.8	156
70	Detecting two-locus associations allowing for interactions in genome-wide association studies. Bioinformatics, 2010, 26, 2517-2525.	1.8	23
71	A Regularized Method for Peptide Quantification. Journal of Proteome Research, 2010, 9, 2705-2712.	1.8	8
72	SNPHarvester: a filtering-based approach for detecting epistatic interactions in genome-wide association studies. Bioinformatics, 2009, 25, 504-511.	1.8	182

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73	MegaSNPHunter: a learning approach to detect disease predisposition SNPs and high level interactions in genome wide association study. BMC Bioinformatics, 2009, 10, 13.	1.2	86
74	Peak bagging for peptide mass fingerprinting. Bioinformatics, 2008, 24, 1293-1299.	1.8	8
75	Optimization-Based Peptide Mass Fingerprinting for Protein Mixture Identification. Nature Precedings, 2008, , .	0.1	0
76	GPC Algorithm and Queuing-selecting for Networked Level Control. , 2007, , .		0
77	eQTL mapping. , 0, , 208-228.		0
78	Introduction to statistical methods in genome-wide association studies. , 0, , 26-52.		0
79	scPI: A Scalable Framework for Probabilistic Inference in Single-Cell RNA-Sequencing Data Analysis. Statistics in Biosciences, 0, , 1.	0.6	0